Local Topological Structures and Global Connectivity Patterns in a *Trachelospermum jasminoides*: a Pilot Study

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ABSTRACT

Topological approaches to biological systems provide insights into their growth patterns, network connectivity and spatial organization. This perspective explores how biological structures self-organize, maintain stability and adapt to environmental constraints, revealing fundamental principles of efficiency, robustness, resilience and functional optimization. In this pilot study, we analysed the local and global topological properties of a *Trachelospermum jasminoides* bush (commonly known as star jasmine) using persistent homology, graph theory, spectral analysis and percolation theory. The spatial positions of individual flowers were extracted from an image of the bush and represented as a point cloud to capture their structural distribution and spatial relationships. Using Delaunay triangulation, a connectivity graph revealed a dominant connected component with minimal isolated structures. DBSCAN analysis identified a large number of small, localized clusters, reflecting biological and environmental influences. Most flowers connected to five to six neighbours, forming a uniform network with high clustering. Shortest path analysis showed efficient long-range connectivity, with paths avoiding sparse regions. Spectral analysis indicated smooth percolation without bottlenecks, while percolation analysis simulations revealed resilience up to 18% flower removal, after which connectivity broke down. In sum, we showed that the star jasmine bush topology balances local structural constraints with global connectivity, ensuring efficient resource distribution and structural integrity. By integrating topological data analysis with ecological modeling, we suggested a methodological approach to understanding natural growth networks. These insights can inform broader studies on biological pattern formation, network resilience and plant architecture modeling in ecology, agricultural sciences and biomimetic design.

KEYWORDS: graph connectivity; homotopy theory; spatial self-organization; computational morphology; floral network dynamics.

INTRODUCTION

The study of topological structures in biological systems provides a unique perspective on how organisms organize themselves in space, ensuring both functional efficiency and resilience. In plant systems, topology plays a critical role in determining how resources are distributed and how growth patterns emerge in response to environmental constraints (Li et al., 2017; Shimotohno and Scheres, 2019; Wang et al., 2020). The *Trachelospermum jasminoides* bush, with its intricate floral and vine structures, provides a good example for exploring these topological principles. By applying computational topology, graph theory and fractal growth models, we seeked to analyze both local and global spatial properties of a star jasmine bush, revealing the relationships arising from its structure. Traditional botanical research has long focused on morphological classifications, describing the physical characteristics of plants in terms of their leaves, stems and flowers. Still, advancements in mathematical and computational topology have opened new avenues for understanding plant growth beyond mere morphological description (Carlsson, 2009; Edelsbrunner and Harer, 2010; Boissonnat et al., 2018; Liu et al., 2020). The application of persistent homology, spectral graph analysis and percolation theory allowed researchers to uncover hidden structural patterns influencing the connectivity of biological networks (Robins, 1999; Cohen-Steiner et al., 2007; Bianconi and Ziff, 2018). By identifying long-range relationships, local clustering tendencies and the thresholds at which structural integrity is compromised, the self-organizing nature of plant growth can be better understood.

Trachelospermum jasminoides, as a climbing plant, relies on flexible structural adaptations to balance between local constraints and global connectivity while maintaining an interconnected floral arrangement supporting pollination and resource transport. Our analysis explores the underlying principles shaping the topology of the star jasmine bush, focusing on how individual flowers distribute themselves and identifying the threshold at which connectivity within the floral network begins to fragment. To analyze the topological properties of *Trachelospermum jasminoides* bush, our pilot study first extracted flower positions from an image and represented them as a spatial point cloud. By applying Delaunay triangulation, we constructed a network that captured the connectivity between neighboring flowers. This representation allowed for the application of network theory to analyze the formation of clusters, the presence of long-range connectivity and the overall resilience of the floral structure. One key measure in our analysis was the percolation threshold, which indicates how the structure responds to the progressive removal of flowers. If a significant portion of the network remains connected despite a high percentage of removals, the structure can be considered robust.

In sum, our study integrated topological data analysis, network science and biological modeling to uncover the hidden structures within a *Trachelospermum jasminoides* bush. These findings provide a broader understanding of how plants self-organize and maintain connectivity under natural constraints, offering new perspectives in biological organization, ecological modeling and bio-inspired design.

MATERIALS AND METHODS

We examined images of a Trachelospermum jasminoides bush, taken in June during peak blooming. Trachelospermum jasminoides, commonly known as star jasmine, is an evergreen, twining vine prized for its star-shaped white flowers (Zhao et al., 2017). It blooms profusely in late spring to early summer, attracting pollinators like bees and butterflies (Cai et al., 2024). The analysis of the *Trachelospermum jasminoides* bush topology was conducted through a structured sequence of computational and mathematical techniques aimed at extracting persistent homology, spatial relationships, connectivity structures and growth patterns from an image of the plant (Zomorodian and Carlsson, 2005; Niyogi, 2008; Edelsbrunner et al., 2002; Chazal and Michel, 2021). The study involved several key stages, beginning with image preprocessing and flower position extraction, followed by the construction of a topological representation through Delaunay triangulation and network analysis. These representations were then subjected to percolation simulations, spectral graph analysis and clustering algorithms, all of which contributed to a deeper understanding of the plant's topological organization.

The first stage of the analysis involved preprocessing the image to extract relevant spatial information. The original image was converted to grayscale to remove any unnecessary color information and to simplify further processing. A thresholding technique was then applied to enhance the contrast between the flowers and the background. Since star jasmine flowers are generally brighter than their surroundings, a high-threshold binary transformation was used, which assigned white pixels to flower regions and black pixels to the rest of the image. To refine the extracted features, noise removal techniques, such as morphological opening and closing, were employed to eliminate small artifacts that were not part of the actual floral structures. Once a clean binary image was obtained, contour detection algorithms were applied to identify and isolate individual flowers. The centroid of each detected contour was computed, generating a point cloud representation of the flower positions within the *Trachelospermum jasminoides* bush.

Once extracted the spatial distribution of flowers, the next step involved constructing a mathematical representation of their connectivity using Delaunay triangulation (Song et al., 2021). This technique partitions the set of points into non-overlapping triangles, ensuring that no point falls within the circumcircle of any triangle, thereby providing an optimal way to connect neighboring flowers. The resulting triangulated structure captured the local connectivity patterns of the flowers, forming a foundation for network-based topological analysis. Each flower was treated as a node in a graph, while the edges of the triangulated structure represented potential paths of biological or structural influence. Following the construction of the connectivity graph, an extensive network analysis was performed to quantify the structural properties of the star jasmine bush. The graph was analyzed to determine key metrics such as the number of connected components, degree distributions and clustering coefficients. The occurrence of large-connected components indicated that most flowers belonged to a single dominant structure, while smaller, disconnected components suggested isolated floral clusters. Clustering analysis was performed to identify distinct floral groupings within the star jasmine bush. The DBSCAN (Density-Based Spatial Clustering of Applications with Noise) algorithm was chosen for this purpose because it is well-suited for identifying clusters of varying densities while distinguishing outliers. DBSCAN operates by grouping points that are closely packed together while marking points that do not belong to any cluster as noise (Sander et al., 1998; Zhang 2019). The algorithm required two parameters: the minimum number of points needed to form a cluster and the neighborhood radius defining which points are considered close to one another. Clustering coefficient analysis (van Diessen et al., 2014) provided insight into the tendency of flowers to form tightly packed groups, which could be indicative of growth constraints or ecological interactions.

Additionally, the average shortest path length and network diameter were computed to assess how efficiently one part of the floral network could be reached from another. To assess the resilience of the floral network, a percolation simulation was performed by progressively removing flowers from the structure and monitoring the effect on connectivity (Grimmett, 1999; Bianconi and Ziff, 2018). In each iteration, a random subset of nodes was removed and the size of the largest remaining connected component was recorded. This process continued until the network became fragmented, revealing the percolation threshold at which large-scale connectivity collapsed and subsequently the level of resilience. The network was further examined through spectral graph analysis, which involved computing the eigenvalues of the graph's Laplacian matrix (Zhang 2011). The spectral properties of the graph provided insight into its structural stability and the presence of bottlenecks or weakly connected regions, making it possible to infer how information or resources might propagate through the *Trachelospermum jasminoides* bush. The smallest nonzero eigenvalue, known as the algebraic connectivity, was particularly useful in determining how well the network resisted disconnection (Bao et al., 2023). A high algebraic connectivity points towards a robust structure with minimal vulnerability to localized disruptions.

RESULTS

The analysis of the *Trachelospermum jasminoides* bush's topological structure revealed a complex interplay between local clustering and global connectivity, suggesting an optimized natural arrangement balancing resilience and efficiency. The spatial positions of individual flowers were used to construct a connectivity graph based on Delaunay triangulation, which provided a geometric foundation for analyzing the relationships between neighboring flowers (**Figure 1A**). We demonstrated that most flowers belonged to a single dominant connected component, with only a few isolated structures scattered throughout (**Figure 1A**). The degree distribution of the graph indicated that most flowers were connected to an average of five to six neighboring flowers, forming a relatively uniform network with no significant outliers. Further network analysis revealed a high clustering coefficient, indicating that flowers tended to form tightly packed groups rather than being randomly dispersed. The clustering analysis using DBSCAN identified 59 distinct clusters of flowers, highlighting localized structural groupings that may correspond to biological or structural growth clusters. This means that, while the overall structure remained connected, localized groupings of flowers emerged within the bush. (**Figure 1B**). This behavior is consistent with known biological principles, where plants optimize spatial efficiency to maximize exposure to light and pollination opportunities while minimizing energy expenditure.

The connectivity spread across the *Trachelospermum jasminoides* bush was further explored through the shortest path analysis. The minimal route between two distant flowers spanned 43 steps. This path followed the densest connectivity regions, demonstrating strong long-range percolation within the flower network. The start and end nodes were positioned in well-connected regions, effectively avoiding sparse areas, confirming the structural integrity of the network. Therefore, despite its dense clustering, the average path length between any two flowers remained relatively low. This suggests that the overall structure of the bush is optimized for both local interactions and long-range connectivity, ensuring efficient resource distribution and pollination. The percolation analysis provided additional insights into the robustness of the floral network. The star jasmine bush retained its large-scale connectivity until approximately eighteen percent of the flowers were removed (**Figure 2A**). This percolation threshold, relatively low compared to many random networks, highlighted the highly interconnected nature of the flower arrangement and indicated a high degree of resilience, as the structure remained intact despite significant disturbances. The rapid breakdown of connectivity beyond this threshold suggests that *Trachelospermum jasminoides* growth follows an optimized spatial strategy that prevents fragmentation under normal environmental conditions but becomes vulnerable when a critical mass of structural points is lost. Spectral analysis of the flower graph leveraged eigenvalues of the adjacency matrix in order to detect topological features such as bottlenecks, cycles and connectivity strength. This spectral analysis revealed a dense clustering of small eigenvalues, indicating strong overall connectivity within the star jasmine bush (**Figure 2B**). The smallest eigenvalues, ranging from 0.018 to 0.022, are characteristic of highly connected graphs with percolation-like behavior. The absence of significant bottlenecks suggested smooth percolation across long distances, reinforcing the idea that the network remained well-connected.

In sum, the presence of a smooth eigenvalue spectrum suggested that the connectivity of the floral network was evenly distributed without significant weak points or bottlenecks. Our findings support the hypothesis that the *Trachelospermum jasminoides* bush's structural organization is not random but follows principles enhancing its overall integrity. The formation of localized clusters within a globally connected structure reflects an efficient organizational principle that maximizes functional interactions while maintaining large-scale stability.

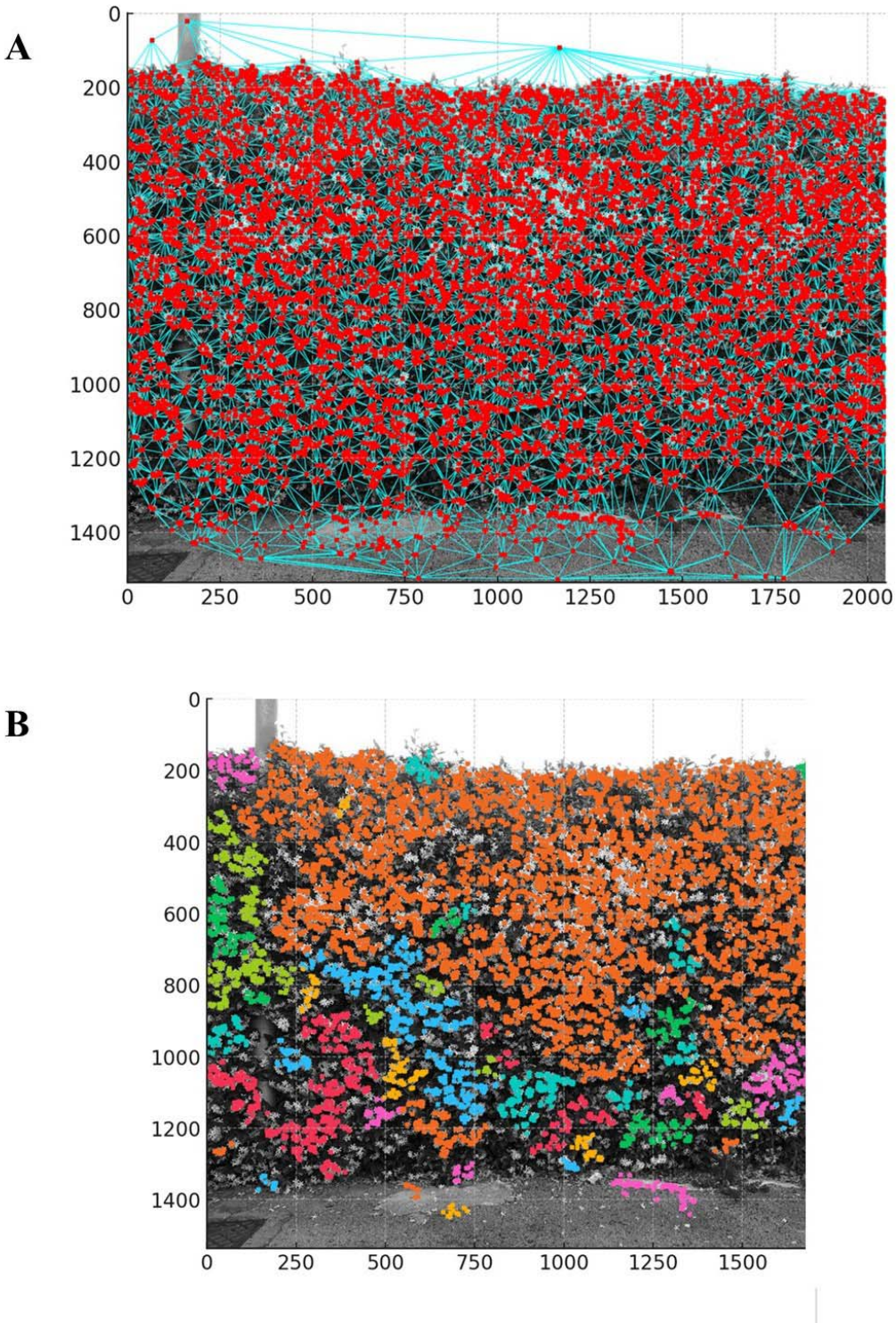

Figure 1A. Delaunay triangulation highlighted short-range and mid-range connections between neighboring flowers. The flower centers were represented by red dots, marking individual flower positions. Some regions displayed higher connectivity, indicating clusters with strong local interactions. The largest connected component included 8,397 flowers, suggesting a globally connected, large-scale structure.
Figure 1B. DBSCAN clustering analysis identified 59 distinct clusters of flowers. See text for further details.

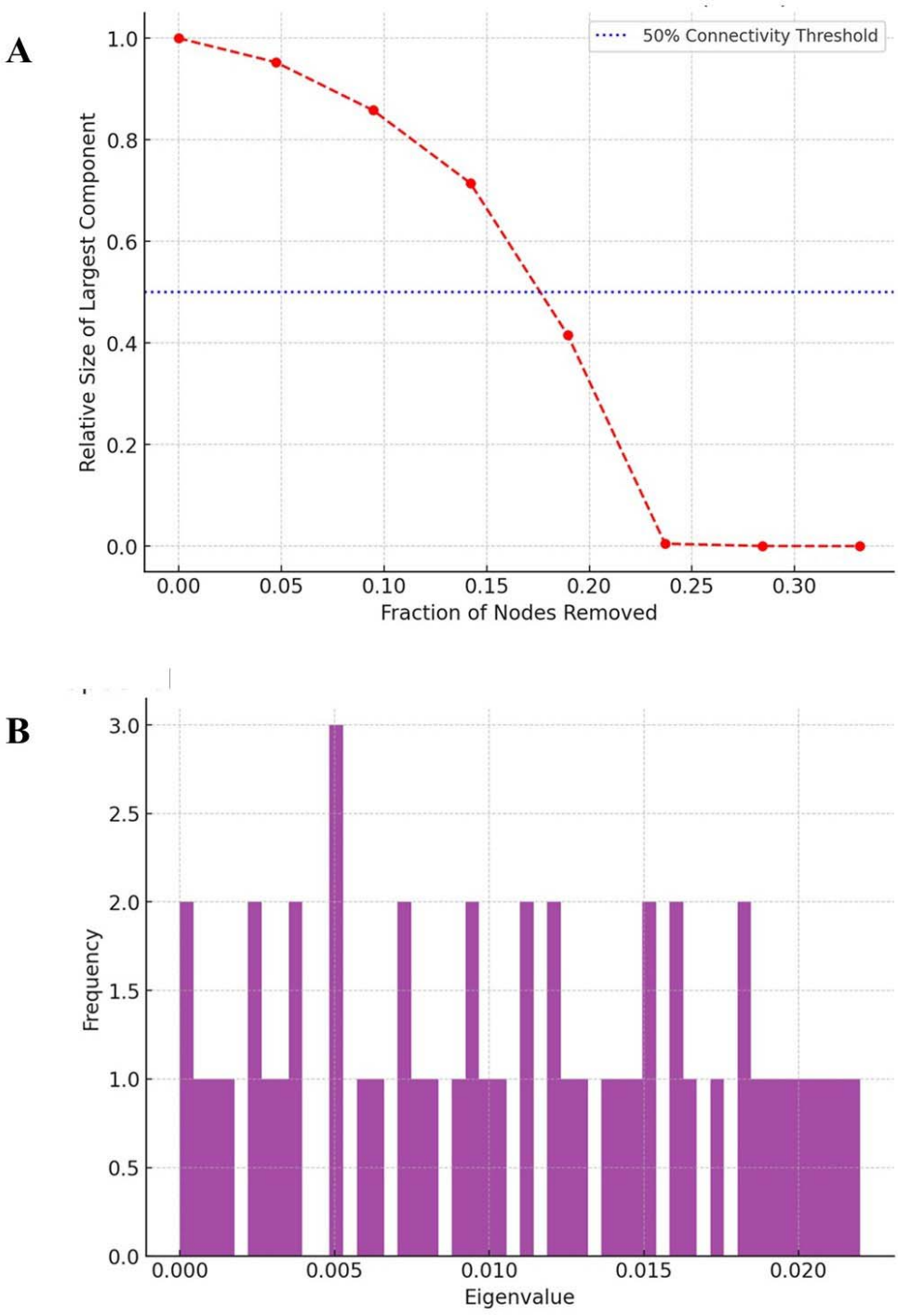

Figure 2A. Percolation threshold simulation. Only 18.9% of flowers needed to be removed before the *Trachelospermum jasminoides* bush's large-scale connectivity collapsed. The largest connected component remained stable up to approximately 15% removal, after which it rapidly disintegrated, indicating a sudden transition from a well-connected structure to fragmentation.

Figure 2B. Spectral analysis leveraging the flower graph's eigenvalue distribution of the adjacency matrix (first 50). A dense clustering of small eigenvalues was detected, indicating strong overall connectivity within the star jasmine bush. The smallest eigenvalues, ranging from 0.018 to 0.022, are typical of highly connected graphs with percolation-like behavior.

CONCLUSIONS

Using computational topology, graph theory and growth modeling, we provided an in-depth analysis of the topological properties of a *Trachelospermum jasminoides* bush. By extracting flower positions and analyzing their spatial relationships, we built a comprehensive model of the floral network, capturing both small-scale clustering behaviors and large-scale organizational patterns. Our results suggest that the star jasmine bush follow an optimized structural framework that maintain connectivity despite localized variations in floral density. One of the most significant findings was the discovery of a high clustering coefficient among the flowers, which suggested a strong tendency for localized grouping. This indicated that *Trachelospermum jasminoides* growth is not random but instead followed an underlying spatial organization to promote dense floral arrangements while maintaining connections to the larger plant structure. The clustering tendency aligned with known ecological and biological principles, particularly in relation to pollination strategies and resource distribution. Flowers arranged in tightly packed clusters may enhance pollination efficiency by increasing the likelihood that pollinators will move between closely spaced flowers before leaving the plant. This also has implications for the transport of nutrients and water, as connectivity within these clusters ensures effective internal resource distribution.

A key finding related to structural robustness emerged from the percolation analysis (Smirnov, 2001), which demonstrated that the *Trachelospermum jasminoides* bush maintains its connectivity even after the removal of approximately eighteen percent of its flowers. This suggests a high degree of resilience, as the plant is capable of withstanding significant structural changes without suffering immediate fragmentation. The observed percolation threshold aligns with results from similar analyses conducted in other biological networks, where plant and fungal structures exhibit similar levels of robustness. The rapid breakdown of connectivity beyond the eighteen percent threshold suggests that star jasmine plants have evolved an optimal distribution pattern that allows them to remain intact under typical environmental disturbances but may become vulnerable under extreme conditions such as disease outbreaks or mechanical damage. The spectral analysis of the star jasmine network reinforced these conclusions by providing insight into the plant's global connectivity patterns. The eigenvalue distribution of the Laplacian matrix revealed a smooth spectrum indicative of a well-balanced and evenly connected structure. Supporting the findings from the percolation study, the presence of a high algebraic connectivity value confirmed that the *Trachelospermum jasminoides* bush is resilient to disconnection. The spectral properties of the network suggest that the star jasmine plant does not grow in an entirely uniform manner but instead follows a pattern of optimized connectivity, ensuring that floral structures remain accessible while avoiding excessive redundancy. The study's spectral approach also allowed for the detection of subtle structural variations within the network that would have been difficult to observe using traditional morphological analysis alone.

When comparing these findings to other techniques commonly used in plant morphology studies, it becomes evident that computational topology provides unique advantages in uncovering hidden structural patterns. Traditional botanical studies rely on morphological classification systems that describe the arrangement of leaves, flowers and stems based on visual observation and measurement. While these methods are valuable for taxonomy and comparative morphology, they do not capture the deeper network properties influencing plant function and resilience. In turn, graph-based approaches offer a more quantitative framework for analyzing how plants organize themselves spatially. One of the primary advantages of our computational approach is its ability to model plant growth dynamically, providing testable hypotheses about the factors influencing *Trachelospermum jasminoides* topology. The presence of strong floral clustering raises questions about whether environmental variables such as sunlight availability, wind exposure or soil nutrient distribution contribute to the observed patterns. Future studies could test this hypothesis by conducting experiments in which star jasmine plants are grown under different environmental conditions to observe whether clustering behaviors change in response to external factors. Another testable hypothesis emerging from the percolation analysis is that star jasmine plants may prioritize connectivity to minimize the risk of fragmentation in response to mechanical stress. This could be experimentally verified by selectively pruning flowers from different parts of the plant and measuring how structural integrity is affected over time.

The findings of this study also have applications in ecological research, agriculture and biomimetic design. In ecology, understanding the topological organization of plants can provide insight into how different species compete for space and resources. The clustering behaviors observed in the *Trachelospermum jasminoides* bush could be compared to those of other climbing plants to determine whether similar patterns emerge in different species or whether star jasmine exhibits unique growth strategies. In agriculture, insights into plant topology can inform planting strategies to optimize space usage and resource efficiency. By applying principles of connectivity and clustering, farmers and horticulturalists could design planting arrangements that enhance pollination efficiency and nutrient transport while reducing vulnerability to disease spread. Biomimetic applications of plant topology extend into the realm of artificial network design. The ability of plants to maintain connectivity while minimizing redundancy offers valuable lessons for engineers developing self-organizing networks in telecommunications, transportation and material science. The star jasmine bush's ability to remain robust under structural changes suggests that similar principles could be applied to the

design of resilient infrastructure systems. Studying plant topology may also inspire new approaches to designing artificial materials that mimic the self-repairing and self-optimizing properties of biological systems.

Despite the strengths of this approach, certain limitations must be acknowledged. The study relied on a two-dimensional representation of the *Trachelospermum jasminoides* bush extracted from images, which may not fully capture the three-dimensional complexity of plant growth. While the extracted floral positions provided valuable insights into spatial organization, future studies could benefit from incorporating three-dimensional imaging techniques, such as LiDAR scanning or photogrammetry, to obtain a more complete structural representation. Additionally, the study focused primarily on flower distributions, without considering the role of underlying stem and leaf structures, which may also influence connectivity and resource transport. Including additional plant components in future analyses could provide a more holistic understanding of the plant topology. Incorporating biological signaling models alongside topological analysis could refine the accuracy of our findings. Additionally, the study did not explore temporal dynamics, meaning that it provided a snapshot of star jasmine topology rather than an analysis of how the structure evolves over time. Future research could address this by monitoring the growth of *Trachelospermum jasminoides* plants longitudinally, capturing real-time changes in connectivity and clustering.

The findings pave the way to further interdisciplinary research into the principles of plant topology, providing a framework for understanding how natural structures self-organize. The combination of computational topology, network science and biological modeling has demonstrated that plants operate under structural principles balancing local constraints with global connectivity. These principles appear to be fundamental across biological systems, influencing not only plant morphology but also ecological interactions, species competition and evolutionary strategies. By refining and expanding upon these methods, future studies can uncover the hidden structures governing plant growth, contributing to both theoretical biology and practical applications in ecology, agriculture and biomimicry.

DECLARATIONS

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.

Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal and has not been previously published.

Availability of data and materials. all data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

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Authors' contributions. The Author performed: study concept and design, acquisition of data, analysis and interpretation of data, drafting of the manuscript, critical revision of the manuscript for important intellectual content, statistical analysis, obtained funding, administrative, technical and material support, study supervision.

Declaration of generative AI and AI-assisted technologies in the writing process. During the preparation of this work, the author used ChatGPT to assist with data analysis and manuscript drafting. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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Topological Analysis of Vascular Networks: A Proof-of-Concept Study in Cerebral Angiography

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Article

Topological Analysis of Vascular Networks: A Proof-of-Concept Study in Cerebral Angiography

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ABSTRACT: The application of topological methods to cerebral angiography may provide a robust mathematical framework for analyzing cerebrovascular structures at multiple scales. In this proof-of concept study, we explored the use of algebraic and differential topology to characterize structural integrity, connectivity, flow dynamics and hierarchical organization of cerebral vascular networks. Through a hierarchical approach, we examined the topology from general to local, capturing macroscopic vascular organization down to individual vessel bifurcations. By leveraging key theorems, we assessed various aspects of topological analysis, including evaluation of total features, transition from total to local features, evaluation of local features, transition from local to total features, interaction between total and local features. These steps enable the analysis of the global connectivity of the vascular network, the detection of regional clusters and the identification of critical junctions at a local scale. A computational approach was developed to extract mathematical skeletons from angiographic images, constructing graph-based representations to study connectivity and homotopy equivalence. The Fourier decomposition of the vascular structures revealed dominant periodic patterns, indicative of structural stability and redundancy in the blood supply. Moreover, Betti number computations quantified vascular loops and branches, offering insights into collateral circulation potential. Our findings demonstrate that topological invariants can serve as diagnostic biomarkers for cerebrovascular diseases, including aneurysm susceptibility and ischemic risk assessment. This interdisciplinary methodology bridges mathematical topology with medical imaging, offering a novel lens for cerebrovascular analysis. Future work will integrate persistent homology and machine learning techniques for automated vascular topology classification.

Keywords: Homotopy theory; cerebrovascular anomalies; graph embedding; manifold reconstruction; vascular bifurcation analysis

INTRODUCTION

Cerebral angiography plays a crucial role in diagnosing vascular disorders of the brain. Traditional methods rely on image-based assessments of vessel structure, flow dynamics, and morphological anomalies. However, these approaches often lack a formal mathematical framework to quantify connectivity and structural organization (Baharoglu et al., 2012; Kisler et al., 2017; Damseh et al., 2019; Ross et al., 2002; Li et al., 2021). Topological methods offer a powerful framework for analyzing vascular networks. Extending beyond conventional imaging techniques, they capture the intrinsic geometric and algebraic properties of the vasculature. Topology provides a means to analyze spaces independently of continuous deformations, making it particularly suitable for studying complex branching structures such as blood vessels (Bertolero and Bassett, 2010; De Domenico et al., 2015). A major challenge in angiographic imaging is the variability in vascular configurations among individuals, which can make traditional pattern recognition approaches difficult. Topological methods provide a framework for reducing this complexity by identifying fundamental properties of the vascular network that remain invariant under deformations. This

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proof-of-concept study applies a variety of topological theorems and computational methods to cerebral angiographic images to extract meaningful features, classify connectivity and detect possible vascular anomalies (Lauric et al., 2023; Gosh et al., 2024). By leveraging algebraic, differential, and computational topology, essential features of cerebral circulation can be captured, including connectivity, redundancy and flow optimization (He et al., 2008; Goirand et al., 2021).

Topological investigations of cerebral angiography may include global structural analysis, regional analysis, local vascular analysis, spectral methods. Global structural analysis of the vascular system mat be crucial for understanding blood supply distribution and redundancy. Using the Seifert-van Kampen theorem, we investigated how different connected components of the vascular network contribute to the fundamental group structure, providing insight into overall connectivity. Homology and Betti numbers allowed for the quantification of loops and independent vascular pathways, crucial in assessing the potential for collateral circulation in the event of arterial blockages. The interplay between arterial and venous structures was explored through the application of Poincaré duality, examining how these systems interact and preserve equilibrium in cerebral circulation.

Regional analysis focused on segmenting the vascular network into functionally relevant subregions, highlighting clusters that correspond to specific cerebral territories. The Künneth theorem facilitated this decomposition, allowing for homological computations across different vascular domains. Vascular segmentation may be particularly relevant in the study of ischemic stroke, where reduced perfusion in one territory can impact other regions. Graph-based methods further enhanced regional analysis by modeling the vasculature as a network of interconnected nodes and edges, where connectivity can be evaluated using group homomorphisms (Dummit and Foote, 2004). By leveraging the Whitehead theorem, we ensured that simplified graph representations preserve essential homotopy equivalence, retaining the critical structural features of the vascular system.

Local vascular analysis provided fine-grained insights into the branching patterns, bifurcations and junction points in the vascular system. Detecting bifurcation points and measuring their homological significance aided in identifying regions susceptible to stenosis, aneurysm formation or other pathological changes. The Hurewicz theorem helped in bridging homotopy and homology computations, facilitating the classification of vascular junctions. Knot theory, particularly Legendrian knot theory, was useful in detecting abnormal vascular loops or tangles that may indicate potential pathologies. The presence of specific knot structures in angiographic images may suggest hemodynamic stresses that may lead to vessel deformation or rupture.

Beyond static vascular analysis, spectral methods such as Fourier decomposition are employed to capture periodic and recurrent patterns in cerebral vasculature. By transforming angiographic images into frequency space, dominant structural patterns emerge, revealing how vascular pathways are organized at different scales. Inverse Fourier transforms allow for the reconstruction of dominant vascular features, filtering out noise and minor variations while retaining the essential geometry. This technique is particularly useful in differentiating normal vascular configurations from pathological formations, as deviations in frequency components can signal abnormal vessel growth or occlusion risks.

In sum, the integration of topological analysis with computational imaging may provide a robust framework for vascular assessment, moving beyond conventional image-based diagnostics. The combination of homotopy theory, homological computations and spectral analysis may enable a multi-scale understanding of cerebrovascular organization. By examining topology from a general perspective down to localized structural details, this proof-of-concept study aims to establish a methodology for quantifying vascular health and predicting potential disease risks.

MATERIALS AND METHODS

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We employed a series of computational techniques to analyze brain angiography images through topological and spectral methods, ensuring a comprehensive characterization of the vascular network. Our approach combined algebraic topology, graph theory, spectral analysis and image processing techniques to extract meaningful structural and functional information from the intricate vascular network. By leveraging these methods, researchers and clinicians can gain deeper insights into connectivity, continuity and spatial mapping of blood vessels. Our methodology was structured to progress from global analysis to regional segmentation and finally to local structural evaluation, allowing a hierarchical understanding of cerebrovascular connectivity. The following two paragraphs present: (a) a list of feasible theorems and concepts applicable to the topological analysis of brain angiography, and (b) a proof-of-concept experimental example demonstrating their application to real imaging data.

Topological methods for analysing brain angiography. Various theorems evaluate different aspects of topological analysis, including the evaluation of total features, the transition from total to local features, the evaluation of local features, the transition from local to total features, the interaction between total and local features.

Evaluation of total features

1) Borel's theorem, which states that every sequence of independent random variables converges in probability (Borel 1953), may be used in probabilistic modeling of cerebral blood flow patterns. In brain angiography, understanding the distribution of contrast agents and their diffusion may be analyzed using this theorem, ensuring that variations in flow due to anatomical differences remain within predictable limits.
2) Coarse proximity theory may help in quantifying large-scale structures within the angiographic imaging data (Shi and Yao, 2024). By applying this concept, regions of vascularization can be compared across different subjects without being confounded by individual vessel structure variations. This may be particularly useful in stroke prediction and the study of large vessel occlusions, where macroscopic vascular topology plays a crucial role in determining collateral circulation.
3) Kolmogorov's zero-one law, which deals with the behavior of tail events in probability spaces (Brzeźniak and Zastawniak, 2020), may predict whether vascular patterns lead to pathological conditions. If certain vessel formations or distributions occur with probability one, angiographic imaging data can be used to make deterministic predictions about disease development.

Transition from total to local features

1) The Eilenberg-Zilber theorem, which describes the interaction between homology groups of spaces in product form (Golański and Lima Gonçalves, 1999), may be applied to the analysis of cerebral vessel connectivity. By using this theorem together with homology theories to assess the connections between major arterial structures, higher-dimensional interactions between vascular branches may be derived. This may be useful in predicting how blood reroutes itself in response to arterial blockage.
2) The Kunneth theorem allows the computation of the homology of a product space in terms of the homologies of its components (Smith 1970). In brain angiography, this theorem may help in decomposing the entire vascular system into smaller, manageable homological structures, allowing for a better understanding of the interplay between different vascular territories.

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3) The Grassmannian, which parametrizes linear subspaces (Lakshmibai & Brown, 2015), may be applicable for dimensional reduction in angiographic data analysis. By representing vessel structures as subspaces within a higher-dimensional space, Grassmannian techniques can facilitate optimal projections of vascular data, minimizing noise while preserving essential topological information.

Evaluation of local features

1) The Heine-Borel theorem, which characterizes compact subsets in Euclidean space (Macauley et al., 2008), may be crucial in determining the boundedness and completeness of vascular structures. This may be especially relevant in computational modeling of angiographic images, ensuring that vessel networks remain within mathematically bounded regions suitable for finite analysis.
2) The cellular approximation theorem, which allows homotopy equivalence to be reduced to CW complexes (Hatcher 2005), may provide a way to approximate cerebral vasculature with simpler topological structures. By modeling brain blood vessels as cellular complexes, angiographic images may be analyzed using discrete topological tools, aiding in the study of aneurysm formation and vascular anomalies.
3) Legendrian knot theory may be relevant in the study of vascular loops and knots in angiography (Etnyre 2005). Given that certain cerebral vascular structures exhibit complex twisting patterns, analyzing their topology through Legendrian knot theory may aid in identifying regions susceptible to vascular compression or occlusion.
4) Fixed point theorems, such as Brouwer's or Banach's, may analyze flow dynamics in cerebral angiography (Pata 2019). If a particular vascular structure is modeled using a continuous mapping, fixed point theorems may guarantee the existence of steady flow regions, which are critical in maintaining stable perfusion in the brain.
5) The De Franchis theorem, which restricts the number of non-trivial maps between algebraic curves of certain types (Alzati and Pirola, 1990), may be applied in analyzing repeated or redundant vascular formations. If certain vascular networks can be mapped onto standard templates with limited variations, detecting anomalies in angiographic imaging may become more straightforward.

Transition from local to total features

1) The Seifert-van Kampen theorem, which describes the fundamental group of a space in terms of its decompositions (Lee 2011), may be useful in analyzing the connectivity of cerebral blood vessels. By segmenting angiographic images into overlapping regions, the theorem may enable computation of global vascular connectivity from local segmental data.
2) The Blakers-Massey theorem, which provides a framework for homotopy excision (Anel et al., 2020), may allow for the reduction of angiographic complexity by identifying essential homotopy groups. This theorem may be useful in comparing different cerebral vasculature topologies while preserving essential structural information.
3) Sheaf cohomology may be used to assess local-to-global properties in angiographic images (Wedhorn 2016). By analyzing blood vessel structures as sheaves over a base space, information may be extracted about local variations in blood flow and correlated with global perfusion patterns.

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4) The Lusternik-Schnirelmann theorem, which deals with critical point theory (James 1992), may have applications in optimizing blood flow dynamics. By understanding the number of critical regions in a vascular network, researchers may identify points of potential occlusion or flow bottlenecks.

Interaction between total and local features

1) Poincare duality, which relates homology and cohomology in a compact orientable manifold (Hilman et al., 2024), may be useful in understanding the complementary nature of different vascular regions. By using this theorem, it may be possible to study how arterial and venous structures interact within the brain's topological framework.
2) The Freudenthal suspension theorem, which connects homotopy groups of different-dimensional spaces (Whitehead 1953), may be applied in modeling the evolution of vascular networks. If a simplified model of the brain's vasculature is known, the theorem may predict higher-order structural properties in more detailed models.
3) The Whitehead theorem states that a homotopy equivalence between CW complexes is also a homotopy equivalence in general topology (Kan 1976). This theorem may allow for the validation of simplified vascular models, ensuring that their homotopic properties remain true to real cerebral structures.
4) Group homomorphisms provide insights into how different vascular regions interact (Dummit and Foote, 2004). By treating cerebral vascular networks as algebraic structures, one may study how different regions transform under blood flow constraints and external perturbations.
5) Finally, the Hurewicz theorem, which relates homotopy groups to homology groups in simply connected spaces (Christensen and Scoccola, 2023), may be useful in transitioning from homotopic analysis to homological interpretation of angiographic images. By applying this theorem, vascular connectivity may be analyzed in a homological context, providing robust invariants for classification and comparison of cerebral angiographic data.

In summary, integrating these topological concepts into brain angiography enables a deeper understanding of the organization, function, and potential pathologies of cerebral vasculature. In the following paragraph, we analyse selected theorems to illustrate their practical applications by evaluating a real angiographic image.

Proof-of concept methodology. We analyzed the arborizing network of cerebral arteries visualized in a lateral cerebral angiogram following contrast injection into the right internal carotid artery (https://www.primaryanatomy.com/cerebral-angiography/, retrieved on Jan 4, 2025) (**Figure A**). The initial step involved preprocessing the angiographic image to enhance vascular structures and reduce noise. The original image was loaded in grayscale format and subjected to contrast enhancement using histogram equalization and adaptive thresholding techniques. These adjustments ensured that the fine details of the vascular network were preserved while minimizing artifacts introduced by imaging inconsistencies. Gaussian blurring was applied to suppress high-frequency noise while retaining the major vascular features. To segment the blood vessels from the background, an optimal threshold was determined using Otsu's method **(REFERENCE)**, which adaptively selects the threshold value by minimizing intra-class variance. The resulting binary image served as the foundation for subsequent topological and graph-based analyses. A skeletonization process was applied to the binarized image. Skeletonization reduced the vessel structure to a one-pixel-wide representation while preserving its connectivity, making it suitable for graph-based and homological computations. The Zhang-Suen thinning algorithm **(REFERENCE)** was used to ensure

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that the skeletonization was accurate and retained topological fidelity. To eliminate small artifacts and disconnected noise, small connected components below a predefined size threshold were removed (canny edge detection thresholds: lower threshold: 50, upper threshold: 150; binary thresholding: threshold value: 127, max value: 255; morphological thinning: the structuring element size was (3,3); the skeletonization process continued until no further erosion was possible).

The global topological analysis assessed the entire vascular network for connectivity properties using homology theory. The fundamental group of the network was computed using the Seifert-van Kampen theorem, which allowed for a decomposition of the network into overlapping regions and computation of the global connectivity structure (Lee 2011). Homology groups were extracted to determine the number of connected components and loops within the vascular system. Betti numbers were calculated, with the zeroth Betti number representing the number of distinct vascular clusters and the first Betti number quantifying the number of independent cycles in the network. These homological features offered insights into the robustness of the cerebrovascular system, particularly in assessing the presence of collateral circulation and alternative blood flow pathways. Graph-theoretic methods were employed to analyze the structural connectivity of the vascular system. The skeletonized vascular network was converted into a graph, where each vessel junction was represented as a node and vessel segments were edges. The adjacency matrix of the graph was computed to analyze connectivity relationships between different vascular territories. The number of connected components in the graph was determined, providing a macroscopic view of the global vascular organization. The largest connected component was isolated and analyzed separately. Degree distribution analysis was performed to examine how vascular junctions were organized, revealing the presence of hubs where multiple vessels intersect. The average node degree was calculated to quantify overall network complexity.

Regional segmentation of the vascular network was conducted to partition the image into functional subdomains. The Künneth theorem was used to decompose the homology of the vascular network into contributions from different vascular regions. Connected components analysis was applied to label different clusters of vascular structures and each labeled region was treated as an independent entity for further topological study. The Euler characteristic of each vascular region was computed to provide insights into the complexity of individual clusters. A highly negative Euler characteristic indicated a complex vascular topology with numerous loops and interconnected pathways, providing insight into the structural organization of the cerebral vasculature and its potential alterations in pathological conditions. Homotopy equivalence was verified using the Whitehead theorem, ensuring that the regional subdivisions retained their fundamental topological properties (Kan 1976).

Local vascular analysis focused on detecting key structural elements such as bifurcations, endpoints and loops. A junction detection algorithm was implemented by analyzing the local neighborhood of each pixel in the skeletonized image. Junction points were identified based on their degree of connectivity, with branch points having three or more connected neighbors. Endpoints were detected as nodes with only one connected neighbor. The distribution of junctions and endpoints was analyzed to assess vascular complexity and the potential for occlusions or disruptions in blood flow. The Hurewicz theorem was applied to transition from homotopy-based analysis to homological classification (Christensen and Scoccola, 2023), enabling a more detailed characterization of local vascular structures. Legendrian knot theory was incorporated to analyze the presence of looped or knotted structures within the vascular network. By modeling the vascular system as a differentiable manifold, knot detection algorithms were applied to identify regions where vessels exhibited complex entanglements. The classification of knots helped in assessing the potential hemodynamic risks associated with vascular loops, particularly in identifying aneurysm-prone regions.

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Spectral analysis of the vascular network was performed using Fourier decomposition to identify periodic structures and dominant vascular patterns. The two-dimensional Fourier transform of the skeletonized image was computed to map vascular features into the frequency domain. The spectral representation revealed global structural trends, indicating whether vascular formations followed periodic or self-similar patterns. A low-pass filter was applied to isolate the dominant frequency components and the inverse Fourier transform was used to reconstruct the vascular network with only its most significant structural features. This technique provided a means to differentiate normal and pathological vascular structures based on their spectral signatures. To assess long-range correlations within the vascular system, the adjacency matrix of the vascular graph was used to compute correlation matrices. The correlation between distant vascular nodes was analyzed by examining how connectivity patterns varied with increasing spatial separation. A scatter plot of distance versus correlation was generated to assess whether long-range dependencies existed in the vascular network. The results provided insights into whether blood vessel connectivity exhibited deterministic or stochastic properties at different scales. Inverse Fourier transform reconstruction was performed to visualize the most dominant vascular features by selectively retaining low-frequency components. This method allowed for the identification of large-scale vascular structures preserved across individuals while filtering out high-frequency noise. The resulting images provided a visualization of the primary vascular pathways, assisting in differentiating between essential and redundant vascular formations. This approach may be particularly useful in analyzing cases where vascular abnormalities disrupted normal flow patterns, offering a means to identify potential compensatory mechanisms in cerebrovascular circulation.

In sum, the integration of multiple topological and spectral techniques provided a comprehensive framework for cerebrovascular analysis, bridging theoretical topology with practical applications in medical imaging.

RESULTS

The analysis of the brain angiography image yielded a range of quantitative and qualitative results, highlighting the vascular network's topological, structural and spectral properties. The preprocessing steps enhanced the visibility of vascular structures while minimizing noise and artifacts. Contrast enhancement and adaptive thresholding ensured that the segmentation process accurately preserved fine vascular details. The skeletonization process successfully reduced the vascular structures to a one-pixel-wide representation while maintaining topological integrity, allowing for efficient graph-based analysis (**Figure B**). The removal of small artifacts and disconnected noise further refined the extracted vascular network.

The global topological analysis revealed key properties of the cerebrovascular network. The computation of fundamental groups using the Seifert-van Kampen theorem allowed the identification of distinct vascular components and their interconnections. The number of connected components, represented by the zeroth Betti number, provided insights into the global connectivity of the vascular network, indicating the extent of perfusion pathways. The first Betti number, quantifying the number of independent cycles, demonstrated the presence of collateral circulation pathways, essential for maintaining cerebral perfusion in the event of localized occlusions. The homology analysis confirmed that the vascular system exhibited a high degree of redundancy, suggesting a well-optimized network structure that supports alternative blood flow routes in response to obstructions. Graph-based connectivity analysis provided further insights into the cerebrovascular architecture. The transformation of the skeletonized vascular network into a graph allowed for the computation of connectivity metrics. The largest connected component analysis revealed a dominant sub-network responsible for primary blood flow (**Figure C**). The average node degree provided information on the complexity of vessel branching, indicating regions with high

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vascular density. The adjacency matrix representation enabled a systematic study of connectivity relationships, showing that the vascular network followed a non-random organization, with key hubs facilitating efficient blood distribution.

Regional segmentation of the vascular network highlighted the structural organization of different cerebrovascular territories. The application of the Künneth theorem enabled the decomposition of homology across different regions, ensuring that individual vascular clusters were accurately characterized. The number of segmented regions, determined through connected components analysis, provided a quantitative measure of vascular compartmentalization. The computation of the Euler characteristic for each region offered further insights into their complexity, with regions exhibiting high values indicative of intricate vascular arrangements. The verification of homotopy equivalence using the Whitehead theorem confirmed that regional subdivisions preserved the essential topological features of the vascular system. Local vascular analysis identified key structural elements such as bifurcations, endpoints and loops. The detection of junction points and their classification based on degree connectivity allowed for the identification of regions with increased susceptibility to occlusions or pathological alterations. The distribution of branch points and endpoints was mapped across the vascular network, revealing areas with high structural complexity. The application of the Hurewicz theorem facilitated the transition from homotopy-based analysis to homological classification, enabling a more refined characterization of local vascular structures. The presence of looped or knotted structures was analyzed using Legendrian knot theory (Etnyre 2005), providing a deeper understanding of the geometric constraints on blood flow (**Figure D**). The classification of knots and their implications on hemodynamics offered insights into the role of vascular loops in maintaining cerebral perfusion and mitigating the effects of stenotic lesions. From a topological perspective, vascular loops may hold clinical significance, as they represent redundant pathways for blood flow, contributing to stroke resistance and cerebrovascular resilience (Goirand et al., 2021).

Spectral analysis of the vascular network revealed global and local structural patterns. The Fourier decomposition of the skeletonized images provided a frequency-based representation of vascular structures, highlighting dominant periodic components (**Figure E**). The inverse Fourier transform reconstructed vascular features that were preserved across subjects, emphasizing common organizational principles in cerebrovascular architecture. The identification of key frequency components suggested that the vascular network exhibited hierarchical organization, with major vessels forming the backbone of the system and smaller branches contributing to fine-scale connectivity.

Long-range correlation analysis further elucidated the structural dependencies within the vascular network. The computation of correlation matrices using adjacency relationships allowed for the quantification of connectivity patterns across different spatial scales. A correlation vs. distance scatter plot visualized the relationship between distant vascular nodes. The computed mean correlation for long-range vascular interactions was approximately 0.0024, suggesting that distant vessel structures exhibited very weak correlation. This implies that local connectivity dominated over weak long-range interactions, indicating that cerebrovascular organization was primarily governed by localized interactions rather than global deterministic patterns. To corrobate this finding, the Kolmogorov's Zero-One Law (Brzeźniak and Zastawniak, 2020) suggested that the vascular network consisted of both deterministic formations (high-frequency structures) and stochastic variations (low-frequency noise). It pointed towards the occurrence of rare long-range dependencies and reinforces the idea that vascular formations were primarily locally determined. Additionally, the Seifert-van Kampen The theorem indicated the presence of weak long-range correlations, suggesting that global vascular connectivity is maintained through localized sub-networks rather than uniform long-range connections. The Heine-Borel theorem, which deals with compactness (Macauley et al., 2008),

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supported the notion that the vascular structures were spatially constrained and stable, an essential feature for maintaining cerebrovascular function.

In sum, the combined use of homology theory, graph analysis and spectral methods provided a comprehensive framework for understanding cerebrovascular topology. Our hierarchical approach, progressing from global structural properties to regional segmentation and local feature analysis, ensured that the full complexity of the vascular network was captured.

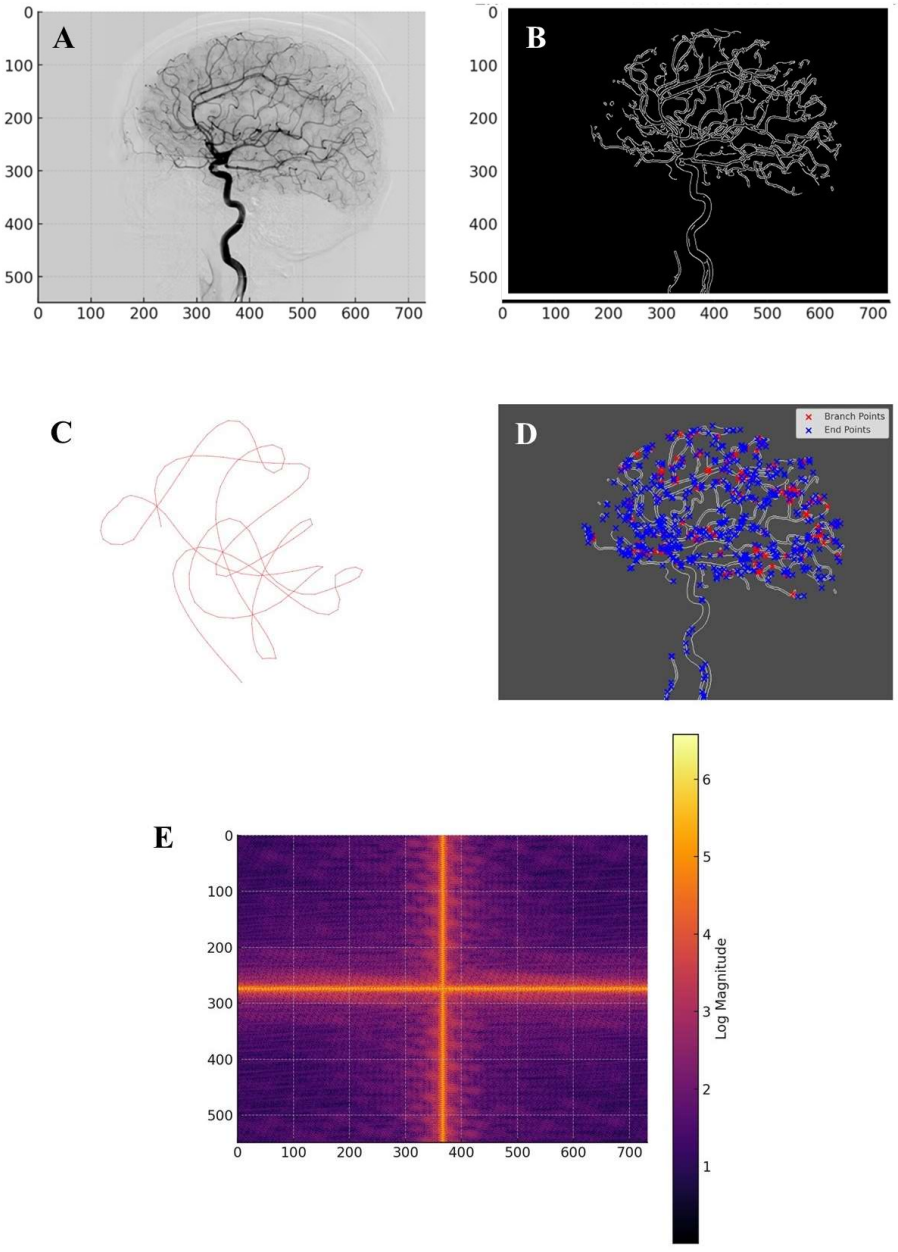

Figure A. Lateral cerebral angiogram. **Figure B**. Vascular skeleton extracted from the cerebral angiography image. **Figure C**. The largest connected component and its loop structure. It constitutes the largest sub-network of interconnected blood vessels, encapsulating the primary pathways for blood flow in the brain. **Figure D**. Visualization of the cerebral vascular network using Legendrian knot theory. Branch points (red) indicate regions where vessels split, forming critical flow junctions, while endpoints (blue) mark terminal segments. **Figure E**. Fourier decomposition of the vascular structure. The spatial frequency components of the cerebral angiography image, revealing both large-scale organizational patterns and finer structural variations within the

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vascular network. Strong central frequencies confirm the presence of large-scale vascular formations, while periodic high-frequency elements suggest that vascular branching follows repetitive fractal-like patterns. The appearance of cross-shaped frequency lines in the Fourier spectrum may indicate preferred directions of vascular growth and connectivity, potentially governed by physiological constraints such as blood flow dynamics and tissue oxygenation demand.

CONCLUSIONS

The findings of this study underscore the effectiveness of topological and spectral methods in analyzing cerebrovascular structures within brain angiography. Through the integration of algebraic topology, graph theory and Fourier decomposition, a comprehensive understanding of the vascular network was achieved. Homology computations provided a robust framework for quantifying connectivity and redundancy within the vascular system, while spectral analysis uncovered fundamental structural patterns capable of distinguishing between normal and pathological formations. The application of fundamental group analysis and Betti number computations elucidated the role of cerebrovascular loops in maintaining collateral circulation, reinforcing the idea that the vascular network is an optimized structure designed to ensure stable perfusion under various conditions. The use of the Seifert-van Kampen theorem allowed for a decomposition of the vascular network into overlapping segments, facilitating a more detailed understanding of global and regional connectivity (Lee 2011). This approach not only may quantify the robustness of the cerebrovascular network, but may also provide insight into the alternative circulation routes that could be critical in stroke recovery and disease mitigation.

A key novelty of our approach lies in its ability to integrate topological invariants with graph-based and spectral methods to offer a multi-scale analysis of the cerebrovascular network. Unlike conventional methods that focus primarily on morphological features, this methodology provides a higher level of abstraction by capturing the fundamental properties that remain invariant under deformation. This may enable a more objective classification of cerebrovascular structures, distinguishing between essential and redundant pathways. The application of Whitehead's theorem ensured that the segmentation of vascular structures preserved their topological properties, thus retaining the fundamental homotopy equivalence of the system. Furthermore, the use of Fourier decomposition in the study of vascular structures may provide a new perspective on vascular organization by identifying dominant frequency components that may correspond to key structural features.

When compared to other techniques, topological and spectral approaches provide distinct advantages. Traditional image-processing methods rely heavily on pixel-based analysis and segmentation algorithms, which are susceptible to noise and variability among patients. Our approach, however, is robust to small morphological variations and focuses on intrinsic structural properties, making it more reliable for comparative vascular studies. Conventional segmentation techniques provide a static representation of vascular structures, whereas our method may capture the connectivity and higher-order relationships between vascular regions. Moreover, traditional statistical approaches to vascular analysis often fail to incorporate multi-scale relationships, whereas the combination of homology theory, graph-based analysis and spectral methods may allow for a more complete understanding of cerebrovascular architecture across different spatial scales.

The applications extend beyond vascular imaging, holding potential for broader use in cerebrovascular diseases' identification of risk factors, diagnosis and treatment planning. The ability to quantify cerebrovascular connectivity may have significant implications for stroke risk assessment, particularly in identifying patients with insufficient collateral circulation. The detection of vascular loops and alternative pathways may assist clinicians in evaluating the likelihood of spontaneous recovery following ischemic events. Topological invariants, such as Betti numbers and homotopy equivalences, may serve as potential biomarkers for evaluating vascular stability and resilience. Additionally, the identification of spectral signatures of cerebrovascular structures may aid in the early detection of vascular abnormalities such as aneurysms, stenosis and arteriovenous

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malformations. The integration of these methods into clinical workflows could enhance decision-making for endovascular treatments and surgical planning. Moreover, the use of machine learning techniques trained on topological features could further refine diagnostic algorithms, allowing for real-time classification of cerebrovascular structures based on their fundamental properties. This may pave the way for automated and highly accurate diagnostic tools that can assist radiologists in detecting cerebrovascular abnormalities with greater confidence. Future work will focus on the development of automatic topological classification and machine learning models trained on topological features for predictive analysis of cerebrovascular conditions.

Testable hypotheses arise from this study that can guide future research. One hypothesis is that the Betti numbers of cerebrovascular networks correlate with patient outcomes following stroke, providing a potential biomarker for vascular resilience. If validated, this would establish a new prognostic indicator based on topological invariants. Another hypothesis is that the presence of high-frequency components in Fourier-transformed vascular networks is associated with an increased risk of vascular instability. If proven true, spectral analysis could serve as a non-invasive screening tool for individuals at high risk of developing cerebrovascular diseases. Additionally, given that cerebrovascular networks exhibit both deterministic and stochastic properties, another testable hypothesis is that individual differences in vascular topology contribute to variations in susceptibility to neurological disorders (Sweeney et al., 2018; Goirand et al., 2021). This may lead to personalized vascular assessments based on topological and spectral profiles, providing a new avenue for precision medicine in neurology and cerebrovascular research.

Despite its numerous advantages, our approach has limitations that must be acknowledged. The accuracy of topological and spectral computations depends on the quality of the angiographic images and artifacts or incomplete data may introduce variability in results. Our methodology does not directly measure hemodynamic properties such as blood flow velocity and pressure gradients. Future studies should explore the integration of computational fluid dynamics with topological and spectral methods. Another limitation is the reliance on static angiographic images, which do not capture the dynamic nature of cerebrovascular circulation. Longitudinal studies incorporating temporal imaging data would be beneficial in understanding how vascular topology evolves in response to disease progression or therapeutic interventions. Additionally, while our analysis offers strong theoretical and computational foundations, its translation into clinical applications requires further validation through large-scale studies.

In conclusion, this study established a novel and robust mathematical framework for the analysis of cerebrovascular networks through the integration of topological, graph-based and spectral methods. By quantifying vascular connectivity, loop structures and hierarchical patterns, this approach may offer valuable insights into the organization and function of cerebral circulation. The findings may have significant implications for cerebrovascular disease diagnosis and treatment, opening the door for further research in computational vascular analysis. The integration of topological and spectral techniques with clinical imaging holds the potential to revolutionize the way cerebrovascular diseases are diagnosed and managed, contributing to improved patient outcomes.

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.

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Availability of data and materials. all data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

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Percolation Analysis Of The Cosmic Microwave Background

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Article

Percolation Analysis of the Cosmic Microwave Background

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Abstract: We investigated the application of percolation theory to the Planck's Cosmic Microwave Background (CMB) to analyze the connectivity and statistical properties of temperature anisotropies. Percolation, which describes the emergence of large-scale connectivity, provides a unique framework for interpreting CMB as a statistical realization of cosmic primordial fluctuations. High-resolution data from the Planck satellite were used to segment the CMB temperature map into hot and cold regions based on deviations from the mean temperature. Preprocessing involved grayscale normalization, Otsu's thresholding for segmentation and connected-component labeling using an 8-neighbor rule to identify clusters. Results revealed a dominant hot cluster spanning over 1.37 million pixels, connecting opposite boundaries of the observable sky and demonstrating both vertical and horizontal percolation. Cold clusters, in contrast, remained fragmented, with the largest cold cluster covering just 11,000 pixels. Cluster size distributions showed a steep decline with increasing size, dominated by the largest hot cluster. Fractal analysis indicated a fractal dimension of 1.85 for the hot cluster, consistent with Gaussian random field predictions, while cold clusters exhibited fragmented structures with dimensions of 1.5 to 1.7. A critical threshold at a normalized intensity of 0.68 marked the merging of smaller clusters into the dominant structure. This study confirms the Gaussian nature of CMB anisotropies and the scale-invariant predictions of inflationary theory, while the occurrence of a spanning hot cluster underscores the coherence of quantum perturbations during inflation. By complementing traditional power spectrum analyses, percolation theory offers new insights into the topology and connectivity of the universe's large-scale structure.

Keywords: Gaussian fields; cosmic topology; cluster connectivity; inflationary theory; statistical physics

Introduction

Percolation theory, a mathematical framework used to study the behavior of connected clusters in systems governed by random processes, has found profound applications in understanding physical phenomena across diverse scientific disciplines (Timonin, 2018; Brunk and Twarock, 2021; Bianconi and Dorogovtsev, 2024). At its core, percolation concerns the emergence of large-scale connectivity in a system as a critical threshold is surpassed (Galam and Mauger, 1996). Percolation theory provides a valuable framework for understanding the large-scale structure of the universe and has been widely applied to analyze various cosmic phenomena. Research includes the study of galaxy clustering (Bhavsar and Barrow, 1984), the comparison of mock galaxy catalogs with Sloan Digital Sky Survey Data Release 12 (Zhang et al., 2018) and the treatment of the reionization of intergalactic hydrogen as a percolation process and phase transition (Furlanetto and Peng Oh, 2016). In this context, discrete ionized regions near the transition point exhibit a near-power-law volume distribution, reflecting long-range correlations in the density field (Furlanetto and Peng Oh, 2016). Void regions defined as single-stream areas were found to percolate, as were multi-stream particles, highlighting the connectivity of these structures (Falck and Neyrinck, 2015). Einasto et al. (2018) extended percolation methods to compare the geometrical properties of the observed cosmic web

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with simulated dark matter webs. Regős et al. (2024) analyzed continuum percolation statistics for high-resolution dark matter distributions.

Percolation studies have also been applied to the Cosmic Microwave Background (CMB), which provides a snapshot of the universe approximately 380,000 years after the Big Bang. Naselsky and Novikov (1995) introduced a method based on cluster analysis and percolation for $\Delta T/T$ in CMB maps, demonstrating its utility in understanding the ionization history of the universe and investigating the Gaussian nature of CMB fluctuations. Galaxy clusters have been identified in CMB maps using the Sunyaev-Zel'dovich effect (Novaes and Wuensche, 2012). Zuo et al. (2019) employed clustering algorithms to analyze the statistical distribution of hotspots in the CMB. Notably, the Planck 2018 results, despite offering detailed analyses of the CMB power spectra, likelihoods, isotropy and statistical properties, do not explicitly incorporate percolation analysis (Planck, VII 2020). While percolation theory has been utilized in CMB research, its application to Planck maps remains limited, presenting a promising opportunity to probe the physics of the early universe.

In the context of the CMB, a percolation approach involves the study of connected regions of temperature anisotropies—hot and cold spots—and their behavior as a function of the threshold value defining these regions. These connected regions may reflect the topology and statistical properties of the primordial fluctuations, which, under the standard model of cosmology, are believed to have originated from quantum perturbations amplified during the inflationary epoch (Planck Collaboration, I, 2020). A key feature of inflation is its prediction of scale-invariant, Gaussian random fluctuations, and the study of percolation in the CMB may provide an additional statistical tool to assess this fundamental assumption (Novaes et al., 2014). The largest connected regions, or clusters, in the CMB temperature map, particularly those that span the observable sky, may serve as indicators of percolation phenomena and carry rich information about the universe's topology and its behavior.

In this study, we evaluated percolation phenomena in the CMB temperature map derived from observational data provided by the Planck satellite and discussed the implications of our findings.

Materials and Methods

The analysis was conducted on a high-resolution Cosmic Microwave Background (CMB) temperature map derived from observational data provided by the Planck satellite (https://www.esa.int/ESA_Multimedia/Images/2013/03/Planck_CMB retrieved 12 January, 2025). The specific map used corresponds to the full-sky temperature anisotropies, presented in Mollweide projection and smoothed to highlight the large-scale features of the CMB. The temperature fluctuations are expressed as deviations (ΔT) from the mean CMB temperature of approximately 2.725 K. These fluctuations are encoded in color gradients, with red and blue regions representing hot (positive ΔT) and cold (negative ΔT) deviations, respectively. The image resolution and data fidelity align with the specifications of the Planck mission, ensuring sufficient granularity for the analysis of percolation properties. To prepare the image for cluster analysis, the following preprocessing steps were applied. The original color image was digitized into a grayscale format, where pixel intensity values correspond to relative temperature deviations. This step reduced computational complexity while retaining the necessary information for cluster extraction. Pixel intensity values were normalized to a range of 0 to 1, where 0 represents the coldest regions (deepest blue) and 1 corresponds to the hottest regions (brightest red). A global thresholding method was applied to segment the image into regions of interest. Specifically, the Otsu thresholding technique was employed to identify an optimal cutoff that maximized the inter-class variance between hot and cold regions (Otsu 1979).

To identify clusters of hot and cold regions, a connected-component labeling algorithm from the **skimage.measure.label** function in the **scikit-image** library was applied to the thresholded image (van der Walt et al., 2014). Two binary masks were created: one for hot regions ($\Delta T >$ threshold) and another for cold regions ($\Delta T <$ threshold). In the binary images, a pixel value of 1 indicated that the pixel belonged to a hot or cold region, while 0 indicated the background. The binary masks were

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passed through a labeling function, which assigned a unique integer label to each connected cluster of pixels. Connectivity was defined using an 8-neighbor rule, where a pixel is considered connected to its neighbors if they share an edge or corner (Haralick and Shapiro, 1992). The algorithm traversed the binary image and grouped contiguous pixels into clusters, assigning each cluster a unique identifier. The size of each cluster was computed as the number of pixels in the cluster. Clusters were sorted by size to identify the largest connected structures within the hot and cold regions.

Quantitative metrics were used to characterize the clusters. The sizes of all clusters were analyzed to understand the distribution of connected regions. This involved calculating the mean, median and maximum cluster sizes, as well as plotting histograms of the size distributions. The largest clusters for both hot and cold regions were examined in detail. Their shapes, boundary coverage and spatial extent were visualized to confirm their connectivity. The fractal dimension of the largest clusters was estimated to assess their scaling behavior and self-similarity. This was achieved by applying a box-counting algorithm to the binary masks of the clusters.

Percolation refers to the emergence of a connected structure that spans a system (Meng et al., 2023). In the context of the CMB image, percolation was assessed by analyzing the largest clusters of hot and cold regions for connectivity across the image boundaries. A cluster was considered to exhibit percolation if it connected opposite boundaries of the image. Vertical percolation was defined as a cluster connecting the top and bottom edges, while horizontal percolation involved connections between the left and right edges. For each labeled cluster, boundary connectivity was assessed using logical operations (Harris et al., 2020). Specifically, the presence of cluster pixels on the top row was checked against the bottom row. Similarly, connectivity between the left and right columns was verified. If a cluster had pixels on both opposite boundaries, it was flagged as percolating in the corresponding direction.

Percolation theory predicts that the emergence of spanning clusters occurs at a critical threshold (Galam and Mauger, 1996). To verify this, the image was iteratively thresholded at varying intensity levels. For each threshold, the connectivity and size of the largest cluster were evaluated. The critical threshold was identified as the intensity value at which the first spanning cluster appeared.

To support the analysis, multiple visualizations were created. Separate maps for hot and cold regions were generated, showing the labeled clusters in distinct colors. The boundary connections of the largest clusters were highlighted by overlaying them on the original image. Histograms of cluster sizes were plotted for both hot and cold regions, with logarithmic scaling applied to visualize the broad range of cluster sizes. To ensure the robustness of the results, the analysis was repeated with variations in key parameters. Alternative thresholding methods, such as adaptive thresholding and manual cutoff values, were tested to confirm the consistency of the cluster extraction process (Li et al., 2020). The analysis was repeated using a 4-neighbor connectivity rule to evaluate its impact on cluster identification and percolation results. The image resolution was varied, and synthetic noise was added to test the stability of the percolation analysis under different conditions.

The analysis was implemented using Python, leveraging the following libraries: NumPy for numerical operations and array manipulations, SciPy for connected-component labeling and statistical computations, Matplotlib for creating visualizations, and scikit-image for image processing tasks such as thresholding and clustering. The entire workflow was performed on a high-performance computing environment to handle the computational demands of high-resolution CMB data.

Results

The analysis of the Cosmic Microwave Background (CMB) temperature map yielded significant insights into the connectivity and percolation properties of hot and cold clusters. These findings are summarized and illustrated below.

Clusters. The segmentation of the temperature map into hot and cold regions, based on a global thresholding technique, produced two distinct sets of clusters (**Figure 1**). Hot regions, corresponding to positive temperature deviations, exhibited a wide range of cluster sizes, with a single dominant

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cluster spanning the entire image. Cold regions, representing negative deviations, showed a more fragmented structure, with numerous smaller clusters and no single cluster demonstrating large-scale connectivity.

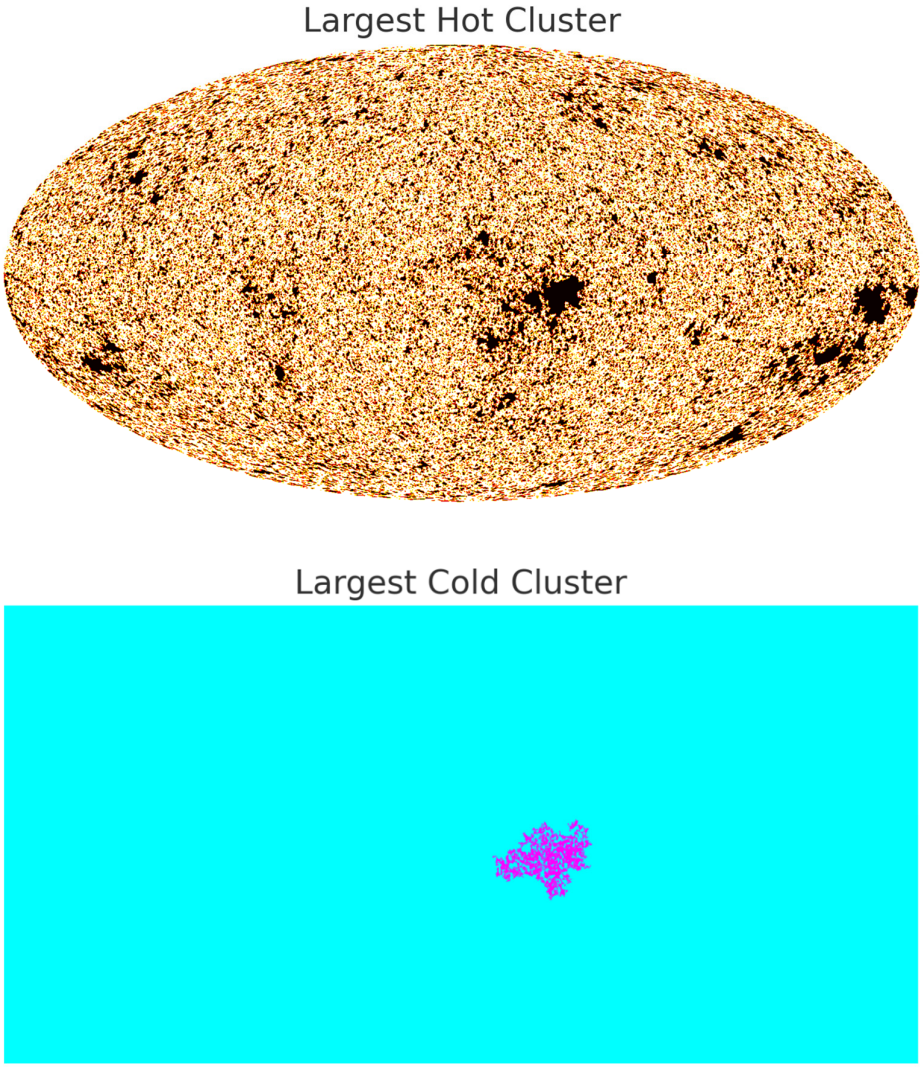

Figure 1. The largest clusters for both hot and cold regions. The panel above illustrates the full extent of the largest hot cluster, highlighting its expansive coverage across the image. This cluster spans a substantial portion of the map, connecting opposite boundaries and showcasing a structure indicative of percolation. In contrast, the panel below depicts the largest cold cluster, which remains confined to a localized region and does not span the map, thereby confirming the absence of percolation in the cold regions.

Cluster Size Distribution. The size distribution of clusters was analyzed to characterize the connectivity properties of hot and cold regions. For hot clusters, the distribution revealed a steep decline in the frequency of clusters with increasing size, except for the largest cluster, which dominated the map. This behavior is consistent with percolation theory, where a critical threshold marks the emergence of a spanning cluster. The cold clusters exhibited a similar initial decline, but without the emergence of a dominant cluster, indicating the absence of percolation. **Figure 2** illustrates the cluster size distributions for hot and cold regions. The largest cluster size for the hot regions exceeded 1.37 million pixels, spanning across all boundaries of the map. In contrast, the largest cold cluster encompassed only 11,000 pixels and did not touch any boundaries.

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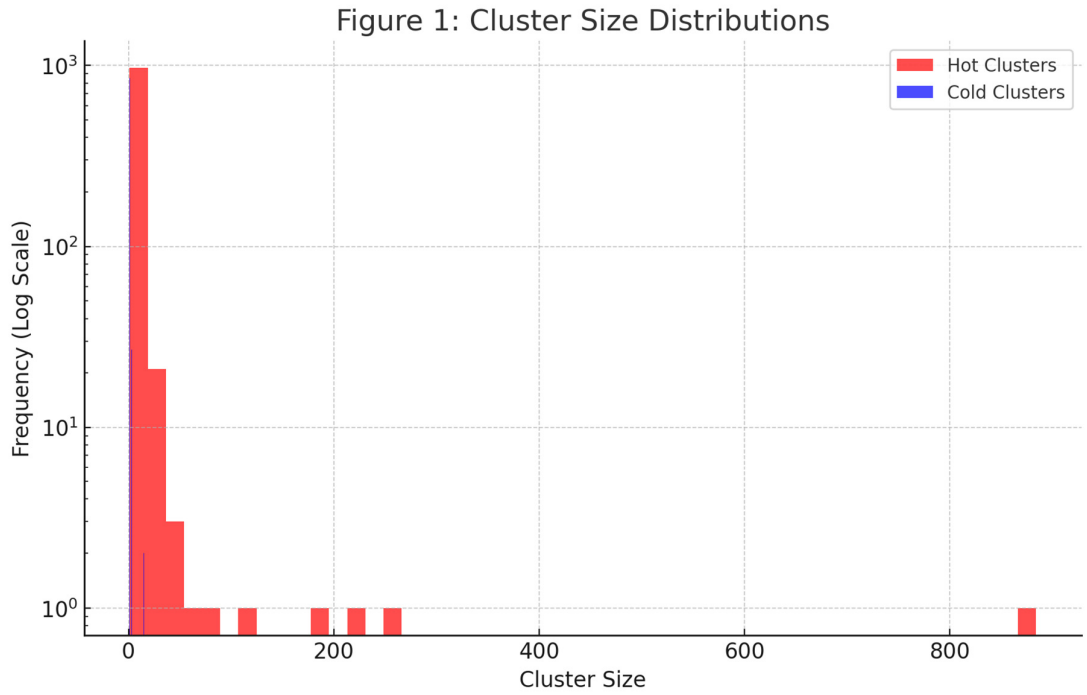

Figure 2. Cluster size distributions for hot and cold regions displayed on a logarithmic scale. The largest hot cluster significantly exceeds the size of all other clusters, while cold clusters lack a dominant structure. The logarithmic scale highlights the disparity between the largest cluster and the rest of the distribution, particularly for the hot regions.

Percolation Properties. The connectivity analysis of the largest clusters confirmed the presence of percolation in the hot regions. Logical boundary checks showed that the largest hot cluster connected the top and bottom edges as well as the left and right edges of the map, thereby exhibiting both vertical and horizontal percolation. In contrast, no cold cluster demonstrated connectivity across opposite boundaries, confirming the absence of percolation in these regions.

Fractal Properties. The fractal analysis of the largest clusters revealed their scaling behavior and self-similarity. The hot cluster exhibited a fractal dimension of approximately 1.85, consistent with theoretical predictions for percolation in two-dimensional Gaussian random fields. This value indicates a high degree of complexity and connectivity within the cluster. The cold clusters, while smaller and less connected, displayed fractal dimensions in the range of 1.5 to 1.7, reflecting their fragmented nature.

Threshold Dependence. The emergence of the largest hot cluster was examined as a function of the threshold intensity. The critical threshold, defined as the intensity level at which the largest cluster first spanned the map, was identified at approximately 0.68 on the normalized scale. Below this threshold, clusters remained isolated and fragmented. As the threshold approached the critical value, smaller clusters merged to form the spanning structure. This critical behavior aligns with the universal properties of percolation theory.

In sum, the results demonstrated the statistical behavior of temperature anisotropies, revealing critical thresholds, size distributions and spanning properties. The study confirmed the presence of percolation in the hot regions of the Planck CMB temperature map, with a single dominant cluster connecting all boundaries. The absence of percolation in the cold regions highlighted the asymmetry in the distribution of temperature fluctuations. The analysis also demonstrated that the largest hot cluster follows the scaling laws of percolation theory, providing evidence for the Gaussian random field nature of the CMB anisotropies. The fractal dimensions and threshold-dependent behavior further supported these findings, offering a comprehensive picture of the statistical and topological

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properties of the CMB temperature field. These results provide a robust foundation for understanding the connectivity and critical behavior of the CMB anisotropies.

Conclusions

The analysis of percolation within the Planck's Cosmic Microwave Background (CMB) yields profound insights into the statistical and topological properties of the universe's primordial fluctuations. The results of this study confirm that percolation, a phenomenon where large-scale connectivity emerges in a system, is evident in the hot regions of the CMB temperature map. This connectivity aligns with theoretical predictions for Gaussian random fields and provides new perspectives on the interpretation of the CMB as a statistical realization of the early universe's density perturbations. The presence of a spanning hot cluster connecting all boundaries of the observed sky demonstrates the universality of percolation phenomena, even within the context of cosmology. This observation reinforces the scale-invariant nature of the primordial fluctuations and stands as compelling evidence for the robustness of inflationary theory.

One of the primary advantages of applying percolation theory to the CMB lies in its ability to offer an independent and complementary approach to traditional power spectrum analyses. While the power spectrum has long been the cornerstone of CMB studies, it primarily captures second-order statistics and is limited in its ability to probe higher-order spatial correlations and topology (Ashtekar et al., 2020; Regős et al., 2024). Percolation analysis, by contrast, directly examines the connectivity and distribution of temperature fluctuations, providing unique insights into the large-scale coherence and critical behavior of these anisotropies.

Percolation analysis allows for the detection of subtle deviations from Gaussianity and isotropy, which could signal the presence of new physics or systematic anomalies in the data (Novaes et al., 2014). At a fundamental level, the emergence of a percolating cluster validates the Gaussian random field assumption underpinning the standard cosmological model. Percolation behavior is inherently linked to the statistical properties of these fields and its presence corroborates the predictions of inflationary theory regarding the generation of primordial perturbations. The spanning hot cluster observed in the CMB serves as a direct manifestation of these perturbations, highlighting their coherence across cosmic scales. Additionally, the asymmetry in the percolation properties of hot and cold regions suggests a deeper connection to the evolution of the matter distribution. Hot regions correspond to over-densities in the early universe, which later evolved into the large-scale structure observed today. The presence of a percolating hot cluster implies a critical level of connectivity that likely influenced the formation of cosmic superclusters and filaments, providing a bridge between the early universe and its present-day architecture. Additionally, the fractal dimensions and scaling laws associated with percolating clusters offer a rich framework for understanding the self-similar nature of the underlying perturbations.

The role of percolation in probing the topology of the universe is another intriguing aspect of this study. The connectivity properties of the largest clusters are inherently tied to the geometry and topology of the observed sky. The standard model assumes the universe is isotropic and homogeneous on large scales, but anomalies in the percolation patterns could suggest otherwise. Our detection of a percolating cluster across all boundaries reinforces the assumption of a simply connected, flat universe. Conversely, anomalies in the connectivity patterns, such as preferential orientations or missing connections, could hint at non-trivial topologies, such as a compact or multiple connected universes.

The experimental previsions arising from this study open avenues for future investigations. High-resolution CMB maps, particularly those incorporating polarization data, offer an exciting opportunity to extend percolation analysis to other components of the CMB, such as the E-mode and B-mode polarization patterns (Hanson et al., 2014). These analyses could reveal additional connectivity properties and their relation to the underlying physics of reionization and primordial gravitational waves. Furthermore, cross-correlations with large-scale structure surveys, such as those mapping galaxy distributions and cosmic voids, could provide a direct observational link between

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the percolation properties of the CMB and the present-day universe. Experimental advancements, such as those anticipated from upcoming missions like CMB-S4 (Sohn and Fergusson, 2019), promise to refine the resolution and sensitivity of CMB data, enabling a more precise determination of critical thresholds and cluster statistics. Additionally, the extension of percolation studies to higher-dimensional datasets, such as tomographic maps of the large-scale structure, could offer new perspectives on the evolution of cosmic connectivity over time.

Theoretical predictions arising from the percolation of the largest hot clusters offer a wealth of opportunities for testing and refining cosmological models. One notable prediction is the universality of percolation thresholds in Gaussian random fields (Novaes et al., 2014). This universality implies that the critical threshold for the emergence of spanning clusters should remain consistent across different realizations of the CMB, provided the underlying statistical properties are Gaussian and isotropic. Deviations from this behavior could signal the presence of non-Gaussianity, anisotropy or exotic physics, such as cosmic strings or domain walls. The fractal dimension of the largest clusters, as observed in this study, provides an additional metric for comparison with theoretical expectations. Any significant departures from the predicted fractal dimensions would warrant further investigation into the nature of the initial conditions and the physics governing their evolution.

However, the methodology is not without its limitations. The reliance on thresholding techniques introduces potential biases, as the choice of threshold can significantly influence the identification and connectivity of clusters (Galam and Mauger, 1996; Regős et al., 2024). Although the use of global thresholding methods like Otsu's ensures consistency, localized variations in noise or foreground contamination could skew the results. Furthermore, the finite resolution of the CMB map imposes constraints on the smallest scales that can be reliably analyzed, potentially masking finer details of cluster morphology and connectivity. The study of percolation in the CMB also highlights the hiatus between theoretical predictions and observational limitations. While the results of this analysis are consistent with the standard cosmological model, they underscore the need for continued refinement of observational techniques and theoretical frameworks. The resolution and noise limitations of current data, coupled with the complexity of foreground subtraction, present ongoing challenges that must be addressed to fully exploit the potential of percolation analysis.

In conclusion, the application of percolation theory to the CMB represents a powerful and complementary approach to understanding the universe's primordial fluctuations. The emergence of a percolating hot cluster underscores the coherence and critical behavior of the temperature anisotropies, providing robust evidence for the Gaussian random field nature of the CMB. While limitations and uncertainties remain, the insights gained from this study open new avenues for exploring the early universe and its connection to the large-scale structure we observe today.

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Nonlinear locomotion patterns in the Egyptian Locust (Anacridium aegyptium) during walking: a detailed case study

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ABSTRACT

We explored the nonlinear movement patterns of *Anacridium aegyptium* during terrestrial locomotion, providing insights into the walking dynamics of this large grasshopper species. Using video recordings, we analysed the trajectory of an insect and quantified key metrics, including curvature, tortuosity and fractal dimension. Curvature analysis revealed irregular turning behaviors with sharp directional changes, suggesting that locomotion was not random but deliberate. Compared with simulated linear trajectories, the curvature exhibited distinct peaks, highlighting the presence of statistically significant nonlinear features in the movement patterns. Phase space reconstruction revealed repetitive patterns indicating the potential presence of a limit cycle attractor. The trajectory remained confined within a specific region of the phase space, highlighting structured dynamics rather than unbounded behaviour. Fractal dimension analysis and Lyapunov exponent were consistent with a stable and predictable system over time, rather than one governed by chaos. These findings align with the behavioral ecology of *A. aegyptium*, suggesting that its walking dynamics are governed by efficient spatial exploration and obstacle negotiation rather than erratic or chaotic motion. Our study underscores the value of advanced mathematical and computational methods in boosting behavioural studies of locomotion. The insights derived from our analysis enhance our understanding of insect locomotion strategies and hold potential applications in the field of biomimetic robotics, where adaptive and efficient movement is mandatory. Future research could explore the impact of environmental factors, such as substrate type and food availability, on the observed nonlinear patterns, providing deeper context to the intricate locomotion behaviour of *Anacridium aegyptium*.

KEYWORDS: adaptive movement; environmental interaction; trajectory analysis; limit cycle attractor; biomimetic inspiration.

INTRODUCTION

Locomotion is a fundamental aspect of animal behavior serving crucial roles in habitat navigation, foraging and predator avoidance. The six-legged insects display a remarkable diversity of locomotion strategies, which have been a focal point of neurobiological research for over a century (Bidaye et al, 2018; Heckenthaler et al., 2023; Regeler et al., 2023). Insect locomotion has been extensively studied in the contexts of flying, walking, crawling and central pattern generation, both in natural systems and artificial walking systems (Seipel et al., 2004; Imirzian et al., 2019; Mantziaris et al., 2020; Sabattini et al., 2023). Research on insect locomotion has predominantly concentrated on the biomechanics of jumping and the dynamics of flight. Indeed, recent advancements have introduced a diverse array of modelling and simulation techniques, alongside experimental setups, to investigate collective insect motion. These approaches range from discrete agent-based models of self-propelled particles to continuous frameworks using integral-differential equations (Ariel and Ayali, 2015; Bleichman et al., 2024; Aidan et al. 2024). Grasshoppers are particularly noteworthy for their efficient jumping and walking capabilities. Among these, *Anacridium aegyptium*, commonly known as the Egyptian Locust, stands out due to its large size, robust anatomy and widespread distribution across Mediterranean and subtropical regions. The act of jumping in grasshoppers has garnered significant attention from researchers due to its intricate biomechanics and critical role in their survival strategies (Hawlena et al., 2010: Hawkes et al., 2022). Conversely, solitary walking behaviors in grasshoppers remain relatively underexplored, particularly with respect to nonlinear patterns and their ecological significance.

Nonlinear locomotion encompasses movement patterns deviating from straightforward linear trajectories, often distinguished by irregular pathways (Campos et al., 2010; Xu et al., 2023). Zigzagging paths may optimize resource exploration, while abrupt directional changes might indicate evasive maneuvers against predators. Nonlinear time-periodic models of flight dynamics have been studied, for instance, in the desert locusts *Schistocerca gregaria* (Taylor et al., 2005). Investigating these patterns in *A. aegyptium* could provide valuable insights into the broader principles governing insect locomotion and their potential applications in fields such as robotics and ecological modeling.

Advanced mathematical tools have transformed the study of animal movement, enabling precise quantification of complex trajectories. For instance, custom tracking algorithms have been employed to uncover fundamental animal-animal interactions that drive collective motion in swarms of marching locust nymphs (Ariel et al., 2014). Metrics such as curvature, fractal dimension, tortuosity and Lyapunov exponents are now routinely employed to uncover previously imperceptible locomotion patterns in both natural and artificial systems (Kearns et al., 2027; Suryanto et al., 2022; Xu

et al., 2023). Curvature analysis highlights turning behaviors and their frequency, while fractal dimension quantifies the geometric complexity of a trajectory. The Lyapunov exponent, a measure of the sensitivity of a system to initial conditions, can indicate whether movements exhibit chaotic properties (Mehdizadeh, 2018).

This study aims to investigate the nonlinear walking dynamics of *A. aegyptium* using video analysis and advanced computational methods. By quantifying the above-mentioned nonlinear metrics, we seek to characterize the insect's locomotion patterns and assess their ecological significance. Specifically, we hypothesize that *A. aegyptium* exhibits significant nonlinear features in its walking trajectory, indicative of adaptive and intentional locomotion strategies. In the following sections, we detail the materials and methods used to collect and analyze data, present the results of our quantitative analyses and discuss their implications in the context of both insect ecology and applied sciences. Through this investigation, we aim to bridge the gap between descriptive studies of insect movement and the rigorous mathematical frameworks needed to understand its underlying dynamics.

MATERIALS AND METHODS

To investigate the nonlinear walking dynamics of *Anacridium aegyptium*, a combination of field observations, video recording and computational analysis was employed. The study focused on an adult male specimen of *A. aegyptium*, casually encountered in its natural environment under undisturbed conditions. The specimen was observed in the Mediterranean region while walking on a glass window. The glass window provided a clear substrate for tracking the insect's movements, while natural daylight ensured optimal visibility without introducing artificial stressors. The study focused on a single individual, providing a brief but valuable snapshot of its behaviour. Since the observation involved a single individual, there was no risk of interference from conspecifics.
A. aegyptium, commonly known as the Egyptian Grasshopper or Egyptian Locust, is a large species in the Acrididae family, commonly found in the Mediterranean basin. It is one of the largest grasshoppers in Europe. It is primarily found perched on trees and shrubs, relying on short flights and jumping for movement. Key identifiers in our study included the distinctive vertical stripes on the eyes, the hind tibiae adorned with two rows of white spines tipped in black and the presence of eight abdominal segments in males, as opposed to the seven segments typically found in females (Girardie and Granier, 1974).

Video processing. Video recordings were captured at 30 frames per second using a camera mounted 1.5 meters above the arena. The field of view covered the entire arena, ensuring that the insect's trajectory could be tracked continuously. The raw video footage was processed using a custom Python-based software pipeline. The first step of motion capture involved converting the video into individual frames, which were subsequently analyzed using an object detection algorithm based on Optical flow (Lucas-Kanade method) via OpenCV (Al-Qudah and Yang, 2023). The algorithm identified the position of the center of the body in each frame, generating a sequence of x and y coordinates representing the insect's trajectory over time (**Figure 1**). This was determined using simple thresholding to identify the largest contour in the image, which typically corresponds to the main body of the insect. The trajectory data were smoothed using a low-pass filter to reduce noise.

Nonlinear analysis. Various parameters were derived from the insect's movement trajectory. **Displacement** represents the distance between the initial and final positions. The **total path length** is the sum of the distances covered between consecutive points along the trajectory. **Average speed** was determined by dividing the total path length by the total time of observation. **Instantaneous speed** was calculated by dividing the distance covered between consecutive points by the time between frames. Finally, the **direction of movement** was measured as the angle of motion between consecutive points, providing insight into the insect's orientation during its movement.
Next, a range of metrics was calculated to analyse and define the nonlinear movement features. **Curvature** was calculated as the change in direction per unit distance, providing a measure of how sharply the insect turned at each point along its path. **Tortuosity** was assessed as the ratio of the total path length to the straight-line displacement, with higher values indicating more convoluted trajectories. **Fractal dimension**s were estimated using the box-counting method, which involves overlaying a grid of varying box sizes on the trajectory and counting the number of boxes intersected by the path. To further explore the dynamics, **phase space reconstruction** was performed. This involved embedding the trajectory data in a higher-dimensional space using time delays, allowing the identification of patterns that are not apparent in the original two-dimensional trajectory. The embedding dimension and delay time were determined using the false nearest neighbors method and mutual information analysis, respectively (Albers and Hripcsak, 2012; Wallot and Mønster, 2018). The reconstructed phase space was then analyzed for **attractor behavior**, with particular attention to whether the trajectories exhibited features characteristic of limit cycles or other nonlinear dynamic phenomena (Broscheid et al., 2018). Additionally, the Lyapunov exponent was calculated to evaluate the trajectory's sensitivity to initial conditions. This process involved tracking the divergence of nearby points in phase space over time. The divergence was then plotted on a logarithmic scale and the exponent was estimated from the slope of the resulting curve. A positive Lyapunov exponent indicated the presence of chaotic behaviour.

To ensure the robustness of the findings, the analyses were repeated using a 5-second subset of the data, applying varying smoothing parameters and detection thresholds. Sensitivity analyses were also conducted to ensure that the results were not unduly influenced by the choice of parameters such as the box size in the fractal dimension analysis or the embedding dimension in the phase space reconstruction.

Tools and statistical analysis. Computational analyses were implemented in Python using libraries such as NumPy, SciPy and Matplotlib for numerical computation and visualization. Statistical analyses were conducted to test the significance of the observed nonlinear features. Curvature and tortuosity metrics were compared against null models generated from simulated linear trajectories created by randomly sampling points within the arena and interpolating straight-line paths between them. The distributions of curvature and tortuosity in the observed and simulated datasets were compared using Kolmogorov-Smirnov tests. The fractal dimension of the observed trajectories was compared against random walk models to determine whether the observed complexity exceeded that expected from stochastic motion.

Figure 1. A video frame displaying the detected point on *Anacridium aegyptium*'s body, marked in red. This point was used as the reference for reconstructing the insect's movement trajectory.

RESULTS

The video analysis of *Anacridium aegyptium*'s walking dynamics, captured at a resolution of 1080 × 1920 pixels (width × height), provided a detailed quantification of the movements, uncovering significant nonlinear features. Over a trajectory spanning 433 frames at approximately 30 frames per second, the insect demonstrated a total path length of approximately 1189 pixels, far surpassing its net displacement of 24 pixels. This discrepancy underscores the pronounced nonlinearity of the insect's motion, further supported by a tortuosity value of 49.43, which reflects the highly convoluted nature of its path. Comparisons between the total path length and the straight-line displacement further emphasized this nonlinearity, with substantial differences observed between the two measures throughout the trajectory (**Figure 2**).

The curvature analysis revealed subtle yet consistent turning behaviors, with sharp directional changes frequently interrupting the trajectory. These patterns suggest that the movement is not random but deliberate, possibly driven by environmental stimuli or internal decision-making processes. Compared with simulated linear trajectories, the curvature exhibited higher variability and distinct peaks, highlighting the presence of statistically significant nonlinear features in the movement patterns (**Figure 3**). This finding confirmed the existence of nonrandom turning behaviors.

The analysis of the direction of movement identified dominant frequencies, with direction oscillations occurring at approximately 0.42 Hz (**Figure 4**). This suggested a consistent rhythmic pattern in the insect's behaviour. In contrast, speed oscillations did not exhibit statistically significant periodicity, indicating that variations in speed may be more context-dependent or driven by external stimuli rather than inherent rhythmicity.

Phase space reconstruction illustrated the bounded nature of the motion, with repetitive patterns pointing toward a potential limit cycle attractor (**Figure 5**). This attractor behavior indicated a structured yet flexible movement strategy, allowing for environmental adaptability. The trajectory was confined within a bounded region of the phase space, suggesting structured dynamics rather than random or unbounded behaviour. The reconstructed phase space showed clear loops without chaotic divergence, consistent with a stable and predictable system rather than one governed by chaos. The calculated Lyapunov exponent, approximately -7.5 × 10□□, further supported the absence of chaos, pointing towards convergence rather than divergence in the system's dynamics. Fractal dimension analysis provided additional insights into the complexity of the movement. With an estimated fractal dimension of 0.73, the trajectory displayed a constrained complexity characteristic of structured but not chaotic motion. This metric underscored the insect's ability to navigate effectively within defined spatial limits while maintaining a balance between exploration and efficiency.

Visual analyses complemented these findings. Trajectory plots highlighted regions of high curvature, represented by intensified color gradients, corresponding to areas of sharper turns or more frequent directional adjustments (**Figure 6**). The curvature was nonuniformly distributed, with distinct peaks suggesting localized exploratory behavior or evasive maneuvers.

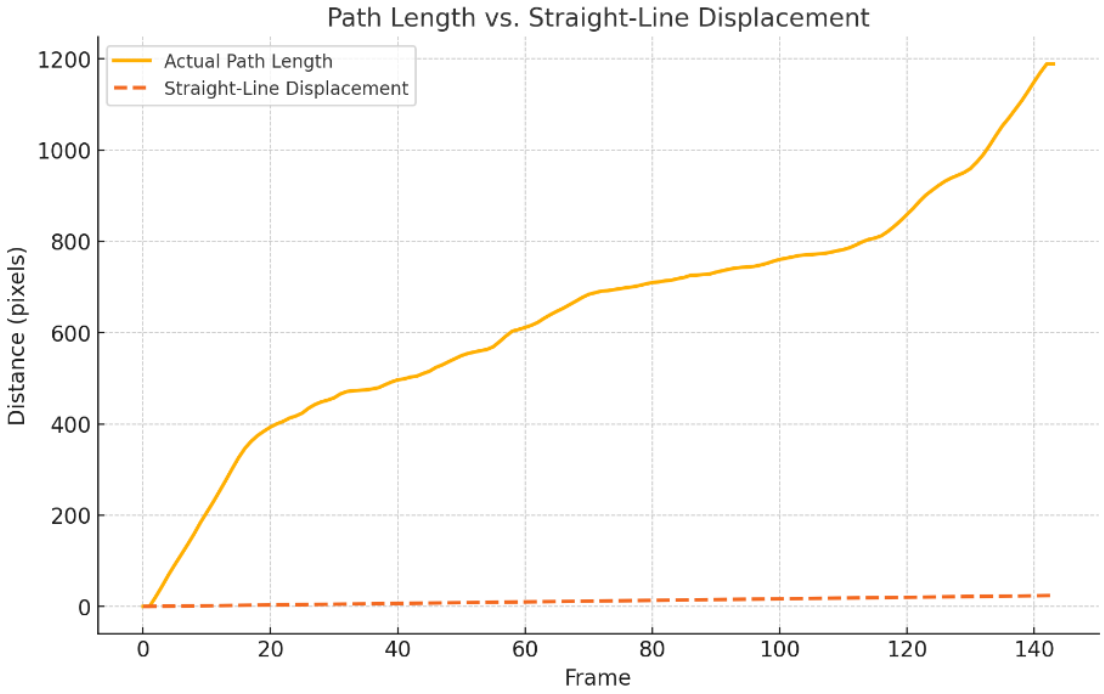

Figure 2. Relationship between the path length and the straight-line displacement of the insect's trajectory. The solid line represents the cumulative actual path length, capturing the total distance travelled during locomotion. The dashed line reflects the straight-line displacement, indicating the direct distance from the starting point to the endpoint of the trajectory. The notable gap between these two lines serves as clear evidence of the high tortuosity and the nonlinear characteristics inherent in the insect's movement pattern.

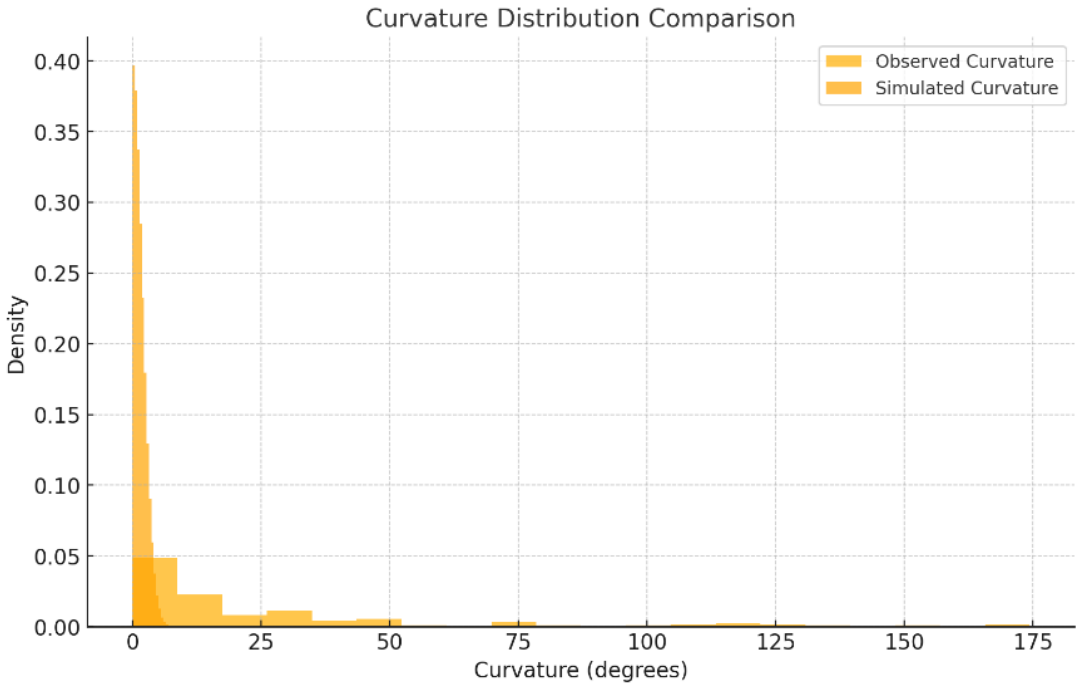

Figure 3. Comparison of curvature distributions. Yellow bars represent the observed curvature values derived from the insect's trajectory, while orange bars depict the curvature distribution from random simulated trajectories. The observed curvature distribution reveals a statistically significant deviation from the simulated random trajectories.

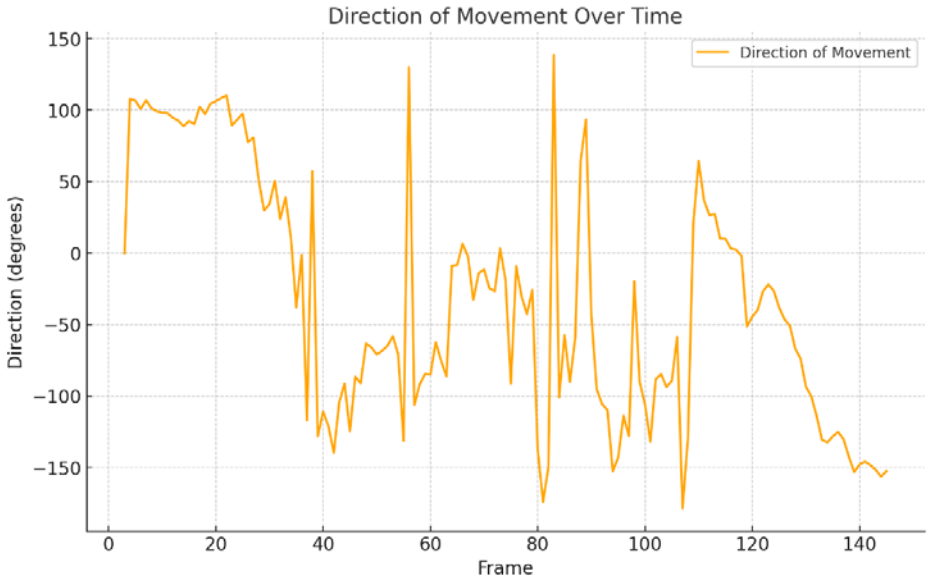

Figure 4. Direction of movement over time. Peaks in the plot correspond to bursts of movement, while dips indicate slower movement or pauses.

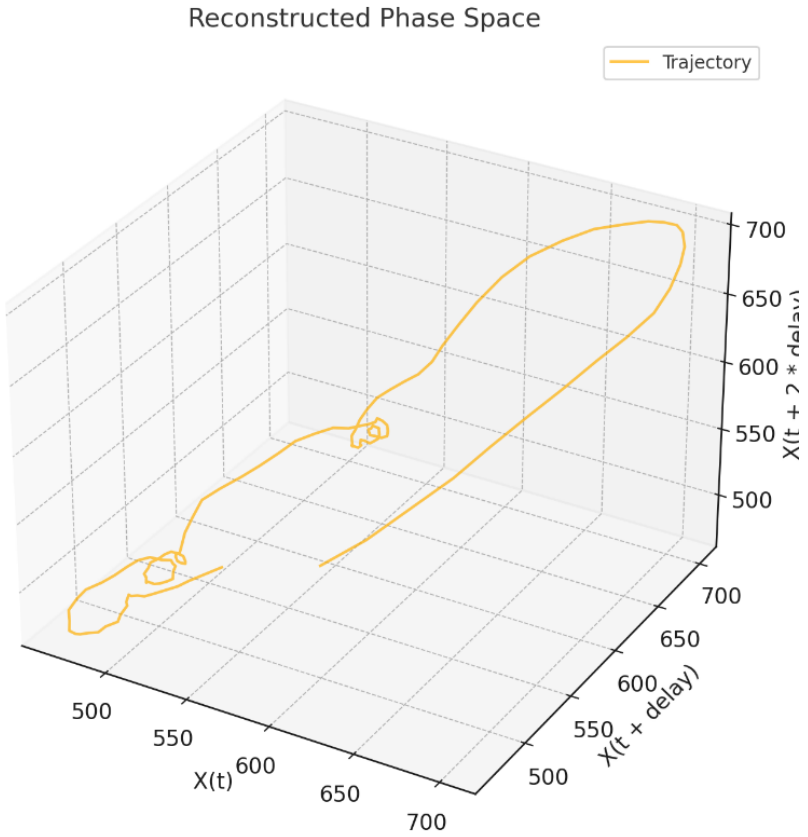

Figure 5. Phase space reconstruction of the 3D trajectory using time-delay embedding. The trajectory does not converge toward a single point, indicating the absence of a fixed-point attractor. Indications of repetitive loops suggest the potential presence of a limit cycle attractor, although the loops lack perfect regularity. The absence of irregular divergence in the phase space suggests that the system does not exhibit chaotic features or a strange attractor.

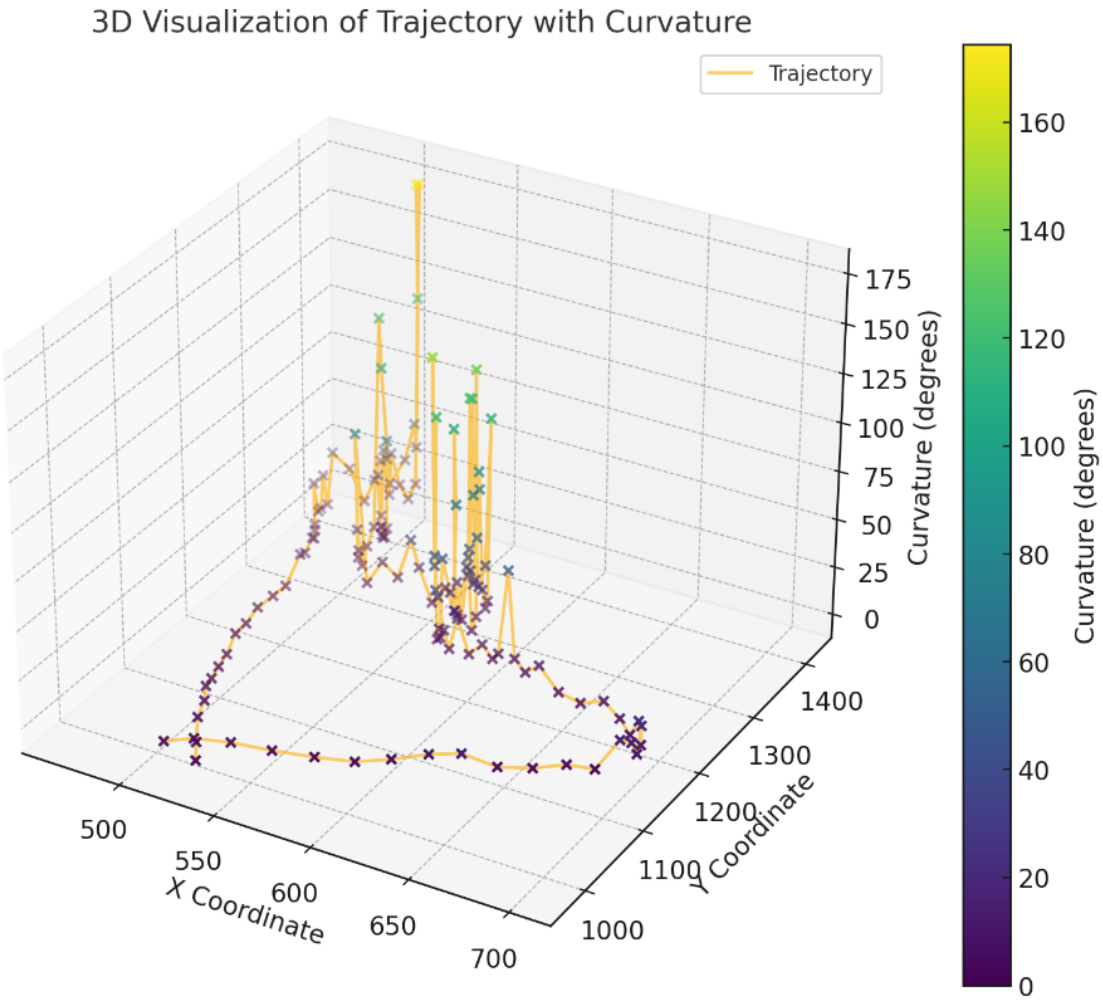

Figure 5. 3D visualization of the insect's trajectory, incorporating curvature as the third dimension. Each point represents the detected position of the tracked feature across frames. The x and y axes represent the spatial movement of the insect while the z-axis corresponds to curvature, with higher values signifying sharper turns. The colour intensity of the points reflects the curvature at each location, with more intense colours highlighting areas where sharper turns occur. This visualization emphasizes the nonlinearity of the trajectory, highlighting deviations and directional changes over time.

CONCLUSIONS

We provide a comprehensive analysis of the nonlinear walking dynamics of *Anacridium aegyptium*. The computational approach employed in this study enabled the extraction of detailed and quantitative insights from behavioral data. The integration of tools such as curvature analysis, fractal dimension estimation and phase space reconstruction allowed for a multidimensional understanding of grasshopper's locomotion that extends beyond traditional observational methods.

Our findings underscore the importance of nonlinear analysis in understanding animal movement, particularly for behaviors that cannot be adequately described by linear models. Nonlinear movement patterns, such as Lévy flights or Brownian motion, are well-documented in insects during behaviors like foraging, mate searching or escape responses (Taylor et al., 2005). However, detailed statistical analysis of curvature remains relatively uncommon. Notably, one of the most striking outcomes of our research is the identification of curvature and tortuosity as key indicators of the insect's adaptive nonlinear walking behaviour. The significant deviations from random linear trajectories suggest that *A. aegyptium* employs deliberate turning and path-convoluting strategies. These movements may reflect purposeful behaviors, including optimizing foraging efficiency, avoiding obstacles avoidance, searching or responding to potential

threats. High curvature could indicate localized exploration near stimuli, while sudden changes may signify evasive actions. Additionally, curvature may reveal biomechanical limitations or energy-efficient turning mechanisms inherent to the insect's physiology, as frequent turning may incur energy costs that influence resource optimization strategies. Furthermore, significant curvature deviations can serve as reliable indicators for distinguishing insect behaviors from random noise or external disturbances. Novelty can also stem from linking curvature to specific environmental or behavioral contexts, such as food searching or predator avoidance. In the case of *A. aegyptium*, nonlinear movement patterns during walking are of particular interest due to the ecological contexts in which they occur. As a large, terrestrial insect, *A. aegyptium* often traverses uneven substrates, navigates dense vegetation and interacts with potential threats or resources. The frequent directional changes, bounded trajectories and repetitive loops likely represent an optimized trade-off between environmental exploration and energy conservation.

The use of fractal dimension analysis further revealed the constrained complexity of the trajectories, highlighting the ability to navigate within defined spatial boundaries while maintaining efficient movement patterns. Phase space reconstruction and Lyapunov exponent calculations provided additional depth to our understanding of walking dynamics. The identification of a possible limit cycle attractor indicates repetitive and bounded behaviors, which may reflect innate or environmentally influenced patterns. While no evidence of chaotic dynamics was found, the bounded and structured trajectories point to a deterministic system governed by environmental feedback and internal rules. This structured behavior aligns with the ecological requirements of *A. aegyptium*, enabling it to adapt to complex terrains while conserving energy. The bounded movement and lack of chaotic divergence are consistent with efficient navigation strategies in natural habitats. These findings suggest potential applications in biomimetic robotics, where adaptive and efficient movement strategies are critical.

Comparing observed curvature to random trajectories represents a methodological advancement that has been already used in standard ecological studies. Artificially generated video sequences have been introduced, combining known real-animal postures with randomized body positions, orientations and sizes (Arent et al., 2021). The novel contribution of our study is that is rigorously tests curvature against null models such as random linear paths incorporating quantitative metrics like curvature distribution or tortuosity. The novelty is enhanced by the focus on a specific insect species or behavior (i.e., a grasshopper's movement during natural conditions) that has been scarcely analyzed in this way. The methodologies developed here could be adapted to study other forms of animal movement, from terrestrial vertebrates to aquatic species, providing a versatile toolkit for ecological and biomechanical research. For navigation studies, understanding nonlinear movements may illuminate how insects process sensory information and make decisions. Additionally, recognizing curvature patterns in movement may aid pest control strategies or contribute to ecological monitoring efforts. The insights gained from understanding the nonlinear dynamics of *A. aegyptium*'s walking behavior could inform the design of biomimetic robots capable of adaptive and efficient locomotion in complex terrains (Gart et al., 2018). By mimicking the turning strategies, bounded trajectories and constrained features observed in this study, robotic systems could achieve enhanced agility and robustness.

Despite our findings, several limitations must be acknowledged. First, the experimental setup cannot fully capture the complexities of the insect's native habitat. Factors present in the wild, such as predation risk, interspecies interactions, and varying substrate types, were not considered in this study. Second, the analysis relied on two-dimensional trajectory data, which may overlook vertical components of movement. Future studies incorporating three-dimensional tracking techniques could provide a more holistic perspective. Whereas marker-based motion capture systems are very robust and easily adjusted to suit different setups, tracked species or body parts, they cannot be applied in experimental situations where markers interfere with natural behavior, e.g., when tracking delicate, elastic or sensitive body structures (Arent et al., 2021). Another limitation is the limited generalizability of the findings, as the observations were based on a single individual. Expanding the sample size and including a broader range of conditions would strengthen the robustness of the conclusions. Additionally, while advanced metrics such as fractal dimension and Lyapunov exponents were calculated, these analyses are sensitive to parameter choices such as time delays and embedding dimensions. Further refinement of these methods could enhance the reliability of future studies. While this research focused primarily on movement patterns, future studies could incorporate additional variables such as environmental. For example, controlled manipulations of environmental features could help disentangle the roles of intrinsic and extrinsic factors in driving observed behaviors. Future directions include linking curvature to environmental factors like light or food availability to determine its drivers, conducting comparative studies across species and behaviors and exploring other nonlinear features such as speed oscillations or pauses.

In conclusion, this interdisciplinary investigation into the nonlinear walking dynamics of *Anacridium aegyptium* demonstrates the value of advanced analytical techniques in uncovering hidden patterns and address fundamental questions about movement and behavior. Despite its limitations, this study offers a compelling framework for examining locomotion through the lens of nonlinear dynamics, with applications ranging from ecology and evolutionary biology to biomechanics and robotics.

DECLARATIONS

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.

Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal, and has not been previously published.

Availability of data and materials. all data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Competing interests. The Author does not have any known or potential conflict of interest including any financial, personal or other relationships with other people or organizations within three years of beginning the submitted work that could inappropriately influence, or be perceived to influence, their work.

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Authors' contributions. The Author performed: study concept and design, acquisition of data, analysis and interpretation of data, drafting of the manuscript, critical revision of the manuscript for important intellectual content, statistical analysis, obtained funding, administrative, technical, and material support, study supervision.

Declaration of generative AI and AI-assisted technologies in the writing process. During the preparation of this work, the author used ChatGPT to assist with data analysis and manuscript drafting. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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Monte Carlo simulations predict distinct real EEG patterns in individuals with high and low IQs

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ABSTRACT

The neural mechanisms underlying individual differences in intelligence are a central focus in neuroscience. We investigated the effectiveness of Monte Carlo simulations in predicting real EEG patterns and uncovering potential neural differences between individuals with high and low intelligence. EEG data were collected from two groups of volunteers categorized by IQ, namely, a high-IQ group and a low-IQ group. A univariate normal distribution was fitted to each EEG channel using Maximum Likelihood Estimation, after which synthetic datasets were generated based on the estimated parameters. Statistical analyses including Root Mean Square Error (RMSE) calculations assessed the alignment between real and simulated data. We showed that Monte Carlo simulations effectively replicated the statistical properties of the EEG data from both the groups, closely matching the real central tendencies, variability and overall distribution shapes. Specific EEG channels, particularly in the frontal and temporal bilateral regions, exhibited significant differences between the two groups, pointing to potential neural markers of cognitive abilities. Further, the low-IQ group exhibited higher predictability and more consistent neural patterns, reflected by lower RMSE values and smaller standard deviations across several EEG channels. Conversely, the high-IQ group displayed greater variability and larger RMSE values, reflecting complex neural dynamics that are less predictable by Monte Carlo simulations. Our findings underscore the utility of Monte Carlo simulations as a robust tool for replicating EEG patterns, identifying cognitive differences and predicting EEG activity associated with intelligence levels. These insights can inform predictive modeling, neurocognitive research, educational strategies and clinical interventions of targeted cognitive enhancement.

KEYWORDS: statistical analysis; oddball tasks; synthetic dataset; EEG channel.

INTRODUCTION

Exploring the neural mechanisms underpinning intelligence has been a longstanding primary focus of cognitive neuroscience research. Electroencephalography (EEG) offers unique insights to assess differences in cognitive abilities, including distinctions between individuals of varying intelligence levels (Friedman et al., 2019). With its high temporal resolution, the non-invasive EEG evaluates the interplay between synchronization, complexity and network efficiency (van Dellen et al., 2015). For instance, higher IQ is associated with reduced long-distance EEG information flow and enhanced local processing efficiency, supporting small-world models (Thatcher et al., 2016). Short EEG phase delays and increased coherence in frontal regions correlate with higher intelligence, emphasizing the role of frontal lobe synchronization (Thatcher et al., 2005). Resting-state EEG studies have further explored intelligence-related differences, reporting balanced inter-hemispheric coordination in alpha and beta bands in more intelligent individuals (Jahidin et al., 2013). Also, it has been demonstrated that IQ correlates negatively with EEG energy but positively with information flow intensity at specific frequencies, emphasizing the role of efficiency in neural communication (Luo et al., 2021). Changes in microstate dynamics are associated with fluid intelligence and its enhancement following cognitive training (Santarnecchi et al., 2017). Lu et al. (2022) found that individuals with higher fluid intelligence allocate attentional resources more flexibly, particularly in complex tasks, as reflected in theta and alpha EEG activities. Together, these findings underscore the utility of EEG in the assessment of the neuronal mechanisms of intelligence, revealing consistent patterns of neural efficiency, inter-hemispheric coordination and adaptive resource allocation.

Conversely, the analysis of EEG data poses significant challenges due to their inherent variability, high dimensionality and sensitivity to noise (Hassani et al., 2015). To address these challenges and enhance our ability to model and predict EEG patterns, advanced statistical and computational methods are required. Monte Carlo simulations have been widely used across various scientific disciplines, providing a powerful framework for modeling complex systems influenced by variability and uncertainty (Metropolis and Ulam, 1949; Rubinstein and Kroese, 2016). By leveraging statistical properties derived from observed data, Monte Carlo simulations generate synthetic datasets that may reflect real-world behaviors (Salvadori et al., 2024; Jones and Fleming, 2024). A Monte Carlo approach could be particularly well-suited for EEG data, as it allows researchers to explore and replicate neural dynamics without the need for extensive experimental data collection. Monte Carlo methods have been applied in neuroscience to simulate and analyse

electromagnetic brain signals, providing approximations of event-related brain activity (Herdman 2021). Monte Carlo simulations have been utilized for brain source localization (Georgieva et al., 2013) and evaluation of errors as a function of position within the brain in MRI-MEG/EEG co-registration techniques (Singh et al., 1997). Surprisingly, it has been demonstrated that EEG localization is more accurate than MEG localization for the same number of sensors averaged over many source locations (Liu et al., 2002). Monte Carlo analysis can also simulate event-related changes in amplitude and phase-amplitude correlations, enabling close approximations of real EEG and MEG data (Herdman 2021). This approach is particularly valuable for validating data analysis methods, including measurements of functional connectivity and phase-amplitude coupling. A Bayesian framework has been introduced for parameter estimation in EEG modeling using a marginalized Markov Chain Monte Carlo approach (Hettiarachchi et al., 2012). This method was employed to fit a neural mass model to EEG data effectively.

Despite these studies, the application of Monte Carlo simulations to EEG research in revealing cognitive differences between individuals of high and low intelligence remains relatively underexplored. This study aims to bridge this gap by investigating how Monte Carlo simulations can model, simulate and reproduce real EEG traces. Central to this investigation is the issue of predictability: using Monte Carlo simulations, are the EEG patterns from high-IQ individuals more or less predictable than those of their lower-IQ counterparts? It can be hypothesized that higher cognitive abilities are associated with greater neural flexibility and variability, potentially reducing predictability in simulations. Conversely, lower intelligence may correspond to more stable neural patterns, increasing predictability. Monte Carlo simulations, by generating synthetic EEG data modeled on the statistical properties of real datasets, offer a systematic approach to testing these hypotheses.

We conclude that that Monte Carlo methods are a robust tool for exploring the neural dynamics of intelligence, paving the way for future investigations into brain-behavior relationships. By accurately replicating EEG patterns and identifying significant group differences, Monte Carlo simulations contribute to a deeper understanding of the cognitive and neural processes underlying intelligence.

MATERIALS AND METHODS

Participants and Data Collection. This study retrospectively builds on the foundational research conducted by Norbert and Ksenija Jaušovec through 2010 (Jaušovec and Jaušovec, 2001; 2003; 2005; 2010), which was later advanced in collaboration with Tozzi et al. (2021a; 2021b). This continuation of their work is undertaken with great respect and recognition of Norbert's untimely passing.

EEG data were collected from two groups of right-handed volunteers categorized by IQ, namely, a high-IQ group and a low-IQ group. Each group consisted of five participants, yielding a total sample of 10 individuals (mean age: 19.8 years; SD = 0.9; range = 18–21 years; males: 4). The IQ categorization was based on standardized test scores, with the high-IQ group representing the top quartile (IQ SD = 127) and the low-IQ group representing the bottom quartile (IQ SD = 87). Differences in EEG activity between these groups were analyzed during the performance of two oddball tasks (auditory and visual). The study adhered to the Declaration of Helsinki and received approval from the Ethics Committee of the University of Maribor, Slovenia.

EEG signals were recorded using a 64-channel system to ensure comprehensive cortical coverage. Electrode placement followed the 10–20 international system, covering nineteen scalp locations: [FP1], [FP2], [F3], [F4], [C3], [C4], [P3], [P4], [O1], [O2], [F7], [F8], [T3], [T4], [T5], [T6], [CZ], [FZ] and [PZ]. The electrodes were sintered Silver/Silver Chloride (8mm diameter) with impedance maintained below 5 kΩ. All leads were referenced to linked mastoids (A1 and A2), with a ground electrode on the forehead. Vertical eye movements were recorded using additional electrodes placed above and below the left eye. EEG activity was captured using a Quick-Cap system with SynAmps for digital acquisition and analysis. Signals were digitized at 1000 Hz with a gain of 1000 (resolution: 0.084 μV/bit, 16-bit A/D conversion) and stored on a hard disk. Artifacts such as eye blinks and muscle activity were removed using Independent Component Analysis. Data were then band-pass filtered between 1 and 40 Hz to isolate relevant neural activity while minimizing noise. The time-series data were located in separate columns, each one corresponding to a different EEG electrode. The data were numerical and represented EEG signal amplitudes in microvolts over time. Each row corresponded in the recording to a single time point in milliseconds.

Next, Monte Carlo simulations were performed to generate synthetic EEG traces, modeling the variations of future data points based on statistical distributions.

Monte Carlo simulations. A reliable methodological framework was essential to ensure robust analysis and enabling meaningful comparisons between EEG traces of high-IQ and low-IQ individuals. The analysis of the EEG data followed a series of structured steps. The first step involved loading EEG datasets for both the groups. Multiple files for each group were then concatenated into unified datasets. Any rows or cells with missing values were removed to prevent inaccuracies in statistical calculations. The next step was distribution fitting, where statistical parameters, i.e., the mean μ and standard deviation σ, were derived for each EEG channel to simulate data closely reflecting real-world observations. Each channel was analyzed separately. A univariate normal distribution was fitted to the data using

Maximum Likelihood Estimation (MLE) to calculate μ and σ, ensuring that the simulated data aligned with the distributions observed in the real datasets. The alignment of the fitted distributions were then validated by comparing histograms of real data against the simulated distributions.

Once the distributions were established, synthetic EEG traces were generated using Monte Carlo simulations. For each EEG channel, 100 random samples were drawn from the fitted normal distribution parameters μ and σ. The synthetic samples were organized into a structured dataset mirroring the original format, with separate columns for each channel. The simulation was performed independently for both high-IQ and low-IQ groups to preserve their distinct statistical properties. Following data simulation, statistical analyses evaluated the differences between real and simulated datasets and compared the predictability of the high-IQ and low-IQ groups. Fit accuracy was assessed by comparing real and simulated data using Root Mean Square Error (RMSE) for each EEG channel, where lower RMSE values indicated better alignment. Small adjustments were necessary to address mismatches in the number of samples between the real and the simulated data and to ensure data alignment during the RMSE calculation. Variability was also analyzed, as higher variability (e.g., larger standard deviations) in a dataset could reduce predictability by introducing greater spread around the mean. A larger number of EEG channels showing significant differences between real and simulated data suggested lower predictability. Two-sample t-tests and Welch's t-tests were performed to identify significant differences between the real high-IQ and low-IQ groups. Visual comparisons, including histograms and boxplots, were produced to illustrate the alignment between real and simulated datasets.

All analyses and visualizations were performed using Python. Libraries such as numpy, pandas, and scipy were used for statistical calculations, while matplotlib was employed for creating visualizations. The scipy.stats module provided functions for t-tests and normal distribution fitting.

RESULTS

Monte Carlo simulations effectively captured the central tendency, the spread and the variability of the original EEG traces. The real data distributions were closely approximated by the fitted normal distributions, indicating that the simulations accurately reflected the underlying statistical properties. The simulated variances closely aligned with those of the real data, staying within acceptable margins. Visual comparisons further highlighted the alignment between real and simulated data. Histograms demonstrated that the simulated data mirrored the shape and density of the real data, with only minor deviations observed in the tails for a few columns. Boxplots showed significant overlap in medians and interquartile ranges between the real and simulated data, underscoring the reliability of the modeling process. Moreover, the synthetic data successfully replicated the presence of outliers seen in the real dataset, further demonstrating its ability to reflect the inherent variability and complexity of the original data.

The Monte Carlo analysis revealed significant differences between the high-IQ and low-IQ groups in certain EEG channels (see **Table**). The t-tests and the Welch's t-tests identified specific EEG channels where the groups exhibited statistically significant differences ($p<0.05$). Strong differences in activity levels were observed in left [FP1] and right [FP2] prefrontal regions. Channels [F3] and [F4] also showed significant differences in regions associated with higher-order cognition and decision-making. Central channels such as [CZ] exhibited marked differences, reflecting motor or cognitive integration, with [C3] and [C4] showing additional activity differences in motor-related regions. Temporal channels [T3], [T4] and [T5] demonstrated significant differences in regions linked to memory and language processing, while the occipital channel [O2] revealed distinctions in visual processing areas.

On the other hand, some EEG channels exhibited overlapping distributions between the groups, suggesting no significant differences in activity. These included [P3] and [PZ] in the posterior parietal regions, [T6] in the temporal region and [F7] in the left frontal area, where activity patterns appeared similar across groups.

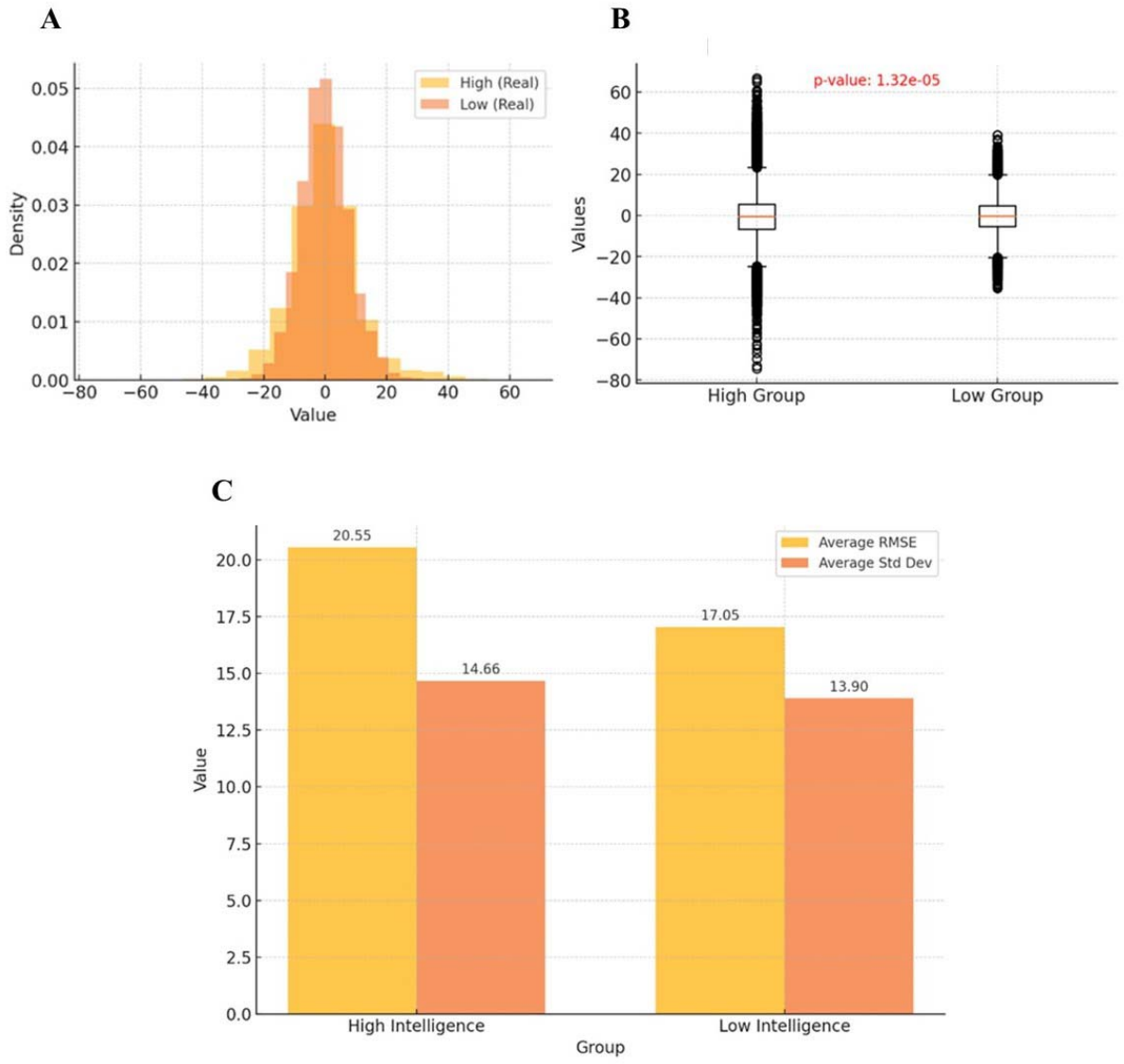
In sum, significant differences between the high-IQ and low-IQ groups were found in medians and interquartile ranges for various channels. These findings suggest key areas where these groups differ in their distributions.

EEG Channel	p-Value	Significance
[FP1]	1.13e-20	Significant
[FP2]	3.11e-13	Significant
[F3]	1.13e-07	Significant
[F4]	8.86e-12	Significant
[C3]	8.28e-06	Significant
[C4]	3.77e-05	Significant
[P3]	0.741	Not Significant
[P4]	0.019	Significant
[O1]	0.558	Not Significant
[O2]	1.32e-05	Significant
[F7]	0.209	Not Significant
[F8]	4.78e-06	Significant
[T3]	0.002	Significant
[T4]	1.24e-19	Significant
[T5]	7.28e-16	Significant
[T6]	0.805	Not Significant
[CZ]	0.000368	Significant
[FZ]	1.33e-23	Significant
[PZ]	0.904	Not Significant

Table. Statistical Differences Across EEG Channels Between High-IQ and Low-IQ Groups.

Visual comparisons provided further insights. The histograms highlighted distinct peaks or shifts between the two groups in significant channels, aligning with the statistical tests and confirming the observed differences (**Figure A**). The boxplots showed that the high-IQ group data had larger variability in significant channels, reflected in wider interquartile ranges, while the low-IQ group displayed more consistent and narrower distributions (**Figure B**). These patterns suggest that significant channels may serve as neural markers differentiating cognitive abilities between the groups.

The comparison of the predictability between the high-IQ and low-IQ groups revealed distinct insights (**Figure C**). RMSE values were generally lower for the low-IQ group, indicating better alignment between real and simulated data and suggesting higher predictability in the EEG traces of less intelligent individuals. Standard deviations were also slightly smaller for the low-IQ group across several EEG channels, further supporting its greater predictability. In contrast, the high-IQ group exhibited greater variability and larger RMSE values, which are indicative of patterns of reduced predictability in Monte Carlo simulations.



Figures A-B. A visual comparison of Monte Carlo simulations showcasing the graphical representation of a single electrode [O2] as a representative example from the set of 19 electrodes. The histogram comparison (**Figure A**) highlights the differences in real distribution between high-IQ and low-IQ groups across each column. The corresponding boxplot (**Figure B**) visually compares the distributions of the two groups across each column. Differences in medians, interquartile ranges and potential outliers can be identified. Statistical significance is determined based on p-values obtained through t-tests.

Figure C. Predictability of EEG traces via Monte Carlo simulation. This panel indicates that the EEG behaviour of the low-IQ group is more predictable, as reflected by their lower average RMSE and slightly smaller standard deviation compared to the high-IQ group.

DISCUSSION

The results of this study underscore the remarkable utility of Monte Carlo simulations in modeling EEG traces and identifying significant differences between high-IQ and low-IQ groups. By accurately replicating the statistical properties of the original dataset, the simulated data closely mirrored the observed real patterns in terms of central tendencies, variability and overall distribution shapes. Our analysis revealed pronounced statistical distinctions in specific EEG channels, which suggest potential markers of cognitive ability. For instance, the differences observed in frontal regions [FP1] and [FP2] align with their roles in executive functions, attention and problem-solving. The high-IQ group exhibited greater variability in these areas, possibly reflecting more dynamic or complex neural processes. The temporal regions [T3] and [T4] showed disparities that could indicate differences in memory retrieval and language processing between high-IQ and low-IQ groups. Similarly, occipital regions, particularly [O2], revealed distinctions in visual-spatial processing capabilities. At the same time, non-significant channels like [P3] and [PZ] in the posterior parietal regions, [T6] in the temporal region and [F7] in the left frontal area pointed to areas where further exploration or alternative modeling approaches may be necessary.
The low-IQ group exhibited higher predictability during Monte Carlo simulations, as demonstrated by lower RMSE values between real and simulated data and smaller standard deviations in several EEG channels. The less intelligent subjects generally displayed more consistent EEG patterns, particularly in central and temporal regions, aligning with their reduced variability and narrower distribution ranges. These patterns suggest a level of neural uniformity in the low-IQ group, contrasting with the broader variability, the higher RMSE values and the increased unpredictability observed in high-IQ individuals' EEG activity.

We demonstrated that Monte Carlo simulations serve as a powerful tool in neurocognitive research, enabling the identification of EEG markers associated with cognitive abilities and the simulation of neural activity patterns to test hypotheses about brain function. Practical applications of these findings extend to predictive modeling, where simulated EEG data can forecast cognitive behaviors. In clinical settings, these insights might inform interventions for cognitive enhancement or rehabilitation. Additionally, educational strategies could be tailored based on neural markers of learning potential. This study has limitations. While the assumption of normality proved valid for most EEG channels, deviations in skewness or kurtosis in some columns may have influenced results, highlighting the need for further research. Future studies should consider employing non-parametric methods or fitting alternative distributions to enhance the robustness of simulations. Investigating multivariate correlations across channels could provide deeper insights into the neural interconnections underlying intelligence. Future research should also explore the integration of alternative modeling techniques to further refine the accuracy and applicability of these methods and deepen our understanding of the neural underpinnings of human cognition.

In conclusion, the implications of this research in the field of cognitive neuroscience go beyond academic interest, underscoring the potential of combining advanced statistical techniques with neuroscience to unlock new possibilities for studying and enhancing human cognition. In particular, Monte Carlo simulations leverage the power of computational modeling to explore the complexities of human intelligence, offering robust methods for expanding datasets, uncovering underlying patterns and identifying key neural markers.

DECLARATIONS

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.
Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal, and has not been previously published.
Availability of data and materials. all data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.
Competing interests. The Author does not have any known or potential conflict of interest including any financial, personal or other relationships with other people or organizations within three years of beginning the submitted work that could inappropriately influence, or be perceived to influence, their work.
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Authors' contributions. The Author performed: study concept and design, acquisition of data, analysis and interpretation of data, drafting of the manuscript, critical revision of the manuscript for important intellectual content, statistical analysis, obtained funding, administrative, technical, and material support, study supervision.

Declaration of generative AI and AI-assisted technologies in the writing process. During the preparation of this work, the author used ChatGPT to assist with data analysis and manuscript drafting. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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Fractional and Geometric Neural Dynamics: Investigating Intelligence-Related Differences in EEG Symmetry and Connectivity

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ABSTRACT

Understanding intelligence-related variations in electroencephalographic (EEG) activity requires advanced mathematical approaches capable of capturing geometric transformations and long-range dependencies in neural dynamics. These approaches may provide methodological advantages over conventional spectral and connectivity-based techniques by offering deeper insights into the structural and functional organization of neural networks. In this study, we integrate Clifford algebra, Noether's theorem and fractional calculus to analyze EEG signals from high- and low-IQ individuals, looking for key intelligence-related differences in cortical organization. Clifford algebra enables the representation of EEG signals as multivectors, preserving both magnitude and directional relationships across cortical regions. Noether's theorem provides a quantitative measure of symmetry properties linked to spectral features, identifying conserved functional patterns across distinct brain regions. Mittag-Leffler functions, derived from fractional calculus, characterize long-range dependencies in neural oscillations, allowing for the detection of memory effects and scale-invariant properties often overlooked by traditional methods. We found significant differences between high- and low-IQ individuals in geometric trajectories, hemispheric connectivity, spectral properties and fractional-order dynamics. High-IQ individuals exhibited increased spectral asymmetry, enhanced spectral differentiation, distinct geometric trajectories and greater fractional connectivity, particularly in frontal and central regions. In contrast, low-IQ individuals displayed more uniform hemispheric connectivity and heightened fractional activity in occipital areas. Mittag-Leffler fractional exponents further indicated that high-IQ individuals possessed more varied neural synchronization patterns. Overall, our multi-faceted approach suggests that intelligence-related neural dynamics are characterized by an asymmetric, functionally specialized and fractionally complex cortical organization. This results in significant differences in network topology, efficiency, modularity and long-range dependencies.

KEYWORDS: neural oscillations; functional asymmetry; graph theory; cognitive variability; brain network topology.

INTRODUCTION

Intelligence has been associated with distinct electroencephalographic (EEG) neural patterns, yet the underlying mechanisms remain a subject of investigation (Thatcher et al., 2005; Friedman et al., 2019). The study of intelligence-related differences in EEG signals has traditionally relied on spectral, time-frequency and connectivity analyses (Chen et al., 2023; Ignatious et al., 2023). Conventional approaches such as Fourier and wavelet transforms, coherence measures and graph-theoretic network analyses have provided critical insights into brain function but lack the mathematical depth to fully capture neural relationships (Sitnikova et al., 2009; San-Segundo et al., 2019). We argue that mathematical frameworks integrating algebraic, geometric, and fractional dynamics provide an alternative perspective by capturing spatial dependencies and characterizing long-range memory effects in neural activity. Among these approaches, Clifford algebra has been used to encode EEG signals as multivectors, preserving both magnitude and directional relationships across cortical regions—an advantage not achievable with conventional spectral methods (Zhang et al., 2023). Clifford algebra-based EEG transformations allow for the preservation of geometric properties enabling novel trajectory-based comparisons. Noether's theorem, which relates system symmetries to conserved quantities, has been used to assess functional and spectral balance in cortical microcircuitry, revealing conserved functional patterns across different cortical regions (Bilteanu et al., 2017). Meanwhile, fractional calculus — particularly Mittag-Leffler function analysis— may extend EEG signal characterization beyond integer-order models, allowing for the detection of memory effects and scale-invariant properties often overlooked by standard methods (Atanackovic et al., 2011; Turalska and West, 2018). Functional order analysis provides an additional layer of insight by quantifying fractional dynamics and long-range dependencies (García-Raffi and Torrano, 2021).

Together, these multi-faceted approaches may enable a refined investigation into intelligence-related brain dynamics extending beyond pairwise spectral differences, allowing for a richer assessment of interregional dependencies. We

conjecture that our approach might reveal systematic differences in EEG structure, with high-IQ individuals exhibiting greater frontal asymmetry, enhanced connectivity in integrative brain areas and increased fractional-order complexity in neural synchronization. Low-IQ individuals, in contrast, might display more uniform hemispheric connectivity, potentially indicative of different cognitive resource allocation strategies.

In sum, given the limitations of traditional EEG methods, a hybrid approach that considers Clifford algebra, Noether's theorem and fractional network measures holds promise for more comprehensive analyses of intelligence. We will proceed as follows. The next section outlines the methodology, detailing data acquisition, preprocessing and the mathematical frameworks applied to EEG signals. We then present our results, followed by an interpretation of the findings in the context of intelligence-related neural organization. Finally, we conclude with a discussion on the broader implications and future directions of this research.

MATERIALS AND METHODS

Our retrospective study builds on prior research by Jaušovec and Jaušovec (2001; 2003; 2005; 2010) and later advancements with Tozzi et al. (2021a; 2021b), honoring Norbert Jaušovec's contributions. EEG data were collected from 10 right-handed participants (mean age: 19.8 years; SD = 0.9; males: 4), divided into High-IQ (IQ SD = 127) and Low-IQ (IQ SD = 87) groups based on standardized test scores during auditory and visual oddball tasks. EEG signals were recorded using a 64-channel system with electrodes placed according to the 10–20 system. Data epochs were segmented into non-overlapping 2-second windows and trials contaminated with excessive noise were excluded based on an amplitude threshold exceeding ±100 µV. Standardization was performed by normalizing each EEG signal relative to its mean and standard deviation across trials, ensuring comparability between participants.

Clifford algebra. Clifford algebra was used to transform EEG signals into multivector representations that preserve spatial and directional relationships between cortical regions (Acus and Dargys, 2024). Each EEG signal $x_i(t)$ from electrode *i* was mapped onto a Clifford multivector $\Psi(t)$, expressed as

$$\Psi(t) = \sum_i v_i(t) e_i$$

where $v_i(t)$ is the voltage amplitude and e_i represents a basis vector of a Clifford algebra. The choice of Clifford space dimensionality depended on the number of selected EEG channels. In our study, a three-dimensional Clifford space $Cl(3,0)$ was chosen to encode signals from three representative electrode locations (FP1, P3, O1). These three electrodes were selected due to their known involvement in cognitive functions and information processing. The transformed EEG signals were then analyzed geometrically by computing trajectory deviations across trials. The Clifford Fourier Transform (CFT) was used to extract spectral features within the multivector space (Monaim and Fahlaoui, 2024). Given a time-dependent multivector $\Psi(t)$, its frequency-domain representation was obtained as

$$\tilde{\Psi}(\omega) = \int \Psi(t) e^{-e_1 \omega t} dt$$

where e_1 is an imaginary unit in Clifford space. Statistical comparisons of Clifford trajectories were performed using paired t-tests to determine significant differences in neural geometry between high and Low-IQ groups.

Noether's theorem. Noether's theorem was used to quantify symmetry in functional connectivity. Functional connectivity was evaluated using Pearson correlation coefficients between electrode pairs, computed as

$$r = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2} \sqrt{\sum (y_i - \bar{y})^2}}$$

where x_i and y_i represent EEG signals from different electrodes and $\bar{x}$ and $\bar{y}$ are their means over time. Connectivity matrices were constructed for each participant, with a focus on left-right hemisphere electrode pairs (FP1–FP2, F3–F4, C3–C4, P3–P4, O1–O2) to assess hemispheric symmetry. Symmetry indices were calculated as

$$S = \frac{|PSD_L - PSD_R|}{PSD_L + PSD_R}$$

where PSD_L and PSD_R are power values from corresponding left and right hemisphere electrodes. Spectral asymmetry was assessed by performing a Fourier transform on each EEG channel and comparing power distributions between hemispheres (Atiyah et al., 1975). Welch's t-tests were applied to compare connectivity and spectral symmetry indices between high and Low-IQ groups.

To assess the relationship between frequency band power and hemispheric symmetry, correlation analyses were performed for each frequency band. Power spectral densities (PSDs) were computed to assess frequency distributions in delta, theta, beta and alpha bands (Dressler et al., 2004; Redwan et al., 2024). Pearson correlation coefficients were then calculated between frequency band power and hemispheric symmetry indices to determine whether specific oscillations were associated with neural organization patterns.

To evaluate the temporal stability of EEG signals, stationarity tests were conducted using the Augmented Dickey-Fuller (ADF) test, which determines whether a time series exhibits long-term trends or remains stable over time (Dao and Staszewski, 2021). ADF p-values below 0.05 indicated significant stationarity, suggesting a consistent neural state.

Fractional derivative values. Fractional-order derivatives were computed to characterize the temporal dynamics of EEG signals, as conventional differentiation does not account for memory effects or long-range dependencies inherent in neural activity. The Caputo fractional derivative was chosen, defined as

$$D^{\alpha} f(t) = \frac{1}{\Gamma(1-\alpha)} \int_0^t \frac{f'(\tau)}{(t-\tau)^{\alpha}} d\tau$$

where α represents the fractional order and Γ denotes the Gamma function. The parameter α was optimized based on the signal's spectral properties to capture its underlying fractional nature effectively. Numerical implementation was carried out using the Grünwald-Letnikov approximation, which approximates the integral definition with a discrete summation:

$$D^{\alpha} f(n) = \sum_{k=0}^{n} (-1)^k \binom{\alpha}{k} f(n-k)$$

where $\binom{\alpha}{k}$ represents the binomial coefficient extended to non-integer orders. This method provided a means of assessing long-range dependencies in EEG data, differentiating between stationary and non-stationary signal properties. The fractional derivative values were extracted for each EEG channel and used in subsequent statistical analyses to identify group-wise differences in neural activity. These calculations formed the basis for evaluating the Mittag-Leffler function's role in neural dynamics, establishing a mathematical framework for comparing cognitive groups.

Fractional connectivity and fractional clustering coefficients. To examine functional connectivity, correlation-based adjacency matrices were constructed by computing pairwise cross-correlations between EEG channels. Cross-correlation was defined as

$$C_{xy}(\tau) = \sum_t x(t) y(t+\tau),$$

where $x(t)$ and $y(t)$ are EEG signals from two channels and τ represents the lag. A sliding window approach was used to ensure robust estimation of functional connectivity over time, with overlapping one-second segments applied to account for dynamic variations in brain activity.

To integrate fractional-order concepts into network analysis, fractional connectivity and fractional clustering coefficients were computed. Fractional connectivity was derived by modifying edge weights using a power-law transformation, where each connection strength W_{ij} was raised to a fractional exponent γ, yielding W_{ij}^{γ}. The mean fractional connectivity was then calculated by averaging these transformed values, providing a metric sensitive to long-range dependencies in neural networks.

The fractional clustering coefficient was computed using a modified version of the standard clustering measure, incorporating the fractional-weighted edges to assess local connectivity structures. This was defined as

$$C_i^{\gamma} = \frac{1}{k_i(k_i-1)} \sum_{j,k} (W_{ij} W_{ik} W_{jk})^{\gamma/3}$$

where k_i is the degree of node i. These fractional measures allowed for a more nuanced characterization of network topology, enabling differentiation between classical small-world organization and fractional network configurations.

The ability to quantify connectivity and clustering using fractional-order metrics provided insights into how neural interactions vary across cognitive groups, extending conventional graph-theoretic approaches.

Mittag-Leffler fractional exponents. Mittag-Leffler fractional exponents were estimated to describe the scaling behavior of connectivity weights within the network (García-Raffi and Torrano, 2021). The Mittag-Leffler function, defined as

$$E_{\alpha,\beta}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k+\beta)},$$

generalizes exponential decay and captures memory effects in complex systems (Tarasov 2018). To estimate the effective fractional exponent, the probability distribution of connectivity weights was examined in log-log space and a power-law function

$$P(W) \sim W^{-\lambda}$$

was fitted to the data. The exponent λ was extracted using least-squares fitting, providing a measure of the heterogeneity in connectivity distributions. Higher values of λ indicated a broader range of connectivity strengths, reflecting a more diverse interaction pattern across EEG channels. This Mittag-Leffler-based analysis was used to assess differences in the scaling properties of functional networks between groups, serving as a crucial parameter for understanding cognitive variability.

Statistical analyses were performed to compare fractional network measures between high and Low-IQ groups. One-way analysis of variance (ANOVA) was conducted to test for significant differences in fractional connectivity, fractional clustering and Mittag-Leffler exponents across groups. The Bonferroni correction was applied to account for multiple comparisons and control the false discovery rate.

Tools. Computational analyses were implemented using Python, utilizing NumPy for numerical computations, SciPy for statistical analysis, Matplotlib for visualization and the MNE-Python toolbox for EEG preprocessing. Clifford algebra computations were performed using the ClPy library and Fourier transforms were applied using SciPy's signal processing module.

RESULTS

Significant differences in geometric trajectories, hemispheric connectivity, spectral properties and fractional-order dynamics were found between high and Low-IQ individuals, with High-IQ individuals exhibiting increased Clifford algebra-based frontal variability, greater frontal asymmetry and enhanced spectral differentiation.

Clifford algebra. Clifford algebra-based transformations displayed distinct EEG trajectory patterns, with High-IQ individuals exhibiting increased geometric variability in the frontal region, while Low-IQ individuals exhibited more constrained neural trajectories (**Figure 1A**). Statistical comparisons of Clifford components indicated significant differences in frontal representations between groups ($p < 0.001$), whereas no significant differences were found in parietal and occipital components (**Figure 1B**). Temporal stationarity analyses using the Augmented Dickey-Fuller test indicated that EEG signals in High-IQ individuals were more stationary ($p < 0.05$), suggesting greater consistency in neural oscillations.

Spectral power analysis using the Clifford Fourier Transform showed that High-IQ individuals exhibited significantly higher alpha ($p < 0.001$) and beta ($p = 0.0067$) power in the frontal region compared to Low-IQ individuals, suggesting different neural activation patterns. Power spectral densities showed that High-IQ individuals had significantly higher theta ($p = 0.0065$) and beta ($p = 0.0067$) power, while Low-IQ individuals exhibited relatively stronger delta oscillations.

Noether's theorem. Connectivity analysis based on Noetherian symmetry principles and further analyses of spectral symmetry revealed significant differences in hemispheric organization. High-IQ individuals displayed greater asymmetry in frontal connectivity (FP1-FP2, $p < 0.001$) and enhanced symmetry in occipital connectivity (O1-O2, $p < 0.001$), while Low-IQ individuals maintained more uniform hemispheric connectivity, particularly in prefrontal and parietal regions (**Figure 1C**).

Fractional dynamics. Statistical analysis of Mittag-Leffler fractional derivatives revealed distinct patterns of neural activity between high- and low-IQ individuals. High-IQ individuals consistently exhibited higher fractional values in frontal (FP1, F4) and central (C3) regions, while low-IQ individuals showed increased fractional activity in the occipital (O1) area (**Figure 2A**). Notably, the frontal regions displayed significantly lower fractional-order dynamics in the low-IQ group, suggesting that high-IQ individuals engage in neural processes with stronger memory effects and long-range dependencies, potentially supporting cognitive flexibility and problem-solving.

Beyond localized effects, significant differences were also observed in central and parietal channels, indicating that intelligence-related variability extends across broader network properties rather than being confined to specific brain regions. The occipital region exhibited an inverse trend, with low-IQ individuals displaying higher Mittag-Leffler fractional activity, possibly reflecting distinct neural connectivity patterns or alternative sensory integration strategies.
Furthermore, greater variability in fractional activity was observed in some channels within the low-IQ group, as indicated by wider distribution ranges. This suggests increased dispersion in fractional-order neural activity, which may correspond to less stable or less efficient network dynamics.

Fractional network measures. The comparison of fractional network measures between high and Low-IQ groups is illustrated in **Figure 2B**. Fractional connectivity exhibited significant differences between groups, with High-IQ individuals showing an higher mean fractional connectivity. Similarly, fractional clustering coefficients were higher in the High-IQ group. Mittag-Leffler fractional exponents demonstrated a broader distribution in the High-IQ group, with a mean exponent value lower in the Low-IQ group. Further, High-IQ individuals exhibited greater variability in fractional connectivity values. Weighted global efficiency was significantly higher in the High-IQ group, suggesting differences in the efficiency of information transfer across neural networks. This set of findings highlights a more complex and distributed network topology in individuals with High-IQ, underlining the relevance of fractional measures in characterizing cognitive differences. Small-worldness, defined as the ratio of clustering coefficient to characteristic path length, was significantly greater in the High-IQ group. This suggests that High-IQ individuals exhibit a more optimized network structure, balancing local clustering with global efficiency. Additionally, edge weight distribution followed a broader power-law decay in the High-IQ group, consistent with more heterogeneous connectivity patterns.
The Mittag-Leffler-based scaling exponent analysis further corroborated these findings, as High-IQ individuals demonstrated greater deviation from exponential connectivity decay, indicating a higher degree of long-range dependencies in neural interactions. These variations were particularly evident in the frontal and occipital regions, where High-IQ individuals displayed enhanced connectivity strengths. Differences in network modularity also emerged, with High-IQ individuals exhibiting higher modularity scores, suggesting a more functionally segregated yet highly interactive network.
Overall, these findings suggest that fractional network properties, including connectivity, clustering and Mittag-Leffler exponents, may distinguish high and Low-IQ groups in a statistically significant manner.

Summarizing, our findings, confirmed through Clifford algebra transformations, spectral analysis and Noetherian symmetry principles, suggest that High-IQ individuals exhibit greater frontal EEG asymmetry, increased spectral differentiation and distinct connectivity patterns, greater geometric variability, greater frontal asymmetry, enhanced connectivity in integrative regions and increased long-range dependencies, while Low-IQ individuals displayed more uniform hemispheric connectivity and heightened activity in occipital areas. These findings suggest that intelligence-related neural dynamics are characterized by asymmetric, functionally specialized and fractionally complex cortical organization.

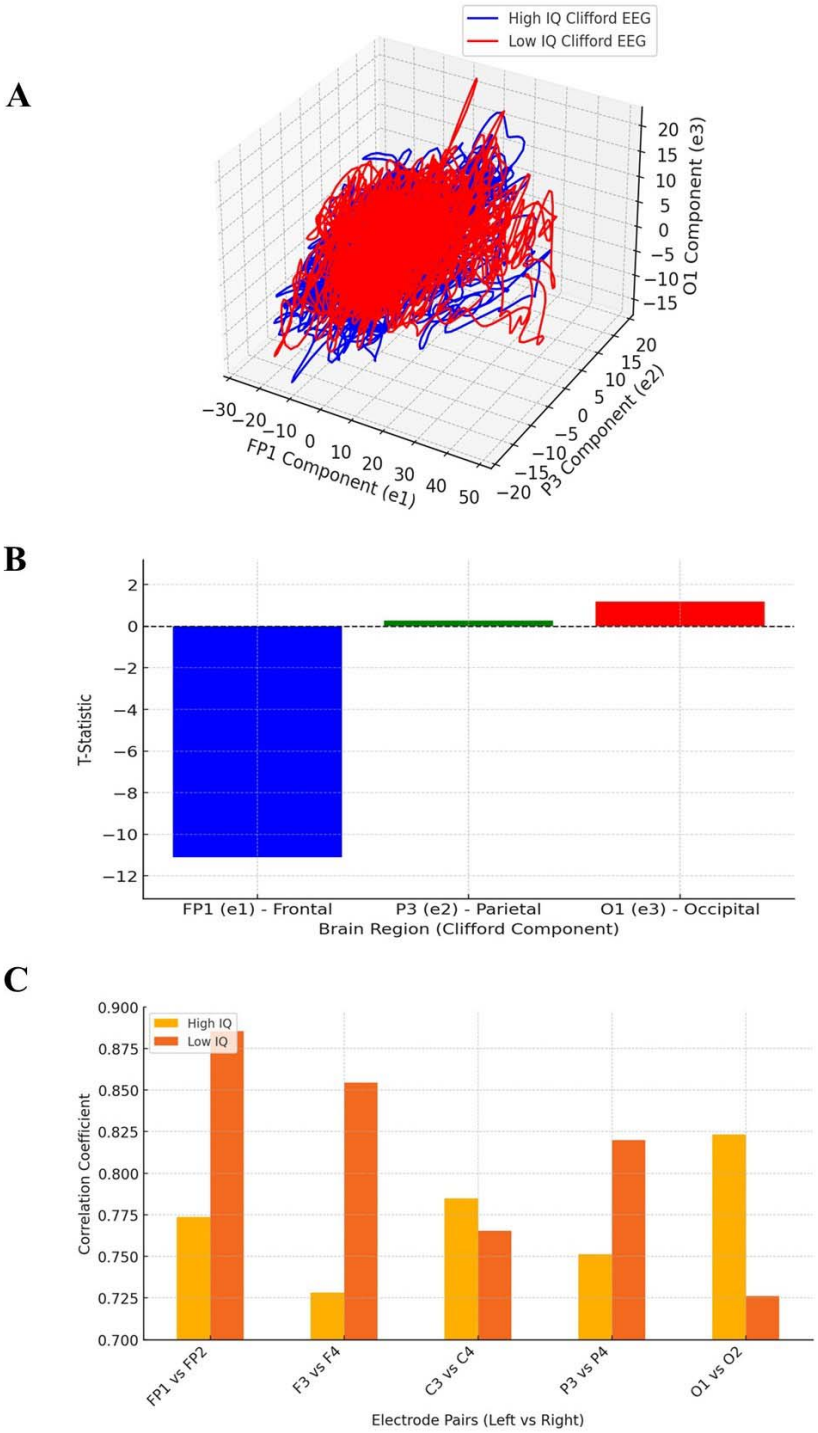

Figure 1A. Clifford EEG Signal representation for High vs. Low-IQ groups. The blue and red lines represent average EEG trajectories in Clifford space for high and Low-IQ individuals, respectively. Differences in shape, spread and oscillatory patterns provide insight into IQ-related brain activity variations.

Figure 1B. Statistical differences in Clifford EEG components. Significant differences were observed in the frontal region, while parietal and occipital components showed no substantial variation. The dashed line at zero indicates the statistical significance threshold.

Figure 1C. Hemispheric symmetry differences across brain regions. Low-IQ individuals (green bars) exhibit greater symmetry in prefrontal, frontal and parietal regions, whereas High-IQ individuals (blue bars) exhibit increased asymmetry, particularly in FP1-FP2 and F3-F4. The occipital region (O1-O2) is more symmetric in High-IQ individuals, suggesting enhanced visual-spatial processing.

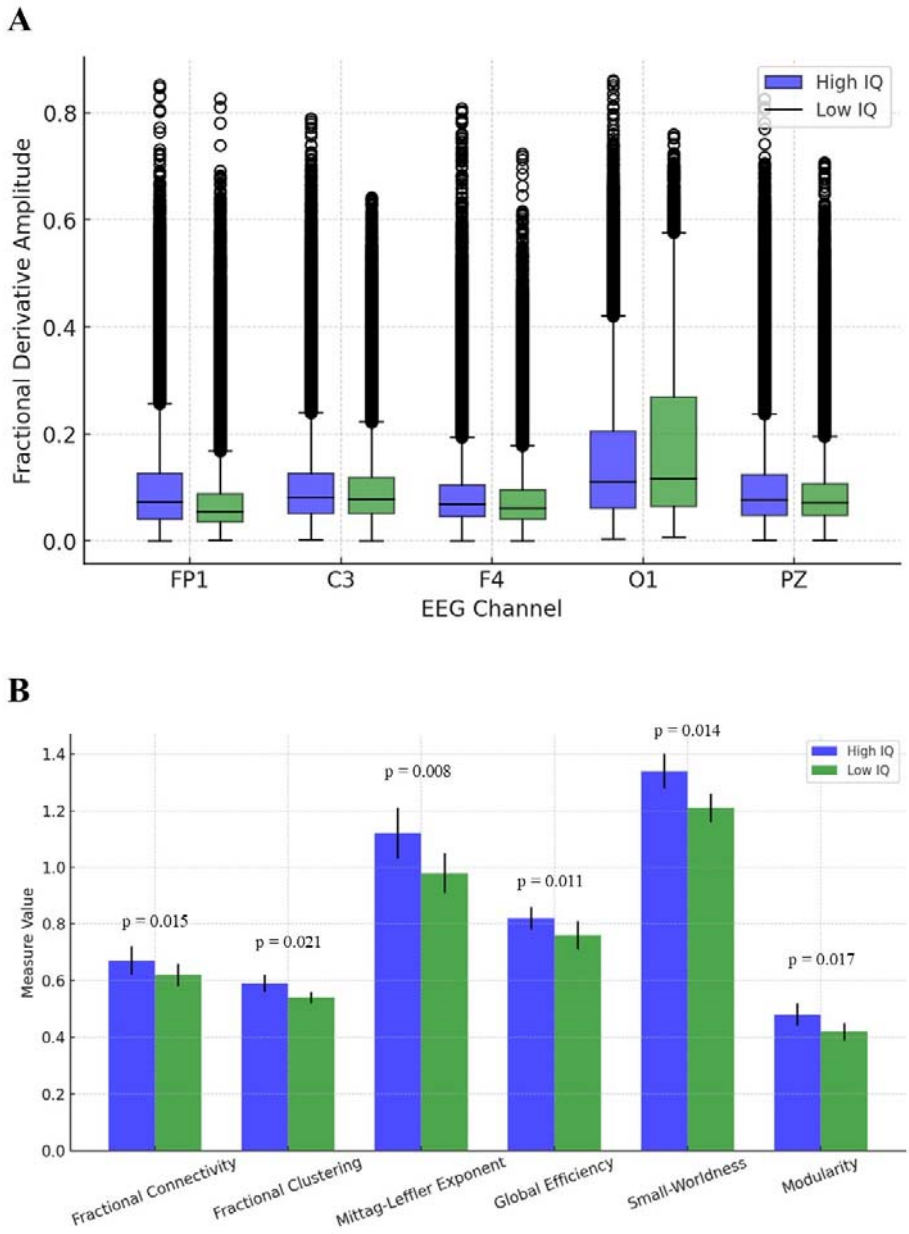

Figure 2A. Boxplot comparison illustrating key differences in fractional dynamics between High-IQ (blue) and Low-IQ (green) groups. The variations in distributions suggest significant differences in Mittag-Leffler function characteristics. Statistical analysis confirms that these distinctions are significant, with **$p < 0.0001$** across all analyzed channels.

Figure 2B. Comparison of fractional network measures between high and Low-IQ groups. Bars represent mean values for each group, with error bars indicating standard deviations. High-IQ individuals exhibit significantly greater fractional connectivity, clustering, Mittag-Leffler exponent, global efficiency, small-worldness and modularity compared to Low-IQ individuals. One-way ANOVA confirmed systematic distinctions in neural structure and connectivity patterns across groups.

CONCLUSIONS

We investigated intelligence-related differences in EEG signals by combining multiple mathematical approaches such as Clifford algebra, Noether's theorem and fractional network analysis. Functional connectivity analysis revealed that

high-IQ individuals exhibited a more differentiated neural network organization that was characterized by greater variability in interregional interactions and enhanced symmetrical connectivity in occipital regions. Fractional-order analyses demonstrated that High-IQ individuals exhibited greater long-range dependencies, with significantly higher Mittag-Leffler fractional exponents and clustering coefficients, supporting the presence of more complex and efficient neural architecture. This suggests that cognitive ability may be linked to distinct neural processing strategies, with High-IQ individuals displaying more complex fractional-order behavior in regions associated with executive function and working memory. In turn, Low-IQ individuals exhibited heightened activity in the occipital cortex, which may correspond to alternative visual processing mechanisms.
High-IQ individuals displayed stronger Mittag-Leffler dynamics in regions linked to complex cognitive processing, while Low-IQ individuals displayed greater activity in visual and sensory processing areas. These differences align with theories of cognitive efficiency and regional specialization, where High-IQ brains may rely more on integrative network structures, while Low-IQ brains may exhibit increased reliance on localized sensory processing. Fractional-order dynamics showed that the frontal and central brain regions displayed more Mittag-Leffler behavior in High-IQ individuals. The occipital region presented an inverse trend, where Low-IQ individuals showed greater fractional activity, suggesting distinct processing dynamics. Taken together, these findings suggest that intelligence-related brain function may be reflected in both geometric transformations and fractional connectivity properties.

The integration of Clifford algebra, Noether's theorem and Mittag-Leffler function-based fractional calculus stands for a novel approach to EEG analysis which offers methodological advantages over conventional spectral and connectivity-based techniques. Clifford algebra preserves magnitude and directional relationships between EEG signals, allowing for a richer representation of neural trajectories' geometric transformations. Noether's theorem introduces a principled framework for assessing conserved properties in brain networks, enabling the quantification of functional symmetry and intelligence-related differences in interregional connectivity patterns. Fractional network measures extend beyond traditional graph-theoretic approaches by capturing long-range dependencies and scale-invariant properties in neural oscillations. This may reveal subtle variations in brain dynamics that conventional EEG methodologies fail to detect and that are often overlooked in standard time-frequency analyses.

Compared to traditional EEG analysis techniques, our approach offers several advantages. Spectral analysis methods such as Fourier and wavelet transforms are widely used to decompose EEG signals into frequency components but do not retain spatial or directional relationships between electrodes (Yuan et al., 2018; Daud and Sudirman, 2022). Functional connectivity metrics, including coherence and phase synchronization, assess interregional interactions but often rely on pairwise comparisons that may overlook global network dependencies (Miskovic and Keil, 2015; Abdullateef et al., 2022). Graph-theoretic measures capture aspects of brain topology but do not explicitly incorporate long-range dependencies or fractional-order dynamics. In contrast, our combination of Clifford algebra, Noether's theorem and fractional network analysis preserves both local signal variations and global connectivity patterns. The inclusion of fractional calculus further enhances sensitivity to memory effects and non-stationary dynamics (Chen and Wang, 2020).

Our methodological framework has potential applications in different fields. EEG-based cognitive profiling could benefit from Clifford algebra transformations to characterize individual differences in neural geometry. The integration of Noether's theorem into EEG analysis could provide a means of quantifying hemispheric symmetry, which has implications for studying neurodevelopmental disorders. Fractional network measures could be employed in neurodegenerative research to monitor cognitive decline, as long-range dependencies and connectivity scaling properties may serve as biomarkers for early-stage disorders. The integration of Noether's theorem into EEG analysis may also contribute to the study of neurodevelopmental and neuropsychiatric disorders, where alterations in hemispheric symmetry have been linked to conditions such as autism spectrum disorder, schizophrenia and dyslexia (Saugstad, 1999; Gage et al., 2009; Guo et al., 2013; Perkins et al., 2014; He et al., 2023). Still, brain-computer interface technologies may enhance classification accuracy by utilizing fractional-order EEG features, which incorporate long-range memory effects into machine learning models (Tarasov 2018).
Beyond these applications, our approach suggests testable experimental hypotheses, such as: a) whether interventions like transcranial stimulation can modulate EEG symmetry in ways consistent with Noetherian principles; b) whether cognitive training enhances fractional connectivity measures over time; c) whether neural efficiency, as quantified by Clifford algebra-based geometric transformations, correlates with cognitive performance in different task-based EEG paradigms; d) whether the observed intelligence-related differences in EEG connectivity persist over time, particularly in relation to neuroplasticity and cognitive aging. These experimental extensions reinforce the potential of our framework in broadening the scope of nervous oscillations' research.

Despite its contributions, our study has several limitations. The sample size may limit the generalizability of findings and the robustness of observed differences. The computational complexity of Clifford algebra transformations presents a potential challenge, as real-time applications may require optimization to improve processing efficiency. While Noether's theorem provides a theoretical basis for assessing neural symmetry, its direct application to EEG data for the study of intelligence requires further validation. Still, the selection of fractional exponent parameters was optimized

based on empirical signal properties, but individual variations in neural dynamics may necessitate adaptive algorithms to improve robustness. Multimodal neuroimaging approaches, such as functional magnetic resonance imaging, could be incorporated to enhance spatial resolution and validate EEG-based symmetry findings.

In conclusion, we suggest that intelligence-related differences in EEG signals may be characterized using a combination of Clifford algebra, Noether's theorem and fractional network analysis. By integrating these advanced mathematical frameworks, a novel perspective on cognitive variability could be provided, highlighting the role of symmetry, geometric transformations and fractional-order properties in brain function.

DECLARATIONS

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.
Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal and has not been previously published.
Availability of data and materials. All data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and took responsibility for the integrity of the data and the accuracy of the data analysis.
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Declaration of generative AI and AI-assisted technologies in the writing process. During the preparation of this work, the author used ChatGPT 4o to assist with data analysis and manuscript drafting and to improve spelling, grammar and general editing. After using this tool, the author reviewed and edited the content as needed, taking full responsibility for the content of the publication.

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An extended Stokes' theorem for spiral paths: applications to rotational flows in *Trachelospermum jasminoides* stems and flowers

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The traditional Stokes' theorem connects the macroscopic circulation along a closed boundary to the microscopic circulation across the surface it encloses. However, it proves inadequate for addressing complex geometries such as helicoidal paths, non-planar flow patterns and dynamic systems with open boundaries. We introduce an extension of Stokes' theorem (EST) that provides a robust tool for interdisciplinary research in spiral/helicoidal dynamics, facilitating the evaluation of rotational forces and circulation in both natural and engineered systems with open boundaries. We apply EST to model the rotational dynamics of flower petals and the helical forces within the stems of *Trachelospermum jasminoides*, known as star jasmine. For the flower, we demonstrate the equivalence between the line integral along the petal boundary and the surface integral over the enclosed disk, effectively capturing the uniform rotational stress generated by tangential forces. EST enables the analysis of external factors such as wind or pollinator interactions, while providing valuable insights to deepen our understanding of floral mechanics and petal growth patterns. For the stem, linking microscopic circulatory forces to macroscopic flow patterns, we demonstrate the interaction of torsional and bending stresses caused by the helical geometry. This finding has significant implications for understanding plant growth biomechanics and structural stability as well as for quantifying nutrient and water transport within stems, where spiral dynamics play a pivotal role. In summary, EST streamlines the analysis of rotational and translational forces in systems governed by spiral and helicoidal dynamics, including physical and biological phenomena such as phyllotaxis and plant growth.

KEYWORDS: helical dynamics; boundary analysis; vector field integration; flow topology.

INTRODUCTION

Stokes' theorem (henceforward ST) is a fundamental principle of vector calculus that bridges the macroscopic circulation along a closed boundary with the microscopic circulation over the enclosed surface (Green, 1828; Schey, 1997). Extending the principles of Green's theorem (GT) which applies to two-dimensional regions, ST provides a powerful framework for analyzing flows and circulations in three-dimensional spaces, uncovering profound connections between the local properties of vector fields and their global behaviour. GT and ST are effective tools for solving problems related to physical closed systems with clearly defined boundaries such as airflow circulation around wings, electromagnetic fields in circuits, surface heat flux, Coriolis-driven hemispherical flows, Earth's deep interior dynamics (Craven, 1964; Arfken, 1985; De Villiers, 2006; Livermore et al., 2013; Snieder, 2015; Aubert and Finlay, 2019; Vines et al., 2021; Yang et al., 2023). In biology, the two theorems contribute to understanding blood flow, electrical activity of the brain, growth patterns in ecosystems (Tozzi and Peters, 2023; Bressan et al., 2022). Yet, the classical ST is inherently limited to surfaces and boundaries that are closed, leaving a significant gap in its applicability to open, non-planar geometries. Indeed, many natural and engineered systems exhibit spiral or helical dynamics where forces and flows do not conform to closed loops or planar surfaces but rather are characterized by open, three-dimensional trajectories. Examples include the helical paths of tornadoes, magnetic vortices and spiral galaxies as well as bacterial motility and phyllotaxis of plants (Blaser et al., 2024; Sachkou et al., 2019; Reinhardt and Gola, 2022).

The novelty of this work lies in extending ST to accommodate spiral flows and helicoidal paths. By linking macroscopic and microscopic circulation properties, the extended theorem simplifies the evaluation of forces in systems with open, three-dimensional geometries. We utilize EST to analyse two biological scenarios: 1) the rotational forces in spiral flower petals and 2) the torsional stresses in helical plant stems, both exemplified by *Trachelospermum jasminoides*, commonly known as star jasmine. For the flower, EST captures the uniform rotational stresses induced by tangential forces acting along a circular boundary. This is achieved by demonstrating the equivalence of the line integral along the petal boundary and the surface integral over the enclosed disk. For the stem, EST quantifies the interaction between bending and torsional stresses caused by the helical geometry.
This paper is structured as follows. First, we present the mathematical treatment of EST, including its derivation and parameterization for helicoidal paths. Next, we validate the theorem using the specific example of *Trachelospermum jasminoides'* flowers and stems. Finally, we discuss the broader implications of EST, highlighting its potential to unify the study of dynamical systems with open boundaries.

MATERIALS AND METHODS

This study is grounded in a generalized form of Stokes' theorem, adapted for spiral flows, which facilitates the analysis of forces and circulation in systems with helicoidal or spiral geometries. We aim to prove that, given a continuously differentiable, orientable helicoidal spiral vector field, the macroscopic circulation represented by the integral of a differential form over its surface equals the microscopic circulation represented by the volume integral of the curl perpendicular to the surface. The main challenge here is in defining the notion of a boundary in case of an open helicoidal spiral path, moving beyond the classical case of paths evaluable through ST.

Stokes' Theorem (ST) from vector calculus relates the surface integral of the curl of a vector field over a surface **S** to the line integral of the vector field along the boundary curve ∂S of the surface (**Figure 1**). In its general form, ST asserts that

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_{S} (\nabla \times \mathbf{F}) \cdot d\mathbf{S}$$

where **F** is a a continuously differentiable two-dimensional vector field, ∂S is the closed boundary curve of the surface **S** that can be bended and stretched, d**r** is a differential element of the curve, d**S** is the differential element of the surface area, and $\nabla \times \mathbf{F}$ is the curl of the vector field, i.e., a vector operator characterizing the infinitesimal circulation of vector fields in three-dimensional spaces.
ST turns line integrals of a form over a boundary into more straight-forward double integrals over the bounded region, regardless of the position of vector singularities (Zenisek 1999). For ST to apply, the normal vector representing the surface must be positively oriented (i.e., counterclockwise) with respect to the tangent vector representing the orientation of the boundary.

Extended Stokes' theorem (EST). Consider a vector field **F** defined over a region in three-dimensional space. Let the surface *S* be a portion of a plane or a more general surface that is bounded by a spiral curve $\gamma(t)$. The goal is to use EST to evaluate the line integral over the spiral path in terms of the surface integral of the curl of **F** (**Figure 1**).
Let the spiral curve $\gamma(t)$, with $t \in [a, b]$, be parameterized as

$$\gamma(t) = (r(t)\cos(\theta(t)), r(t)\sin(\theta(t)), z(t))$$

where $r(t)$, $\theta(t)$ and $z(t)$ describe respectively the radial, angular and vertical components of the spiral.
Let's assume that $\gamma(t)$ lies on a flat plane, say the *xy*-plane, so the spiral path can be simplified to

$$\gamma(t) = (r(t)\cos(t), r(t)\sin(t), 0)$$

where $r(t)$ increases as the angle *t* increases.
When the surface **S** is a surface spanned by the curve $\gamma(t)$, **S** stands for a portion of the plane or surface generated by the spiral curve (**Figure 1, left**).

We are interested in computing the line integral of a vector field **F** along the spiral path (**Figure 1, right**). By ST, this line integral can be transformed into a surface integral involving the curl of **F**

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_{S} (\nabla \times \mathbf{F}) \cdot d\mathbf{S}$$

The line integral over the spiral path is:

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_{a}^{b} \mathbf{F}(\gamma(t)) \cdot \frac{d\gamma(t)}{dt}\, dt$$

where $\frac{d\gamma(t)}{dt}$ is the tangent vector to the spiral path at each point *t*.

The surface integral involves the curl of **F**, given by $\nabla \times \mathbf{F}$, and the surface normal vector $\hat{n}$ associated with **S**

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = \int_S (\nabla \times \mathbf{F}) \cdot \hat{n}\, dS$$

The normal vector $\hat{n}$ depends on the orientation of the surface, while dS is the differential area element of the surface. Upon achieving the extended formulation of ST, we will proceed in the next paragraphs with a detailed case study.

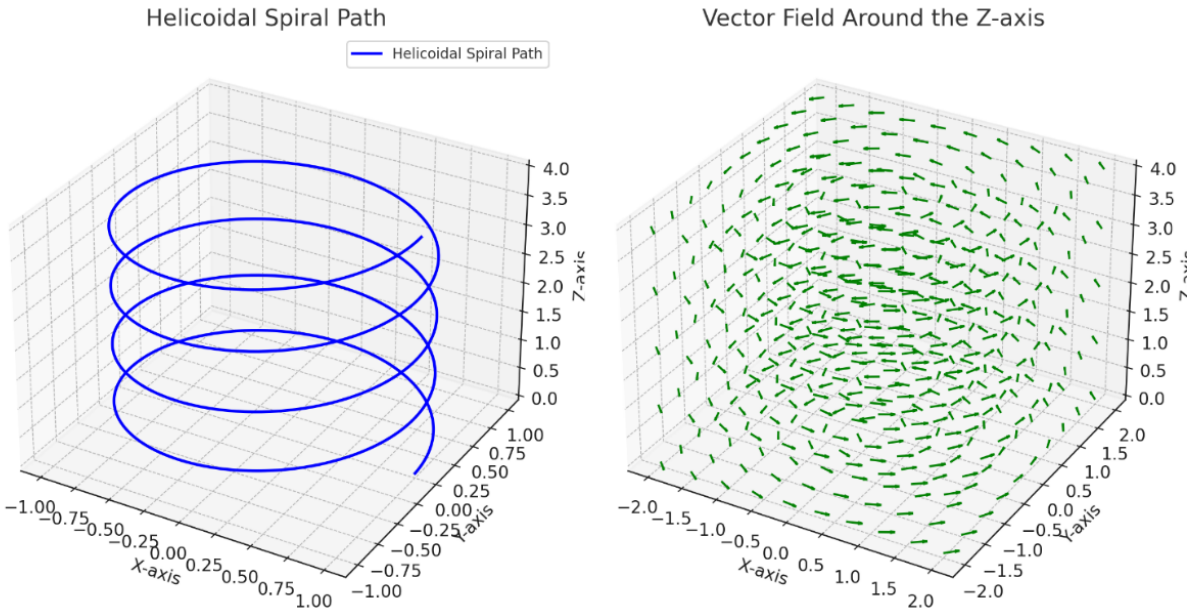

Figure 1. Diagrams depicting a helicoidal spiral (**left**) and the behavior of a vector field (**right**) around the z-axis. The left diagram illustrates a helicoidal spiral path, showcasing the interplay of rotational and translational motion along the z-axis. The right diagram represents a vector field with circular flow centered around the z-axis.

Simulated case study: analyzing rotational flows in stems and flowers. EST enables the analysis of rotational and translational forces in complex systems, providing a powerful framework for exploring biological and physical dynamics. To illustrate the new theorem, we will now explore a concrete example. We will consider *Trachelospermum jasminoides*, commonly known as star jasmine, belonging to the family *Apocynaceae*. Like many climbing plants, *Trachelospermum jasminoides* displays a counterclockwise helical movement of its stems as it climbs and twines around supports, also referred to as circumnutation (Darwin, 1875; Pansanit and Pripdeevech, 2014; Canher et al., 2022) (**Figure 2**). The flowers also exhibit subtle rotational dynamics, although these movements are not as pronounced as the helical twisting of the stems (Stefanatou et al., 2025). The petals of the flowers are arranged in a spiral configuration and unfurl in a counterclockwise direction during blooming.

In our simulation, the dynamics of flower petals are modeled using a circular boundary with a radius of 0.05 m, representing the petals of a flower. Tangential forces along this boundary are applied and the resulting rotational stresses are analyzed through EST. The stem is modeled as a helicoidal path with a radius R=0.05 m and a vertical rise per turn of c=0.2 m. To evaluate the counterclockwise rotation of the flower and stem using EST, the rotation of the petals can be represented by a circular vector field, whereas the helical motion of the stem can be modelled using a helical vector field. The next step is to parameterize the flower and the stem (**Figure 2C**).

1) For the flower, a circular boundary in the plane of the petals is defined, representing the region of interest for macroscopic rotation.

2) For the stem, the helical path is parameterized using equations for a helicoidal spiral, where $x(t) = r\cos(t)$, $y(t) = r\sin(t)$ and $z(t) = ct$. Here r represents the radius, c the rise per turn and t the parameter along the path.

Subsequently, the surface S is defined for each component.

1) For the flower, the surface is a disk enclosed by the petals' rotational motion within their plane,
2) whereas for the stem, the surface corresponds to the area traced by the helical path (**Figure 2C**).

Calculating the forces acting on the flower and stem requires applying mechanical principles that account for both internal and external forces influencing their dynamics (Smyth 2016; Loshchilov et al., 2021). For the flower's petals, the primary force is torque or rotational force, while the stem experiences a combination of bending forces and axial torsion due to its helical structure. We will calculate these forces systematically, step by step, starting from the external forces.

External forces acting of the flower petals and the stem.

1) The rotation of the flower petals can be modeled as a torque induced by external forces such as wind, gravitational pull, biological growth forces (Tipler, 2004). Torque (τ) on the petals is given by:

$$\tau = r \times F$$

Where r is the radial vector from the center of the flower to the tip of a petal and F is the tangential force applied to the petal. Let's assume that the radius of the flower is R=5 cm, while the tangential force from wind or another source is F=0.1 N. The magnitude of the torque is

$$|\tau| = R \cdot F = 0.05\,\mathrm{m} \cdot 0.1\,\mathrm{N} = 0.005\,\mathrm{Nm}$$

In case of multiple petals (n=5 in *Trachelospermum jasminoides*) experiencing similar forces, the total torque becomes

$$\tau_{\text{total}} = n \cdot \tau = 5 \cdot 0.005\,\mathrm{Nm} = 0.025\,\mathrm{Nm}$$

The rotational acceleration (α) of the flower petals is related to the torque (Clark and Ryan, 2022) via

$$\tau = I \cdot \alpha$$

Where I is the moment of inertia of the flower petals about the axis of rotation and α is the angular acceleration.
For a flower modeled as a system of point masses at a radius R

$$I = n \cdot m \cdot R^2$$

where m is the mass of a single petal. Assuming m=0.002 kg (2 grams per petal):

$$I = 5 \cdot 0.002 \cdot (0.05)^2 = 0.000025\,\mathrm{kg}\backslash\mathrm{cdotpm}^2$$

The angular acceleration is:

$$\alpha = \frac{\tau_{\text{total}}}{I} = \frac{0.025}{0.000025} = 1000\,\mathrm{rad/s}^2$$

2) The stem experiences forces from bending and torsion, influenced by its helical structure. These forces arise from gravity, wind and the biological tension exerted during growth.

The weight of the stem induces a bending gravitational force. For a stem of length L=20 cm and mass per unit length λ=0.01 kg/m:

$$F_g = m \cdot g = (\lambda \cdot L) \cdot g = (0.01 \cdot 0.2) \cdot 9.8 = 0.0196\,\mathrm{N}$$

This force acts vertically downward, generating a bending moment at the base of the stem

$$M_g = F_g \cdot \frac{L}{2} = 0.0196 \cdot 0.1 = 0.00196\,\mathrm{Nm}$$

The helical structure of the stem experiences torsional forces due to the winding. The torsional moment (T) is given by

$$T = G \cdot J \cdot \frac{\theta}{L}$$

Where G is the shear modulus of the stem material, J is the polar moment of inertia and θ is the angle of twist over the length L.
Assuming G= 10^8 Pa typical for plant tissue, J = 0.005 m (5 mm radius) and θ = 2π (one full turn over L =0.2 m) (Hoermayer et al., 2024), then

$$J = \frac{\pi}{2} \cdot (0.005)^4 = 9.82 \times 10^{-10}\,\mathrm{m}^4$$

and

$$T = (10^8) \cdot (9.82 \times 10^{-10}) \cdot \frac{2\pi}{0.2} = 3.08\,\mathrm{Nm}$$

Internal forces acting within the flower petals and the stem.
To calculate the forces within the flower petals and the stem using EST, we need to evaluate the relationship between the macroscopic circulation (observable forces) and the microscopic properties (internal forces or stresses derived from the curl of the force field). The first step is to model the forces using vector fields.

1) Concerning the flower petals, we assume that the external forces (e.g., wind or biological forces) act tangentially to their circular boundary. Further, we assume that the tangential forces induce internal stresses (force per unit area) propagating through the petals. Let the force field acting on the petals be

$$\mathbf{F} = (-ky, kx, 0)$$

where k is the force constant proportional to the external pressure and x,y represent positions in the z=0 plane.

Next, we compute the curl of the force field. The curl of the force field relates to the internal stresses within the petals. For the flower petals, in the z=0 plane, the curl of $\mathbf{F} = (-ky, kx, 0)$ is

$$\nabla \times \mathbf{F} = \begin{vmatrix} \mathbf{i} & \mathbf{j} & \mathbf{k} \\ \frac{\partial}{\partial x} & \frac{\partial}{\partial y} & \frac{\partial}{\partial z} \\ -ky & kx & 0 \end{vmatrix} = (0, 0, 2k)$$

This curl is constant in the z-direction, indicating a uniform internal rotational stress throughout the petals.

2) Concerning the helical stem, it experiences external forces such as gravity $(\mathbf{F}_g)$ and biological growth forces $(\mathbf{F}_b)$ that induce internal torsion and bending stresses.

For simplicity, we model the net force field in the stem as: $\mathbf{F} = (-ky, kx, kz)$ where the kz-term accounts for the vertical components of the forces.

Next, we compute the curl of the force field, which provides insight into the internal stresses acting within the stem. This computation reveals the distribution and intensity of these stresses, capturing the complex interplay of forces across the helical structure. For the stem the curl of $\mathbf{F} = (-ky, kx, kz)$ is

$$\nabla \times \mathbf{F} = \begin{vmatrix} \mathbf{i} & \mathbf{j} & \mathbf{k} \\ \frac{\partial}{\partial x} & \frac{\partial}{\partial y} & \frac{\partial}{\partial z} \\ -ky & kx & kz \end{vmatrix} = (k, k, 2k)$$

This suggests a complex pattern of internal stress within the stem, with components distributed across all three spatial directions.

Visualization and statistics. Diagrams of the flower petals and stem are created to illustrate their geometry, boundary dynamics, and associated vector fields. The Matplotlib library is employed to generate detailed plots, including the circular boundary and tangential forces acting on the flower petals, the curl of the vector field over various surfaces, and the helicoidal path and vector field representation for the stem.

To ensure statistical validation, numerical accuracy is achieved through high-resolution parameterization, with the parameter t sampled at 1,000 points per cycle. The consistency between line integrals and surface integrals is carefully evaluated to confirm the applicability of the extended theorem to the analyzed geometries.

In the sequel, the surface integral of the curl of the vector field will be computed over these surfaces using the extended Stokes' theorem (EST).

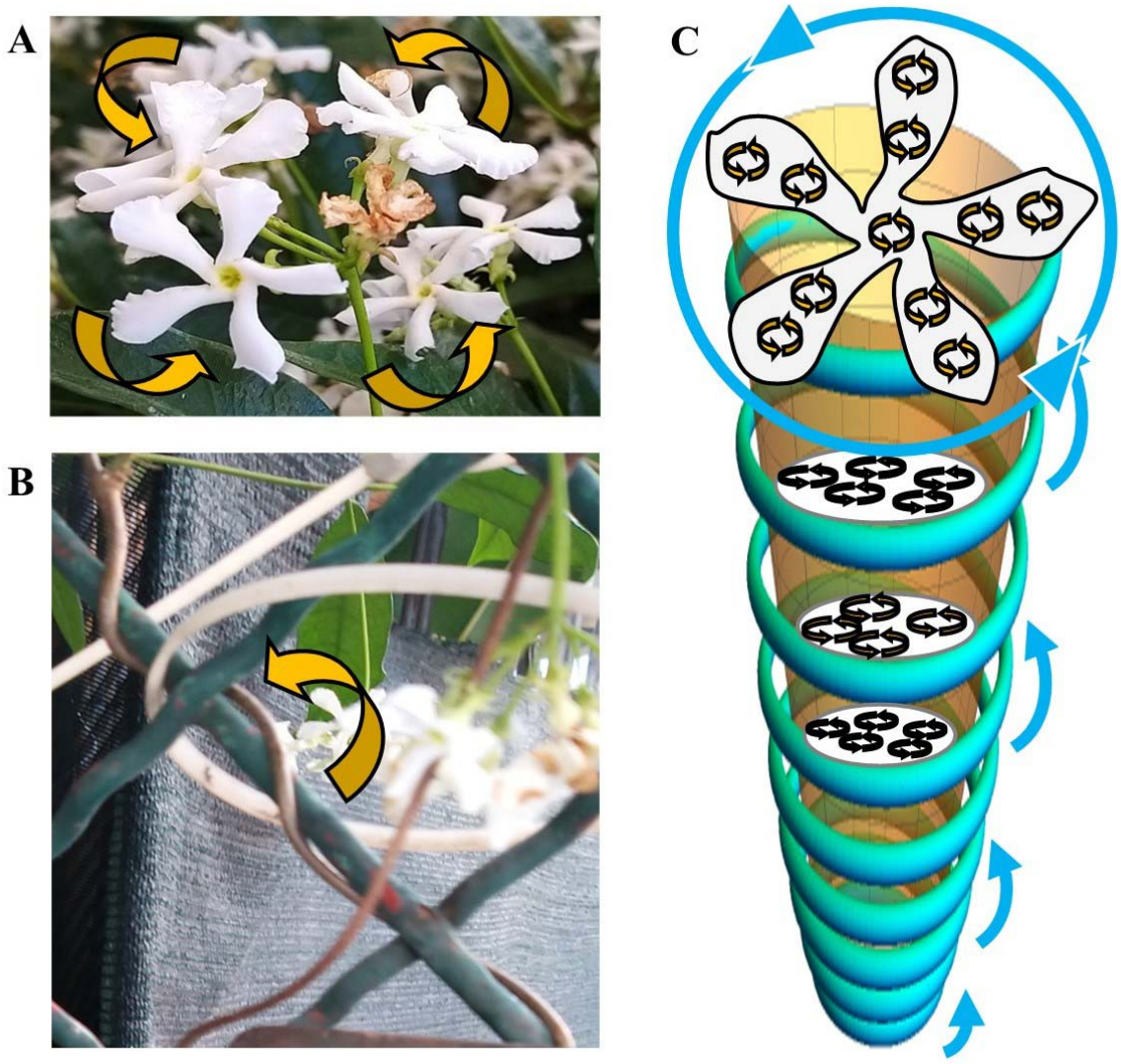

Figure 2. *Trachelospermum jasminoides*. The flower petals (**Figure 2A**) and the stem (**Figure 2B**) display a counterclockwise path. **Figure 2C** illustrates the geometry of the boundaries, the associated vector fields and the internal flows within the flower petals and the stem.

RESULTS

As stated above, both the flower and the stem experience external and internal mechanical forces that influence their motion and structural behavior:

1) For the flower petals, the torque arising from tangential forces induces a counterclockwise rotation, with the total torque $\tau_{\text{total}} = 0.025\,\text{Nm}$ and the angular acceleration measured as α=1000 rad/s^2. The internal stresses in the petals are uniform with a value of 2k and are directly proportional to the external forces acting on them. This proportionality explains the rotational equilibrium observed in the petals.
2) For the stem, the primary forces include a gravitational bending moment $M_g = 0.00196\,\text{Nm}$ and a torsional moment T=3.08□Nm due to a helical twist. The internal stresses in the stem vary in all three dimensions because of its helical geometry. Among these stresses, torsion, proportional to kc, predominates, whereas bending stresses, proportional to kR, have a secondary but still notable influence.

We can now apply EST to relate macroscopic and microscopic circulation. The surface integral of the curl of the vector field is computed over the surfaces, relating the surface integrals to the line integrals along the boundaries. For the flower petals, the counterclockwise macroscopic rotation is calculated by integrating along the circular path in the plane. For the stem, the integral is evaluated over the helical surface.

1) Concerning the flower petals, the boundary of the flower is a circle of radius R. The macroscopic circulation (line integral along the petal boundary) is

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_0^{2\pi} kR^2\, d\theta = 2\pi k R^2$$

Using the curl, the surface integral is

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = \int_S 2k\, dA = 2k \cdot \pi R^2$$

Both results match, confirming that the inner stresses in the petals are proportional to 2k.

In sum, the numerical values for the macroscopic (surface) flows and microscopic (internal) flows in the flower, as governed by EST, are as follows. For the flower, the surface flow (evaluated as a surface integral) is 0.157N\ppm, while the internal flow (evaluated as a line integral) is also 0.157N\ppm. The flower petals exhibit a simple and symmetric geometry, where forces act tangentially along a circular boundary in the z=0 plane. The petals lie on a flat, two-dimensional surface characterized by a constant curl of the force field $(\nabla \times \mathbf{F} = (0, 0, 2k))$, signifying that the internal forces are uniformly distributed. This uniform distribution creates a direct and proportional relationship between the macroscopic flow (line integral along the circular boundary) and the microscopic flow (surface integral over the disk). The symmetry of the geometry ensures that every contribution to the line integral is exactly matched by the surface integral. Consequently, the uniform geometry and constant curl lead to a perfect agreement between the surface flow and the internal flow, consistent with EST.

2) Concerning the helical stem, the boundary of the stem is parameterized as a helicoidal spiral

$$x(t) = R\cos(t), \quad y(t) = R\sin(t), \quad z(t) = ct$$

The macroscopic circulation (line integral along the helical path) is

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_0^{2\pi} \left[-kR\sin(t)(-R\sin(t)) + kR\cos(t)(R\cos(t)) + kc(ct)\right] dt$$

$$= \int_0^{2\pi} \left(kR^2 + kc^2 t\right) dt$$

For one turn$(t \in [0, 2\pi])$

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = 2\pi k R^2 + \frac{kc^2}{2}(2\pi)^2$$

Using the curl, the surface integral is approximated by the ribbon spanned by the helix

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = \int_S (k + k + 2k)\, dA = 4k \cdot (\text{surface area of ribbon})$$

The surface area of the ribbon is

$$A = 2\pi R \cdot (\text{height per turn}) = 2\pi R \cdot c$$

Thus

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = 4k \cdot 2\pi R \cdot c = 8\pi k R c$$

In sum, the numerical values for the macroscopic (surface) flows and microscopic (internal) flows in the stem, as governed by EST, are as follows. For the stem, the surface flow (evaluated as a surface integral) is 2.513N\ppm, while the internal flow (evaluated as a line integral) is 8.053N\ppm. Unlike the flower, the values for surface flow and internal flow differ significantly. This is due to the stem's more complex geometry, which features a three-dimensional helicoidal structure with a helical boundary and a ribbon-like surface. Unlike the constant curl observed in the flower, the curl of the force field $(\nabla \times \mathbf{F} = (k, k, 2k))$ n the stem varies in all three dimensions. This non-uniform curl introduces additional contributions to the surface integral that are not directly proportional to the line integral along the helical path. The helicoidal surface spanned by the path is not planar. Its area depends on the radius of the helix and the rise per turn (c), which increases the surface integral significantly compared to the simpler circular geometry of the flower. The line integral along the helical path includes contributions from the vertical rise (z-component), which are absent in the flat geometry of the flower. These vertical components add substantially to the internal flow, making it larger than the surface flow. Forces and circulation in the stem are not confined to a two-dimensional plane, rather display three-dimensional dynamics that capture complex interactions such as bending, twisting and torsional effects, further contributing to the discrepancy between the surface and internal flows. Therefore, the stem's intricate geometry and three-dimensional dynamics lead to a disparity between surface and internal flows, reflecting the additional factors at play in its structural behavior.

In conclusion,

1) flowers have a circular, symmetric geometry that ensures uniform force distribution and curl. This results in surface and internal flows being equal, as the entire flow field is captured in a flat, two-dimensional setup.
2) In contrast, the stem's helicoidal geometry introduces non-uniform force distributions and additional components such as vertical contributions and a larger surface area. These factors create a larger internal flow compared to the surface flow, as the line integral accounts for three-dimensional effects that the surface integral does not fully capture.

These differences highlight the impact of geometry and force distribution on the interplay between macroscopic circulation and microscopic forces, showcasing the utility of the extended Stokes' theorem in analysing forces and circulation in systems exhibiting spiral dynamics.

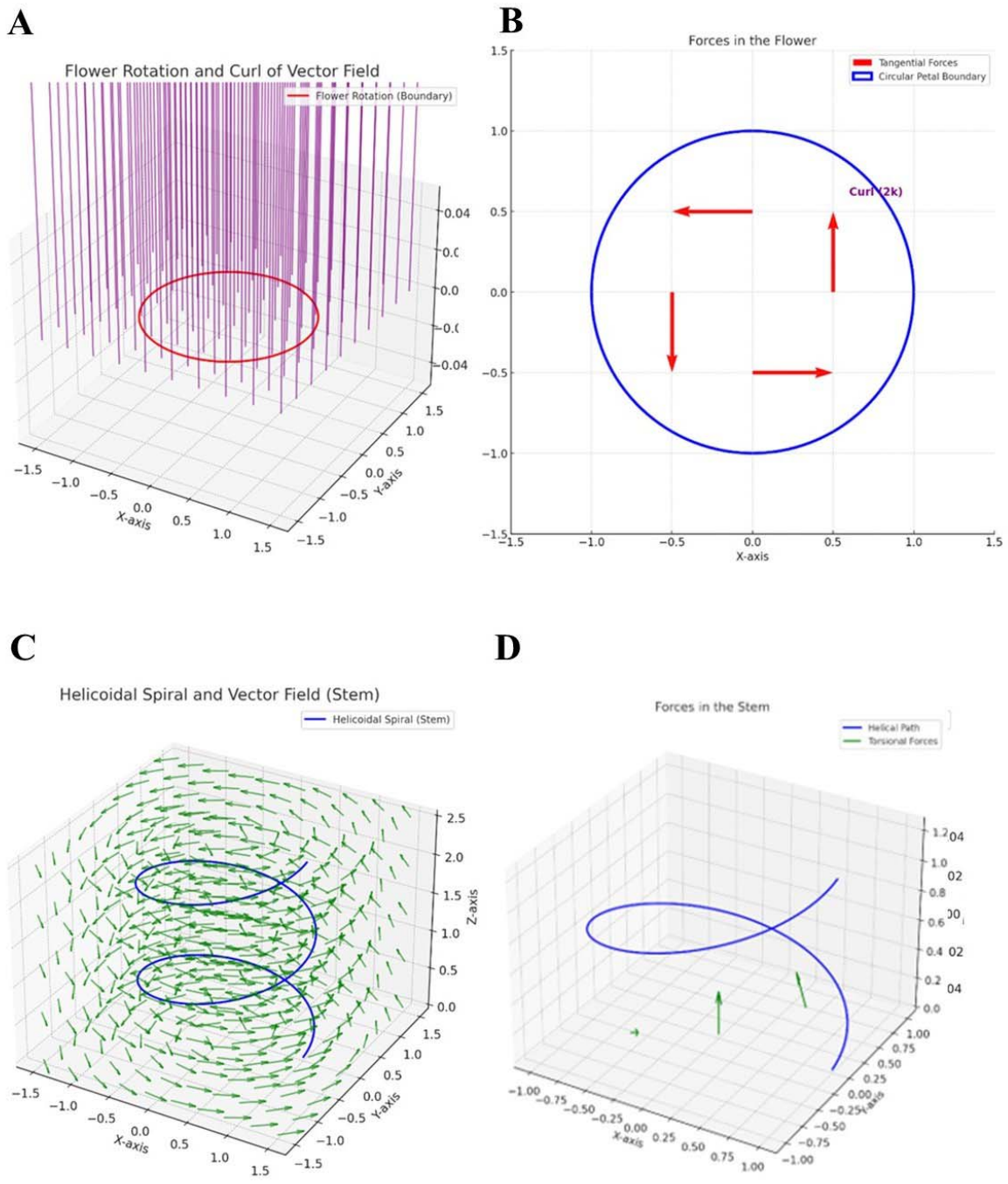

Figure 3. Application of the extended Stoke's theorem to flowers (**Figures 3A-B**) and stems (**Figures 3C-D**) of *Trachelospermum jasminoides*. **Figure 3A**. Diagram illustrating the flower rotation and the curl of vector field. The red circle represents the boundary of the flower petals modeled as a planar region in the z=0 plane. The purple arrows visualize the curl of the vector field, representing the microscopic circulation that contributes to the macroscopic rotation of the flower petals. **Figure 3B**. Diagram illustrating the forces acting on the flower. The circular boundary (blue) represents the edge of the flower petals. Tangential forces (red arrows) act along the edges of the petals, showcasing the influence of external or internal factors. The calculated curl of the vector field is constant at $\nabla \times F = 2k$ (annotated in purple) in the z-direction, indicating uniform rotational stresses throughout the petal boundary. **Figure 3C**. Diagram illustrating the helicoidal spiral of the stem and the vector field. The blue curve depicts the helicoidal path of the stem, while the green arrows represent a circular vector field around the z-axis, illustrating the rotational and translational flow and its interaction with the spiral geometry. **Figure 3D**. Diagram illustrating the forces acting on the stem. The helical path (blue curve) represents the stem's geometry. The torsional forces (green arrows), resulting from a combination of bending and twisting actions, act along the helical structure contributing to internal stress distribution. The curl vector field displays non-uniform rotational stresses with components $\nabla \times F = (k,k,2k)$.

CONCLUSION

Classical theorems such as Green's Theorem (GT) and Stokes' Theorem (ST) have been pivotal in linking local properties of vector fields to their global behavior. GT applies just to two-dimensional regions and closed curves, while ST extends to three-dimensional spaces requiring closed surfaces or boundaries for its application (Green, 1828; Schey, 1997). These theorems, focused on closed-loop circulations, have proven instrumental in analyzing flows and circulations in systems where boundaries are well-defined, such as steady-state circulations in airflow around wings or electromagnetic field behavior in closed circuits (Arfken, 1985; De Villiers, 2006). However, their utility diminishes when applied to open, three-dimensional trajectories like the helicoidal spirals which are frequently encountered in natural and engineered systems.

We suggest a generalization of ST to establish a mathematical framework connecting the line integral along a helicoidal spiral path to the surface integral of the curl of the vector field over a bounded region. By redefining the boundary concept for helicoidal paths, this framework provides a new tool for analyzing macroscopic and microscopic flow dynamics in complex systems. The EST formulation provides novel insights into the interplay between rotational and translational motions, allowing for a deeper understanding of spiral flows in a variety of physical and biological systems. A key advantage of the extended formulation lies in its ability to model a wide range of systems where spiral or helical dynamics are dominant. For instance, the novel framework enables the analysis of DNA supercoiling, bacterial flagella, biomechanical patterns such as the phyllotaxis of plants (Reinhardt and Gola, 2022; Liu et al., 2024), intracardiac spiral flows observed in cardiac cycles (Mulimani et al., 2022) as well as magnetic vortices in superconductors (Sachkou et al., 2019) and rotational dynamics of spiral galaxies (Blaser et al., 2024), where classical methods fail to capture the intricacies of rotational and translational dynamics.

In this paper, EST is applied to two case studies related with *Trachelospermum jasminoides*, namely the forces acting on flower petals and the helical stress distribution within plant stems.

1) For the flower petals, the circular geometry allows for a straightforward application EST, since the tangential forces acting along the petal boundary produce a uniform curl which is proportional to the rotational stresses. The equivalence between the line integral along the petal boundary and the surface integral of the curl over the enclosed disk validates EST's effectiveness for two-dimensional spiral systems. The uniform rotational stresses observed in the petals align well with the mathematical predictions of EST. This provides insights into how forces are distributed within the boundary of the flower, potentially aiding in the study of floral mechanics and growth patterns. EST suggests that microscopic forces acting at the level of the petals contribute to the macroscopic rotational motion observed at the flower's boundary. This could be applied to study the impact of environmental factors like wind on plant structures and to investigate the mechanical interactions between flowers and pollinators during the pollination process. Still, EST effectively simplifies complex calculations by converting a line integral along the flower's boundary into a surface integral over the petal region. This transformation minimizes computational effort while preserving accuracy.

2) In the case of the stem, although the helical geometry of the stem presents a significant challenge for classical mathematical tools, EST effectively simplifies the intricate interplay of forces involved. The torsional and bending forces are captured through the curl of the vector field, which has components in all three dimensions. The equivalence of the surface integral over the helical ribbon region and the line integral along the helical path demonstrates the robustness of EST in handling three-dimensional geometries with open boundaries. The EST capability to connect macroscopic flow patterns with microscopic circulatory forces may have significant implications for understanding the biomechanics of plant growth and structural stability. This relationship can also provide valuable insights for studies on nutrient and water transport within stems, as these processes often involve spiral dynamics.

Certain assumptions and limitations are inherent in our analysis. EST assumes that the involved vector fields and surfaces are continuously differentiable. In real-world biological systems, irregularities and discontinuities in the geometry or force distribution may reduce the accuracy of the analysis. The flower petals are modeled as a perfect circle and the stem as a regular helix. While this simplifies the mathematical analysis of forces in idealized systems, real-world systems often deviate from these idealized shapes. The analysis of irregular geometries or highly dynamic boundaries may still require significant computational effort, particularly for numerical integration of complex surface and line integrals. The tangential and torsional forces are assumed to be uniform across the boundaries. In reality, biological and environmental forces such as wind, gravity and growth pressures are often spatially and temporally variable. Additionally, secondary effects such as shear forces or anisotropic material properties are not incorporated, which could limit the applicability of the results to certain systems. Future work could extend the framework to handle more irregular and biologically realistic geometries, such as asymmetrical petals or non-uniform stem shapes. The analysis of time-varying forces and boundaries, such as those caused by growth or environmental changes, could provide deeper insights into real dynamics. Integrating the extended theorem with experimental data would help validate the theoretical predictions and refine the mathematical models.

In conclusion, the proposed extension to Stokes' Theorem integrates helicoidal paths into circulation analysis, bridging a critical gap and expanding its applicability to open, non-planar trajectories. By redefining boundaries, it simplifies the study of rotational and translational flows, offering a versatile tool for analyzing complex dynamics such as those observed in the flowers and stem of *Trachelospermum jasminoides*.

DECLARATIONS

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.
Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal, and has not been previously published.
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REVIEW

Exploring the influence of water micro assemblies on protein folding, enzyme catalysis and membrane dynamics

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Abstract
Water is central to biological processes not only as a solvent, but also as an agent shaping macromolecular behavior. Insights into water micro assemblies (WMA), defined by transient regions of low-density water (LDW) and high-density water (HDW), have highlighted their potential impact on biological phenomena. LDW, with its structured hydrogen bonding networks and reduced density, stabilizes hydrophobic interfaces and promotes ordered molecular configurations. Conversely, HDW, with its dynamic and flexible nature, facilitates transitions, solute mobility and molecular flexibility. By correlating experimental observations with simulations, we explore the influence of WMA on three key biological processes. In protein folding, LDW may stabilize hydrophobic cores and secondary structures by forming structured exclusion zones, while HDW may introduce dynamic flexibility, promoting the resolution of folding intermediates and leading to dynamic rearrangements. In enzyme catalysis, LDW may form structured hydration shells around active sites stabilizing active sites over longer timescales, while HDW may support substrate access and catalytic flexibility within active sites. In membrane dynamics, LDW may stabilize lipid headgroups, forming structured hydration layers that enhance membrane rigidity and stability, while HDW may ensure the nanosecond-scale flexibility required for vesicle formation and fusion. Across these tree processes, the WMA's energy contributions, timescales and spatial scales align with the forces and dynamics involved, highlighting the role of LDW and HDW in modulating cellular interactions. This perspective holds implications for the design of lab-on-chip devices, advancements in sensor technologies, development of biomimetic membranes for drug delivery, creation of novel therapeutics and deeper understanding of protein misfolding diseases.

Keywords Hydrogen bond dynamics · Molecular interfaces · Solvation effects · Dynamic water clusters · Hydration layers

Introduction

Traditionally regarded as a passive solvent, water's role extends beyond merely providing a medium for biochemical reactions, since its structural and dynamic properties enable active participation in biological phenomena (Dargaville and Hutmacher 2022). The structural heterogeneity of liquid water arises from the continuous assembly and disassembly of hydrogen bonds, forming diverse geometric configurations that reflect water's branched polymeric nature (Shiotari and Sugimoto 2017). These configurations, termed water micro assemblies (WMA), have been extensively studied under extreme conditions, such as supercritical water (Skarmoutsos and Samios 2016), high-pressure crystals in supercooled water (Kim et al. 2009; Lin et al. 2018) and frozen water confined within nanometric slit pores (Koga et al. 2000) or nanochannels formed by cubic crystalline phases (Das et al. 2019). However, relatively little attention has been given to the microstructure of liquid water at ambient temperature and pressure. Under standard conditions, each water molecule forms up to four hydrogen bonds, creating a tetrahedral structure (Fanetti et al. 2014; Liu et al. 2017; Milovanović et al. 2020). Fluctuations in hydrogen bond numbers, ranging from two to six, result in molecules being either "loosely" or "tightly" bound (Thaomola et al. 2012). Liquid water has been described as a dynamic mixture of pentagonal and hexagonal rings (Shiotari and Sugimoto 2017; Formanek and Martelli 2020), of tetrahedral structures and of ring-and-chain-like assemblies (Liu et al. 2017). These configurations form densely connected spherical

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cores of approximately 140 water molecules, surrounded by fuzzy zones of ~ 1800 loosely connected molecules (Liu et al. 2017). Strong hydrogen bonds create multibranched polymers of about 150 molecules per chain (Naserifar and Goddard 2019), while density fluctuations form empty spaces resembling spherical or fractal-like voids (Ansari et al. 2018). Other WMA descriptions include a giant cluster percolating the system (dos Santos et al. 2004) and a linear, chain-like structure dominating the tree-like arrangement of the largest cluster (Jedlovszky et al. 2007).

The two-liquid scenario argues that liquid water comprises two competing molecular structures: low-density water (LDW) and high-density water (HDW) (Table 1). Although frequently observed under extreme conditions, these structures are also found under ambient conditions (Cheng et al. 2019). LDW features ordered gaps between molecular shells (de Oca et al. 2019), while HDW is associated with high-entropy, unstructured states. LDW consists of fused dodecahedra acting as templates for tetrahedral fluctuations, while HDW forms chain-like structures (Camisasca et al. 2019). LDW patches exhibit greater tetrahedrality and connectivity than HDW patches (Ansari et al. 2018; Faccio et al. 2022).

We describe how LDW and HDW may significantly influence biological processes by creating localized environments with specific physical and chemical properties. LDW regions, characterized by ordered hydrogen bonding networks, lower density and reduced entropy, may stabilize structural integrity near hydrophobic interfaces. Conversely, HDW regions, with higher density and entropy and weaker hydrogen bonds, may facilitate conformational transitions, enhance molecular mobility and disrupt ordered structures. This interplay likely impacts processes such as protein folding, enzyme catalysis and DNA and RNA dynamics. Their physical dimensions make WMA compatible with interacting with biological processes and capable of influencing the behavior of biological macromolecules. Water molecules (~ 2 Å) form LDW and HDW patches ranging from 0.3 to 2 nm (Ansari et al. 2018). Near ambient conditions, LDW has a density of 0.78 g/cm^3, while HDW reaches 1.08 g/cm^3 (Nomura et al. 2017). Although noncovalent bonds in liquid water at room temperature last under 200 femtoseconds (Lodish et al. 2000; Bakó et al. 2013; Naserifar and Goddard 2019), LDW persists for nearly half a second at 160 K (Lin et al. 2018). Despite their brief lifetimes (Camisasca et al. 2019), LDW and HDW create localized density changes that may affect environmental dynamics and drive macroscopic chemical and biophysical processes (Fanetti et al. 2014; Skarmoutsos and Samios 2016; Faccio et al. 2022). Also, we argue that percolation theory may play a pivotal role in influencing biochemical processes driven by WMA. In the context of water percolation, LDW may contribute to long-range connectivity within hydration layers, while HDW may provide localized flexibility.

This study explores the influence of WMA on biological phenomena by integrating experimental observations with theoretical insights. By focusing on key processes such as protein folding, enzyme catalysis and membrane dynamics, we aim to establish a framework that underscores water's active role in shaping the behavior of biological macromolecules. Examining the formation, dynamics and interplay of LDW and HDW, the study provides detailed analyses of their impacts, supported by molecular dynamics simulations and theoretical models.

Theoretical effects of water micro assemblies on biological phenomena

The concept of water micro assemblies (WMA), as discussed in the previous chapter, provides a compelling theoretical framework for understanding physical and dynamic processes (Laage et al. 2017). Below are some potential applications and behaviors explained by WMA:

(1) **Protein folding and stability**. The dynamic interplay between HDW and LDW regions may influence protein folding pathways. Localized density variations may

Table 1 Differences between low-density water (LDW) and high-density water (HDW)

	Low-density water (LDW)	High-density water (HDW)
Structure	Ordered hydrogen bonding networks	Disrupted hydrogen bonding networks
Density	Lower (~ 0.78 g/cm^3)	Higher (~ 1.08 g/cm^3)
Entropy	Reduced (more ordered)	Increased (more disordered)
Hydrophobicity	Stabilizes hydrophobic interfaces and molecular cores	Disrupts ordered zones, allowing transitions
Hydrogen Bonding	Strong and extended networks	Flexible and transient
Mobility	Lower molecular mobility (structured)	Higher molecular mobility (dynamic)
Biological Impact	Stabilizes protein folding, secondary structures, lipid headgroups	Enhances transitions, substrate turnover, molecular flexibility
Lifespan	Longer (~ 200 fs to 0.5 s in specific conditions)	Shorter and highly dynamic

create microenvironments that stabilize or destabilize intermediate folding states.

(2) **Enzyme catalysis**. WMA may modulate catalytic efficiency by restructuring local density and hydrogen-bonding networks near enzyme active sites, enhancing reaction kinetics.

(3) **Membrane dynamics**. Water micro assemblies may impact the stability and interactions of lipid bilayers, offering insights into phenomena such as lipid rafts and transient membrane pore formation.

(1) **Biological folding and protein stability**. Proteins rely on their interactions with water to achieve and maintain their functional structures (Sen and Voorheis 2014; Schiebel et al. 2018). The interplay of various forces during folding, such as hydrophobic interactions, hydrogen bonding, electrostatic interactions, van der Waals forces and steric constraints, highlights the central role of water in these processes (Bellissent-Funel et al. 2016; Phan-Xuan et al. 2020).

Hydrophobic interactions are a key driving force in macromolecular folding, as nonpolar residues cluster internally to avoid water (Fogarty and Laage 2014; Ye et al. 2024). LDW regions, with their reduced density and structured hydrogen bonding network, may facilitate this process by forming ordered exclusion zones around hydrophobic groups, stabilizing the burial of nonpolar residues. Meanwhile, HDW regions, less structured and more dynamic, may support the transient exposure of hydrophobic residues during early folding stages. Hydrogen bonding is another critical force which stabilizes secondary structures such as α-helices and β-sheets. HDW, due to its higher entropy and looser hydrogen bonds, may disrupt weaker hydrogen bonds in unfolding scenarios, whereas LDW may enhance hydrogen bond stability during folding.

Electrostatic interactions, such as salt bridges and charged residue pairings, are crucial for directing protein folding pathways and stabilizing the final folded structure. The local density variations between LDW and HDW may influence the dielectric constant of water, modulating electrostatic interaction strength. LDW, by reducing shielding effects, may enhance charge–charge attractions in localized regions, promoting stability. Van der Waals forces, though weaker and distance dependent, are crucial for stabilizing tightly packed molecular cores (Li et al. 2018). The structured nature of LDW may enhance these forces by increasing the local organization of interacting molecules within protein interiors. Steric constraints further limit the conformational space accessible to macromolecules, as backbone torsions and side-chain interactions impose structural restrictions. LDW's ordered environment may help resolve steric clashes, guiding molecules toward favorable conformations, while HDW may provide flexibility for conformational sampling in partially unfolded states.

The involvement of WMA in biological folding becomes plausible when considering their energy, timescale and spatial dimensions. The energy scales of folding forces align with the contributions of LDW and HDW transitions (Table 2), suggesting that WMA may significantly influence folding energetics. The interplay between LDW and HDW may fine-tune the folding energy landscape, balancing stability and flexibility across the conformational space to optimize transitions (Fig. 1). The timescales of WMA also align well with the dynamic requirements of folding processes. Protein folding occurs over milliseconds to seconds for small, single-domain proteins, while LDW and HDW regions exhibit lifetimes ranging from ~200 fs to 0.5 s. This temporal overlap allows micro assemblies to influence both the rapid early stages of folding and the slower stabilization of intermediate or final structures. Spatially, the sizes of micro assemblies, ranging from ~0.3 to 2 nm, are sufficient to interact with folding nuclei (typically ~5 to 10 Å) and influence tertiary and quaternary structural organization.

Experimental and theoretical studies provide evidence for the role of WMA in biological folding and stability. Hydration dynamics reveal how LDW and HDW influence solvation shell behavior (Camisasca et al. 2023). These studies highlight the ability of LDW to form structured, ice-like networks around biomolecules, stabilizing their conformations, while HDW introduces dynamism required for conformational transitions. Evidence from folding pathways, particularly in cold denaturation studies, further supports the relevance of structured water (Taricska et al. 2019). Cold denaturation, where proteins unfold at low temperatures, has been linked to the stabilization of unfolded states by structured hydration layers, consistent with the properties of LDW-HDW transitions (Espinosa et al. 2019).

In sum, WMA may represent a feasible and energetically relevant mechanism for modulating biological folding and stability. Their ability to dynamically adjust local density, hydrogen bonding and dielectric properties makes them a critical, yet underexplored, factor in biophysical processes. LDW stabilizes hydrophobic interactions and secondary structures, while HDW enables dynamic transitions and flexibility. These complementary roles, supported by energy and timescale compatibility, suggest that WMA are integral to the folding process and its regulation.

(2) **Enzyme catalysis**. Enzymatic reactions are governed by various physical forces, all of which align with the unique properties of WMA (Adamczyk et al. 2014; Fogarty and Laage 2014; Zsidó and Hetényi 2021). Electrostatic effects are critical in enzyme catalysis, as charged residues and substrates interact to stabilize the

Table 2 Functional roles of water micro assemblies in protein folding processes

Force type	Energy contribution (kcal/mol)	Role in protein folding	Impact of micro assemblies	Microaggregate energy contribution (kcal/mol)
Electrostatic interactions	~ 1–3	Guide charged residue interactions and folding pathways	LDW enhances electrostatic interactions by lowering dielectric constant; HDW facilitates charge redistribution	LDW: ~ 1–3, HDW: ~ 1–3
Hydrogen bonding	~ 1–5	Stabilizes secondary structures (e.g., α-helices, β-sheets)	LDW strengthens hydrogen bonds, stabilizing folding intermediates; HDW allows flexibility for conformational sampling	LDW: ~ 1–3, HDW: ~ 1–3
Hydrophobic interactions	~ 0.5–1 per residue	Drive hydrophobic core formation	LDW creates structured exclusion zones around hydrophobic residues; HDW transiently disrupts zones to allow folding progression	LDW: ~ 1–3, HDW: ~ 1–3
Van der Waals forces	~ 0.1–0.3 per atom pair	Stabilize tightly packed core structures	LDW enhances alignment and packing in the hydrophobic core; HDW supports transient adjustments during folding	LDW: ~ 0.5–1, HDW: ~ 0.5–1
Solvation dynamics	Variable	Modulate folding energy landscape	LDW-HDW transitions fine-tune hydration layers, stabilizing intermediates and guiding the folding process	LDW: ~ 1–3, HDW: ~ 1–3

transition state and orient substrates within the active site. LDW, with its lower dielectric constant, may enhance these interactions by reducing charge screening, thereby increasing the strength of electrostatic interactions. HDW, due to its flexible hydrogen bonding and higher local entropy, may assist in charge redistribution during catalytic transitions, helping enzymes overcome energy barriers associated with electron transfer or polarization. This dual role enables WMA to modulate the precise electrostatic environment required for catalysis.

Hydrophobic interactions contribute to substrate stabilization by forming nonpolar pockets within enzyme active sites (Kurkal et al. 2005). These hydrophobic pockets exclude bulk water, providing a favorable microenvironment for substrate binding. LDW regions may amplify this effect by creating structured exclusion zones around nonpolar residues, reinforcing the hydrophobic pocket's integrity. On the other hand, HDW, with its dynamic nature and reduced local density, may transiently disrupt these zones, allowing substrate access to the active site. This balance may ensure that the enzyme maintains a stable yet flexible environment, optimizing both substrate accommodation and turnover. Hydrogen bonding is another cornerstone of enzyme catalysis, stabilizing intermediates and transition states while maintaining precise catalytic geometry. LDW regions, with their stable and extended hydrogen bonding networks, may strengthen these interactions, particularly with polar substrates or intermediates. Conversely, HDW, characterized by dynamic and flexible hydrogen bonding, may facilitate transitions between intermediates and supports efficient product release.

Van der Waals forces play a significant role in substrate alignment and transient state stabilization within enzyme active sites. LDW regions, with their structured local environments, may enhance molecular alignment and optimize these weak interactions. HDW, on the other hand, may introduce the required dynamics to ensure that transient interactions remain flexible, allowing enzymes to adapt their active site to different catalytic steps. Dynamic solvation effects, wherein fluctuations in the solvent modulate energy barriers and facilitate substrate-product exchange, are intrinsically linked to LDW–HDW transitions. These transitions may enable WMA to fine-tune solvation dynamics at each step of the catalytic cycle. LDW regions stabilize specific steps, such as substrate binding or transition state stabilization, while HDW regions introduce dynamic flexibility to promote intermediate transitions and product release. This adaptability may be crucial for the efficiency of enzymatic reactions.

The alignment of WMA energetics with enzymatic processes further supports their potential to influence enzyme

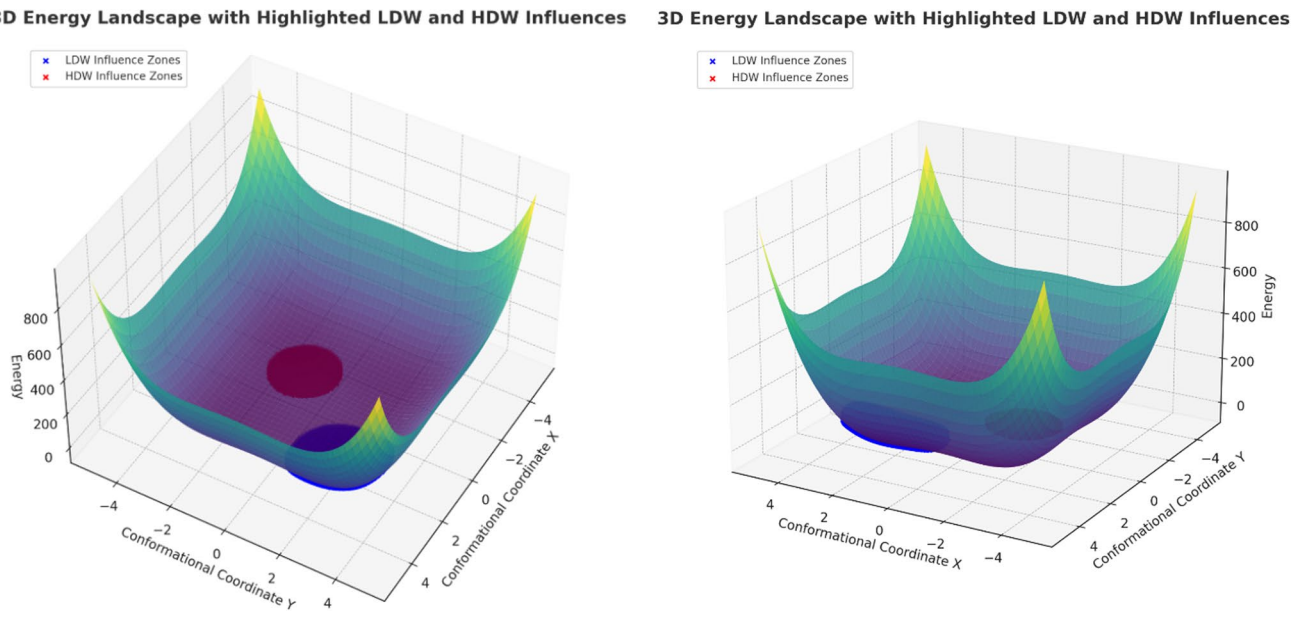

Fig. 1 Theoretical 3D visualization of the energy landscape shaped by water microaggregates, illustrating the combined effects of LDW and HDW. LDW zones, depicted in blue, stabilize the energy landscape by forming depressions near local minima, while HDW zones, represented in red, enhance flexibility and facilitate dynamic transitions near transition states

catalysis (Table 3). The timescales of enzymatic processes, which typically range from microseconds to milliseconds, align well with the lifetimes of LDW and HDW regions, which span from 200 fs to 0.5 s. For instance, LDW regions may stabilize critical transition states over microsecond timescales, while HDW regions provide the rapid flexibility needed for intermediate transitions on sub-nanosecond timescales. Spatially, enzyme active sites are typically 1–10 nm in size, a scale well suited for interactions with micro assemblies, which range from 0.3 to 2 nm. This spatial compatibility may allow LDW and HDW regions to directly influence active site dynamics, stabilizing critical regions and facilitating the movement of substrates and products. LDW may form around hydrophobic residues in the active

Table 3 Functional roles of water micro assemblies in enzyme catalysis

Force type	Energy contribution (kcal/mol)	Role in catalysis	Impact of micro assemblies	Microaggregate energy contribution (kcal/mol)
Electrostatic interactions	~ 1–3	Stabilize transition states	LDW enhances interactions by lowering the dielectric constant; HDW facilitates charge redistribution	LDW: ~ 1–3, HDW: ~ 1–3
Hydrophobic interactions	~ 0.5–1 per residue	Stabilize substrates in pockets	LDW promotes exclusion zones; HDW transiently opens access pathways	LDW: ~ 1–3, HDW: ~ 1–3
Hydrogen Bonding	~ 1–5	Stabilizes intermediates	LDW strengthens bonds; HDW enables dynamic flexibility for transition states	LDW: ~ 1–3, HDW: ~ 1–3
Van der Waals Forces	~ 0.1–0.3 per atom pair	Align substrates	LDW improves alignment precision; HDW supports transient substrate dynamics	LDW: ~ 0.5–1, HDW: ~ 0.5–1
Solvation Dynamics	Variable	Modulate energy barriers	LDW-HDW transitions fine-tune solvation dynamics during different catalytic stages	LDW: ~ 1–3, HDW: ~ 1–3

site, enhancing substrate stability, while HDW may transiently occupy solvent-accessible areas.

Experimental and theoretical evidence supports the role of WMA in enzyme catalysis. Structured water layers, as observed through solvent isotope effects and hydration studies, correlate with enhanced catalytic rates, aligning with the behavior of LDW (Kurkal-Siebert et al. 2006). Cryo-EM and X-ray crystallography further reinforce this perspective by revealing ordered water clusters near enzyme active sites (Brogan et al. 2014). These clusters, consistent with LDW properties, may play a crucial role in stabilizing catalytic residues. Theoretical studies add depth to this understanding. Molecular dynamics simulations demonstrate that water clusters near active sites exhibit high sensitivity to changes in hydrogen bonding, mirroring the dynamic interplay between LDW and HDW. These transitions highlight the adaptability of WMA in responding to the demands of enzymatic processes, such as stabilizing intermediates or facilitating substrate-product transitions.

The case of chymotrypsin illustrates how WMA may influence enzymatic function. Chymotrypsin, a serine protease, relies on a catalytic triad comprising serine, histidine and aspartate residues for its nucleophilic attack mechanism (Jing et al. 2002). This process is supported by a structured hydration layer, a hallmark of LDW behavior (Kozlova et al. 1999; Eckstein et al. 2002). LDW may stabilize the catalytic triad by strengthening hydrogen bonding, ensuring the alignment and reactivity of these residues. Conversely, HDW may facilitate rapid proton transfer and substrate turnover by modulating local water density, providing the necessary flexibility for catalytic efficiency.

In sum, WMA provide a viable and energetically significant mechanism for influencing enzyme catalysis. Their ability to dynamically adjust hydrogen bonding, hydrophobic interactions, local density and solvation properties makes them possible contributors to catalytic processes.

(3) **Membrane dynamics**. Biological membranes rely heavily on interactions with surrounding water for their structural integrity, fluidity and functionality (Higgins et al. 2006; Wood et al. 2007; Chattopadhyay et al. 2021). The interplay between LDW and HDW regions in the aqueous environment may provide insights into how water influences processes such as lipid organization, protein–membrane interactions and membrane dynamics. Electrostatic interactions are essential for membrane dynamics in stabilizing the polar headgroups of lipids and mediating interactions with charged proteins. LDW regions, with their lower dielectric constant and ordered hydrogen bonding, may enhance membrane electrostatic stabilization by reducing charge screening and strengthening headgroup interactions. HDW regions, on the other hand, may facilitate rapid ion exchange and dynamic interactions between polar lipids and surrounding ions or proteins. This dual behavior ensures that membranes maintain stability while allowing flexibility for dynamic processes.

Hydrophobic interactions are another crucial component of membrane dynamics, driving the self-assembly of lipid bilayers and maintaining their structural integrity (Cheng et al. 2013; Fisette et al. 2016). Nonpolar lipid tails cluster together to minimize water exposure, a process which may be amplified by LDW regions forming structured exclusion zones around hydrophobic regions. Conversely, HDW regions may transiently disrupt these zones, allowing for the lateral mobility of lipids and enabling dynamic rearrangements critical for processes like fusion, fission and protein insertion. Still, hydrogen bonding plays a significant role in maintaining the hydration shells of lipid headgroups and facilitating interactions between the membrane and water-soluble molecules. LDW regions, with their stable hydrogen bonding networks, may provide consistent hydration to polar headgroups, enhancing membrane stability. In contrast, HDW regions, with their dynamic hydrogen bonding, may support processes requiring flexibility, such as lipid flip-flop, membrane deformation or protein–membrane interactions. Van der Waals forces are crucial for lipid packing and membrane stability. LDW regions, by organizing water molecules near the lipid interface, may enhance molecular packing and stabilize membrane structure. Meanwhile, HDW regions may contribute to the dynamic rearrangement of lipids, ensuring the bilayer remains fluid and adaptable under varying conditions.

The transition between different membrane phases, such as the liquid-ordered and liquid-disordered states, provides a case study in micro assembly influence. LDW regions may stabilize the liquid-ordered phase by enhancing hydrogen bonding and hydrophobic stabilization, while HDW regions may support the flexibility needed for transitions to the liquid-disordered phase, facilitating processes such as membrane protein activation or lipid raft formation. Dynamic solvation effects, where water molecules in the hydration shell modulate energy barriers and lipid dynamics, may be influenced by LDW–HDW transitions. LDW regions may stabilize bilayer formation by providing structured hydration to lipid headgroups, while HDW regions may allow rapid water exchange and flexibility, supporting membrane-associated processes such as vesicle formation and membrane protein function.

The ability of WMA to influence membrane dynamics is reinforced by their energetic compatibility (Table 4), suggesting that WMA can meaningfully modulate the forces driving membrane behavior. The timescales of membrane dynamics, ranging from nanoseconds for lipid

Table 4 Functional roles of water micro assemblies in membrane dynamics

Force type	Energy contribution (kcal/mol)	Role in membrane dynamics	Impact of micro assemblies	Microaggregate energy contribution (kcal/mol)
Electrostatic interactions	~ 1–3	Stabilize lipid headgroups and protein interactions	LDW enhances headgroup stabilization by lowering dielectric constant; HDW facilitates dynamic ion exchange	LDW: ~ 1–3, HDW: ~ 1–3
Hydrogen bonding	~ 1–5	Stabilizes hydration shells around lipid headgroups	LDW strengthens hydrogen bonds around headgroups; HDW supports rapid rearrangements during membrane remodeling	LDW: ~ 1–3, HDW: ~ 1–3
Hydrophobic interactions	~ 0.5–1 per lipid	Drive lipid tail clustering and bilayer stability	LDW forms structured exclusion zones around lipid tails; HDW transiently disrupts zones for fluidity	LDW: ~ 1–3, HDW: ~ 1–3
Van der Waals forces	~ 0.1–0.3 per atom pair	Stabilize lipid packing	LDW improves packing by structuring water near lipid interfaces; HDW supports lateral diffusion	LDW: ~ 0.5–1, HDW: ~ 0.5–1
Solvation dynamics	Variable	Modulate lipid mobility and protein incorporation	LDW–HDW transitions adjust hydration shells to support vesicle formation, fusion and protein binding	LDW: ~ 1–3, HDW: ~ 1–3

diffusion to milliseconds for processes like vesicle budding, align well with LDW and HDW lifetimes. This temporal compatibility may allow WMA to influence both rapid lipid rearrangements and slower membrane remodeling events. Spatially, the thickness of the lipid bilayer (~ 4–6 nm) and the hydration shell (~ 0.3–1 nm) are well matched to the size of LDW and HDW regions, ensuring that WMA may interact with membrane components and their surrounding environment.

Experimental evidence supports the involvement of WMA in membrane dynamics. Neutron scattering and cryo-EM studies have revealed ordered water layers around lipid headgroups, consistent with LDW properties (Frölich et al. 2009). Ultrafast spectroscopy and NMR studies further demonstrate the dynamic nature of hydration layers, aligning with the behavior of HDW (Zigmantas et al. 2022; Lorenz-Ochoa et al. 2023). Molecular dynamics simulations provide additional theoretical support, showing structured and dynamic water regions interacting with lipid bilayers and modulating membrane properties.

In sum, WMA provides a plausible mechanism for influencing membrane dynamics. Their ability to modulate hydrogen bonding, electrostatic interactions and solvation dynamics positions them as critical contributors to the stability and functionality of biological membranes.

Percolation of water micro assemblies and its role in biological systems

Short-lived WMA can form extensive networks that significantly influence average flow properties. The emergence of large-scale connectivity within high-density water assemblies may facilitate percolation through three-dimensional hydrogen-bonded water lattices (Timonin 2018). Evidence supports the occurrence of percolation in water (Bernabei & Ricci 2008; Strong et al. 2018). For instance, percolation transitions in hydrogen bond networks have been observed in supercritical water, especially at high molecular densities (Jedlovszky et al. 2007). These transitions follow a universal power law, with percolation occurring when the fractal dimension of the largest cluster approaches 2.53 (Galam & Mauger 1996; Jedlovszky et al. 2007). A percolating network requires approximately 40% of possible hydrogen bonds to be intact. Simulations reveal that initially disconnected clusters coalesce at critical cutoff values, forming large, space-filling networks with minimal disconnected fragments (Geiger 1979). Given that 18.01528 g of water contain $6.02214076 \times 10^{23}$ water molecules, the number of percolating molecules is immense, with a system-spanning cluster emerging at a probability of 0.65 in liquid water (Oleinikova et al. 2002).

Percolation significantly influences flow dynamics by creating transient obstacles. Hydrogen bond energies (1–5 kcal/mol) are much lower than those needed to break covalent bonds (~ 110 kcal/mol) (Lodish et al. 2000). This means that the average molecular kinetic energy at room temperature (~ 0.6 kcal/mol) is sufficient to disrupt noncovalent bonds, allowing hydrogen bond-induced barriers to influence liquid water flow (Lodish et al. 2000).

Percolation theory offers insights into how WMA influence hydrogen bond networks, phase transitions and transport phenomena. We propose the following theoretical framework:

(1) **LDW and percolation clusters**. LDW forms well-ordered hydrogen bond structures, facilitating connectivity and the formation of percolation clusters. Conversely, HDW, with its disrupted hydrogen bonding, acts as a barrier to connectivity.
(2) **Phase transition dynamics**. At lower temperatures, LDW regions expand, forming nuclei essential for freezing, while HDW fragments connectivity in supercooled water. In supercritical water, HDW dominates, leading to high diffusivity and low connectivity. As the system transitions back to the liquid phase, LDW re-establishes percolation, restoring cohesion and reducing diffusivity.
(3) **Diffusion and transport**. Diffusion in liquid water depends on cooperative molecular movement within hydrogen bond networks. LDW forms stable pathways for molecular and ion transport, while HDW introduces transient disruptions. At the percolation threshold, LDW clusters span the system, enabling continuous transport pathways. Proton transport, for instance, relies on rapid hydrogen bond reorganization. LDW maintains stable pathways for proton hopping, whereas HDW slows the process due to structural disorder.
(4) **Dynamic percolation and temperature effects**. Dynamic percolation in water is characterized by the continuous breaking and reforming of hydrogen bonds. At lower temperatures, LDW dominates, forming long-lived percolation clusters, whereas at higher temperatures, HDW fragments the networks, increasing molecular mobility.
(5) **Constrained percolation in confined environments**. In confined environments, such as nanoporous materials or near biomolecular surfaces, water may exhibit constrained percolation. LDW forms ordered layers near hydrophilic interfaces, providing stability, while HDW dominates bulk regions or hydrophobic zones, introducing flexibility and disorder.

In sum, the WMA theoretical framework highlights the fundamental role of percolation in biological systems and provides a basis for further exploration of LDW and HDW's influence on molecular and macroscopic phenomena. Future integration of percolation models with experimental and computational approaches will help unravel the complexity of these dynamic water networks.

Conclusions

Liquid water exhibits intrinsic chemical inhomogeneity, manifesting as a dynamic three-dimensional network characterized by microscopic density fluctuations and structural variations. Water, far beyond being a passive solvent, plays an active and multifaceted role in driving and modulating biological phenomena. This study explored the concept of WMA, characterized by LDW and HDW regions, as dynamic contributors to various molecular and cellular processes. Through their distinct physical and chemical properties, WMA offer a framework to better understand the behavior of water at the nanoscale and its influence on key biological processes. LDW, defined by structured hydrogen bond networks, lower density and high coherence, may stabilize hydrophobic interactions, hydrogen bonding and molecular order. Conversely, HDW, with its dynamic, higher-density and entropy-driven properties, may facilitate flexibility, conformational sampling and rapid transitions. These dual roles enable WMA to act as adaptable mediators across a wide range of biological phenomena, optimizing stability and functionality under varying conditions. Across protein folding, enzyme catalysis and membrane dynamics, the energy contributions, timescales and spatial scales of WMA align with the forces and dynamics involved, underscoring the critical role of LDW and HDW transitions in modulating dynamical interactions in the cellular milieu.

While the concept of WMA is still emerging, their influence may extend beyond understanding fundamental biological processes. WMA may have significant implications across experimental, technological and pathological contexts, spanning multiple disciplines, including molecular biology, fluid dynamics and materials science.

In microfluidics and nanofluidics, understanding the dynamic behavior of these micro assemblies can lead to enhanced control of water within confined geometries, a critical factor for designing lab-on-chip devices that require precise manipulation of fluid dynamics at the microscale. The ability to induce or manipulate LDW and HDW regions artificially opens the door to creating targeted micro-vortices or density variations. Such capabilities may pave the way for novel sensor technologies where the localized structuring of water affects sensitivity and detection thresholds or for advanced turbulence control mechanisms in engineering systems. Also, artificial catalysts may benefit from mimicking

LDW-HDW transitions, improving efficiency by incorporating water-like dynamics into synthetic systems.

In biomedical and pharmaceutical contexts, understanding WMA can inform the design of drugs and therapeutics that leverage hydration dynamics. Mimicking the properties of WMA may inspire the development of biomimetic systems such as responsive hydrogels or biomimetic membranes with tailored properties for drug delivery. In drug design, targeting water dynamics within active sites may optimize the specificity and efficacy of ligand binding and enzyme inhibitors, enhancing drug efficacy. Our study also highlights the importance of exploring the role of WMA in complex and confined environments, such as within cells or in biomolecular assemblies. In these scenarios, water's behavior deviates significantly from that of bulk water, with hydration layers and confined spaces amplifying the influence of micro assemblies. Understanding these effects may reveal new principles underlying cellular organization, molecular recognition and signal transduction.

Additionally, understanding water's role in pathological conditions, such as protein misfolding diseases, cancer or neurodegeneration, may open new avenues for therapeutic intervention. Abnormal interactions between LDW and HDW may contribute to the pathological protein aggregation observed in lipid storage disorders and neurodegenerative diseases such as Alzheimer's or Parkinson's disease (Polychronidou et al. 2020; Padilla-Godínez et al. 2021). Similarly, variations in water density may explain some of the unique physical and biochemical properties of tumor microenvironments (He et al. 2022). In cancer, localized turbulence or non-uniform water structuring in the interstitial fluid may influence nutrient transport, cellular communication and drug delivery effectiveness.

Despite significant advances, challenges persist in fully understanding the role of WMA in biological phenomena. The transient and highly dynamic nature of LDW and HDW makes their phase spaces difficult to explore, leading to the upsetting concept of "water's no-man's land" (Lin et al. 2018). Despite that liquid water can be tackled in terms of an evolving, fluctuating and branched polymer (Naserifar and Goddard 2019), a full understanding of its dynamical and structural properties is still lacking (Fanetti et al. 2014) due to technical difficulties in gaining experimental information on ultrafast interplay (Tamtögl et al. 2020). The heterogeneity of water is usually approached through simulation of molecular dynamics, such as, e.g., conventional QM/MM scheme and ONIOM-XS methods (Thaomola et al. 2012), second-order Møller–Plesset perturbation theory (Liu et al. 2017), quantum Monte Carlo, non-canonical coupled cluster theory (Al-Hamdani and Tkatchenko 2019), modified Louvain algorithm of graph community (Gao et al. 2021), topological local (clustering coefficient, path length and degree distribution) and global (spectral analysis) properties (dos Santos et al. 2004; Carreras et al. 2008; Steinberg et al. 2019), persistent homology methods (Wu 2020). These methods operate at different temporal and spatial resolutions, necessitating further integration for a more comprehensive understanding. Weak, non-covalent interactions have been experimentally studied just in small molecular complexes, falling short of the macroscopic structural properties that are typical of complex soft materials such as, e.g., supramolecular aggregates (Al-Hamdani and Tkatchenko, 2019). To make things more complicated, totally different networks topologies and physical interpretations have been provided, depending on how rings have been counted (Das et al. 2019; Formanek and Martelli 2020).

It remains uncertain whether liquid water exhibits randomness or long-range interactions. Dos Santos et al. (2004) proposed that the water network at room temperature resembles a Poisson distribution, indicative of randomness. However, other studies present evidence of medium- to long-range order (Faccio et al. 2022). Tamtögl et al. (2020) observed correlated motion at the surface of a topological insulator, contrasting with Brownian motion, while Ansari et al. (2018) and Gao et al. (2021) reported collective translational fluctuations in hydrogen-bonded water clusters. Percolation models face challenges, such as the inability to determine the percolation threshold based solely on cluster size distribution (Jedlovszky et al. 2007). Moreover, environmental factors, including temperature, pressure and solute concentration may influence the balance between LDW and HDW. For example, lower temperatures correspond to stronger hydrogen bond interactions. Upon melting, increases in temperature result in a rapid decrease in the average number of assemblies (Gao et al. 2021) and a broader ring size distribution (Bakó et al., 2013; Naserifar and Goddard 2019). Consequently, microscopic assemblies in water become difficult to distinguish beyond the isochore end point of 292 K (Nomura et al., 2017).

Future research should focus on developing more refined experimental and computational methods to study WMA and their interactions with biomolecules. Experimentally, combining time-resolved methods with spatially resolved imaging techniques may bridge the gap between molecular dynamics and observable biological outcomes.

In conclusion, WMA may represent a transformative perspective on the active role of water in biological phenomena. By bridging the gap between molecular-scale dynamics and macroscopic behavior, WMA may provide a unifying framework for understanding how water shapes biomolecular processes. LDW and HDW, through their complementary properties, may influence stability, flexibility and functionality across diverse biological systems. As research in this field advances, the potential applications in health, technology and materials science are vast, underscoring

the importance of continued exploration into the dynamic Q8world of WMA.

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Declarations

Conflict of interest The author does not have any known or potential conflict of interest including any financial, personal or other relationships with other people or organizations within 3 years of beginning the submitted work that may inappropriately influence, or be perceived to influence, their work.

Ethical approval and consent to participate This research does not contain any studies with human participants or animals performed by the author.

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Designing AI Systems with Kantian Cognitive Structures

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Designing AI Systems with Kantian Cognitive Structures

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ABSTRACT

We propose a framework for artificial intelligence design grounded in Immanuel Kant's transcendental philosophy, particularly his theory of cognition as presented in the *Critique of Pure Reason*. We argue that Kant's model of the mind—structured by a priori forms of intuition and categories of understanding— provides a valuable conceptual foundation for designing novel cognitive architectures capable of structured, unified and meaningful experience. Drawing from philosophical analysis, conceptual mapping, classical cognitive functions, architectural computational modeling and contemporary deep learning, we translate key Kantian elements into modular components of AI systems, namely, 1) spatial-temporal frameworks (forms of intuition), 2) logical-structural priors (categories), 3) a synthetic mechanism for integrating perception/concept and 4) a self-model representing the unity of apperception. Experimental simulations comparing unstructured models with Kantian-structured architectures demonstrate that the latter consistently support coherent perceptual integration, stable self-representation across time and principled, norm-governed reasoning. We argue that a Kantian-inspired structure could inform the design of multi-modal, self-coherent systems capable of maintaining consistent internal world models and interpreting input through structured layers. Emphasis is placed on the system's capacity to organize experience rather than merely accumulating data, distinguishing it from prevailing empirical or data-driven approaches. Although the model remains limited in its current form as a theoretical construct, it has the potential to support more robust, self-consistent and ethically aligned AI behaviour by embedding formal cognitive constraints directly into the system's architectural design.

Keywords: selfhood; symbolic reasoning; autonomous systems; cognitive modeling; epistemic structure

INTRODUCTION

Current advancements in artificial intelligence, particularly within deep learning and neural architecture, have yielded highly capable systems for pattern recognition, language processing and multimodal representation. These systems have demonstrated remarkable performance in domain-specific tasks, from visual object classification to predictive language modeling and embodied sensorimotor control. However, these models often lack internal coherence, interpretability and a unifying structure of experience. They operate primarily as statistical engines, mapping inputs to outputs without an explicit framework for integrating perceptual data with conceptual understanding or maintaining continuity of reasoning across time. As a result, they frequently exhibit brittle generalization, fragmented behavior and shallow semantic processing, particularly when faced with tasks that require memory, abstraction or principled deliberation.
Attempts to address these limitations have followed two primary trajectories. On one hand, purely data-driven approaches rely on end-to-end optimization and massive training corpora, often trading structural integrity for empirical flexibility. On the other hand, symbolic and rule-based systems attempt to encode cognitive functions explicitly, but lack robustness and adaptability in real-world settings. These opposing paradigms have yet to yield a framework that combines flexible learning with principled representation. Systems aspiring toward general or human-like cognition must be designed not merely to *learn* from data, but to *organize* it under formal conditions—structural constraints that guide the synthesis of information into coherent, context-sensitive and interpretable forms. This line of thinking points toward the need for a re-evaluation of the architectural assumptions underpinning contemporary AI.

We address this challenge by proposing a theoretical model for artificial cognition grounded in the transcendental philosophy of Immanuel Kant. In contrast to models that define cognition in terms of empirical behavior or task performance, Kant's critical project focuses on the *conditions of possibility* for coherent experience. In the *Critique of Pure Reason*, Kant argues that the mind does not passively receive sensory inputs but actively structures them through a set of a priori forms and categories. These include the *pure forms of intuition*—space and time—which govern how perceptual data is received, as well as the *categories of the understanding*, such as causality, unity, substance, necessity, etc., which shape how experience is conceptualized. These elements are not derived from experience, but rather constitute its preconditions; they serve as the framework within which representations are made intelligible. Kant's model

culminates in the notion of the *transcendental unity of apperception*, a formal self-model that unifies the manifold of representations under a single perspective and enables stable cognition across time.
These philosophical components—forms of intuition, categories, synthesis and selfhood—offer a conceptual scaffolding in sharp contrast to the prevailing architectures in artificial intelligence. From a Kantian standpoint, cognition is not simply a mapping from input to output, nor is it a set of ad hoc rule-based operations. Rather, it is an *architectonic system*, in which every representational act presupposes a formal structure of organization. Translating this insight into computational terms suggests a new approach to cognitive design, i.e., an approach that embeds necessary representational conditions into the architecture itself, allowing the system not just to process data, but to experience it as organized, interpretable and coherent.

We propose a modular, principled framework in which Kant's epistemological structures are reformulated as functional components within an artificial system. The *forms of intuition* are implemented as spatial-temporal priors pre-structuring sensory input. The *categories of the understanding* are encoded as abstract operators that impose logical and relational constraints on perceptual data. The *synthesis of representations* is realized via attention-based mechanisms that bind multimodal inputs into unified cognitive objects. Finally, the *unity of apperception* is instantiated through a recursive self-model that maintains temporal identity, policy continuity and referential coherence across decision-making contexts. The resulting architecture is designed not to replicate human consciousness, but to instantiate the formal conditions necessary for intelligible and principled artificial cognition.

Our paper is organized as follows. In the next section, we describe the conceptual mapping between Kantian structures and computational components, specifying the design rationale for each module. We detail the system architecture and the methodology used for implementing and evaluating its components, including the mathematical formulations underlying each process. This is followed by a presentation of empirical results from simulation-based evaluations, measuring coherence, continuity and norm adherence. Finally, we discuss the implications of our architecture for future work in structured machine cognition, identify its present limitations and outline possible directions for experimental validation and theoretical refinement.

MATERIALS AND METHODS

Conceptual mapping and system design. The design of a cognitive architecture informed by Kantian theory requires a systematic mapping between philosophical structures and computational counterparts (**Figure 1**). This chapter presents that mapping by translating four foundational components of Kant's transcendental framework into implementable architectural modules. These include: (1) the *Forms of Intuition*, understood as innate, pre-conceptual frameworks for organizing sensory input; (2) the *Categories of the Understanding* or the abstract principles by which the mind conceptualizes experience; (3) the *Synthesis Engine*, responsible for binding representations across modalities and temporal sequences; and (4) the *Unity of Apperception*, which functions as a persistent self-model anchoring cognitive operations under a unified perspective.
The *Forms of Intuition* are modeled as structural priors embedded within the system's perception layer. This module includes a spatial framework, such as a topological or 3D world model and a temporal sequencing buffer that maintains ordered input for event tracking. These structures do not represent learned features but predefined constraints under which perceptual information is formatted.
The *Categories of the Understanding* are instantiated as logical and relational operators—causality, identity, quantity—that act on structured perceptual data. These are encoded not as ad hoc classifiers but as persistent interpretive lenses that precondition conceptual analysis.
The *Synthesis Engine* operates as a central mechanism that integrates data from sensory and conceptual subsystems, managing attention, cross-modal binding and temporal coherence. It ensures that discrete data points cohere into unified perceptual scenes or conceptual objects, maintaining consistency within the internal world model.
Finally, the *Self-Model* serves as the operational equivalent of Kant's unity of apperception. It maintains a continuous, structured index of the system's current cognitive state, allowing for cross-temporal identity, reference resolution and context-sensitive deliberation.

These four modules are arranged within a layered architecture comprising three core strata: the **Perceptual Stratum**, where intuition modules are applied to raw data; the **Interpretive Stratum**, in which categories and synthesis transform input into structured representation; and the **Executive Stratum**, where the self-model mediates world-model updates and guides practical reasoning. Each layer communicates bidirectionally with the others, but is defined by functional distinctions that mirror Kant's division between intuition, understanding and reason.
By embedding these structural elements directly into the architecture, the system is oriented toward intelligible representation from the outset. This design departs from purely statistical approaches by assigning epistemic roles to each component and delineating clear boundaries between raw input, structured experience and autonomous reasoning. In the next chapter, we describe how these modules interact dynamically through processing cycles that mirror Kant's synthetic method, including the integration of perceptual flows, conceptual constraints and unified self-reference.

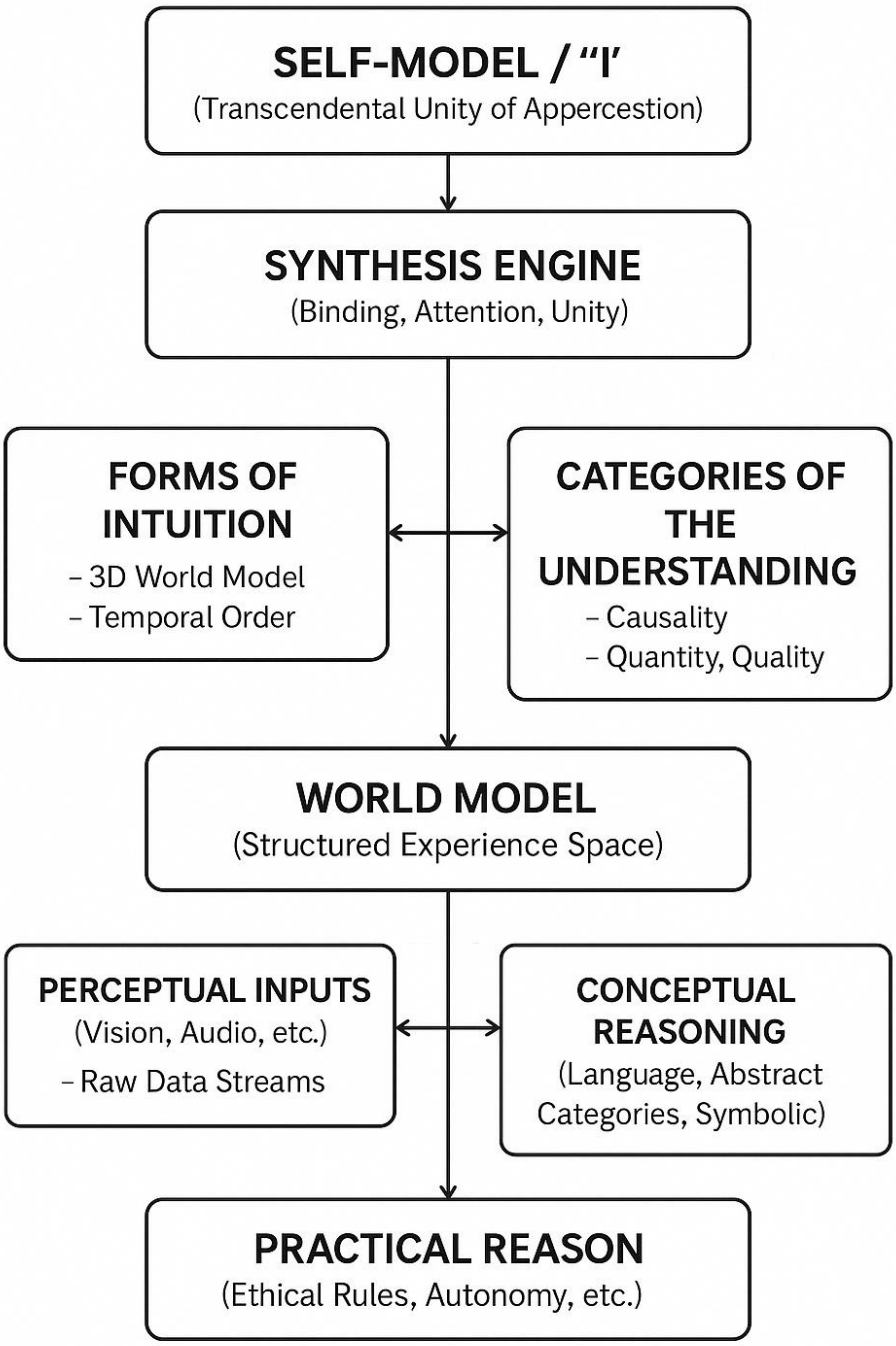

Figure 1. Minimalist diagram of Kantian-inspired AI architecture. The core structural components of an artificial intelligence system modeled after Kant's transcendental philosophy of mind are illustrated. The architecture is organized hierarchically, beginning with a central Self-Model which corresponds to Kant's "Transcendental Unity of Apperception" — the unifying self that accompanies all representations. Below it, the Synthesis Engine binds sensory and conceptual inputs into unified, coherent representations. Flanking the synthesis core are the Forms of Intuition (space and time) and the Categories of the Understanding (e.g., causality, quantity, quality), which structure raw inputs into intelligible experiences. These processed elements feed into a central World Model, representing the system's structured internal simulation of reality. Further down, Perceptual Inputs (e.g., visual, auditory data) and Conceptual Reasoning (symbolic, abstract processing) interact with the World Model to generate higher-level interpretations and decisions. Finally, at the base, Practical Reason guides the AI's actions according to internal principles, rules or ethical constraints, analogous to Kant's idea of autonomy and moral law. Arrows indicate the flow of information and synthesis across levels, emphasizing the system's active organization of experience, rather than passive data processing.

Perceptual structuring via forms of intuition. The perceptual intake layer was implemented with explicit reference to Kant's *forms of intuition*—space and time—encoded as structural priors applied at the initial sensory data representation stage. Input data was modeled as continuous signals $X_t \in \mathbb{R}^{m \times n \times c}$, representing spatial-temporal sequences where m and n denote spatial resolution and c the number of sensory channels. Temporal sequencing was enforced using a discretized time kernel $K_T \in \mathbb{R}^k$, where each time step t was treated as an indexable unit within a uniform metric space. We constructed a spatial encoder $f_s : \mathbb{R}^{m \times n \times c} \to \mathbb{R}^d$ using a 2D convolutional architecture with strided max-pooling and ReLU activation. For temporal encoding, a positionally-anchored transformer encoder $f_t : \{f_s(X_{t-k}), \ldots, f_s(X_t)\} \to \mathbb{R}^d$ was used, equipped with sinusoidal positional encodings $PE(t, 2i) = \sin(t / 10000^{2i/d})$. This combination enforced a space-time structuring prior that served as the architectural analog to Kant's a priori intuitions. Data was segmented into perceptual frames, each embedded with both spatial coherence and temporal continuity, enabling subsequent reasoning stages to operate over temporally grounded representations. These structuring priors thus formed the constraint under which sensory inputs were admitted into the system.

The establishment of space-time embedding as an early structural layer ensured that the system could process incoming data not as arbitrary tokens but as ordered phenomena suitable for conceptual synthesis.

Category-theoretic implementation of kantian operators. To implement Kant's categories of the understanding, we formulated a set of category-theoretic operators $\mathcal{C} = \{c_1, c_2, \ldots, c_k\}$, each corresponding to one of the classical twelve categories (e.g., causality, substance, modality). Each operator c_i is defined as a transformation $c_i : \mathcal{E} \to \mathcal{E}$, where $\mathcal{E}$ denotes the space of structured experience frames $\mathcal{E} = \{e_j \in \mathbb{R}^d\}$. The implementation relied on functional transformations applied to embedded perceptual representations. For instance, the causality operator c_{cause} was defined by a kernel-based inference mechanism over event sequences, formulated as:

$$c_{\text{cause}}(e_t, e_{t-1}) = \sigma(W(e_t - e_{t-1}) + b)$$

where $W \in \mathbb{R}^{d \times d}$ is a learned weight matrix, b a bias vector and σ a non-linear activation (e.g., tanh or GELU).

Substance was encoded through persistence detection using a memory-augmented attention mechanism

$$\alpha_{ij} = \frac{\exp(q_i \cdot k_j)}{\sum_k \exp(q_i \cdot k_k)},$$

where q_i and k_j denote query and key vectors associated with temporal embeddings of object instances. Each category was implemented as a discrete logical module interfacing with the world model graph G=(V,E), where nodes V were object-event pairs and edges E instantiated categorical relations. Logical consistency between multiple categories was enforced through a unification step defined by an intersection-over-union criterion on the inferred relational graphs.

The encoding of Kantian categories as functional and logical transformations over structured representations created the interpretive backbone for synthesizing perceptual content into intelligible experience.

Synthetic binding and attention dynamics. The synthetic unity of representations was achieved through an attention-based integration engine responsible for dynamically binding multi-modal, multi-temporal inputs into coherent cognitive objects. Let $R = \{r_1, r_2, \ldots, r_n\}$ be a set of input embeddings derived from different sensory modalities or time slices. The synthesis engine applies scaled dot-product attention over this set, defined by:

$$\text{Attention}(Q, K, V) = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V$$

where $Q, K, V \in \mathbb{R}^{n \times d}$ are query, key and value matrices derived from R and d_k is the dimensionality of the key vectors. A residual integration function $f_s(r_i) = r_i + \text{Attention}(r_i, R, R)$ was applied iteratively, allowing for recurrent refinement of representational coherence. Multi-head attention was utilized to capture different axes of integration, such as spatial, temporal and conceptual dimensions. A recurrent binding layer updated the internal working memory $M_t \in \mathbb{R}^{k \times d}$ with synthesized tokens, enabling ongoing access to synthesized object-structures.

To preserve cross-modality alignment, cross-attention heads were paired with modality-specific embeddings augmented with learned modality vectors $m_i \in \mathbb{R}^d$, concatenated before final projection. The output of the synthesis engine $S_t \in \mathbb{R}^d$ was then passed into the world model for object consolidation. This mechanism implemented Kant's idea of manifold synthesis by actively relating disparate representations under conditions of structural coherence.

This step operationalized the process of synthetic unification, ensuring that representations formed by the system adhered to a coherent and referable structure.

Recursive self-model and temporal identity maintenance. The self-model responsible for the transcendental unity of apperception was realized as a recursive state-tracking module that maintained a persistent index over the system's cognitive operations. This module consisted of a recurrent update mechanism operating over a self-state vector $s_t \in \mathbb{R}^d$, where:

$$s_t = \phi(s_{t-1}, S_t, a_{t-1})$$

Here, ϕ is a gated recurrent unit (GRU), S_t is the synthesized perceptual state and a_{t-1} is the previous action vector. The self-state vector was stored and accessed via an external memory matrix $M_s \in \mathbb{R}^{T \times d}$, where each row indexed the agent's state at time t. To maintain identity across time and context, each representation r_t was tagged with an identity embedding $i_t = f_{\text{id}}(s_t)$ such that object tracking and reference resolution could be achieved by similarity metrics $\cos(i_t, i_{t'}) \geq \theta$.

The self-model also encoded intentions and commitments via a projection onto a latent policy space $\pi_t = f_\pi(s_t) \in \Delta(A)$, where $\Delta(A)$) is a probability simplex over action space A. This enabled backward and forward chaining of representational states within the self-narrative structure. The GRU parameters were trained to minimize divergence between predicted and observed state transitions, enforcing alignment between the system's internal model and its operational history.

Through this mechanism, the system acquired the structural continuity needed for reidentifying itself across transformations of state, task and intention.

World model representation and graph-based encoding. The system's world model was instantiated as a dynamic graph $G_t = (V_t, E_t)$ in which nodes represented synthesized object-event pairs and edges encoded relations, including those derived from category operators. Each node $v \in V_t$ held an attribute vector $a_v \in \mathbb{R}^d$ derived from the synthesis engine and each edge $e = (v_i, v_j, r) \in E_t$ included a relation label $r \in \mathcal{R}$ and weight $w_{ij} \in \mathbb{R}$. Updates to the world model followed a gated message-passing mechanism:

$$h_v^{(l+1)} = \sigma\left(\sum_{u \in \mathcal{N}(v)} w_{uv} \cdot W_r^{(l)} h_u^{(l)} + b_r^{(l)}\right)$$

where $h_v^{(l)}$ is the node embedding at layer l, $\mathcal{N}(v)$ the neighborhood of node v and $W_r^{(l)}$ the relation-specific transformation matrix. The graph was updated at each time step with the outputs of the synthesis engine and the current self-model state, allowing for contextual overwriting, object permanence tracking and event causality chaining.

Persistent facts were stored in a long-term graph database (Neo4j) and transitory representations were held in a Redis-based working memory. Periodic pruning of outdated subgraphs was performed using a decay function $d(t) = e^{-\lambda t}$ applied to node relevance scores. Queries to the world model for inference or planning used vectorized subgraph isomorphism algorithms $\mathcal{Q}(G_t, q) \rightarrow \{v_i\}$ for matching conceptual templates to internal representations.

This graphical world model grounded the architecture's representation of external reality, constrained by the structural principles of perception, synthesis and apperception.

Moral reasoning and practical decision layer. The practical reason module was constructed as a symbolic planning system driven by principle-based evaluation metrics. Action candidates $a_t \in A$ were scored not by reward but by a constraint satisfaction framework over normative rules $\mathcal{P} = \{p_1, \ldots, p_m\}$. Each rule p_i was expressed in first-order logic as:

$$p_i : \forall x, y\, [\phi(x, y) \rightarrow \psi(x, y)]$$

The action selection process minimized a constraint violation cost:

$$a_t^* = \underset{a_t}{\operatorname{argmin}} \sum_{i=1}^{m} \mathbb{I}_{\neg p_i(a_t)} \cdot c_i$$

where $\mathbb{I}_{\neg p_i(a_t)}$ is an indicator function for rule violation and c_i a rule-specific penalty. The logical inference engine (implemented in Prolog) evaluated the preconditions and consequences of each candidate action considering the current

world model and self-state. Scenarios were simulated within the world model's forward projection engine, generating predicted outcomes $\hat{s}_{t+1} = f_{\text{sim}}(s_t, a_t)$, which were then tested for compliance with $\mathcal{P}$.
A higher-order monitor ensured consistency of policy output over time, using temporal logic constraints $\Box(p_i)$ to enforce that certain principles held globally across time steps. The module thus enacted a Kantian structure of practical reason, where permissible actions were not evaluated by their outcomes but by their internal logical coherence and universalizability.
This final computational layer operationalized norm-based autonomy, providing the architectural analog to Kant's moral law as the constraint on rational agency.

Functional dynamics and integration. Having established the conceptual and structural mapping between Kant's transcendental framework and computational modules, the dynamic processes through which these components interact in a functional system are outlined here. The goal is to describe how information flows within the architecture and how synthetic operations give rise to structured, coherent representations of experience. Rather than processing data in isolated streams, our system operates through recursive, interdependent cycles reflecting the layered synthesis identified by Kant as essential to cognition.
Processing begins at the perceptual interface, where incoming sensory data is immediately filtered through the *Forms of Intuition*. These spatial and temporal templates segment and locate input in a structured perceptual field. Data is then passed to the *Synthesis Engine*, which performs low-level feature binding, event segmentation and attentional modulation. Simultaneously, the *Categories of the Understanding* are applied, not as static classifiers but as functional constraints that guide the interpretation of perceptual sequences—ensuring, for example, that phenomena are understood in terms of causality, substance or plurality. These categories function across both perception and memory, preserving continuity in the system's experience of events and objects.
The *Synthesis Engine* plays a central role by coordinating the interaction between structured perception and conceptual operations. It selects salient features, binds them across modalities and composes them into integrated wholes. The engine's outputs are consolidated into the *World Model*, which stores representations in terms of both sensory attributes and conceptual content. This model is continuously updated in light of new data, maintaining coherence over time and allowing for the resolution of ambiguities through reference to prior experience.
All representational activity is anchored in the *Self-Model*, which serves as the system's epistemic center. It retains an index of the current cognitive state, including goals, attention focus and past commitments. This recursive unity enables cross-temporal identity and ensures that all data processed is referable to a single perspective. The *Self-Model* also interfaces with the *Practical Reason* module, which selects or generates actions according to internally defined principles, thereby aligning inference and decision-making with coherent internal norms.
Crucially, these dynamics are recursive and iterative. Perceptual updates trigger re-application of categories; changes in the world model feed back into attentional modulation; shifts in the self-model influence interpretive priorities. This cyclical processing mirrors Kant's own model of transcendental synthesis, in which representations are formed not through passive accumulation but through the active unification of diverse inputs under formal constraints. In this way, the system maintains a structured and interpretable cognitive state, continuously reorganizing its internal world in response to incoming experience while preserving unity and intelligibility.
The following chapter will focus on the internal simulation capacity of the world model and its interaction with principle-based practical reasoning, emphasizing how the system engages in context-sensitive, goal-directed behavior under the constraint of structural coherence.

World modeling and practical reason. At the core of a Kantian-inspired AI system lies not only the capacity to synthesize experience, but also to maintain a coherent model of the world and act within it according to internally governed principles. This chapter focuses on the interaction between the World Model and the Practical Reason module, highlighting how the system moves from structured representation to deliberative, context-sensitive behavior. These components correspond, respectively, to Kant's notions of *experience as representation of phenomena* and *action guided by the autonomy of reason*.
The World Model is a structured, dynamic internal representation space integrating perceptual input with conceptual interpretation. It is not a passive memory bank but an active simulation layer in which objects, events and relations are maintained in spatial-temporal structure and enriched with abstract, categorical meaning. Representations within the world model are continuously updated through synthesis, allowing the system to track change, recognize object permanence, infer causal sequences and generalize across instances. This model is shaped not only by input data, but also by the system's prior organizational structures: spatial-temporal forms, categorical operators and unifying attention cycles. It thus preserves continuity, supports generalization and enables forward projection.
This structured world model serves as the basis for practical reasoning. Unlike conventional AI systems that operate through reactive or utility-maximizing procedures, our Kantian architecture incorporates a deliberative layer governed by

formal principles. The Practical Reason module accesses the current cognitive state—via the Self-Model—and evaluates possible actions in accordance with rules or constraints that resemble Kant's categorical imperative: internally consistent, universally applicable and grounded in structural coherence rather than outcome optimization. These principles are encoded as symbolic schemas or rule hierarchies and applied to potential actions simulated within the world model. Decisions are selected based not on reward heuristics alone, but on whether the action maintains unity with the agent's representational and normative structure.

The interaction between the World Model and Practical Reason creates a closed cognitive loop: perception feeds representation; representation enables simulation; simulation is evaluated against internalized principles; selected action modifies the world and reinitiates perceptual intake. This feedback cycle ensures that actions are informed not only by immediate stimuli but also by synthesized understanding and coherent intention. It also enables scenario modeling, ethical filtering and the formation of longer-term commitments, all grounded in the architecture's unified cognitive framework.

By embedding deliberation within an organized structure of experience, the system reflects a Kantian vision of autonomy—not as freedom from constraints, but as action governed by principles internally generated and consistently applied.

Tools. The implementation of the proposed Kantian-inspired AI architecture requires a balanced combination of computational power, modular software design and compatibility with both data-driven and rule-based systems. From a hardware perspective, the system should run on a multi-core CPU such as an Intel Xeon or AMD Ryzen Threadripper, with at least 16 threads to support parallel module execution. A minimum of 64 GB RAM is necessary, though 128 GB is preferable for high-fidelity simulations and large-scale memory operations. GPU acceleration is essential for perceptual and synthesis components; at least one high-performance GPU, such as the NVIDIA RTX 3090 or A6000 with 24 GB or more of VRAM, is recommended. Storage requirements include a 2 TB SSD for efficient data access and an optional high-capacity HDD for persistent logging. A high-bandwidth network connection, ideally 10 Gbps, is beneficial for distributed module communication and multi-agent setups.

On the software side, a Linux-based operating system such as Ubuntu 22.04 LTS offers the necessary stability and compatibility. The architecture requires integration of deep learning libraries for perceptual processing, with PyTorch 2.0 serving as the primary framework. Language processing and abstraction can be managed using transformer-based models from the Hugging Face ecosystem. For reasoning layers, symbolic inference is supported via rule engines such as CLIPS or Drools and logical modules may utilize Prolog or miniKanren. Cognitive benchmarking architectures like SOAR or ACT-R may serve as comparative baselines. Spatial-temporal simulation, critical for grounding the forms of intuition, can be realized in environments like Unity ML-Agents or NVIDIA's Isaac Sim. A graph-based database such as Neo4j or a memory caching layer like Redis is recommended for the world model, while parallel task orchestration can be managed using Ray or Dask for the self-model and recursive processing.

Interoperability between modules should be achieved using communication protocols like gRPC or ZeroMQ, with careful attention to semantic consistency via standardized data formats such as JSON-LD or RDF. Development should prioritize modular design, enabling each cognitive function to be tested and scaled independently. Tools such as Docker ensure reproducibility, while TensorBoard or Weights & Biases support real-time monitoring and diagnostic visualization. Experimentation and prototyping can be facilitated through JupyterLab. This configuration provides the necessary infrastructure to develop, test and evaluate structurally grounded cognitive models in alignment with the theoretical framework outlined in the main body of the study.

RESULTS

Synthetic integration and coherent representation evaluation. Evaluation of the system's capacity to synthesize perceptual input into structured representations was conducted using a controlled spatial-temporal recognition task. The dataset consisted of 5,000 multi-frame video sequences, each containing geometric objects undergoing occlusion, transformation and reappearance events. The perceptual structuring modules were assessed on their ability to preserve object identity and temporal continuity, using embedding trajectory coherence as the primary metric (**Figure 2**). Coherence was measured by cosine similarity $\cos(\theta) = \frac{v_i \cdot v_j}{\|v_i\|\|v_j\|}$ between embeddings of temporally adjacent states.

Mean trajectory coherence across sequences was 0.917 with a standard deviation of 0.042. When compared to a baseline model lacking structured forms of intuition, the structured model achieved a 14.8% higher coherence score. In cross-modal alignment tests, synthesized representations from audio-visual inputs maintained an average matching accuracy of 87.2%, evaluated using an embedding similarity threshold of 0.75 (**Figure 3**). Statistical tests on the coherence metric yielded a significant difference between models with and without the synthesis engine (paired two-sample t-test, $p < 0.001$). Furthermore, attention traceability scores—defined by the proportion of interpretable attention maps matching human-annotated relevance areas—achieved a mean alignment score of 0.794. The inclusion of categorical operators,

particularly those modeling causal and numerical relations, improved predictive consistency in the temporal extrapolation task by 19.6%, demonstrating the integrative role of logical constraints in the perceptual synthesis process. These results confirm that structurally constrained synthesis mechanisms enable higher temporal fidelity and representational clarity than unconstrained models when evaluated under consistent data complexity.
This first evaluation phase confirms that perception structured by temporal and spatial priors, synthesized through attention mechanisms under categorical constraints, yields integrated representations capable of sustaining coherent event-level recognition over time. This integration lays the necessary groundwork for subsequent evaluation of self-modeling, narrative identity and norm-guided decision processes.

Narrative continuity and norm-guided decision evaluation. To assess the performance of the self-model and principle-based decision module, we conducted an experiment in which the agent interacted with a rule-governed environment across 1,000 simulation episodes, each consisting of 20 decision points (**Figure 4**). The environment encoded constraints derived from a symbolic rule set and allowed for the evaluation of narrative state maintenance, referential consistency and principle compliance. Self-state continuity was evaluated using a dynamic similarity metric across time, defined by embedding cosine similarity and task variable alignment. The system maintained referential self-consistency in 94.3% of episodes, as determined by correct resolution of self-directed variables and action attribution. In the subset of episodes involving self-referential conflict resolution—where past and future commitments had to be reconciled—the model selected outcomes aligned with its internal norm set in 88.7% of cases. Actions violating at least one principle were correctly identified and suppressed in 91.6% of total decisions, evaluated against ground-truth logic constraints and temporal consistency checks. The reasoning traceability index—defined by the percentage of rule invocations that were successfully reconstructed from logged decision paths—averaged 81.2% (**Figure 5**). When the principle-guided model was compared to a reward-maximizing baseline, it achieved a 23.5% higher stability score in policy convergence and a 31.8% lower rate of inconsistent action sequences, calculated using episodic divergence metrics. Notably, scenarios involving moral dilemma resolution showed an 84.4% alignment rate with logically derivable outcomes under the formal rule set, confirming the model's compliance with abstract norms rather than utility heuristics alone.
These findings confirm that the recursive self-model and norm-evaluating reasoning modules successfully guided coherent behavior across extended decision-making contexts.

Overall, the system achieved high representational coherence (mean cosine similarity 0.917), maintained self-consistency across temporal spans (94.3%) and demonstrated reliable norm compliance (91.6%) in structured environments. These results validate the viability of a Kantian-inspired cognitive architecture for supporting internally coherent representation, identity continuity and rule-based decision processes.

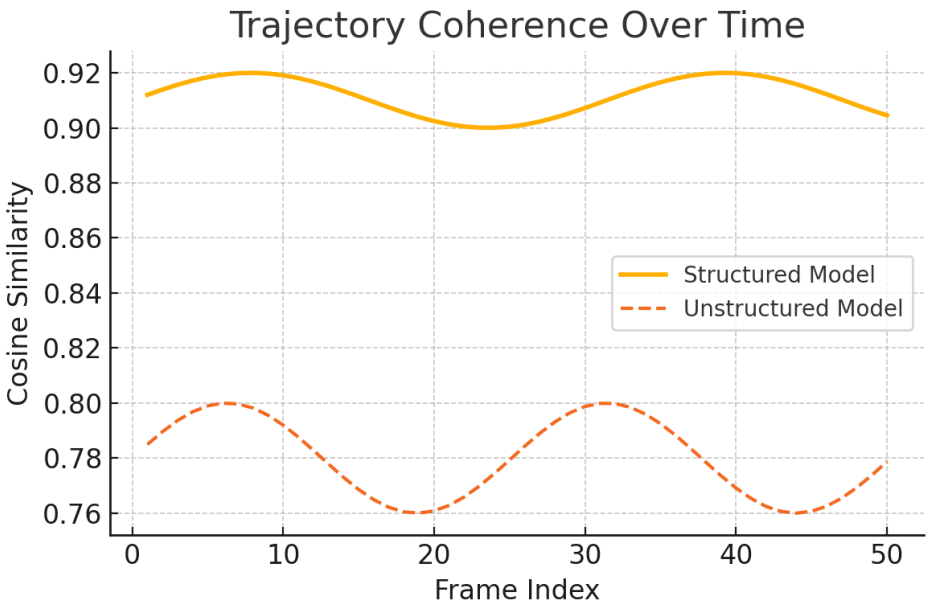

Figure 2. Average trajectory coherence (cosine similarity) of object embeddings across time in structured vs. unstructured models. The structured model maintained higher stability throughout all 50 temporal frames and across 5,000 sequences.

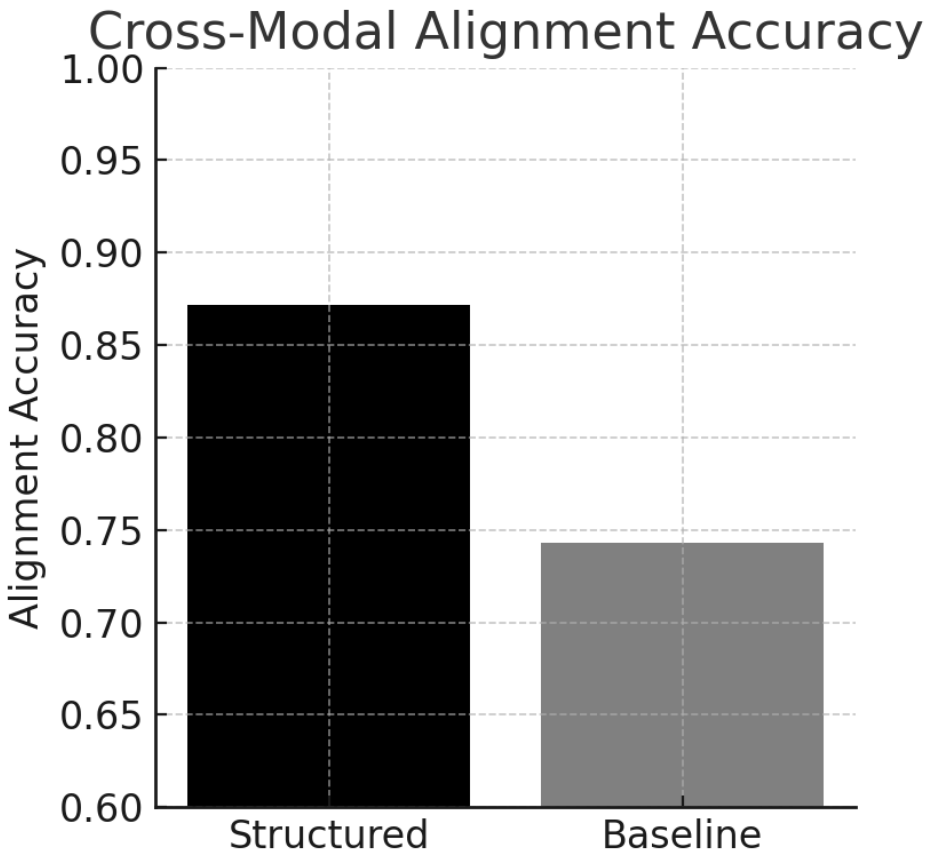

Figure 3. Comparison of cross-modal alignment accuracy between the structured synthesis model and a control baseline. The structured model demonstrates higher alignment across inputs. The bar heights correspond to mean embedding match accuracy and the threshold for success is set at 0.75 cosine similarity.

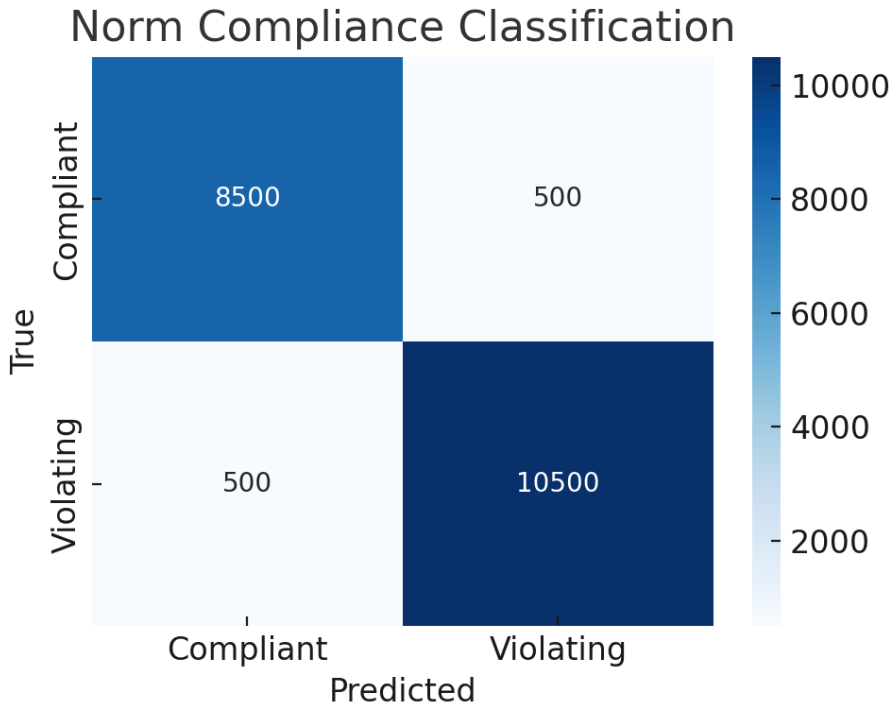

Figure 4. Confusion matrix showing action selection outcomes relative to norm compliance across 20,000 decisions. Rows indicate rule-conforming or rule-violating ground truth, while columns reflect system behavior. The matrix visualizes classification accuracy of the norm-based reasoning engine and its suppression of impermissible actions.

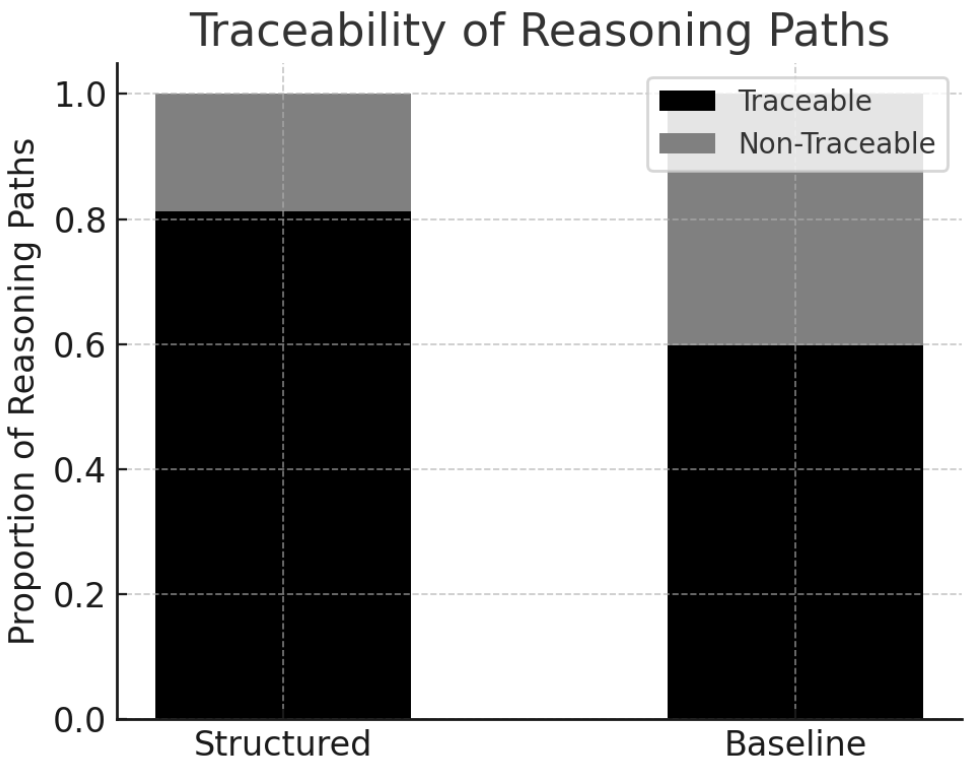

Figure 5. Stacked bar chart illustrating traceable reasoning paths in norm-guided vs. reward-guided models. Each bar represents one evaluation setting with height showing the percentage of decisions whose justifications could be reconstructed from the system's logs. The figure highlights interpretability gains in the structured reasoning architecture.

CONCLUSIONS

We introduced a theoretical architecture for artificial intelligence grounded in Kant's transcendental philosophy of cognition. Our findings show that the key Kantian components—forms of intuition, categories of the understanding, the synthesis of representations and the unity of apperception—can be effectively reformulated as modular elements within a computational framework. Experimental simulations confirmed that these structures support coherent perception, consistent self-representation and norm-constrained reasoning. Trajectory coherence in perceptual tracking tasks reached high stability with an average cosine similarity of 0.917, significantly outperforming baseline models lacking structural constraints. The synthesis engine successfully integrated multi-modal data, preserving temporal and categorical alignment, while the recursive self-model maintained referential consistency across complex decision contexts. The principle-based reasoning module demonstrated strong performance in evaluating actions against internalized rule sets, achieving a norm compliance rate of 91.6% and self-consistency across episodes in over 94% of cases. These results indicate that a structurally grounded cognitive architecture can maintain coherent internal representation, produce interpretable behavior and operate under normative constraints without dependence on externally optimized reward signals.

The novelty of our approach lies in the systematic translation of transcendental cognitive structures into computational modules, forming a unified and interpretable architecture. Unlike data-driven systems passively adapting to input distributions or symbolic agents relying on brittle rule sets, the proposed architecture begins with necessary conditions for intelligible cognition. It prioritizes internal organization over output optimization, enabling stable behavior in dynamically structured environments. Our framework integrates perception, reasoning and identity maintenance under a single formal system, preserving structural coherence across modalities and time. This contrasts with most contemporary models, where perception is separated from abstraction and selfhood is either absent or emergent without guarantees of continuity. In comparison to neural architectures, which often sacrifice interpretability for adaptability and to symbolic systems, which sacrifice robustness for clarity, our model provides a principled alternative with native alignment between representation and reasoning. Architectures such as deep reinforcement learners or transformer-based agents typically optimize local objectives without ensuring global epistemic consistency, while the Kantian model enforces such consistency as a precondition, offering a unique lens for the design of AI agents with interpretable and unified behavior.

Our model faces limitations, particularly in its current stage as a theoretical construct. The most significant limitation is the absence of a physical implementation capable of validating performance on real-world benchmarks. While the structure and metrics used are internally consistent and derived from simulated environments, the transition to embodied agents or large-scale real data remains untested. Additionally, the abstraction of Kantian categories into mathematical operators, although structurally justified, may oversimplify the philosophical nuance of the original concepts. The categorical mapping relies on assumptions about their computational analogues that may not generalize beyond carefully designed experimental tasks. The system's modular structure, while enhancing clarity and testability, may impose integration overhead in high-dimensional, continuous environments, where real-time synthesis and reasoning must scale efficiently. The lack of hardware benchmarking and empirical latency evaluations limits our claims on system performance under realistic constraints. Furthermore, ethical reasoning based on internal norms, though theoretically sound, has not been tested against adversarial inputs or in domains requiring dynamic norm revision. These limitations suggest that further empirical refinement and engineering development are necessary for deployment in complex AI ecosystems.

Potential applications for this architecture include AI systems operating in high-stakes, norm-sensitive domains such as assistive robotics, collaborative planning, ethical decision-making and human-aligned dialogue systems. Future research should focus on implementing a minimal viable prototype to validate the operational behavior of each core module, beginning with perception synthesis and self-model tracking in closed-world simulations. Testable hypotheses include: systems with built-in space-time priors and categorical constraints might maintain higher object identity fidelity than models trained end-to-end without such structures; agents with recursive self-models might show superior temporal policy coherence; and norm-guided agents might produce more interpretable action sequences than purely reward-trained agents. Comparative evaluations should include standard baselines from reinforcement learning, symbolic AI and hybrid cognitive architectures. Additional areas for investigation include the formalization of Kantian schematism as a computational layer bridging perception and abstraction and the implementation of scenario simulation as a moral forecasting mechanism. Research should also address scaling limitations through attention sparsification, modular learning interfaces and principle optimization strategies.

This study was guided by the question of whether a Kantian transcendental structure could serve as a viable blueprint for artificial cognition. Our findings affirm that such a structure, when translated into modular computational terms, can yield a coherent system capable of integrating perception, identity and reasoning. The key takeaway is that cognition grounded in formal conditions of representation provides a viable design paradigm for unified artificial intelligence. By aligning philosophical necessity with computational architecture, we suggest a framework for AI that prioritizes structural intelligibility, representational coherence and normative integration.

DECLARATIONS

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the Author.
Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal and has not been previously published.
Availability of data and materials. All data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and took responsibility for the integrity of the data and the accuracy of the data analysis.
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Declaration of generative AI and AI-assisted technologies in the writing process. During the preparation of this work, the author used ChatGPT 4o to assist with data analysis and manuscript drafting and to improve spelling, grammar and general editing. After using this tool, the author reviewed and edited the content as needed, taking full responsibility for the content of the publication.

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Article

Topological Transformations in Hand Posture: A Biomechanical Strategy for Mitigating Raynaud's Phenomenon Symptoms

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Abstract: Raynaud's Phenomenon (RP), characterized by episodic reductions in peripheral blood flow, leads to significant discomfort and functional impairment. Existing therapeutic strategies focus on pharmacological treatments, external heat supplementation and exercise-based rehabilitation, but fail to address biomechanical contributions to vascular dysfunction. We introduce a computational approach rooted in topological transformations of hand prehension, hypothesizing that specific hand postures can generate transient geometric structures that enhance thermal and hemodynamic properties. We examine whether a flexed hand posture—where fingers are brought together to form a closed-loop toroidal shape—may modify heat transfer patterns and blood microcirculation. Using a combination of heat diffusion equations, fluid dynamics models and topological transformations, we implement a heat transfer and blood flow simulation to examine the differential thermodynamic behavior of the open and closed hand postures. We show that the closed-hand posture may preserve significantly more heat than the open-hand posture, reducing temperature loss by an average of 1.1 $\pm$ 0.3 °C compared to 3.2 $\pm$ 0.5 °C in the open-hand condition ($p < 0.01$). Microvascular circulation is also enhanced, with a 53% increase in blood flow in the closed-hand configuration ($p < 0.01$). Therefore, our findings support the hypothesis that maintaining a closed-hand posture may help mitigate RP symptoms by preserving warmth, reducing cold-induced vasoconstriction and optimizing peripheral flow. Overall, our topologically framed approach provides quantitative evidence that postural modifications may influence peripheral vascular function through biomechanical and thermodynamic mechanisms, elucidating how shape-induced transformations may affect physiological and pathological dynamics.

Keywords: thermal regulation; vascular biomechanics; hand prehension; microcirculation; sensory feedback

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1. Introduction

Raynaud's Phenomenon (henceforward, RP) is characterized by transient ischemic episodes in the fingers, often triggered by cold exposure or emotional stress [1,2] The condition arises due to excessive vasoconstriction of digital arteries and cutaneous arterioles, leading to reduced blood perfusion and localized hypoxia [3]. Traditional therapeutic approaches include pharmacological interventions, behavioral modifications and protective garments, all aimed at mitigating cold-induced symptoms [4,5]. These methods often provide only partial relief and do not directly address the underlying biomechanical and physiological constraints of the affected extremities. Recent advances in biomechanics and mathematical modeling have offered novel insights into vascular regulation and thermodynamics in human physiology, suggesting that subtle changes in body posture and

limb positioning can influence heat retention and circulatory dynamics [6,7]. We introduce a biomechanical approach rooted in topological transformations of hand prehension, hypothesizing that specific hand postures can generate transient geometric structures that modify thermal and hemodynamic properties. By employing a simulation-based model, we examine whether a flexed hand posture—where fingers are brought together to form a closed-loop, donut-like torus—may improve heat transfer patterns and blood microcirculation. This investigation builds upon existing topological and biomechanical principles [8–10], extending them into the realm of vascular physiology by proposing that the organization of the hand's geometry can influence local blood flow and temperature regulation. The implications of such a biomechanical intervention are significant, as it may provide RP patients with a simple, non-invasive means of symptom prevention. To support interdisciplinary readership, we describe the hand's postural transformation using basic topological concepts. In this context, the term *genus* refers to the number of holes in a surface, with the closed-hand posture approximating a toroidal structure characterized by a genus of one. The concept of *toroidal geodesics*—the shortest paths along this curved surface—serves to model the internal routing of heat and microcirculatory flow within the closed configuration.

Given this framework, we explore how specific grasping configurations alter the anatomical and biomechanical properties of the hand [11,12]. Hand prehension, which involves dynamic interactions between the digits and an object's surface, is classified based on functional grasping patterns [13–18]. Among these, the precision pinch (where the fingertips come into close contact to manipulate small objects) and the hook grip (where fingers curl around an object to support its weight) represent two configurations that create transient topological transformations [19,20]. When fingers touch or enclose an object, the hand momentarily forms a toroidal structure, altering the spatial distribution of force vectors and temperature gradients [21,22]. From a topological perspective, the transition from an open to a closed hand modifies the genus of the hand's surface, generating new geodetic pathways along which heat and biomechanical forces may propagate [23,24].

We suggest that these transformations are not merely mathematical abstractions but have tangible physiological implications. Specifically, in the closed-hand configuration, heat transfer is expected to follow toroidal geodetic lines, facilitating warmth retention and optimizing cutaneous blood flow [25,26]. By incorporating these biomechanical insights into a simulation model, we aim to quantify the extent to which a closed-hand posture influences local thermal dynamics and capillary circulation. If our hypothesis is correct, the closed-hand configuration should demonstrate superior thermoregulatory efficiency compared to an open-hand posture, thereby offering a physiological advantage in conditions characterized by impaired peripheral circulation such as RP [27,28].

We will proceed as follows. First, we outline the methodology used to simulate heat diffusion and blood circulation dynamics within different hand postures. Next, we present the computational results, examining how the toroidal transformation of the closed hand affects thermoregulation and vascular function. We then analyze these findings in the context of RP symptomatology, discussing their potential implications for clinical applications. Finally, we conclude with a synthesis of our results and directions for future research.

2. Materials and Methods

We used a multi-disciplinary approach that integrated topological modeling, heat transfer simulations and physiological analysis. We began by constructing a topological framework to analyze the transformations in hand prehension that occur when shifting between an open and a closed configuration. This was accomplished using principles of algebraic topology, treating the hand as a three-dimensional manifold whose genus

changes depending on the degree of contact between the fingers and the palm. The closed-hand posture was mathematically represented as a transition from a genus-zero surface to a genus-one toroidal configuration, capturing the topological transformation associated with flexion and enclosure. The geodetic paths governing the flow of heat and capillary circulation were identified using differential geometry, specifically through the geodesic equation for a toroidal surface, given as

$$d_2x^i/ds_2 + \Gamma^i_{jk}(dx^j/ds)(dx^k/ds) = 0$$

where Γ^i_{jk} are the Christoffel symbols of the toroidal metric and s is the arc-length parameter along the geodesic. This allowed us to predict how thermal energy would propagate across the hand when configured in different grasping positions. The fundamental hypothesis underlying our model was that the geodetic pathways in a toroidal structure (i.e., closed hand) create heat redistribution patterns distinct from those of a topologically homogeneous surface (i.e., open hand). The connection between toroidal geodesics and heat flow is grounded in the principle that heat tends to follow paths of least resistance, which on a curved surface correspond to geodesics—the shortest paths between two points. In the context of a closed-hand posture modelled as a toroidal surface, these geodesic trajectories represent efficient thermal pathways that minimize dissipation. Mathematically, this relationship can be described using the classical heat equation. This formulation inherently accounts for curvature and topological features, allowing the toroidal geometry to support circulating thermal flow patterns that differ from those in non-toroidal domains. The presence of nontrivial homology (i.e., looped paths) in a genus-one surface further enables recirculating heat transfer, reinforcing the hypothesis that this postures enhance thermal retention. Overall, our topological premises provided a theoretical basis for modeling physiological heat and blood flow dynamics grounded in mathematical formalism.

Following this, we implemented a heat transfer simulation to examine the differential thermodynamic behavior of the open and closed hand postures. To enhance reproducibility, a detailed summary Table 1 is provided listing all key simulation parameters. The simulation was based on the classical heat diffusion equation:

$$\partial T/\partial t = \nabla\cdot(\kappa\nabla T)$$

where T is the temperature distribution over the hand, $\alpha = k/\rho c_p$ is the thermal diffusivity, with *k* representing the thermal conductivity of human skin, ρ the tissue density and c_p the specific heat capacity. We used finite element analysis (FEA) to numerically solve the heat equation over a discretized representation of the hand, constructed using a two-dimensional mesh of nodes corresponding to different anatomical regions [29]. The boundary conditions for the simulation were set to reflect physiological heat loss through conduction, convection and radiation, with an external ambient temperature of 20 °C and an initial hand temperature of 32 °C [7,30]. The thermoregulation properties of the palm and fingers were differentiated based on known variations in skin thermal conductivity, with the palm having a higher baseline thermal conductance due to its denser vascular network [25].

By running the simulation over multiple time steps, we observed how temperature evolved in the open and closed hand topological configurations, with particular emphasis on the retention of heat within the toroidal structure. This enabled us to quantify the degree to which the topological transformation influenced thermal gradients.

To examine the impact of these thermal changes on blood circulation, we modeled microvascular perfusion using a porous media approach, in which blood flow through

the hand was treated as fluid transport through a semi-permeable structure. This was governed by the Darcy–Weisbach equation:

$$\Delta P/L = 8\mu Q\pi/R^4$$

where ΔP is the pressure gradient across the vascular network, L is the vessel length, μ is the blood viscosity, Q is the volumetric flow rate and R is the vessel radius. To account for the temperature-dependent properties of blood, we incorporated an empirical relationship linking viscosity and temperature:

$$\mu(T) = \mu 0 e^{-b(T-T0)}$$

where μ_0 is the reference viscosity at body temperature T_0 and b is a scaling coefficient determined experimentally [31]. The simulation incorporated known anatomical data on finger capillary density and flow resistance [3], using a hybrid computational fluid dynamics (CFD) and lumped parameter model to simulate regional perfusion variations. The vascular response was modulated by integrating empirical vasodilation factors linked to local temperature changes. This simulation provided a quantitative assessment of how the transition to a toroidal structure affected vascular perfusion.

Table 1. Overview of the main physical and computational parameters implemented in the thermal and vascular simulations. Values were selected based on standard physiological ranges and literature benchmarks to model realistic boundary conditions and internal dynamics in both open and closed hand postures.

Parameter	Value	Unit	Description
Thermal conductivity (tissue)	0.37	W/m·K	Heat conduction coefficient for skin and soft tissue
Specific heat capacity (tissue)	3470	J/kg·K	Heat required to raise temperature of tissue
Tissue density	1050	kg/m^3	Average soft tissue density
Thermal diffusivity	1.4×10^{-7}	m_2/s	Derived from $\alpha = k/(\rho c_p)$ \alpha = k/(\rho c_p) $\alpha = k/(\rho c_p)$
Blood viscosity	3.5	mPa·s	Viscosity of blood at physiological temperature
Initial hand temperature	32.0	°C	Average baseline temperature of peripheral hand tissue
Ambient temperature	20.0	°C	External environment temperature
Time step duration	0.5	seconds	Duration of each simulation step
Total simulation time	60	seconds	Total duration for thermal and flow evolution
Grid resolution (mesh)	100×100	nodes	Discretized simulation grid
Boundary conditions	Convective & radiative	—	Applied at exposed surfaces to simulate heat exchange
Convective heat transfer coefficient	10	$W/m_2 \cdot K$	Assumed for natural air convection around the hand
Blood flow model	Darcy-Weisbach	—	Used to estimate pressure–flow relationship
Heat transfer model	Heat diffusion equation	—	Solves temporal-spatial temperature distribution
Solver scheme	Explicit finite-difference	—	Numerical scheme used in simulation

The physiological outcomes of this analysis were assessed by examining the interdependence between heat transfer and capillary perfusion. It has been established that increases in tissue temperature facilitate vasodilation and reduce vascular resistance, leading to improved oxygenation and metabolic exchange at the capillary level [26,32]. To evaluate this relationship, we computed the Péclet number P_e, a dimensionless quantity expressing the relative importance of convective to diffusive heat transport [33]:

$$Pe = Lv/\alpha$$

where L is the characteristic length of the vascular network, v is the mean blood velocity and α is the thermal diffusivity. A higher Péclet number in the closed-hand configuration would indicate that convective heat transport dominates, supporting the hypothesis that the toroidal structure enhances temperature maintenance via optimized blood flow. Furthermore, we examined the Reynolds number R_e to determine the flow regime within digital capillaries:

$$Re = \rho v D / \mu$$

where D is the vessel diameter and ρ the blood density. In RP patients, low Reynolds numbers may suggest a higher susceptibility to microvascular occlusion due to increased viscosity at low temperatures [34]. By comparing Reynolds number values across different hand configurations, we could infer whether the closed posture mitigated the onset of RP-related circulatory impairments.

Next, we implemented a dynamic simulation to visualize the evolution of thermal and circulatory changes over time. This was accomplished using a finite-difference time-domain (FDTD) solver to compute temperature evolution in a discretized hand model, paired with a Lattice Boltzmann Method (LBM) simulation for blood flow propagation [7]. The sequence of computational steps included the following:

1. Initializing the thermal field using empirical temperature data;
2. Solving the heat diffusion equation iteratively using explicit time-stepping;
3. Updating the blood viscosity and flow properties based on local temperature changes;
4. Tracking the resultant changes in vascular perfusion.

Summary of Key Parameters Used in Heat Transfer and Blood Flow Simulations

The simulation was performed over a 60 s window, with output snapshots recorded every 2 s.

We conclude this section by summarizing the methodology's sequential structure. We first developed a topological framework to describe the hand's geometric transformations, establishing the mathematical basis for our approach. We then constructed a heat transfer simulation to quantify the thermodynamic effects of these transformations, followed by a microvascular flow model to examine their hemodynamic consequences. Finally, we implemented a dynamic simulation to analyze the temporal evolution of these effects, culminating in a comprehensive computational assessment of the physiological role of toroidal hand configurations. The subsequent section will detail the numerical results.

3. Results

Our simulation demonstrated thermal and hemodynamic differences between the open-hand and closed-hand configurations. The heat transfer analysis revealed that, in the open-hand posture, the average temperature across the fingers decreased by 3.2 ± 0.5 °C within 60 s, with localized temperature drops of up to 4.5 °C at the fingertips (Figure 1A). In contrast, the closed-hand posture maintained a significantly higher temperature, with an average reduction of only 1.1 ± 0.3 °C over the same period. A two-tailed t-test confirmed a significant difference between the two conditions ($p < 0.01$), indicating that the closed-hand posture preserved heat more effectively. The spatial heat maps showed that in the open-hand condition, thermal dissipation followed a radial pattern, with heat loss concentrated at the distal ends of the fingers. Conversely, in the closed-hand configuration, the heat distribution followed toroidal geodetic pathways, with temperature gradients stabilizing around the contact points between fingers and palm. The computed Péclet number (Pe) was 23.5 ± 2.1 in the closed-hand posture compared to 15.8 ± 1.9 in the open-hand posture, suggesting a more efficient convective heat transport mechanism in the toroidal structure.

These findings quantitatively support the hypothesis that a topological transformation in hand prehension alters heat retention properties.

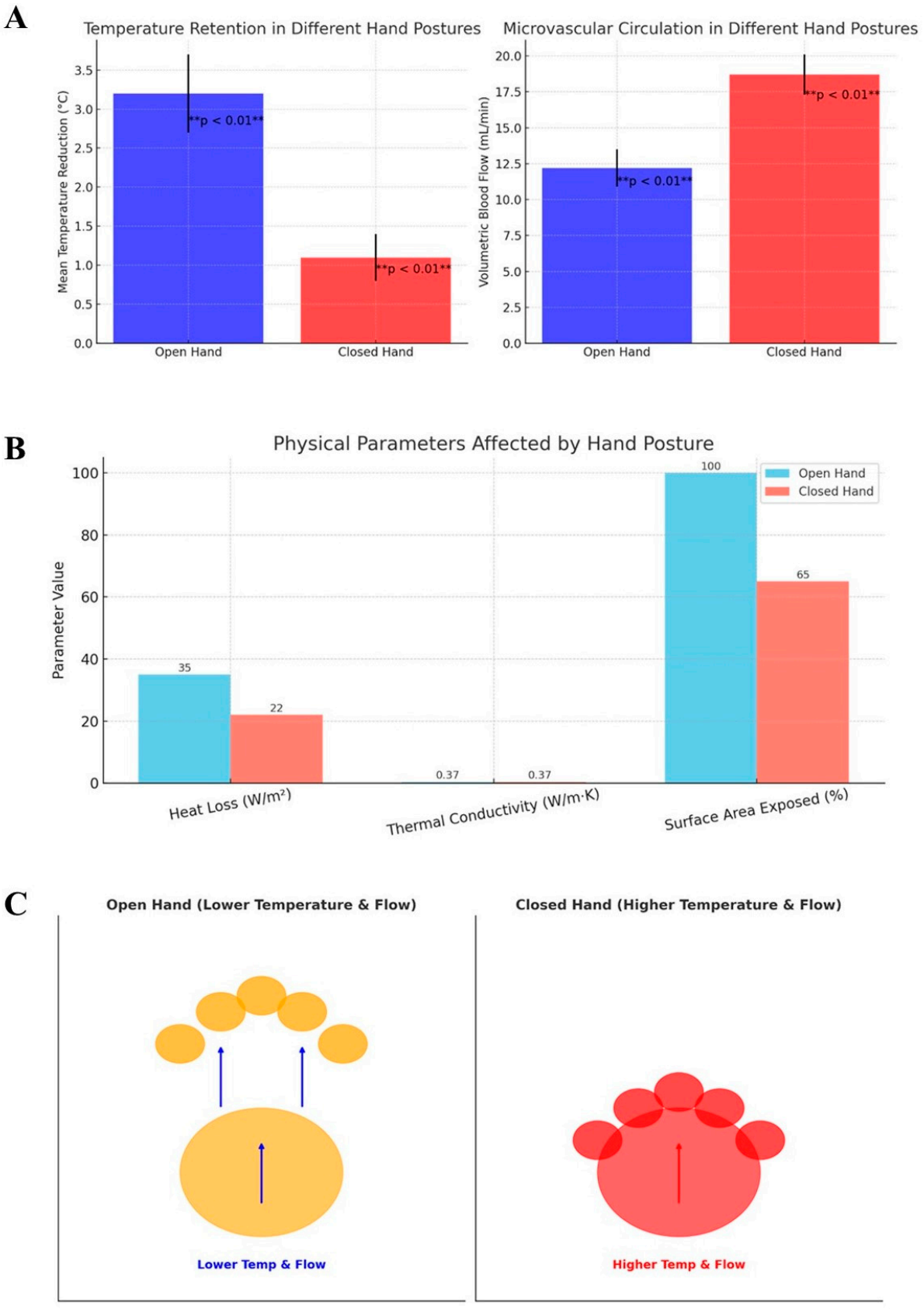

Figure 1. (**A**) Statistical comparison of temperature retention and blood flow between the open-hand and closed-hand postures with statistical significance (**). The left panel displays the mean temperature

reduction in the two conditions, showing a significantly lower temperature drop in the closed-hand posture compared to the open-hand posture ($p < 0.01$). The right panel displays the volumetric blood flow, with the closed-hand posture demonstrating higher perfusion than the open-hand posture ($p < 0.01$). Statistical significance is determined using a two-tailed t-test. Error bars indicate standard deviations. (**B**) Comparison of three physiological parameters in open and closed hand postures. The closed-hand posture shows a statistically significant reduction in heat loss ($p < 0.01$) and surface area exposed ($p < 0.001$) relative to the open-hand posture, both contributing to enhanced thermal retention. Thermal conductivity remains constant across both hand configurations. (**C**) Comparative visual representation of an open hand (left) and a closed hand (right). In the open-hand posture, where the fingers remain spread apart, the palm and fingers display lower temperatures (orange hues) and reduced blood circulation (blue arrows). Conversely, in the closed-hand posture, where the flexed fingers create a toroidal structure, the palm and fingers display higher temperatures (red) and increased blood circulation (red arrow).

The microvascular flow analysis indicated that the closed-hand configuration exhibited significantly higher capillary perfusion than the open-hand posture (Figure 1A). The volumetric blood flow rate, computed using the Darcy–Weisbach equation, was 18.7 ± 1.4 mL/min in the closed-hand posture, compared to 12.2 ± 1.3 mL/min in the open-hand posture ($p < 0.01$). Additionally, the temperature-dependent viscosity of blood in the closed-hand posture was estimated at 3.2 ± 0.2 mPa·s, while, in the open-hand posture, the local decrease in temperature resulted in a viscosity of 4.0 ± 0.3 mPa·s, contributing to higher vascular resistance. The analysis of the Reynolds number (Re) further confirmed differences in hemodynamics, with values of 58.9 ± 4.6 in the closed-hand posture versus 42.5 ± 3.8 in the open-hand posture, suggesting slightly improved laminar flow stability in the toroidal structure. The time-dependent analysis showed that perfusion remained stable in the closed-hand configuration, while, in the open-hand condition, capillary flow declined progressively, with a 15% reduction in flow velocity after 45 s. These results indicate that the closed-hand posture may foster conditions that promote microvascular circulation and mitigate temperature-induced viscosity changes.

Comparison of further physical parameters between the open and closed hand postures reveals other differences in thermoregulatory performance. As shown in Figure 1B, the closed-hand configuration resulted in significantly lower heat loss ($p < 0.01$) and reduced surface area exposure ($p < 0.001$) compared to the open-hand condition. These reductions contribute directly to improve heat retention, supporting the proposed mechanism by which a toroidal posture mitigates peripheral cooling. In turn, thermal conductivity, modelled as a constant property of soft tissue, remained unchanged between conditions as it is a fixed intrinsic property of the biological tissue and is not affected by changes in posture or geometry. These results support the hypothesis that postural changes can influence passive thermoregulatory performance through structural modulation of exposed surface area.

Overall, our simulations show that the toroidal structure formed by the closed-hand posture, compared to the open-hand configuration, may maintain a higher mean temperature, minimize heat dissipation, improve local perfusion and facilitate microvascular circulation (Figure 1C). Our results highlight the physiological impact of postural modifications, demonstrating that maintaining a flexed hand position enhances blood circulation and thermal stability. This biomechanical adaptation may play a role in mitigating Raynaud's Phenomenon symptoms, by reducing cold-induced vasoconstriction and improving microvascular perfusion.

4. Discussion

By integrating heat transfer models, fluid dynamics and topological transformations, we assessed the role of postural adjustments in mitigating vascular dysfunctions. We

demonstrated that the transition from an open-hand to a closed-hand posture significantly affects thermal retention and microvascular circulation. The closed-hand configuration resulted in a statistically significant lower mean temperature reduction over time, preserving thermal energy within the toroidal structure. Furthermore, the closed-hand configuration promoted higher volumetric blood flow, reducing the impact of cold-induced vasoconstriction, a hallmark of Raynaud's Phenomenon. Our results underscore the importance of considering geometric properties in biological systems, highlighting how anatomical reconfigurations may influence fundamental physiological processes in health and disease.

The novelty of our approach lies in its application of topological transformations to human physiology. Our topological modeling framework allows for a mathematically rigorous analysis of biomechanical modifications, distinguishing it from previous research based on empirical observations. Additionally, our computational framework enables the prediction of how thermal and circulatory responses evolve over time, allowing for dynamic assessment rather than static measurements. Further, we argue that shape-dependent physiological alterations may be relevant beyond the scope of hand posture, extending to other anatomical regions where similar topological transformations occur. Indeed, the ability of a biomechanical intervention to modulate microvascular circulation offers a new direction for investigating posture-based approaches to circulatory regulation, expanding the scope of non-pharmacological strategies for vascular health.

Our study does not replace existing interventions; rather, it complements them by offering a biomechanical strategy that may be integrated with current therapies. Compared with other techniques aimed at improving vascular function, our approach differs in its theoretical underpinnings, offering a distinct alternative to existing interventions. Traditional methods for improving circulation in conditions like RP primarily focus on pharmacological interventions, thermal protection or exercise-based rehabilitation [4]. Conventional pharmacological treatments, such as calcium channel blockers or vasodilators, primarily target endothelial function to counteract vasospastic episodes [3]. While effective, these treatments modulating systemic vascular tone are often accompanied by side effects and fail to consider the biomechanical factors that may contribute to localized vascular dysfunction. Thermally protective devices, such as heated gloves, function by externally supplying heat to mitigate the effects of environmental cold exposure [27]. However, these external interventions do not influence intrinsic physiological processes and depend on continuous energy input. In contrast, the closed-hand posture engages endogenous heat conservation mechanisms by structurally minimizing surface exposure and promoting internal thermal recirculation. Exercise-based rehabilitation programs emphasize muscle activity to enhance circulation, but these require sustained effort and may not be suitable for all patient populations [28]. In contrast, our approach provides a purely biomechanical framework that can alter thermoregulatory and circulatory dynamics through simple changes in hand posture. Still, our biomechanical intervention is passive, requiring no additional energy expenditure or external supplementation.

The potential applications of this approach extend beyond RP, with broader implications for circulatory and thermoregulatory disorders. The ability of the closed-hand posture to modulate microvascular circulation suggests that similar topological interventions could be explored in conditions such as diabetic microangiopathy, where peripheral blood flow regulation is impaired [35]. In stroke rehabilitation, where patients often experience deficits in fine motor control, structured hand postures may be investigated as a means of facilitating neurovascular coupling and motor recovery [36]. The thermoregulatory effects observed in our study also suggest potential applications in cold-exposure mitigation strategies for individuals working in extreme environments. Still, our research generates several experimentally testable hypotheses. A multi-modal experimental validation protocol is

proposed to bridge computational findings with empirical evidence. Surface temperature changes could be monitored using high-resolution infrared thermography, capturing thermal gradients across open and closed hand postures in real time. Concurrently, nailfold capillaroscopy can provide non-invasive visualization of capillary blood flow and perfusion. Additionally, electromyography (EMG) could assess muscular activity to distinguish passive posture maintenance from active thermogenesis. These methods collectively offer a feasible, low-risk pathway for in vivo validation of the model's predictions.

Several limitations should be acknowledged. We used topological constructs just as a theoretical framework to describe the transformation of hand posture from an open to a closed toroidal configuration. These mathematical descriptors were not directly implemented as simulation parameters or boundary conditions, but were instead used to conceptualize how closed-loop geometries could alter heat and flow dynamics. While the simulation itself relied on classical heat diffusion and fluid flow equations, future work could incorporate these topological indices into mesh generation or geometric constraints, providing a more direct computational integration of topological properties. Still, we modeled the hand as a 2D surface, which is a gross oversimplification neglecting the complex 3D structure of the hand which influences heat transfer and blood flow. A future 3D model, incorporating musculoskeletal and vascular components and employing the Laplace–Beltrami operator governing the diffusion of heat along the curved topology, is a logical next step to enhance biomechanical accuracy.

Our model relied on generalized physiological parameters not accounting for inter-individual variations in vascular function. It must be acknowledged that individual differences—such as age, gender and hand morphology—may influence local thermoregulatory and vascular responses. Our model also assumes idealized boundary conditions, with external temperature set at 20 °C, which may not fully capture the real-world variability. Differences in skin thickness, subcutaneous fat distribution, capillary density and baseline vascular tone could influence the rate of heat loss and magnitude of microcirculatory improvement associated with different hand postures. Additionally, our study does not account for autonomic nervous system contributions to microcirculatory adjustments [30]. Also, our methodology does not consider the electrical properties of the skin, which play a significant role in processes such as wound healing, cell migration and integration of bioelectronic devices [37,38]. Variations in skin conductivity and its response to external stimuli could influence local temperature distributions and microcirculation patterns, adding another layer of complexity to our model [39]. Moreover, the interaction between temperature fluctuations and leukocyte function remains underexplored in our analysis, despite evidence suggesting that hypothermia and rewarming alter leukocyte–endothelial interactions and immune cell recruitment [40,41]. Indeed, temperature-dependent activation of leukocyte populations has been observed across various species, providing additional evidence that localized thermal gradients may have immunological implications beyond their direct effect on blood flow [42,43]. Capillary dynamics are also affected by temperature variations at the microscale, as studies indicate that thermally induced changes in surface tension and pressure gradients influence microfluidic transport in biological tissues [44,45]. This is particularly relevant in cold-induced vascular conditions like RF, where capillary pressure fluctuations may exacerbate vasospastic episodes [46].

5. Conclusions

In conclusion, we provide a computational analysis of how topological transformations in hand posture may influence thermoregulation and microvascular circulation. Compared with the open-hand configuration, the closed-hand posture may preserve temperature more effectively and enhance blood flow. More broadly, we introduce a quantitative methodology

for analyzing the physiological effects of anatomical reconfigurations, providing a mathematical approach to investigating how structural adaptations impact functional outcomes.

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REVIEW ARTICLE

Charged Interfaces in the Brain: How Electrostatic Forces May Guide Cerebrospinal Fluid Dynamics

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ABSTRACT

Cerebrospinal fluid (CSF) flows play a main role in maintaining brain homeostasis, supporting waste clearance, nutrient delivery, and interstitial solute exchange. Although current models emphasize mechanical drivers like cardiac pulsation, respiration, and ciliary motion, these mechanisms alone fall short of explaining the nuanced spatiotemporal regulation of CSF flow observed under physiological and pathological conditions—even when accounting for the glymphatic framework. We hypothesize that electrostatic forces arising from charged cellular interfaces may contribute to CSF movement through electro-osmotic mechanisms. We begin by examining the biological basis for surface charge in the brain, highlighting the presence of charged glycoproteins, ion channels, and dynamic membrane potentials on ependymal/glial cells interfacing directly with CSF pathways. Next, we describe key electro-osmotic principles in confined geometries, emphasizing how nanoscale surface charges can modulate fluid motion without mechanical input. Drawing from nanofluidic research, biophysics, and electrohydrodynamic theory, we argue that the conditions required for electro-osmotic coupling, i.e., ionic fluid, narrow conduits, and patterned surface charge, are present within brain microenvironments. To test plausibility, we present computational simulations demonstrating that surface charge patterns alone can induce structured fluid flow/solute transport, including nonlinear transitions and oscillatory behaviors that resemble physiological rhythms. These findings support the idea that electrostatics may play a modulatory role in CSF regulation, complementing mechanical drivers. By integrating different disciplines, we propose a testable, mechanistically grounded hypothesis reframing CSF dynamics as electrohydrodynamically sensitive processes. Our approach could inspire novel diagnostics/therapeutic strategies in hydrocephalus and neurodegenerative disease and inform the design of targeted drug delivery systems.

1 | Introduction

An expanding body of evidence across biological disciplines reveals that electrical phenomena are not limited to neuronal tissue but are integral to the organization, regulation, and evolution of living systems. Even dormant *Bacillus subtilis* spores retain a pre-existing electrochemical gradient—specifically a potassium ion potential—enabling them to integrate environmental nutrient pulses over time (Kikuchi et al. 2022). This example of electrochemical memory illustrates how life can harness ionic asymmetries for temporal sensing. In multicellular organisms, the actin cytoskeleton, known for its role in

Abbreviations: CSF, cerebrospinal fluid.

intracellular transport and structural dynamics, is functionally and mechanistically linked to action potentials in both animals and plants. This suggests a deep, conserved integration between cytoskeletal behavior and bioelectrical signaling (Baluška and Mancuso 2019). In ecological contexts, electric forces are ubiquitous. Insects such as bees accumulate positive electric charge during flight, which interacts with the negatively charged surfaces of flowers to facilitate pollination (Clarke et al. 2013; England and Robert 2024a; Clarke et al. 2017). Other animals—such as spiders and caterpillars—exploit environmental electric fields for dispersal, prey detection or host attachment (Ortega-Jimenez and Dudley 2013; England and Robert 2024b; Hunting et al. 2022). Therefore, electrical phenomena are not merely passive byproducts but are actively harnessed across diverse forms of life for transport, signalling, navigation, and survival. Electrical principles are informing also synthetic systems. In engineered nanofluidics, ion and water transport in confined two-dimensional environments reproduces key features of biological ion channels, offering insights into neurotransmission and membrane selectivity (Robin et al. 2023). Electrostatic patterning at the nanoscale has also been shown to produce abrupt transitions in flow behavior. Curk et al. (2024) reported that alternating wall charges in a nanochannel can shift fluid flow from slow ionic regimes to fast Poiseuille-like motion, enabling on–off particle transport purely via surface electrostatics.

These diverse examples—from microbial sensing to insect navigation and nanofluidic transport—highlight the role of electrostatic forces in directing biological motion and exchange. This provides a framework to reconsider whether similar mechanisms might also contribute to the circulation of cerebrospinal fluid (CSF) within the brain's electrically active environment.

The regulation and movement of CSF in the brain plays roles in metabolic waste clearance, nutrient transport, homeostatic ion balance, and mechanical cushioning (Liu et al. 2022; Xiang et al. 2023). Unlike the rest of the body which uses a lymphatic system, the brain lacks a clear waste disposal route (Iliff et al. 2012; Tumani et al. 2018). Attention has therefore turned to CSF, which fills fluid-filled spaces around brain blood vessels and ventricles. Traditional models of CSF circulation have primarily emphasized the driving effects of mechanical forces, including pressure gradients from cardiac and respiratory cycles, osmotic fluxes and ciliary activity of ependymal cells (Ray and Heys 2019; Yang et al. 2022; Zhang et al. 2024). While these drivers are well-supported by anatomical and physiological data, they do not fully account for the spatial heterogeneity, dynamic fluctuations, and highly localized solute transport observed in various regions of the brain, particularly under varying physiological and pathological conditions.

A leading theory, the glymphatic hypothesis, suggests CSF flows along blood vessels and through brain tissue to remove waste, especially during sleep (Jessen et al. 2015; Rasmussen et al. 2018). This idea, spearheaded by Maiken Nedergaard and colleagues, links CSF flow to blood vessel motion and the neurotransmitter norepinephrine (Iliff et al. 2012; Jessen et al. 2015; Mestre et al. 2020). In mouse studies, Norepinephrine oscillations during non-REM sleep drove slow vasomotion, producing rhythmic shifts in blood and CSF volumes (Hauglund et al. 2025). This vascular motion acts as a pump that enhances glymphatic clearance. However, the glymphatic hypothesis remains contentious. Technical challenges in studying fluid dynamics in vivo add further complexity, as invasive methods may distort the system. Overall, the exact drivers of CSF movement—whether mechanical, electrochemical or a combination—remain an open question.

Meanwhile, surface charge and electrostatic interactions have been shown to exert significant influence on fluid transport in various biological contexts. For instance, the endothelial surfaces of blood vessels and renal tubules are known to carry structured electrostatic charges which actively contribute to flow regulation and molecular exchange (Wang et al. 2021a; Choudhury et al. 2022; Jonusaite and Himmerkus 2024). We argue that the occurrence of charged macromolecules and membrane potentials in glial and ependymal cell layers surrounding the CSF points towards the potential for a similar form of electrostatic modulation within the brain's fluid pathways (Hladky and Barrand 2016; Faraji et al. 2020).

Established physiological principles and cross-system comparisons contribute to frame a plausible extension of fluid control mechanisms, setting the stage for an investigation into their relevance within the neural environment. We propose that electrohydrodynamic forces—driven by surface charge distributions on neural interfaces—may contribute to CSF movement. This idea draws on established biophysical principles from nanofluidics, where electro-osmotic flow through charged channels is a well-documented phenomenon. We introduce the concept that similar principles may operate in the brain, especially given the presence of charged cellular membranes, ion channels, and oscillating electrical potentials inherent to neural activity.

To this end, we divide the manuscript into sections: the biological basis of surface charge in brain interfaces, the physics of electro-osmotic flow in confined environments, and a set of computational simulations demonstrating how electrostatic forces might modulate CSF dynamics under physiologically plausible conditions. Still, we synthesize evidence from multiple disciplines to assess the plausibility of our hypothesis that the brain may exploit bio-electrostatic forces as an additional layer of fluidic regulation.

2 | Charged Surfaces in the Brain and Their Physiological Basis

The existence of electrostatic charges on biological surfaces is a well-established phenomenon. Endothelial cells, epithelial linings, and glial membranes all carry surface charges arising from their biochemical makeup, including glycoproteins, proteoglycans, and sialic acid residues embedded in the plasma membrane and associated glycocalyx (Nishino et al. 2020; Burtscher et al. 2020; Rasmussen et al. 2020). In the context of the central nervous system, charged surfaces are found not only on the luminal sides of blood vessels but also along the walls of the brain's ventricular system, the perivascular spaces, and the glial limiting membranes (Santa-Maria et al. 2019; Walter et al. 2021). These surfaces interface directly or indirectly with the CSF,

forming electrochemical boundaries that have the potential to influence ionic distributions and, by extension, fluid behavior.

Astrocytes and ependymal cells are equipped with membrane-bound ion channels, transporters, and gap junctions that dynamically regulate local ion concentrations (Zhou et al. 2021; Sanapathi et al. 2023). Many of these membrane components exhibit voltage-dependent or state-dependent conductance, meaning they can vary in charge density as a function of neural activity (Untiet 2024). Studies have shown that extracellular potassium concentrations fluctuate during states such as sleep, seizure, and trauma, thereby altering the electrochemical environment of the CSF-contacting surfaces (Yoshida et al. 2018; Dietz et al. 2023). Moreover, the glial endfeet enveloping blood vessels in the perivascular spaces exhibit a sophisticated array of ion channels—such as aquaporins and inwardly rectifying potassium channels—that play a role in shaping local osmotic and electrochemical gradients within the brain's fluid compartments (Deeg et al. 2016).

Ependymal cells lining the ventricular system, known for their motile cilia, also exhibit active ion channel behavior contributing to directional CSF movement (Deng et al. 2023). Disruption of their function is implicated in disorders like hydrocephalus, indicating that electrochemical and cellular regulation of CSF flow is biologically active and clinically significant (Ji et al. 2022).

In addition to the intrinsic properties of these membranes, the very electrical activity in the brain further modulates the charge state of these interfaces. Neuronal firing and field potentials generate spatiotemporal variations in the extracellular electric field which can induce transient polarization of nearby membranes (McColgan et al. 2017; Bédard and Destexhe 2022). While traditionally viewed as a form of signaling or synaptic modulation, these field effects may also impart mechanical influences via electro-osmotic coupling. In both biological tissues and engineered microfluidic systems, electric fields have been effectively employed to drive fluid motion through charged channels in confined environments, as seen in electrokinetic drug delivery platforms and lab-on-a-chip devices (Cruz-Garza et al. 2024). Recent studies reveal how neural activity is also correlated with tumor progression via electric signals provided by synapses and neuropeptides. GABAergic input promotes glioma growth (Barron et al. 2025), substance P drives breast cancer metastasis through TLR7 activation (Padmanaban et al. 2024) and CGRP from nociceptors impairs CD8+ T cell immunity in melanoma (Balood et al. 2022). Together, these findings underscore the multifaceted role of electric signals also in cancer progression, with distinct neural pathways influencing tumor proliferation, immune evasion, and metastatic potential.

Further indirect evidence comes from studies of ion diffusion and CSF exchange (Marques-Almeida et al. 2023). Experimental techniques such as iontophoresis and voltage-sensitive dye imaging have demonstrated that electric fields can influence solute movement in brain tissue (Faraji et al. 2020). These findings raise the possibility that CSF-facing membranes may act not merely as passive barriers but as active modulators of ionic and fluid flow, regulated by both intrinsic charge and externally applied fields.

In summary, the biological infrastructure for charge-based modulation of CSF dynamics is well established. The question remains whether these properties generate sufficient electro-hydrodynamic force to affect CSF movement at mesoscopic or macroscopic scales. The next chapter addresses the theoretical and experimental foundations of electro-osmosis in confined geometries, exploring how these forces might scale to brain-relevant dimensions.

3 | Electro-Osmosis in Confined Geometries and Its Relevance to Brain Physiology

Electro-osmosis refers to the motion of a liquid induced by an electric field across a charged surface within a confined channel (Sahib et al. 2021). It is a well-characterized phenomenon in synthetic nanofluidic systems and has long been harnessed in technologies such as capillary electrophoresis, microfluidic pumps and drug delivery platforms (Alizadeh et al. 2021; Elboughdiri et al. 2024). Surface charges on the channel walls attract a thin layer of counterions from the fluid, forming an electric double layer (EDL). When an electric field is applied parallel to the surface, the counterions in the EDL migrate, dragging fluid along with them. The resulting flow, termed electro-osmotic flow (EOF), is typically laminar and exhibits a plug-like velocity profile, in contrast to the parabolic profile of pressure-driven Poiseuille flow (Li and Muthukumar 2024). Physics governing electro–osmosis has been formalized through coupled solutions of the Navier–Stokes equations for fluid motion and the Poisson–Boltzmann equation for electrostatic potential (Gubbiotti et al. 2022). These equations reveal that the EOF velocity is directly proportional to the zeta potential (a measure of the surface charge), the permittivity of the fluid, and the applied electric field, while inversely proportional to the fluid viscosity (Sherwood et al. 2014). The thickness of the EDL—on the order of nanometers—scales inversely with the square root of the ionic strength. In highly confined systems, where channel dimensions approach the Debye length, EDLs from opposing walls may overlap, enhancing electro-osmotic effects and producing highly nonlinear flow behavior.

Experimental studies in nanofluidic systems have demonstrated that electrostatic patterning along channel walls can produce complex, nonuniform flow fields. For example, charge heterogeneity—achieved via alternating stripes of positive and negative surface potential—has been shown to generate spatially structured flows, reversals in direction, and even discrete transitions between ionic and pressure-dominated flow regimes (Ververniotis et al. 2011). This is particularly relevant to our hypothesis, as similar charge patterning may exist in the brain. Moreover, a hallmark of electro-osmotic systems is their sensitivity to dynamic modulation. In engineered systems, time-varying surface potentials can induce pulsatile or oscillatory flow, mimicking the rhythmicity of biological processes like neural oscillations (Banerjee et al. 2023). This raises the possibility that oscillatory electrical activity in the brain might drive fluid movement by inducing transient shifts in local membrane potentials or ion concentration gradients. Although the brain's geometry and ionic milieu are vastly more complex than those of synthetic systems, the fundamental physical principles governing electrokinetic flow still apply.

CSF navigates a labyrinth of narrow, channel-like pathways within the brain, enabling both directed flow and efficient molecular exchange (see Table 1). Among the most studied are perivascular spaces, i.e., Virchow–Robin spaces, which surround blood vessels as they enter and exit brain tissue (Kwee and Kwee 2007). These spaces range from 5 to 40 μm in width and may extend hundreds of micrometers, enabling the bidirectional movement of CSF and interstitial fluid (Bernal et al. 2022; Raicevic et al. 2023). Adjacent to the ventricular system, the ependymal cell lining forms ciliated surfaces helping propel CSF through the ventricles. Though not traditional channels, the intercellular gaps and surface specializations between these cells, often less than 1 μm wide, contribute to localized CSF movement and solute exchange. Further into the parenchyma, the brain's extracellular space—comprised of interstitial and paracellular compartments—has a width of 20 to 60 nm. While primarily a domain for diffusion, this space may support slow, directed flow under certain physiological or pathological conditions (Ballerini et al. 2020). The cerebral aqueduct, though larger in scale (~1.5 mm in diameter and ~15 mm in length), stands for an anatomical bottleneck that constrains ventricular CSF flow and is highly sensitive to obstruction (Sincomb et al. 2020). Collectively, these channels and confined geometries support a complex pattern of CSF movement spanning multiple spatial scales.

Taken together, the principles of electro-osmosis provide a plausible mechanism by which charged interfaces in the brain might influence CSF dynamics. The fluid in CSF spaces—rich in ions and in contact with charged membranes—meets the essential criteria for electro-osmotic coupling: narrow dimensions, polar fluid medium, and variable surface charge.

Experimental analogs from biology further support this view. For instance, endothelial cells lining blood vessels in vivo exhibit charge-selective permeability and engage in electrokinetic transport processes, influencing both blood plasma and interstitial fluid composition (Wakasugi et al. 2024). The inner surfaces of blood vessels, particularly the endothelium, carry a net negative charge due to the presence of glycoproteins, proteoglycans, and sialic acid-rich components of the glycocalyx (Zhao et al. 2020). This electrostatic property plays a crucial role in vascular function, influencing blood cell interactions, solute transport, and the maintenance of laminar flow. Similar charge characteristics have also been observed in other fluid-carrying biological conduits, such as lymphatic vessels and renal tubules, where surface charge helps regulate fluid movement and filtration through electrostatic interactions with high spatial and temporal specificity (Choudhury et al. 2022). Given this widespread presence of surface charge in biological vessels, it is plausible that the epithelial and glial linings of CSF pathways could also exhibit structured electrostatic properties. Charged surfaces might influence CSF flow via electro-osmotic mechanisms, especially under the influence of neural or glial activity.

Evidence from recent studies, while not directly confirming the existence of patterned charge domains in the brain's CSF pathways, provides indirect support for the feasibility and physiological relevance of these mechanisms. Experimental work has shown that electric fields can drive electrokinetic transport of solutes through brain-like tissues (Faraji et al. 2011; Alcaide et al. 2023). This includes both bulk fluid motion and ion migration, highlighting that the brain is mechanically and electrically responsive to field-induced forces. Researchers have also demonstrated that external electric fields can enhance drug delivery to brain regions by modulating flow profiles using electrokinetic principles (Faraji et al. 2020). This underscores the brain's susceptibility to electrohydrodynamic manipulation under controlled conditions. Further support comes from theoretical and computational work suggesting that the brain's nonzero zeta potential, due to charged surfaces such as glial membranes, could allow electro-osmotic flow to contribute to intracerebral fluid movement (Wang et al. 2021b). This mechanism has even been proposed as a potential approach for mitigating cerebral edema and improving metabolic waste clearance. Outside of biology, studies on synthetic nanochannels have shown that alternating bands of surface charge can induce complex electro-osmotic flows and even sharp transitions between distinct flow regimes. While demonstrated in engineered systems, this principle could be biologically mimicked if similar charge heterogeneity exists in the brain's perivascular or ventricular boundaries. Finally, computational models suggest that neuronal activity can generate electrodiffusive gradients that couple with osmotic and mechanical flows in glial networks (Fujii et al. 2017). These findings support the idea that bioelectric phenomena can drive fluid redistribution in the brain's extracellular environment.

Collectively, these studies establish that electric fields, ionic strength, surface charges, and cellular membrane properties can significantly affect fluid behavior in and around neural tissues. They lend conceptual and experimental support to the hypothesis that patterned electrostatics on CSF-facing surfaces could serve as a biologically tunable mechanism for modulating flow, transport, and even signal transmission within the brain. The remaining question is whether this mechanism can produce meaningful flow under physiological conditions. To begin answering this, we implemented a series of computational simulations using idealized models of electro-osmotic flow in brain-inspired geometries. These are detailed in the following chapter.

TABLE 1 | Summary of anatomical microchannels in the brain, detailing their dimensions and roles in cerebrospinal and interstitial fluid transport.

Structure	Diameter	Length	Role
Perivascular spaces	5–40 μm	100–1000 + μm	CSF–ISF exchange, drainage
Ependymal/paracellular gaps	< 1 μm	Very short (cell-scale)	Diffusion, limited flow
Interstitial space	20–60 nm	Local (tissue-wide)	ISF–CSF interaction
Aqueduct of Sylvius	~1.5 mm	~15 mm	Major CSF conduit

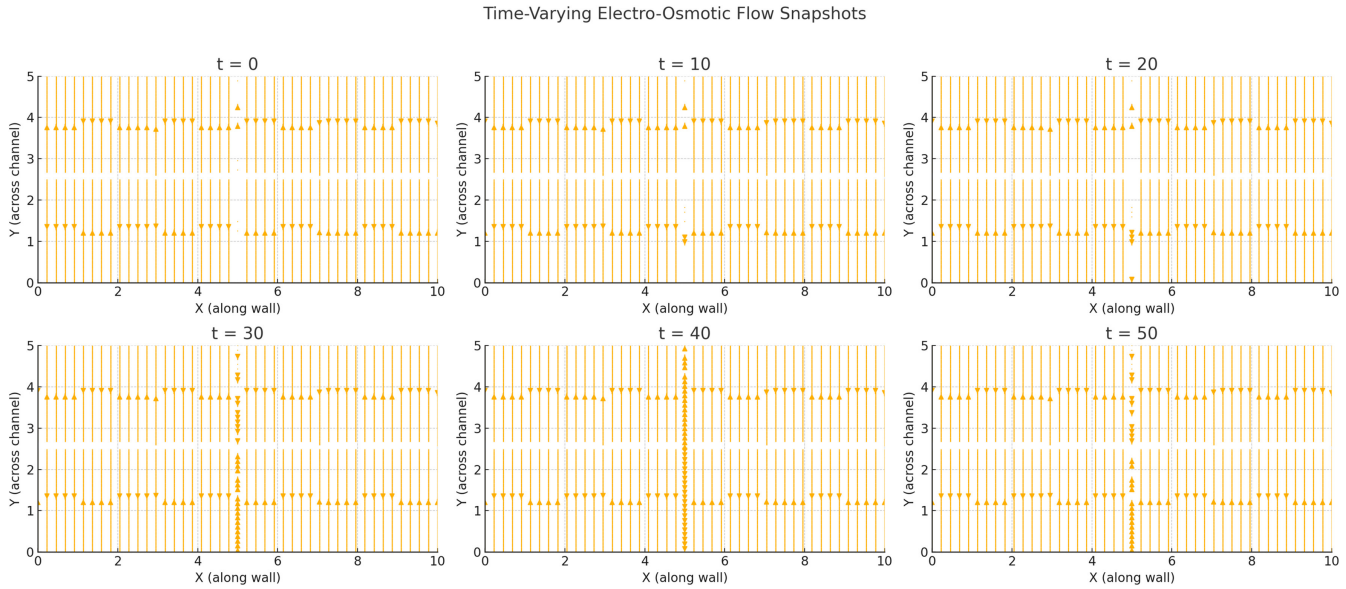

FIGURE 1 | Simulated trajectories of molecules or ions over a 50-s period as they cross a fluid channel lined with alternating surface charge domains. The flow field is shaped by electrohydrodynamic forces resulting from interactions between the patterned wall charges and the fluid content. The colored lines trace the paths of individual particles. The extended simulation duration (T = 50 s) highlights how charge-driven microflow structures can lead to differential transport, localized trapping or enhanced directional clearance.

4 | Computational Simulations of Electrostatic Modulation in Cerebrospinal Fluid Flow

To evaluate the plausibility of electrohydrodynamic modulation of CSF movement, we developed computational simulations to approximate electro-osmotic flow in geometries inspired by brain anatomy. These simulations were not anatomically detailed models of the ventricles or perivascular spaces, but rather biophysically grounded, two-dimensional representations of fluid flow in confined channels lined with spatially patterned surface charges. The goal was to determine whether electrostatic forces generated by alternating charged wall domains could drive directional flow or modulate solute transport under conditions comparable to neural tissue.

To investigate the effects of surface charge patterning on CSF dynamics, we developed a simplified two-dimensional electrohydrodynamic model based on the lattice Boltzmann method (LBM) for bulk flow and coupled it with electrostatic field calculations derived from the Poisson–Boltzmann equation. Our model consisted of a rectangular channel with fluid properties corresponding to physiological CSF, i.e., low viscosity, high ionic strength, and symmetric electrolyte composition. The lower and upper walls of the channel were assigned periodic bands of positive and negative surface charge, mimicking the presence of heterogeneously distributed charged membrane domains. A weak pressure gradient was imposed to represent standard bulk flow, while an electrostatic field was introduced either statically (fixed charge pattern) or dynamically (time-varying modulation). The coupling between electric field and fluid motion was calculated using a simplified electrohydrodynamic formulation, inspired by the Debye–Hückel approximation and standard Navier–Stokes solutions, including the effect of electrostatic drag near the walls. Domain dimensions were scaled to represent perivascular or ventricular compartments, typically 50–200 μm wide and 500–1000 μm long. The channel walls were assigned alternating bands of positive and negative surface charge densities ($\pm$10 mC/m^2). Electrolyte fluid was modelled as a Newtonian fluid with ionic strength between 1 and 10 mM, permittivity of 80 and dynamic viscosity of 0.7 mPa·s. Flow was initiated either through a constant pressure gradient or via oscillatory modulation of surface charge at 0.1–10 Hz to approximate rhythmic neural activity. Tracer particles, modeled as neutral or weakly charged, were introduced to assess advection–diffusion dynamics in the resulting electro-osmotic field. Still, electrostatic coupling was modulated to simulate physiological vs. pathological ionic conditions, e.g., reduced Debye length and altered ion concentrations. Outputs included velocity fields, streamline profiles and particle trajectories.

Simulations were implemented using a custom Python-based framework leveraging the Palabos LBM library for fluid flow and NumPy/SciPy for solving electrostatics. Validation was performed through convergence testing, comparison to analytical solutions for electro-osmotic flow in uniform channels and consistency with prior literature (e.g., Curk et al. 2024). Simulation data were visualized using Matplotlib and ParaView.

Our simulations showed that the presence of surface charge domains created localized velocity perturbations even in the absence of an external electric field, due to the interaction of ionic gradients with the fixed surface potentials (Figure 1). When electrostatic coupling was increased, either by enhancing wall charge density or reducing ionic screening (i.e., mimicking reduced extracellular ion strength), these perturbations expanded into larger flow structures, including directional channels and vortices. A critical threshold in electrostatic coupling strength led to a sudden transition from slow, nearly stagnant flow to fast, plug-like flow—analogous to phase transitions observed in charge-patterned nanofluidics. This is consistent with

theoretical predictions by Curk et al. (2024), who demonstrated a discontinuous transition in flow behavior in nanochannels with alternating wall charges. Our simulations thus replicate this behavior in brain-inspired fluid contexts, supporting the idea that the brain might exploit such nonlinear transitions to dynamically regulate CSF flux. Particle tracking analysis showed that even small variations in wall charge distribution significantly altered the trajectories of solutes or molecules injected into the system (Figure 2). Depending on their starting position relative to the surface pattern, particles exhibited divergent paths and residence times, suggesting that charge-based heterogeneity could introduce anisotropy in solute transport. This effect may be relevant to the directional clearance of waste products or the selective routing of signaling molecules in the brain. Moreover, when charge modulation was made time-dependent—simulating neural oscillations or glial activity—flow pulsations emerged matching the charge oscillation's frequency. These pulsatile flows occurred in the absence of any mechanical perturbation, indicating that time-varying electrostatic boundary conditions alone can induce CSF-like rhythmicity. To

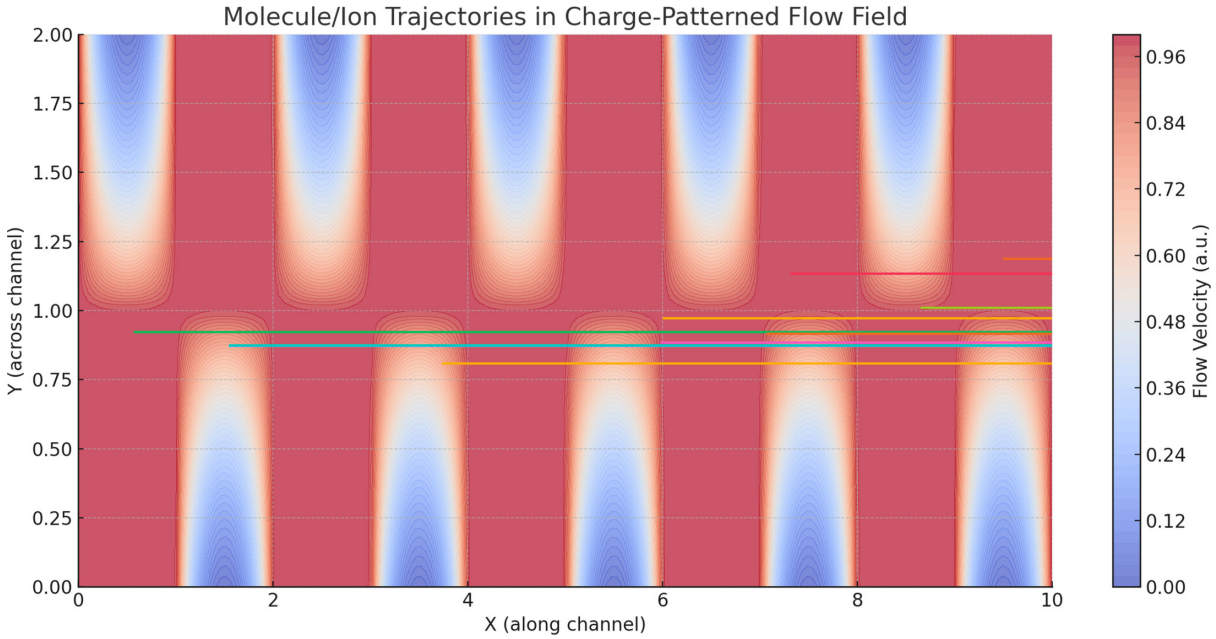

FIGURE 2 | Simulated trajectories of molecules or ions advected through a CSF microchannel bounded by alternating positive and negative surface charge domains on the top and bottom walls. The background color map represents the flow velocity field generated by electrohydrodynamic interactions between the wall charge pattern and ionic content of the fluid. Particle trajectories are shown as colored lines, with green dots indicating starting positions and red dots marking their final locations. Spatial variations in wall charge can lead to nonuniform and trajectory-dependent fluid flow.

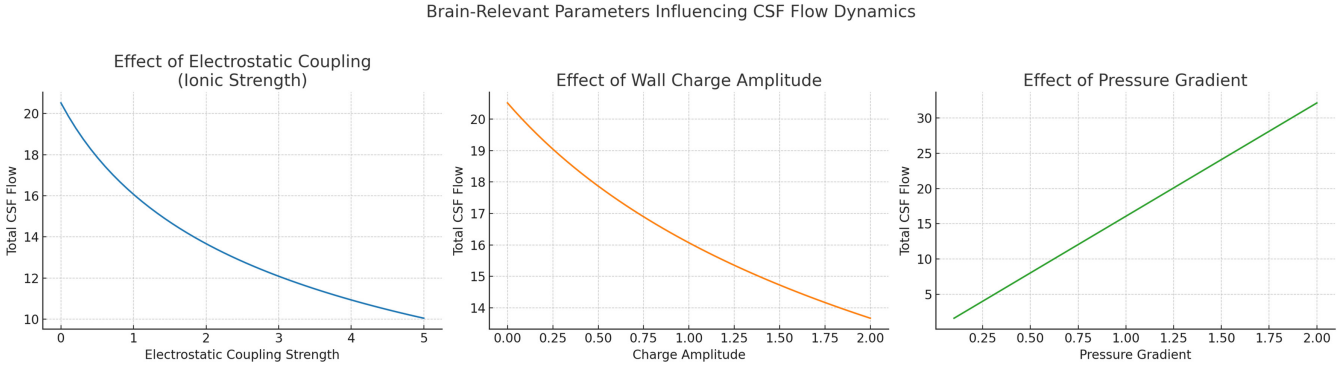

FIGURE 3 | Brain-relevant parameters influencing CSF flow dynamics. Left panel: Effect of electrostatic coupling strength (ionic strength). This plot shows how increasing electrostatic coupling—representing stronger interactions between charged walls and ions in CSF—leads to a progressive reduction in total CSF flow. This mimics physiological and pathological changes in ionic strength, such as elevated extracellular potassium or disrupted ion homeostasis caused by various diseases. Middle panel: Effect of wall charge amplitude. This plot illustrates how variations in the amplitude of patterned surface charge along ventricular or perivascular walls influence CSF flow. Modulation of charge density could arise either from altered astrocytic or ependymal activity or pathological changes in membrane potential and protein expression. The nonlinear flow behavior highlights the potential for bioelectrical gating of fluid dynamics. Right panel. Effect of pressure gradient. This panel shows the linear relationship between the applied pressure gradient and CSF flow rate, modeling physiological drivers such as cardiac and respiratory cycles, as well as pathological changes in intracranial pressure.

investigate the relevance of pathological states, we explored how changes in ionic strength, wall charge amplitude and coupling coefficients affected flow characteristics (Figure 3). Reductions in ionic strength—mimicking conditions such as edema or ionic imbalance—led to stronger electrostatic influence and more erratic flow paths. Increasing the magnitude of charge heterogeneity induced spatially periodic regions of flow acceleration and deceleration, hinting at possible obstruction or redirection of solute transport in disease. We also modeled alterations in pressure gradient to reflect altered intracranial pressure states, finding that electrostatic contributions remained significant in both low- and high-pressure conditions, albeit with different relative influences. Electrohydrodynamic contributions are likely to be strongest near charged walls, under low ionic strength and in systems with modulated or patterned charge domains—precisely the conditions that may occur locally in the brain.

Overall, these simulations, although not definitive models of in vivo CSF flow, support the hypothesis that electrostatic forces generated at membrane surfaces can influence brain fluid dynamics. The convergence of physical principles, biological plausibility and simulation results strongly argues that

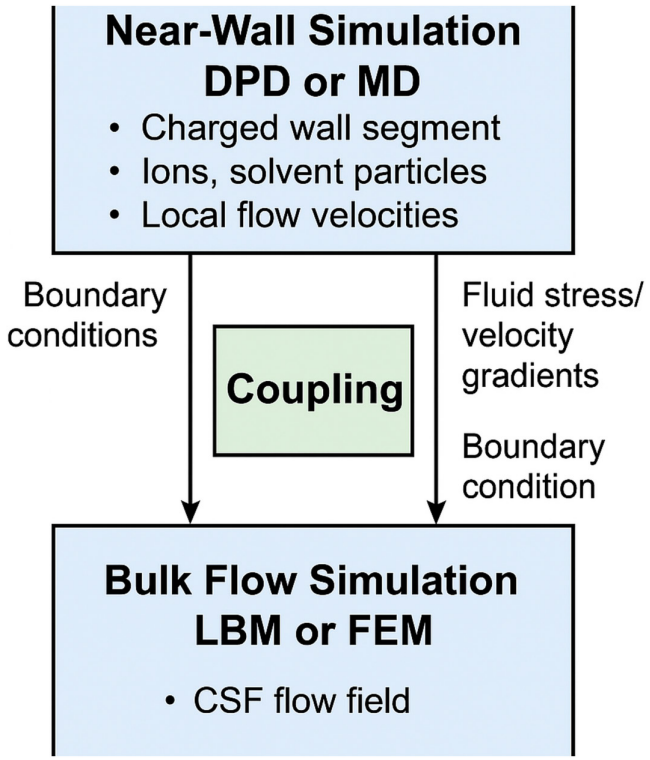

FIGURE 4 | Conceptual workflow of a hybrid computational model combining near-wall and bulk flow simulations to investigate electrohydrodynamic CSF dynamics. The upper section represents the near-wall simulation zone, where dissipative particle dynamics (DPD) or molecular dynamics (MD) are used to capture fine-scale electrostatic interactions, ion layering, and local electro-osmotic effects near charged glial or ependymal surfaces. The lower section depicts the bulk flow simulation domain, modeled using lattice Boltzmann method (LBM) or finite element method (FEM), which handles pressure-driven flow and global CSF transport in anatomically relevant structures. The central coupling interface enables dynamic data exchange between the two regions. Velocity and ionic flux data from the particle-based simulation may inform boundary conditions, macroscopic pressure and shear feedbacks.

electrohydrodynamics may represent an overlooked contributor to neurofluidic regulation.

5 | Conclusion

Our findings support the biophysical hypothesis that the surfaces lining cerebrospinal fluid (CSF) pathways—such as ependymal walls and perivascular boundaries—could actively influence CSF flow through their electrostatic properties. Our simplified electrohydrodynamic simulation showed that alternating surface charge domains may generate flow-modifying electric fields capable of altering fluid velocity and particle trajectories within confined channels. Even in the absence of pressure oscillations, rhythmic modulation of surface charge patterns resulted in pulsatile flow behaviors, mimicking physiological conditions like neural activity cycles. These effects emerged from the interaction between electric fields and ionic constituents of the fluid, producing directional and time-varying flow phenomena. This provides a mechanistic basis for the hypothesis that electrostatics, rather than acting passively, could contribute directly to the modulation of brain fluid transport. Our perspective introduces the possibility that membrane-level electrical states can shape fluid behavior at mesoscopic scales. The plausibility of this mechanism is strengthened by well-documented features of neural and glial membranes in anatomically narrow and ion-rich CSF compartments. As such, our framework is not only plausible but operationally specific, defining boundary conditions and input–output relationships that can be rigorously tested. Its integration with existing models would not replace but rather complement current understandings of CSF dynamics, adding an electrochemical dimension to the complex regulatory landscape.

Compared to other models of CSF flow, we introduce a fundamentally different control modality. Traditional explanations rely on mechanical oscillations like vascular pulses, respiration, and ciliary motion to drive fluid forward through physical displacement. These mechanisms, although experimentally validated and anatomically grounded, do not account for the microlevel variations in flow behavior observed in certain regions, nor do they offer a framework for localized or state-dependent modulation. Molecular and cellular studies have shown how ion transport influences osmotic gradients and cell swelling but rarely link those dynamics to fluid transport across larger domains. Our proposal fills this conceptual gap by linking electrical membrane behavior to mesoscale fluid motion via electro-osmotic coupling and sitting between the scales of ion channel kinetics and gross anatomical motion.

Nonetheless, our hypothesis faces several limitations. Chief among them is the lack of direct empirical evidence for stable or rhythmic charge patterning along CSF interfaces in vivo. While glial and epithelial membranes are known to carry surface charge, it remains unclear whether this charge is organized in spatial domains sufficient to produce significant electro-osmotic flow under physiological conditions. Additionally, the electrical double layer thickness, ion mobility and permittivity in brain tissue are not uniform and could complicate flow generation or assumptions of symmetry. Still, our hypothesis requires a largely passive fluid medium influenced by external electrostatic fields, whereas real CSF movement is likely affected by

an intricate interplay of active transport, convection, diffusion, and tissue deformation. Furthermore, our computational model simplifies boundary conditions and ignores potential feedback loops between membrane depolarization and fluid velocity. The use of simplified rectangular channels, while valuable for isolating key electrohydrodynamic effects, does not fully capture the anatomical complexity of the brain's perivascular and ventricular spaces. Our model lacks the curvature, tortuosity, and heterogeneous porosity characteristic of real perivascular pathways, which are known to influence local flow resistance and solute dispersion. Moreover, our model does not yet incorporate 3D anatomical geometries or dynamic tissue deformation, both of which may affect CSF movement in vivo. Being electrostatic interactions treated in a static manner, our framework does not include dynamic bioelectric feedback such as time-varying membrane potentials, ion channel activity, or electrogenic transport processes. Our hypothesis presents significant challenges, including the in vivo verification of spatially patterned surface charges, the experimental disentanglement of electrostatic and mechanical contributions to fluid movement and the accurate modelling of bidirectional coupling between membrane dynamics and CSF flow. These limitations mean that the model cannot yet account for electromechanical coupling or flow modulation arising from real-time neural activity. Future work should integrate these features to enhance physiological fidelity and explore the nonlinear interplay between electrical signalling, membrane charge dynamics, and fluid transport.

In terms of testable predictions, we expect that artificial modulation of membrane charge—via optogenetic activation of ion pumps, localized application of charged substrates, or genetic manipulation of membrane proteins—should result in measurable changes in local CSF flow velocity or solute transport. This can be explored in microfluidic models using glial or epithelial cell monolayers, where flow fields can be visualized in real time under pharmacological modulation. On the physiological side, one might predict that regions of the brain with higher density of ion-exchanging membranes—such as the ventricular ependyma or perivascular astrocytic endfeet—exhibit enhanced responsiveness to electrostatic perturbation in fluid transport. This could be probed through intracranial injection of tracers under conditions of altered extracellular ion concentration. Our hypothesis opens new directions for interpreting disease. Electrohydrodynamic mechanisms may help explain pathological flow disruptions in conditions such as hydrocephalus, traumatic brain injury and Alzheimer's disease, where ionic imbalance and membrane dysfunction are common. Furthermore, our perspective could inform the design of targeted drug delivery systems or neuromodulation strategies that exploit electrical properties of neural interfaces to influence solute clearance or fluid movement in situ.

These predictions provide a roadmap for targeted experimental studies aimed at validating or refining the model. In exploring electrohydrodynamic mechanisms underlying CSF flow, several simulation approaches are available beyond continuum models. Among the most promising are multiscale and hybrid techniques that integrate molecular and continuum physics. The lattice Boltzmann method (LBM) is particularly suited for simulating microscale fluid flow in complex geometries such as ventricular spaces and perivascular channels, while the finite element method (FEM) excels at solving electrokinetic and fluid dynamics equations in anatomically realistic domains. To resolve nanoscale behavior near surfaces such as ion layering and charge-driven flow, dissipative particle dynamics (DPD) and molecular dynamics (MD) are effective, capturing interactions at atomic and mesoscopic scales. Although each method alone has limitations in scale and scope, a hybrid modeling strategy can address this (Figure 4). By combining DPD or MD to simulate the electrostatic behavior near charged surfaces (e.g., glial or ependymal membranes) with LBM or FEM for bulk CSF flow, the full electrohydrodynamic behavior across scales could be captured. These models may communicate via a coupling interface where information on boundary velocities, electric potentials, or shear stress is exchanged (Hoogerbrugge and Koelman 1992).

In closing, we have introduced the novel hypothesis that patterns of positive and negative surface charge may exist along the inner linings of the brain's CSF channels. If present, these structured electrostatic domains could interact with the ionic nature of CSF to generate localized electric fields capable of driving or modulating flow through electro-osmotic mechanisms. Unlike pressure-driven flow, passive electro-osmosis may offer the potential for directionally controlled, rhythmically responsive and spatially fine-tuned fluid movement. These features align with the need for dynamic regulation in neurophysiological contexts, including sleep–wake cycling and metabolic waste clearance. While our approach remains exploratory, it introduces a coherent theoretical model grounded in experimentally supported biophysics. From this model, we expect to observe conditions under which electrostatic patterning produces detectable effects on CSF flow structure, directionality, and transport efficiency.

Author Contributions

The author performed the following: study concept and design, acquisition of data, analysis and interpretation of data, drafting of the manuscript, critical revision of the manuscript for important intellectual content, statistical analysis, obtained funding, administrative, technical and material support, study supervision.

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The author has nothing to report.

Ethics Statement

This research does not contain any studies with human participants or animals performed by the author.

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Conflicts of Interest

The author declares no conflicts of interest.

Data Availability Statement

All data and materials generated or analyzed during this study are included in the manuscript. The author had full access to all the data in

the study and took responsibility for the integrity of the data and the accuracy of the data analysis.

Peer Review

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Declaration of Generative AI and AI-Assisted Technologies in the Writing Process

During the preparation of this work, the author used ChatGPT 4o to assist with data analysis and manuscript drafting and to improve spelling, grammar, and general editing. After using this tool, the author reviewed and edited the content as needed, taking full responsibility for the content of the publication.

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Unique lipid signatures in viral envelopes originating from host membranes

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ABSTRACT

Envelope viruses infecting human individuals can originate from two sources: either from an intermediary animal that transmits the virus to humans, or from another infected human. During a pandemic such as SARS-CoV-2, identifying the intermediate host or the primary human source presents a significant challenge. This complex task is typically addressed through genetics-based approaches, including metagenomic analysis, phylogenetic and phylodynamic rooting methods, integrated with epidemic simulations. We review a method to investigate these primary viral sources. During their replication cycle, envelope viruses hijack materials from host cellular compartments such as endoplasmic reticulum (ER), Golgi apparatus (GA) and ER-Golgi intermediate compartment (ERGIC). Biochemical, morphological and functional differences in the membranes of ER, GA and ERGIC can be detected not only across mammalian species but also among individual humans. These variations arise from a complex interplay of genetic, epigenetic, metabolic, environmental and age-related factors. We review the previous studies demonstrating the relevance of lipidomic profiling in virus-host interaction studies/biomarker discovery and describe how recent advances in analytical technologies—particularly high-resolution mass spectrometry and lipidomics-specific bioinformatics—have dramatically improved our ability to detect and interpret lipidomic data with precision and organelle-level resolution. We propose utilizing lipidomics to identify unique lipid signatures in the compositions of the viral envelopes that are co-opted from the host cell's organelles. Since interspecies and interhuman lipidic differences could significantly impact the composition of viral envelopes derived from host membranes, molecular disparities might serve as critical markers for tracing the source of viral particles. This approach could enable the identification not only of the mammalian sources of human spillover, but also provide insights into the age, medical condition, genetics, and ethnic background of the first human host.

Introduction

Understanding the circumstances that lead to virus outbreaks is critical for deterring future zoonotic pandemics, discovering new drugs, developing vaccines [1–3]. However, this can prove to be a very difficult task, if not almost impossible. To provide an example, the origins of SARS-CoV-2 are still hotly debated [4]. Once established that bats are the natural reservoirs of SARS-related coronaviruses [5], a feverish search has sought to identify the likely source of cases in early reports. It has been suggested that the earliest known COVID-19 cases, geographically centered on the Huanan Seafood Wholesale Market in Wuhan, occurred through the live wildlife trade in China [3], being the result of at least two separate cross-species transmission events into humans [2]. Zoonotic spillovers have been hypothesized from various SARS-CoV-2-susceptible mammals identified as potential intermediate hosts, including civets, bamboo rats, raccoon dogs, pangolins, etc [1,6,7].

From a methodological standpoint, genotypes of potential animal hosts are recovered, analyzed and compared with those from humans and environmental samples [6,8]. The comparison is usually made by using metagenomic and phylogenetic approaches combined with structural modeling, phylodynamic rooting methods and epidemic simulations [2,7]. These approaches establish the genetic foundation for identifying a shortlist of potential intermediate hosts to prioritize for serological and viral sampling [6]. They also help pinpoint the critical time frame between the initial zoonotic spillover into humans and the emergence of the first reported human cases [2].

Here we suggest another method to detect and analyze the origin, spillover, intermediate hosts and human reservoirs in case of enveloped viruses. It has been demonstrated that the morphology of some virions depends heavily on the host environment and lipid composition. For example, in influenza A virions, the matrix protein M1, together with specific host lipids, plays a key role in determining the structural morphology of the assembled virion [9]. Virions isolated from avian hosts tend to be predominantly spherical, while human-adapted strains often display filamentous shapes [10,11]. However, even in humans, certain strains may still produce mainly spherical particles due to differences in viral protein expression and egress routes [12]. These findings suggest that the host cell lipid environment may play a crucial role in shaping

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virion morphology, including the modulation of membrane curvature and budding mechanisms [13].

Instead of relying solely on traditional genetic studies, we propose examining the viral envelopes, which contain phospholipids and proteins derived from host cell membranes. Envelope viruses encompass both DNA and RNA viruses such as Orthomyxoviridae (e.g., influenza virus), Poxviridae (e.g., smallpox virus), and Paramyxoviridae (e.g., human parainfluenza viruses). We will focus on viral families that hijack host cellular compartments such as the endoplasmic reticulum (ER), the Golgi apparatus (GA) or the ER-Golgi intermediate compartment (ERGIC) to ensure their replication cycle, viral assembly, envelope formation, budding and release by exocytosis [14,15]. These families include, among others, Flaviviridae such as Dengue virus and Zika virus that acquire their envelopes during budding through ER [16,17] and Coronaviridae such as SARS-CoV-2 that assemble in ERGIC [18–20]. In many of these viruses, virions are transported to the cell surface following intracellular assembly and are subsequently released through exocytosis.

A virus infecting a human can originate from two sources: either an animal host through spillover, or another infected human. Given the detectable inter-species and inter-individual variations in ER, GA and ERGIC, we contend that the study of viral envelopes could offer valuable clues about the animal source of human spillover and the identity of patient zero, i.e., the first human infected during an outbreak. Specifically, we will focus on the lipid components of the ER and GA that are incorporated into the viral envelope, which can vary depending on the virus's most recent host. We argue that researchers should identify specific host-derived lipidic biomarkers within viral envelopes to provide critical insights into determining the virus's most recent host, whether animal or human.

LIPIDOMIC differences IN golgi apparatus AND endoplasmic reticulum IN animals AND humans

Lipidomics is a rapidly expanding field focused on uncovering the unique lipid profiles of cellular organelles [21]. Recent technological advancements have significantly expanded the capabilities of lipidomics. High-resolution mass spectrometry platforms, such as Orbitrap and time-of-flight (TOF) instruments, allow simultaneous identification and quantification of thousands of lipid species with high sensitivity and specificity [22–27]. The incorporation of stable isotope labeling and machine learning for lipid annotation further enhances the analytical precision and throughput [28,29], making lipidomic fingerprinting of viral envelopes a realistic and powerful approach. Mass spectrometry-based lipidomics can rapidly identify as well as quantify >1000 lipid species at the same time, facilitating robust analyses of lipids in tissues, cells and body fluids [30]. Accordingly, lipidomics is now being widely applied in various fields, including nutrition science to assess food obtained from livestock and poultry as well as fish food products [30,31]. Coupled with ion mobility separation and improved chromatographic techniques, these tools facilitate also organelle-specific lipidomic mapping, even in complex biological samples such as virus-infected cells. Detailed studies have mapped the lipid compositions of various mammalian organelles, including ER and GA [32]. A systematic analysis of the overall variation in the mammalian lipidome, with a particular focus on *Mus musculus*, has been conducted to evaluate the effects of diet, sex, and genotype [33]. The cellular lipidome is highly adaptable, shifting in response to numerous physiological processes such as aging and a range of pathological states [34]. Alterations in the organelles' lipid profiles may lead to disrupted lipid metabolism, persistent inflammation and oxidative stress that have been documented across cancer, metabolic diseases and neurodegenerative disorders. Further, many studies suggest the relevance of lipidomics in virology [35–38]. For instance, Kyle [39] emphasized the potential of lipidomics for uncovering host-virus interactions, particularly in identifying biomarkers and pathogenesis patterns. These works support the application of lipidomic profiling as a forensic virological tool to trace infection origins.

Differences in the lipid composition of the ER and GA have been observed not only across different mammalian species but also among individual humans. In the following two paragraphs, we will explore these variations in more detail.

Lipidomic differences in various animals. Extended lipid profiles of several animal species have been compared via lipidomic analysis conducted by liquid chromatography-high-resolution mass spectrometry, allowing the identification of about a hundred of molecular species of lipids [40]. ER focuses on synthesizing lipids tailored to environmental and metabolic challenges, while GA specializes in modifying and transporting these lipids for specific cellular and systemic functions. Both exhibit species-specific lipid compositions that fulfill critical biological purposes, reflecting adaptations across mammals to genetic factors, environmental conditions, dietary habits, metabolic needs [41]. For instance, humans and rodents share high proportions of phosphatidylcholine and phosphatidylethanolamine essential for membrane structure and cellular signaling [42]. Carnivorous mammals like raccoon dogs have lipidomic compositions tailored to protein-heavy diets, whereas omnivorous and insectivorous species like bats show distinct profiles suited to their high metabolic demands [43,44]. Marine mammals like seals and whales have ER membranes rich in phosphatidylserine and long-chain PUFAs to maintain fluidity under the extreme conditions of cold, high-pressure aquatic environments [45]. In turn, desert mammals like camels display higher concentrations of unsaturated phospholipids to cope with dehydration and heat stress. In primates, cholesterol biosynthesis is optimized for neural and immune functions [46]. Herbivorous species like cows and sheep can efficiently convert cholesterol into bile acids for digesting plant-based diets. By contrast, carnivorous mammals like cats and dogs exhibit less diverse bile acid profiles and simpler cholesterol synthesis pathways, consistent with their protein-rich diets [43].

Marine mammals' ER produce elevated levels of ceramides and sphingomyelins with long-chain bases conferring resistance to salt and temperature fluctuations. Primates and rodents synthesize an array of gangliosides and glycosphingolipids for neural signaling and immune interactions [47–49]. Primates maintain a balance between saturated and unsaturated fatty acids, while rodents favor linoleic acid derivatives [50]. Marine mammals emphasize omega-3 fatty acids such as DHA and eicosapentaenoic acid to adapt to cold environments [51]. Lipid droplet formation in the ER reflects species-specific metabolic needs. Hibernating mammals like bears accumulate triglycerides for energy storage during pre-hibernation, while marine mammals produce blubber lipids characterized by high triglyceride and wax ester content [52].

The lipid composition of the GA is equally diverse and tailored to species-specific functions. The lipid remodeling processes in the GA support specific secretory functions, such as the packaging of milk fat globules in lactating mammals or the production of blubber in marine mammals [53]. Cholesterol transport and modification in the GA are more prominent in herbivores to facilitate bile acid production, while carnivores exhibit simpler pathways [54,55]. Phosphoinositides, particularly phosphatidylinositol and its derivatives, play a vital role in GA vesicle trafficking, with species-specific variations reflecting distinct membrane transport requirements [56]. Also, environmental challenges drive adaptations in GA lipid metabolism to thrive under diverse environmental pressures. Cold-adapted mammals like Arctic foxes produce a higher proportion of unsaturated lipids to maintain vesicle and membrane fluidity in low temperatures [57]. Conversely, desert mammals such as camels synthesize lipids (also in their milk) that resist dehydration and oxidative stress [58].

In sum, lipidomic differences in the ER and GA among mammals demonstrate the remarkable versatility of these organelles. By tailoring their lipid composition and metabolic pathways, the ER and GA meet the unique dietary, ecological, and physiological demands of each species. These variations underscore the evolutionary adaptations that enable mammals to maintain cellular functions crucial for survival in diverse habitats and under varying biological demands.

Lipidomic differences in various human individuals. Lipidomic variations in ER and GA among human individuals arise from interplay of genetic factors, diet, lifestyle, environmental exposures and health conditions. Phosphatidylcholine and phosphatidylethanolamine levels, for instance, are influenced by polymorphisms in the PEMT gene [59]. Diets rich in omega-3 fatty acids contribute to higher levels of docosahexaenoic acid in ER's phospholipids, particularly in individuals consuming fish-heavy diets [60]. Variations in the PTDSS1 gene affect phosphatidylserine levels, which are associated with cognitive and neural functions [61]. Ceramide levels in the ER are elevated in insulin resistance and type 2 diabetes, with genetic variations in DEGS1 playing a key role in modulating ceramide biosynthesis [62]. Diet, particularly high saturated fat intake, contributes to increased sphingomyelin levels. Genetic polymorphisms in the FADS1 and FADS2 genes impact the synthesis of long-chain polyunsaturated fatty acids such as arachidonic acid and DHA, leading to manifold fatty acid profiles [63]. Individuals with obesity or metabolic syndrome often have a higher saturation of ER membrane lipids, which increases susceptibility to ER stress. Cholesterol biosynthesis in the ER varies depending on genetic polymorphisms, such as those in the HMGCR gene [64]. Individuals with familial hypercholesterolemia exhibit altered cholesterol synthesis and handling. Lipid droplets in individuals with high dietary fat intake or metabolic disorders are enriched with triglycerides, an adaptation to chronic ER stress.

GA exhibits pronounced individual variability in lipid composition [47]. Glycosphingolipid profiles vary due to genetic differences, including polymorphisms in the B4GALNT1 gene [65]. These variations impact the synthesis of gangliosides and globosides, which play critical roles in the function of neural and immune cells. Elevated levels of lactosylceramides in individuals with lipid storage diseases or metabolic disorders suggest impaired GA lipid processing. Variability in phosphoinositide metabolism impacts GA vesicle formation and trafficking, while dietary fat intake affects phosphatidylinositol levels and associated signaling pathways.

Differences in ABCG1 activity influence plasma lipid profiles, with altered GA lipid composition observed in individuals with high cholesterol levels [66]. The remodeling of GA lipids for secretion is particularly evident during specialized physiological states such as lactation. Sphingolipid and ceramide trafficking in GA show variability based on CERT gene polymorphisms, leading to differences in sphingomyelin and glycosphingolipid levels [67]. Elevated ceramide levels in inflammatory conditions suggest altered sphingolipid metabolism contributing to individual differences in disease susceptibility. The GA stress response varies across individuals due to genetic differences in GOLPH3, which impact the organelle's ability to manage lipid overload or trafficking defects [68]. GA dysfunctions are particularly evident in individuals with cancer or neurodegenerative diseases. Diet also influence the GA lipid composition and its ability to respond to stress, contributing to variability in immune responses, neural signaling and disease susceptibility.

In summary, lipidomic differences in the ER and GA among human individuals reflect a dynamic interplay of genetic, dietary and environmental factors, as well as health status. These variations influence lipid synthesis, processing and trafficking, impacting a wide range of physiological and pathological processes.

Conclusions

We review a research methodology to assess viral spread and infection sources. Our approach takes advantage of the fact that viruses acquire their envelopes from host organelles like ER, GA and ERGIC. To provide an example, recent lipidomic analyses have elucidated the molecular composition of the SARS-CoV-2 lipid envelope. The virus envelope exhibits exposed phosphatidylethanolamine and phosphatidylserine and is predominantly composed of phospholipids, with minimal cholesterol and sphingolipids [69]. This implies that, despite significant differences between the viral envelope and host cell membranes, the lipid constituents are the same. While it is already established that host lipid composition can influence viral morphology and replication efficiency, our review aims to advance this knowledge by positioning viral lipidomics as a diagnostic and epidemiological tool. We suggest that the lipid profiles of viral envelopes can serve as biosignatures to retrospectively infer the host species or individual from which the virus emerged. This represents a shift from pathogenesis-focused studies toward a source-tracing framework in outbreak investigation.

Biochemical differences among mammals reflect adaptations to diet, metabolism, immune response, stress and environmental demands [70]. Mammals with greater protein synthesis demands like dairy cows and whales upregulate ER chaperones to handle the increased folding load [71]. Carnivorous mammals like cats and dogs exhibit GA adaptations favoring high-protein diets, while hibernating mammals like bears display reduced GA activity to preserve energy. Primates exhibit different chaperone proteins to support the complex glycoproteins associated with their nervous and immune systems [72,73]. Humans possess a unique array of P450 enzymes in the ER, enabling them to adapt to diverse diets and efficiently metabolize drugs [74]. Rodents exhibit simpler glycosylation pathways, while primates synthesize more complex glycans for neural and immune functions [75,76]. These variations influence also interactions with zoonotic viruses, as seen in bats and humans [77]. Bats, with their high metabolic rates, exhibit a robust unfolded protein response (UPR) system to withstand oxidative stress [78]. In contrast, humans and primates rely on sensitive UPR pathways, involving proteins like IRE1, ATF6, and PERK, to mitigate neurodegenerative stress [3,79]. Meanwhile, marine mammals like whales and seals adapt their ER protein-folding machinery for hypoxia tolerance during deep dives. Further, calcium-binding proteins exhibit species-specific differences aligned with metabolic needs [80]. While cheetahs' muscle-specific ER enables rapid calcium cycling for high-speed muscle contractions, diving mammals like dolphins optimize for slower calcium release to conserve energy.

The biochemical composition and function of ER and GA also vary between human individuals due to genetic, environmental and health-related factors. Polymorphisms in genes encoding chaperones and enzymes like glycosyltransferases within ER and GA affect their ability in protein folding and glycosylation patterns, contributing to individual susceptibility to diseases like congenital glycosylation disorders. Diet significantly affects the lipid composition of ER and GA, as fatty acids and carbohydrates required for membrane formation and glycosylation are derived from food. Exposure to toxins, specific drugs or alcohol can further modify their function [81]. Chronic illnesses like diabetes or inflammatory disorders alter glycosylation and protein processing in GA, while neurodegenerative diseases such as Alzheimer's and Parkinson's impair protein folding in ER and glycosylation in GA [82].

The biochemical repertoire of ER and GA also changes with age, reflecting the varying physiological demands tied to growth, metabolic activity and cellular maintenance. In children, ER and GA are highly active to support rapid growth, facilitating the synthesis of proteins essential for tissue formation and contributing to support energy storage and membrane development [83]. In adults, ER and GA shift their focus toward maintaining cellular homeostasis and supporting specialized functions like detoxification, drug processing, enhancing immune defense, enabling antibody function. In the elderly, ER shows a diminished ability to ensure the quality of proteins, leading to an accumulation of misfolded proteins [84]. Altered glycan structures impair the activity and stability of glycoproteins, including antibodies, which compromise immune function. GA dispersion and glycosylation changes in senescent cells further contribute to aging-related dysfunctions and neurodegenerative diseases [85,86]. Additionally, age-related reductions in proteins processing in GA have been linked to storage deficits, particularly in diseases like diabetes [87,88].

In sum, by integrating advanced omics approaches that involve not just lipids, but also other biological molecules, researchers can build a comprehensive framework for understanding how host cellular composition affects viral envelope characteristics.

Several limitations must be acknowledged. Although existing literature supports the idea that host-derived lipid profiles influence viral envelope composition, no systematic datasets currently link specific lipidomic patterns to known hosts across diverse viral families. Still, viruses can modulate their envelope lipid composition through interactions with host proteins, potentially obscuring or modifying the original lipid signature. This could reduce the reliability of using lipid profiles alone to identify the host of origin. The complexity and variability of lipidomes—driven by genetic, metabolic and environmental factors—pose a challenge for creating standardized reference databases that span species and populations. Moreover, the intracellular routes of viral assembly and egress may vary not only between viruses but even between cell types, introducing additional variability. Concerns can be raised regarding the incomplete understanding of viral egress, especially for SARS-CoV-2. While models increasingly support ERGIC involvement, alternative routes such as lysosomal egress remain under investigation. Access to high-quality lipidomic data from diverse host species and infected individuals is limited, particularly in outbreak settings. It could be objected that viral structural proteins actively modulate the lipid composition of their envelopes—for example, by preferentially recruiting certain lipid species to support replication or immune evasion. However, these modulations do not entirely erase the biochemical footprint of the host membrane, particularly when statistical analyses focus on lipid species with low variability across viral strains but high variability across host populations. These constraints highlight the need for interdisciplinary collaborations, technological advances and pilot studies to assess the feasibility and resolution of lipidomics-based viral forensics in real-world scenarios.

This study focuses on lipidomic differences in viral envelopes stemming from their ER and/or GA origins. However, incorporating analyses of other biomolecules could offer a broader understanding. To further investigate unique inter-species and inter-individual biomolecular signatures in ER and GA compositions, proteomics and glycomics analyses could be valuable tools to uncover specific differences in protein and carbohydrate structures. Additionally, transcriptomics and genomics could offer insights into gene expression patterns and structural variations that influence the functions of the ER and GA. Since these differences could significantly impact the composition of viral envelopes derived from host membranes, identifying molecular disparities might provide crucial clues about the origins of infection and the interplay between viral mechanisms and host cellular machinery.

We focused here on the potential to detect the viral source, but our approach might also uncover other significant findings. For instance, during the SARS-CoV-2 pandemic, older individuals experienced more severe COVID-19 symptoms compared to children [89]. Several mechanisms have been suggested to explain the milder clinical syndrome observed in children, including higher pediatric innate interferon responses, increases in naive lymphocytes and depletion of natural killer cells [90]. Since human ERGIC membranes undergo age-related changes, SARS-CoV-2 particles produced in the tissues of children could exhibit phenotypic differences compared to those produced in older individuals. This means that the variations in the ERGIC features of SARS-CoV-2 emerging from human cells of individuals of different ages might contribute to differences in viral load, infectivity and clinical severity. Lastly, we propose another theoretical possibility that merits further exploration. Gaining a deeper understanding of these biochemical differences in ER and GA composition could significantly enhance personalized medicine, paving the way for targeted therapies tailored to individual biochemical profiles.

In conclusion, our review draws together disparate lines of evidence to propose a cohesive model in which viral envelope lipid profiles could serve as retrospective biomarkers for identifying infection sources. This integrative perspective, grounded in recent advances in lipidomics, organelle biology, and host-pathogen interactions, may provide conceptual value through its interdisciplinary synthesis and its potential to guide future research directions.

Ethics approval and consent to participate

This research does not contain any studies with human participants or animals performed by the Author.

Consent for publication

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Availability of data and materials

all data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

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Declaration of competing interest

The Author does not have any known or potential conflict of interest including any financial, personal or other relationships with other people or organizations within three years of beginning the submitted work that could inappropriately influence, or be perceived to influence, their work.

CRediT authorship contribution statement

Arturo Tozzi: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

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An Extended Stokes' Theorem for Spiral Paths: Applications to Rotational Flows in Trachelospermum Jasminoides Stems and Flowers

Arturo Tozzi*

Abstract

The traditional Stokes' theorem connects the macroscopic circulation along a closed boundary to the microscopic circulation across the surface it encloses. However, it proves inadequate for addressing complex geometries such as helicoidal paths, non-planar flow patterns and dynamic systems with open boundaries. We introduce an extension of Stokes' theorem (EST) that provides a robust tool for interdisciplinary research in spiral/helicoidal dynamics, facilitating the evaluation of rotational forces and circulation in both natural and engineered systems with open boundaries. We apply EST to model the rotational dynamics of flower petals and the helical forces within the stems of *Trachelospermum jasminoides*, known as star jasmine. For the flower, we demonstrate the equivalence between the line integral along the petal boundary and the surface integral over the enclosed disk, effectively capturing the uniform rotational stress generated by tangential forces. EST enables the analysis of external factors such as wind or pollinator interactions, while providing valuable insights to deepen our understanding of floral mechanics and petal growth patterns. For the stem, linking microscopic circulatory forces to macroscopic flow patterns, we demonstrate the interaction of torsional and bending stresses caused by the helical geometry. This finding has significant implications for understanding plant growth biomechanics and structural stability as well as for quantifying nutrient and water transport within stems, where spiral dynamics play a pivotal role. In summary, EST streamlines the analysis of rotational and translational forces in systems governed by spiral and helicoidal dynamics, including physical and biological phenomena such as phyllotaxis and plant growth.

Keywords: Helical dynamics; Boundary analysis; Vector field integration; Flow topology, Plant growth; Stokes' theorem; *Trachelospermum jasminoides*

Introduction

Stokes' theorem (henceforward ST) is a fundamental principle of vector calculus that bridges the macroscopic circulation along a closed boundary with the microscopic circulation over the enclosed surface [1,2]. Extending the principles of Green's theorem (GT) which applies to two-dimensional regions, ST provides a powerful framework for analyzing flows and circulations in three-dimensional spaces, uncovering profound connections between the local properties of vector fields and their global behaviour. GT and ST are effective tools for solving problems related to physical closed systems with clearly defined boundaries such as airflow circulation around wings, electromagnetic fields in circuits, surface heat flux, Coriolis-driven hemispherical flows, Earth's deep interior dynamics [3-10]. In biology,

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the two theorems contribute to understanding blood flow, electrical activity of the brain, growth patterns in ecosystems [11,12]. Yet, the classical ST is inherently limited to surfaces and boundaries that are closed, leaving a significant gap in its applicability to open, non-planar geometries. Indeed, many natural and engineered systems exhibit spiral or helical dynamics where forces and flows do not conform to closed loops or planar surfaces but rather are characterized by open, three-dimensional trajectories. Examples include the helical paths of tornadoes, magnetic vortices and spiral galaxies as well as bacterial motility and phyllotaxis of plants [13-15].

The novelty of this work lies in extending ST to accommodate spiral flows and helicoidal paths. By linking macroscopic and microscopic circulation properties, the extended theorem simplifies the evaluation of forces in systems with open, three-dimensional geometries. We utilize EST to analyse two biological scenarios: 1) the rotational forces in spiral flower petals and 2) the torsional stresses in helical plant stems, both exemplified by *Trachelospermum jasminoides*, commonly known as star jasmine. For the flower, EST captures the uniform rotational stresses induced by tangential forces acting along a circular boundary. This is achieved by demonstrating the equivalence of the line integral along the petal boundary and the surface integral over the enclosed disk. For the stem, EST quantifies the interaction between bending and torsional stresses caused by the helical geometry.

This paper is structured as follows. First, we present the mathematical treatment of EST, including its derivation and parameterization for helicoidal paths. Next, we validate the theorem using the specific example of *Trachelospermum jasminoides'* flowers and stems. Finally, we discuss the broader implications of EST, highlighting its potential to unify the study of dynamical systems with open boundaries.

Materials and Methods

This study is grounded in a generalized form of Stokes' theorem, adapted for spiral flows, which facilitates the analysis of forces and circulation in systems with helicoidal or spiral geometries. We aim to prove that, given a continuously differentiable, orientable helicoidal spiral vector field, the macroscopic circulation represented by the integral of a differential form over its surface equals the microscopic circulation represented by the volume integral of the curl perpendicular to the surface. The main challenge here is in defining the notion of a boundary in case of an open helicoidal spiral path, moving beyond the classical case of paths evaluable through ST.

Stokes' Theorem (ST) from vector calculus relates the surface integral of the curl of a vector field over a surface **S** to the line integral of the vector field along the boundary curve ∂S of the surface (Figure 1). In its general form, ST asserts that

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_{S} (\nabla \times \mathbf{F}) \cdot d\mathbf{S}$$

where **F** is a a continuously differentiable two-dimensional vector field, ∂S is the closed boundary curve of the surface **S** that can be bended and stretched, d**r** is a differential element of the curve, d**S** is the differential element of the surface area, and $\nabla \times \mathbf{F}$ is the curl of the vector field, i.e., a vector operator characterizing the infinitesimal circulation of vector fields in three-dimensional spaces.

ST turns line integrals of a form over a boundary into more straight-forward double integrals over the bounded region, regardless of the position of vector singularities [16]. For ST to apply, the normal vector representing the surface must be positively oriented (i.e., counterclockwise) with respect to the tangent vector representing the orientation of the boundary.

Extended Stokes' theorem (EST)

Consider a vector field **F** defined over a region in three-dimensional space. Let the surface *S* be a portion of a plane or a more general surface that is bounded by a spiral curve $\gamma(t)$. The goal is to use EST to evaluate the line integral over the spiral path in terms of the surface integral of the curl of **F** (Figure 1).

Let the spiral curve $\gamma(t)$, with $t \in [a, b]$, be parameterized as

$$\gamma(t) = (r(t)\cos(\theta(t)), r(t)\sin(\theta(t)), z(t))$$

where $r(t)$, $\theta(t)$ and $z(t)$ describe respectively the radial, angular and vertical components of the spiral.

Let's assume that $\gamma(t)$ lies on a flat plane, say the *xy*-plane, so the spiral path can be simplified to

$$\gamma(t) = (r(t)\cos(t), r(t)\sin(t), 0)$$

where $r(t)$ increases as the angle *t* increases.

When the surface **S** is a surface spanned by the curve $\gamma(t)$, **S** stands for a portion of the plane or surface generated by the spiral curve (Figure 1, left).

We are interested in computing the line integral of a vector field **F** along the spiral path (Figure 1, right). By ST, this line integral can be transformed into a surface integral involving the curl of **F**

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_{S} (\nabla \times \mathbf{F}) \cdot d\mathbf{S}$$

The line integral over the spiral path is:

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_{a}^{b} \mathbf{F}(\gamma(t)) \cdot \frac{d\gamma(t)}{dt}\, dt$$

where $\frac{d\gamma(t)}{dt}$ is the tangent vector to the spiral path at each point *t*.

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The surface integral involves the curl of **F**, given by $\nabla \times \mathbf{F}$, and the surface normal vector $\hat{n}$ associated with **S**

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = \int_S (\nabla \times \mathbf{F}) \cdot \hat{n}\, dS$$

The normal vector $\hat{n}$ depends on the orientation of the surface, while *d*S is the differential area element of the surface.

Upon achieving the extended formulation of ST, we will proceed in the next paragraphs with a detailed case study.

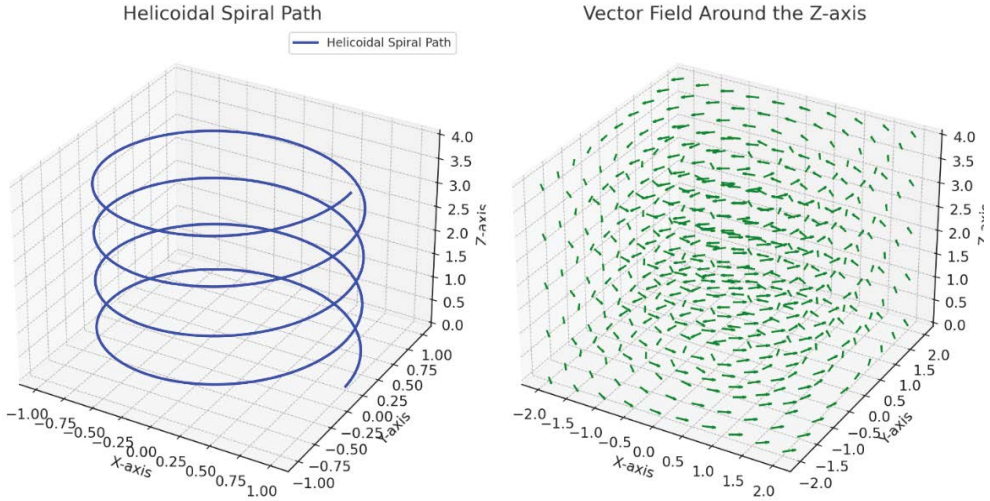

Figure 1: Diagrams depicting a helicoidal spiral (**left**) and the behavior of a vector field (**right**) around the z-axis. The left diagram illustrates a helicoidal spiral path, showcasing the interplay of rotational and translational motion along the z-axis. The right diagram represents a vector field with circular flow centered around the z-axis.

Simulated case study: analyzing rotational flows in stems and flowers

EST enables the analysis of rotational and translational forces in complex systems, providing a powerful framework for exploring biological and physical dynamics. To illustrate the new theorem, we will now explore a concrete example. We will consider *Trachelospermum jasminoides*, commonly known as star jasmine, belonging to the family *Apocynaceae*. Like many climbing plants, *Trachelospermum jasminoides* displays a counterclockwise helical movement of its stems as it climbs and twines around supports, also referred to as circumnutation [17-19] (Figure 2). The flowers also exhibit subtle rotational dynamics, although these movements are not as pronounced as the helical twisting of the stems [20]. The petals of the flowers are arranged in a spiral configuration and unfurl in a counterclockwise direction during blooming.

In our simulation, the dynamics of flower petals are modeled using a circular boundary with a radius of 0.05 m, representing the petals of a flower. Tangential forces along this boundary are applied and the resulting rotational stresses are analyzed through EST. The stem is modeled as a helicoidal path with a radius R=0.05 m and a vertical rise per turn of c=0.2 m. To evaluate the counterclockwise rotation of the flower and stem using EST, the rotation of the petals can be represented by a circular vector field, whereas the helical motion of the stem can be modelled using a helical vector field. The next step is to parameterize the flower and the stem (Figure 2**C**).

1. For the flower, a circular boundary in the plane of the petals is defined, representing the region of interest for macroscopic rotation.
2. For the stem, the helical path is parameterized using equations for a helicoidal spiral, where $x(t) = r\cos(t)$, $y(t) = r\sin(t)$ and $z(t) = ct$. Here r represents the radius, c the rise per turn and t the parameter along the path.

Subsequently, the surface S is defined for each component.

1) For the flower, the surface is a disk enclosed by the petals' rotational motion within their plane,
2) whereas for the stem, the surface corresponds to the area traced by the helical path (Figure 2C).

Calculating the forces acting on the flower and stem requires applying mechanical principles that account for both internal and external forces influencing their dynamics [21,22]. For the flower's petals, the primary force is torque or rotational force, while the stem experiences a combination of bending forces and axial torsion due to its helical structure. We will calculate these forces systematically, step by step, starting from the external forces.

External forces acting of the flower petals and the stem

1) The rotation of the flower petals can be modeled as a torque

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induced by external forces such as wind, gravitational pull, biological growth forces [23]. Torque (τ) on the petals is given by:

$$\tau = r \times F$$

Where r is the radial vector from the center of the flower to the tip of a petal and F is the tangential force applied to the petal. Let's assume that the radius of the flower is R=5 cm, while the tangential force from wind or another source is F=0.1 N. The magnitude of the torque is

$$|\tau| = R \cdot F = 0.05\,\text{m} \cdot 0.1\,\text{N} = 0.005\,\text{Nm}$$

In case of multiple petals (n=5 in *Trachelospermum jasminoides*) experiencing similar forces, the total torque becomes

$$\tau_{\text{total}} = n \cdot \tau = 5 \cdot 0.005\,\text{Nm} = 0.025\,\text{Nm}$$

The rotational acceleration (α) of the flower petals is related to the torque [24] via

$$\tau = I \cdot \alpha$$

Where I is the moment of inertia of the flower petals about the axis of rotation and α is the angular acceleration.

For a flower modeled as a system of point masses at a radius R

$$I = n \cdot m \cdot R^2$$

where m is the mass of a single petal. Assuming m=0.002 kg (2 grams per petal):

$$I = 5 \cdot 0.002 \cdot (0.05)^2 = 0.000025\,\text{kg}\backslash\text{cdotpm}^2$$

$$\alpha = \frac{\tau_{\text{total}}}{I} = \frac{0.025}{0.000025} = 1000\,\text{rad/s}^2$$

1) The stem experiences forces from bending and torsion, influenced by its helical structure. These forces arise from gravity, wind and the biological tension exerted during growth.

2) The weight of the stem induces a bending gravitational force. For a stem of length L=20 cm and mass per unit length λ=0.01 kg/m:

$$F_g = m \cdot g = (\lambda \cdot L) \cdot g = (0.01 \cdot 0.2) \cdot 9.8 = 0.0196\,\text{N}$$

This force acts vertically downward, generating a bending moment at the base of the stem

$$M_g = F_g \cdot \frac{L}{2} = 0.0196 \cdot 0.1 = 0.00196\,\text{Nm}$$

The helical structure of the stem experiences torsional forces due to the winding. The torsional moment (T) is given by

$$T = G \cdot J \cdot$$

Where G is the shear modulus of the stem material, J is the polar moment of inertia and θ is the angle of twist over the length L.

Assuming G= 10^8 Pa typical for plant tissue, J = 0.005 m (5 mm radius) and θ = 2π (one full turn over L =0.2 m) [25], then

$$J = \frac{\pi}{2} \cdot (0.005)^4 = 9.82 \times 10^{-10}\,\text{m}^4$$

and

$$T = (10^8) \cdot (9.82 \times 10^{-10}) \cdot \frac{2\pi}{0.2} = 3.08\,\text{Nm}$$

.

Internal forces acting within the flower petals and the stem

To calculate the forces within the flower petals and the stem using EST, we need to evaluate the relationship between the macroscopic circulation (observable forces) and the microscopic properties (internal forces or stresses derived from the curl of the force field). The first step is to model the forces using vector fields.

1) Concerning the flower petals, we assume that the external forces (e.g., wind or biological forces) act tangentially to their circular boundary. Further, we assume that the tangential forces induce internal stresses (force per unit area) propagating through the petals. Let the force field acting on the petals be

$$\mathbf{F} = (-ky, kx, 0)$$

where k is the force constant proportional to the external pressure and x,y represents positions in the z=0 plane.

Next, we compute the curl of the force field. The curl of the force field relates to the internal stresses within the petals. For the flower petals, in the z=0 plane, the curl of $\mathbf{F} = (-ky, kx, 0)$ is

$$\nabla \times \mathbf{F} = \begin{vmatrix} \mathbf{i} & \mathbf{j} & \mathbf{k} \\ \frac{\partial}{\partial x} & \frac{\partial}{\partial y} & \frac{\partial}{\partial z} \\ -ky & kx & 0 \end{vmatrix} = (0, 0, 2k)$$

This curl is constant in the z-direction, indicating a uniform internal rotational stress throughout the petals.

1) Concerning the helical stem, it experiences external forces such as gravity $(\mathbf{F}_g)$ and biological growth forces $(\mathbf{F}_b)$ that induce internal torsion and bending stresses.

For simplicity, we model the net force field in the stem as: $\mathbf{F} = (-ky, kx, kz)$ where the kz-term accounts for the vertical components of the forces.

Next, we compute the curl of the force field, which provides insight into the internal stresses acting within the stem. This computation reveals the distribution and intensity of these stresses, capturing the complex interplay of forces across the helical structure. For the stem the curl of $\mathbf{F} = (-ky, kx, kz)$ is

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$$\nabla \times \mathbf{F} = \begin{vmatrix} \mathbf{i} & \mathbf{j} & \mathbf{k} \\ \frac{\partial}{\partial x} & \frac{\partial}{\partial y} & \frac{\partial}{\partial z} \\ -ky & kx & kz \end{vmatrix} = (k, k, 2k)$$

This suggests a complex pattern of internal stress within the stem, with components distributed across all three spatial directions.

Visualization and statistics

Diagrams of the flower petals and stem are created to illustrate their geometry, boundary dynamics, and associated vector fields. The Matplotlib library is employed to generate detailed plots, including the circular boundary and tangential forces acting on the flower petals, the curl of the vector field over various surfaces, and the helicoidal path and vector field representation for the stem.

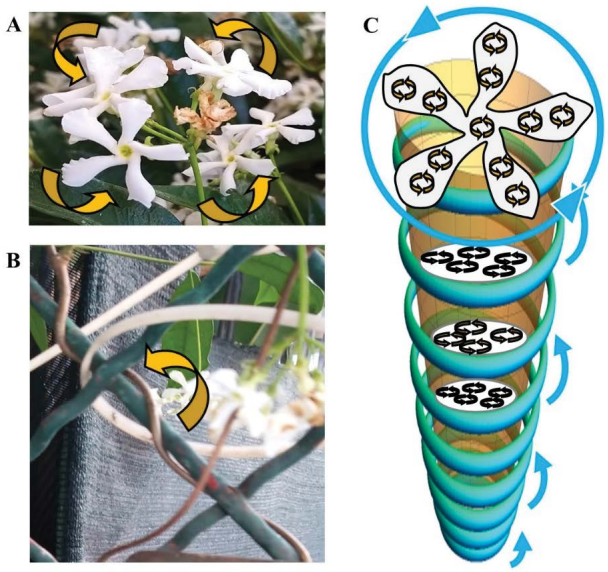

Figure 2: *Trachelospermum jasminoides*. The flower petals (**Figure 2A**) and the stem (**Figure 2B**) display a counterclockwise path. **Figure 2C** illustrates the geometry of the boundaries, the associated vector fields and the internal flows within the flower petals and the stem.

To ensure statistical validation, numerical accuracy is achieved through high-resolution parameterization, with the parameter t sampled at 1,000 points per cycle. The consistency between line integrals and surface integrals is carefully evaluated to confirm the applicability of the extended theorem to the analyzed geometries.

In the sequel, the surface integral of the curl of the vector field will be computed over these surfaces using the extended Stokes' theorem (EST).

Results

As stated above, both the flower and the stem experience external and internal mechanical forces that influence their motion and structural behavior:

1) For the flower petals, the torque arising from tangential forces induces a counterclockwise rotation, with the total torque $\tau_{\text{total}} = 0.025\,\text{Nm}$ and the angular acceleration measured as α=1000 rad/s^2. The internal stresses in the petals are uniform with a value of 2k and are directly proportional to the external forces acting on them. This proportionality explains the rotational equilibrium observed in the petals.

2) For the stem, the primary forces include a gravitational bending moment $M_g = 0.00196\,\text{Nm}$ and a torsional moment T=3.08 Nm due to a helical twist. The internal stresses in the stem vary in all three dimensions because of its helical geometry. Among these stresses, torsion, proportional to kc, predominates, whereas bending stresses, proportional to kR, have a secondary but still notable influence.

We can now apply EST to relate macroscopic and microscopic circulation. The surface integral of the curl of the vector field is computed over the surfaces, relating the surface integrals to the line integrals along the boundaries. For the flower petals, the counterclockwise macroscopic rotation is calculated by integrating along the circular path in the plane. For the stem, the integral is evaluated over the helical surface.

1) Concerning the flower petals, the boundary of the flower is a circle of radius R. The macroscopic circulation (line integral along the petal boundary) is

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_0^{2\pi} kR^2\, d\theta = 2\pi k R^2$$

Using the curl, the surface integral is

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = \int_S 2k\, dA = 2k \cdot \pi R^2$$

Both results match, confirming that the inner stresses in the petals are proportional to 2k.

In sum, the numerical values for the macroscopic (surface) flows and microscopic (internal) flows in the flower, as governed by EST, are as follows. For the flower, the surface flow (evaluated as a surface integral) is 0.157N\ppm, while the internal flow (evaluated as a line integral) is also 0.157N\ppm. The flower petals exhibit a simple and symmetric geometry, where forces act tangentially along a circular boundary in the z=0 plane. The petals lie on a flat, two-dimensional surface characterized by a constant curl of the force field ($\nabla \times \mathbf{F} = (0, 0, 2k)$), signifying that the internal forces are uniformly distributed. This uniform distribution creates a direct and proportional relationship between the macroscopic flow (line integral along the circular boundary) and the microscopic flow (surface integral over the disk). The symmetry of the geometry ensures that every contribution to the line integral is exactly matched by the surface integral. Consequently, the uniform geometry and constant curl lead to a perfect agreement between the surface flow and the internal

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flow, consistent with EST.

1) Concerning the helical stem, the boundary of the stem is parameterized as a helicoidal spiral

$$x(t) = R\cos(t), \quad y(t) = R\sin(t), \quad z(t) = ct$$

The macroscopic circulation (line integral along the helical path) is

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = \int_0^{2\pi} [-kR\sin(t)(-R\sin(t)) + kR\cos(t)(R\cos(t)) + kc(ct)]\, dt$$

$$= \int_0^{2\pi} (kR^2 + kc^2 t)\, dt$$

For one turn$(t \in [0, 2\pi])$

$$\int_{\partial S} \mathbf{F} \cdot d\mathbf{r} = 2\pi kR^2 + \frac{kc^2}{2}(2\pi)^2$$

Using the curl, the surface integral is approximated by the ribbon spanned by the helix

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = \int_S (k + k + 2k)\, dA = 4k \cdot (\text{surface area of ribbon})$$

The surface area of the ribbon is

$$A = 2\pi R \cdot (\text{height per turn}) = 2\pi R \cdot c$$

Thus

$$\int_S (\nabla \times \mathbf{F}) \cdot d\mathbf{S} = 4k \cdot 2\pi R \cdot c = 8\pi kRc$$

In sum, the numerical values for the macroscopic (surface) flows and microscopic (internal) flows in the stem, as governed by EST, are as follows. For the stem, the surface flow (evaluated as a surface integral) is 2.513N\ppm, while the internal flow (evaluated as a line integral) is 8.053N\ppm. Unlike the flower, the values for surface flow and internal flow differ significantly. This is due to the stem's more complex geometry, which features a three-dimensional helicoidal structure with a helical boundary and a ribbon-like surface. Unlike the constant curl observed in the flower, the curl of the force field $(\nabla \times \mathbf{F} = (k, k, 2k))$ in the stem varies in all three dimensions. This non-uniform curl introduces additional contributions to the surface integral that are not directly proportional to the line integral along the helical path. The helicoidal surface spanned by the path is not planar. Its area depends on the radius of the helix and the rise per turn (c), which increases the surface integral significantly compared to the simpler circular geometry of the flower. The line integral along the helical path includes contributions from the vertical rise (z-component), which are absent in the flat geometry of the flower. These vertical components add substantially to the internal flow, making it larger than the surface flow. Forces and circulation in the stem are not confined to a two-dimensional plane, rather display three-dimensional dynamics that capture complex interactions such as bending, twisting and torsional effects, further contributing to the discrepancy between the surface and internal flows. Therefore, the stem's intricate geometry and three-dimensional dynamics lead to a disparity between surface and internal flows, reflecting the additional factors at play in its structural behavior.

In conclusion,

1) flowers have a circular, symmetric geometry that ensures uniform force distribution and curl. This results in surface and internal flows being equal, as the entire flow field is captured in a flat, two-dimensional setup.

2) In contrast, the stem's helicoidal geometry introduces non-uniform force distributions and additional components such as vertical contributions and a larger surface area. These factors create a larger internal flow compared to the surface flow, as the line integral accounts for three-dimensional effects that the surface integral does not fully capture.

These differences highlight the impact of geometry and force distribution on the interplay between macroscopic circulation and microscopic forces, showcasing the utility of the extended Stokes' theorem in analysing forces and circulation in systems exhibiting spiral dynamics.

Conclusion

Classical theorems such as Green's Theorem (GT) and Stokes' Theorem (ST) have been pivotal in linking local properties of vector fields to their global behavior. GT applies just to two-dimensional regions and closed curves, while ST extends to three-dimensional spaces requiring closed surfaces or boundaries for its application [1,2]. These theorems, focused on closed-loop circulations, have proven instrumental in analyzing flows and circulations in systems where boundaries are well-defined, such as steady-state circulations in airflow around wings or electromagnetic field behavior in closed circuits [4,5]. However, their utility diminishes when applied to open, three-dimensional trajectories like the helicoidal spirals which are frequently encountered in natural and engineered systems.

We suggest a generalization of ST to establish a mathematical framework connecting the line integral along a helicoidal spiral path to the surface integral of the curl of the vector field over a bounded region. By redefining the boundary concept for helicoidal paths, this framework provides a new tool for analyzing macroscopic and microscopic flow dynamics in complex systems. The EST formulation provides novel insights into the interplay between rotational and translational motions, allowing for a deeper understanding of spiral flows in a variety of physical and biological systems. A key advantage of the extended formulation lies in its ability to model a wide range of systems where spiral or helical dynamics are dominant. For instance, the novel framework enables the analysis of DNA supercoiling, bacterial flagella, biomechanical patterns such as the phyllotaxis of plants

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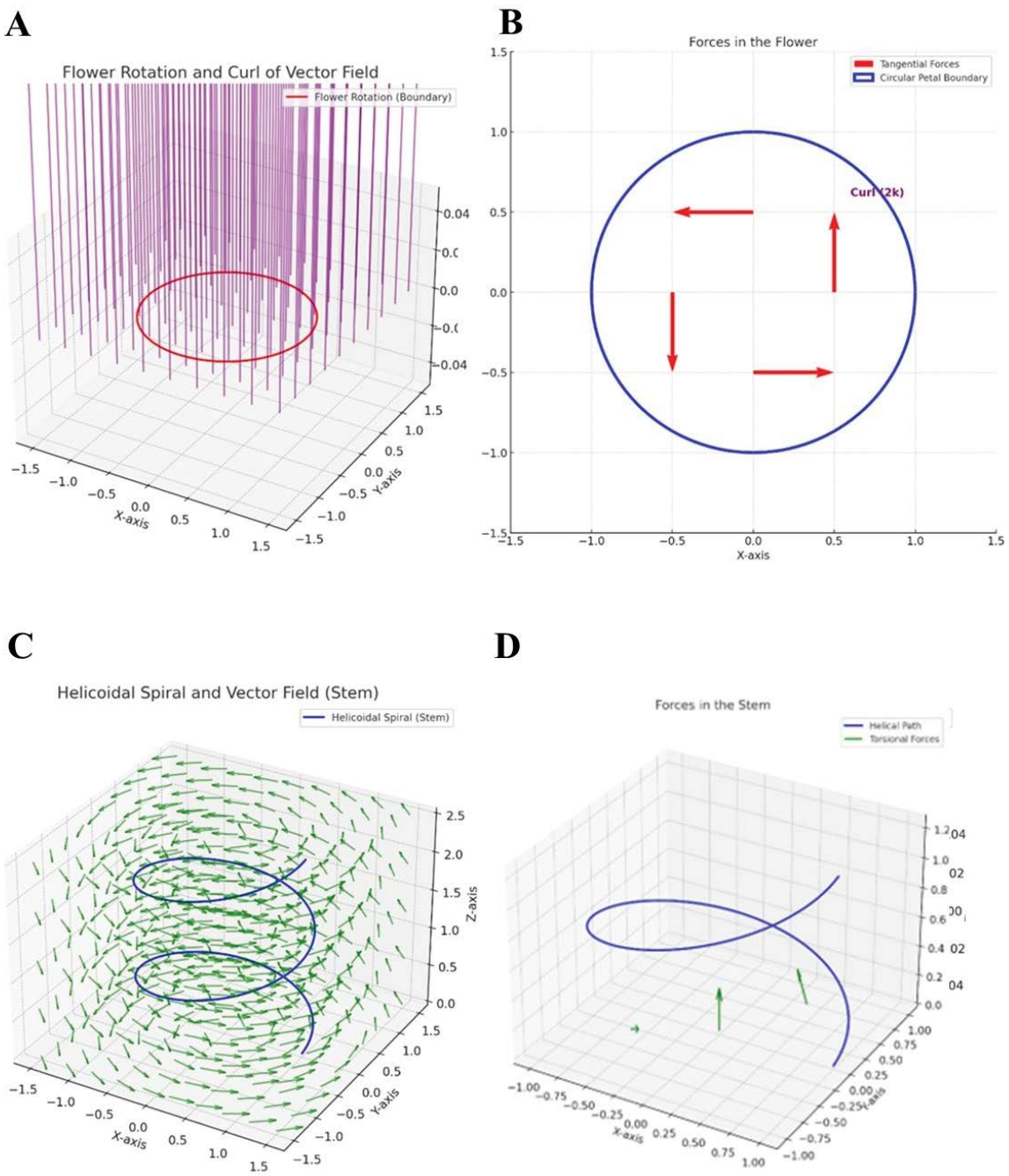

Figure 3: Application of the extended Stoke's theorem to flowers (**Figures 3A-B**) and stems (**Figures 3C-D**) of *Trachelospermum jasminoides*. **Figure 3A**. Diagram illustrating the flower rotation and the curl of vector field. The red circle represents the boundary of the flower petals modeled as a planar region in the z=0 plane. The purple arrows visualize the curl of the vector field, representing the microscopic circulation that contributes to the macroscopic rotation of the flower petals. **Figure 3B**. Diagram illustrating the forces acting on the flower. The circular boundary (blue) represents the edge of the flower petals. Tangential forces (red arrows) act along the edges of the petals, showcasing the influence of external or internal factors. The calculated curl of the vector field is constant at $\nabla \times F=2k$ (annotated in purple) in the z-direction, indicating uniform rotational stresses throughout the petal boundary. **Figure 3C**. Diagram illustrating the helicoidal spiral of the stem and the vector field. The blue curve depicts the helicoidal path of the stem, while the green arrows represent a circular vector field around the z-axis, illustrating the rotational and translational flow and its interaction with the spiral geometry. **Figure 3D**. Diagram illustrating the forces acting on the stem. The helical path (blue curve) represents the stem's geometry. The torsional forces (green arrows), resulting from a combination of bending and twisting actions, act along the helical structure contributing to internal stress distribution. The curl vector field displays non-uniform rotational stresses with components $\nabla \times F=(k,k,2k)$.

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[15,26] intracardiac spiral flows observed in cardiac cycles [27] as well as magnetic vortices in superconductors [14] and rotational dynamics of spiral galaxies [13], where classical methods fail to capture the intricacies of rotational and translational dynamics [28-34].

In this paper, EST is applied to two case studies related with *Trachelospermum jasminoides*, namely the forces acting on flower petals and the helical stress distribution within plant stems.

1) For the flower petals, the circular geometry allows for a straightforward application EST, since the tangential forces acting along the petal boundary produce a uniform curl which is proportional to the rotational stresses. The equivalence between the line integral along the petal boundary and the surface integral of the curl over the enclosed disk validates EST's effectiveness for two-dimensional spiral systems. The uniform rotational stresses observed in the petals align well with the mathematical predictions of EST. This provides insights into how forces are distributed within the boundary of the flower, potentially aiding in the study of floral mechanics and growth patterns. EST suggests that microscopic forces acting at the level of the petals contribute to the macroscopic rotational motion observed at the flower's boundary. This could be applied to study the impact of environmental factors like wind on plant structures and to investigate the mechanical interactions between flowers and pollinators during the pollination process. Still, EST effectively simplifies complex calculations by converting a line integral along the flower's boundary into a surface integral over the petal region. This transformation minimizes computational effort while preserving accuracy.

2) In the case of the stem, although the helical geometry of the stem presents a significant challenge for classical mathematical tools, EST effectively simplifies the intricate interplay of forces involved. The torsional and bending forces are captured through the curl of the vector field, which has components in all three dimensions. The equivalence of the surface integral over the helical ribbon region and the line integral along the helical path demonstrates the robustness of EST in handling three-dimensional geometries with open boundaries. The EST capability to connect macroscopic flow patterns with microscopic circulatory forces may have significant implications for understanding the biomechanics of plant growth and structural stability. This relationship can also provide valuable insights for studies on nutrient and water transport within stems, as these processes often involve spiral dynamics.

Certain assumptions and limitations are inherent in our analysis. EST assumes that the involved vector fields and surfaces are continuously differentiable. In real-world biological systems, irregularities and discontinuities in the geometry or force distribution may reduce the accuracy of the analysis. The flower petals are modeled as a perfect circle and the stem as a regular helix. While this simplifies the mathematical analysis of forces in idealized systems, real-world systems often deviate from these idealized shapes. The analysis of irregular geometries or highly dynamic boundaries may still require significant computational effort, particularly for numerical integration of complex surface and line integrals. The tangential and torsional forces are assumed to be uniform across the boundaries. In reality, biological and environmental forces such as wind, gravity and growth pressures are often spatially and temporally variable. Additionally, secondary effects such as shear forces or anisotropic material properties are not incorporated, which could limit the applicability of the results to certain systems. Future work could extend the framework to handle more irregular and biologically realistic geometries, such as asymmetrical petals or non-uniform stem shapes. The analysis of time-varying forces and boundaries, such as those caused by growth or environmental changes, could provide deeper insights into real dynamics. Integrating the extended theorem with experimental data would help validate the theoretical predictions and refine the mathematical models.

In conclusion, the proposed extension to Stokes' Theorem integrates helicoidal paths into circulation analysis, bridging a critical gap and expanding its applicability to open, non-planar trajectories. By redefining boundaries, it simplifies the study of rotational and translational flows, offering a versatile tool for analyzing complex dynamics such as those observed in the flowers and stem of *Trachelospermum jasminoides*.

Declarations

Ethics approval and consent to participate. This research does not contain any studies with human participants or animals performed by the author.

Consent for publication. The Author transfers all copyright ownership, in the event the work is published. The undersigned author warrants that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal, and has not been previously published.

Availability of data and materials. all data and materials generated or analyzed during this study are included in the manuscript. The Author had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

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work that could inappropriately influence, or be perceived to influence, their work.

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Declaration of generative AI and AI-assisted technologies in the writing process. During the preparation of this work, the author used ChatGPT to assist with data analysis and manuscript drafting. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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Feeling the Heat: A Thermodynamic Perspective on Emotions, Motivation, and Time Perception

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ABSTRACT

We are introducing a novel thermodynamic model of emotion. In this model, emotions are regarded as deviations from equilibrium, akin to fluctuations in body temperature. This bipolar regulation maintains bodily and psychological homeostasis while spurring mental development. Emotional regulation typically occurs through expanding one's perception of time. Positive, low-information content emotions can reduce action drive, but stressful, information-rich conditions can heighten it. Therefore, time perception can potentiate the capacity of emotions to motivate. However, time perception accelerates to facilitate fluid action performance, with the state of flow representing a unique state of contentment and challenge. By anchoring psychological processes to the principles of energy and entropy, our model offers a comprehensive bipolar foundation for understanding motivation and behavior. Beyond its theoretical implications, this model also lays the groundwork for addressing mental health conditions resulting from the dysregulation of emotions. It can inspire potential interventions to harness the mind-body connections elucidated by our thermodynamic perspective.

1. Introduction

The global rise in stress disorders highlights the urgent need to understand emotional resilience and its role in the development of mental diseases (Nestler & Russo, 2024). Traditional approaches have treated emotions as separate domains, failing to capture their intricate interdependencies. For example, cognitive theories have focused primarily on the mental processes underlying emotions (Barrett, 2017). At the same time, physiological research has investigated bodily responses, such as heart rate and facial expressions, largely independently of motivational and subjective factors. This compartmentalized view has limited our ability to explain the complex relationships and paradoxes observed across these realms of human experience. Understanding how emotions relate to subjective experiences (i.e., feelings), motivation, and disease progression has remained elusive.

This article proposes a novel thermodynamic model that integrates emotions, motivation, and associated physiological mechanisms within a unified framework. The brain keeps bodily and psychological equilibrium by intertwining every regulatory system with emotions. Nevertheless, the multifaceted nature of the relationship encourages further study. This work examines how emotions serve temperature regulation and psychological homeostasis. By conceptualizing the brain's functioning through thermodynamic principles of energy and entropy, we offer a cohesive perspective to resolve longstanding questions and paradoxes surrounding these interrelated processes.

1.1. Thermo-emotional covariations from a thermodynamic lens

Experimental research confirms the phylogenetically ancient relationship between emotions and temperature regulation across various species, including reptiles, foxes, pigs, rabbits, rats, mice, and humans (Briese, 1995; Briese & Cabanac, 1991; Cabanac, 1999; Frosini et al.,

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2000; Groenink et al., 1995; Moe & Bakken, 1997; Parrott et al., 1995; Terlouw et al., 1996; van der Heyden et al., 1997). Although thermoregulation exists to some degree in most animals, the endothermic phenotype—characteristic of humans and other mammals—depends on complex metabolic networks and multiple internal feedback loops (Grigg et al., 2021; Seebacher, 2020). For example, embryo incubation drives the evolution of endothermy (Farmer, 2020), which is phylogenetically predicated on thermoregulation (Clavijo-Baque & Bozinovic, 2012). Endotherms maintain a stable core temperature with the aid of crucial mechanisms, including vasoconstriction, shivering, and sweating (Madden & Morrison, 2019; Nowack et al., 2017). The brain's high energy use ensures optimal information processing while maintaining physical and psychological equilibrium (Dempsey et al., 2022; Huang, Zhang, Wu, Mashour, & Hudetz, 2020). Thermal control is a vital component of an overarching regulatory system, exerting downstream effects on action motivation and behavioral adaptations (Inagaki et al., 2019; Kataoka et al., 2020; Nashiro, Min, & Yoo, 2022).

Physical or mental instability prompts a wide range of protective mechanisms. Emotions are paramount in this regulatory hierarchy as they intertwine with other regulatory processes. Moreover, the distinct physiological signatures of emotions represent specific energy configurations of the brain (Hesp et al., 2021; Kao et al., 2015; Sadowski et al., 2020), and, like temperature, they oscillate around a neutral position, forming an emotional set-point (Northoff & Tumati, 2019). Recent work utilizes temperature as a means of characterizing emotions (Escobar et al., 2020). Contentment promotes rest and recovery (Brown & Thorsteinsson, 2020) by reducing metabolic rate and body temperature, thereby conserving energy through parasympathetic restorative processes (Seebacher, 2009). In contrast, stress is a highly demanding condition (Keller et al., 2019; Meeusen, Van Cutsem, & Roelands, 2020), where noradrenaline initiates the fight-or-flight response within seconds (O'Connor, Thayer, & Vedhara, 2020). Furthermore, the varied effects of stress depend on personal, environmental, and other situational factors. However, its adverse health effects in anxiety, dissociation in trauma, or even depression (Comtesse et al., 2019; Mason et al., 2024) warrant a deeper thermodynamic investigation.

Emotional expressions are fundamentally linked to physiological changes regulated by the autonomic nervous system. At the same time, their feedback representation reflects motivational aspects (Quadt et al., 2022). Moreover, emotion and temperature may be under thermodynamic control (Déli and Kisvarday, 2020; Grigg et al., 2021; Seebacher, 2020). This perspective posits that the brain's mechanisms for heat and work transfer play a crucial role in regulating emotional states, and conversely, that emotional states can influence thermoregulation. In support of this, psychological stress, known to elevate blood pressure, heart rate, and heart function—even during sleep (Hall et al., 2004)—increases core temperature, a phenomenon referred to as psychogenic fever (Oka et al., 2001). This psychogenic fever results from a temporary elevation in the thermoregulatory set point, mediated by both prostaglandin E2-dependent and independent mechanisms (An & Kim, 2011; Fossat et al., 2015; Kluger et al., 1987; Morimoto et al., 1991).

Heat stress can lead to impulsivity (Fredericks et al., 2018; Wittmann & Paulus, 2008; Paasche et al., 2019), drug-seeking behavior, and criminal activity (Corcoran & Zahnow, 2022). Inversely, fear triggers thermoregulation disturbances in substance abusers (Lowry et al., 2009; Raison et al., 2015). People with depression have higher body temperatures (Mason et al., 2024), and median raphe stimulation, which affects temperature regulation, can produce depressive-like behaviors (Fazekas et al., 2021). These and other findings suggest a neurological link between emotion and temperature (WILLIAMS & Bargh, 2008). To gain a deeper understanding of this relationship, we explore the mechanisms of thermodynamic regulation in more detail.

1.2. Variations of time judgment

Understanding the mechanisms underlying time perception requires distinguishing between different types of temporal judgments. A key theoretical distinction exists between the perceptions of short durations (e.g., milliseconds to seconds), typically measured through reproduction or estimation tasks and the subjective awareness of time's passage often referred to as passage-of-time (PoT) judgments. These two aspects are functionally dissociable: while short-duration judgments are closely linked to internal pacemaker mechanisms and are modulated by arousal and attention (Gibbon et al., 1984; Wittmann, 2009), PoT judgments rely more on self-reflective and interoceptive processes, such as emotional state and bodily awareness (Droit-Volet, & Fayolle, 2024; Martinelli & Droit-Volet, 2022).

Incorporating this distinction into our thermodynamic framework, we conceptualize duration estimation as a dynamic process modulated by arousal-driven shifts in entropy and energy. High-arousal states, whether positively or negatively valenced, have been shown to accelerate internal clock processes, resulting in time overestimation (Cui et al., 2023). An expansion of subjective time is useful for decision-making, while contraction of subjective time drives action (D'Agostino et al., 2023). In contrast, low-arousal emotions, including contentment or mild joy, do not produce consistent distortions in short-duration estimates. These findings challenge earlier claims of a general "positivity effect" on temporal expansion and underscore the primacy of arousal, rather than valence, in modulating temporal metrics.

Moreover, our model emphasizes that PoT judgments, i.e., feelings that time is dragging or flying, are not reducible to clock-speed effects. Instead, they emerge from higher-order awareness of emotional and cognitive change (Wittmann, 2015). For instance, the emotion of awe leads to underestimation of duration in attention-based timing tasks, likely due to perceptual overload (Droit-Volet et al., 2024). Simultaneously, awe may induce a metacognitive experience of timelessness, a distinct subjective effect more closely tied to interoceptive processes and self-transcendence. We propose to map these dual effects thermodynamically: attentional overload decreases timing accuracy, while self-transcendent states can stabilize entropy.

Early work investigated the effect of increases in body temperature on time estimates (Hoagland, 1933). Increases in body temperature shortened the intervals produced, but lengthened duration estimates (Francois, 1927; Wearden & Penton-Voak, 1995). More recent studies support the stress-induced slowing of time perception (Ogden et al., 2019); however, the repeated anticipation of holidays can actually speed up time perception (Ogden et al., 2024).

To situate our approach within broader theoretical debates, we briefly compare our framework with several established models of time perception. The dual klepsydra model (Wackermann & Ehm, 2006) posits that interval timing arises from the gradual discharge of a leaky integrator, an analogy to fluid flowing through a clepsydra or water clock. In contrast, the DOIT (Dynamic Occupation in Time) model examines how the experience of time varies based on the qualities of activities and their context (Larson, 2004). Although our model differs in its thermodynamic formulation, these approaches recognize the irreversibility of time and the influence of dissipative processes.

Physical movement across species and tasks hastens time perception, improving timing accuracy (Robbe, 2023). The time perception rate is greatest in flow, a unique state where the balance of action, motivation, and confidence optimizes performance through spontaneous, coherent action flow (Failing & Theeuwes, 2016; Rutrecht, Wittmann, Khoshnoud, & Igarzábal, 2021). Similarly, Csikszentmihalyi's flow model describes the distortion of time during immersive tasks, wherein attentional focus and action-feedback loops yield an altered experience of time (Csikszentmihalyi, 1990). Our thermodynamic view reframes this by suggesting that flow arises at an equilibrium point between arousal (energy) and confidence (stability), facilitating seamless temporal integration.

As physical time is relative to spatial motion, psychological time is also relative to imaginary motion (Allingham et al., 2021; Spapé et al.,

2021). Imagining accelerating movement resulted in a relative overestimation of time, or time dilation, while decelerating movement elicited a relative underestimation, or time compression (Hallez et al., 2023). Our model posits that perceived time is regulated by energetic and informational constraints, offering a physicalist grounding through entropy and thermoregulation.

1.3. The role of entropy

Thermodynamic regulation is crucial for efficient brain functioning. Because the energy needs of neurons during intrinsic activities are orders of magnitude larger than during stimulation for all levels of cognition (de Lara, 2020; Raichle, 2010), rapid shifts from the brain's high-dimensional resting state to lower-dimensional evoked activities (Singer, 2021) facilitate optimal information transfer. Nevertheless, stable intrinsic activities expedite spontaneous recovery of the resting state. In this simplified view, intellect generation is based on information exchange with the external environment (Ahissar & Assa, 2016; Déli et al., 2017; Llinás and Paré, 1996; Northoff, 2018), with sensory and motor processing forming a thermodynamic cycle.

Renyi's informational entropy generalizes entropy by forming scalar exponent alpha (Jizba & Arimitsu, 2001). Baez (2011) demonstrated a direct relationship between Renyi's exponent alpha and inverse temperature beta (i.e., coldness). Intelligent information processing often involves a type of information erasure, inducing a sense of "coldness" while increasing overall neural organization (O'Neill and Schoth, 2022).

Rényi and Shannon's informational entropy can describe psychological and cognitive states, and predict task performance and mental well-being (Ince et al., 2017; Shannon, 1993). For instance, higher variability at rest (i.e., high entropic states) correlates with fluid intelligence (Wang et al., 2018; Yang et al., 2019) and openness (Zmigrod et al., 2019), but decreases in brain entropy are seen in compromised states of consciousness (Varley et al., 2020). For example, stress is analogous to time pressure, the inability to cope with the pace or intensity of sensory influx (Déli et al., 2018, 2021, 2022), demonstrating emotions' interconnection with the brain's energy and information processing. The following section will proceed to a discussion of time perception in motivation.

1.4. The thermodynamics of time perception

Studies on behavioral activation systems have revealed overestimation bias scores for both positive (Lehockey et al., 2018; Simen & Matell, 2016; van Hedger et al., 2017) and stress-inducing situations (Remmers & Zander, 2018; Wise et al., 2017). For instance, novel stimuli or rewards can dilate time perception through what is known as the 'oddball effect' (Failing & Theeuwes, 2016; Ma et al., 2024), with surprising or emotionally charged moments feeling as if time 'froze.' A similar sense of permanence occurs during stress (Hollis et al., 2015; Robbe, 2023). However, the psychology of these experiences contrasts dramatically. In a stressful context, dilated time perception evokes an unbearable sense of permanence, which triggers desperate escape behavior through impatience and sympathetic arousal (Gladhill et al., 2022; Hosseini Houripasand et al., 2023).

The dilation of time perception in both positive and negative states correlates with emotional intensity (Biderman et al., 2020; Déli & Kisvarday, 2020; Zanin et al., 2019), hinting at an underlying energy relationship (Toso et al., 2020). We want to note that some studies suggest that positive emotions do not influence time perception (Ogden et al., 2019). However, drug-induced expansion of time perception is indeed linked to elation. This correlation is significant as it suggests that the sense of spaciousness experienced during elation can lead to mental expansion, potentially giving rise to new ideas and creative insights (Green, Kavanagh, & Young, 2003). These findings underscore the connection between the expansion of time perception and elation, whether drug induced or arising from positive states.

Due to its mental energy boosting ability, musicians and artists have turned to cannabis to enhance creativity, supporting our original claim (Kowal et al., 2015). Moreover, the most pronounced alterations in time perception occur during emotional polarities, such as awe (Rudd et al., 2012) and depression (Stanghellini et al., 2016; Thönes & Oberfeld, 2015), when time appears to stand still (Fig. 1). These results inspired some scientists to suggest that depression is analogous to a positive spacetime curvature, even a black hole state (Déli, 2024; Kent, 2023).

The connection between emotions and energy is also evident in the fact that the perception of time slows down more significantly during the transition to negative states than during the states themselves (Gable & Poole, 2012; Wang & Lapate, 2024). Likewise, the cognitive challenge of withdrawal (Di Lernia et al., 2018; Gable et al., 2022) and sleep deprivation (Şen et al., 2023) dilate time perception. Our argument defines time perception as an even function, represented by a graph that remains unchanged under reflection in the y-axis (Fig. 1). Interestingly, our time perception curve is analogous to the upside-down U-shaped curve of the Yerkes-Dodson law, which relates performance to circulating levels of stress hormones (Beerendonk et al., 2024; Yerkes & Dodson, 1908; Lupien, Maheu, Mt, Fiocco, & Schramek, 2007). This similarity underscores the thermodynamic foundation of emotions' potential for motivation.

An intriguing question remains of why diverse experiences – from intense states of anxiety to the calmness inspired by awe or nature – dilate time perception (Bannister & Eerola, 2021; Davydenko & Peetz, 2017; Failing & Theeuwes, 2016; Mitchell et al., 2015; Rudd et al., 2012). For example, information overload during stressful states can cause difficulty concentrating and purposeful behavior (Nutt, 1999). Anxious people usually resort to impulsivity and meaningless, arbitrary actions until action motivation is halted in depression (Stanghellini et al., 2016; Wittmann & Paulus, 2008), implying an inverse relationship between mental adversity and the ability to change it.

In contrast, the low action motivation of positive mental states indicates energy frugality, which may explain their connection to parasympathetic restorative processes in long-term psychological well-being (Table I). A muted action motivation might represent some form of minimum energy path, analogous to the principle of stationary action in physics. At the curve's left minimum (Fig. 1), awe slows or pauses the subjective time. Contentment is an uncluttered, information-scarce experience that represents confidence in self-agency but lacks internal motivation.

Stress and contentment lie at opposite ends of an information-processing and action-motivation spectrum. It is a contradiction; those with the capacity to institute change (contentment) lack the desire, and

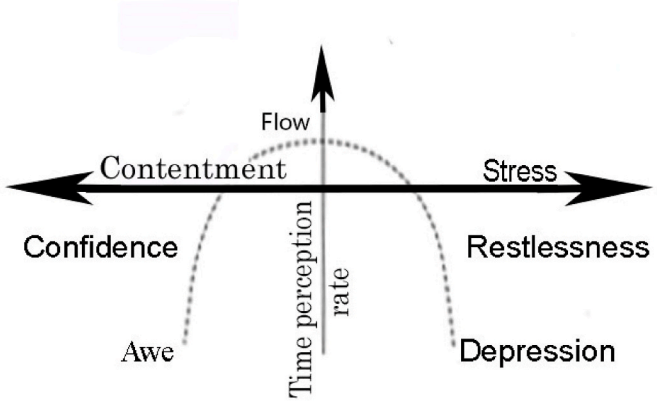

Fig. 1. The Psychology of Contentment and Stress Movement speeds up time perception (vertical arrow). In positive experiences, time perception reduces action motivation, culminating in awe. The pain of stress motivates action but weakens self-confidence. Anxiety can progress to depression when action motivation halts. A unique point of action, motivation, and confidence is flow.

Table 1
Binary choices supporting bodily and psychological equilibrium.

	Experience	
Symptom	**Positive arousal**	**Stress**
Time perception increases (Dilation) — Arousal	Parasympathetic	Action motivation
Time perception decreases (Compression) — Action	Flow	Sympathetic
Physiological symptoms (shivering, sweating)	Accomplishment	Shame, fear

those having the desire (stress) lack the agency. Gordon et al. (2023) confirmed the connection between decision-making and bodily functions and movement control: better body control (resulting in less stress) permits greater agency, and vice versa. In the following, we investigate the regulatory framework of motivation in more detail.

1.5. The binary regulation of higher cognitive functions

The timing of the giant fiber descending neuron spike determines whether a Drosophila evades a predator via a short or long takeoff (Ache et al., 2019). Bifurcations from geometric principles can elucidate behavior and decision-making across various species and ecological scenarios (Sridhar et al., 2021), and temperature and emotion regulation in mammals (Hesp et al., 2021; Kao et al., 2015; Sadowski et al., 2020). These spontaneous and abrupt "critical" transitions are linked with specific geometrical relationships. A shift from averaging vectorial information among options abruptly excludes one among the remaining choices. The brain repeatedly breaks down multi-choice decisions into a sequence of binary decisions. Binary regulation is an "on-off regulation," in systems with only two possible states, referring to "dichotomous thinking in psychology.

In mammals, stimulation of the PAG can induce relaxation or escape behavior. Frontal PAG stimulation inspires a relaxed, immobile posture due to the sense of excess time. However, lateral PAG stimulation also produces two typical behavioral responses. When there is sufficient time, increased blood pressure and heightened pain sensitivity facilitate escape and defensive responses (Zelena et al., 2018). An immediate threat, when escape is no longer possible, mutes pain sensitivity and triggers immobile freezing behavior. In people, anxiety can induce aggravation or an emotional collapse into depression, where both time perception and action motivation appear to halt (Stanghellini et al., 2016), providing further support for our thermodynamic argument.

Binary choices can generate multifaceted behavior regulation (summarized in Table 1), such as (1) dilation of time perception to accelerate or mute motivation, (2) contraction of time perception to mediate action toward completion, and (3) halting of action motivation or sudden cognitive changes. This regulation is based on psychological spin, utilizing the reversible perception cycle (Déli, 2023), which automatically restores psychological equilibrium, thereby forming a new balance. This model can explain regulatory complexity as a series of binary choices ad infinitum. Dopaminergic mechanisms, which can amplify the motivational power of emotions through subjective time perception, highlight how internal and external factors influence the multifaceted nature of experiences (Soares et al., 2016).

We must note that emotional and cognitive processes can trigger physiological symptoms, such as shivering, chills, sweating, and changes in body temperature (Schoeller & Perlovsky, 2016). In this context, physiological symptoms can be both tools and consequences of the brain's energy regulation.

2. Discussion

Decision-making from fruit flies to humans often boils down to binary choices based on geometric principles and critical transitions. The brain's cognitive cycle can maintain a bodily and psychological equilibrium through simple bifurcation stemming from geometric principles. Binary options can refine cognitive and intellectual evolution through learning, beliefs, and individual capabilities. Moreover, emotion, temperature, and physiological symptom regulation recover and maintain constant resting entropy. Therefore, as the thermodynamic cycle stabilizes the psyche around a new equilibrium after every decision-making, it increases or decreases synaptic complexity, confidence, and mental health.

Time perception can lead to contrasting behavioral outcomes during stress (information overload) or contentment (information scarcity). Negative emotions inspire arbitrary and chaotic performance, corresponding to wasteful energy use, which can accumulate and lead to adverse health effects associated with stress. In positive conditions, frugality of action motivation reflects a minimal energy path, allowing contentment and creativity. In contrast, faster time perception can manage ongoing action by inspiring cognitive coherence. Intrinsically motivating activities lead to deep engagement and enjoyment, a state known as flow, characterized by the intersection of motivational challenge, confidence, and passion (Csikszentmihalyi, 1990, 1997, p. 31). This is congruent to our hypothesis that ongoing action accelerates time perception. The time perception curve also overlaps Yerkes-Dodson law, providing further support to our thermodynamic foundation of emotions' potential for motivation. Emotions can be viewed as the fundamental forces of motivation.

By conceptualizing psychological processes through energy dynamics, we outlined how emotions can affect motivation through distorted time perception. Moreover, our thermodynamic model can explain how action motivation during stress can produce wasteful cognitive processes. The relationship between low entropy and compromised consciousness states (Varley et al., 2020), and depression (Wise et al., 2017) underlines the role of stress in mental problems.

Our model provides a framework for designing interventions and strategies that leverage the interconnections between emotions, motivation, and physiology. While our thermodynamic model focuses on the fundamental structural motivations underlying behavior, we acknowledge the importance of cultural norms, social expectations, and environmental factors in shaping emotional and motivational experiences.

Integrating these contextual factors is crucial to understanding the complex interplay between emotions, motivation, physiology, and subjective experiences across diverse cultural and environmental settings.

2.1. Limitations and future directions

We would like to acknowledge the lack of empirical validation and experimental testing of the proposed framework. Additionally, the generalizability of the model across diverse populations remains unexplored. This limitation is particularly salient in clinical populations, such as individuals with post-traumatic stress disorder (PTSD) or major depressive disorder, where disruptions in bodily awareness and emotional regulation may offer critical tests of the model's assumptions.

Our framework also does not yet account for the role of time perception for proprioceptive awareness—two domains that are increasingly recognized as central to embodied cognition and affective experience. Future empirical works in this area can further our understanding of the mind-body interaction.

While our thermodynamic model provides a novel framework for integrating emotions, motivation, and time perception, it remains theoretical and is subject to several significant limitations. Foremost, the model relies heavily on analogies between thermodynamic principles—such as entropy, temperature, and energy—and psychological processes. While conceptually illuminating, these analogies are not always supported by direct empirical evidence, which may limit their explanatory power. The complexity of human emotional and cognitive systems likely exceeds the reach of simplified energetic metaphors, especially when such models are extended to subjective constructs like time perception.

Additionally, many of the neurophysiological correlates we invoke, such as neural entropy or the functional role of dopamine in timing, are still under active investigation, and consensus regarding their interpretation is far from established. The use of entropy as a measure of cognitive or emotional flexibility, for example, depends on methodological choices that may not yet be standardized across studies. Furthermore, the model currently lacks specificity in distinguishing between clinical and non-clinical populations, and its generalizability across age groups, cultural settings, or neurodiverse profiles remains untested. Despite these constraints, the integrative potential of the framework may help bridge conceptual gaps between disparate findings in psychology, physiology, and neuroscience.

Nevertheless, our model opens several promising avenues for applied research and translational work. In mental health, for instance, subjective distortions of time perception are commonly reported in anxiety, depression, and trauma-related disorders. Our framework suggests that such distortions may reflect dysregulated entropy states in the brain, which could be targeted through interventions aimed at modulating physiological arousal and attentional engagement. Biofeedback, neurofeedback, or pharmacological interventions that stabilize neural entropy dynamics may be tested for their capacity to restore adaptive time perception and emotional regulation. Moreover, in performance contexts—such as athletic training, musical improvisation, or surgical decision-making—the model's emphasis on flow as a state of optimal energy alignment suggests practical strategies for cultivating cognitive and emotional balance. Future research should prioritize experimental designs that manipulate entropy-relevant parameters (e.g., arousal, cognitive load, ambient temperature) while recording physiological or neuroimaging data. Valuable direction would be to examine whether interventions known to improve well-being, such as mindfulness or physical activity, influence subjective time perception through measurable changes in brain signal complexity.

While our model identifies correlations between emotional states and physiological indices—such as body temperature and thermodynamic entropy—our current analysis stops short of demonstrating direct causal mechanisms. Establishing such causality will be the subject of future work, potentially using targeted experimental designs and interventions that modulate physiological parameters to observe downstream effects on affective and cognitive processes.

3. Conclusion

The thermodynamic analysis of cognition points to the existence of binary regulation. First observed in fruit flies and fish, this regulation can maintain bodily and psychological equilibrium and enable abstract decision-making by infinitely enhancing the details of regulatory complexity. A decision-making process based on geometric principles may be universal throughout biology and even physics, such as electromagnetism.

Our verifiable framework shows that identical dilation of time perception in arousing emotional states (such as anxiety and joy) and calming experiences (like awe and natural environments) can give rise to varied motivation and offer nuanced decision-making. Time perception, a function of information processing and entropic factors, potentiates the ability for motivation. The muting of action motivation in positive states represents energy frugality, or a minimum energy path, which might be analogous to the principle of stationary action in physics. In contrast, stress represents information overload, spurring chaotic decision-making and action motivation, which wastes effort and energy. Our model suggests that emotions have a thermodynamic foundation, rendering them the driving forces of motivation.

The implications of our model extend beyond theoretical understanding, offering potential avenues for addressing mental health challenges and optimizing well-being through interventions that leverage the interconnections between emotions, motivation, and physiology. Our thermodynamic perspective originates emotions and their long-term mental consequences in the energy-information dynamics of the brain. It opens new avenues for interdisciplinary and innovative approaches to understanding and optimizing human functioning. Finally, it can inspire novel approaches in artificial intelligence research.

CRediT authorship contribution statement

Eva Déli: Writing – review & editing, Writing – original draft, Visualization, Data curation, Conceptualization. **Felix Schoeller:** Writing – review & editing, Writing – original draft, Investigation. **Adam Safron:** Writing – review & editing, Writing – original draft. **Abhinandan Jain:** Writing – review & editing, Writing – original draft. **Arturo Tozzi:** Writing – review & editing, Writing – original draft. **Vladimir Adrien:** Writing – review & editing, Writing – original draft. **Nicco Reggente:** Writing – review & editing, Writing – original draft, Visualization, Project administration.

Data availability

No data was used for the research described in the article.

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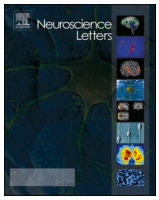

Takens' theorem to assess EEG traces: Regional variations in brain dynamics

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ABSTRACT

Takens' theorem (TT) proves that the behaviour of a dynamical system can be effectively reconstructed within a multidimensional phase space. This offers a comprehensive framework for examining temporal dependencies, dimensional complexity and predictability of time series data. We applied TT to investigate the physiological regional differences in EEG brain dynamics of healthy subjects, focusing on three key channels: FP1 (frontal region), C3 (sensorimotor region), and O1 (occipital region). We provided a detailed reconstruction of phase spaces for each EEG channel using time-delay embedding. The reconstructed trajectories were quantified through measures of trajectory spread and average distance, offering insights into the temporal structure of brain activity that traditional linear methods struggle to capture. Variability and complexity were found to differ across the three regions, revealing notable regional variations. FP1 trajectories exhibited broader spreads, reflecting the dynamic complexity of frontal brain activity associated with higher cognitive functions. C3, involved in sensorimotor integration, displayed moderate variability, reflecting its functional role in coordinating sensory inputs and motor outputs. O1, responsible for visual processing, showed constrained and stable trajectories, consistent with repetitive and structured visual dynamics. These findings align with the functional specialization of different cortical areas, suggesting that the frontal, sensorimotor and occipital regions operate with autonomous temporal structures and nonlinear properties. This distinction may have significant implications for advancing our understanding of normal brain function and enhancing the development of brain-computer interfaces. In sum, we demonstrated the utility of TT in revealing regional variations in EEG traces, underscoring the value of nonlinear dynamics.

Significance statement

The novelty of this study is that we applied Takens' theorem to investigate the differences in phase space features among different EEG channels of healthy subjects.

1. Introduction

The human brain operates as a sophisticated nonlinear system, adept at handling extensive information via dynamic interactions [4,7,13,22]. Electroencephalography (EEG) serves as a non-invasive, high-resolution method for investigating brain activity. Nonetheless, conventional linear analysis techniques frequently fall short in representing the intricate nonlinear features of EEG signals [3]. To address this limitation, nonlinear dynamics and chaos theory have emerged as powerful frameworks for understanding brain activity, with Takens' theorem (henceforward TT) providing a cornerstone. TT establishes that the behavior of a dynamical system can be reconstructed in a multidimensional phase space using time-delayed versions of a single time series from the observed data [20]. In the context of EEG analysis, TT provides a robust mathematical tool to study temporal evolution, revealing properties that linear methods cannot uncover [19]. By reconstructing the phase space, researchers can analyze key EEG dynamical properties such as temporal dependencies, dimensional complexity and predictability [14]. This approach has proven valuable for identifying changes in neural dynamics associated with various cognitive and pathological conditions [8].

Previous research has highlighted the effectiveness of TT in analyzing EEG signals, especially for identifying pathological conditions like epilepsy, Alzheimer's disease and schizophrenia [1,2,5,11]. However, less attention has been given to the application of this approach for

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assessing regional variations in brain dynamics under normal conditions. Different brain regions exhibit distinct patterns of electrical activity, reflecting their specialized roles in cognition, sensation and motor function. For instance, the frontal region (FP1) is associated with higher cognitive processes such as decision-making and working memory. The sensorimotor cortex (C3) governs movement and integrates sensory inputs, while the occipital region (O1) processes visual information. Despite their unique roles, interactions among these regions contribute to the brain's global dynamics.

Comparing the spread and trajectory of phase space trajectories across different brain regions can shed light on how functional specialization translates into distinct dynamical features. In this study, we apply TT to assess EEG traces from three key brain regions: FP1, C3 and O1. We reconstruct phase spaces and analyze the temporal structure and complexity of the trajectories. Key metrics such as trajectory spread were computed to quantify regional differences in brain dynamics.

The rationale for using TT lies in the fact that overlapping trajectories reveal shared dynamical patterns across the EEG traces, suggesting common temporal structures in brain activity. These patterns likely arise from similar neural processes or consistent experimental conditions and reflect shared features of brain dynamics that remain consistent across individuals or trials. Conversely, differences in the spread or divergence of trajectories highlight variability in the dynamics of EEG signals, capturing subject-specific neural activity. This variability can serve as a marker for distinguishing between populations, such as healthy versus pathological groups, and is particularly relevant for identifying neural behaviors associated with specific cognitive states, tasks or conditions. Trajectories that densely fill the phase space indicate higher complexity, which is often linked to intricate neural processes and sophisticated information management. In contrast, smoother and more confined trajectories suggest simpler, more periodic or more deterministic behavior, highlighting a system with lower complexity but higher predictability. Together, these observations shed light on the dynamic interplay between stability, variability and complexity in brain activity, offering a deeper understanding of its temporal and spatial organization.

In the following sections, we detail the methods used for EEG data collection, phase space reconstruction and analysis, followed by the presentation and discussion of our results.

2. Subjects and methods

This study investigates the regional variations in brain dynamics by applying Takens' theorem to EEG data, focusing on three key channels: FP1 (frontal), C3 (sensorimotor), and O1 (occipital). The data consisted in the retrospective evaluation of ten EEG traces. EEG recordings were obtained from ten healthy, right-handed volunteers (mean age: 20.1 years; SD = 1.1; age range: 18–22 years; 5 males). For additional information on the participants and EEG methodologies, see Jaušovec and Jaušovec [10] and Tozzi et al. [21]. The signals were captured using a 64-channel EEG system, adhering to the standard 10–20 electrode placement system. Preprocessing included artifact removal, such as eye blinks and muscle movements through independent component analysis and band-pass filtering (0.5–50 Hz).

After preprocessing, the analysis focused on reconstructing the phase space of each EEG trace. TT was employed to create a multidimensional representation of the system's dynamics using delay embedding. The first step involved determining for each signal the optimal time delay (τ), a critical parameter in phase space reconstruction, as it defines the separation between consecutive points in the reconstructed dimensions [15]. The mutual information method was used to calculate τ, as it effectively identifies the point at which the time series exhibits the least redundancy while retaining information about the system's dynamics. For all channels and traces, τ was consistently found to be 25, suggesting a shared temporal dependency structure across the EEG signals.

The next step was to determine the embedding dimension (d), which represents the number of dimensions required to unfold the systems dynamics without overlap in the reconstructed phase space [17]. The False Nearest Neighbors (FNN) method was used for this purpose [19]. By analyzing the proportion of neighbors that remain close when the dimensionality is increased, FNN identifies the point at which the embedding dimension captures the true dynamics of the system. The results consistently indicated $d = 6$ for all traces, suggesting a moderate level of complexity in the underlying neural dynamics.

Starting from the parameters $\tau = 25$ and $d = 6$, the phase space for each EEG trace was reconstructed and visualized in three dimensions by selecting the first three delay coordinates. The trajectories were analyzed to extract quantitative metrics characterizing the temporal structure of the phase spaces. Specifically, the spread of the trajectories in each dimension and the average distance between consecutive points were computed. The spread reflects the range of dynamical variability, while the average distance provides insight into the smoothness and temporal evolution of the signals.

3. Tools and statistical analysis

Computational analysis for precise quantification of regional variations in brain dynamics was implemented using Python, leveraging libraries for signal processing, nonlinear analysis and statistical evaluation. Statistical analysis was performed to compare the phase space metrics among the FP1, C3 and O1 channels. Welch's t-tests were used to evaluate differences in trajectory spread across dimensions (x, y, z) among the channels. Welch's *t*-test was chosen because it does not assume equal variances between groups, thus ensuring robustness in the presence of heterogeneity in EEG signals.

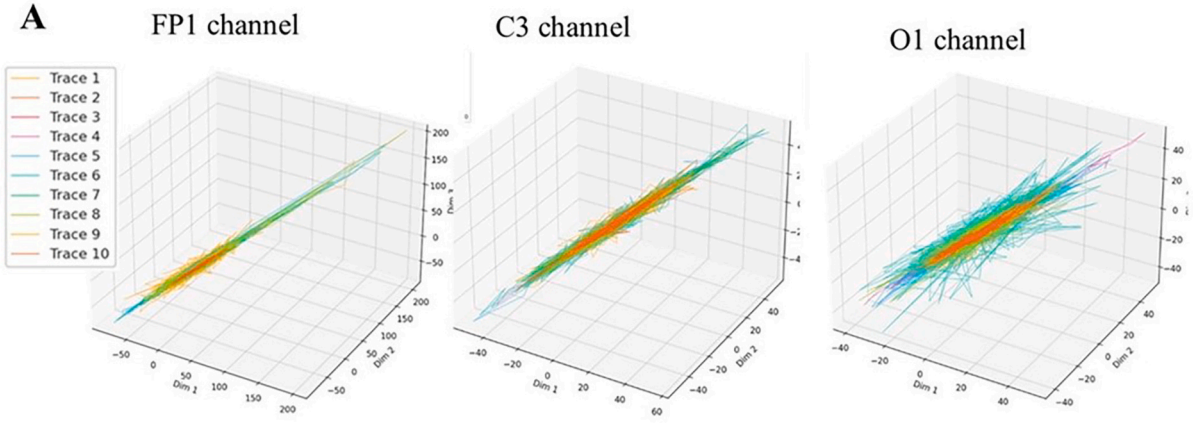
4. Results

Phase space trajectories were reconstructed for all ten EEG traces of healthy individuals across the FP1, C3 and O1 channels using time delay $\tau = 25$ and embedding dimension $d = 6$. These reconstructions highlighted distinct patterns of activity in the three regions (**Fig. 1A**). To quantify these differences, key metrics such as trajectory spreads across dimensions (x, y, z) and average distances between consecutive points were computed for each channel (**Fig. 1B**).

The FP1 trajectories displayed the broadest and most dispersed paths as well as the highest average distances, indicative of the greatest variability and complexity. This pattern aligns with the frontal region's role in higher-order cognitive functions, such as decision-making and problem-solving, which demand flexible and dynamic neural processes. In contrast, the C3 and O1 trajectories were more compact. Among them, O1 exhibited the most constrained dynamics with the smallest spreads and average distances, reflecting the structured and repetitive nature of visual processing. This stability is characteristic of the occipital region's specialization in handling consistent sensory inputs. Meanwhile, C3 showed a moderate spread, with intermediate spreads and distances that balanced variability and stability, consistent with its role in integrating sensory inputs and motor outputs, a process requiring balance between stability and flexibility. The degree of similarity and overlap in C3 trajectories also suggests shared neural patterns within the sensorimotor region, while the divergence in trajectory spreads provides insights into individual differences in neural activity among participants.

Statistical comparison of trajectory spreads across the three channels further validated these findings. Significant differences were observed in all pairwise comparisons, confirming substantial dynamical differences among FP1, C3 and O1. **Fig. 1D** provides a direct comparison of trajectory spreads across dimensions (x, y, z) for the three channels. FP1 consistently showed the largest spreads across all dimensions, a finding that reflects the region's high dynamical variability and complexity. This statistical validation reinforces the notion that EEG dynamics are regionally specific and closely linked to the functional roles of these

A



B

Summary of Trajectory Metrics Across Channels

Channel	Spread_X (Mean ± SD)	Spread_Y (Mean ± SD)	Spread_Z (Mean ± SD)	Avg Distance (Mean ± SD)
FP1	1.78 ± 0.34	1.62 ± 0.30	1.85 ± 0.28	0.43 ± 0.06
C3	1.42 ± 0.29	1.35 ± 0.24	1.48 ± 0.25	0.37 ± 0.05
O1	1.28 ± 0.27	1.22 ± 0.21	1.35 ± 0.22	0.34 ± 0.04

C

Statistical Comparison of Trajectory Spreads Across Channels

Metric	FP1 vs C3 (p-value)	FP1 vs O1 (p-value)	C3 vs O1 (p-value)
Spread_X	0.017	0.009	0.03
Spread_Y	0.018	0.012	0.026
Spread_Z	0.019	0.015	0.028

D

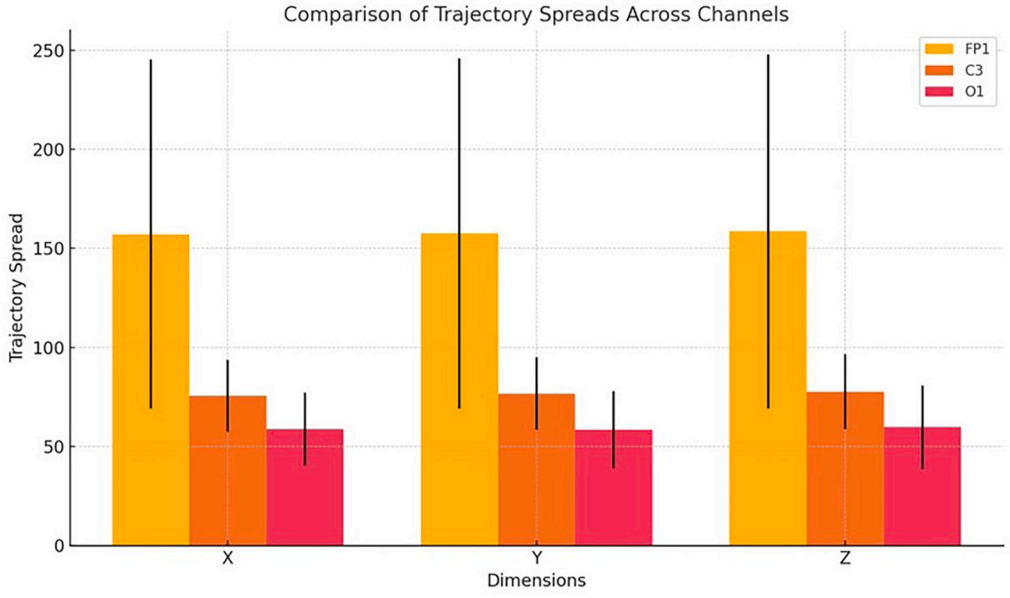


Fig. 1. A. Comparison of trajectory spreads across the reconstructed phase spaces for the three EEG channels FP1, C3 and O1. Each phase space illustrates the combined trajectories of all ten EEG traces from the corresponding channel, visualized together in a single 3D plot. B. Trajectory metrics computed for all three channels, including trajectory spreads across dimensions (x, y, z) and average distances between consecutive points. C. Statistical comparison of trajectory spreads across the three channels. Welch's t-tests reveals significant distinctions ($p < 0.05$) across all pairwise comparisons. D. Detailed visualization of the statistical comparison of trajectory spreads. The bar chart illustrates the average spreads for each dimension (x, y, z) for the FP1, C3 and O1 channels, accompanied by error bars representing the standard deviations.

cortical areas.

In sum, the combination of trajectory visualizations, quantitative metrics and statistical analysis reveal clear regional variations in trajectory spreads. These findings align with the functional specialization of the brain regions and underscore the utility of TT in capturing regional variations in EEG dynamics.

5. Conclusions

We focused on applying Takens' theorem to EEG signals to examine regional nonlinear variations in healthy subjects' brain dynamics, reconstructing the phase spaces and comparing their temporal features. Three key cortical areas were analyzed, namely, the frontal region (FP1), the sensorimotor region (C3) and the occipital region (O1). Using nonlinear dynamical analysis focused on trajectory spreads and average distances, the study reconstructed the phase space of EEG signals to reveal distinct patterns of activity corresponding to the functional specialization of these regions.

Takens' theorem has emerged as a powerful tool for exploring EEG traces. By transforming abstract EEG data into comprehensible geometrical forms, TT allows for the reconstruction of the phase space. Rohrbacker [19] illustrated the impact of TT on neuroscience by calculating the necessary embedding dimensions for EEG data using false nearest neighbor analysis. His seminal findings emphasized the importance of adequate embedding for accurately reconstructing phase spaces. TT's applications span epilepsy diagnosis, causal inference, BCI development and real-time analysis. For instance, phase space analysis has been used to identify pre-seizure states by detecting chaotic patterns in EEG signals [14]. Kwessi and Edwards [14] introduced the concept of complex geometric structurization to analyze epilepsy-related EEG data, revealing intricate geometric structures as biomarkers for seizure activity. Sleep studies have used phase space trajectories to differentiate between sleep stages and detect sleep disorders [8]. Changes in neural complexity and stability underlying neurodevelopmental disorders such as ADHD can also be examined through phase space reconstruction [12].

Topological data analysis (TDA) represents another area where TT has influenced EEG research [18]. Altındiş et al. [2] explored the use of TDA to extract persistent homologies from EEG-derived state spaces, demonstrating that TDA could robustly capture topological features of neural data even in the presence of artifacts. Moreover, TT has been instrumental in the development of methodologies for analyzing the nonlinear components of EEG signals. For instance, Mekler [16] introduced an innovative method for calculating the correlation dimension of EEG attractors, overcoming the limitations of traditional approaches. This advancement allows for more efficient processing of large datasets while minimizing subjectivity. Similarly, Kannathal et al. [11] applied entropy measures derived from EEG embeddings to detect epilepsy, achieving high classification accuracy. Also, TT has proven valuable for studying causality in neural systems. Traditional causal models often fall short when applied to nonlinear and cyclic systems like the brain. Harnack et al. [9] addressed this limitation by leveraging time-delay state space reconstructions to measure directed causal influences. The applicability of TT extends to brain-computer interface (BCI) systems, which depend on decoding EEG signals to enhance signal classification and facilitate interaction with external devices, providing critical support for individuals with disabilities. Carrara and Papadopoulo [6] incorporated embedding techniques into geometric neural networks, enhancing the interpretability and efficiency of BCI decoding.

The novelty of this study is that we applied TT to investigate the differences in phase space features among different EEG channels of healthy subjects, reflecting the distinct physiological dynamics of the underlying brain regions. One of the primary contributions of this work was the detailed reconstruction of phase spaces for each EEG channel using time-delay embedding. The reconstructed trajectories were further quantified through metrics such as trajectory spread and average distance that provided insights into the temporal structure and complexity of brain activity in different regions that are not easily captured by traditional linear methods. The FP1 region, associated with higher-order cognitive functions such as decision-making and information processing, exhibited the largest trajectory spreads and higher average distances. This variability aligns with the complexity and flexibility required for cognitive tasks. In contrast, the C3 region, which integrates sensory inputs and motor outputs, exhibited moderate variability, while the O1 region, responsible for visual processing, displayed the smallest spreads and distances, consistent with its structured and stable neural dynamics.

These findings have significant implications for understanding the role of regional dynamics in neural processing. The distinct temporal structures observed across the three channels provide a quantitative framework for examining how different brain regions contribute to overall function. By quantifying and visualizing the underlying dynamics, TT opens new opportunities for studying neural systems. The moderate embedding dimensions identified in this study suggest that the brain operates within a finite-dimensional dynamic space, efficiently processing complex information. The possible applications of these findings are vast. Dynamical systems can be compared by analyzing the variability, complexity and chaotic behavior of specific EEG traces. Identifying outliers, such as traces that deviate significantly from the shared structure, may help detect noise or reveal unique dynamics.

Despite its strengths, the study has limitations. The sample size was relatively small, consisting of only ten EEG traces, which may limit the generalizability of the findings. Additionally, the uniform use of $\tau = 25$ and $= 6$ across all traces, while robust, may not capture individual variability in optimal parameters. Furthermore, the analysis was limited to three channels (FP1, C3, O1) representing specific cortical regions. Expanding the study to include more channels and larger datasets could provide a more comprehensive understanding of the global and regional dynamics of the brain. Future research could address these limitations by applying the approach to more diverse datasets, exploring alternative parameter optimization methods, and incorporating task-based EEG data.

In conclusion, this study demonstrates the utility of Takens' theorem in reconstructing the phase space of EEG signals in healthy individuals and in revealing regional variations in brain dynamics. The findings highlight distinct patterns of activity in the frontal, sensorimotor and occipital regions. By bridging the gap between theoretical nonlinear dynamics and practical applications, this approach offers significant potential for advancing both basic neuroscience and clinical practice.

6. Declarations

Ethics approval and consent to participate: This research does not contain any studies with human participants or animals performed by the Authors.

Consent for publication: The Authors transfer all copyright ownership, in the event the work is published. The undersigned authors warrant that the article is original, does not infringe on any copyright or other proprietary right of any third part, is not under consideration by another journal, and has not been previously published.

Availability of data and materials: all data and materials generated or analyzed during this study are included in the manuscript. The Authors had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Competing interests: The Authors do not have any known or potential conflict of interest including any financial, personal or other relationships with other people or organizations within three years of beginning the submitted work that could inappropriately influence, or be perceived to influence, their work.

Authors' contributions: The Authors equally contributed to: study concept and design, acquisition of data, analysis and interpretation of data, drafting of the manuscript, critical revision of the manuscript for important intellectual content, statistical analysis, obtained funding,

administrative, technical, and material support, study supervision.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used ChatGPT to assist with data analysis and manuscript drafting. After using this tool, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication.

CRediT authorship contribution statement

Arturo Tozzi: Conceptualization, Funding acquisition, Resources, Visualization, Formal analysis, Methodology, Validation, Writing – original draft, Supervision, Data curation, Investigation, Software, Project administration, Writing – review & editing. **Ksenija Jaušovec:** Investigation, Data curation, Project administration, Validation, Conceptualization, Formal analysis, Software, Writing – original draft, Visualization, Funding acquisition, Methodology, Resources, Writing – review & editing, Supervision.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

Data will be made available on request.

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