

On a Characterization of Discrete Homotopy Distance

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Abstract

Brain chains [1] have emerged as a powerful tool for distinguishing subtypes of Alzheimer’s disease, offering a topological perspective on how network structure reflects disease progression. Central to this framework is the discrete homotopy distance; prior work established that this distance is bounded below by the number of positions in which maximal chains differ, but the precise conditions under which this bound is achieved remained open. In this work, we provide a characterization for general posets, identifying exactly when the discrete homotopy distance coincides with the number of differing positions between maximal chains.

1 Introduction

Graph posets arise naturally in many areas of network dynamical systems such as information propagation in social networks, population dynamics in ecology, and the study of graph percolation. In particular, studying the properties of such posets has been fruitful in distinguishing different subtypes of Alzheimer’s disease [1]; however, as the authors remarked, constructing $\mathcal{H}(N)$, the spanning subgraph poset of the complete graph on N vertices quotiented by homotopy equivalence, suffers from the limitation of computational complexity. Consequently, the distance defined in [1] (c.f. definition 1.3) is currently computationally intractable for large N because it relies on constructing the entire $\mathcal{H}(N)$ poset. In this manuscript, we provide a characterization that, in some cases, decreases the computation time of the discrete homotopy distance presented in definition 1.3. We also provide a GitHub repository, <https://github.com/B-Vigil/discrete-homotopy>, that contains the following:

- a Python implementation of Algorithm 1 and Algorithm 2 from [1] to construct $\mathcal{H}(N)$ and
- a Boolean function that indicates when two maximal chains in $\mathcal{H}(N)$ satisfy theorem 2.2.

We recall three definitions such that the reader may become familiar with the discrete homotopy distance; all three of these definitions can be found on page 1275 in [1].

Definition 1.1 (pg. 1275, Def. 5.1 in [1]). *Two maximal chains \mathcal{F}_1 and \mathcal{F}_2 are **adjacent** if they differ in exactly one position.*

This notion of adjacency captures a local relation between maximal chains, determined by a single deviation in their respective positions. This relation is a key property to define the discrete homotopy distance; an example of two adjacent maximal chains is depicted in Figure 1.

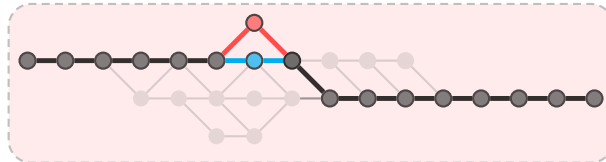


Figure 1: Two adjacent chains differing only at the red and cyan nodes.

Definition 1.2 (pg. 1275, Def. 5.2 in [1]). Let $\{\mathcal{F}_i\}_{i=1}^d$ be a sequence of maximal chains in a graded poset such that \mathcal{F}_k and \mathcal{F}_{k+1} are adjacent for all $k \in \{0, 1, \dots, d-1\}$. The sequence $\{\mathcal{F}_k\}$ is a **discrete homotopy** of length d .

Definition 1.3 (pg. 1275, Def. 5.3 in [1]). Let \mathcal{F}_I and \mathcal{F}_F be maximal chains in a graded poset. The **discrete homotopy distance** $d_H(\mathcal{F}_I, \mathcal{F}_F)$ between \mathcal{F}_I and \mathcal{F}_F is the length of the shortest discrete homotopy $\{\mathcal{F}_i\}_{i=0}^d$ with $\mathcal{F}_0 = \mathcal{F}_I$ and $\mathcal{F}_d = \mathcal{F}_F$.

The authors remarked in [1] that the discrete homotopy distance between two maximal chains in a graded poset is bounded below by the number of positions in which they differ. We characterize precisely when this lower bound is obtained, i.e. when the discrete homotopy distance equals the number of differing positions between two maximal chains.

2 Characterizing discrete homotopy distance

In the study of discrete homotopy distance, a fundamental problem is to determine when the natural lower bound for the distance between two maximal chains is achieved. Recall that Goodbrake et al. remarked that this lower bound is given by the number of positions in which the chains differ. While this bound is immediate, equality is not guaranteed; the combinatorial structure of the poset may impose constraints that force additional steps in any admissible homotopy. Thus, a characterization of when the lower bound is attained is essential, as it identifies precisely the circumstances under which the *geometry* of the poset allows for the most efficient deformation between chains.

The notion of interleaving provides such a characterization. By requiring the elements of the two chains to alternate in a coherent order, interleaving ensures that the discrepancy between the chains is distributed in a way that permits the homotopy to realize the lower bound without additional detours. Theorem 2.2 formalizes this intuition, showing that interleaving is both necessary and sufficient for the discrete homotopy distance to equal the number of differing positions. This result not only gives a sharp condition for equality, but also highlights the structural interplay between combinatorial order and discrete homotopy theory. Figure 2 depicts four posets such that any two maximal chains in the posets are interleaved.

Definition 2.1. Let \mathcal{F} and \mathcal{G} be two maximal chains of length n . \mathcal{F} and \mathcal{G} are **interleaved** if

$$z_k^{\mathcal{F}} \prec z_{k+1}^{\mathcal{G}} \quad \text{or} \quad z_k^{\mathcal{G}} \prec z_{k+1}^{\mathcal{F}}$$

for all $k \in \{0, 1, \dots, n-1\}$.

Theorem 2.2. Let P be a poset and let \mathcal{F} and \mathcal{G} be maximal chains of length n . The discrete homotopy distance $d_H(\mathcal{F}, \mathcal{G})$ equals the number of locations where \mathcal{F} and \mathcal{G} differ if and only if \mathcal{F} and \mathcal{G} are interleaved.

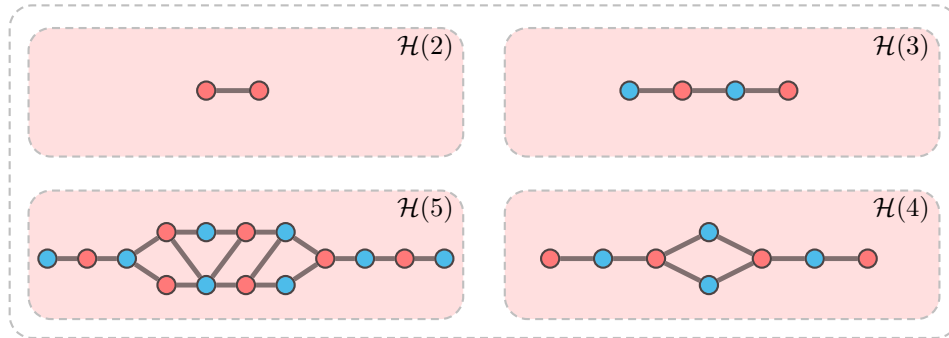


Figure 2: Four posets with the property that any two maximal chains are interleaved.

Theorem 2.2 provides a characterization of when the discrete homotopy distance between two maximal chains is exactly the number of positions in which they differ, namely when the chains are interleaved. Although this statement is a complete characterization, it can be made more practical by recognizing that interleaving is only nontrivial in the positions where the chains actually differ. Indeed, whenever \mathcal{F} and \mathcal{G} agree at a position, the interleaving condition is automatically satisfied. Thus, to verify interleaving in the sense of Theorem 2.2, it suffices to restrict one's attention to the set of differing, or discrepant, positions.

This observation naturally leads to Theorem 2.3, which reformulates the condition of interleaving entirely in terms of the discrepancy set $D = \{i \mid z_i^{\mathcal{F}} \neq z_i^{\mathcal{G}}\}$. In doing so, the theorem makes explicit the fact that the homotopy distance attains the lower bound precisely when the differences between the two chains can be ordered in a compatible way across the poset. The reformulation has one main advantage: it provides a sharper, more computationally tractable criterion for checking equality of the distance for large chains. Moreover, this equivalence underpins the proof of Theorem 2.2, as the restricted condition of D captures exactly the essence of the interleaving relation while avoiding redundancies introduced by identical positions. It is straightforward to see that Theorem 2.2 and Theorem 2.3 are equivalent.

Theorem 2.3. *Let P be a poset. Let \mathcal{F} and \mathcal{G} be maximal chains of the same finite length in P and $D = \{i \mid z_i^{\mathcal{F}} \neq z_i^{\mathcal{G}}\}$ the set where \mathcal{F} and \mathcal{G} differ. The discrete homotopy distance $d_H(\mathcal{F}, \mathcal{G})$ equals $|D|$, the number of locations where \mathcal{F} differs from \mathcal{G} , if and only if $\mathcal{F} = \mathcal{G}$, $|D| = 1$ or*

$$z_k^{\mathcal{F}} \prec z_{k+1}^{\mathcal{G}} \quad \text{or} \quad z_k^{\mathcal{G}} \prec z_{k+1}^{\mathcal{F}}$$

for all $k \in D \setminus \{m_D\}$, where $m_D = \max\{i \mid i \in D\}$.

Proof. (\Leftarrow) If $\mathcal{F} = \mathcal{G}$, then we are done, so suppose that $|D| = 1$. Without loss of generality, take $F_0 = \mathcal{F}$ and $F_1 = \mathcal{G}$. Note that F_0 and F_1 are adjacent by definition; therefore, we have constructed a discrete homotopy of length $|D| = 1$. Now, suppose $|D| > 1$ and let \mathcal{F} and \mathcal{G} be maximal chains in P such that

$$z_k^{\mathcal{F}} \prec z_{k+1}^{\mathcal{G}} \quad \text{or} \quad z_k^{\mathcal{G}} \prec z_{k+1}^{\mathcal{F}}$$

for all $k \in D \setminus \{m_D\}$. Let p be the first position where either $z_p^{\mathcal{F}} \prec z_{p+1}^{\mathcal{G}}$ or $z_p^{\mathcal{G}} \prec z_{p+1}^{\mathcal{F}}$ but not both. Suppose $z_p^{\mathcal{F}} \prec z_{p+1}^{\mathcal{G}}$, in this case we take $F_0 = \mathcal{F}$ and $F_{|D|} = \mathcal{G}$. There are two main cases to examine; $z_{m_D-1}^{\mathcal{F}} \prec z_{m_D}^{\mathcal{G}}$ or $z_{m_D-1}^{\mathcal{G}} \prec z_{m_D}^{\mathcal{F}}$. We first consider the case where $z_{m_D-1}^{\mathcal{F}} \prec z_{m_D}^{\mathcal{G}}$; take $F_1 = F_0(z_{m_D}^{F_0} \rightarrow z_{m_D}^{\mathcal{G}})$ where $F_0(z_{m_D}^{F_0} \rightarrow z_{m_D}^{\mathcal{G}})$ indicates that we only replace $z_{m_D}^{F_0}$ with $z_{m_D}^{\mathcal{G}}$ in F_0 . Since $z_{m_D-1}^{\mathcal{F}} \prec z_{m_D}^{\mathcal{G}}$, it follows that F_0 and F_1 are adjacent. Let $l_1 \in D \setminus \{m_D\}$ be the smallest element such that $z_{l_1}^{\mathcal{G}} \prec z_{l_1+1}^{F_1}$, take $F_2 = F_1(z_{l_1}^{F_1} \rightarrow z_{l_1}^{\mathcal{G}})$. By the minimality of l_1 it follows that $z_{l_1-1}^{F_2} \prec z_{l_1}^{\mathcal{G}}$; therefore, F_1 and F_2 are adjacent. Let $l_2 \in D \setminus \{m_D, l_1\}$ be the smallest element such that $z_{l_2}^{\mathcal{G}} \prec z_{l_2+1}^{F_2}$, if no such element exists, then we have constructed a discrete homotopy between \mathcal{F} and \mathcal{G} of length $|D|$ and we are done. So suppose such an element exists. Take $F_3 = F_2(z_{l_2}^{F_2} \rightarrow z_{l_2}^{\mathcal{G}})$, again by the minimality of l_2 it follows that $z_{l_2-1}^{F_3} \prec z_{l_2}^{\mathcal{G}}$; therefore, F_2 and F_3 are adjacent. Continuing this process will construct a discrete homotopy between \mathcal{F} and \mathcal{G} of length $|D|$; therefore, the discrete homotopy distance is equal to $|D|$, the number of locations where \mathcal{F} and \mathcal{G} differ. Now consider the case where $z_{m_D-1}^{\mathcal{G}} \prec z_{m_D}^{\mathcal{F}}$. Let $l_1 \in D \setminus \{m_D\}$ be the smallest element such that $z_{l_1}^{\mathcal{G}} \prec z_{l_1+1}^{F_0}$ and take $F_1 = F_0(z_{l_1}^{F_0} \rightarrow z_{l_1}^{\mathcal{G}})$. By the minimality of l_1 , it follows that $z_{l_1-1}^{F_1} \prec z_{l_1}^{\mathcal{G}}$; therefore, F_0 and F_1 are adjacent. Moreover, if $l_1 = m_D - 1$, then we are in the same case as before where we treat $m_D - 1 = m_D$ and we can construct a discrete homotopy between \mathcal{F} and \mathcal{G} of length $|D|$ because the last maximal chain from the $m_D - 1$ construction, will only differ from \mathcal{G} at $z_{m_D}^{\mathcal{G}}$ and is thus adjacent to \mathcal{G} , so suppose $l_1 \neq m_D$. Let $l_2 \in D \setminus \{m_D, l_1\}$ be the smallest element such that $z_{l_2}^{\mathcal{G}} \prec z_{l_2+1}^{F_1}$, take $F_2 = F_1(z_{l_2}^{F_1} \rightarrow z_{l_2}^{\mathcal{G}})$. By the minimality of l_2 , it follows that $z_{l_2-1}^{F_2} \prec z_{l_2}^{\mathcal{G}}$, thus F_1 and F_2 are adjacent. If $l_2 = m_D - 1$, then we can follow the same construction as in the previous case, and we are done. Note that by continuing this process, there must be an ℓ_s such that $\ell_s = m_D - 1$, either $s = |D| - 1$ and F_s is adjacent to \mathcal{G} , or $s < |D| - 1$ and by the minimality of ℓ_s , we can construct $|D| - 1$ sequentially adjacent maximal chains, where the last chain in this sequence is adjacent to \mathcal{G} ; therefore, we can construct a discrete homotopy between \mathcal{F} and \mathcal{G} of length

$|D|$. The case where p is such that $z_p^{\mathcal{G}} \prec z_{p+1}^{\mathcal{F}}$ follows dually to the above argument. If no such p exists, take either $F_0 = \mathcal{F}$ or $F_0 = \mathcal{G}$ and follow the same construction as above.

(\rightarrow) We prove this direction using the contrapositive. Suppose $|D| > 1$ and there exists a $k \in D \setminus \{m_D\}$ such that neither $z_k^{\mathcal{F}} \prec z_{k+1}^{\mathcal{G}}$ nor $z_k^{\mathcal{G}} \prec z_{k+1}^{\mathcal{F}}$ holds. Since neither $z_k^{\mathcal{F}} \prec z_{k+1}^{\mathcal{G}}$ nor $z_k^{\mathcal{G}} \prec z_{k+1}^{\mathcal{F}}$ holds, it follows that $z_{k+1}^{\mathcal{F}} \neq z_{k+1}^{\mathcal{G}}$; therefore, we must have a maximal chain that replaces $z_{k+1}^{\mathcal{F}} \rightarrow z_{k+1}^{\mathcal{G}}$ or $z_{k+1}^{\mathcal{G}} \rightarrow z_{k+1}^{\mathcal{F}}$. However, this cannot happen because neither $z_k^{\mathcal{F}} \prec z_{k+1}^{\mathcal{G}}$ nor $z_k^{\mathcal{G}} \prec z_{k+1}^{\mathcal{F}}$ holds; therefore, we must have at least $|D| + 1$ sequentially adjacent maximal chains and thus a discrete homotopy distance of at least $|D| + 1$. \square

To aid in the intuition of the previous proof, Figure 3 illustrates a discrete homotopy of length 4 between two interleaved maximal chains in $\mathcal{H}(6)$; the homotopy is constructed via the construction provided in the previous proof.

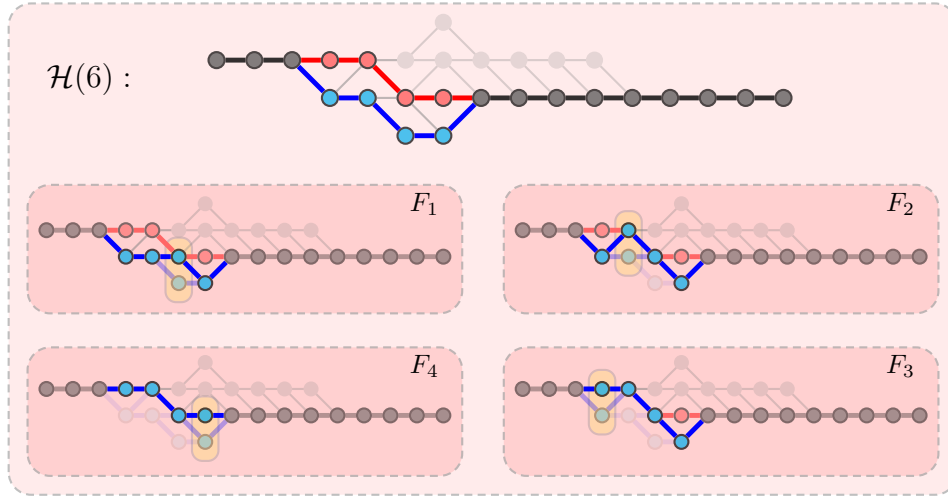


Figure 3: A discrete homotopy of length 4 between two maximal chains in $\mathcal{H}(6)$.

We note that in the specific setting of $\mathcal{H}(N)$, the spanning subgraph poset of the complete graph on N vertices quotiented by homotopy equivalence, this poset is finite and has a unique minimal and maximal element; therefore, every maximal chain has the same length [3]. This leads to the following corollary tailored specifically to $\mathcal{H}(N)$.

Corollary 2.4. *The discrete homotopy distance between two maximal chains \mathcal{F}_1 and \mathcal{F}_2 in $\mathcal{H}(N)$ is equal to the number of locations where \mathcal{F}_1 and \mathcal{F}_2 differ if and only if $\mathcal{F}_1 = \mathcal{F}_2$, they are adjacent, or for every $k \in D \setminus \{m_D\}$*

$$z_k^{\mathcal{F}_1} \prec z_{k+1}^{\mathcal{F}_2} \text{ or } z_k^{\mathcal{F}_2} \prec z_{k+1}^{\mathcal{F}_1}$$

where $D = \{i \mid z_i^{\mathcal{F}_1} \neq z_i^{\mathcal{F}_2}\}$ and $m_D = \max\{i \mid i \in D\}$.

Remark 2.5. *Observing Figure 2 and applying the above corollary, we immediately see that in the context of $\mathcal{H}(N)$, $N = 6$ is the smallest N such that the poset $\mathcal{H}(N)$ contains at least two maximal chains that are not interleaved, i.e. there exists two maximal chains in $\mathcal{H}(6)$ such that the discrete homotopy distance is strictly greater than the number of places where they differ.*

As mentioned previously, Goodbrake et al. noted the limitation to efficiently compute the full poset $\mathcal{H}(N)$ for large N . As N grows, the size of $\mathcal{H}(N)$ increases quite rapidly, making the direct construction of the entire poset currently computationally infeasible in practice. In some cases, Corollary 2.4 provides a more tractable alternative to efficiently compute the discrete homotopy distance between two maximal chains in $\mathcal{H}(N)$. Specifically, it is sufficient to examine only the positions in which the two maximal chains differ and

to check whether the successors of the corresponding graph homotopy polynomials satisfy the interleaving condition. This approach reduces the computational burden by avoiding unnecessary exploration of regions of the poset unrelated to the chains under comparison. It is important to emphasize that the corollary does not provide a general algorithm for computing the discrete homotopy distance between two arbitrary maximal chains. Rather, it determines when the distance between maximal chains is equal to the number of differing positions without constructing the entire poset $\mathcal{H}(N)$. For example, the chains studied in [1] corresponding to the Alzheimer’s disease subtypes Limbic, MTL, Posterior and Temporal are interleaved for each $N = 4, 6, 8, 12$, for $N = 15$ the subtypes Limbic and MTL are interleaved; the subtypes MTL, Posterior, and Temporal are also interleaved. Therefore, by applying Corollary 2.4, the discrete homotopy distance between these chains can be determined without constructing the entire poset. While computing $\mathcal{H}(N)$ for $N = 4, 6, 8, 12, 15, 18$ is still feasible (see Figure 4), the corollary offers a scalable alternative that extends beyond these moderate cases. In particular, it provides a practical avenue to study the full brain connectome consisting of $N = 83$ nodes, where direct computation of the entire $\mathcal{H}(83)$ poset would be infeasible.

To assess the computational complexity of computing the entire poset $\mathcal{H}(N)$ and verifying the interleaving conditions, we measured their execution times as a function of the number of nodes. Execution times were obtained using Python’s built in *time* module; for each measurement of constructing the poset $\mathcal{H}(N)$, the clock commenced immediately before the function call and stopped immediately after its completion. The difference between these two values was recorded as the execution time for that run. In the left plot of Figure 4 we compared the interleaving procedure with the construction of the homotopy polynomial poset $\mathcal{H}(N)$. For each value of $N \in \{0, 1, \dots, 21\}$, two random maximal chains of graphs were generated from which the corresponding chains of homotopy polynomials were constructed. The interleaving procedure was then applied to these chains, and the total execution time of this process was recorded, including the construction of the chains of graphs and homotopy polynomials. The homotopy polynomial poset $\mathcal{H}(N)$ was constructed for the same values of N , and its execution time was recorded in the same way. The results illustrate that as N increases, the computation time for $\mathcal{H}(N)$ grows rapidly; naturally, one might wonder how the interleaving procedure grows. The plot on the right of Figure 4 we focused exclusively on the interleaving procedure where we consider $N \in \{20, 30, 40, 50, 60, 70, 80, 90\}$. The execution time was recorded in the same way as previously described.

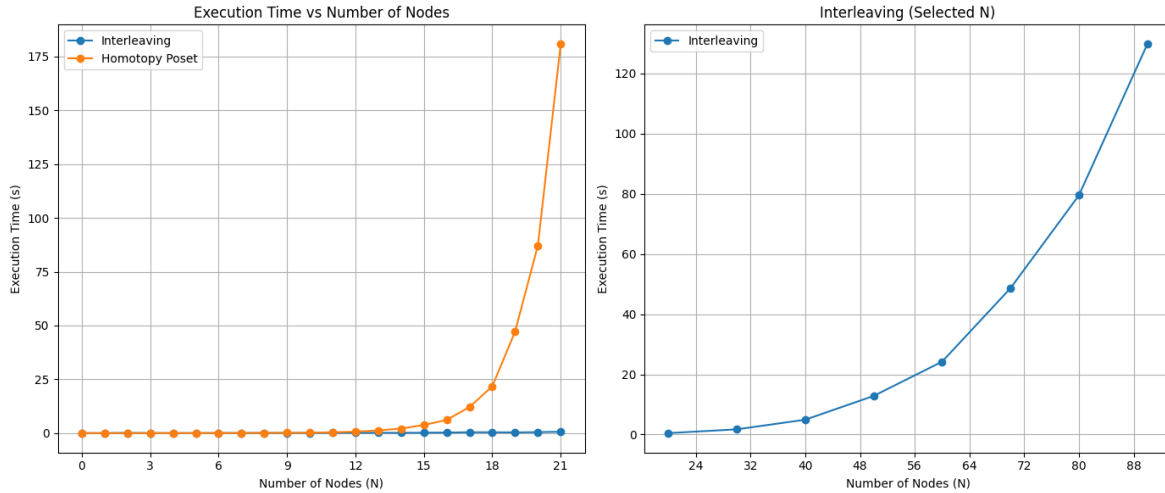


Figure 4: An execution time analysis comparing the construction of the full homotopy poset to the interleaving procedure as the number of nodes, N , increases (left panel), and an execution time analysis of the interleaving procedure as the number of nodes, N , increases (right panel).

The execution time analysis reinforces the earlier discussion of Corollary 2.4, highlighting how interleaving-based checks can bypass the need for the full poset construction. Although the corollary does not yield the

discrete homotopy distance for arbitrary pairs of maximal chains, it nevertheless provides a powerful tool in cases where the interleaving condition is satisfied. The timing experiments illustrate this trade-off by illustrating that constructing the entire homotopy polynomial poset becomes rapidly infeasible as N grows, whereas the interleaving test scales much more gracefully, even for larger graphs. Thus, these computational results serve as a practical validation of the theoretical framework developed earlier, demonstrating how structural characterizations of maximal chains translate into efficient procedures that can be applied to large-scale data, such as brain connectomes.

3 Discussion

In this manuscript, we expounded upon some observations made in [1] by providing a characterization of the discrete homotopy distance grounded in the notion of interleaving between maximal chains. Building on the theoretical results, we provide a GitHub repository that contains (1) a Python implementation of Algorithm 1 and Algorithm 2 presented in [1], and (2) a function indicating when two maximal chains in $\mathcal{H}(N)$ are interleaved. To assess the practical implications of these new theoretical approaches, we performed an execution time analysis comparing the cost of computing the entire poset $\mathcal{H}(N)$ with the cost of performing the interleaving check. Together, these contributions elucidate the practical utility of interleaving in enabling scalable computations for complex posets, in particular, for $\mathcal{H}(N)$.

The characterization provided by Theorem 2.2 has several important consequences for discrete homotopy distance and its application to network dynamical systems, in particular, to brain networks. From a computational perspective, the theorem identifies precisely when the discrete homotopy distance between two maximal chains can be obtained directly from the number of positions in which they differ. In some instances, Theorem 2.2 allows one to compute the discrete homotopy distance between two maximal chains in $\mathcal{H}(N)$ without having to compute the entire poset. This is significant because calculating the discrete homotopy distance between two maximal chains in $\mathcal{H}(N)$ required constructing the poset explicitly, a process that, as we have seen (see Figure 4), can become combinatorially intensive as the complexity of the poset increases. By establishing interleaving as the condition for equality, the theorem offers a principled shortcut for efficient computation.

3.1 Future directions

In the context of brain network applications explored in [1], the characterization provided in Theorem 2.2 may provide valuable information regarding Alzheimer’s disease subtypes. Maximal chains represent hierarchical pathways in the connectivity patterns of the brain, and determining whether two such chains are interleaved illustrates how these pathways differ in a minimally coherent way. Interleaving, therefore, not only marks when chains differ in the most efficient sense but also illuminates which chains are intimately connected. This distinction may enhance our ability to interpret homotopy distance as a biologically meaningful descriptor. For instance, interleaved chains may correspond to functional pathways that exhibit similar patterns of signal propagation, reflecting coordinated or conserved activity across regions. This naturally leads to the following inquiries: why are the MTL and Limbic subtypes interleaved in $\mathcal{H}(N)$ for $N = 4, 6, 8, 12, 15$? Will they always be interleaved in $\mathcal{H}(N)$? What causes the Posterior and Limbic subtypes to not be interleaved? Are these phenomena caused by the structure of the structural brain connectome, or by the Alzheimer’s model used [2]? Can interleaving be used as a proxy in future models? By focusing on positions where chains are interleaved, we may be able to identify portions of the network where alterations are meaningful, potentially indicative of pathological disruption, while filtering out variations that do not affect the overall propagation dynamics. These ideas suggest avenues for further exploration.

Another promising direction for future exploration lies in leveraging the structural properties of interleaving to further accelerate computations of discrete homotopy distance between any two arbitrary chains in $\mathcal{H}(N)$. In particular, interleaved segments of maximal chains motivate the question of defining ‘collapsible chains’, and if by collapsing these sections could one potentially reduce the effective size of the poset that must be constructed or analyzed, limiting computations to only the noninterleaved regions that contribute

to the homotopy distance. This approach could yield significant reductions in computational cost. The less speculative future directions consider the parallelization of the interleaving verification and its extension to arbitrary posets with arbitrary orderings. Exploring theoretical conditions that identify and exploit such collapsible structures represents a natural extension of the current work and could open new avenues for scalable computation and analysis of $\mathcal{H}(N)$.

References

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