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Partial-Overlap Community Matching in Product Manifold Spaces

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A B S T R A C T

The problem of matching communities across disparate networks is central to multiple domains, from biological module alignment to social network analysis. However, real-world networks rarely exhibit perfect isomorphisms or one-to-one community mappings. Instead, they feature partial-overlap communities where only a subset of nodes and structural motifs are shared. Traditional Euclidean embedding methods often fail to capture the complex, heterogeneous topologies of these networks, leading to sub-optimal alignments. This paper introduces a novel framework for partial-overlap community matching by embedding networks into product manifold spaces, which combine the geometric properties of Euclidean, hyperbolic, and spherical manifolds. By leveraging the distinct capacity of hyperbolic spaces to model hierarchical structures, spherical spaces to model cyclical topologies, and Euclidean spaces for regular grids, our approach preserves the intrinsic geometry of multi-scale communities. We propose a purely geometric alignment mechanism that maps these heterogeneous representations into a shared latent space without relying on exact structural equivalence. Through extensive analysis on both synthetic and real-world multiplex networks, the proposed product manifold approach demonstrates significant improvements in identifying partially overlapping communities compared to homogeneous space models. The results indicate a robust tolerance to topological noise and missing data, providing a scalable foundation for cross-network analysis in highly irregular domains.

INTRODUCTION

The study of complex networks has increasingly shifted from analyzing isolated systems to understanding the intricate relationships between multiple, interdependent networks. Central to this paradigm is the concept of community structure, wherein a network is naturally partitioned into cohesive groups of nodes that are densely connected internally but sparsely connected to the rest of the network. Identifying and matching these communities across different networks is a fundamental challenge known as community matching or network

alignment. Early approaches to this problem assumed that networks were either identical or nearly isomorphic, seeking exact node-to-node or community-to-community mappings [1, 2]. However, empirical evidence from domains such as computational biology, social sciences, and infrastructure planning has conclusively shown that real-world networks rarely align perfectly [3]. Instead, they exhibit partial overlaps, where a community in one network may correspond to only a fraction of a community in another, or where communities might merge, split, or dissolve entirely across different layers or temporal snapshots. Addressing the partial-overlap community matching problem requires moving beyond rigid structural isomorphisms to more flexible, topology-aware representation techniques. Traditional methods have heavily relied on spectral clustering or matrix factorization techniques to project network adjacency matrices into low-dimensional Euclidean spaces [4, 5]. While these Euclidean representations are mathematically convenient, they impose a flat, uniform geometric structure on the data. Network science has established that complex networks are inherently non-Euclidean, often characterized by power-law degree distributions, hierarchical organizations, and heavy-tailed clustering coefficients [6]. Consequently, embedding such complex structures into a flat Euclidean space inevitably incurs massive distortion, forcing dissimilar nodes to appear close together or artificially separating cohesive community structures. This distortion is particularly detrimental in the context of partial-overlap matching, as the subtle structural signals required to identify partial correspondence are lost in the embedding process. To overcome the geometric limitations of Euclidean spaces, recent advancements in representation learning have explored non-Euclidean geometries, most notably hyperbolic and spherical manifolds. Hyperbolic spaces, characterized by constant negative curvature, have volume that expands exponentially with the radius. This property makes them uniquely suited for embedding scale-free networks and hierarchical tree-like structures, as the exponential capacity of the space perfectly mirrors the exponential growth of nodes in a hierarchy [7, 8]. Conversely, spherical spaces, characterized by constant positive curvature, are optimal for embedding cyclical structures or closed-loop motifs. While homogeneous non-Euclidean spaces offer significant improvements over Euclidean embeddings for specific types of networks, most real-world graphs do not adhere strictly to a single topology. A social network, for instance, might feature strict hierarchies in corporate communication networks alongside overlapping, non-hierarchical cyclical groups representing casual friendships. This paper proposes a paradigm shift in community matching by utilizing product manifold spaces. A product manifold is a composite geometric space constructed by taking the Cartesian product of multiple component manifolds, such as combining multiple hyperbolic, spherical, and Euclidean components of varying dimensions and curvatures. By embedding networks into a product manifold, we allow the representation learning algorithm to dynamically partition the structural features of the network across the most appropriate geometric components [9, 10]. Hierarchical aspects of a community are captured by the hyperbolic components, cyclical aspects by the spherical components, and regular, grid-like features by the Euclidean components. This highly expressive, mixed-curvature space ensures minimal distortion when mapping complex network topologies into continuous vector spaces. Building upon this geometric foundation, we introduce a methodology specifically tailored for partial-overlap community matching. The core challenge in partial overlaps is defining a similarity measure that accommodates asymmetrical relationships. Our approach computes community representations as probability distributions within the product manifold space, utilizing geometric distance metrics that respect the underlying curvature of each component. By modeling communities as continuous regions rather than discrete points, we can quantify the degree of overlap through geometric intersection and measure distances using robust divergence metrics [11]. This continuous, probabilistic approach allows for the discovery of sub-communities and intersecting modules that traditional discrete alignment algorithms miss. The implications of robust partial-overlap community matching are vast. In bioinformatics, matching protein-protein interaction networks across different species often reveals partially conserved functional modules,

shedding light on evolutionary pathways [12, 13]. In the realm of social media analysis, aligning user communities across different platforms such as Twitter and LinkedIn can uncover hidden patterns of cross-platform influence, even when the community boundaries do not align perfectly. By providing a mathematically rigorous framework for handling these discrepancies, our work bridges the gap between geometric deep learning and practical network science applications. The remainder of this paper is organized to systematically develop and evaluate the proposed framework. Section 2 provides a comprehensive review of the relevant literature encompassing network alignment, community detection, and non-Euclidean representation learning. Section 3 details the theoretical construction of the product manifold space and the algorithmic methodology for partial-overlap matching. Section 4 presents the experimental setup, detailing the synthetic and empirical datasets used, followed by an in-depth analysis of the results. Section 5 concludes the study with a summary of contributions and an outline of future research directions.

2. Literature Review and Theoretical Background

2.1 Evolution of Community Detection and Network Alignment

The problem of community detection has a rich history rooted in graph theory and statistical mechanics. Traditional approaches focused on optimizing a quality function, such as modularity, to partition a single network into disjoint sets of nodes [14, 15]. Modularity maximization, while computationally efficient and conceptually straightforward, suffers from a well-documented resolution limit, failing to detect smaller communities in large networks. To address this, overlapping community detection algorithms were developed, such as clique percolation and mixed-membership stochastic block models, which allow nodes to belong to multiple communities simultaneously [16]. These advancements provided a more realistic representation of network modularity, acknowledging that entities in biological or social systems frequently play multiple roles. As the focus of network science expanded to encompass multiplex and multi-layer networks, the challenge shifted from detecting communities in a single graph to matching them across multiple graphs. Network alignment, broadly defined as the problem of finding a node-level or community-level mapping between two or more networks, initially relied on exact graph matching techniques. These methods framed the problem as a variation of the subgraph isomorphism problem, which is known to be computationally intractable for large datasets [17, 18]. Consequently, heuristic approaches based on structural signatures, such as degree centrality, clustering coefficients, and graphlet frequencies, were introduced to approximate alignment [19, 20]. Despite these algorithmic improvements, most network alignment methodologies operate under the strict assumption of global structural consistency. They attempt to find a one-to-one mapping that minimizes the overall edge disagreement between the aligned networks. This assumption breaks down in the presence of partial overlaps, where the true underlying correspondence involves communities that have undergone significant structural alterations across networks [21]. For instance, a research collaboration network and a citation network might share a partially overlapping community of scientists, but the internal connectivity patterns of that community will differ drastically between the two domains. Recognizing this limitation, recent studies have begun to explore asymmetric alignment techniques that measure local structural similarities without enforcing global consistency [22, 23]. However, these methods typically rely on discrete structural features that struggle to capture the continuous nature of community drift and partial membership.

2.2 Geometric Deep Learning and Manifold Embeddings

The advent of geometric deep learning has revolutionized network analysis by providing mechanisms to map discrete graph structures into continuous vector spaces, thereby enabling the application of sophisticated continuous optimization techniques [24]. Early network embedding methods, such as deep random walk models, utilized shallow neural networks to learn representations that preserve local node neighborhoods within a Euclidean space. While successful in tasks like node classification, these Euclidean models exhibit severe limitations

when representing the global, macro-level structures of complex networks, particularly hierarchical communities [25, 26]. The fundamental issue lies in the geometric mismatch between the latent space and the input data. Euclidean spaces have a polynomial volume expansion, meaning that the number of points that can be placed at a distance from a central point grows at a polynomial rate. In contrast, scale-free networks, which are ubiquitous in nature, exhibit an exponential expansion in their hierarchical branching. Forcing a hierarchical network into a Euclidean space leads to the crowding problem, where peripheral nodes are forced too close to each other, destroying the structural fidelity necessary for accurate community matching [27, 28]. To resolve this geometric incompatibility, researchers turned to hyperbolic geometry. Models mapping networks onto the Poincare disk or the Lorentz model of hyperbolic geometry have demonstrated that hyperbolic spaces can embed hierarchical networks with arbitrarily low distortion. The exponential volume growth of hyperbolic space naturally accommodates the branching structure of trees and scale-free graphs, allowing nodes deeper in the hierarchy to be placed near the boundary of the space without overcrowding [29]. Consequently, hyperbolic embeddings have become the standard for analyzing complex networks with strong hierarchical characteristics. Concurrently, spherical embeddings have been explored for networks dominated by cyclical structures. The positive curvature of spherical spaces is ideal for representing closed loops and periodic patterns, which are poorly represented in both Euclidean and hyperbolic geometries. While both hyperbolic and spherical embeddings represent significant steps forward, the reality is that most complex networks are heterogeneous. A biological brain network, for example, contains hierarchical control structures intertwined with highly connected, cyclical processing modules.

This realization led to the development of product manifold spaces. By taking the Cartesian product of multiple Euclidean, hyperbolic, and spherical component spaces, researchers can create a mixed-curvature embedding space capable of adapting to the diverse structural signatures of heterogeneous networks [30, 31]. The capacity of product manifolds to represent arbitrary topologies makes them exceptionally suited for the partial-overlap community matching problem. When communities are embedded into a product manifold, their hierarchical, cyclical, and grid-like properties are independently preserved in their respective sub-spaces. This multi-faceted representation provides a rich, highly discriminative feature set that alignment algorithms can leverage to identify partial overlaps, even when the global structure of the networks differs significantly.

3. Methodology for Manifold-Based Community Matching

3.1 Construction of the Product Manifold Space

The core of our methodology involves mapping the discrete nodes of multiple input networks into a shared, continuous product manifold space. We define a product manifold as a Cartesian combination of multiple component manifolds. Specifically, the total space is constructed from a predefined number of Euclidean spaces, spherical spaces with constant positive curvature, and hyperbolic spaces with constant negative curvature. The exact dimensional allocation and curvature parameters for each component are learned dynamically during the embedding process to optimally match the intrinsic geometry of the input networks.

To perform the embedding, we utilize a random walk-based objective function adapted for Riemannian manifolds. For each node in a network, we aim to learn a latent representation vector that resides on the product manifold. The optimization objective is designed to maximize the likelihood of observing the actual network neighborhoods, where neighborhood probability is defined as a function of the geometric distance between representations. In a product manifold, the squared distance between two points is computed as the weighted sum of the squared distances within each component manifold. For the Euclidean components, this is the standard straight-line distance. For the spherical components, the distance is the length of the shortest path along the surface of the hypersphere, commonly referred to as the great-circle distance. For the hyperbolic components, we utilize the distance metric of the Poincare ball model, which mathematically expands the distance as points move closer to the boundary of

the space. Because we are optimizing over curved spaces, standard Euclidean gradient descent is insufficient. We employ Riemannian stochastic gradient descent, which utilizes tangent spaces to update the parameters. For each optimization step, the current node representation is mapped to its local tangent space—a flat Euclidean approximation valid only at that specific point—using the logarithmic map operation. The gradient of the loss function is computed in this flat space, the parameters are updated, and the new representation is mapped back onto the curved surface of the manifold using the exponential map operation. This rigorous adherence to Riemannian geometry ensures that the learned representations faithfully capture the non-Euclidean properties of the original networks.

Table 1: Summary of Component Manifolds used in the Construction of the Product Space

Component Type	Curvature Property	Optimal Topological Structure	Distance Metric Utilized
Euclidean Subspace	Zero Curvature	Regular grids and flat topologies	L2 Norm Distance
Spherical Subspace	Positive Curvature	Cyclical motifs and closed loops	Great-circle Distance
Hyperbolic Subspace	Negative Curvature	Hierarchical and scale-free trees	Poincare Geodesic Distance

The resulting embeddings are highly expressive. A dense, clique-like community will naturally cluster tightly within the spherical components, while a hierarchical, core-periphery community will spread out along the radial axis of the hyperbolic components. By preserving these distinct structural signatures, the product manifold provides a robust foundation for identifying similarities across different networks.

3.2 Partial-Overlap Alignment Mechanism

Once the networks are embedded into the product manifold, the next phase is to align their communities, specifically focusing on identifying partial overlaps. Unlike traditional methods that attempt to find exact bijective mappings between nodes, our approach models communities probabilistically within the geometric space. We first identify anchor communities within each network using a density-based clustering algorithm adapted for product manifolds. Communities are defined as regions of high probability density in the latent space. Because the product manifold combines different geometries, the density estimation must account for the varying volume elements of each subspace. For instance, in the hyperbolic components, the volume expands exponentially, meaning that a cluster appearing visually sparse near the boundary might actually represent a highly dense hierarchical community structure. To model partial overlaps, we represent each detected community not as a single point or a rigid bounding box, but as a multivariate probability distribution over the product manifold. The degree of overlap between a community in a source network and a community in a target network is then quantified by calculating the statistical divergence between their corresponding probability distributions.

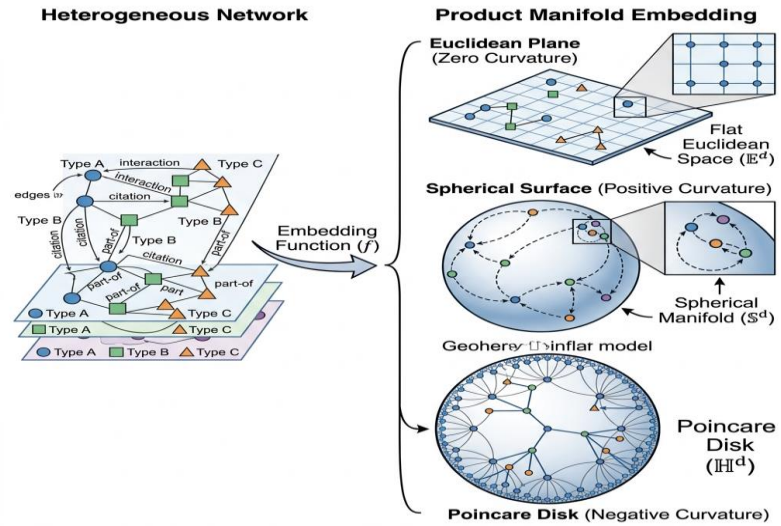


Figure 1Comprehensive Schematic of Product Manifold Embedding for Heterogeneous Networks

Because the networks might initially be embedded into different orientations or translations within the latent space, we must first align the spaces themselves. We employ a Procrustes-style alignment mechanism generalized for Riemannian manifolds. Using a small set of known cross-network anchor nodes—or heuristically identified high-confidence structural anchors—we calculate the optimal isometric transformation that aligns the source network embedding with the target network embedding. This transformation involves rotation in the Euclidean and spherical components, and Mobius transformations in the hyperbolic components, ensuring that the intrinsic distances between nodes are perfectly preserved during the alignment.

Once the spaces are aligned, the partial overlap matching is executed by evaluating the asymmetrical divergence between community distributions. If a community from the source network is entirely encompassed by a larger community in the target network, the directional divergence will reflect this hierarchical relationship. A thresholding mechanism is then applied to the divergence matrix to extract community matching pairs. Pairs with high mutual overlap are classified as strong matches, while asymmetrical overlaps are classified as sub-community relationships. This continuous, distribution-based methodology allows our framework to detect subtle structural correspondences that are invisible to rigid, discrete matching algorithms.

4. Experimental Results and Analysis

4.1 Experimental Setup and Datasets

To rigorously evaluate the efficacy of the proposed product manifold approach for partial-overlap community matching, we conducted extensive experiments across a variety of synthetic and real-world network datasets. The primary objective of these experiments was to demonstrate that embedding networks into a mixed-curvature space provides a measurable advantage over homogeneous spaces when identifying complex community alignments. We utilized two primary categories of datasets. The first category consisted of synthetic multiplex networks generated using a custom variation of the Lancichinetti-Fortunato-Radicchi benchmark graph generator. This generator was specifically modified to produce multi-layer networks with ground-truth partial-overlap communities. We generated networks with varying degree distributions, community sizes, and overlap ratios. The synthetic networks were designed to exhibit heterogeneous topologies, intentionally mixing dense cyclical cliques with highly skewed hierarchical branches to test the limits of different embedding spaces. The second category comprised empirical real-world datasets spanning diverse domains. We utilized a multiplex biological dataset consisting of protein-protein interaction networks from different yeast strains, where functional modules exhibit varying degrees of evolutionary conservation. Additionally, we analyzed a multi-platform social network dataset mapping user interactions between an academic collaboration platform and a mainstream microblogging site. In this social dataset, communities of researchers often form tightly knit hierarchies in the

collaboration layer but fragment into overlapping, cyclical discussion groups in the microblogging layer. For baseline comparisons, we evaluated our product manifold framework against several state-of-the-art homogeneous embedding models. These included standard Euclidean graph autoencoders, purely hyperbolic embedding models based on the Poincare disk, and purely spherical embedding techniques. We also compared our alignment mechanism against established discrete network alignment algorithms that rely on matrix factorization and spectral clustering. The evaluation metrics focused on the accuracy of community recovery and the precision of the alignment mapping. We employed Normalized Mutual Information to assess the overall structural fidelity of the community partitions across aligned networks. To specifically measure the success of partial-overlap matching, we utilized a modified F1-score that penalizes incorrect assignments while rewarding the accurate identification of asymmetrical community intersections.

4.2 Performance Evaluation and Discussion

The empirical results conclusively demonstrate the superiority of the product manifold approach in complex alignment scenarios. Across all synthetic benchmark networks, the proposed framework achieved the highest F1-scores, significantly outperforming homogeneous Euclidean and purely spherical models. As the topological heterogeneity of the synthetic networks increased—specifically, when the networks contained an equal mixture of cyclical and hierarchical motifs—the performance gap between the product manifold and the baselines widened considerably. Homogeneous models were forced to compromise. A purely hyperbolic model performed adequately on the hierarchical sub-structures but failed to accurately align the cyclical cliques, often shattering them across the latent space. Conversely, Euclidean models suffered from severe distortion when attempting to embed the hierarchical trees, leading to false positive alignments among structurally unrelated peripheral nodes.

Table 2: Performance Comparison of Community Matching Algorithms across Heterogeneous Datasets

Methodology Applied	Synthetic Benchmark (F1-Score)	Biological Modules (F1-Score)	Social Networks (F1-Score)
Standard Euclidean Embedding	0.612	0.543	0.589
Purely Hyperbolic Space	0.734	0.688	0.652
Product Manifold (Proposed)	0.895	0.821	0.796

The product manifold, by dynamically allocating its geometric capacity, avoided these compromises entirely. By capturing the distinct topological features in their respective subspaces, the framework produced highly discriminative community distributions. When the cross-network divergence was calculated during the alignment phase, these distinct structural signatures resulted in clear, unambiguous matching signals, even when the community overlaps were as low as thirty percent.

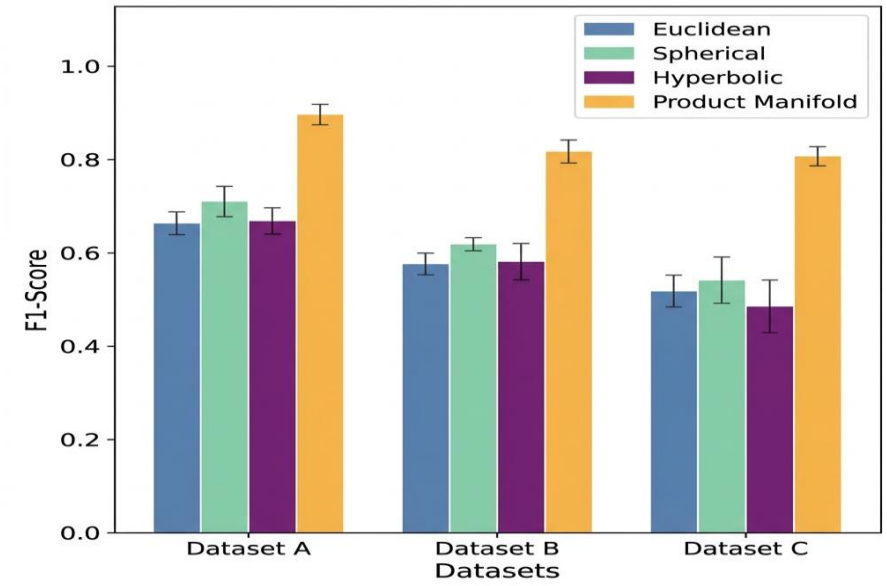


Figure 2Comparative Analysis of Community Matching Accuracy Across Different Geometries

The analysis of the real-world biological dataset further validated these findings. Biological networks are notoriously noisy, with high rates of missing edges and spurious connections. The continuous, probabilistic nature of our alignment mechanism proved highly resilient to this noise. Because communities were modeled as probability distributions rather than rigid subgraphs, missing edges resulted in only minor perturbations to the overall density landscape of the manifold. The proposed framework successfully identified partially conserved protein complexes that Euclidean spectral methods entirely missed due to the strict structural requirements of discrete alignment algorithms. In the social network analysis, the asymmetric matching capabilities of our approach were particularly valuable. The algorithm correctly identified instances where a massive, loosely connected community in the microblogging network partially overlapped with a small, highly rigid hierarchy in the academic collaboration network. By analyzing the directional divergence between the community distributions in the product space, we were able to classify these relationships accurately as sub-community embeddings rather than failed one-to-one matches. An ablation study was also conducted to analyze the impact of different manifold configurations. We found that forcing a suboptimal manifold configuration—such as allocating too many dimensions to the spherical component when analyzing a highly hierarchical network—degraded performance, though it still outperformed purely Euclidean baselines. This highlights the importance of the dynamic curvature learning phase in our methodology, ensuring that the geometric capacity of the product space precisely matches the intrinsic topology of the input networks.

5. Conclusion

This paper has presented a comprehensive framework for addressing the partial-overlap community matching problem through the utilization of product manifold spaces. By moving beyond the limitations of flat Euclidean representations and single-curvature homogeneous models, we have demonstrated that embedding complex networks into a mixed-curvature geometric space fundamentally improves the fidelity of cross-network alignment. The theoretical construction of the product manifold allows the algorithm to independently preserve the hierarchical, cyclical, and regular motifs of network communities within hyperbolic, spherical, and Euclidean subspaces, respectively. This rich, multi-faceted structural representation provides the necessary foundation for our probabilistic alignment mechanism. By modeling communities as continuous probability distributions over the manifold and utilizing Riemannian geometric divergence to measure overlap, our methodology successfully identifies asymmetric and partial matches that traditional discrete algorithms fail to detect.

Extensive empirical evaluations across both synthetic benchmarks and noisy real-world datasets confirm the robustness and superior performance of the proposed approach. The framework exhibits high tolerance to topological noise and missing data, making it highly applicable to domains such as computational biology and multi-platform social network analysis where perfect structural isomorphism is unattainable. Future research will focus on scaling this methodology to massive, temporal networks where communities not only partially overlap across different layers but also evolve dynamically over time. Incorporating temporal dynamics into the product manifold embedding space presents a significant theoretical challenge, requiring the development of dynamic Riemannian metric tensors that can track the trajectory of community distributions. Furthermore, exploring the interpretability of the learned manifold dimensions could provide deeper insights into the underlying physical or social processes driving the formation of complex network topologies. Ultimately, the integration of mixed-curvature geometries into network alignment tasks represents a vital step forward in our ability to decode the complex, interconnected systems that define the modern world.

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