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Topology-Based Detection and Modularity Analysis of Communities in Email Communication Networks

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Abstract

This study investigates the structural organization of an email communication network constructed from the SNAP Enron dataset, where nodes represent individual email addresses and edges correspond to communication links between them. Communities within the network were identified using the Label Propagation Algorithm (LPA), yielding 35 distinct groups. To evaluate the structural coherence and significance of these communities, we integrated two complementary analytical frameworks: Persistent Homology, from Topological Data Analysis (TDA), and Modularity, a key metric in network theory. Persistent homology was utilized to detect enduring topological features—such as connected components, loops, and voids—that characterize the intrinsic structure of each community across varying filtration scales. Modularity analysis, in turn, quantified the relative density of intra- and inter-community connections. Combining these approaches enabled the classification of communities as non-significant, significant, influential, or highly influential. The findings reveal a strong correlation between persistent topological features and high modularity scores, offering deeper insights into the stability, cohesion, and influence of communities in large-scale social communication networks.

Keywords: Email communication network; Community detection; Label propagation algorithm; Persistent homology; Modularity; Topological data analysis

1. Introduction

Understanding community structure in social networks is fundamental to analyzing communication patterns, organizational behavior, and influence dynamics. Traditional network analysis has relied heavily on graph-theoretic measures such as degree centrality, betweenness centrality, and modularity to quantify relationships and connectivity. While these metrics provide valuable insights, they often overlook higher-order relationships and the intrinsic topological robustness that characterize complex social systems.

In recent years, Topological Data Analysis (TDA)—particularly the use of Persistent Homology—has emerged as a powerful framework for uncovering multi-scale structural features that persist across different levels of network filtration. By incorporating TDA into community detection, researchers can reveal subtle patterns and hierarchical relationships that are not easily captured by conventional graph-based approaches. This integration offers a complementary perspective that enhances our understanding of structural stability and the persistence of information flow within social systems.

Social networks are inherently complex and heterogeneous, comprising subsets of densely connected nodes known as communities. These communities play a crucial role in maintaining social cohesion, facilitating communication, and shaping the emergence of collective identities. Consequently, community detection has become a central problem in

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network science and social media analysis. Its primary objective is to identify groups of nodes that are more densely connected internally than externally, thereby uncovering the modular organization underlying large-scale networks.

A wide range of methods has been proposed for community detection, each addressing specific challenges such as the resolution limit associated with modularity-based algorithms. For instance, Guo et al. (2023) introduced a generalized modularity density function and corresponding benchmark tests to mitigate the resolution limit problem. Similarly, Zhang et al. (2024) and Rustamaji et al. (2024) proposed alternative quality functions that better capture local community cohesiveness and node potentiality within communities.

Recent studies have shifted toward identifying influential communities, which not only exhibit strong internal connectivity but also play a pivotal role in influence propagation throughout the network. The Top-L Most Influential Community Detection (TopL-ICDE) framework proposed by Zhang et al. (2024) combines structural cohesiveness with influence dynamics to rank the most influential communities. Likewise, Li et al. (2017) developed a maximal *kr*-clique community model supported by an efficient C-Tree index structure to enhance computational performance in influential community detection. In overlapping networks, Aparna and Nairt (2018) emphasized the need to account for both internal and external influences to better understand information diffusion across community boundaries.

Several other studies have extended these concepts to diverse domains such as interest-based (Ahajjam et al., 2016) and academic (Islam et al., 2016; Lei & Wei, 2020) networks, where new influence metrics like the Weighted State of Critical Functionality (WSCF) have been introduced to evaluate community importance. Beyond social systems, community detection has been applied to software and biological networks, uncovering modular structures in method-call relationships and protein interaction networks (Vragović & Louis, 2006).

Complementary approaches, including spectral clustering (Newman, 2006; Wang et al., 2014), topic-integrated community detection (Ding, 2011), and Nonnegative Matrix Factorization (NMF) (Lu et al., 2022), have further diversified the methodological landscape. Collectively, these studies underscore the versatility and significance of community detection, while highlighting the untapped potential of topological approaches in advancing structural network analysis.

Building upon this foundation, the present study integrates modularity-based community detection with topological data analysis to achieve a deeper understanding of the internal organization and influence of communities in social networks. While modularity measures the density-based cohesion of communities, persistent homology captures higher-order topological features—such as connected components, loops, and voids—that persist across network filtrations. The combined framework thus provides a more comprehensive assessment of community robustness, stability, and influence.

In this research, we apply the integrated modularity–TDA framework to the Enron email communication network, a widely used benchmark dataset in social network analysis (Leskovec et al., 2009). Using the Label Propagation Algorithm (LPA), we detected 35 distinct communities, which were subsequently analyzed through persistent homology and modularity optimization. This dual analysis enables the classification of communities as *non-significant*, *significant*, *influential*, or *highly influential*, offering a unified perspective that bridges structural and topological insights in complex network analysis.

2. Dataset Description

2.1. Construction of the Enron Email Network Subset

The dataset utilized in this study is derived from the **Stanford Large Network Dataset Collection (SNAP)**, specifically the **Enron Email Network** (Leskovec et al., 2009; Klimt, 2004). This dataset captures the communication structure among Enron employees and external contacts through email exchanges recorded over several years.

The network is modeled as an undirected graph, where:

- **Nodes** represent individual email addresses (both Enron and external).
- **Edges** represent communication links between two addresses, indicating at least one email exchange.
- **Network size:** The original dataset consists of approximately *500,000 email exchanges*.
- **Representation:** Each node i is *connected* to node j by an edge if there exists at least one email correspondence between them. External email addresses serve as *peripheral sources* or *sinks* of information flow.

For this study, we focused primarily on *internal communications* to ensure the integrity of community structures within the organization.

2.2. Data Preprocessing

To enable efficient computation and meaningful topological analysis, a random sampling technique was applied to extract a representative subnetwork from the full dataset. From the original graph containing *36,692* nodes and *183,831* edges, a subset of *4,001* nodes and their corresponding edges was selected. This sampled network retains the essential connectivity patterns and structural diversity of the full Enron network while allowing tractable community detection and topological computations.

3. Methodology

3.1. Network Construction

An undirected graph $G = (V, E)$ was constructed to represent the Enron email communication network. Each vertex $v_i \in V$ corresponds to an individual email address, and an edge $e_{ij} \in E$ denotes the existence of at least one email exchange between v_i and v_j. To focus on the structural connectivity rather than the frequency of communication, multiple email exchanges between the same pair of nodes were reduced to a single undirected edge.

3.2. Community Detection

Community structures within the Enron email network were identified using the Label Propagation Algorithm (LPA), chosen for its efficiency and non-parametric nature. Initially, each node is assigned a unique label. During each iteration, a node updates its label to the one most frequently observed among its neighbors. This process continues until label assignments stabilize, resulting in a natural partition of the network into 35 distinct communities.

The LPA is computationally lightweight, making it well-suited for large-scale networks where more complex algorithms such as Louvain or Infomap may become computationally expensive. Although LPA's non-deterministic nature can yield variable results, its simplicity and scalability provide strong advantages for exploratory analysis.

3.3. Label Propagation Approach (LPA):

The Label Propagation Algorithm (Garza, 2019) operates through an iterative majority-voting mechanism where nodes adopt the most common label among their immediate neighbors, thus forming cohesive clusters.

3.3.1. Algorithmic Steps:

- *Initialization:* Assign a unique label to every node in the network.
- *Label Propagation:* Iteratively update each node's label to match the most frequent label among its neighbors. In the event of a tie, one label is selected randomly.
- *Convergence:* The process repeats until label assignments no longer change, indicating the stabilization of community structures.

While the Louvain method offers higher modularity optimization accuracy, the LPA provides greater computational efficiency and simplicity, particularly beneficial for large datasets such as the Enron network.

3.4. Modularity Analysis

Modularity (Q) is a fundamental metric used to assess the quality of a network's division into communities. It quantifies how well a network is partitioned by comparing the actual density of edges within communities to the expected density in a randomized network that preserves the original node degree distribution. In essence, modularity evaluates whether the observed community structure is significantly stronger than what might occur by chance.

Formally, for a network $G = (V, E)$ with $m = \mid E \mid$ total edges, modularity is defined as:

$$Q = \frac{1}{2m} \sum_{i,j} [A_{ij} - \frac{k_i k_j}{2m}]\, \delta(c_i, c_j),$$

where

$$A_{ij} = \begin{cases} 1, & if\ there\ is\ an\ edge\ between\ nodes\ i\ and\ j \\ 0, & otherwise \end{cases};$$

k_i and k_j denote the degrees of nodes i and j, respectively; c_i represents the community assignment of node i, and

$$\delta(c_i, c_j) = \begin{cases} 1, & \text{if nodes } i \text{ and } j \text{ belong to the same community} \\ 0, & \text{otherwise} \end{cases}.$$

A higher modularity value indicates that a network exhibits dense intra-community connections and sparse inter-community links, reflecting a well-defined and cohesive community structure. Conversely, lower modularity suggests weaker or less distinct community organization.

3.5. Persistent Homology Analysis

To gain deeper insights into the structural properties of the detected communities, we employ Persistent Homology (PH), a key tool in Topological Data Analysis (TDA). For each community subgraph, we construct a Vietoris–Rips filtration and compute the Betti numbers ($\beta_0, \beta_1, \beta_2, \ldots$) using established TDA software such as GUDHI or Ripser where

β_0: Number of connected components;
β_1: Number of loops or cycles; and
β_2: Higher-dimensional voids.

Persistent homology captures the evolution of these topological features across different filtration scales. Communities exhibiting long-lived homology classes are considered structurally significant, reflecting stable and robust connectivity patterns beyond simple edge density. These features are visualized through persistence barcodes and diagrams, which map the "birth" and "death" of topological structures, enabling a multi-scale assessment of community organization.

3.5.1. PH Computation from Point Cloud Data

The computation of persistent homology begins with point cloud data, representing the network nodes in a metric space. The process proceeds as follows:

- *Simplicial Complex Construction*: Nodes are connected to form simplices (vertices, edges, triangles, etc.), representing higher-order relationships among points.
- *Chain Groups and Boundary Operators*: Simplices are grouped by dimension, and boundary operators map higher-dimensional simplices to their boundaries, identifying cycles and voids.
- *Homology Group Computation*: Chain complexes are used to compute homology groups, capturing topological features such as connected components (0D), loops (1D), and voids (2D) at a given scale.
- *Persistence Analysis*: Features are tracked across filtration scales to distinguish persistent structures (significant topological features) from short-lived noise.
- *Visualization*: Persistence diagrams or barcodes illustrate the birth and death of topological features, providing a clear representation of the intrinsic shape and structure of the community (Shiraj et al., 2024).

This approach allows us to quantify structural stability and detect higher-order patterns that traditional graph-theoretic measures may overlook.

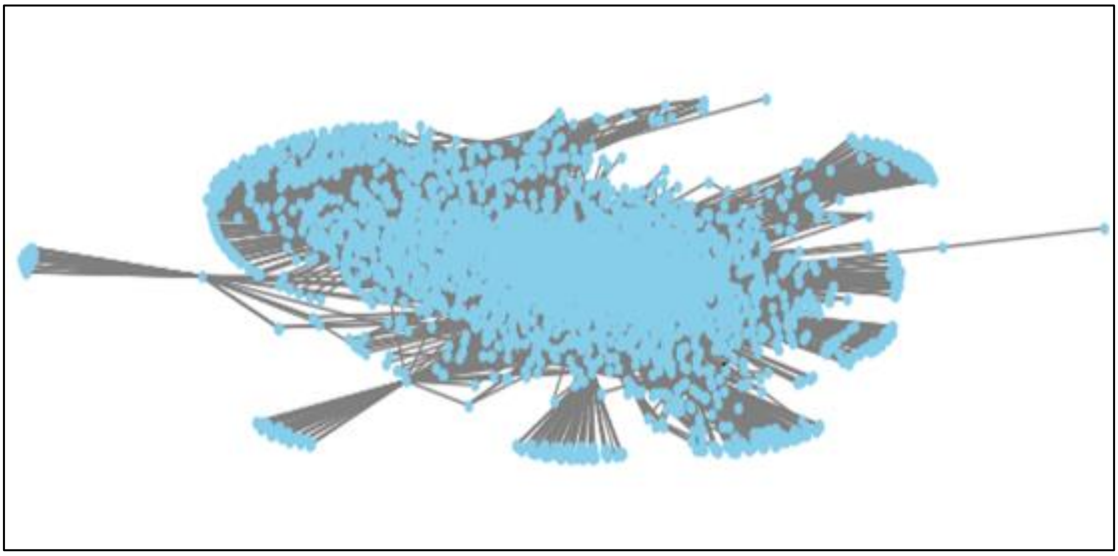

Figure 1 Email user's network graph

3.6. Classification of Communities

We classify communities based on combined metrics:

- ***Most Influential***: High modularity and persistent homological features (high β_1 persistence);
- ***Influential***: High modularity but moderate persistence;
- ***Significant***: Stable topological features with moderate modularity; and
- ***Non-significant***: Low modularity and weak persistence.

This dual-framework classification captures both structural cohesion and topological robustness, offering a comprehensive assessment of community importance and influence within the network.

Table 1 Different Email user's communities and their respective member counts

Community Label	Number of Community member		Community Label	Number of Community member		Community Label	Number of Community member
0	35		12	2		24	2
1	3468		13	2		25	2
2	3		14	2		26	3
3	28		`15	2		27	2
4	320		16	2		28	2
5	2		17	3		29	2
6	2		18	3		24	2
7	2		19	58		30	4
08	2		20	5		31	3
09	4		21	3		32	4
10	4		22	2		33	3
11	4		23	5		34	11

4. Results and Discussion

We analyzed a network of 4,001 email users, organizing them into 35 distinct communities using the Label Propagation Algorithm (LPA), following Louvain's modularity-based approach. Traditional community detection methods often identify community structures but fail to highlight influential communities. In contrast, our framework integrates topological and modularity-based analyses to classify communities based on structural stability and influence. The results are presented in the following subsections.

Table 2 Details of the calculated loops of each clusters of the influential and significant cluster group

Community Groups	Community No.	Lifetimes of the significant loops	No. of loops
Influential & Significant (Lifetimes of the significant loops ≥ 0.01)	1	0.02	>122
	4	0.01	57
Significant	0	0.002	5
	3	0.0004	01
	19	0.004	7

4.1. Community Structure

Figures 1 and 2 visualize the overall network and the 35 detected communities. Each community is assigned a distinct color to facilitate visual differentiation and highlight connectivity patterns.

As shown in Table 1, community 1 is the largest, containing 3,468 nodes, while communities 0, 3, 4, and 19 have 35, 28, 320, and 58 nodes respectively. The remaining communities are much smaller, illustrating the network's heterogeneous community size distribution. The community detection process completed in approximately 0.8 seconds, achieving a modularity score of 0.7368, indicating strong intra-community cohesion.

4.2. Identification of Significant Communities

To distinguish significant from non-significant communities, we examined the topological features of each community using persistent homology. Communities with at least one loop or higher-dimensional feature were considered significant, reflecting stronger internal connectivity and structural stability. Conversely, communities without loops were classified as non-significant.

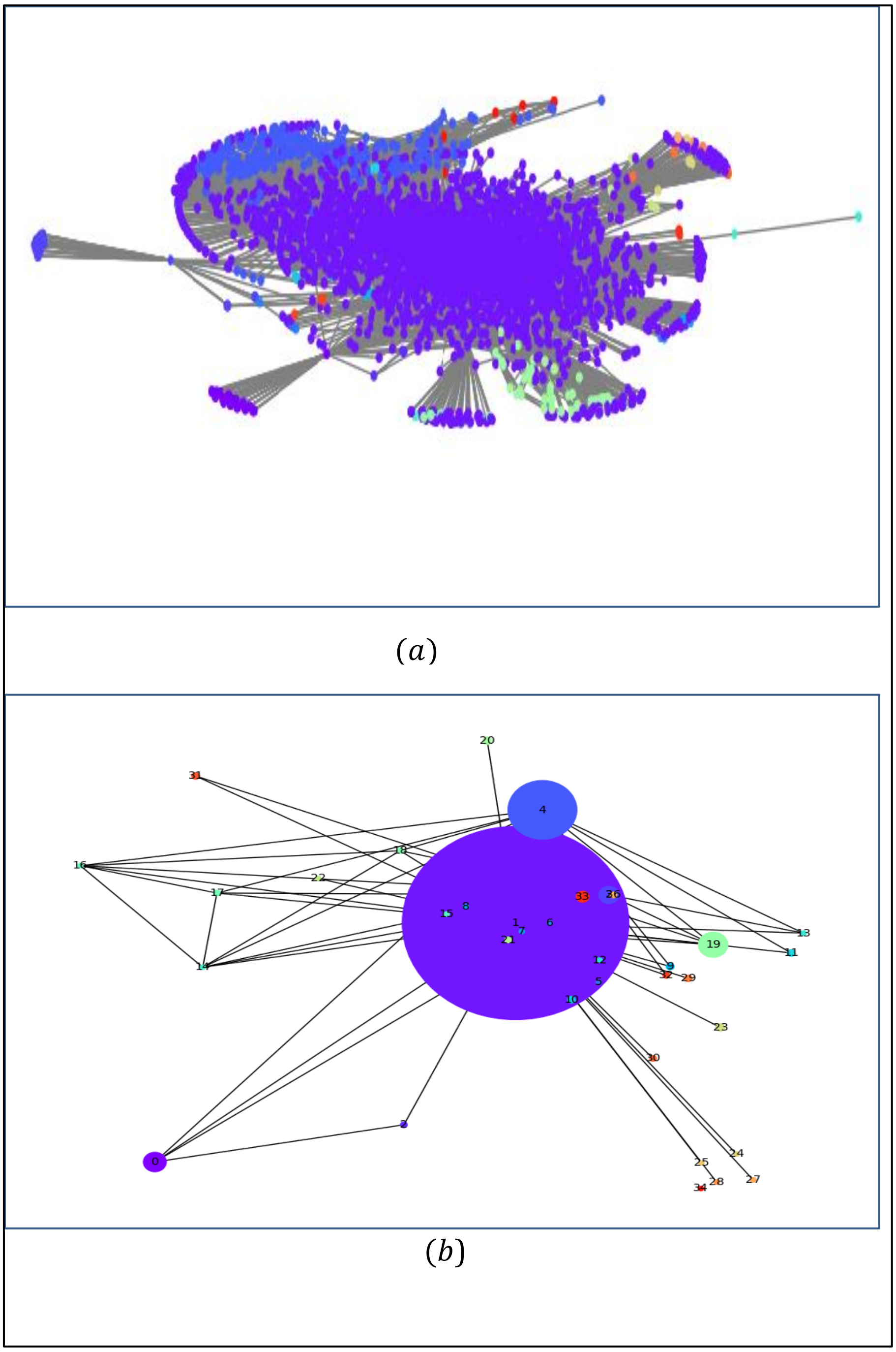

Figure 2 Different Email user's communities with their connectivity

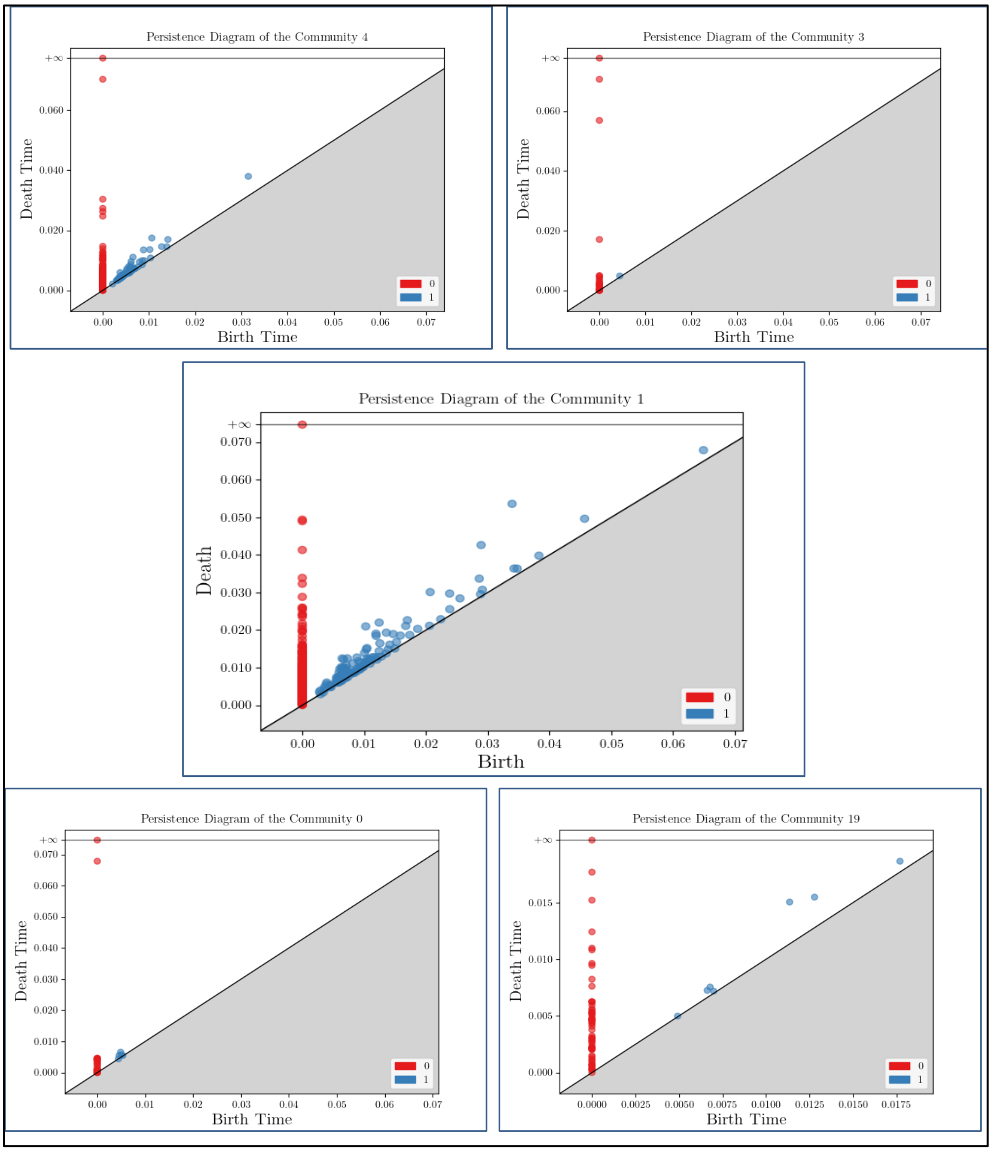

Figure 3 Persistent diagrams of the most influential communities and significant communities

Figure 4 presents persistent diagrams for non-significant communities, including 2, 5, 7, 9–11, 13–18, 20–21, 23, and 33, which lack loops. Based on this analysis, communities 0, 1, 3, 4, and 19 were identified as significant, as illustrated in Figure 3.

4.3. Identification of Influential Communities:

Among significant communities, the lifetime of loops serves as a measure of influence: longer-lived loops indicate that more nodes are involved in stable structures. Table 2 summarizes the loop lifetimes for each significant community:

- **Community 1**: longest loop lifetime of 0.02;
- **Community 4**: loop lifetime of 0.01; and
- **Community 3**: shortest significant loop lifetime of 0.0004.

We classified communities into two groups:

- **Influential Communities**: communities with loop lifetimes > 0.01 (communities 1 and 4)
- **Significant Communities**: remaining communities with loops (0, 3, and 19).

To reduce computational complexity in larger communities, 500 nodes were randomly selected from community 1 for detailed analysis. Figure 3 displays persistence diagrams of the influential community loops, with blue dots representing loops and red dots representing connected components.

4.4. Most Influential Communities:

To determine which among the two identified influential communities holds the highest level of influence, the modularity scores of all 35 detected communities were calculated, as presented in Table 3. Communities with higher modularity values indicate stronger internal cohesion and a greater degree of structural significance within the overall network.

Table 3 Evaluation of each the communities score combining internal edge, external edge, loops lifetime and number of nodes

Community Label	Number of Internal Edges of the Community	Modularity (Q) of the Community	Life Time
0	34	0.000575	0.0017
1	56737	0.024267	0.0196
2	3	0.000051	0.0000
3	31	0.000524	0.0004
4	1163	0.019075	0.0068
5	1	0.000017	0.0000
6	1	0.000017	0.0000
7	1	0.000017	0.0000
8	1	0.000017	0.0000
9	6	0.000102	0.0000
10	6	0.000102	0.0000
11	4	0.000068	0.0000
12	1	0.000017	0.0000
13	1	0.000017	0.0000
14	1	0.000017	0.0000
15	1	0.000017	0.0000
16	1	0.000017	0.0000
17	3	0.000051	0.0000
18	3	0.000051	0.0000
19	133	0.002243	0.0037
20	10	0.000169	0.0000
21	3	0.000051	0.0000
22	1	0.000017	0.0000
23	5	0.000085	0.0000
24	1	0.000017	0.0000
25	1	0.000017	0.0000
26	3	0.000051	0.0000
27	1	0.000017	0.0000
28	1	0.000017	0.0000
29	6	0.000102	0.0000
30	3	0.000051	0.0000

31	6	0.000102	0.0000
32	3	0.000051	0.0000
33	25	0.000423	0.0000
34	1	000017	0.0000
Total	59062	0.0484	

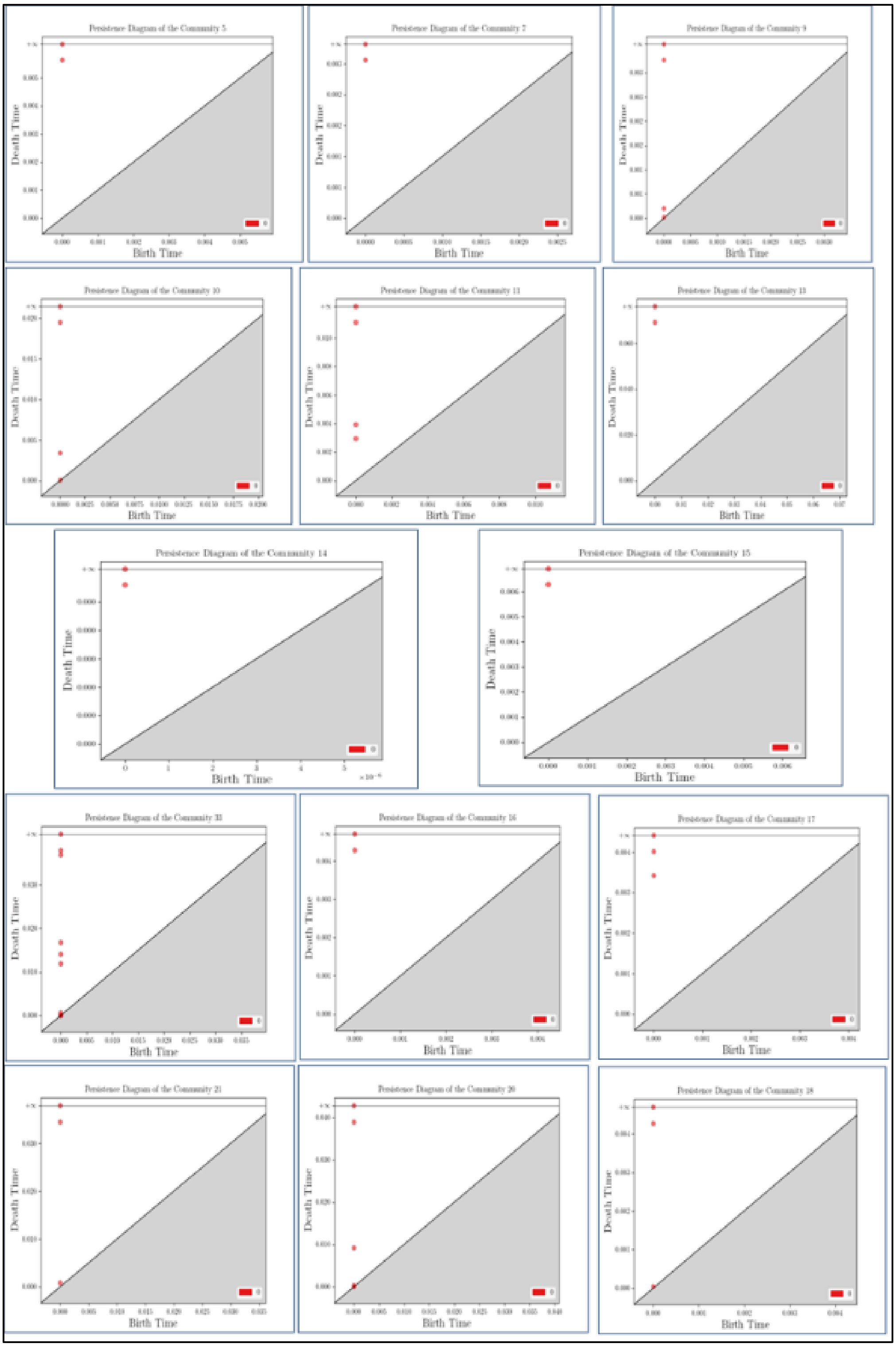

Figure 4 Persistent diagrams of some non-significant communities

Among the two influential communities, Community 1 exhibits the highest modularity score of 0.0243 and a loop lifetime of 0.02, indicating its dominant structural and topological importance in the network. Community 4, with a modularity score of 0.0191 and a loop lifetime of 0.01, ranks as the second most influential community.

This ranking confirms that Community 1 is the most influential within the network, demonstrating both strong internal connectivity and persistent loop structure.

These findings provide valuable insights for practical applications such as targeted marketing, information propagation, or public health awareness campaigns, where identifying and engaging the most influential communities can significantly enhance communication efficiency. The proposed framework thus offers a robust approach for quantifying and ranking influence within complex social networks.

5. Conclusion

This study applied Topological Data Analysis (TDA) and Persistent Homology (PH) to explore the structural organization and connectivity patterns within an email communication network. From the original dataset containing 36,692 users and 183,831 edges, a representative subnetwork of 4,001 nodes was extracted for computational tractability. The Louvain-based community detection process identified 35 distinct communities, forming the foundation for subsequent modularity and topological analyses.

Through the examination of connected components and loop structures, the topological characterization revealed key insights into the organization and resilience of communication communities. While most communities exhibited a single dominant connected component, several contained persistent loops, indicating cyclical information flow and structural robustness—features often overlooked by conventional graph-theoretic approaches.

The network achieved a global modularity score of 0.73684, confirming a strong degree of community cohesion. Communities were further categorized as significant or non-significant based on the persistence of loop structures. Among them, communities 0, 1, 3, 4, and 19 demonstrated significant topological features. The analysis of loop lifetimes revealed that community 1 exhibited the most persistent loop (0.02), followed by community 4 (0.01). When combining topological persistence with modularity metrics, community 1 emerged as the most influential, with a modularity score of 0.0243, while community 4 ranked second (0.0191). This hybrid evaluation framework successfully integrates topological and modular measures to identify influential communities within large-scale communication networks.

Despite these promising results, the study acknowledges computational challenges in scaling persistent homology to larger and more dynamic datasets. Future research should emphasize the development of computationally efficient algorithms, improved filtration optimization, and the extension of this methodology to temporal or evolving networks, enabling the tracking of community formation and transformation over time. Additionally, incorporating machine learning techniques for automated feature extraction and classification may enhance scalability and analytical precision in high-dimensional network analyses.

The proposed framework holds substantial potential across diverse application domains:

- **Social Media Analytics:** Detecting cohesive and influential user clusters to analyze information diffusion dynamics.
- **Targeted Marketing:** Identifying key influencer communities for optimized engagement and campaign strategies.
- **Recommendation Systems:** Improving personalization by leveraging structurally cohesive user subgroups.
- **Network Security:** Locating highly connected or vulnerable communities to mitigate risks related to misinformation or cyber threats.

In summary, this research demonstrates that the integration of persistent homology with modularity optimization provides a robust, multidimensional perspective on community structure, stability, and influence in complex communication systems. The classification of communities into significant, non-significant, influential, and most influential categories introduces a novel interpretative dimension for network analysis. Future investigations will aim to capture the temporal evolution of communities and examine higher-dimensional topological features, further advancing the understanding of the topological backbone of social interactions in large-scale networks.

Compliance with ethical standards

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Disclosure of conflict of interest

The authors declare that there are no known conflicts of interest, financial or otherwise, that could have influenced the outcomes or interpretations presented in this paper.

Statement of ethical approval

This research was conducted in full compliance with established ethical standards.

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