Microscopic Structural Analysis of Complex Networks: An Empirical Study using Motifs

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ABSTRACT Complex Networks can depict a clear image of real-world systems. A real-world scenario can be represented a graph with interconnected layers - called a multi-layer network. Finding motifs can give an idea of the topology of complex systems and helps to understand the dynamics in the graphs. Looking at motifs as atoms of the network is helpful to analyze the relationship between nodes, and between layers. In this work, we suggest a sub-graph enumeration approach to find and count the motifs in multi-layer network. The proposed work has many application in graph mining, particularly to structure and dynamics of complex networks.

INDEX TERMS complex networks , isomorphism , graph enumeration , motifs.

I. INTRODUCTION

Real-world systems, like social or biological and technological systems such as transportation networks, protein networks, citation networks are easier to represent by complex networks. Each of the systems has multiple subsystems. As the data associated with the complex networks evolved to be more heterogeneous and complex, the demand for organizing the complex network into a multilayer network grew [1], [2], [3]. Research in Complex networks has transformed the real-world entities represented from single layer network to multilayer networks by combining the set of nodes exhibiting identical behavior [4].

A multilayer graph consists of a set of nodes, edges, organised in layers. The number of layers and their interpretation differs from graph to graph based on the application scenario. The edges represent the relationships or interactions with nodes in the same or different layers as shown in [1].

The motifs are tiny well-connected substructures that act as the basic building units of every network graph. Milo et al. [5] defines network motifs to be subgraph patterns that occur significantly more often in the network. It corresponds to a randomized version of the network, which reflects specific properties of the network. A graph H is called a subgraph of G whenever V(H) ⊆ V(G). A Network motif are recurrent pattern subgraph. In other words, motifs are subgraphs with triad. Network motifs are studied to understand either individual nodes or the network as a whole. For understanding the network structure or network topology, identification and analysis of motifs and their implications are essential to network science [6]. Identifying a network motif is a computationally hard problem, as it demands matching with all possible subgraph patterns. Research on the detection of motifs on subgraphs is extensively done in [7].

Finding the similarity of structure among graphs is termed graph matching. Detecting a common subgraph is helpful to measure the similarity of two graphs. If a maximum common subgraph of G_A and G_B exists, the more similar the two graphs are. Given two graphs G_A = (V_A, E_A) and G_B = (V_B, E_B), with |V_A| = |V_B|, if a one-to-one mapping f : V_A → V_B such that (u, v) ∈ E_B iff (f(u), f(v)) ∈ E_A exists, we infer an isomorphism, i.e G_D is said to be isomorphic to G_A. This type of problem is said to be exact graph matching.

Graph isomorphism establishes the fact that two graphs are structurally equal disregarding the labels of the original graph. Two multilayer networks are structurally equivalent if
the vertices in one of them can be relabeled so that the first network is bijective to the second one. The structural analysis of a real-world network will be feasible with sub-graph enumeration where we enumerate sub-graph with different size. Graph Isomorphism is used for identifying the motifs. Sub-graph Isomorphism is computationally NP-complete [3]. The problem for computing network motifs using subgraph isomorphism is intractable. Identifying isomorphism for multilayer networks yields establishing relations among various networks represented as layers in a multi-layer network. Motif of any size is broken down into smaller consisting of three nodes. This can be called as the stable size of the motif in the complex networks.

This article proposes a new algorithmic approach for the subgraph enumeration procedure for isomorphism multilayer complex networks. The motif discovery and its analysis have benefited the study of graph isomorphism. The subgraph enumeration methods on a multilayer network are done as motif enumeration using G-Trie (Graph reTRIeval) [10]. A G-Trie is a multiway (m-way) tree capable of storing graphs. The nodes of the m-way hold details like the graph vertex and its corresponding edges to ancestor nodes. A path from the root to any node resembles one single distinct graph. A common subgraph is shared among the descendants of a G-Trie nodes. G-tries are proved to be a feasible and very efficient data structure for network motifs discovery on single layer graph [9]. We are extending the motif discover over the multilayer network using the G-Trie.

The main contributions of this article are:

- We propose the use of the G-Trie data-structure over the multilayer network to perform the subgraph matching and counting the motif.
- We then propose a sub-graph enumeration procedure for identifying isomorphism in multilayer networks.

We mathematically prove that the exact subgraph counting is possible with our proposed solution. Our contributions will help in the discovery of motifs and the popularization of multilayer networks such as Twitter. The paper is organized as follows. Section II illustrates the background studies. The proposed work and its analysis is explained in Section III. The proof of correctness is explained in Section IV. Finally, the article concluded in Section V.

II. BACKGROUND STUDY

A. MULTILAYER NETWORK: DEFINITIONS AND NOTATIONS

We define a multilayer graph $G_M$ as quadruple

$$G_M = (V_M, E_M, V, L)$$

where $V$ is the complete set of vertices, $L$ represents the total number of layers, $V_M$ is the set of vertices in each layer, and $E_M$ is the interconnecting edges. The layer $L = \{L_a\}$ represents a number of layers with $d$ aspects. Integrating all the elementary layers $L_1 \times \ldots \times L_d$ results in a multilayer network. The vertices in a layer $\alpha$ is represented as $V_\alpha = \{v_1^\alpha, v_2^\alpha, \ldots, v_n^\alpha\}$ and the edges interconnecting the layer $\alpha$ and $\beta$ can be represented as $E_M = \{E_{\alpha \beta} \subseteq V_\alpha \times V_\beta; \alpha, \beta = \{1, 2, \ldots, m\}, \alpha \neq \beta\}$. 

![Figure 1: Spectral diagram of a graph: multilayer network.](image-url)
The group of vectors are collectively organized by a summation up of the scalar multiplication of corresponding vectors. It is a linear combination of span of each vector in the set \([12], [13]\):

\[
\text{span}\{v_1, \ldots, v_m\} = \langle \{v_1, \ldots, v_m\}\rangle
\]

Given the set \(\{v_1, v_2, \ldots, v_N\}\) and \(\{l_1, \ldots, l_m\}\) are basis of \(V\) and \(L\) respectively. There for

\[
\{v_i \otimes l_j; 1 \leq i \leq N, 1 \leq j \leq m\}
\]

\[
M_A = \begin{pmatrix}
A_{L1} & I_1 \\
I_2 & A_{L2}
\end{pmatrix}
\]

\[
\begin{array}{cccccc}
x \otimes l_1 & y \otimes l_1 & z \otimes l_1 & x \otimes l_2 & y \otimes l_2 & z \otimes l_2 \\
0 & 0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 \\
0 & 0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 0
\end{array}
\]

**TABLE 1**: Supra-adjacency matrix for the multiplex network shown in Fig. 2.

### C. MOTIF

The motifs are tiny connected substructures that act as the basic building units of every network graph [5]. It appears in an undoubtedly much larger number of occurrences in the network. It has given much importance to the structural analysis of complex networks. The motif discovery and analysis benefit the study of graph isomorphism, in which the enumerated subgraphs are brought together into isomorphism classes and reviewed [14], [15], [16]. The small isomorphism classes help to manage computation and clarify the result of such computation. We realize the advantage of limiting the size of a subgraph, the number of vertices, and the number of layers.

The multilayer isomorphism classes increase as the function of the number of vertices and number of layers. The elementary component of a network is an edge: either a directed or undirected connection between pair of nodes. Nodes reside either in the same layer or between layers. It is described as a tuple \((v_i^\alpha, v_j^\beta)\) is described in the set \(E\), where \(i = 1, 2, \ldots, n; \alpha = 1, 2, m; \beta = 1, 2, \ldots, m\).

In [21], the authors present an algorithm for estimating the frequency of subgraphs in random networks that enumerates all size \(k\) subgraphs. The algorithm starts with a vertex \(v\) from the input graph and adds only those vertices to the considered set \(V_{\text{extension}}\) that satisfies two properties. Firstly labels must be larger than that of \(v\), and secondly they may only be neighbor to the newly added vertex \(w\) but not to a vertex already in \(V_{\text{subgraph}}\).

In [13], the authors developed a statistical theory for estimating motif counts from a bigger graph. The authors focused on only a fraction of vertices for sampling. The authors have used Horvitz-Thompson type estimation approach.
and Neighborhood sampling approach. For the subgraph sampling, the sampling ratio \( p \) is \( \theta_k \left( \max \left( \left( s e \right)^2 - \frac{1}{\epsilon}, \frac{2}{\epsilon s e} \right) \right) \), where \( d \) is the maximal degree of parent graph for any connected motif \( h \) on \( k \) vertices and \( s(g, G) \) denote the number of induced subgraph of \( G \) with \( \epsilon \) as the multiplicative error. In the neighborhood sampling method, authors labeled neighbors of all vertices in \( S \), denoted by \( G \). In this approach, the sample of rows of the adjacency matrix of \( G \) independently with probability \( p \) and then observe the rows together with the row indices and the neighborhood information is acquired for each sampled vertex. Since this method consider only a fraction of vertices, there is a chance that the triad structures are unidentified. This disadvantage is overcome in the proposed algorithm.

Graph matching and motif analysis are key research activities in complex network analysis. The inherent properties are discovered through motif analysis. The subgraph matching based on the structural parameter such as adjacency matrix is a feasible technique. Parallel algorithms have been designed on layered graphs that address computationally challenging problems like Minimum vertex cover, Maximum Independent Set, etc. These problems pave the way to solve many social network problems [19, 20]. The nearest neighborhood trust properties and second hop-neighborhood are discovered through its supra-adjacency matrix or tensor algebra. Since our graph matching algorithm entirely relies upon algebraic connections, the proposed work leaves a great outlook in complex network research, particularly structural analysis.

**D. GRAPH MATCHING ALGORITHMS**

The graph matching process compares two graphs or subgraphs for any similarity or duplicates. There are two types of matching process, namely exact matching and inexact matching algorithms. The authors in [17] suggests two approaches that are able to generate candidate structures without redundant structures from a complex graph

Ullmann’s Algorithm

It is an exact matching algorithm for graph isomorphism and subgraph isomorphism. DFS strategy is applied to deploy the algorithm. Let us consider two graphs, \( G_A(V_A, E_A) \) and \( G_B(V_B, E_B) \), \( |V_A| = n \) and \( |V_B| = m \). An \( n \times m \) permutation matrix, \( M \), is to be constructed. It contains only 0 or 1, exact 1 in each row and not more than 1 in each column. A permutation matrix is to be generated by repeatedly changing the row and column of an identity matrix. \( M \times B : \) move row \( j \) changes to row \( i \). \( (MB)^T : \) move column \( j \) to column \( i \). \( M(MB)^T : \) move column \( j \) to column \( i \) and row \( j \) to row \( i \). It is a popular graph isomorphism and subgraph isomorphism. An isomorphic subgraph can be enumerated from graph B by relabels the nodes [18].

VF2 Algorithm

The VF2 algorithm is considers under the category of inexact algorithm in which adds a pair of nodes to each stage and compare the threshold [22].

The process of finding similarity among two graphs \( G_i \) and \( G_j \) are done by a function, \( M_{iso} \) which budding of nodes of \( G_i \) and \( G_j \). There are many graph similarity checking procedures available and all are of complex in terms of execution time. The one which is used for sub graph isomorphism is in NP-complete in nature. A most feasible and preferably an linear time algorithms has some bottleneck for performance while considering graph with large nodes and high average degree. The function for comparison, mapping function \( M_{iso} \) is performed as a set of pairs \((v_i, v_j)\) explicit. where \( v_i \in G_i \) and \( v_j \in G_j \); measuring the similarity of nodes in the spectrum. \( v_i \) of \( G_i \) with \( v_j \) of \( G_j \).

A mapping \( M_{iso} \subset N_i \times N_j \) is said to be an isomorphic only when the mapping function \( M_{iso} \) shows the bijective character which uphold the spectral properties of the two graphs under consideration. A mapping \( M_{iso} \subset N_i \times N_j \) is said to be a graph-subgraph isomorphic only when the mapping function \( M_{iso} \) shows the bijective character which uphold the spectral properties of the two sub graphs, \( G_i \) and \( G_j \), under consideration.

Each state \( s \) of the similarity checking process is describe by the help of State Space Representation(SSR). The similarity function associated a partial solution for mapping between samples, which is a function of \( s \) of SSR. The solution \( M_{iso}(s) \) is subset of \( M_{iso} \) and label the samples, as subgraph of \( G_i \) and \( G_j \).

The transition from usual state \( s \) to \( s' \) is addition of pair \((v_i, v_j)\) of matched nodes to generic \( s \) of SSR. A few subset of the SSR require only the similarity of isomorphism that there are limited environment for attaining solutions. It is to be proven that the consistency conditions, isomorphism or subgraphs isomorphism, the mapping is based on consistency conditions. So that specifically define that the partial graphs \( G_i(s) \) and \( G_j(s) \) correlated to \( M_{iso}(s) \) are isomorphic. All the consistency properties are maintained by subgraph isomorphism and state which is generated in SSR is a consistent state and has no consistent successors.

The function \( F(s, v_i, v_j) \) check the feasibility such that whether it is true or not. The state \( s \) with pair of nodes is accepting the feasibility rules and it depends only on the spectrum of the graph as sample. The feasibility function is depicted as :

\[
F(s, v_i, v_j) = F_{syn}(s, v_i, v_j) \land F_{sem}(s, v_i, v_j)
\]

where Syntactic feasibility, \( F_{syn}() \) depends structure of the graph given only, and semantic feasibility,\( F_{sem}() \) rely upon the attributes.

VF3 algorithm

VF3 uses tree search method for generating subgraph isomorphism. VF3 employs depth first strategy to reach the goal. VF3 also employs SSR (State Space Representation) in which each state \( s \) of the SSR represents a partial mapping with the matching constraints; and a goal state is a state whose mapping is complete, when covers all the nodes in graph [23].
In the proposed method, we introduce an m-way tree to hold all the subgraph nodes that are being considered. The subgraph enumeration methods on a multilayer network are done as motif enumeration using G-Trie. This approach overcomes the additional task of relabeling when a match pattern is found. The proposed algorithm generates a match in the motif pattern considering an intra-link or interlink among the layer in the multilayer network.

### III. PROPOSED WORK

Isomorphic properties of a graph formulate the concept that two graphs have equivalent structures [24][25]. Two graphs are isomorphic if the first graph can be transformed into another by renaming the vertices [26]. There is no labeling on the edges. Vertex labels at the two endpoints identify the edges. The transformation updates the labels as well. Two multilayer graphs $M_1$ and $M_2$, are isomorphic such that we introduce a bijective function $\psi : V_1 \rightarrow V_2$ that maps $M_1^\psi = M_2$. We can define isomorphism in multilayer networks in the same way as of plain graph. If two multilayer graphs are isomorphic, one can be transformed into another by renaming the vertices [26]. There is no labeling among the layer in the multilayer network.

The subgraph enumeration methods on a multilayer network hold all the subgraph nodes that are being considered. Each element of all groups is to be verified.

**MULTIPLEX NETWORKS**

We use computational methods to analyze the isomorphism in multi-layer networks. The leading and most common type of multi-layer network is multiplex networks, most suitable for dealing with empirical data. [27][28][29][30]. Multiplex Networks illustrate the advantages of isomorphism. There are multiple types of interactions between vertices, either within a layer or between layers. Multiplex networks are represented using an array of graphs.

$$\{M_x\}_m = \{V_x, E_x\}_m$$ (11)

The main feature of a multiplex network is that each layer has the same cardinality of vertices, $V_\alpha = V_\beta$ for all layers $\alpha, \beta$. The characteristic behavior of the multiplex network is called *vertex-aligned*. In order to bridge the conceptual rifting, a multiplex network describes by choosing a single aspect, $M_\alpha$, considered as linking each vertex to its corresponding replica in neighboring layers. The method by which each vertex establishes a connection with its counterparts in another layer is known as coupling. The isomorphism is facilitated by establishing either categorical coupling or by the inter-layer connections established. The isomorphism classes are well defined in multiplex networks. The relabelling of the vertex is permuted in vertex-isomorphism by preserving the types of edges, and the layer isomorphism is also preserving relabelling of layers to monotonic nature. The matching process performs graph isomorphism, which works best in computational complexities when the number of subgraphs to be compared is relatively tiny. The motif analysis is the best example. The subgraphs enumeration problem is matching and counting non-isomorphic subgraphs [31].

While extending the same to multiplex networks, counting the subgraphs are tabulated with $n$ vertices and aspect $b$ is $2^{\binom{n}{b}}$.

**Definition 1:** Two multilayer networks $M_1$ and $M_2$ are:

1. isomorphic with respect to vertex if there is a mapping function, $\psi$, which maps vertex such that $M_1^\psi = M_2$;
2. isomorphic with respect to layers if there is a mapping function, $\tau$ such that $M_1^\tau = M_2$;
3. isomorphic with respect to both vertex and layer if a mapping function $\delta = (\psi, \tau)$ such that $(M_1^\psi)^\tau = (M_2^\tau)^\psi$.

The complete picturization of isomorphism concerning vertex, layer, and both is shown in Fig[5] The actual practice, computation of various types of isomorphism is executed simply with minimum computational complexity. The induced graph enumeration process is complicated while we move on to multiple layers, called *aspects*, denoted as $d$. Complexity increases with the number of aspects increases. The auxiliary graph construction is defined as $2^d$ types of isomorphism. The small subgraph, which is the basic building blocks, are called *motifs*. All sub-graphs of a given graph need to be verified and classified into different graph classes for motif analysis. Each element of all groups is to be verified.
A. CANDIDATE PAIR

The pair of node which is to be considered for adding with the existing mapping function $m_{map}$ in the given state is $P_{map}$. Let us consider $T_{(a)}^{1} = \{v_1 \in V_{1}^{l_1} \setminus D(m_{map}) : \exists \tau_1 \in D(m_{map}) : (v_1, \tau_1) \in E_{1}^{l_1}\}$, and $T_{(b)}^{2} = \{v_1 \in V_{2}^{l_2} \setminus R(m_{map}) : \exists \tau_2 \in R(m_{map}) : (v_2, \tau_2) \in E_{2}\}$.

The set candidate pair $P_{(map)}$ includes the pair of open neighbours of closed branch nodes, and if there is no such combination of nodes, all the mapped combinations of nodes supplements with two un-mapped nodes.

$$
P_{(map)} = \begin{cases} T_{(a)}^{1} \times T_{(b)}^{2} & \text{if } T_{(a)}^{1} \neq \emptyset \text{ and } T_{(b)}^{2} \neq \emptyset, \\ V_{1}^{l_1} \setminus D(m_{map}) \times V_{2}^{l_2} \setminus R(m_{map}), & \text{otherwise} \end{cases}
$$

B. CHECK CONSISTENCY

While adding a candidate pair $P_{(map)}$ to an existing mapping function for node labelling by the given problem of subgraph isomorphism. A function $\text{ConS}(P_{(map)}, m)$ check whether adding candidate pair $P_{(map)}$ into $m$ leads to consistent mapping by the given problem.

Proof 1: $\text{ConS}(P_{(map)}, m) := \text{ConS}((v_1, v_2) \setminus m)$ where $\text{ConS}((v_1, v_2) \setminus m) := \text{ConS}(m) \land \psi(v_1) = \psi(v_2) \land (v_1, v_2) \in E_{1} \cap R(m_{map}) : (v_1, m_{map}(v_2)) \in E_{1} \land (v_2) \in \Gamma(v_1) \cap D(m) : (v_1, m_{map}) \in E_{2}$

Definition 6: Let $\text{argmax}_f(s') := \{v_1 \in S : f(v_1) = \max_{v_2 \in S} \{f(v_2)\} \}$ $\text{argmin}_f(s') := \text{argmax}_{-f}(S)$, where $S$ is a finite set, $f : S \rightarrow R$, $F_{match}(\varphi) := |\{v_2 \in V_2 \} - |\{v_1 \in M : \varphi(\psi(v_1))\}|$ and $\varphi$ is a node label and arbitrary elements of Matching function and $M \subseteq V_1^l$.

C. SUB GRAPH ENUMERATION

Definition 7: The subgraph, $M_k$ is derived from a multilayer graph $M$ if and only if $M_k$ is a subgraph of size $k$ from a graph $M$. $V(M_k) \subseteq V(M)$ and $E(M_k) \subseteq E(M)$. For any pair of vertices $(u_\alpha, v_\alpha) \in E(M_k)$ and $(u_\alpha, v_\alpha) \in E(M)$.

The procedure for analyzing and counting motifs from a multilayer graphs is different from frequent subgraphs. The procedure for subgraph enumeration shown in Algorithm [1] This is different from frequent subgraphs. The steps for counting a subgraph progresses in two different approaches, measuring the size and performing isomorphism. We cannot give up any part of the main graphs for subgraph matching. So we are wasting time by searching all portions of the tree and allowing us to drain a lot of time while considering subgraphs one by one.
Algorithm 1 Matching of subgraph and counting

Input: \( G = (V_M, E_M, V, L) \); \( T = \emptyset \); A sub graph, \( G_i \);
Output: Check \( T \equiv \text{Trie} \) & motif count, \( c \);

procedure MATCH(G, g_k)
  for all subgraph \( c \) of \( T \).root do
    match(\( g_k, G, k, V_m \))
  end for

procedure match(g_k, G, k, V_m)
  if \( V_m = \emptyset \) then
    \( G_{\text{sub}} := V(G) \)
    \( G_{\text{sub}} = \{ V_m[a] : T.data[a] = 1 \} \)
  else
    \( n := n \in G_{\text{sub}} : |N(n)| \leq |N(m)| \)
    \( G_{\text{sub}} := \{ n \in N(m) : m \notin G_{\text{sub}} \} \)
  end if
  for all \( m \in G_{\text{sub}} \) do
    Add \( v \) to end of \( G_{\text{part}} \)
  end for
  if \( T.isLeaf() \) then
    ReportGraph()
    for all children \( c \) of \( T \) do
      match(\( c, G, k + 1, G_{\text{sub}} \))
    end for
  end if
end procedure

Remove \( m \) from \( G_{\text{sub}} \)

D. G-TRIES

We are making use of the advantages of tree data structure in the process of the mining-induced subgraph. All the subgraphs are loaded in the tree and follow the common topology. We recognize and label the importance of predecessors in the family of tree nodes to present the typical arrangement and pattern image. We utilize the advantages of the topology of the data structure G-Tries[Graph reTRIEval].

The G-Trie is the form of a multiway tree that can make used to store a collection of graphs, it is shown in Fig. 5. Each tree node accommodates information of a single graph vertex and traverses through predecessors. Traversal from root to leaf represents a single graph. Nodes in the path of the ancestry of a G-Trie contribute a common subgraph.

1) G-Trie construction

Every node in a G-Trie can store information for a newly created vertex connected to the ancestry path. The most common graph representation is the adjacency matrix because of the simplicity of representation. For the representation, 1 is for connection between two vertices and 0 for its non-occupancy.

The rows of a matrix represent the vertices and their connections. Each tree node represents a new vertex, where
we can store in it the equivalent row. When we increment the total number of predecessor structures, the size of the tree becomes decreases. The compression rate depends on the number of nodes and vertices in the G-Trie. The G-Trie compression ratio is termed as \( G - \text{Trie}_{cr} \)

\[
G - \text{Trie}_{cr} = 1 - \frac{\# \text{nodes in the tree}}{\# \text{nodes of stored graph}}
\] (13)

The objective of first subtask is to enumerate all subgraphs for the given size \( k \). It seems to be computationally higher in magnitude due to subgraphs ranging from small to largest. The second subtask is induced subgraph enumeration technique which is explained in the section. As we move on to the last part, we are explicitly identifying size of each subgraph classes for a given \( k \) and given degree.

All-natural, biological and engineered systems have interconnected subsystems. A multilayer graph represents such complex networks. Nodes reside at each layer. Such multilayer models are called multiplex graphs. But all nodes may not be available at all layers in almost all complex systems. Such graph representation is called a multilayer graph in general. Nodes interconnect with each other in the layer and between layers. Such graphs have complex topology and structural properties. The microscopic structure repeats in the systems help to study the structural and dynamical behavior of the systems. The self-repeating structure of the systems is called a motif. The study of motif helps to discover complex networks.

The most stable structure is the trie - the relation between three nodes. The isomorphic structure of the trie is depicted in Fig.8. When we consider layered structure, there are two possibilities for the layout. The first case is that all three modes are in the same layer. The properties of a simple graph are helpful for the study. But the latter one is, any one of the nodes resides in one layer, and the other two reside in another layer. The connection or relationship established between layers is as shown in Fig.9.

The isomorphic view of the motif in multilayer networks are shown in the Fig.9. The Layer 1 have three nodes, \( V_1 = A, B, C \) and Layer 2 has three nodes namely, \( V_2 = D, E, F \). Different motif can be formed between layer1 and layer2 and some of them are < A, D, E > , < A, D, F > , < A, E, F > , < A, B, D > < A, B, E > , < A, B, F > , < A, C, D > , < A, C, E > and < A, C, F > . The motif has three nodes where the other two nodes are in layer two, and the third node in layer one or the first nodes in layer two, and the other two in layer 1. The motif with tree nodes repeats throughout the entire structure. The structural analysis of the complex networks and dynamics can be easily studied through motif analysis, especially with the help of Trie.

The detailed study of motifs occurrence and its frequencies is the direct application of isomorphism that also addressed. More extensive networks and more complex motifs are possible to analyze; G-tries reduce computational and space complexity. Studying the microscopic structure of the complex network helps to model applications across domains like brain network, DNA network, food web, transportation network. Exploration of the structure of networks helps in discovering the dynamic nature of the real-world network. The microscopic structures help in discovering properties like symmetry, transitivity or clustering, reciprocity among the nodes. This study will further help in the spatial perception of real-world networks.

For a multi layer graph \( G_M \), the Algorithm 2 finds a
Algorithm 2 \( M_x \text{Graph}: \text{Multilayer Graph Enumeration Algorithm} \)

**Input:** \( M = ((V, E), E_{a,b}) \): A social graph; \( M_{map}(s_0) = \emptyset \); An Intermediate state, \( s' \)

**Output:** Result of the Similarity Check: between two graph, \( M_1 \) and \( M_2 \)

**procedure** \( M_x \text{Graph}(m_{map}, P_{map}) \)

\[
M_{map}(s_0) = \emptyset, \quad V_{M_x} = \emptyset
\]

while \( V_1 \setminus M_{map} \neq \emptyset \)

\[
v_r \in \arg\max_{x} (V_1 \setminus M_{map})
\]

Compute \( T_1^a \times T_2^a \); \( G \)-Tries PR QuadTree

Follows a BFS Tree Traversal

end while

for Each \( p \) in \( P(s) \) do

for \( x = 0, 1, \ldots \); BFS depth \( (T_1^a \times T_2^a) \) do

\[
V_{M_x} := \text{is the node at each depth}
\]

end for

\[
m \in \arg\min_{F_{M_x}} (\arg\max_{d} (\arg\max)_{x} (V_{M_x}))
\]

\[
V_{M_x} := V_{M_x} \setminus M_{map}
\]

end for

Refresh \( F_{M_x} \) and Restore

end procedure

matching and counts the number of motifs in the sub graph using a G-Trie.

**IV. PROOF OF CORRECTNESS**

**Theorem 4.1:** Consider a multilayer network defined as a quadruple \( G_M = (V_M, E_M, V, L) \) where \( V \) is the complete set of vertices, \( L \) represents the total number of layers, \( V_M \) is the set of vertices in each layer, and \( E_M \) is the interconnecting edges and \( G_{sub} \) denotes a subgraph.

Let \( T \) be the triad such that \( T \in G_{sub} \) with \( T = \sum^n_i T_i \) exists for \( i = 1, 2, 3 \ldots n \).

Let \( G_{part} \) denotes the set all the identified triads as follows.

\[
T_j \notin V_m \text{ for } i \neq j \Rightarrow \text{mismatch and } T_i \notin G_{part} \text{.}
\]

Hence \( G_{sub} = G_{part} \cup G_{part}^c \)

**Proof 2:** The above theorem is proved by induction.

Consider the minimum \( |G_{sub}| = 2 \Rightarrow \) no triad and \( T \in G_{sub} \).

Hence \( G_{part} = \emptyset \).

Let \( |G_{sub}| = 3 \).

For \( i \neq j, T_i \neq T_j \Rightarrow T_i \in G_{part} \) and \( \notin G_{part}^c \).

Now lets assume \( |G_{sub}| = k, k > 3 \), then there exists at least one triad \( T_i \in G_{part}^c \).

The procedure \textit{match} considers a subgraph as input and looks for the triad structure. It picks a matching structure and is marked into the set \( G_{part} \) in Algorithm 1. The algorithm guarantees to find a triad if there exists. A trie structure is repeatedly constructed among the adjacent pair of vertices within and across the layers. Algorithm 1 also ensures that no duplicate triad is considered. As the subgraph \( G_{sub} \) size increases, the complexity increases in exponential time. The Algorithm 2 gets all the matching subgraphs from \( G_{part} \), and enumerates the matching motifs.

**V. CONCLUSION**

The research work on isomorphisms makes an excellent foundation for many analyses in the fields of multilayer networks. An exceptional application of isomorphism in multilayer networks is the analysis of the structural portrayal of defining the equivalency between multilayer networks. In this article, we look into the analysis and counting motifs detection in multilayer networks. We have performed the induced subgraph enumeration method efficiently to show an outstanding result in the multilayer network explicitly. We defined motifs and accounted for them concerning the isomorphism classes—structure for enumerating subgraph and counting. Experiments on complex real-world networks show that our methodology performed much more efficiently in magnitude than others. By concentrating on the algorithmic view of motif detection, our proposed work concentrates not on simply enumerating and counting but on analyzing large and multilayer complex networks. The matching algorithm and counting network motif is NP-hard in nature. The pattern to be compared performs a match with all induced subgraphs which are enumerated. The complexity of the motif analysis grows as exponentially as the number of nodes in increases.

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