Epsilon Equitable Partitions based Approach for Role & Positional Analysis of Social Networks

A THESIS

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THESIS CERTIFICATE

This is to certify that the thesis entitled **Epsilon Equitable Partitions based Approach for Role & Positional Analysis of Social Networks**, submitted by **Pratik Vinay Gupte**, to the Indian Institute of Technology, Madras, for the award of the degree of **Master of Science (by Research)**, is a bona fide record of the research work carried out by him under my supervision. The contents of this thesis, in full or in parts, have not been submitted to any other Institute or University for the award of any degree or diploma.

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To my teachers

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ABSTRACT

In social network analysis, the fundamental idea behind the notion of *position* is to discover actors who have similar structural signatures. Positional analysis of social networks involves partitioning the actors into disjoint sets using a notion of equivalence which captures the structure of relationships among actors. Classical approaches to Positional Analysis, such as Regular equivalence and Equitable Partitions, are too strict in grouping actors and often lead to trivial partitioning of actors in real world networks. An ϵ-Equitable Partition (ϵEP) of a graph is a useful relaxation to the notion of structural equivalence which results in meaningful partitioning of actors. All these methods assume a single role per actor, actors in real world tend to perform multiple roles. For example, a Professor can possibly be in a role of "Advisor" to his PhD students, but in a role of "Colleague" to other Professors in his department. In this thesis we propose ϵ-equitable partitions based approaches to perform scalable positional analysis and to discover positions performing multiple roles. First, we propose and implement a *new scalable distributed* algorithm based on MapReduce methodology to find ϵEP of a graph. Empirical studies on random power-law graphs show that our algorithm is highly scalable for sparse graphs, thereby giving us the ability to study positional analysis on very large scale networks. Second, we propose a new notion of equivalence for performing positional analysis of networks using *multiple* ϵ-equitable partitions. These multiple partitions give us a better bound on identifying equivalent actor "positions" performing multiple "roles". Evaluation of our methods on multi-role ground-truth networks and time evolving snapshots of real world social graphs show the importance of *epsilon equitable partitions* for discovering positions performing multiple roles and in studying the evolution of actors and their ties.

KEYWORDS: Equitable Partition, Positional Analysis, Multiple Role Analysis, Structural Equivalence, Distributed Graph Partitioning

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LIST OF SYMBOLS

$\triangle$	The symmetric set difference operator
$\cap$	The set intersection operator
$\cup$	The set union operator
ϵ	The value of relaxation allowed
$\equiv$	The equivalence relation
γ	The power-law exponent
$\mu(\pi)$	The mean-of-mean cell distance of partition π
$\overrightarrow{deg}(v)$	The degree vector of vertex v
π	The partition of vertex set
π_{init}	The ordered equitable partition with *initial* cell ordering
π_{pert}	The ordered equitable partition with *permuted* cell ordering
$\preccurlyeq$	The *finer* than relation
$\vec{r_v}$	The role label vector of vertex v
a_t	The property value of vertex a at time t
$a_{t+\delta t}$	The property value of vertex a at time $t + \delta t$

c_a	The current active cell
c_i	The i^{th} cell/block of a partition
$cooc(a, b)$	The co-occurrence value of nodes a and b
$deg(v_i, c_j)$	The degree of vertex v_i to cell c_j
$dist(a, b)$	The distance between nodes a and b
E	The edge set of a graph
G	The graph
G_t	The graph at time t
$G_{t+\delta t}$	The graph at time $t + \delta t$
$sim(\pi_1, \pi_2)$	The similarity score between partitions π_1 and π_2
$sim(a, b)$	The similarity between nodes a and b
V	The vertex set of a graph
Z	The hierarchical clustering linkage data structure

ABBREVIATIONS

EP	Equitable Partition
ϵEP/EEP	ϵ-Equitable Partition
MϵEPs/MEEPs	Multiple ϵ-Equitable Partitions
SNA	Social Network Analysis
PA	Positional Analysis
SE	Structural Equivalence
RE	Regular Equivalence
DV	Degree Vector
DP	Degree Partition
SBM	Stochastic Blockmodel
MR	MapReduce
HC	Hierarchical Clustering
HAC	Hierarchical Agglomerative Clustering
CL	Complete-link
SL	Single-link
IMDb	Internet Movie Database
WϵEP	Weighted ϵ-Equitable Partition

CHAPTER 1

Introduction

In social network analysis, the notions of social **position** and social **role** have been fundamental to the structural analysis of networks. These dual notions discover actors who have similar structural signatures. This involves identifying social position as collection of actors who are similar in their ties with others and modelling social roles as system of ties between actors or between positions. As an example, head coaches in different football teams occupy the **position** *manager* by the virtue of the similar kind of relationship with players, assistant coaches, medical staff and the team management. It might happen that an individual coach at the position *manager* may or may not have interaction with other coaches at the same position. Further, the actors at the position *manager* can be a **role** of "Coach" to actors at the position *player* or a "Colleague" to the actors at the position *assistant coach*. Similarly, the actors at position *medical staff* can be in a role of "Physiotherapist" or a "Doctor" to actors at the position *player*. Positional Analysis (PA) of social networks involves partitioning the actors into disjoint sets using a notion of equivalence which captures the structure of relationships among actors. While PA is a very intuitive way of understanding interactions in networks, this hasn't been widely studied to model *multiple roles* performed by actors, neither has it been studied for large networks due to the difficulty in developing tractable algorithms. In this thesis, we propose *ϵ-equitable partition* (ϵEP) based positional analysis approaches for the two problems as follows:

- **Scalable Positional Analysis:** We propose a new algorithm with better heuristics to find the ϵ-equitable partition of a graph and focus on scaling this algorithm. We present the results of our algorithm on time evolving snapshots of the `facebook` and `flickr` social graphs. Results show the importance of positional analysis on large dynamic networks.

- **Discovering Positions Performing Multiple Roles:** We propose a new notion of equivalence for performing PA of social networks. Given a network, we find its Multiple ϵ-Equitable Partitions (MϵEPs) to analyze *multiple* roles. These multiple partitions give us a better bound on identifying equivalent actor "positions" performing multiple "roles". Evaluation of our method on *multi-role ground-truth* networks and time evolving snapshots of real world social graphs show the importance of multiple epsilon equitable partitions for discovering positions performing multiple roles and also in studying the evolution of actors and their ties.

1.1 Motivation

The key element in finding positions, which aid in the meaningful interpretation of the data is the notion of *equivalence* used to partition the network. Classical methods of finding equivalence like structural equivalence [2], regular equivalence [3], automorphisms [4] and equitable partition [5, 6] often lead to trivial partitioning of the actors in the network. This trivial partitioning of actors is primarily attributed due to either their strictness in the case of structural, automorphisms and equitable equivalence, which results in largely singleton position; or their leniency in the number of connections the actors at each position can possibly have with the actors at another position, as in the case of regular equivalence, which results in a giant equivalence class. An ϵ-equitable partition (ϵEP) [7] is a notion of equivalence, which has many advantages over the classical methods. ϵEP allows a leeway of ϵ in the number of connections the actors at a same position can have with the actors at another position. In the Indian movies dataset from IMDb, authors in [7] have shown that actors who fall in the same block of the partition, tend to have acted in similar kinds of movies. Further, the authors also show that people who belong to a same position of an ϵEP tend to evolve similarly. In social networks, tagging people who belong to the same position has potentially many advantages, both from business and individual perspective, such as, position based targeted promotions, ability to find anomalies, user churn prediction and personalised recommendations.

Though efficient graph partition refinement techniques and their application in finding the regular equivalence of a graph are well studied in the graph theoretic literature [8, 9], the application of these techniques for doing positional analysis of very large social graphs and networks is so far unknown. In this thesis, we propose a new algorithm to find the ϵ-equitable partition of a graph and focus on scaling this algorithm.

Further, an observation we made from ϵ-equitable partitioning method was that the ϵEP of a graph is not unique and many such partitions exist. In this thesis, we exploit these multiple ϵ-equitable partitions to analyze *multiple* roles and positions. We define a new notion of equivalence based on these multiple ϵEPs to perform PA of social networks.

1.2 Organization of the thesis

- Chapter 2 covers detailed background work on Role and Positional Analysis in Social Network Analysis (SNA) literature.
- Chapter 3 presents our contribution of a *new, scalabale and distributed* algorithm for finding ϵ-equitable partition of a graph. We discuss about the algorithm complexity, implementation, evaluation methodology and our contribution on *parallelizing* the algorithm using MapReduce paradigm.
- In Chapter 4 we discuss about the non-uniqueness of ϵEP of a graph and subsequently propose the notion of Multiple ϵ- Equitable Partitions (MϵEPs) and an algorithm to find MϵEPs for a graph. We present the notion of Positional Equivalence in MϵEPs along with the algorithm, its implementation, ground-truth network evaluation methodology, dataset details and results on real world networks.
- Chapter 5 concludes the thesis. A summary of the work and future directions are provided here. We also present preliminary results on the notion of structural equivalence for weighted graphs.

1.3 Major contributions of the thesis

The major contributions of the thesis are as follows:

- We propose a new algorithm with better heuristics to find the ϵ-equitable partition of a graph and implement its *scalable distributed algorithm* based on MapReduce methodology [10]. This allows us to study the Positional Analysis on large dynamic social networks. We have successfully validated our algorithm with detailed studies on *facebook* social graph, highlighting the advantages of doing positional analysis on time evolving social network graphs. We present few results on a relatively large component of the *flickr* social network. Further more, the empirical scalability analysis of the proposed new algorithm shows that the algorithm is highly scalable for large sparse graphs. We also compare the positions given by our proposed algorithm with the ϵEP algorithm as suggested by authors in [7] on an example toy network.

- We propose a new notion of equivalence using multiple ϵ-equitable partitions of a graph. These multiple partitions give us a better bound on grouping actors and better insights to the "roles" of actors. We compute a similarity score for each actor-pair based on their co-occurrence at a same position across multiple ϵEPs. We define a new notion of equivalence using these pairwise similarity scores to perform agglomerative hierarchical clustering to identify the set of equivalent actors. Evaluation of our method on multi-role ground truth IMDb co-cast network shows that our method correctly discovers positions performing multiple roles; empirical evaluation on time evolving snapshots of JMLR co-citation and co-authorship graphs show the importance of MϵEPs in studying the evolution of actors and their ties.

CHAPTER 2

Overview of Role and Positional Analysis

The notions of social *position* and social *role* have been fundamental to the structural analysis of networks. These dual notions, are key techniques in identifying actors which are similarly embedded in a network and in finding out the pattern of relations, which exist among these similarly embedded actors.

This chapter is organized as follows. Section 2.1 explains the notion of *position* and *roles*. Section 2.2 explains mathematical preliminaries. Section 2.3 introduces the classical methods of role and positional analysis. Section 2.4 speaks about the *Stochastic Blockmodels* approach to positional analysis.

2.1 Position and Role

In SNA, the fundamental idea behind the notion of *position* is to find out actors which have similar structural signature in a network. Actors who have same structural correspondence to other actors in a network are said to occupy same "*position*". On the other hand, the fundamental idea behind the notion of *role* is to find out similar pattern of relations among different actors or positions. Actors at same position tend to perform same "*role*" to actors at another position ([11], [12], [13]).

Wasserman and Faust [11] state "key aspect in role and position analysis is: identifying social position as collection of actors who are similar in their ties with others and modelling social roles as system of ties between actors or between positions".

Example, professors in different universities occupy the *position* "Professor" by the virtue of similar kind of relationship with students, research scholars and other professors. Though individual professors may not know each other. Also, since the notion of *role* is dependant formally & conceptually on the notion of *position*, in the same example a professor could be in a *role* of "Guide" to his research scholars and in the *role* of a "Colleague" to fellow professors of his department.

2.2 Mathematical Preliminaries

Positional Analysis (PA) [11] of a social network aims to find similarities between actors (vertices) in the network. It is about dividing set of actors into subsets, such that actors in a particular subset are structurally similar to other actors. PA tries to identify actors which are similarly embedded in the network. PA also helps in analyzing the evolution of networks [14], actors at a particular position tend to evolve in a similar fashion.

Mathematically, PA is finding a partition of the graph on the basis of some *equivalence* relation. The subsequent section (2.3) discusses few important *equivalence* relations in detail. Before that, we present few mathematical definitions in the following subsection (2.2.1).

2.2.1 Partition and Ordered Partition

Definition 2.1. (*partition of a graph*) Given, graph G ≡ ⟨V, E⟩, V is the vertex set and E is the edge set. A partition π is defined as $\pi = \{c_1, c_2, ..., c_n\}$ such that,

- $\cup c_i = V, i = 1$ to n and
- $i \neq j \Rightarrow c_i \cap c_j = \phi$

Thus, the definition of a *partition* of a graph G means that we have *non-empty* subsets of the vertex set V, such that all subset pairs are *disjoint* to each other. These subsets $c_1, c_2, ..., c_n$ are called *cells* or *blocks*[*] of the partition π.

A cell with cardinality of one is called *trivial* or *singleton* cell. A partition in which all the cells are *trivial* is called the *discrete* partition. On the other hand, a partition which has all the vertices in a *single* cell is called the *unit* partition.

Finer and Coarser partitions: If π_1 and π_2 are two partitions, then π_1 is *finer* than π_2 ($\pi_1 \preccurlyeq \pi_2$) and π_2 is *coarser* than π_1, if every cell of π_1 is a subset of some cell of π_2 (*finer* than also includes the case when π_1 and π_2 are equal). Example,

$$\begin{array}{|c|c|c|c|}\hline a & b & c & d \\ \hline\end{array} \preccurlyeq \begin{array}{|c|cc|c|}\hline b & a & c & d \\ \hline\end{array} \preccurlyeq \begin{array}{|cccc|}\hline a & b & c & d \\ \hline\end{array}$$

Figure 2.1: Example of a "*finer*" than relation

A *refinement* of a *non-discrete* partition π is an action which gives a partition π', such that π' is a subset of π. Example, the partition [{*a*,*b*},{*c*},{*d*,*e*}] is a *refinement* of

[*]In this thesis, we use the terms *cell, block* and *position* interchangeably.

the partition [{*a*,*b*,*c*},{*d*,*e*}], but [{*a*,*b*,*c*,*d*},{*e*}] isn't, since the cell {*a*,*b*,*c*,*d*} is not a subset of either of the cells {*a*,*b*,*c*} or {*d*,*e*}. Precisely, a *refinement* action on a partition π maintains the *finer* than property.

Definition 2.2. (*ordered partition*) Given, a partition π and a *refinement* action R on π. Suppose, the successive application of R on π leads to partitions $\pi_i, \pi_{i+1}, ..., \pi_{i+n}$ respectively, then we say that each of the π_{i+1} is an *order preserving refinement* of π_i ($i \in 1, 2, ..., n$) if and only if the relative order of vertices in each cell is preserved after the application of the *refinement* action R. Mathematically, given a partition $\pi_1 = \{c_1, c_2, ..., c_i, c_j ..., c_n\}$ and let $\pi_2 = \{z_1, z_2, ..., z_k, z_l, ..., z_m\}$ be the partition after the refinement action R on π_1, then we say π_2 is an *ordered* partition of π_1 if and only if:

- π_2 is *finer* than π_1, and
- if $i \leq j$, $z_k \subseteq c_i$ and $z_l \subseteq c_j$; *implies* $k \leq l$.

Example,

Let, π_1=[$\{a\}, \{b, c, d\}$], further let π_2=[$\{a\}, \{b, c\}, \{d\}$] and π_3=[$\{d\}, \{a\}, \{b, c\}$] be the partitions of π_1 after application of two different refinement actions. π_2 maintains the relative cell order *w.r.t.* the vertices of π_1 and hence is an *ordered* partition of π_1, but π_3 isn't, since the cell $\{a\}$ is located before the cell containing d (*i.e.* $\{b, c, d\}$) in partition π_1.

The set of *ordered* partitions over the relation "*finer*" than ($\preccurlyeq$), on the vertex set V form a *partially ordered set*, wherein the unique maximal element is the *unit* partition and the minimal element being the *discrete* partition. We misuse terminology and call an order preserving refinement of π as a ordered partition of π.

2.3 Classical Methods of Role and Positional Analysis

Historically, the notion of social *"role"* dates back to Nadel's work *"The Theory of Social Structure"* (1957) [15]. A key idea from Nadel's work projected the use of pattern of relations among concrete entities to model social structure, rather than the use of abstract entities or attributes on these entities. He also suggested that to model a social structure properly, one needs to aggregate these interaction patterns in a way which is consistent with their inherent network structure. Nadel's ideas were first mathematically formalized by Lorrain and White (1971) [2], in this seminal paper, they introduced the notion of *Structural Equivalence* (SE), which is discussed in the following subsection (2.3.1).

2.3.1 Structural Equivalence

Two actors are structurally equivalent if they have exactly same set of ties to and from other actors in the network. Mathematically, SE is defined as follows ([2]):

Definition 2.3. (*structural equivalence*) Given a graph $G \equiv \langle V, E \rangle$, a and b are *structurally equivalent* if,

- $(a, c) \in E$ if and only if $(b, c) \in E$ and
- $(c, a) \in E$ if and only if $(c, b) \in E$

Example in Figure 2.2 depicts structurally equivalent nodes in same colours. The partition of the graph according to SE is [{A,B}, {C,D,E}, {F,G}, {H,I,J}]. It is

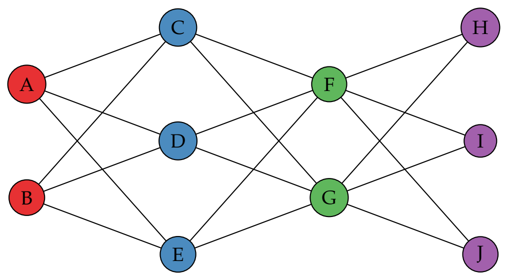


Figure 2.2: Example of Structural Equivalence. Structurally equivalent actors are coloured in same colour, which are {A,B}, {C,D,E}, {F,G}, {H,I,J}. A and B are equivalent since they have identical ties with the cell {C,D,E}, same is true for other cells accordingly.

worth mentioning here that, nodes in same cell connect exactly with same set of nodes in other cells.

Discussion

Since two structurally equivalent actors exactly connect to *identical* actors in other cells, they are perfectly *substitutable* for each other. Also, they have same set of node properties like: same degree, same centrality, same number of triangles etc. Though actor substitutability may make sense in small sized networks (like in scenarios where systematic redundancy of actors needs to be studied), perfect SE in real-world networks is often rare and mostly leads to trivial partitioning of the network. For example in the university scenario, two professors would be equivalent only if they "guide" exactly same set of research scholars, and are "colleagues" with exactly same set of individuals.

Computing Structural Equivalence

Two structurally equivalent actors will have identical correspondence among rows (or columns) in their graph adjacency matrix. Since exact SE is rare in most social networks, measures that estimate an approximate notion of structural equivalence among two nodes make more sense, *i.e.* estimating the degree to which their columns are identical. Burt's STRUCTURE ([16]) program achieves this by computing the values of *Euclidean distance* among each pair of actors (nodes) in the network, the program then merges nodes which are within threshold distance of each other incrementally, until all nodes end up in a single cluster (*i.e.* performs hierarchical clustering in an agglomerative fashion). Breiger, Boorman and Arabie (1975) came up with a divisive hierarchical clustering algorithm CONCOR ([17]) to estimate SE. The CONCOR (CONvergence of iterated CORrelations) algorithm computes the *Pearson's product moment correlation* among every pair of rows (or columns) and divides the data in two sets. The process is repeated over the iterated correlation matrix and in each iteration, all the sets having more that two elements are split into two parts.

Sailer in 1979 proposed a way to relax the strict definition of SE, which he called "*structural relatedness*" (SR). The notion of SR was paraphrased by John Boyd ([18]) as "two points are structurally equivalent if they are related in the same ways to points that are structurally equivalent". Example, for two professors to be equivalent, they need to "guide" some research scholar (as opposed to the same research scholar in SE), since all research scholars are structurally equivalent. The ideas from Sailer's work paved way for notions of *equivalence* which captured position and role in a better way, we discuss them in following subsections.

2.3.2 Regular Equivalence

White and Reitz in 1983 proposed the notion of Regular Equivalence (RE). RE is a widely accepted and studied notion of PA. Two actors are regularly equivalent if they have same set of ties to and from equivalent others. Mathematically, RE is defined as follows ([3]):

Definition 2.4. (*regular equivalence*) Given a graph $G \equiv \langle V, E \rangle$ and let $\equiv$ be an equivalence relation on V. Then, $\equiv$ is a *regular equivalence* if and only if for all a, b, c and d $\in$ V, $a \equiv b$ implies:

- $(a, c) \in E$ implies there exists $d \in V$ such that $(b, d) \in E$ and $d \equiv c$ and
- $(c, a) \in E$ implies there exists $d \in V$ such that $(d, b) \in E$ and $d \equiv c$.

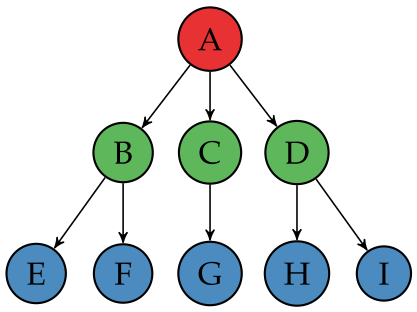


Figure 2.3: Example of Regular Equivalence. Regularly equivalent actors are depicted in same colour, which are {A}, {B,C,D}, {E,F,G,H,I}.

Example in Figure 2.3 depicts regularly equivalent nodes in same colour. Let us consider the node A being a parent fast-food chain company. A gives franchisees to B, C and D, and let (E,F), (G) & (H,I) be the employees appointed by them respectively. Now, by the definition of RE we have: regularly equivalent actors have similar set of ties to & from other regularly equivalent actors. Hence, the positions for actors in example 2.3 are {A} (*parent company*), {B,C,D} (*franchisees*), {E,F,G,H,I} (*employees*). Here, the RE relation doesn't try to distinguish among the employees of B with those of either C or D and vice versa. Here, all the "*employees*" belong to a single set because of the virtue of their connections to the "*franchisees*" set. SE on the other hand would have distinguished the employees of B, C & D from each other. An important observation from the "*employees*" set is that, the RE relation *doesn't* consider the *number of connections* from other sets, it just considers the *similar* nature of ties. Possibly in our example (2.3), the single employee "G" might have been overloaded in work than others, but RE would have failed to make that distinction.

Discussion

RE may be understood as partition of actors into classes, *s.t.* actors who belong to same class are surrounded by same classes of actors. Marx and Masuch ([19]) showed that RE from social networks theory is closely related to the notion of *bisimulation* in modal logic from computer science theory. The notion of *bisimulation* is used to indicate indistinguishability between two states of two different state transition systems. Everett and Borgatti in 1991 ([20]) proposed an alternate definition of RE based on *vertex colouring*, they coined the term "*role colouring*" for this definition. Under this definition, two regularly equivalent vertices belong to same colour class, and neighbourhoods of each of these vertices (which are also regularly equivalent) will also belong to different sets of same colour classes respectively.

White and Reitz ([3]) also defined the notion of *multiplex regular equivalence*

(MPXRE)[†]. MPXRE requires equivalent actors to have same set ('bundle') of relations with equivalent others. Example, suppose in a 5-relation ($R_1, R_2, ..., R_5$) network, node x has outgoing links to node y on R_1 and R_4, then for any node z to be equivalent to node x, z needs to have an alter equivalent to node y with exactly these two relations (R_1 and R_4). Everett and Borgatti in 1993 ([22]) extended the definition of "regular colouring" to directed graphs and networks, in addition to that, they also define the notion of MPXRE in terms of *multiplex regular colouring*.

The RE of a graph is not unique. The set of all the regular equivalences of a graph forms a *lattice* ([23]). The *supremum* element of the lattice is called *maximal regular equivalence* (MRE). In the next subsection we discuss what these multiple regular equivalences mean.

Computing Regular Equivalence

The earliest algorithm to compute RE was REGE, which was due to the efforts of White and Reitz from their unpublished manuscripts from University of California, Irvine archives (1984 and 1985)[‡]. The idea behind working of REGE algorithm, as explained by K. Faust ([24]), could be summarized in 3 steps as follows:

- Step 1: Divide the vertex set into three sets (classes): *source, sink* or *repeaters* (others). If the graph has no distinct source or sink vertices, then the result has a single equivalence class.
- Step 2: Combine all vertices which have same set of alters *w.r.t.* other classes.

[†]White and Reitz originally called it 'bundle equivalence' and later used the same term to define a distinct notion (page 208 & 214 of [3]). Hence, we use the term MPXRE as coined by [21] for clarity.

[‡]For more details about these manuscripts, readers are advised to look-up these references [24], [23] and [21].

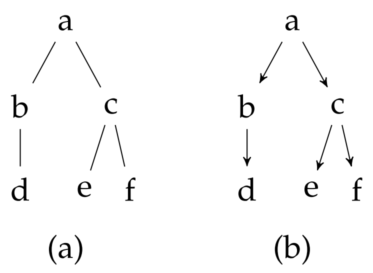


Figure 2.4: Example graph for equivalence given by REGE Algorithm. (a) Undirected graph (b) Directed graph

Step 2 is repeated until the equivalence classes do not change.

- Step 3: Output the equivalence classes.

The output of the REGE algorithm for graph in Figure 2.4 (a), is [{a,b,c,d,e,f}]. Whereas, the equivalence classes for the directed graph of Figure 2.4 (b), are [{a},{b,c},{d,e,f}]. The REGE algorithm finds only the *maximal regular equivalence* for any given graph. Also, for the example in Figure 2.4 (a), following are few partitions which are all valid *regular equivalences*:

- *Partition*1 : [{a,b,c,d,e,f}]
- *Partition*2 : [{a},{b,c},{d,e,f}]
- *Partition*3 : [{a},{b},{c},{d},{e,f}]

*Partition*1 being the output of the REGE algorithm (the MRE). *Partition*3 being the *maximal structural equivalence* (MSE). An important point to note here is that, SE also satisfies the definition of RE. All structurally equivalent actors are regularly equivalent, but the reverse is not always true. Intuitively, *Partition*2 might look like a better fit for the motivation behind RE. Which suggests that both MRE and MSE fail to capture essence for *undirected* graphs. On the other hand, the

REGE output for the *directed* graph from Figure 2.4 (b), captures the notion well. To overcome the disadvantage of a trivial partition under MRE for undirected graphs, Doreian proposed algorithm for finding RE for symmetric graphs ([25]). The idea behind Doreian's algorithm[§] was to *split* a symmetric structure into two asymmetric structures by using *centrality* scores as attribute on nodes, and then use REGE to find out the RE on each of these asymmetric pairs. Doreian's algorithm on the example of Figure 2.4 (a) would still yield *Partition*3, *i.e.* the MSE of the graph, which suggests that Doreian's algorithm may not always output a 'best-fit' RE for all undirected graphs. Precisely, Doreian's algorithm finds the RE from the *lattice* which is somewhere in between Lorrain and White's SE ([2]) and the MRE of White and Reitz ([3]). The reason of its closeness to SE being the dependence of the initial *Doreian's split* on the *centrality* of the nodes, which (centrality) in turn depends on the degree of the nodes. Steve Borgatti's paper from 1988 ([26]) discusses in detail, the changes to Doreian's algorithm, so as to make it more suitable for finding better and degree independent RE, these ideas influenced the REGE/A algorithm. In the same paper, Borgatti advocated the need to address the problem of finding the RE of graph as a *hierarchical clustering problem*. Rather than finding an unknown RE (as in the case of Doreian's algorithm) or finding the MRE (as with REGE), he proposed looking at the complete tree of the regular equivalences and pick a level, which suits the level of reduction required based on the data in hand. The REGE/A algorithm ([23]) overcomes the disadvantages of *Doreian's split* by finding out a MRE which preserves any *point-attribute* (node attribute) as chosen by the user, rather than just the *centrality* attribute. Few example point-attributes can be centrality or degree (network theoretic attributes) or even information like education or age

[§]We use the term *Doreian's split* interchangeably to refer to Doreian's algorithm.

(background attributes). The authors also showed the utility of REGE/A algorithm to *"regularize"* partitions generated by other equivalences such as the *Winship & Mandel* ([27]) equivalence or *orbit* partitioning ([28]). These partitions are given as attribute input to REGE/A, the resulting partition is therefore a MRE preserving that structure. Borgatti and Everett in 1993 ([21]), proposed the algorithm CATREGE (CATegorical REGE), extending the notion of RE to work with *categorical* data. Two actors are regularly equivalent in CATREGE if in addition to the normal definition of RE, they also relate to equivalent others in the same category. The input to CATREGE is nominal data, *i.e.* integer valued adjacency matrix amongst actors, where the integer values represent relationship in terms of categories. For example, we can use 1 to represent a close friend, 2 to represent a office colleague and 3 to represent an acquaintance. It should be noted here that these values do not capture the *strength* of a relationship, rather they simply indicate categories. CATREGE is a *divisive* HC algorithm, the algorithm starts with all the nodes in the same equivalence class. First iteration splits the nodes according to basic relational patterns, which classify the nodes as sources, sinks and repeaters. Second iteration onwards, the immediate neighbourhoods of the nodes are considered for a split. A split happens only when their neighbourhoods do not belong to same categories. Nodes which never split, are perfectly equivalent. CATREGE can also handle data with *multiplex* relations. Batagelj *et al.* ([29]) proposed the use of a criterion function which estimates RE and provides a measure of how far a given structure is from exact regular equivalence, they then use a local optimization procedure to find a partitioning which minimizes this criterion function. That is, given the final number of blocks, the algorithm then uses a greedy approach to optimize a cost function, which estimates the degree to which a partition is regularly equivalent.

The authors advocated the efficacy of the local optimization procedure on smaller graphs as an obvious advantage of the proposed method on larger networks, though the claim was not supported by any studies. It is very likely, *esp.* for large graphs, that a local optimization procedure might terminate at a local minima, than at a desired global minima. Few authors have also used simulated annealing ([30, 31]), tabu search ([32, 33]) *etc.* as optimization routines. The use of combinatorial optimization procedures to approximate RE with user-defined number of classes makes the problem non-trivial in nature. Roberts and Sheng ([34]) proved that the problem of finding *2-role* regular equivalence belongs to the *class-NP*. John P. Boyd in 2002 ([35]) proposed a mechanism to estimate the goodness-of-fit of a given equivalence to regularity, and then used *permutation test* and an optimization routine based on the adaptation of Kernighan-Lin variable-depth search algorithm (Kernighan and Lin 1970 [36]) to approximate regular equivalence for a given network. Kernighan-Lin search works better than greedy search, where local increase in the fitness score leads to creation of a new class. It is also faster than exhaustive search over all possible equivalences, but this method also does not guarantee an optimal solution. The experimental studies based on this method and Boyd & Jonas's ([37]) work on the validity of RE as a measure to precisely model/evaluate social relations reject regularity decisively, both suggested the need for a new model of defining equivalence.

2.3.3 Automorphisms

Definition 2.5. (*automorphisms*) Given a graph $G \equiv \langle V, E \rangle$, an *automorphism* is a bijective function f from $V \rightarrow V$ such that $(a, b) \in E$ if and only if $(f(a), f(b)) \in E$.

Discussion

Automorphism can also be understood as an isomorphism from a graph to itself. Automorphism finds symmetries in the network. The orbits of an automorphism group form a partition of the graph and each block of this partition indicates a position. The problem of finding all automorphically equivalent vertices is computationally hard (it is not known whether it is NP-complete or not) and it has been shown to be Graph Isomorphism Complete. However, efficient graph automorphism solvers like NAutY - No Automorphisms, Yes? [38] and Saucy [39] exist which are widely used for solving this problem. Automorphism is also a strict notion for position as it is a bijective function. Real world networks are quite irregular and hence existence of symmetries is very rare. In the hospital scenario, two doctors will be automorphically equivalent only if they relate to the same number of patients, nurses, and colleagues in the same way. Thus automorphism too fails to characterize the real world notion of similarity.

2.3.4 Equitable Partition

Definition 2.6. (*equitable partition*) A partition $\pi = \{c_1, c_2, ..., c_n\}$ on the vertex set V of graph G is said to be *equitable* [5] if,

$$\text{for all } 1 \le i, j \le n, deg(u, c_j) = deg(v, c_j) \text{ for all } u, v \in c_i \tag{2.1}$$

where,

$$deg(v_i, c_j) = sizeof\{v_k \mid (v_i, v_k) \in E \text{ and } v_k \in c_j\} \tag{2.2}$$

The term $deg(v_i, c_j)$ denotes the number of vertices in cell c_j adjacent to the vertex v_i. Here, cell c_j denotes a position and therefore $deg(v_i, c_j)$ means the number of connections the actor v_i has to the position c_j.

The equitable partition (EP) for the TA Network is shown in Figure 2.5(c). EP leads to a trivial partitioning of the network. The EP for this network has 7 positions, it treats each of the TAs and their respective student groups separate from each other.

Discussion

Equitable partitions are relaxations of automorphism since the partitions formed by automorphism are always equitable but the reverse is not true. Polynomial time algorithms exist for finding the coarsest equitable partition of a graph [5]. It can be observed that equitable partition is a regular partition with an additional constraint that the number of connections to the neighbouring positions should be equal for equivalent nodes. This constraint is too strict for complex large graphs and hence results in trivial partitioning. For example, in the hospital scenario, two doctors would be equivalent only if, say one of them interacts with n_1 nurses, n_2 other doctors and n_3 patients, then the other also is connected to n_1 nurses, n_2 other doctors and n_3 patients.

2.3.5 Computing Equitable Partition

The procedure to find the equitable partition of a graph is given in *Algorithm* 1. Given the initial colouring of vertices, the output of the procedure is the *coarsest* equitable partition of the input graph.

Algorithm 1 Equitable Refiner

```
Input: graph $G$, coloured partition $\pi$
Output: Equitable partition $R(G,\pi)$
 1: $f : V \to \mathcal{N}$
 2: active = indices($\pi$)
 3: while (active $\neq \phi$) do
 4:     $idx = min$(active)
 5:     active = active $\setminus \{idx\}$
 6:     $f(u) = deg_G(u, \pi[idx]) \; \forall u \in V$
 7:     $\pi' = \textsc{split}(\pi, f)$
 8:     active = active $\cup$ [ordered indices of new split cells from $\pi'$, while replacing
    (in place) the indices from $\pi$ which were split]
 9:     $\pi = \pi'$
10: end while
11: return $\pi$
```

Equitable Refinement Function *R* The key element in the equitable refinement function illustrated in *Algorithm* 1 is the procedure SPLIT.

SPLIT takes as input an *ordered* partition π on V and a function f, which maps every vertex $u \in V$ to its degree to a subset $c_a \subseteq V$ of the vertex set. c_a is the vertex set of the current *active* cell of the partition π. Mathematically, f is defined as follows:

$$\begin{aligned} &f : V \to \mathcal{N} \\ &f(u) = deg(u, c_a) \; \forall u \in V \end{aligned} \tag{2.3}$$

The SPLIT procedure then sorts (in ascending order) the vertices in each cell of the partition using the value assigned to each vertex by the function f as a key for comparison. The procedure then *"splits"* the contents of each cell wherever the keys differ. An important point to note here is that, the SPLIT operation at each iteration of the algorithm results in a partition π' which is both *ordered* and *finer* than the partition from the previous step.

2.4 Stochastic Blockmodels

Two actors are stochastic equivalent if they have same probability of linking to other actors at each of the positions. The early work on stochastic blockmodeling [40, 41] generalized the deterministic concept of structural equivalence to probabilistic models. In these, given the relational data of n actors and their attribute vector $\vec{x} = (x_1, x_2, ..., x_n)$, where x_i is the attribute value of i^{th} actor from a finite set ϱ of *positions*; the observed relational structure $\vec{y} = (y_{ij})_{1 \leq i \neq j \leq n}$ is modelled conditionally on the attribute vector $\vec{x}$, where y_{ij} is the observed relation between each ordered pair of actors i and j of the network. Approaches for modeling the cases where the attributes are known are called a priori stochastic blockmodel, in that, the roles are known in advance. Modeling for relational data in the absence of observed attributes falls under the class of a posteriori stochastic blockmodel [42, 43]. In these, the position structure is identified a posteriori based on the relational data $\vec{y}$ and the attribute structure $\vec{x}$ is unobserved or *latent*, in that, the model identifies the latent role an actor plays. The latent stochastic blockmodel (LSB) [43] limit the membership of each of the actors to a single position or to play a single latent role. The authors in [44], extend the LSB method to support multiple roles. The authors assume that the roles are separated into categories and that each actor performs one role from each category. They evaluate their proposed method using synthetically generated networks. The authors in [45] relax the single latent role per actor as in LSB [43]. They propose *mixed membership stochastic blockmodels* (MMSB) for relational data, thereby allowing the actors to play multiple roles. The authors evaluate their method on social and biological networks. The limitation of this model is in generating actors with higher degrees or with networks having skewed degree distributions.

2.5 Overview of ϵ-Equitable Partition

The notion of ϵ-Equitable Partition (ϵEP) was proposed by Kate and Ravindran in 2009 [1, 7]. The section highlights the advantages of ϵEP over classical approaches like structural and regular equivalences which lead to trivial partitions for undirected graphs. We also discuss in detail the definition, concepts and algorithm for ϵEP of graphs as proposed by Kate and Ravindran.

2.5.1 ϵ-Equitable Partition

Motivation Positional analysis based on structural equivalence, automorphism, regular equivalence and equitable partition of complex social networks results in trivial partitioning of the graph. Few of the drawbacks associated with these methods are listed below:

1. Regular equivalence does not take the number of connections to other positions into account. For example, node a_1 having 10 connections to position p_1 is considered equivalent to node a_2 having just 1 connection to position p_1.

2. Regular equivalence, however, is strict when comparing two actors based on the positions in the neighbourhood. For example, if node a_1 has a single connection to position p_1 and node a_2 does not have any connection to position p_1, then a_1 and a_2 will end up in separate blocks.

3. Definition of equitable partition rectifies the limitation 1 of regular equivalences, but it imposes a strict condition that the number of connections to other positions should be exactly equal for two nodes to be equivalent. This notion is too strict requirement for real world complex networks.

Kate and Ravindran [1, 7] proposed a relaxation to equitable partitioning of complex graphs.

Definition 2.7. (*ϵ-equitable partition*) A partition $\pi = \{c_1, c_2, ..., c_K\}$ of the vertex set $\{v_1, v_2, ..., v_n\}$, is defined as *ϵ-equitable partition* if:

$$\text{for all } 1 \leq i, j \leq K, |deg(u, c_j) - deg(v, c_j)| \leq \epsilon, \text{ for all } u, v \in c_i \tag{2.4}$$

where,

$$deg(v_i, c_j) = sizeof\{v_k \mid (v_i, v_k) \in E \text{ and } v_k \in c_j\} \tag{2.5}$$

The *degree vector* of a node u is defined as

$$\overrightarrow{deg}(u) = [deg(u, c_1), deg(u, c_2), ..., deg(u, c_K)] \tag{2.6}$$

Thus, the *degree vector* of a node u is a vector of size K (the total number of cells in π), where each component of the vector is the number of neighbours u has in each of the member blocks of the partition π.

Also, *slack* of a node v_i is defined as,

$$slack_{v_i} = \left\| \frac{1}{sizeof(c_{v_i}) - 1} \sum_{v_j \in c_{v_i} i \neq j} (\vec{\epsilon} - \mid \overrightarrow{deg}(v_i) - \overrightarrow{deg}(v_j) \mid) \right\|_1 \tag{2.7}$$

where,

$\overrightarrow{deg}(v_i)$ = the degree vector of node v_i (Equation 2.6)

c_{v_i} = the block to which node v_i belongs and

$\vec{\epsilon}$ = K dimensional vector such that $\epsilon_k = \epsilon$, for $k = 1, 2, ..., K$.

$\| \|_1$ is the l_1 norm of a vector (sum of the components)

The above definition (Equation 2.4) proposes a relaxation to the strict partitioning condition of equitable partition, an error of ϵ in the number of connections of an actor is allowed for it to be equivalent to an actor at another position.

The *slack* (Equation 2.7) computes how close a node is to other nodes in the block. Larger value of *slack* indicates a smaller within block distance. Kate and Ravindran also proposed the notion of *maximal* ϵEP, which is defined as follows.

Definition 2.8. (*maximal ϵ-equitable partition*) Given a graph G ≡ ⟨V, E⟩, partition $\pi = \{c_1, c_2, ..., c_K\}$ is *maximal ϵ-equitable* if,

1. for all $1 \leq i, j \leq K, |deg(u, c_j) - deg(v, c_j)| \ \leq \ \epsilon,$ for all $u, v \in c_i$
2. (K - $\sum_{v_i} slack_i$) is minimum, $i = 1, 2, ..., n$, n = number of nodes in the graph

A *maximal* ϵEP is a one in which no two blocks can be further merged without violating the ϵ property of the partition. The second condition of Definition 2.8. tries to optimize such that the number of blocks in the partition are minimum and the sum of slacks of all the vertices are maximum.

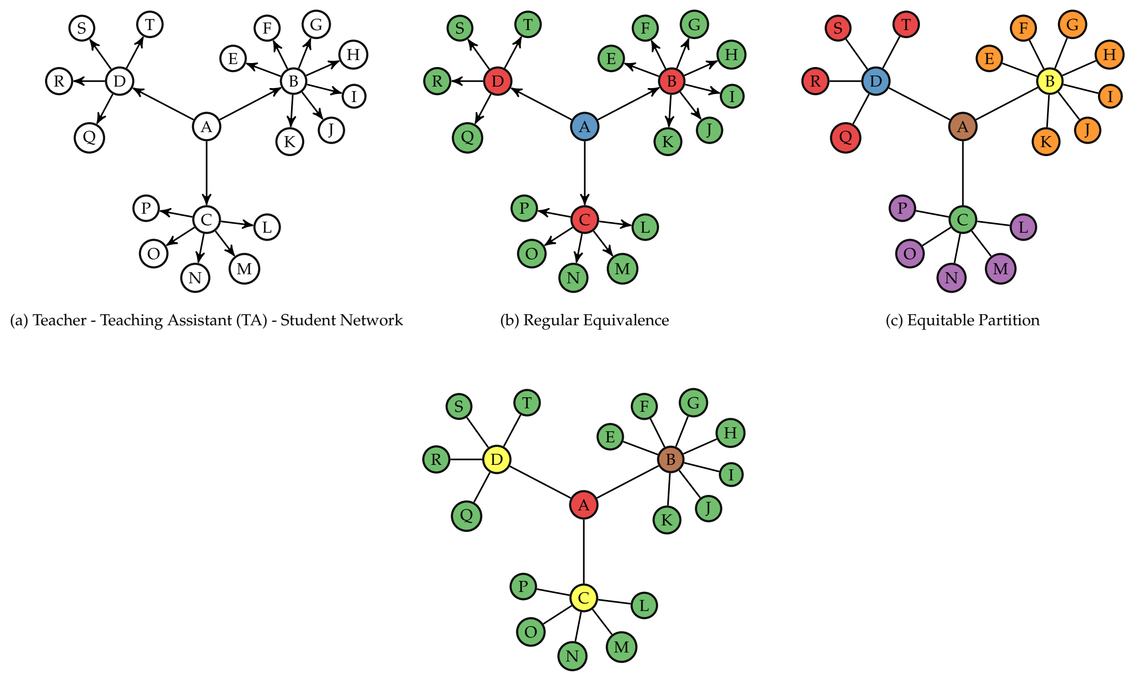
Example:

We use the Teacher-TA-Student example network from [7] to show the *positions* captured by various equivalence relations. Figure 2.5 (a) shows the TA Network, the network depicts an example classroom scenario in a department of an university having *three* positions, wherein the node A is a *teacher* who teaches a class of 16 *students* (nodes E – T), A is assisted by 3 *teaching assistants* B, C and D, each of them assists a group of 7, 5 and 4 students respectively. Figure 2.5 (b) and (c) show the partitions of the TA network under RE and EP respectively. RE successfully captures three positions, which are teacher, TAs and the students. EP on the other hand leads to a trivial partitioning with 7 positions, treating each of the TA and their respective student groups separate from each other. For this example, SE also leads to the same partitioning as that of EP. Finally, Figure 2.5 (d) shows the *maximal* ϵEP for an ϵ value of 1. The partition has 4 positions namely a teachers position (block {A}), a students position (block {E–T}) and two TAs positions (blocks {B} and {C,D}). Here, one might argue that the logical TAs position is split into two positions, but interestingly on an intuitive thought we may counter argue that the teaching assistant B was relatively overloaded that his counterparts C and D. Hence, the ϵ-equitable partitioning of a graph corresponds to more intuitive notions by considering the number of connection one has to the other positions in the network.

2.5.2 Advantages of ϵ-Equitable Partition

1. The ϵEP is an useful relaxation for large networks than the equitable partition. Example, with an ϵ value of 2 in the university network, a professor with 8 colleagues in the 'professor' position and guiding 6 individuals at the 'research scholars' position is equivalent to a professor having 10 colleagues and 4 research scholars.

2. ϵ value allows us to tweak the amount of relaxation required depending on given context and use-case under study. Also, $\epsilon = 0$ corresponds to the *coarsest* equitable partition.



(a) Teacher - Teaching Assistant (TA) - Student Network

(b) Regular Equivalence

(c) Equitable Partition

(d) Maximal 1-Equitable Partition

Figure 2.5: (a) The TA Network [7]. (b) TA network under Regular Equivalence, the partition is [{A},{B,C,D},{E-T}]. (c) Undirected TA network under Equitable Partition is [{A},{B},{C},{D},{E-K},{L-P},{Q-T}]. (d) Maximal ϵ-Equitable Partition on the TA Network, the partition for $\epsilon = 1$ is [{A},{B},{C,D},{E–T}].

3. It is both strict and lenient than regular equivalence. Strict due to the fact that ϵEP requires the number of connections between two nodes to a position to be atmost ϵ apart for them to be called equivalent. RE on the other hand does not care about the number of connections, it simply requires some connection. Lenient than RE since, ϵEP considers a node having no connection to a position as equivalent with another node having ϵ connections to the same position.

4. ϵEP of a graph corresponds to intuitive notions.

2.5.3 Algorithm for finding an ϵEP from [1]

Kate ([1], Chapter 4) discusses 4 different algorithms to find the ϵEP of a graph. Two of them find the *maximal* ϵEP, while the other two find the ϵEP for a given input graph. We discuss the algorithm #4 briefly here, since it is used for experimental validation of the proposed method. The pseudo code for Algorithm 4 (Chapter 4 [1]) is shown in Algorithm box 2. Input to this algorithm is (*i*) the graph, (*ii*) the *coarsest equitable partition* of graph [5] and (*iii*) a value of ϵ. The cells in the input equitable partition are arranged by ascending order of their *block degrees*[¶]. The algorithm then computes the *degree vector* (Equation 2.6) for each of the vertices in the graph G. The algorithm then tries to merge these cells by taking two consecutive cells at a time. If the degree vectors of the member nodes from these two cells are within ϵ distance of each other, they are merged into a single new cell. For further merging, this new cell becomes the current cell, which is then compared with the next cell for a possible merger. If the merging fails, the next cell becomes the current cell. The algorithm exits if no further merging of cells is possible. Also, the degree vectors need to be updated whenever two cells are merged. The time complexity of this algorithm to find ϵEP of a graph is $O(n^3)$.

[¶]*Cell or block degree* of a cell of an equitable partition is the degree of the member nodes in that block.

Algorithm 2 Algorithm to find ϵ-equitable partition from [1]

```
1: Sort the input equitable partition according to ascending order of the degree of the blocks (degree of the block of an equitable partition is same as the degree of the member nodes of that block)
2: for $i = 0 \rightarrow \epsilon$ do
3:     merge all the blocks having $degree = i$ into a single block and update the partition by deleting the merged blocks and by adding the new block
4:     update the variable $K$ according to the resulting partition
5: end for
6: for each node $v_i$ of the graph do
7:     calculate the degree vector $\overrightarrow{deg}(v_i)$                ▷ Equation 2.6
8: end for
9: $currentBlock$ = the first block in the ordered partition having degree > $\epsilon$
10: for each block in the currentPartition do
11:     check if it can be merged with currentBlock without violating the $\epsilon$ criterion, where $\epsilon = \epsilon/2$
12:     if True then
13:         merge it with currentBlock and update the partition, $K$ and the degreeVectors
14:     else
15:         make the block as currentBlock and continue
16:     end if
17: end for
```

CHAPTER 3

Scalable Positional Analysis: Fast and Scalable Epsilon Equitable Partition Algorithm

In this chapter we propose and implement a *new, scalable and distributed* algorithm based on the MapReduce methodology to find ϵEP of a graph. Empirical studies on random power-law graphs show that our algorithm is highly scalable for sparse graphs, thereby giving us the ability to study positional analysis on very large scale networks. We also present the results of our algorithm on time evolving snapshots of the *facebook* and *flickr* social graphs. Results show the importance of positional analysis on large dynamic networks.

The rest of the chapter is organized as follows. In Section 3.2 we propose a new algorithm with better heuristics for finding the ϵ-equitable partition of a graph. Section 3.3 describes the Parallel ϵEP algorithm along with its implementation. We present the scalability analysis, evaluation methodology, dataset details and experimental results in Section 3.4.

3.1 Motivation

An ϵ-equitable partition (ϵEP) [1] is a notion of equivalence, which has many advantages over the classical methods. ϵEP allows a leeway of ϵ in the number of connections the actors at a same position can have with the actors at another position. In the Indian movies dataset from IMDb, authors in [7] have shown that actors who fall in the same cell of the partition, tend to have acted in similar kinds of movies. Further, the authors also show that people who belong to a same position of an ϵEP tend to evolve similarly. In large social networks, tagging people who belong to the same position has potentially many advantages, both from business and individual perspective, such as, position based targeted promotions, ability to find anomalies, user churn prediction and personalised recommendations.

Though efficient graph partition refinement techniques and their application in finding the regular equivalence of a graph are well studied in the graph theoretic literature [8, 9], the application of these techniques for doing positional analysis of very large social graphs and networks is so far unknown. In this work, we propose a new algorithm to find the ϵ-equitable partition of a graph and focus on scaling this algorithm. We have successfully validated our algorithm with detailed studies on *facebook* social graph, highlighting the advantages of doing positional analysis on time evolving social network graphs. We present few results on a relatively large component of the *flickr* social network. Further more, the empirical scalability analysis of the proposed new algorithm shows that the algorithm is highly scalable for very large sparse graphs.

3.2 Fast ϵ-Equitable Partition

Our proposed new algorithm with better heuristics to find an ϵ-equitable partitioning of a graph is given in *Algorithm* 4. The implementation of our Fast ϵEP algorithm is directly based on the modification of McKay's original algorithm [5] to find the equitable partition of a graph, which iteratively refines an ordered partition until it is equitable (Chapter 2, 2.3.4). The key idea in our algorithm is to allow splitting a cell only when the degrees of the member nodes of a cell are more than ϵ apart. To achieve that, we first modify the SPLIT procedure of *Algorithm* 1, such that, it captures the definition of ϵ-equitable partition as defined by Equation 2.4. The new SPLIT function is listed in *Algorithm* 3. The key modifications are listed as follows:

- The input coloured partition π to Algorithm 1 is the *ordered unit* partition of G (*i.e.* all vertices belong to a *single cell*). The initial ordering of the unit partition is done by sorting the contents of the partition based on the output of function f, considering the unit partition as the active cell.
- An additional input parameter ϵ is passed to the algorithm.
- The default SPLIT procedure on line 7 of Algorithm 1 is replaced by the SPLIT procedure from Algorithm 3.

Key difference between the SPLIT procedure of *Algorithm* 1 (Chapter 2, 2.3.4) and SPLIT from *Algorithm* 3 is the fact that the later "*splits*" each cell of partition π **only** when their *sorted keys* as assigned by the function f (Equation 2.3), *w.r.t.* the current *active* cell are **more** than ϵ apart.
The algorithm for finding ϵ-equitable partition of G is given in *Algorithm* 4.

3.2.1 Description of Algorithm 4

The algorithm starts with the *unit* partition of the graph G and the current active cell c_a having the entire vertex set V. It then computes the function f (line 5,

Algorithm 3 Function SPLIT for finding ϵ-equitable partition

Input: epsilon ϵ, function f, partition π
Output: split partition π_s

```
 1: $idx = 0$                                                  ▷ index variable for $\pi_s$
 2: for each $currentCell$ in $\pi$ do
 3:     $sortedCell$ = SORT($currentCell$) using $f$ as the comparison key    ▷ i.e. if
    $f(u) < f(v)$ then $u$ appears before $v$ in $sortedCell$
 4:     $currentDegree = f(sortedCell[0])$
 5:     for each $vertex$ in $sortedCell$ do
 6:         if $(f(vertex) - currentDegree) \leq \epsilon$ then
 7:             Add $vertex$ to cell $\pi_s[idx]$
 8:         else
 9:             $currentDegree = f(vertex)$
10:             $idx = idx + 1$
11:             Add $vertex$ to cell $\pi_s[idx]$
12:         end if
13:     end for
14:     $idx = idx + 1$
15: end for
16: return $\pi_s$
```

Algorithm 4 Fast ϵ-Equitable Partition

Input: graph G, *ordered unit* partition π, epsilon ϵ
Output: ϵ-equitable partition π

```
 1: active = indices($\pi$)
 2: while (active $\neq \phi$) do
 3:     $idx = min$(active)
 4:     active = active $\setminus \{idx\}$
 5:     $f(u) = deg(u, \pi[idx]) \; \forall u \in V$                  ▷ $f : V \rightarrow \mathcal{N}$
 6:     $\pi' =$ SPLIT($\pi, f, \epsilon$)                            ▷ Algorithm 3
 7:     active = active $\cup$ [ordered indices of newly split cells from $\pi'$, while replacing
    (in place) the indices from $\pi$ which were split]
 8:     $\pi = \pi'$
 9: end while
10: return $\pi$
```

Algorithm 4) for each of the vertices of the graph. The algorithm then calls the SPLIT function (Algorithm 3). The SPLIT function takes each cell from the partition π and sorts the member vertices of these cells using the function f as the comparison key (Equation 2.3). Once a cell is sorted, a linear pass through the member vertices of the cell is done to check if any two consecutive vertices violate the ϵ criteria. In case of violation of the ϵ condition, the function *splits* the cell and updates the partition π and the active list accordingly. The algorithm exits either when the active list is empty or when π becomes a *discrete* partition, *i.e.*, all cells in π are singletons.

Explanation: The algorithm starts with *"splitting"* the *ordered* unit partition wherever the ϵ property to *"itself"* is violated and updates the partition π accordingly. In the second iteration, *second cell* of π is marked *active*, the function f is then populated *w.r.t.* this cell. Again, the algorithm *"splits"* each of the cells in π which violate the ϵ criteria (Eq. 2.4) to the second cell, updates π and so on. The algorithm terminates when no further splits of π are possible. At each iteration of the algorithm, the *ordered*[*] property of the partition is preserved, this is achieved by updating the list of *active* indices *in-place*. Example,
let $\pi = \{c_1, c_2, ..., c_i, ..., c_n\}$ be a partition at some intermediate iteration of Algorithm 4 and the current *active* list = *indices*$[c_2, c_3, ..., c_i, ..., c_n]$. Now suppose, the new partition π' generated by the procedure SPLIT (line 6, Algorithm 4) is,
$\pi' = \{c_1, c_2, ..., c_{i-1}, s_1, s_2, ..., s_j, c_{i+1}, ..., c_n\}$, *i.e.* cell c_i of π is *"split"* to cells $(s_1, s_2, ..., s_j)$ in π', then new *active* list = *indices*$[c_2, c_3, ..., c_{i-1}, s_1, s_2, ..., s_j, c_{i+1}, ..., c_n]$ (line 7, Algorithm 4).

[*]Mathematically, the definition of a partition doesn't force an ordering on the member *cells/blocks*. We abuse the *cell index* preserving partition as an *ordered* partition.

3.2.2 A note on running time complexity of Algorithm 4

Let n be the size of the vertex set V of G. The *while* loop of line 2 can run at most for n iterations: the case when SPLIT leads to the *discrete* partition of π, hence *active* will have n indices from $[0, 1, ..., (n-1)]$. The computation of the function $f(u) = deg(u, c_a)$ $\forall u \in V$ (line 5, Algorithm 4), either takes time proportional to the length of the current active cell c_a or to the length of the adjacency list of the vertex u[†]. The SORT function inside SPLIT procedure (line 3, Algorithm 3) is bound to $O(n \log n)$. Also, the *"splitting"* (line 4 to line 13, Algorithm 3) is a linear scan and comparison of vertices in an already sorted list, hence is bound to $O(n)$. Hence, the total running time of the function SPLIT is bound to $O(n \log n)$.

The maximum cardinality of the current active cell c_a can at most be n. Further, for *dense* undirected simple graph, the maximum cardinality of the adjacency list of any vertex can also at most be $(n-1)$. Therefore for n vertices, line 5 of Algorithm 4 performs in $O(n^2)$. For *sparse* graphs, the cardinality of the entire edge set is of the order of n, hence line 5 of algorithm 4 performs in the order $O(n)$.

Therefore, the total running time complexity of the proposed *Fast ϵ-Equitable Partitioning* algorithm is $O(n^3)$ for *dense* graphs and $O(n^2 \log n)$ for *sparse* graphs. In reality this would be quite less, since subsequent *splits* would only reduce the cardinality of the current *active* cell c_a. Which implies that we can safely assume that the cardinality of set c_a will be less than the cardinality of the *adjacency list* of the vertices of the graph. This analysis is only for the serial algorithm. Empirical

[†]Finding the *degree* of a vertex to current active cell translates to finding the *cardinality* of the *intersection set* between the current *active cell c_a* and the *adjacency list* of the vertex u. With a good choice of a data structure, the time complexity of intersection of two sets is usually proportional to the cardinality of the smaller set.

scalability analysis on random power-law graphs shows that our parallel algorithm (Section 3.3, Algorithm 5) is an order faster in time for sparse graphs.

3.3 Scalable and Distributed ϵ-Equitable Partition

This section describes the parallel implementation of the *Fast* ϵ-EP Algorithm 4 by the MapReduce methodology.

3.3.1 Overview of MapReduce

MapReduce (MR) [10] is a programming model to process large amounts of data using distributed computing nodes and algorithms that can be parallelized based on this paradigm. The MR paradigm is based on two main steps:

- *Map* step - Master node divides the input into smaller sub-problems and distributes amongst worker nodes in the cluster. Workers process the smaller problem and send back the result to the master node.
- *Reduce* step - The master combines the individual results from each of the worker nodes to generate the output.

3.3.2 Logical/Programming View of the MR Paradigm

Both the *Map* and *Reduce* procedures are defined *w.r.t.* as set of (*key,value*) pair.

The *Map* function is applied in parallel to each of the input record pairs at the worker nodes, which in turn generate an *intermediate* (*key,value*) pair. All these intermediate records are sent back to the master node, which groups the records for each *intermediate key* and then passes it to the *reduce* function.

The *Reduce* function accepts an intermediate key and a set of values for that key. It merges together these values to form a (possibly) smaller set of values. The return of these *reduce* functions is collected as the result list.

Mathematically,

- $Map(k_1, v_1) \rightarrow list(k_2, v_2)$
- $Reduce(k_2, list(v_2)) \rightarrow list(v_2)$

The input $(key, value)$ pairs are drawn from a different domain than the output $(key, value)$ pairs. Furthermore, the intermediate $(key, value)$ pairs are from the same domain as the output $(key, value)$ pairs. Thus, the MR paradigm transforms input $(key, value)$ pairs into list of values.

3.3.3 An analogy to MapReduce - "Mumbai's Dabbawalas"

The *dabbawalas* [46, 47] are one of its kind century old service industry based in Mumbai, India, who collect freshly prepared food in lunch boxes from homes and then deliver them at offices around lunch time using the city's rail network. An average working professional in Mumbai has to leave home early to reach office due to longer commute times and hence the lunch would loose its freshness by noon. The dabbawalas (person carrying the boxes) come to rescue by picking up the food much later in time and delivering the boxes just in time for lunch. A process which sounds fairly simple, actually involves these sequence of steps:

- A dabbawala collects lunch box from each home
- Dabbawalas then meet at a designated place where the boxes get sorted and grouped into different carriages for different destinations
- The carriages are then loaded onto trains according to respective destination areas
- The boxes in carriages are unloaded from trains and dispatched for final delivery address

The accuracy in collecting and delivering about 1.5 – 2 lakh boxes everyday is achieved using a code which is marked on each box lid. The code is comprised of a resident pick-up group code, resident railway station code, destination railway station code, destination pick-up group code and the destination address code.

Here's how the *dabbawalas*[‡] working sequence translates to the MapReduce paradigm:

- Picking up the lunch box from home and marking with an unique code: the *map* phase
- Meeting at a designated place and loading boxes marked for same destination into same carriages: the *intermediate* sort and shuffle phase
- Unload from the carriage and deliver the box to office address: the *reduce* phase

[‡]This analogy is inspired from the talk given by Janakiram M.S.V. (ex-AWS Technology Evangelist at Amazon, http://www.janakiramm.net/) at the Amazon Web Services Cloud Tour India 2011 [48] event held at Chennai, India.

3.3.4 Parallel ϵ-Equitable Partition

In the Parallel ϵEP Algorithm, we have implemented the most computationally intensive step of the ϵEP algorithm, namely, computation of function f (Equation 2.3), as a MAP operation. Each *mapper* starts by initializing the *current active cell* c_a for the current iteration (*line* 3 Algorithm 5). The *key* input to the MAP phase is the node id n and the node data corresponding to the node n is tagged along as the *value* corresponding to this key. The MAP operation involves finding the degree of the node n to the current active cell c_a, which translates to finding the size of the intersection of the adjacency list of n and the member elements of c_a (*line* 5, Algorithm 5). The MAP phase *emits* the node id n as the *key* and the degree of n to the current active cell c_a as a *value*. This corresponds to the value of function f (Equation 2.3) for the node n. Finally, a single *reducer* performs the *split* function (*line 6*, Algorithm 4) as described in the previous Section 3.2. The output of the REDUCE phase is used by the (*i*) *mapper* to initialize the active cell c_a and the (*ii*) *reducer* itself to update the partition π and the *active* list. Single MapReduce step of the algorithm is depicted in Algorithm 5. The *iterative* MR job continues till the *active* list becomes empty or the partition becomes *discrete*.

Implementation of the Parallel ϵEP Algorithm 5

The proposed Parallel ϵEP algorithm is *iterative* in nature, which implies that, the output of the current iteration becomes the input for the next one. The number of iterations in the Parallel ϵEP Algorithm for sparse graphs having a million nodes is in the range of few ten thousands. The existing MapReduce framework implementations such as Hadoop and Disco [49, 50] follow the programming

Algorithm 5 MapReduce step of the Parallel ϵ-Equitable Partition

```
1: class MAPPER
2:   method INITIALIZE()
3:     $c_a \leftarrow$ Current Active Cell                                   ▷ active[0]
4:   method MAP(id $n$, vertex $N$)
5:     $d \leftarrow |N.AdjacencyList \cap c_a|$   ▷ $d$ corresponds to the value of function $f(n)$,
   Equation 2.3
6:     EMIT(id $n$, value $d$)
```

```
1: class REDUCER                                                  ▷ Single Reducer
2:   method REDUCE()
3:     SPLIT($\pi, f, \epsilon$)                                       ▷ Algorithm 3
4:     UPDATE(active)                                        ▷ Algorithm 4, line 7
5:     UPDATE($\pi$)
```

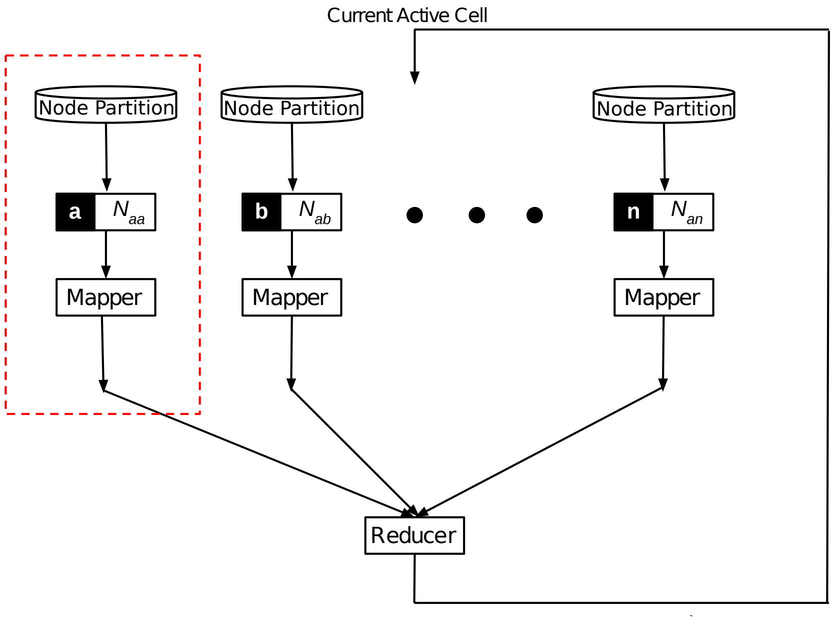
model and its architecture from the original MapReduce paradigm [10]. Hence, these implementations focus more on data reliability and fault tolerance guarantees in large cluster environments. This reliability and fault tolerance is usually associated with high data copy and job setup overhead costs. Although these features are suited for programs with a single MAP & a single REDUCE operation, they introduce high job setup overhead times across the *iterative* MR steps [51, 52, 53]. To circumvent this, we implemented a bare minimum MapReduce framework using open source tools GNU Parallel and rsync [54, 55]. We used GNU Parallel to trigger parallel map and reduce jobs on the cluster, rsync was used for data copy across the cluster nodes. We were able to achieve job setup overhead time in the range of **few milliseconds** using the custom framework, as opposed to ˜30 − 45 seconds for Hadoop on a 10 node cluster isolated over a Gigabit Ethernet switch. Conceptual and detailed overview of our Lightweight MapReduce Framework implementation is depicted in Figure 3.1. We intelligently *sharded* the input graph data across the distributed computing nodes. The *node data partitioning* is performed based on the number of nodes n in the input graph and the number of cores p available for computation; the methodology is depicted in Figure 3.1(b). The *node partition* splits the input graph into nearly equal sized vertex groups for processing on each of the available cores, we cache the vertex data for each of these groups on the corresponding compute nodes. This is conceptually similar to the user control on *data persistence* and *data partitioning* in the Resilient Distributed Datasets in the *Spark* MapReduce framework [53, 56]; though our implementation was inspired independently of the Spark framework and realized before that. This helped us achieve locality in reading the input graph. Execution time empirical studies on random power-law graphs for the proposed Algorithm 5 are presented in Section 3.4.5.

3.4 Experimental Evaluation

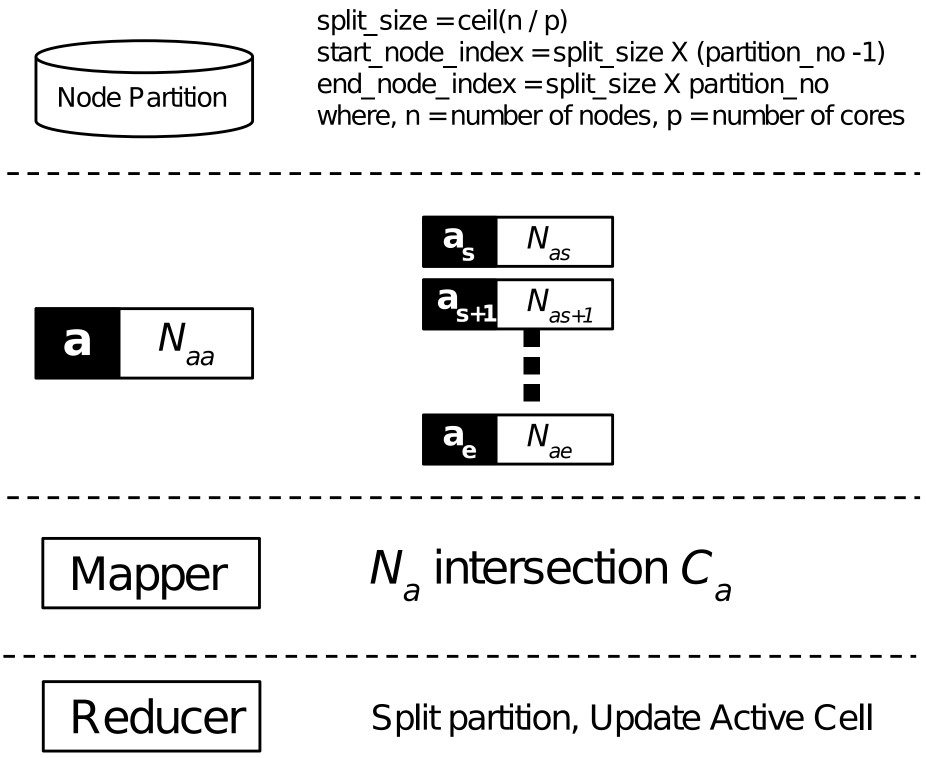
In this section we first present the results of our Fast ϵEP algorithm on a small example toy network. Later we briefly talk about the datasets used for evaluating our proposed algorithm. We also discuss the evaluation methodology and present our results. Finally, we do the scalability analysis of the proposed Parallel ϵEP algorithm.

3.4.1 Evaluation on an Example Toy Network

We performed static analysis of the ϵ-equitable partition algorithm on the TA Network using the ϵEP Algorithm from [7] and the proposed Fast ϵEP Algorithm 4 for $\epsilon = 1$. The TA Network depicts an University classroom scenario in which the node A signifies the position *professor*, the nodes B, C and D represent the

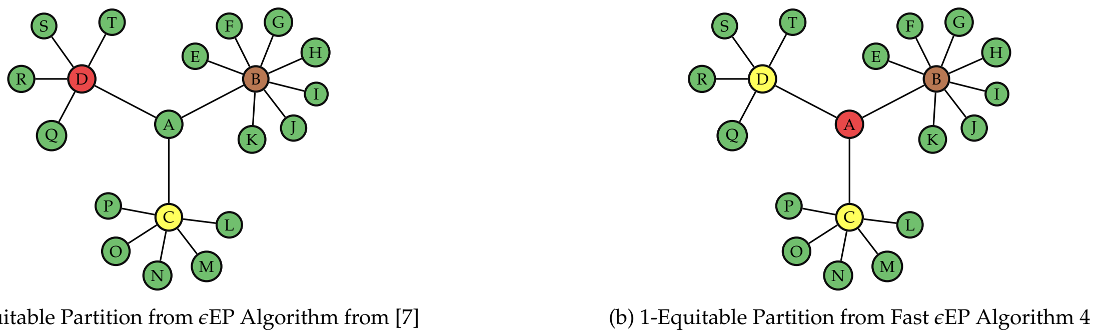


(a) Conceptual Overview of our Lightweight MapReduce Implementation


Node Partition
split_size = ceil(n / p)
start_node_index = split_size X (partition_no -1)
end_node_index = split_size X partition_no
where, n = number of nodes, p = number of cores
a
N_{aa}
a_s N_{as}
a_{s+1} N_{as+1}
a_e N_{ae}
Mapper
N_a intersection C_a
Reducer
Split partition, Update Active Cell

(b) Detailed View of our MapReduce Implementation

Figure 3.1: (a) Conceptual overview of our Lightweight MapReduce implementation. (b) Detailed view of our MapReduce implementation. The data partition number *partition_no* is in the range of $[1, p]$, where p is the number of available cores. The *node partition* splits the input graph into nearly equal sized vertex groups for processing on each of the available cores, we cache the vertex data for each of these groups on the corresponding compute nodes.



S
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(a) 1-Equitable Partition from ϵEP Algorithm from [7]
(b) 1-Equitable Partition from Fast ϵEP Algorithm 4

Figure 3.2: (a) The TA Network [7] 1-Equitable Partition under ϵEP Algorithm from [7] is [{A,E–T},{B},{C},{D}]. (b) 1-Equitable Partition under the proposed Fast ϵEP Algorithm 4 is [{A},{B},{C,D},{E–T}].

position *teaching assistant* (TA) and the nodes $E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S$ and T signify the position *student*. The result is depicted in Figure 3.2 (a) and (b). Our Fast ϵEP Algorithm 4 has successfully captured all the intuitive positions $[\{A\}, \{B\}, \{C, D\}, \{E{-}T\}]$, it has captured the relatively under loaded teaching assistants $\{C, D\}$, as a separate position than the overloaded teaching assistant B. Also, the partitioning of the TA Network given by our algorithm is the *maximal* ϵ-equitable partition§. On the other hand, partition given by ϵEP Algorithm from [7] for the TA Network leads to non-intuitive positions. It is quiet evident that, given a graph, its ϵEP is *not unique* and many such partitions which satisfy the ϵ-equitable equivalence may exist. We are primarily interested in studying the ϵEP which is either maximal or as coarse as possible, though we suspect that our Algorithm 4 may not always result in the *maximal* ϵEP of the graph.

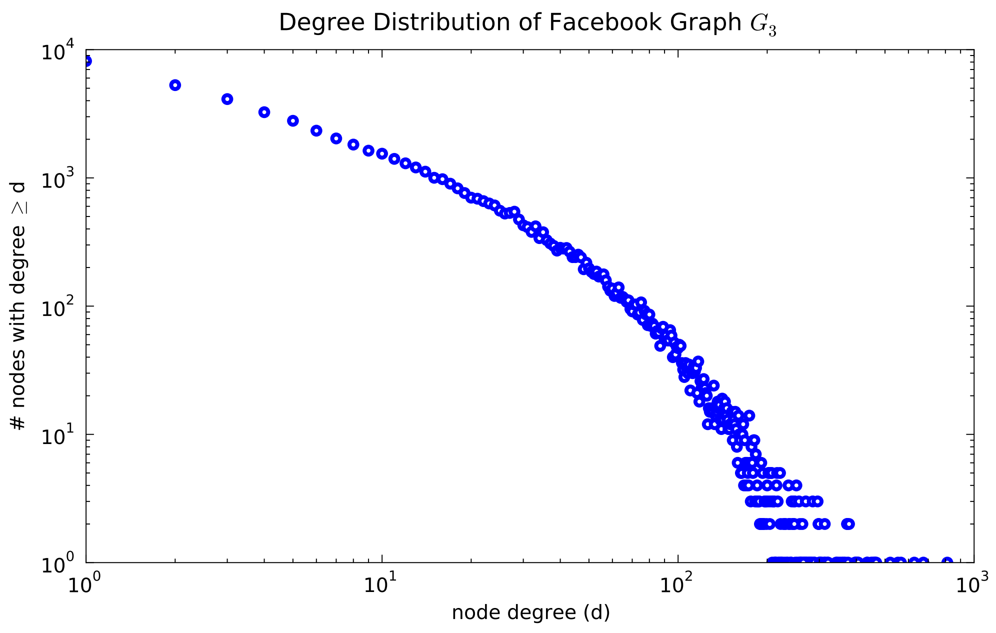
3.4.2 Datasets used for Dynamic Analysis

We have used the `Facebook` (New Orleans regional network) online social network dataset from [57]. The dataset consists of timestamped friendship link formation information between September 26th, 2006 and January 22nd, 2009. We created

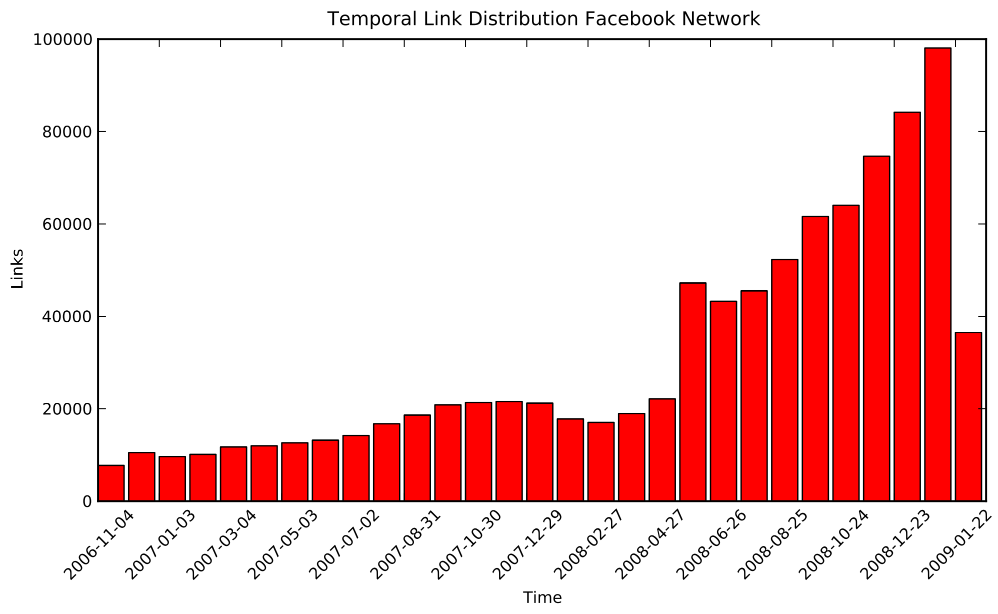
§Partition is *maximal* ϵEP if no two cells can be merged together without violating the ϵ property of the partitioning.

three time evolving graph snapshots for the facebook network, the base network consists of all the links formed between September 26th, 2006 and June 22nd 2007. The remaining *two* graphs are created such that, the graph at evolved point of time $t + \delta(t)$ has the graph at time t, along with the new vertices and edges that were added to the graph between time t and time $t + \delta(t)$, with $\delta(t)$ being 290 days. Table 3.1 tabulates the dataset properties. The degree distribution and the temporal distribution of link formation time for the `Facebook` graph G_3 is shown in Figure 3.3.

The second dataset that we used is the `Flickr` social network dataset from [58], which consists of a total of 104 days (November 2nd - December 3rd, 2006, and February 3rd - May 18th, 2007) of crawl data. This dataset consists of the timestamped link formation information among nodes. Since the nature of contact links in Flickr are directional in nature, we create an undirected dataset as described next. For each outgoing link from user $a \rightarrow b$, if user b reciprocates the link $b \rightarrow a$, we create an undirected edge (a, b). The time of link reciprocation by b is marked as the timestamp of the link formation. Further, we create a time evolving snapshot from this graph. The base graph G_1 has data from the first crawl, *i.e.*, between Nov 2nd - Dec 3rd, 2006. The second graph is created in a similar fashion as the `Facebook` graphs, with G_2 being G_1 plus the augmented data from the second crawl, *i.e.*, between Feb 3rd - May 18th, 2007. Table 3.2 tabulates the dataset properties. The degree distribution and the link reciprocity time plot for the `Flickr` graph G_2 is shown in Figure 3.4. The *link reciprocity* plot shows that most of the people connect back within a day of getting an incoming link request.

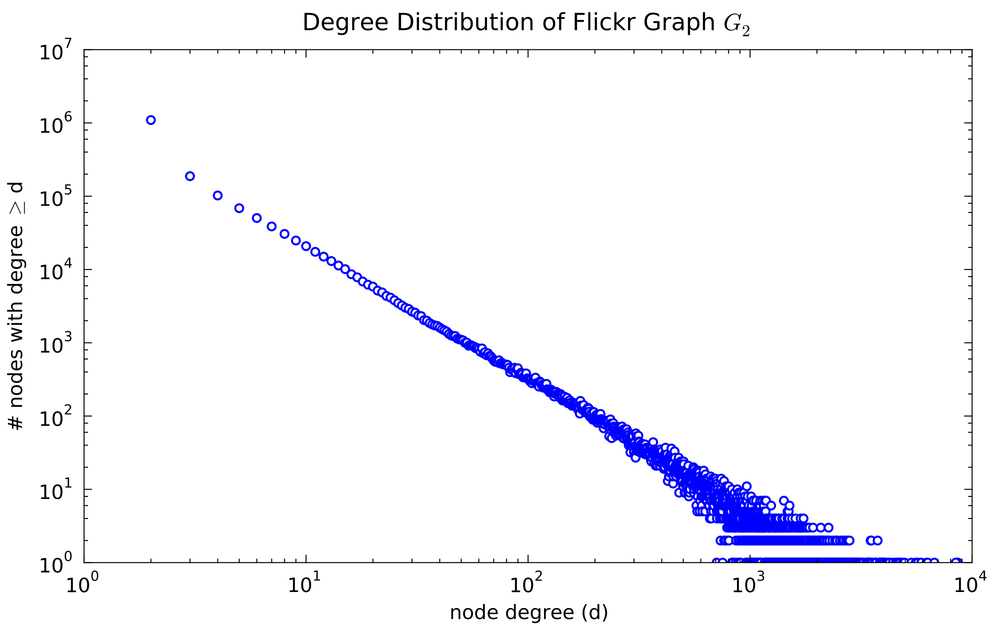


(a) Degree Distribution for Facebook graph G_3

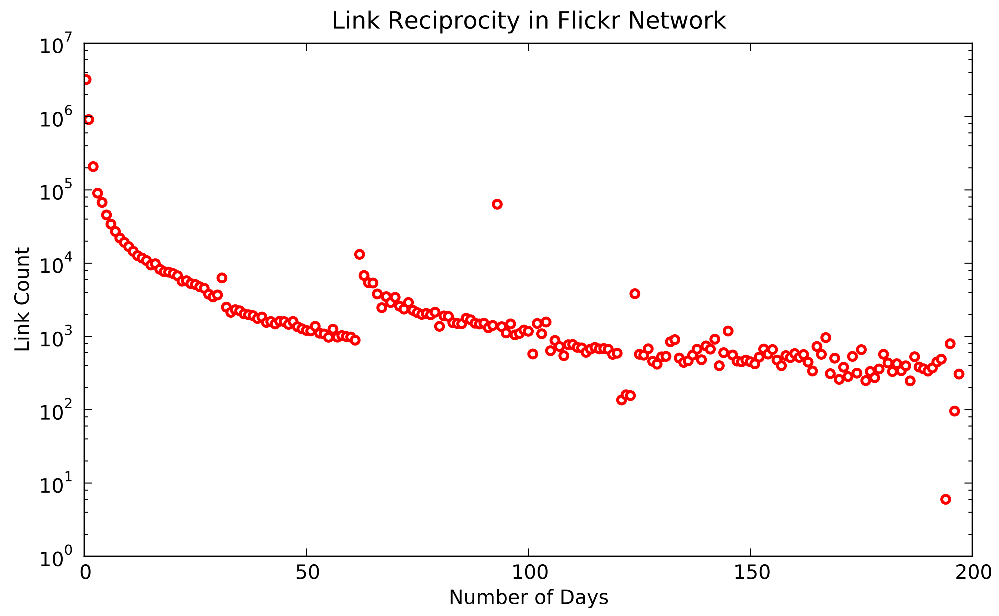


(b) Temporal Link Distribution of Facebook graph G_3

Figure 3.3: (a) Degree Distribution for Facebook graph G_3. (b) Temporal Distribution of link formation time for the Facebook graph G_3, a considerable number of new links have been added to the network in the last 120 days.



(a) Degree Distribution for Flickr graph G_2



(b) Link reciprocity time plot for Flickr graph G_2

Figure 3.4: (a) Degree Distribution for Flickr graph G_2. (b) Link Reciprocity time plot for Flickr graph G_2, most of the people connect back within a day of getting an incoming link request.

Table 3.1: Facebook Dataset Details

Graph	Vertices	Edges	Upto Date
1	15273	80005	2007-06-22
2	31432	218292	2008-04-07
3	61096	614796	2009-01-22

Table 3.2: Flickr Dataset Details

Graph	Vertices	Edges	Upto Date
1	1277145	6042808	2006-12-03
2	1856431	10301742	2007-05-19

3.4.3 Evaluation Methodology

We are primarily interested in studying the effect of PA on dynamic social networks and to characterize what role PA plays in the co-evolution of nodes in the networks. Given, a social network graph G_t at time t and its evolved network graph $G_{t+\delta t}$, our algorithm would return an ϵ-equitable partitioning π_t for G_t and $\pi_{t+\delta t}$ for $G_{t+\delta t}$. The methodology used to evaluate our proposed ϵEP algorithm is as follows.

i. **Partition Similarity**: We find the fraction of actors who share the same position across the partitions π_t and $\pi_{t+\delta t}$ using Equation 3.1. The new nodes in $G_{t+\delta t}$, which are not present in G_t are dropped off from $\pi_{t+\delta t}$ before computing the partition similarity score.

$$sim(\pi_t, \pi_{t+\delta t}) = \frac{1}{2}\left[\left(\frac{N - |\pi_t \cap \pi_{t+\delta t}|}{N - |\pi_t|}\right) + \left(\frac{N - |\pi_t \cap \pi_{t+\delta t}|}{N - |\pi_{t+\delta t}|}\right)\right] \tag{3.1}$$

where, N is the size of the *discrete* partition of π_t. The quantity $|\pi_t \cap \pi_{t+\delta t}|$ is the size of the partition obtained by doing *cell-wise* intersection among the cells of π_t and $\pi_{t+\delta t}$. In equation 3.1, if the number of actors who share positions across π_t and $\pi_{t+\delta t}$ is large, the value of $|\pi_t \cap \pi_{t+\delta t}|$ will be almost equal to the size of either π_t or $\pi_{t+\delta t}$. Hence, the resulting partition similarity score will be close to 1. On the other hand, if the overlap of actors between π_t and $\pi_{t+\delta t}$ is very small, $|\pi_t \cap \pi_{t+\delta t}|$ will be a large number, resulting in a similarity score close to 0. The terms in the denominator of the equation essentially provide a normalization *w.r.t.* the size of partitions π_t and $\pi_{t+\delta t}$. The value of $sim(\pi_t, \pi_{t+\delta t})$ given by Equation 3.1 is always between $[0, 1]$. We provide a detailed note on the partition similarity and its computation in Appendix A.

ii. **Graph theoretic network centric properties**: Given co-evolving vertex pairs (a, b) which occupy the same position in the partition π_t, we study the evolution of network centric properties corresponding to the vertex pairs in the time evolved graph $G_{t+\delta t}$. We study the following properties which are widely used for characterizing the graph structure:

   - *Betweenness centrality* of a node v is the number of shortest paths across all the node pairs that pass through v. This signifies the importance of a node, for routing, information diffusion, etc.
   - *Degree centrality* of a node is the number of nodes it is connected to in a graph. It quantifies the importance of a node *w.r.t.* the number of connections a node has.
   - Counting the *number of triangles* a node is part of, is an elementary step required to find the clustering co-efficient of a node in a graph. Clustering co-efficient of a node signifies how strongly-knit a node is with its neighbourhood. There is a scalable algorithm to count the number of triangles in a graph [59].
   - *Shapley value centrality* corresponds to a game theoretic notion of centrality. This models the importance of a node in information diffusion [60], it is also efficiently computable for large graphs.

We evaluate the co-evolution of nodes in various positional analysis methods using these four *network centric* properties as follows. For each pair of nodes (a, b) which occupy same position in a partition, we compute the difference $(a_t - b_t)$. Where, a_t and b_t correspond to the score of either of these four properties described previously. For the same pair of nodes, we also compute the difference $(a_{t+\delta t} - b_{t+\delta t})$. The scores $a_{t+\delta t}$ and $b_{t+\delta t}$ correspond to the property score at time $t + \delta t$. Finally, we take an absolute value of the difference of these two quantities, *i.e.*, $|(a_t - b_t) - (a_{t+\delta t} - b_{t+\delta t})|$. A low value of this quantity therefore signifies that for a co-evolving node pair (a, b) at time t, the network centric property of node a and b at time $t + \delta t$ have also evolved similarly. Note that we are not partitioning based on the centrality scores, hence our comparisons are across timestamps.

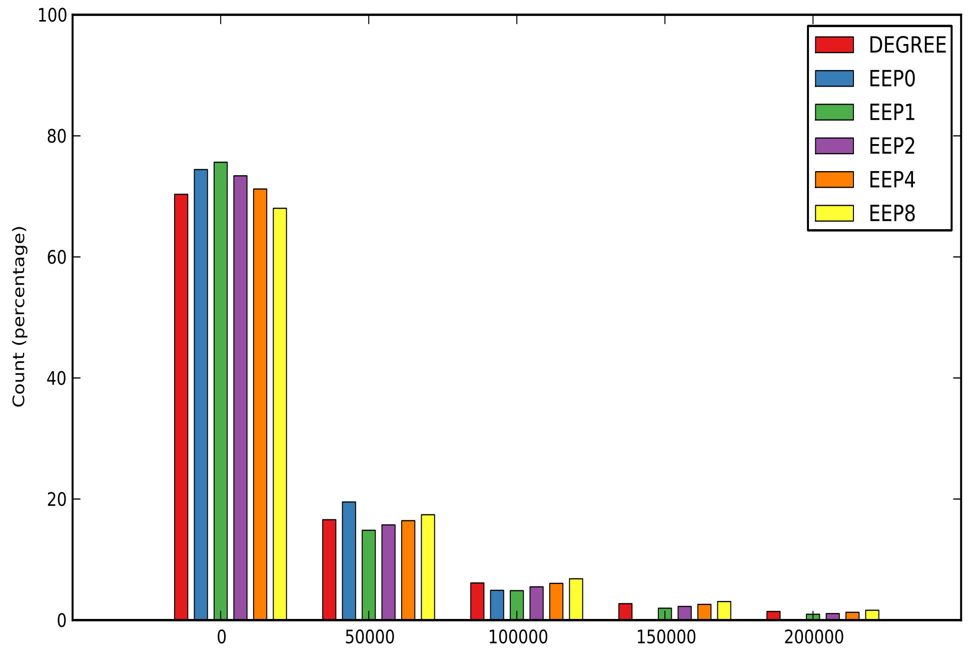
Epsilon (ϵ)	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**d***
G_1 **with** G_2	59.59	66.19	76.60	83.00	86.57	89.43	91.29	92.88	94.18	86.93
G_1 **with** G_3	54.11	57.17	69.33	76.61	80.85	84.37	86.60	88.95	90.72	79.42
G_2 **with** G_3	56.88	67.18	76.80	82.12	85.55	87.99	89.87	91.48	92.93	78.11

Table 3.3: Percentage of ϵEP overlap using the Partition Similarity score (Equation 3.1) for time evolving graphs of the Facebook Network. ϵ varied from 0 to 8, $\epsilon = 0$ corresponds to an equitable partition. d* denotes the partition based on degree.

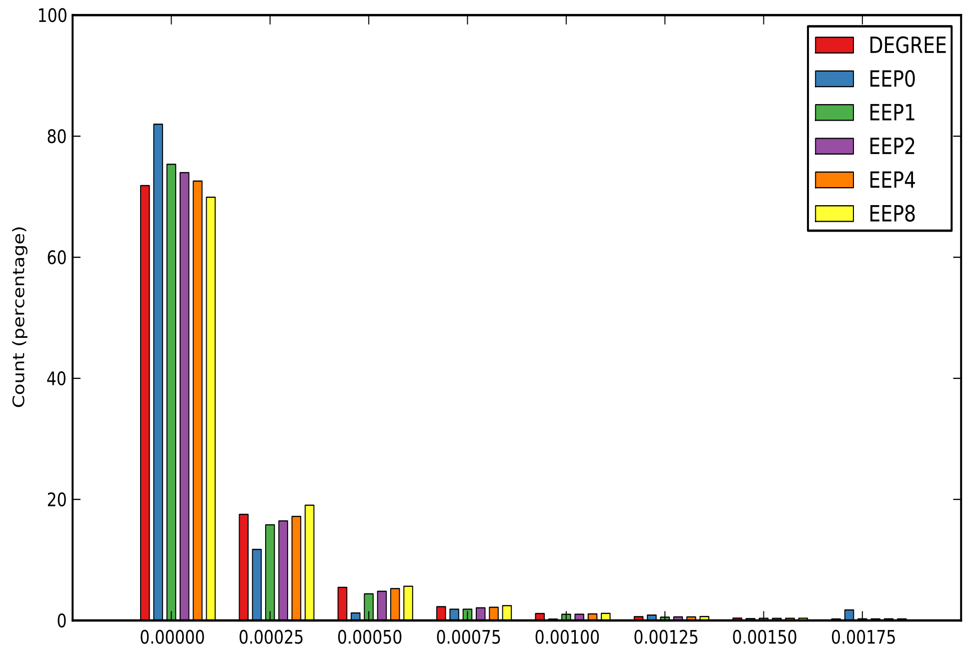
3.4.4 Results of Dynamic Analysis

We present the evaluation of our proposed algorithm using the methodology described in the previous subsection. The results of the *partition similarity* score in percentages are tabulated in Table 3.3. We compare our method with *equitable partition* (EP) and the *degree partition*[¶] (DP) for the `Facebook` dataset. We study

[¶]Nodes having same degree occupy same position in the partition.

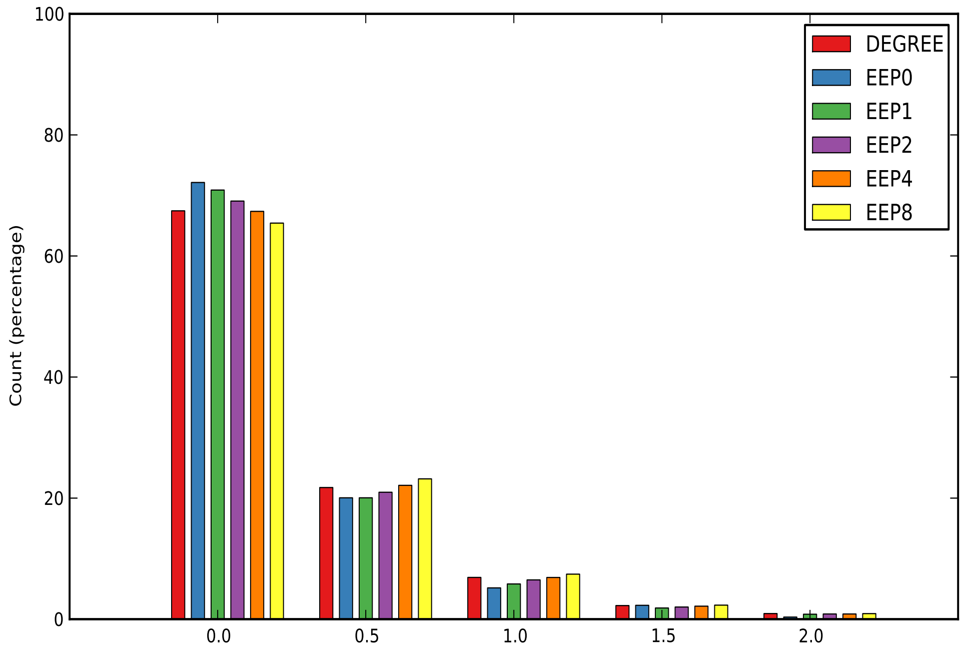


(a) Difference of Betweenness Centrality

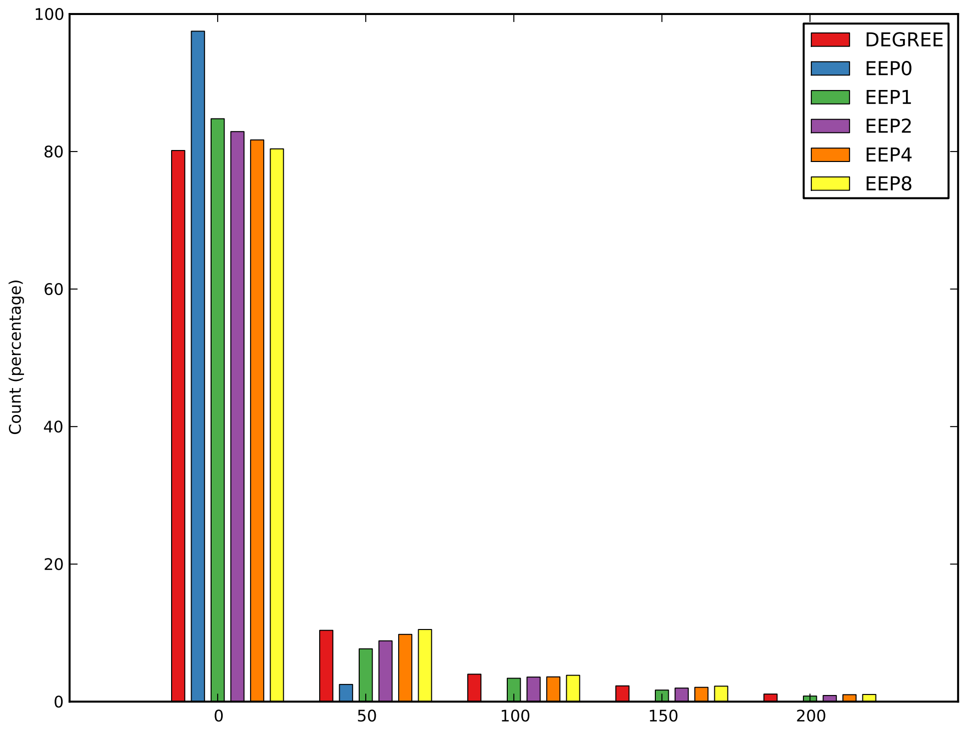


(b) Difference of Normalized Degree Centrality

Figure 3.5: Co-evolving node pairs for Facebook Graph $G_1 \rightarrow G_2$. (a) Difference of Betweenness Centrality. (b) Difference of Normalized Degree Centrality.

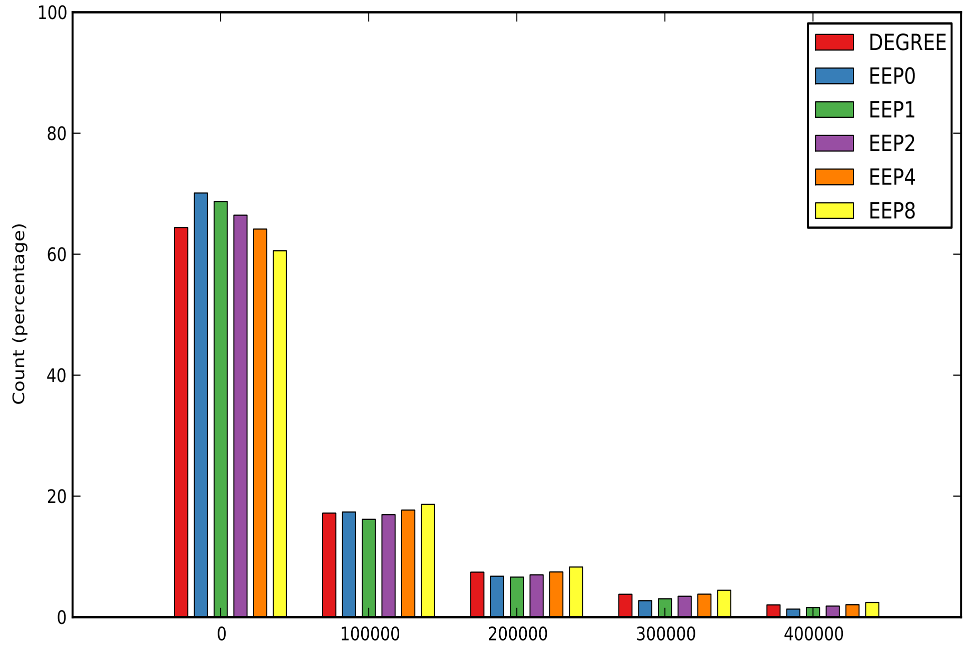


(c) Difference of Shapley Value Centrality

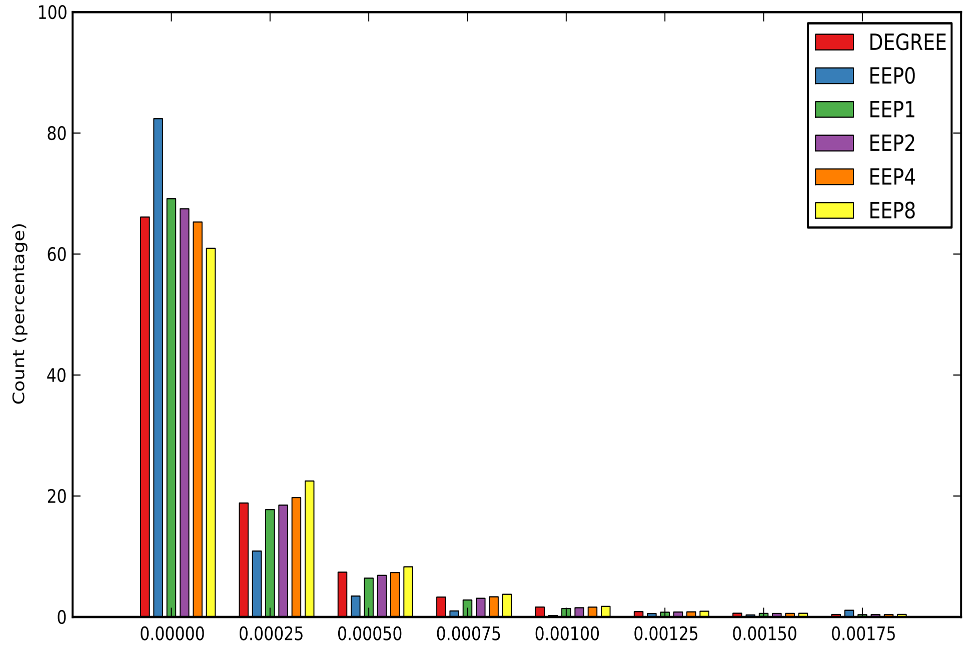


(d) Difference of Triangles

Figure 3.5: Co-evolving node pairs for Facebook Graph $G_1 \rightarrow G_2$. (c) Difference of Shapley Value Centrality. (d) Difference of Triangles.

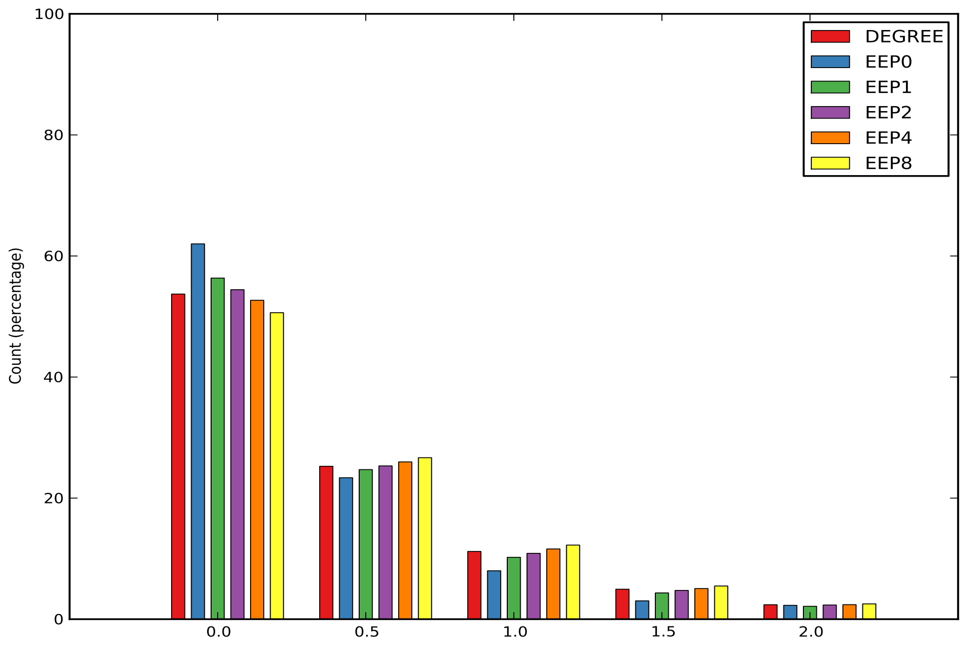


(a) Difference of Betweenness Centrality

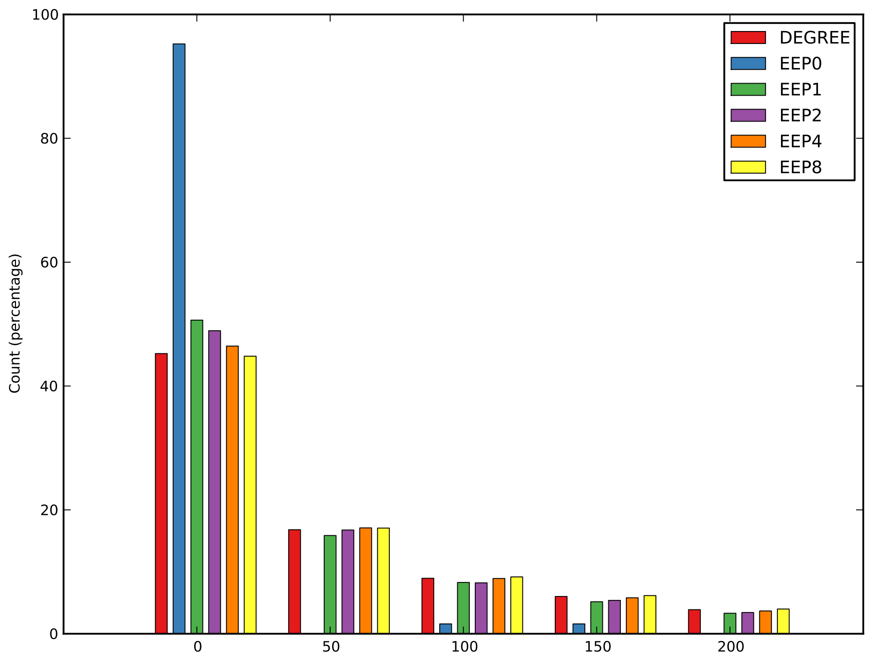


(b) Difference of Normalized Degree Centrality

Figure 3.6: Co-evolving node pairs for Facebook Graph $G_1 \rightarrow G_3$. (a) Difference of Betweenness Centrality. (b) Difference of Normalized Degree Centrality.



(c) Difference of Shapley Value Centrality



(d) Difference of Triangles

Figure 3.6: Co-evolving node pairs for Facebook Graph $G_1 \rightarrow G_3$. (c) Difference of Shapley Value Centrality. (d) Difference of Triangles. A low value of difference signifies that for a co-evolving node pair (a, b) at time t, the network centric property of node a and b at time $t + \delta t$ have also evolved similarly.

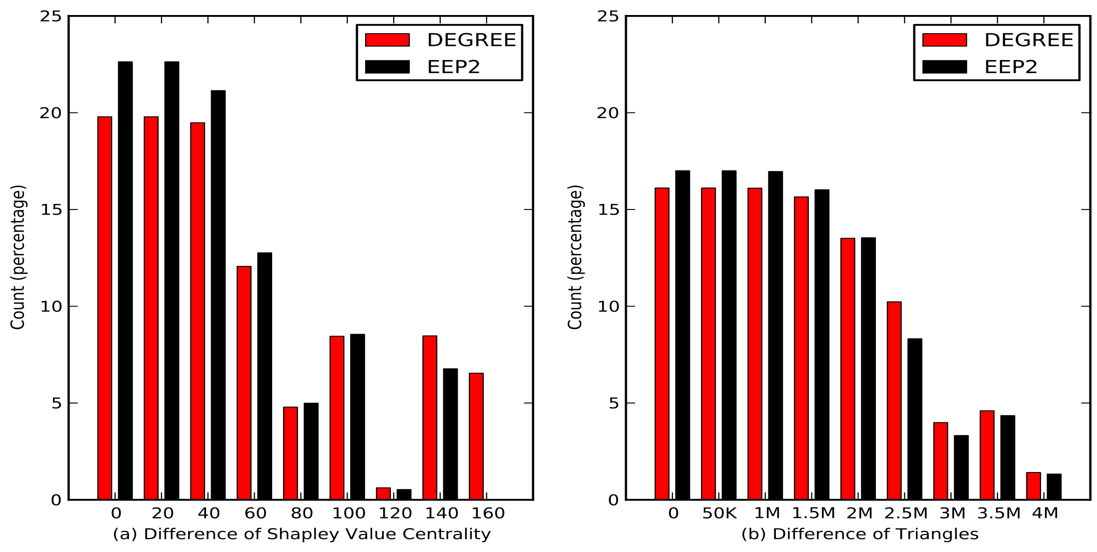


Figure 3.7: Co-evolving node pairs for Flickr graph $G_1 \rightarrow G_2$. (a) Difference of Shapley Value Centrality. (b) Difference of Triangles. A low value of difference signifies that for a co-evolving node pair (a, b) at time t, the network centric property of node a and b at time $t + \delta t$ have also evolved similarly.

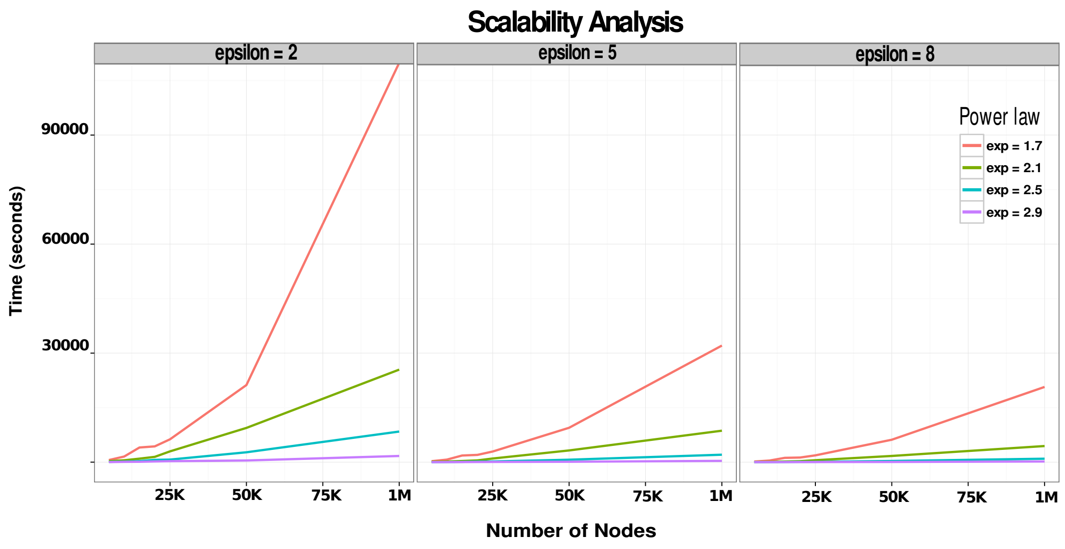


Figure 3.8: Scalability Curve for Size of the input versus Time, for varying Power law exponents and $\epsilon = 2, 5, 8$. Higher values of power-law exponent γ signify *sparse graphs*, this implies, our algorithm is linearly scalable for large sparse graphs, irrespective of the choice of ϵ.

the evolution of actors from graph $G_1 \to G_2$, $G_1 \to G_3$ and $G_2 \to G_3$, under these three partitioning methods. The ϵ-equitable partition and the degree partition display a high percentage of overlap among positions than the equitable partition. The poor performance of the EP under the partition similarity score is attributed due the strict definition of equivalence under EP. As an example, consider two nodes a and b occupy same position under EP for graph G_1, implies that both have exactly the same degree vector. Suppose, in G_2, the number of connections of b remained exactly the same, but node a added one extra link to another position, implies that a and b will now belong to different positions under EP. The ϵEP consistently performs better than the DP for higher values of ϵ. The higher values of ϵ, correspond to greater bounded relaxation under the definition of ϵEP. In most of the cases for a given graph, the number of positions under ϵEP would decrease as we increase the ϵ. Therefore, given two ϵEPs π_1 and π_2, both of them would have relatively less number of positions at higher values of ϵ. This explains the higher partition similarity percentages for ϵEP. The high values of partition similarity score for degree partition could be attributed due to the nodes in the network which don't evolve with time.

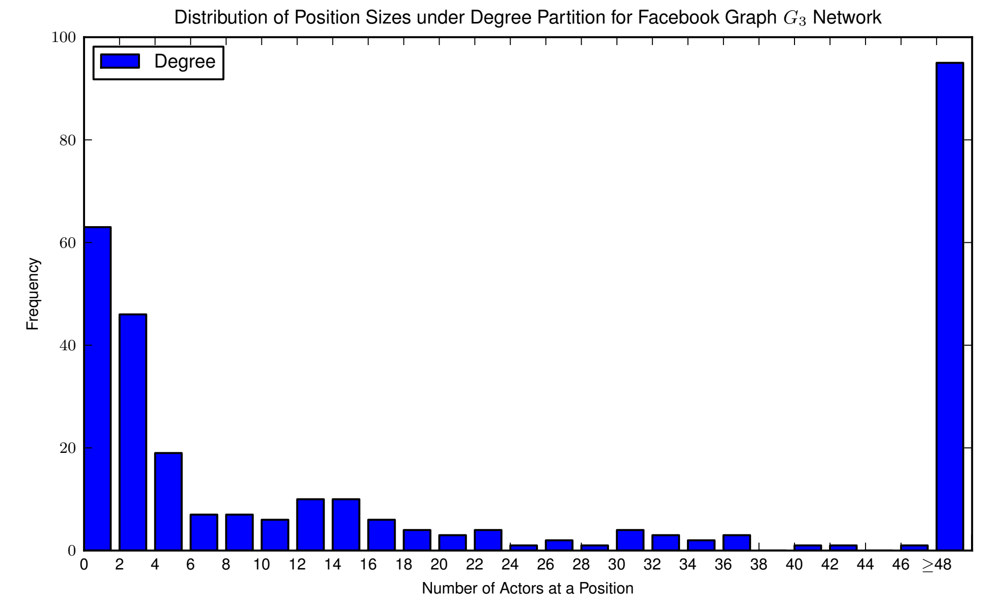
The question on choosing a correct value of ϵ, which corresponds to suitable notion of positions, while satisfying stronger cohesion among actors occupying these positions in dynamic networks is beyond the purview of this work. Nevertheless results from Table 3.3 highlight a very important property of ϵ-equitable partition, namely "*tunability*".

The study of the various *network centric properties* for co-evolving node pairs of the `Facebook` and the `Flickr` datasets, for different positional analysis methods is presented in Figure 3.5, Figure 3.6 and Figure 3.7 respectively. The *x-axis* corresponds to the bins containing the difference of a network centric property. The *y-axis* corresponds to the frequency of node pairs that belong to a particular bin, as a percentage of the total number of node pairs that occupy the same position in the partition. The results show that equitable partitioning outperforms both the ϵEP and the DP for each of the network centric properties, which implies that they model positions of co-evolving node pairs pretty well. But the fact that equitable partition leads to trivial partitioning of nodes in a network, makes it the least suitable method for performing PA on real-world networks. Let us consider the example of the equitable partition for the graph G_3 from the `Facebook` dataset which has 61096 nodes. The EP of G_3 has 59474 cells, out of which 58494 (˜96%) cells are singletons. The co-evolving node pairs under the ϵEP outperform the DP in most of the cases for the `Facebook` networks $G_1 \rightarrow G_2$ and $G_1 \rightarrow G_3$, especially for smaller values of ϵ. The ϵEP with smaller values for ϵ perform better because of their closeness to the equitable partition. It is worth mentioning here that, the number of positions given by ϵEP for $\epsilon = 1$ for G_3 is 8783. This implies that, ϵEP guarantee a high degree of confidence on the values of network centric properties of the co-evolving node pairs, along with a partitioning of a reasonable size. Also, the degree partition has too few positions, most of them having large number of nodes. The distribution of *position sizes* and their respective counts for each of these methods is shown in Figure 3.9.

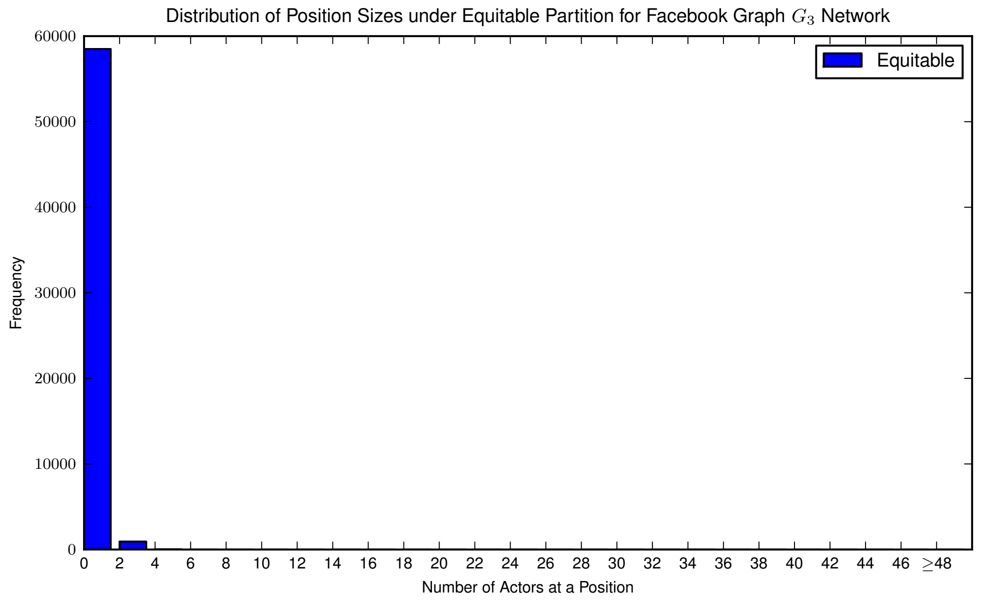
The `Flickr` dataset results in Figure 3.7 also follow a similar trend, the ϵEP partition performs better than the DP. The percentage counts of both the properties is more spread out across initial few bins for the `Flickr` dataset. The ϵEP for $\epsilon = 2$ has higher percentage counts for co-evolving node pairs in the bins, which correspond to smaller difference values, whereas, the co-evolving node pairs from the DP have relatively lower percentage counts in the bins closer to a difference of zero and high percentage of nodes towards the tail end of the *x-axis*, especially, for the shapley value centrality, which is not desirable. Also, the degree based partition has very few positions. Therefore, ϵEP is a consistent performer, both from the perspective of node co-evolution characteristics and number of positions it gives.

3.4.5 Scalability Analysis of the Parallel ϵEP Algorithm

In this section we present empirical studies on the scalability of our proposed parallel algorithm 5. The algorithm execution was done on a single machine having eight cores; utilizing all the eight cores for the program. We study the effect of increasing the size of the input, on the running time of the algorithm. We do this analysis on *random power law* graphs by varying the power law exponent γ between $1.7 \leq \gamma \leq 2.9$. Figure 3.8 shows the various scalability curves. The size of the input varies from 25 thousand nodes to 1 million nodes. The running time of the algorithm increases as we decrease the value of ϵ, this is attributed due to the fact that for small values of ϵ, the number of SPLITS which we do (Algorithm 4, *line 11*) is quite large, which directly translates to increase in the number of iterations for the algorithm. Also, decreasing the power law exponent γ, increases the running time of the algorithm. Since, a lower value of γ corresponds to *denser* graphs, for dense graphs, the computation of the degree of each vertex to the current active cell c_a, therefore, becomes a costly operation. It is evident from the graph that the algorithm scales almost linearly with increase in the input graph

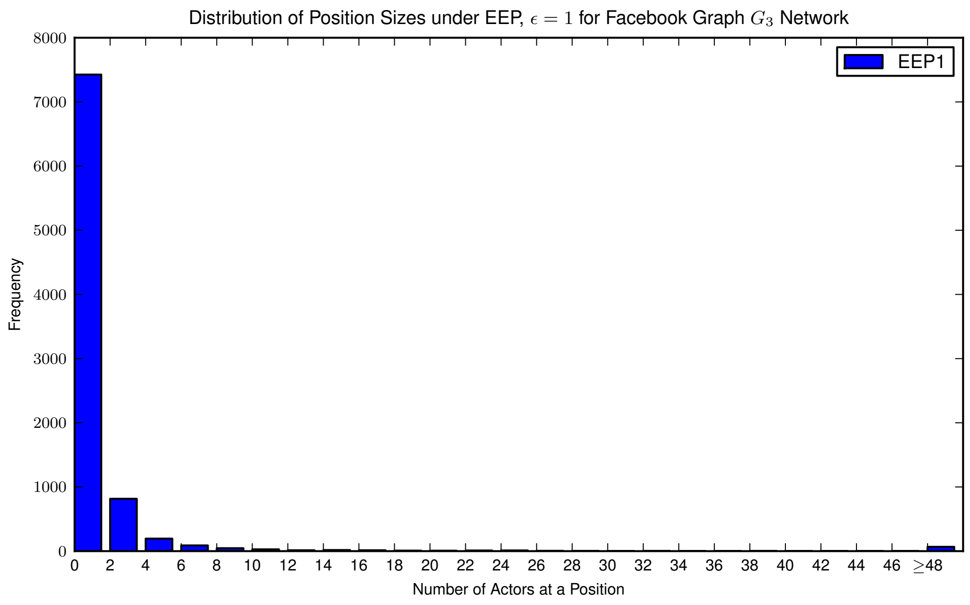


(a) Position Size Distribution for Degree Partition

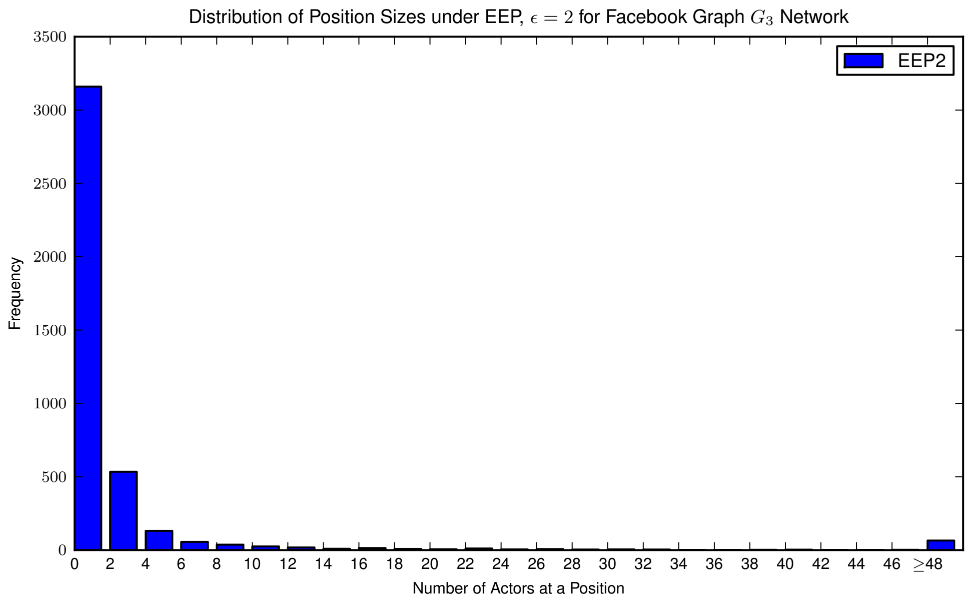


(b) Position Size Distribution for Equitable Partition

Figure 3.9: Position Size Distribution for Facebook graph G_3. (a) Degree Partition. (b) Equitable Partition. DP has problem of fewer positions having large number of nodes. On the contrary, EP has too many positions, mostly singletons.

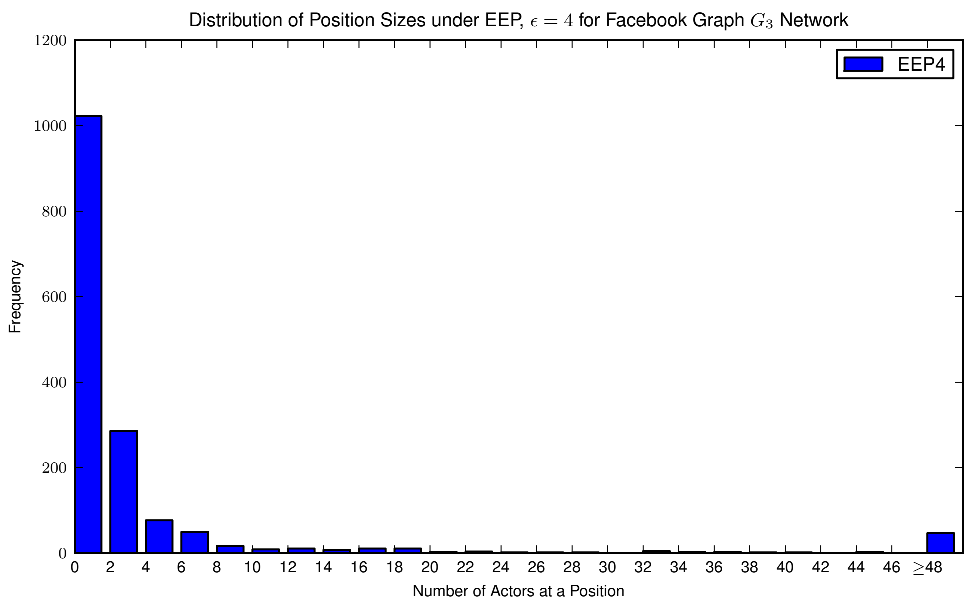


(c) Position Size Distribution for EEP, $\epsilon = 1$

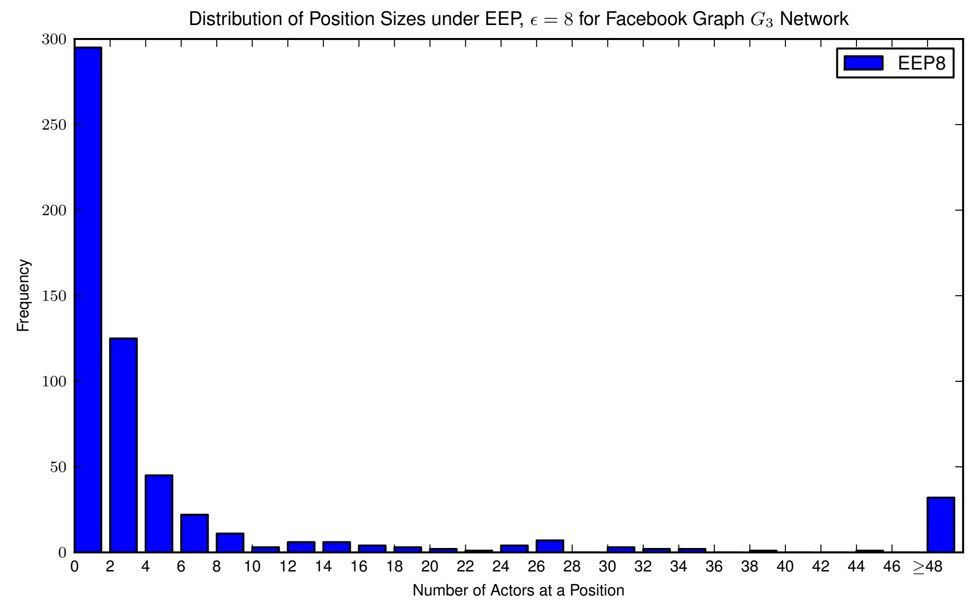


(d) Position Size Distribution for EEP, $\epsilon = 2$

Figure 3.9: Position Size Distribution for Facebook graph G_3. (c) EEP, $\epsilon = 1$. (d) EEP, $\epsilon = 2$.



(e) Position Size Distribution for EEP, $\epsilon = 4$



(f) Position Size Distribution for EEP, $\epsilon = 8$

Figure 3.9: Position Size Distribution for Facebook graph G_3. (e) EEP, $\epsilon = 4$. (f) EEP, $\epsilon = 8$. ϵ-Equitable Partition strikes a balance between fewer positions, as in case of DP and trivial positions as with EP. It gives us the ability to *tune* the number of positions by varying the ϵ according to the level of abstraction required in the study.

size for the values of $2.1 \leq \gamma \leq 2.9$. It is worth mentioning here that, for most of the real-world graphs, γ lies between 2 and 3, with few exemptions [61, 62]. We also performed curve-fitting using polynomial regression to get a complexity bound on the algorithm for $\epsilon = 5$. We get a running time bound of $O(n)$, $O(n \log n)$ and $O(n^2)$ for random power law graphs generated using $\gamma = 2.9$, 2.5 and 2.1 respectively. The results are tabulated in Table 3.4. It is worth noting that, the sum squared residual for $\gamma = 2.1$ and the curves $n \log n$ and n^2 was quiet marginal.

γ	2.9	2.5	2.1
Complexity	$O(n)$	$O(n \log n)$	$O(n^2)$

Table 3.4: Computational Aspects of the Scalable EEP Algorithm: Curve Fitting Results, $\epsilon = 5$

We also compare the running time of our *sequential* ϵEP algorithm 4 with the MapReduce based *parallel* algorithm 5 for sparse graphs. We perform the study using random power-law graphs for node sizes between $[5000, 75000]$, for the power-law exponent $\gamma = 2.9$. The results are depicted in Figure 3.10. It is evident from the graph that as the size of the input increases, the execution time of the *parallel* algorithm decreases significantly as compared to the *sequential* algorithm. For the power-law graph of 75000 nodes, we achieve a speed-up of $5X$ and $14X$ with the *parallel* algorithm for ϵ values of 2 and 4 respectively. A smaller value of ϵ in the ϵ-equitable partitioning algorithm translates to more number of iterations, thereby increasing the execution time. This implies that our *parallel* ϵEP algorithm gives us significant speed-ups over the *sequential* algorithm for large sparse graphs.

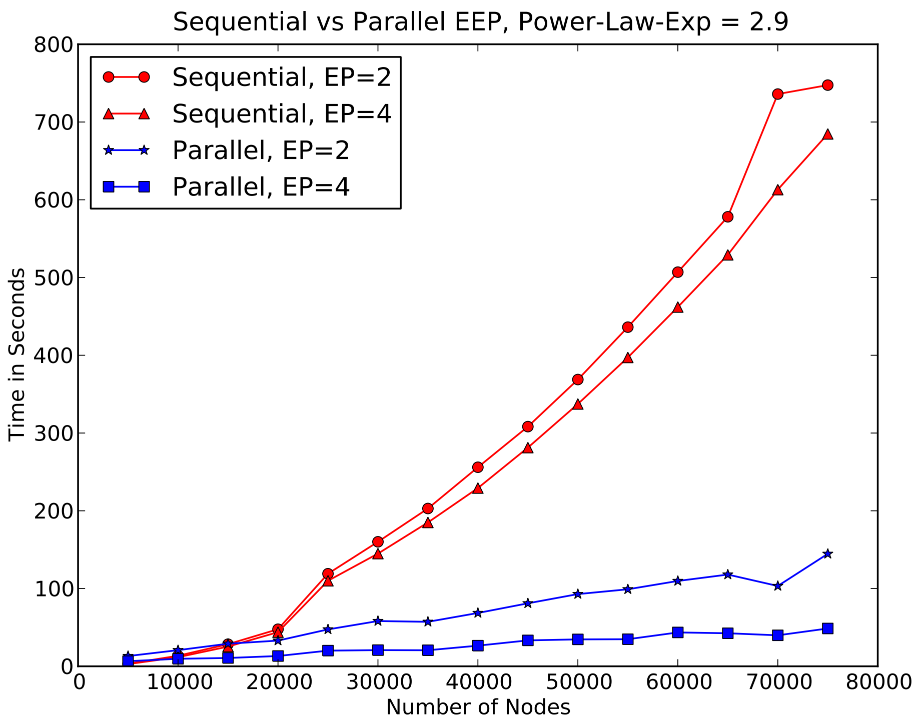


Figure 3.10: Sequential versus Parallel EEP Algorithm. Comparison of the running times for various input sizes for the Fast ϵEP Algorithm 4 versus the Parallel ϵEP Algorithm 5 for $\epsilon = 2, 4$. The exponent for random power-law graphs is $\gamma = 2.9$. The speed-up in execution time for sparse graphs using the Parallel Algorithm is evident in the plot.

3.5 Conclusions

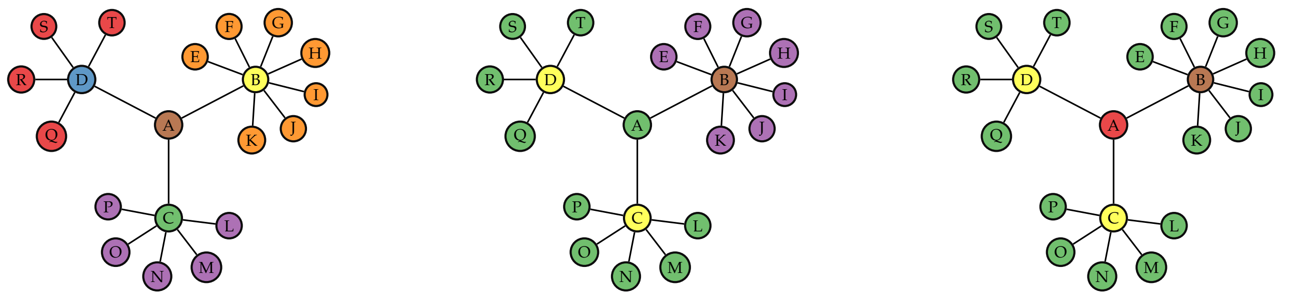
In this chapter we have presented a scalable and distributed ϵ-equitable partition algorithm. To the best of our knowledge, this is the first attempt at doing positional analysis on a large scale online social network dataset. We have been able to compute ϵEP for a significantly large component of the `Flickr` social graph using our Parallel ϵEP algorithm and its implementation. Further, the results of our algorithm on the `Facebook` and `Flickr` datasets show that ϵEP is a promising tool for analyzing the evolution of nodes in dynamic networks. Empirical scalability studies on random power law graphs show that our algorithm is highly scalable for very large *sparse* graphs.

CHAPTER 4

Discovering Positions Performing Multiple Roles: Multiple Epsilon Equitable Partitions

In the previous chapters we have seen that ϵ-equitable partitioning of a graph corresponds to intuitive positions in networks and overcomes a lot of problems associated with the traditional approaches of positional analysis. In this chapter we discuss about the fact that ϵ-equitable partitioning of a graph is not unique and multiple such partitions exist for a given graph. We exploit these multiple ϵ-equitable partitions to analyze *multiple* roles and positions. We define a new notion of equivalence based on these multiple ϵ-equitable partitions (MϵEPs) to perform positional analysis of social networks.

The rest of the chapter is organized as follows. In section 4.1 we show using an example that the ϵEP of a graph is not unique. Section 4.2 speaks about motivation behind multiple role analysis in networks. We discuss the MϵEPs algorithm and its implementation in section 4.3. In section 4.4 and 4.5, we define a new notion of equivalence using the *actor-actor similarity score* derived from these multiple ϵEPs. We present a detailed description on the evaluation methodology, ground-truth & temporal datasets used for evaluation, and qualitative & dynamic analysis of our proposed method in section 4.6.



(a) Equitable Partition (b) First 1-Equitable Partition (ϵEP-1) (c) Second 1-Equitable Partition (ϵEP-2)

Figure 4.1: (a) The TA Network under Equitable Partition is [{A},{B},{C},{D},{E-K},{L-P},{Q-T}]. (b) First 1-Equitable Partition is [{A,L-P,Q-T},{B},{C,D},{E-K}]. (c) Second 1-Equitable Partition is [{A},{B},{C,D},{E–T}]. The ϵ-equitable partition of a graph is not unique.

4.1 On Non-Uniqueness of ϵ-Equitable Partition

The evaluation of the proposed Fast ϵEP Algorithm 4 on the TA Network Chapter 3, Figure: 3.2 showed that the ϵEP of a graph is not unique. In this section, we work an example on the TA Network to get two different ϵEPs. We achieve this by starting with two different cell orderings of the *node degree vectors* (Equation 2.6) of the input equitable partition. Primarily, we *ignore* the sort by cell degrees step - *line* 1 of the Algorithm 2 and shuffle the cells of the input equitable partition (EP) randomly. The *degree vectors* (DVs) of the nodes of the input equitable partition in sorted order their of block/cell degrees for the TA Network, Figure: 4.1a, are depicted in Table 4.1.

Since the nodes $E, F, G, ..., K$ all belong to the same cell of the equitable partition of the TA Network, their DV to all the other cells of the EP are exactly the same. Same applies to the nodes $L, ..., P$ and $Q, ..., T$.

The equitable partition and the two 1-equitable partitions are shown in Figure: 4.1. For generating the first 1-equitable partition ϵEP-1, we start with the *shuffled cell order* $[\{L, ..., P\}, \{Q, ..., T\}, \{A\}, \{C\}, \{B\}, \{D\}, \{E, ..., K\}]$. We take two consecutive cells and try to merge them into a single cell if they are within $\epsilon = 1$ of each

Cell Order → **DV of Nodes ↓**	1 {E,...,K}	2 {L,...,P}	3 {Q,...,T}	4 {A}	5 {D}	6 {C}	7 {B}
$\overrightarrow{deg}(E-K)$	0	0	0	0	0	0	1
$\overrightarrow{deg}(L-P)$	0	0	0	0	0	1	0
$\overrightarrow{deg}(Q-T)$	0	0	0	0	1	0	0
$\overrightarrow{deg}(A)$	0	0	0	0	1	1	1
$\overrightarrow{deg}(D)$	0	0	4	1	0	0	0
$\overrightarrow{deg}(C)$	0	5	0	1	0	0	0
$\overrightarrow{deg}(B)$	7	0	0	1	0	0	0

Table 4.1: Node DVs of the TA Network's Equitable Partition (Figure: 4.1a) in sorted order of their cell degrees

other. For further merging, this new cell becomes the current cell and is compared with next cell for possible merger. If the merging fails, the next cell becomes the current cell. The algorithm exits if no further merging of cells is possible. Also, the degree vectors need to be updated whenever two cells are merged[*]. The cell mergers and the corresponding DVs for ϵEP-1 (Figure: 4.1b) and ϵEP-2 (Figure: 4.1b) are depicted in Table: 4.2 and Table: 4.3 respectively. The *shuffled cell order* for generating the second 1-equitable partition is $[\{E,...,K\},\{L,...,P\},\{Q,...,T\},\{C\},\{D\},$ $\{B\},\{A\}]$. At each step, the *degree vectors* of only those nodes which take part in merging, or, are possible candidates for a merge operation are shown.

[*]A detailed note on the Algorithm is given in Chapter 2, Section 2.5.3

DV of Equitable Partition before merge-

Cell Order → **DV of Nodes ↓**	1 {L,...,P}	2 {Q,...,T}	3 {A}	4 {C}	5 {D}	6 {B}	7 {E,...,K}
$\overrightarrow{deg}(L-P)$	0	0	0	1	0	0	0
$\overrightarrow{deg}(Q-T)$	0	0	0	0	1	0	0

DV of 1-Equitable Partition after first merge-

Cell Order → **DV of Nodes ↓**	1 {L,...,P,Q,...,T}	3 {A}	4 {C}	5 {D}	6 {B}	7 {E,...,K}
$\overrightarrow{deg}(L-T)$	0	0	1	1	0	0
$\overrightarrow{deg}(A)$	0	0	1	1	1	0

DV of 1-Equitable Partition after second merge-

Cell Order → **DV of Nodes ↓**	1 {L,...,T,A}	4 {C}	5 {D}	6 {B}	7 {E,...,K}
$\overrightarrow{deg}(A, L-T)$	0	6	5	1	0
$\overrightarrow{deg}(C)$	6	0	0	0	0
$\overrightarrow{deg}(D)$	5	0	0	0	0

DV of 1-Equitable Partition after third (final) merge-

Cell Order → **DV of Nodes ↓**	1 {L,...,T,A}	4 {C,D}	6 {B}	7 {E,...,K}
$\overrightarrow{deg}(C-D)$	6	0	0	0
$\overrightarrow{deg}(B)$	1	0	0	7
$\overrightarrow{deg}(E-K)$	0	0	1	0

Table 4.2: Epsilon equitable partition of a graph is **not unique**. First 1-Equitable Partition ϵEP-1 is shown in Figure 4.1b. We derive this from the shuffled starting cell order: $[\{L,...,P\},\{Q,...,T\},\{A\},\{C\},\{B\},\{D\},\{E,...,K\}]$ of the Equitable Partition depicted Figure 4.1a.

DV of Equitable Partition before merge-

Cell Order → **DV of Nodes ↓**	1 {E,...,K}	2 {L,...,P}	3 {Q,...,T}	4 {C}	5 {D}	6 {B}	7 {A}
$\overrightarrow{deg}(E-K)$	0	0	0	0	0	1	0
$\overrightarrow{deg}(L-P)$	0	0	0	1	0	0	0

DV of 1-Equitable Partition after first merge-

Cell Order → **DV of Nodes ↓**	1 {E,...,K,L,...,P}	3 {Q,...,T}	4 {C}	5 {D}	6 {B}	7 {A}
$\overrightarrow{deg}(E-P)$	0	0	1	0	1	0
$\overrightarrow{deg}(Q-T)$	0	0	0	1	0	0

DV of 1-Equitable Partition after second merge-

Cell Order → **DV of Nodes ↓**	1 {E,...,Q,...,T}	4 {C}	5 {D}	6 {B}	7 {A}
$\overrightarrow{deg}(E-T)$	0	1	1	1	0
$\overrightarrow{deg}(C)$	5	0	0	0	1
$\overrightarrow{deg}(D)$	4	0	0	0	1

DV of 1-Equitable Partition after third (final) merge-

Cell Order → **DV of Nodes ↓**	1 {E,...,T}	4 {C,D}	6 {B}	7 {A}
$\overrightarrow{deg}(C-D)$	9	0	0	2
$\overrightarrow{deg}(B)$	7	0	0	1
$\overrightarrow{deg}(A)$	0	2	1	0

Table 4.3: Epsilon equitable partition of a graph is **not unique**. Second 1-Equitable Partition ϵEP-2 is shown in Figure 4.1c. We derive this from the shuffled starting cell order: $[\{E,...,K\},\{L,...,P\},\{Q,...,T\},\{C\},\{D\},\{B\},\{A\}]$ of the Equitable Partition depicted in Figure 4.1a.

4.2 Motivation

In Chapter 2 we saw that the Classical approaches to Positional Analysis, such as Structural Equivalence, Regular equivalence, Graph Automorphisms and Equitable Partitions, are too strict in grouping actors and often lead to trivial partitioning of nodes in real world networks. An ϵ-equitable partition of the graph is a useful relaxation to the notion of structural equivalence and often corresponds to intuitive notions of roles and positions. All these methods assume a single role per actor, which may not be always true in the real world. For example, a Professor can possibly play the role of "Advisor" to students, but the role of "Colleague" to his fellow professors. An observation we made from ϵEP method in the previous section was that the initial order in which the algorithm groups actors may affect the final position of an actor. A different starting order for the algorithm may therefore allow us to analyze these "multiple" roles and positions in a better way.

This drives us to explore the fact that ϵEP of a graph is not unique and many such partitions exist. These multiple partitions give us a better bound on grouping actors and better insights into the "roles". We propose a similarity score for two actors based on their co-occurrence at a same position across multiple ϵEPs. We define a new notion of equivalence using these pairwise similarity scores to perform hierarchical clustering and identify the set of equivalent actors.

4.3 Algorithm for finding Multiple Epsilon Equitable Partitions

The implementation of our algorithm is based on the modification of Kate's [1] Algorithm 2 to find an ϵEP of a graph. The algorithm to find the multiple ϵ-equitable partitions of a graph is presented in Algorithm box 6. Input to our algorithm is (*i*) the graph, (*ii*) the *coarsest equitable partition* of graph, (*iii*) a value of ϵ and (*iv*) r - the number of ϵEPs required.

The algorithm performs a common *pre-processing* step (Algorithm 6, *lines* $1-10$) for all the r MϵEPs it returns. Pre-processing involves merging all the cells of the EP which have cell degrees between $[0, \epsilon/2]$. We derive this heuristic by combining the two observations[†] made by the author in [1]. The two observations are as follows:

- **Observation 1:** Merging the cells of an equitable partition having same degree such that it is less than ϵ does not violate the ϵ condition of an ϵ-equitable partition.
- **Observation 2:** Merging cells according to the criterion with $\epsilon = \epsilon/2$ does not violate the ϵ condition for other cells.

The pre-processing step of our Algorithm 6 differs from the pre-processing step (*lines* $2-5$) of Kate's Algorithm 2. In Algorithm 2, for each degree $i \in 0 \to \epsilon$, a new cell corresponding to the degree i merges all the cells from EP having a *cell degree* $= i$. Further, these $(\epsilon+1)$ new cells are excluded for subsequent merge operations of

[†]For details and proofs, interested readers may please refer Chapter 4, Section 4.3.4 of [1].

Algorithm 6 MϵEPs: Algorithm to find multiple ϵ-equitable partitions

Input: Graph G, its equitable partition π, r - the number of multiple ϵ-equitable partitions required

Output: r multiple ϵ-equitable partitions: $[\pi_1, \pi_2, ..., \pi_r]$

```
 1: {Pre-processing}
 2: startCell ← []                                          ▷ Initialize as empty cell
 3: for each cell ∈ $\pi$ do
 4:     degree = cellDegree(cell)                           ▷ Block/Cell degree
 5:     if ($0 \le cellDegree \le \lfloor \epsilon/2 \rfloor$) then
 6:         startCell ← startCell + nodesFrom(cell)         ▷ Append nodes from cell to startCell
 7:         $\pi \leftarrow \pi \setminus cell$                ▷ Remove cell from the equitable partition $\pi$
 8:     end if
 9: end for
10: {Pre-processing Ends}
11: maxCellDegreeInPi = MAX[cellDegree($c_i$)], $\forall i \in \{1, 2, ..., k\}$   ▷ $\forall c_i \in \pi$, $\pi = \{c_1, c_2, ..., c_k\}$. Find maximum cell degree in $\pi$
12: for each $i \in 1 \rightarrow r$ do
13:     $\pi_p \leftarrow \{startCell\}$                     ▷ Initialize partition with startCell
14:     for each currDegree ∈ (($\lfloor \epsilon/2 \rfloor + 1$) → maxCellDegreeInPi) do
15:         Permute at random, all the cells of the equitable partition $\pi$ with cell degree = currDegree to generate a shuffled cell sequence
16:         Add the shuffled cell sequence from the above step to $\pi_p$
17:     end for
18:     for each node $v_i$ of the graph do
19:         calculate the degree vector $\overrightarrow{deg}(v_i)$      ▷ Equation 2.6
20:     end for
21:     currentCell = startCell
22:     for each cell ∈ $\pi_p$ do
23:         check if cell can be merged with currentCell without violating the $\epsilon$ criterion, where $\epsilon = \epsilon/2$
24:         if true then
25:             merge it with currentCell and update the $\pi_p$ and the degree vectors
26:         else
27:             make cell as currentCell
28:             continue
29:         end if
30:     end for
31:     $\pi_i \leftarrow \pi_p$                               ▷ $i^{th}$ $\epsilon$-equitable partition
32: end for
```

the algorithm. In our Algorithm 6, we combine the above two observations. First, we create a single new *startCell* having the nodes from all the cells whose *cell degree* $i \in 0 \rightarrow \epsilon/2$. Second, we allow this cell to be a valid starting cell for subsequent merge comparisons. Since the *cell degree* of *startCell* is at most $\epsilon/2$, it follows from *Observation 2* that the *startCell* does not violate the ϵ condition for other cells in the subsequent merges. The cells which are added to the *startCell* are removed from the input EP (*line* 7, Algorithm 6). The algorithm then generates r random cell order permutations within *cell degrees* for all the remaining cells of the input EP (*lines* $12-17$, Algorithm 6). This corresponds to generating r different starting *shuffled cell order sequences* for finding multiple ϵEPs. We restrict the *shuffling* of the cells within each *cell degree* of the input EP π. We adopt this heuristic to maximize the chances of possible cell merges according to the ϵ criterion, since the likelihood of merging two cells with an equal cell degree is more than the cells with differing cell degrees. The algorithm then computes the DVs of all the nodes (*lines* $18-20$, Algorithm 6). The algorithm then tries to merge these cells by taking two consecutive cells at a time. If the degree vectors of the member nodes from these two cells are within $\epsilon/2$ distance of each other, they are merged into a single new cell. For further merging, this new cell becomes the current cell, which is then compared with the next cell for a possible merger. If the merging fails, the next cell becomes the current cell (*lines* $21-30$, Algorithm 6). Also, the degree vectors need to be updated whenever two cells are merged. If no further merging of cells is possible, the partition is returned as the i^{th} ϵ-equitable partition π_i (*line* 31, Algorithm 6). A loose bound on the running time complexity of Algorithm 6 is $O(r.n^3)$, where r is the number of ϵ-equitable partitions and n being the size of the vertex set $V \in G$. We present an efficient *parallel* implementation of the algorithm in the following subsection.

4.3.1 Implementation of the MϵEPs Algorithm 6

In the previous section we discussed that generating *multiple* ϵEPs is computationally expensive. The Multiple ϵEPs algorithm generates the permutations of the initial cells given by the equitable partition algorithm, and then computes an ϵEP for each one of these permuted cell orderings. The initial computation of *degree vectors* (Equation 2.6) of all the vertices of the input social graph is computationally intensive (*line* $18-19$, Algorithm 6). These degree vectors are also large in size.

We address the problem as follows: Given, the cell ordering $\{c_1, c_2, ...c_K\}$ of the *initial equitable partition* π_{init} of a graph G, we compute the degree vectors of the vertex-set $V \in G$ corresponding to this cell order. We persist these DVs on a hierarchical data format (HDF) file [63, 64]. HDF files are used to store and organize large amounts of numerical data, while providing efficient access, storage and platform independence capabilities. In the implementation of the Multiple ϵEPs algorithm, for each permuted cell of π_{init} (*lines* $14-17$, Algorithm 6), we maintain and persist a mapping corresponding to its original cell number in π_{init}. In other words, for each permuted cell of the current ϵEP iteration, we also maintain a mapping of its cell index in the saved HDF file. Now given, (*i*) the permuted cell ordering and (*ii*) its mapping to the initial cells of the equitable partition, each MϵEPs algorithm iteration can execute independently in **parallel**. With this, we are also able to run this in a distributed setting by simply copying the HDF file to each computing node and triggering the MϵEPs algorithm using *GNU Parallel* [54]. The following example depicts the working of shared degree vectors and a mapping of permuted cells.

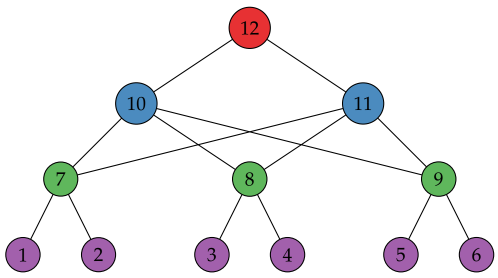


Figure 4.2: Equitable partition for an example network. Equivalent actors are coloured in same colour. We use this example to explain the implementation of MϵEPs Algorithm 6 using shared degree vectors and cell order mapping.

MϵEPs Implementation Example: The example network in Figure 4.2 depicts the equitable partition and the connections among the nodes. Equivalent actors are coloured using same colours. Let us assume the initial partition cell ordering is $\pi_{init} = \{(1,2,3,4,5,6),(7,8,9),(10,11),(12)\}$ and the permuted cell ordering is $\pi_{pert} = \{(1,2,3,4,5,6),(12),(7,8,9),(10,11)\}$. Given, π_{init} and π_{pert}, we compute the following:

1. We compute the ϵEP of π_{pert} for an $\epsilon = 3$ using its degree vectors.
2. We compute the ϵEP of π_{pert} for an $\epsilon = 3$ using the degree vectors of π_{init} and cell-to-cell mapping between π_{pert} and π_{init}.

(i) 3-equitable partition of π_{pert} from its DVs: The degree vectors of π_{pert} = $\{(1,2,3,4,5,6), (12),(7,8,9),(10,11)\}$ are depicted in Table 4.4. The subsequent cell merges for $\epsilon = 3$ are depicted in Table 4.5.

The 3-*equitable partition* using DVs of π_{pert} is:

$$\{(1,2,3,4,5,6,7,8,9,12),(10,11)\} \tag{4.1}$$

Cell Order $\rightarrow$ **DV of Nodes** $\downarrow$	$Cell_1$ $\{1,2,...,6\}$	$Cell_2$ $\{12\}$	$Cell_3$ $\{7,8,9\}$	$Cell_4$ $\{10,11\}$
$\overrightarrow{deg}(1)$	0	0	1	0
$\overrightarrow{deg}(12)$	0	0	0	2
$\overrightarrow{deg}(7)$	2	0	0	2
$\overrightarrow{deg}(10)$	0	1	3	0

Table 4.4: The cell DVs of the example network of Figure 4.2, corresponding to the cell order of π_{pert}.

(ii) 3-equitable partition of π_{pert} from DVs of π_{init} and cell mapping: The degree vectors of $\pi_{init} = \{(1,2,3,4,5,6),(7,8,9),(10,11),(12)\}$ are depicted in Table 4.6. The *cell-to-cell mapping* between the cells of π_{init} and π_{pert} is shown in Table 4.7. The subsequent cell merges for $\epsilon = 3$ are depicted in Table 4.8.

The 3-*equitable partition* using DVs of π_{init} and cell-to-cell mapping between π_{init} and π_{pert} is:

$$\{(1,2,3,4,5,6,7,8,9,12),(10,11)\} \tag{4.2}$$

The example shows that the ϵEP computed using the node DVs of the initial equitable partition cell ordering and a cell-to-cell mapping (Eq. 4.2), is **exactly same**, as the ϵEP computed using the node DVs of the permuted cell ordering (Eq. 4.1) of the input graph's equitable partition.

This implementation helped us achieve parallelism and a significant reduction in the memory footprint. Since, for generating n multiple ϵEPs, we only save n mapping files and a single instance of the node degree vectors HDF file on disk. Thus, we avoid *recomputation* and *storage* of n times the size of degree vectors of the vertex-set V.

DV after 1st Merge: $Cell_1 \leftarrow Cell_1 + Cell_2$

Cell Order $\rightarrow$ / **DV of Nodes** $\downarrow$	$Cell_1$ $\{1, 2, ..., 6\}$	$Cell_3$ $\{7, 8, 9\}$	$Cell_4$ $\{10, 11\}$
$\overrightarrow{deg}(1)$	0	1	0
$\overrightarrow{deg}(12)$	0	0	2
$\overrightarrow{deg}(7)$	2	0	2
$\overrightarrow{deg}(10)$	1	3	0

DV after 2nd Merge: $Cell_1 \leftarrow Cell_1 + Cell_3$

Cell Order $\rightarrow$ / **DV of Nodes** $\downarrow$	$Cell_1$ $\{1, 2, ..., 6\}$	$Cell_4$ $\{10, 11\}$
$\overrightarrow{deg}(1)$	1	0
$\overrightarrow{deg}(12)$	0	2
$\overrightarrow{deg}(7)$	2	2
$\overrightarrow{deg}(10)$	4	0

Table 4.5: Cell merge sequence of the example network of Figure 4.2 for $\epsilon = 3$. The cell order corresponds to that of the partition π_{pert} (Table 4.4).

Cell Order $\rightarrow$ / **DV of Nodes** $\downarrow$	$Cell_1$ $\{1, 2, ..., 6\}$	$Cell_2$ $\{7, 8, 9\}$	$Cell_3$ $\{10, 11\}$	$Cell_4$ $\{12\}$
$\overrightarrow{deg}(1)$	0	1	0	0
$\overrightarrow{deg}(7)$	2	0	2	0
$\overrightarrow{deg}(10)$	0	3	0	1
$\overrightarrow{deg}(12)$	0	0	2	0

Table 4.6: The cell DVs of the example network of Figure 4.2, corresponding to the cell order of π_{init}.

π_{init}	$Cell_1$	$Cell_2$	$Cell_3$	$Cell_4$
π_{pert}	$Cell_1$	$Cell_4$	$Cell_2$	$Cell_3$

Table 4.7: Cell-to-cell mapping between π_{init} and π_{pert} for the cell orderings of Example Network of Figure 4.2.

DV after 1st Merge: $Cell_1 \leftarrow Cell_1 + Cell_4$

Cell Order $\rightarrow$	$Cell_1$	$Cell_2$	$Cell_3$
DV of Nodes $\downarrow$	$\{1,2,...,6\}$	$\{7,8,9\}$	$\{10,11\}$
$\overrightarrow{deg}(1)$	0	1	0
$\overrightarrow{deg}(7)$	2	0	2
$\overrightarrow{deg}(10)$	1	3	0
$\overrightarrow{deg}(12)$	0	0	2

DV after 2nd Merge: $Cell_1 \leftarrow Cell_1 + Cell_2$

Cell Order $\rightarrow$	$Cell_1$	$Cell_3$
DV of Nodes $\downarrow$	$\{1,2,...,6\}$	$\{10,11\}$
$\overrightarrow{deg}(1)$	1	0
$\overrightarrow{deg}(7)$	2	2
$\overrightarrow{deg}(10)$	4	0
$\overrightarrow{deg}(12)$	0	2

Table 4.8: Cell merge sequence of the example network of Figure 4.2 for $\epsilon = 3$. The cell order corresponds to that of the partition π_{init} (Table 4.6) and each merge sequence is mapped to π_{pert} using the cell-to-cell mapping from the Table 4.7.

4.4 Actor-Actor Similarity Score

In this section we define the notion of *actor-actor similarity score*, which forms the basis for the definition of a "**Position in MϵEPs**". Given, nodes $v_i, v_j \in G$ and n multiple ϵ-equitable partitions $\{\pi_1, \pi_2, ..., \pi_n\}$ of G. We define the following definitions:

Definition 4.1. (*common cell members*) Given, nodes v_i, v_j and partition $\pi = \{c_1, c_2, ..., c_k\}$. We define a `boolean` function $cellMembers_\pi(v_i, v_j)$ on the partition π as follows:

$$cellMembers_\pi(v_i, v_j) = \begin{cases} 1, & \text{if } (v_i \in c_r \textbf{ and } v_j \in c_r), \text{ for some } c_r \in \pi. \\ 0, & \text{otherwise.} \end{cases} \tag{4.3}$$

The function $cellMembers_\pi$ returns a value of 1 (`true`), if the nodes v_i and v_j both belong to the same *cell* or *block* of the partition π.

Definition 4.2. (*actor-actor co-occurrence*) Given, two nodes v_i, v_j and the partitions $\{\pi_1, \pi_2, ..., \pi_n\}$. We define the co-occurrence function $cooc(v_i, v_j)$ as follows:

$$cooc(v_i, v_j) = \sum_{k=1}^{n} cellMembers_{\pi_k}(v_i, v_j) \tag{4.4}$$

This function essentially returns the count of the number of partitions in which the node-pair v_i, v_j occupies a same *position* in the partition.

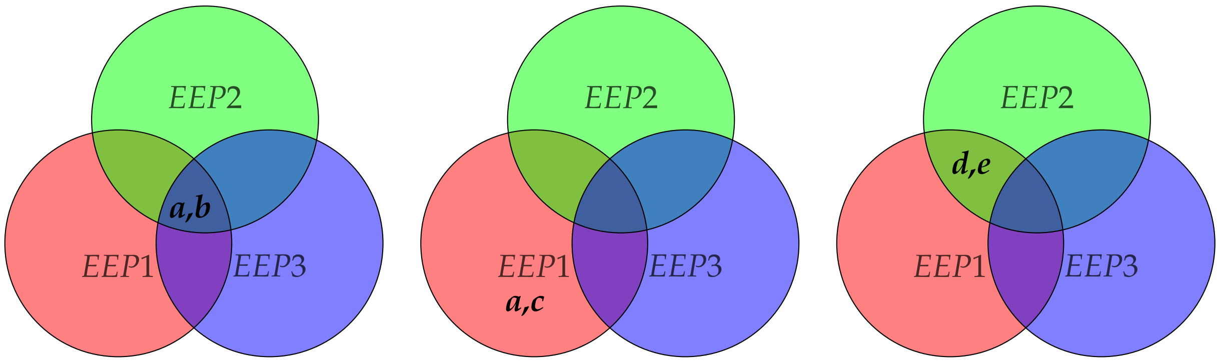


Figure 4.3: Example of Actor-Actor Similarity for three ϵ-equitable partitions using Equation 4.5. (a) $sim(a,b) = 1$. (b) $sim(a,c) = 1/3$. (c) $sim(d,e) = 2/3$.

Definition 4.3. (*actor-actor similarity and distance*) Given, a nodes $v_i, v_j \in G$ and the partitions $\{\pi_1, \pi_2, ..., \pi_n\}$. The *similarity* and *distance* between two nodes v_i and v_j is defined as:

$$sim(v_i, v_j) = \frac{cooc(v_i, v_j)}{n} \tag{4.5}$$

$$dist(v_i, v_j) = 1 - sim(v_i, v_j) \tag{4.6}$$

Thus, the *similarity* score of two actors v_i and v_i is defined as the number of ϵEPs in which both v_i and v_j occupy a same position, divided by the total number of multiple ϵ-equitable partitions generated for the graph G.

Following example illustrates the *actor-actor similarity* for three $\epsilon-$equitable partitions. The example is also depicted in the Figure 4.3.

- EEP1: {(a,b,c),(d,e),(f)}
- EEP2: {(a,b),(d,e),(c,f)}
- EEP3: {(a,b),(c,d),(e,f)}
- $sim(a,b) = 1, sim(a,c) = 1/3, sim(a,d) = 0$
- $dist(a,b) = 0, dist(a,c) = 2/3, dist(a,d) = 1$

4.5 Definition of a "Position" in Multiple ϵ-Equitable Partitions

In this section, we define the notion of a *"Position"* in MϵEPs. Before that, we define some preliminaries in the coming subsections.

4.5.1 Hierarchical Clustering

Hierarchical Clustering (HC) [65] builds a hierarchy of clusters which are used to perform cluster analysis. The strategies to perform HC fall under two categories:

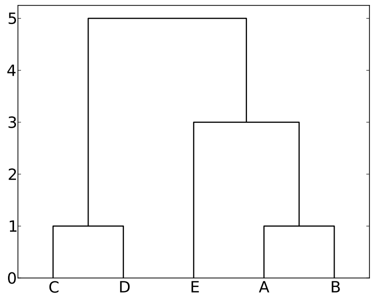
1. **Hierarchical Agglomerative Clustering**: This is a bottom-up approach at creating cluster hierarchies. Hierarchical Agglomerative Clustering (HAC) starts with each node as a singleton cluster at the outset and then successively merge/agglomerate pairs of clusters using a *linkage criterion* based on the node similarity/distance scores. The merge terminates when all clusters have been merged into a single cluster that contains all the nodes.

2. **Hierarchical Divisive Clustering**: This is a top-down approach to create cluster hierarchies. Divisive clustering starts with a single cluster containing all the nodes at the outset. It proceeds by splitting clusters recursively at each step until individual nodes are reached.

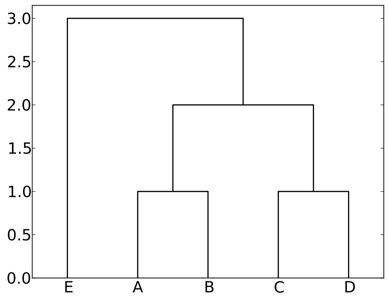
Linkage Criteria for HAC: The HAC algorithm depends on a *linkage criterion* to agglomerate a pair of clusters at each level of hierarchy. Given, the $n \times n$ distance matrix *dist* which contains the pairwise distance between each of the n node-pairs

$$\begin{array}{c|ccccc} & A & B & C & D & E \\ \hline A & 0 & 1 & 2 & 2 & 3 \\ B & 1 & 0 & 2 & 4 & 3 \\ C & 2 & 2 & 0 & 1 & 5 \\ D & 2 & 4 & 1 & 0 & 3 \\ E & 3 & 3 & 5 & 3 & 0 \end{array}$$

(a) Distance Matrix



(b) Complete-link



(c) Single-link

$$\begin{array}{c|cccc} & 1 & 2 & 3 & 4 \\ \hline 1 & [(C)] & [(D)] & 1 & [(A),(B),(C,D),(E)] \\ 2 & [(A)] & [(B)] & 1 & [(A,B),(C,D),(E)] \\ 3 & [(A,B)] & [(E)] & 3 & [(A,B,E),(C,D)] \\ 4 & [(A,B,E)] & [(C,D)] & 5 & [(A,B,C,D,E)] \end{array}$$

(d) Linkage Data Structure of (b)

Figure 4.4: Example of Linkage Criteria for HAC. (a) Shows an example distance matrix *dist* for 5 nodes. (b) Shows the dendrogram for the HAC on *dist* using Complete-link linkage. (c) Shows the dendrogram for the HAC on *dist* using Single-link linkage. (d) Linkage data structure Z of (b). Columns 1 & 2 have the clusters which would be merged, column 3 has the corresponding *combination distance*, column 4 has the corresponding clustering/partition at that level of hierarchy. Thus, each row of the linkage data structure depicts the two clusters that were merged with the corresponding combination distance.

and two clusters A and B, two commonly used *linkage criterion* are as follows:

- *Single-link* (SL): $\textsc{min}\{dist(x, y) : x \in A \text{ and } y \in B\}$
- *Complete-link* (CL): $\textsc{max}\{dist(x, y) : x \in A \text{ and } y \in B\}$

A HAC is typically visualized using a *dendrogram*. Each merge is represented by a horizontal line. The y-coordinate of the horizontal line is the *distance/similarity* of the two clusters that were merged, this is called **combination distance/similarity**. Figure 4.4 shows the dendrograms for an example distance matrix of five nodes using both *complete-link* and *single-link* linkage. In Figure 4.4(b), the actors (C, D) and (A, B) were both merged with a *combination distance* of 1.

We represent the output of the HAC as a **linkage data structure** Z. Z has $(n-1)$ rows and 4 columns, with n being the number of nodes. The columns 1 and 2 of the data structure Z contain the clusters which would be merged to form a single cluster. The third column has the value of the *combination distance* based on the *linkage criterion* that was used. The forth column has the partition/clustering at that level of hierarchy. The linkage data structure of example for complete-link linkage is depicted in Figure 4.4(d).

4.5.2 Positional Equivalence in Multiple ϵ-Equitable Partitions

The HAC performed using the *similarity* measure computed using pairwise actor-actor similarity scores (Equation 4.5) signifies **positional equivalence** in MϵEPs.

The actor *dendrogram* created from the hierarchical clustering based on the actor-actor pairwise similarity scores is a rich structure depicting the actor position merges at each level of the hierarchy. To obtain the most relevant partition, we need to find the *best level* for cutting the dendrogram tree. The algorithm to find the best clustering level from the HAC is given in Algorithm 7. Prior to that, we define the notion of mean-of-mean cell distance of a partition as follows:

Definition 4.4. (*mean-of-mean cell distance of a partition*) Given, the distance matrix *dist* and a clustering (partition) $\pi = \{c_1, c_2, ...c_m\}$. We compute the *mean-of-mean cell/block distance* of π as follows:

$$\mu(\pi) = \frac{1}{m} \sum_{i=1}^{m} \frac{1}{\binom{|c_i|}{2}} \sum_{v_j, v_k \in c_i} dist(v_j, v_k) \tag{4.7}$$

For each unique pair of vertices in a cell, we compute the mean of distances between these pairs and then we compute the mean of these means.

Algorithm 7 Best Level to Cut the Dendrogram Tree

Input: (*i*) HAC linkage data structure Z and (*ii*) threshold range $[\tau_1, \tau_2]$
Output: Clustering π of G

```
1: $d_1 = 0.0$                                   ▷ Initialize previous combination distance
2: $\mu_1 = 0.0$                                 ▷ Initialize previous mean-of-mean cell distance of $\pi$
3: $max\_slope = 0.0$                            ▷ Initialize maximize slope
4: $best\_level = 0$                             ▷ Initialize best clustering level
5: for each level in Z do                        ▷ Iterate over each row in the HAC linkage matrix Z
6:     $\pi = clusteringAt(level) = Z[level][4]$  ▷ $\pi$ is the clustering/partition at the level: level in Z
7:     $\mu_2 = \mu(\pi)$                         ▷ mean-of-mean cell distance of $\pi$, Equation 4.7
8:     $d_2 = Z[level][3]$                        ▷ the combination distance at level: level of HAC
9:     $slope = \frac{\mu_2 - \mu_1}{d_2 - d_1}$  ▷ rate-of-change of mean-of-mean cell distance w.r.t combination distance
10:    if $(\tau_1 \le \mu_2 \le \tau_2)$ and $(slope > max\_slope)$ then
11:        $max\_slope = slope$                   ▷ Update max_slope
12:        $best\_level = (level - 1)$            ▷ best_level is previous level, since there was a change of slope between the current level and previous level
13:    end if
14:    $\mu_1 = \mu_2$                            ▷ Update $\mu_1$ and $d_1$ for next iteration
15:    $d_1 = d_2$
16: end for
17: $\pi = clusteringAt(best\_level) = Z[best\_level][4]$
18: return $\pi$                                  ▷ Return the best clustering from HAC
```

Algorithm 7: Best Level to Cut the Dendrogram Tree The algorithm to find the best clustering from the dendrogram tree is given in Algorithm 7. The input to the algorithm is (*i*) HAC linkage data structure and (*ii*) threshold range $[\tau_1, \tau_2]$. The algorithm iterates over each level of the HAC linkage structure Z and evaluates the following. At each level of the hierarchy, algorithm takes the partition π corresponding to the clustering at that level of HAC. It computes the *mean-of-mean*

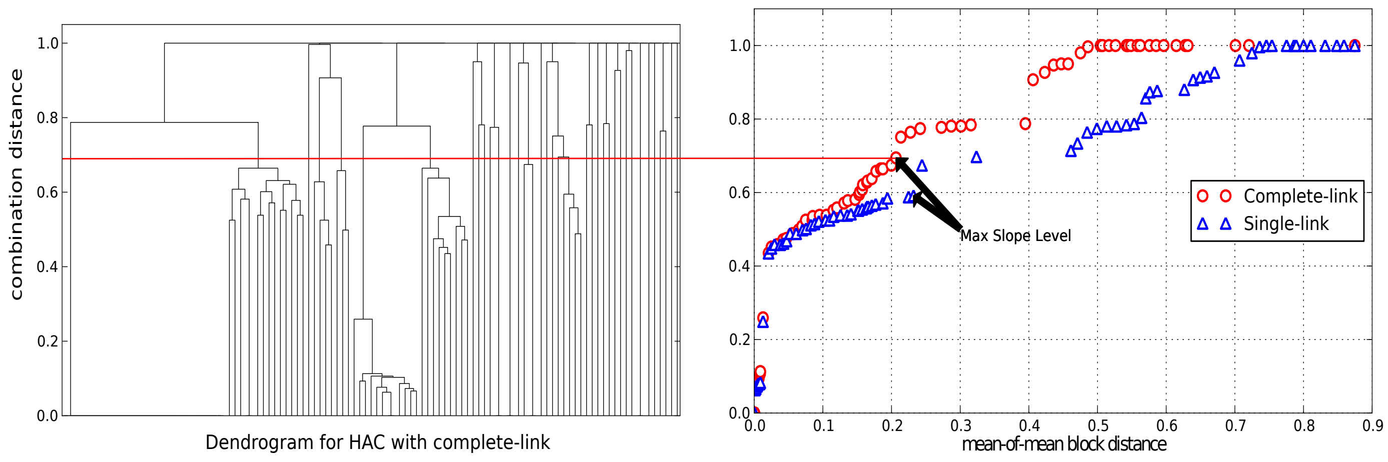


Figure 4.5: Best level to cut the dendrogram tree: An example plot showing the best cutting criteria. The dendrogram on left depicts HAC with complete-link linkage on the example network. The plot on the right depicts the graph for mean-of-mean distance vs the combination distance for both complete-link and single-link clustering. The **maximum slope** points for MϵEPs-CL and MϵEPs-SL are annotated with arrows. The red line maps the corresponding best complete-link clustering level onto the dendrogram.

block distance of the partition π using Equation 4.7 (Algorithm 7, *lines 6-7*). The algorithm then determines whether the rate-of-change of *mean-of-mean cell distance of* π, with respect to the *combination distance* is (*i*) *greater* than the previously computed *slope and* (*ii*) is within a *threshold range* $[\tau_1, \tau_2]$. The algorithm updates the *maximum slope* and the *best clustering level* seen so far accordingly (Algorithm 7, *10-13*). The algorithm returns the clustering/partition π at the level corresponding to the *best level*. The actors at each of the positions of this partition π correspond to the *best set of equivalent actors in MϵEPs*.

Significance of the Cutting Criteria

Our measure to find best clustering is purely based on the distance between the data points. The goal of a clustering algorithm is to find clusters which have high similarity among cluster members, at the same time, clusters which are well separated. To achieve this goal, at each level of the hierarchy, we compute the *mean-of-mean block distance* of the partition using Equation 4.7. We compute the *rate-of-change* of *mean-of-mean block distance*, with respect to the change in cluster *combination distance* (Section 4.5.1). The comparison of the current *slope*, with the *slope* computed for the previous level of clustering hierarchy iteratively capture the drastic changes in the *slope* as *maximum slope*. The updates to *maximum slope* also update the *best level* in the dendrogram tree seen so far. We also restrict the *threshold range* for the *mean-of-mean cell distance of partition* as $[\tau_1 = 0.15, \tau_2 = 0.35]$. Note that, from Equation 4.5 and 4.6, these thresholds correspond to a bound on mean-of-mean cell *similarity* of a partition in the range $[0.65, 0.85]$. Therefore, the *slope* and *threshold range* correspond to an objective function which finds a level in the tree having the following significance:

- The mean of "the intra-position actor-actor similarity mean" for the all the positions in the partition is at least 65%.

- Cut the dendrogram tree at a level prior to the level which has the **maximum** slope. This level corresponds to a level after which there was a drastic change in the *slope*. Hence implies that, the merge between two clusters at this level according to the *combination similarity* has resulted in a drastic change in the intra-position similarities.

The manuscripts [66, 67] discuss various measures for cluster quality analysis. Evaluation of MϵEPs on multi-role ground-truth networks shows that our method correctly discovers positions performing multiple roles.

4.6 Experimental Evaluation

The datasets used for evaluation are described in Section 4.6.1, followed by the evaluation methodology in Section 4.6.2. Finally, we present the results in Section 4.6.3.

4.6.1 Datasets used for Evaluation

Multi-Role Ground-truth Datasets:

1. Internet Movie Database Co-Cast Network The Internet Movie Database (IMDb) [68] is an online database of movies, television shows and video games. The database has the information related to the actors, production crew, release date, trivia, genre, plots etc. to name a few. We create a movie Co-Cast network as follows: The cast members are from *English* movies of "Action" *genre* between the year 2003 to 2013 form the nodes of the Co-Cast network. Using the complete IMDb database, two nodes i and j are linked with a weight w_{ij}, if they have cast together in w_{ij} movies. We discard links whose weight is less than 10, corresponding isolate nodes are also discarded. We assign a *role label vector* for each node in the Co-Cast network based on the *role(s)* they have performed while casting in movies. For example, if we have three roles: *actor, director* and *writer*; a node i has worked in 5 movies as an *actor*, 6 movies as a *director* and 2 movies as a *writer*. Therefore, the role label vector for a node i will be $\vec{r_i} = \{5, 6, 2\}$. Further, the components in the role label vector of a node having values less than 5 are considered 0. In our example, the final role label vector for node i is $\vec{r_i} = \{5, 6, 0\}$, this essentially means that we would only consider node i in roles of *actor* and *director*. The role label

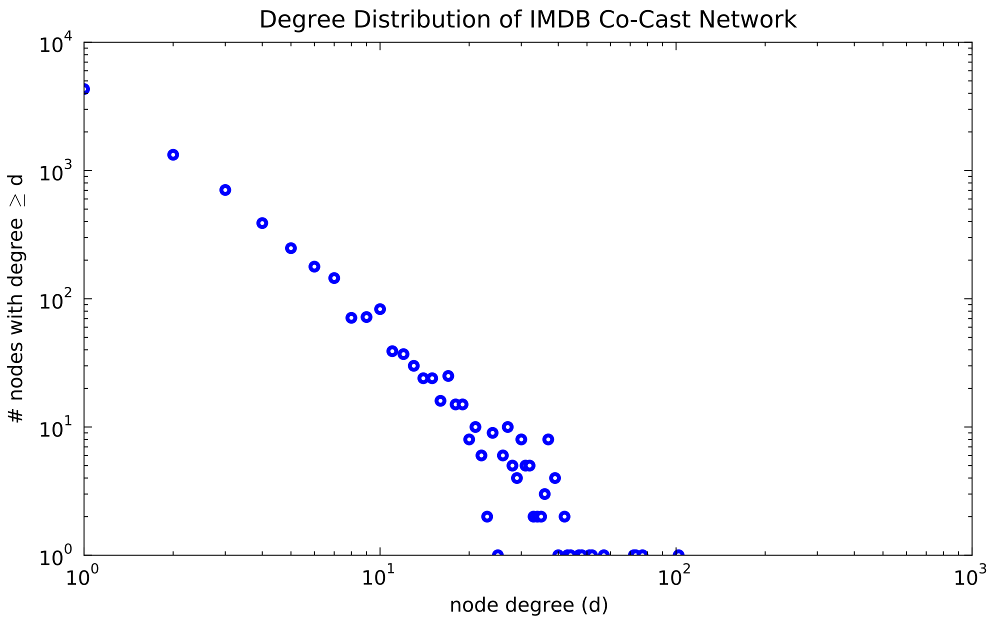


Figure 4.6: Degree distribution plot of the IMDb Co-Cast Network for English Action movies, between year 2003 to 2013.

vector corresponds to the *ground-truth roles*. Our IMDb dataset has 10 defined roles. The IMDb Co-Cast network consists of 7874 vertices and 11393 edges. The degree distribution plot of the IMDb Co-Cast Network is shown in Figure 4.6.

2. Summer School Network This is a network derived from a survey taken at a doctoral summer school [69]. The Summer School Network (SSN) is a network of attendees based on a survey questionnaire, which primarily asked them about the people they knew before and after the summer school. We use the combined network, which takes the union of links of people who knew each other (*i*) before the summer school and (*ii*) after the summer school. The network has a link from vertex A to vertex B, if person A responded to know person B. For our evaluation, we assume the links to be symmetric and hence we convert the network to an undirected graph. This graph has 73 vertices and 1138 edges. Further, for each vertex v in the network, the dataset has corresponding "roles" performed by the person. Few roles defined for a person are: *Senior Organizer, Local Organizer, Visitor, Speaker* etc., these correspond to the ground-truth roles.

Datasets used for Dynamic Analysis

1. JMLR Dataset We extracted the Co-Authorship and Co-Citation networks for the Journal of Machine Learning Research (JMLR) for the years spanning from 2001 to 2011. The dataset was extracted from Thomson Reuters Web of Science Portal [70] and processed using the Science of Science (Sci^2) toolbox [71].

We create 6 time evolving snapshots for the Co-Citation network from year 2006 to year 2011, such that, the snapshot for year 2006 network has paper co-citation data from year 2001 to year 2006. The snapshot for year 2007 network includes the data from year 2001 to year 2007 and so on for years up to 2011. Similarity, we generate 2 time evolving snapshots for the Co-Authorship network for years 2010 and 2011. Further, edges with number of co-authored or co-cited papers together with edge-weights less than 4 were pruned in the study. The dataset properties of the final network have been tabulated in Table 4.9.

Dataset	Vertices	Edges
Co-Authorship	1356	2363
Co-Citation	541	5672

Table 4.9: JMLR Dataset Properties

2. DBLP Co-Authorship Network We parsed the DBLP bibliographic database [72] to extract the author details from the conference proceedings of KDD, VLDB and ICML between year 1999 to year 2013. We generate 2 time evolving snapshots

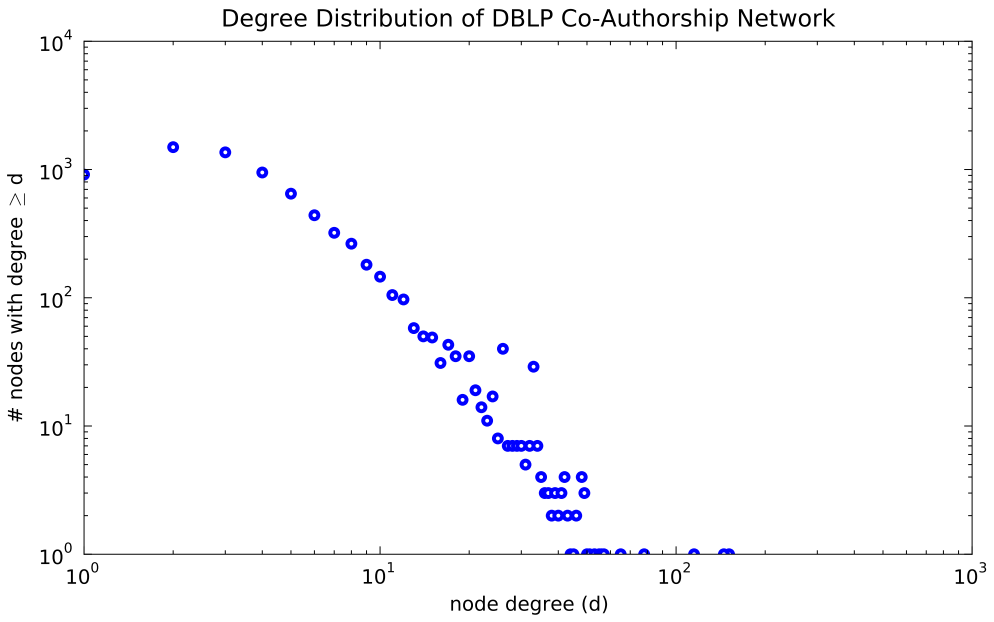


Figure 4.7: Degree distribution plot of the DBLP Co-Authorship Network from conference proceedings of KDD, VLDB and ICML, between year 1999 to 2013.

of the co-authorship network, using the same methodology as described for the JMLR dataset. The first network has all the co-authorship links between the years 1999 to 2008, the evolved network consists all the links between year 1999 to year 2013. The dataset details are tabulated in Table 4.10. The degree distribution plot of the DBLP graph G_2 is shown in Figure 4.7.

Graph	Vertices	Edges	Year Range
G_1	5103	12448	$1999 \rightarrow 2008$
G_2	7468	19929	$1999 \rightarrow 2013$

Table 4.10: DBLP Co-Authorship Network Details

4.6.2 Evaluation Methodology

Evaluation Methodology for Multi-Role Ground-Truth Networks

In multi-role networks, the actors can perform more than one *role*. To evaluate the positions performing *multiple roles*, we extend the evaluation metrics used for studying *multi-label classification*. In multi-label classification [73], each example $x_i \in X$ is associated with a set of ground-truth labels $Y \subseteq L$, with $|L| > 2$. The *multi-label classifier* H predicts a set of labels $Z_i = H(x_i)$, for each of the examples $x_i \in X$. The evaluation metrics that we use are as follows:

1. **Hamming Loss:** This was used by the authors in [74], it is defined as follows.

$$HammingLoss(H,D) = \frac{1}{|D|}\sum_{i=1}^{|D|}\frac{|Y_i \vartriangle Z_i|}{|L|} \tag{4.8}$$

   where, $|D|$ is the number of examples, $|L|$ is the number of labels, Y_i is the ground-truth label set of example x_i and Z_i is the predicted label set of x_i. $\vartriangle$ is the *symmetric difference* of two sets. *Hamming loss* evaluates how many times an example and its label pair are misclassified. Smaller the value of hamming loss, better is the performance.

2. **Precision:** This along with recall and accuracy were used by authors in [75].

$$Precision(H,D) = \frac{1}{|D|}\sum_{i=1}^{|D|}\frac{|Y_i \cap Z_i|}{|Z_i|} \tag{4.9}$$

   Precision is the fraction of the labeled examples which are correctly labeled. Bigger the value of precision, better is the performance.

3. **Recall:** Is defined as follows.

$$Recall(H, D) = \frac{1}{|D|} \sum_{i=1}^{|D|} \frac{|Y_i \cap Z_i|}{|Y_i|} \tag{4.10}$$

Recall is the fraction of the labeled examples which are relevant. Bigger value of recall is better. But getting a recall value of 1 in Equation 4.10 is trivial by labeling the predicted label set Z_i of x_i with the entire label set L. Hence recall alone is not a good measure.

4. **Accuracy:** Is defined as follows.

$$Accuracy(H, D) = \frac{1}{|D|} \sum_{i=1}^{|D|} \frac{|Y_i \cap Z_i|}{|Y_i \cup Z_i|} \tag{4.11}$$

Accuracy symmetrically measures how close the actual labels are to the predicted labels. Bigger the value of accuracy, better it is.

5. **F1 Score:** Is defined as follows.

$$F1 = \frac{2 \times precision \times recall}{precision + recall} \tag{4.12}$$

F1 score weights recall and precision equally. A good algorithm will maximize both precision and recall.

Notion of Predicted Labels for Evaluating MϵEPs Since multi-label classification is a supervised learning approach and MϵEPs is an unsupervised approach, we extend the evaluation metrics as follows. The *predicted label set* Z of a vertex u, corresponds to the union of all the ground-truth labels of the vertices which belong to the position occupied by u. This can be mathematically defined as follows. Given, a vertex $u \in c_j$, where c_j is the cell of the partition π given by our method. The predicted label Z is defined as:

$$Z = \bigcup_{v \in c_j} \{r | r \in \vec{r_v} \text{ and } r \neq 0\} \tag{4.13}$$

where, $\vec{r_v}$ is the role vector of vertex v.

We **discard** the *singletons* from the study while computing each of these evaluation metrics. We do this to avoid an evaluation bias, since the predicted label and the actual label for singletons would always be the same.

Additional Measures to Evaluate Multi-Role Networks In addition to the evaluation measures discussed above, we also use the following two measures:

1. N_p - the number of positions correctly identified performing multiple roles. Given, a position c_i and the actors $a_j \in c_i$, where $j \in 1 \rightarrow |c_i|$, $i \in 1 \rightarrow K$ and the partition $\pi = \{c_1, c_2, ..., c_K\}$ (K is the number of positions in π). Then,

$$N_p = sizeof\{\, c_i \mid \forall a_j, a_k \in c_i \implies \vec{r_{a_j}} = \vec{r_{a_k}}\} \tag{4.14}$$

where, $\vec{r_v}$ is the role label vector of vertex v.

2. N_a - the number of actors correctly identified performing multiple roles. Given, a position c_i and the actors $a_j \in c_i$, where $j \in 1 \rightarrow |c_i|$, $i \in 1 \rightarrow K$ and the partition $\pi = \{c_1, c_2, ..., c_K\}$ (K is the number of positions in π). Then,

$$N_a = \sum_{i=1}^{K} \{sizeof(c_i) \mid \forall a_j, a_k \in c_i \implies \vec{r_{a_j}} = \vec{r_{a_k}}\} \tag{4.15}$$

Evaluation Methodology for Dynamic Analysis

Since we are primarily interested in studying the effect of PA on dynamic social networks and to characterize what role PA plays in the co-evolution of nodes in the networks. We follow the same evaluation strategies as discussed in the previous Chapter 3, Section 3.4.3. In addition to the evaluation measures discussed previously, we also study the evolution of ties of actor-pairs. We discuss this in the following subsection.

Evolution of Ties/Links of Actor-Pairs We are primarily interested in finding out how the ties of actor pairs, which have common membership to a position in the network at time t, evolve over time with respect to their ties to other positions. For each pair of nodes that share a position in the time t network, we create a *difference degree vector* of their number of connections to all the other positions. For example, if node a has two connections to position p_1 and three connections to position p_2, and node b has one connection to position p_1 and four connections to position p_2, their *difference degree vector* $\vec{a} - \vec{b}$ would be $[1, -1]$. For same pair of actors, we compute their *difference degree vector* for the time $t + \delta t$ network. A natural way to compare the degree vectors of the t and $t + \delta t$ networks is using *cosine similarity*.

We pad the smaller of the two vectors with *zeros* to make its dimension equal to the other one. Cosine similarity is the normalized dot product of two vectors and is defined as follows:

$$similarity(a, b) = \cos(\theta) = \frac{a \cdot b}{||a|| * ||b||} \tag{4.16}$$

The resulting similarity ranges from -1 meaning exactly opposite, to 1 meaning exactly the same. 0 usually indicating independence, and in-between values indicating intermediate similarity or dissimilarity.

4.6.3 Results

Evaluation Results on Ground-Truth Networks

We compare the results of positions given by MϵEPs with four other positional analysis approaches, namely, *equitable partition*, *degree partition* (DP), *ϵ-equitable partition* algorithm from [7] and *stochastic blockmodel* (SBM) [69]. The notion of SBM is similar in spirit to the notion of ϵEP, in that both approaches permit a bounded deviation from perfect equivalence among actors. The primary difference between these two methods is that ϵEP determines equivalences purely from a structural equivalence aspect, where as SBM addresses the same using probabilistic models.

We use *complete-link* (CL) and *single-link* (SL) distance measures as *linkage criterion* for performing HAC in MϵEPs. The results for the IMDb ground-truth network are depicted in Table 4.11. For number of actors N_a and number of positions N_p correctly identified playing multiple roles, both MϵEPs with *CL*

Method	**Hamming Loss**	**Precision**	**Recall**	**Accuracy**	**F1**	$\mathbf{N_p}$	$\mathbf{N_a}$
EEP (ϵ = 10)	0.78	17.85	98.71	17.85	30.23	16	37
EEP (ϵ = 5)	0.71	19.28	95.56	19.28	**32.09**	22	51
Degree	0.82	15.82	**99.78**	15.82	27.32	0	0
Equitable	**0.30**	**25.22**	66.44	**25.22**	**36.57**	**27**	**58**
MEEPs-CL (ϵ = 10)	0.74	18.22	95.26	18.22	30.59	22	48
MEEPs-CL (ϵ = 5)	**0.60**	**19.58**	84.9	**19.58**	31.82	**28**	**60**
MEEPs-SL (ϵ = 10)	0.75	16.12	93.21	16.12	27.49	12	28
MEEPs-SL (ϵ = 5)	0.76	16.85	95.22	16.85	28.63	16	37
SBM	0.81	15.94	**100**	15.94	27.5	0	0

Table 4.11: Evaluation on IMDb Co-Cast Network. The best two results for each of the evaluation measures are shown in bold.

ϵ = 5 clustering and equitable partition perform better than other approaches. On the contrast, both SBM & DP perform badly and fail to predict actors and exact positions performing multiple roles. The *hamming loss* measure is best in case of EP and the performance of other methods is nowhere close to EP. This implies that most of the positions in EP performing multiple roles, have fewer incorrect roles labeled. This is primarily attributed due to the fact that the non-singleton positions in EP have fewer number of actors as compared to other methods, hence the predicted labels assigned to a position are also smaller as compared to other methods. The *precision* measure is best for EP, followed by MϵEPs with CL linkage, ϵ = 5. The ϵEP with ϵ = 5 from [7] is not far behind in performance. SBM and DP are the best performers when it comes to the *recall* measure. The high recall in these two methods is attributed due to the fewer number of final positions, 40 and 51 in SBM and DP respectively. This implies that both these methods are not suitable to perform the PA of larger networks, since they create a generalization around the actors in the network. The values of *accuracy* measure are exactly same as *precision* for all the methods, this essentially implies that the actual label set is a subset of the predicted label set. Since the *F1 score* gives equal weights to *precision* and *recall*, it gives a bias to the methods having high recall in our evaluation. This is due to the fact that all methods have high recall except for EP and MϵEPs-CL with $\epsilon = 5$ and all of them have precision values in a comparable range. From these evaluation metrics, equitable partition is a clear winner, followed by MϵEPs-CL with $\epsilon = 5$. A point worth mentioning here is that the EP of the Co-Cast Network of 7874 nodes has 1971 singleton positions, compared to 874 and 293 singletons in MϵEPs with complete-link and single-link clustering respectively for $\epsilon = 5$. Since the singleton positions don't provide any useful insights, ϵ-equitable partition based approaches are *tunable* according to the level of abstraction required in the study.

The results for the Summer School Network are tabulated in Table 4.12. We don't compare our method with equitable partition for this network since the EP for the SSN network with 73 nodes has 73 singletons. The *hamming loss* measure

Method	**Hamming Loss**	**Precision**	**Recall**	**Accuracy**	**F1**
EEP ($\epsilon = 4$)	**0.19**	47.26	90.41	47.26	62.07
EEP ($\epsilon = 8$)	0.22	48.26	97.26	48.26	64.51
MEEPs-CL ($\epsilon = 4$)	0.21	**50.66**	97.26	**50.66**	**66.62**
MEEPs-CL ($\epsilon = 8$)	0.26	44.59	**100**	44.59	61.68
MEEPs-SL ($\epsilon = 4$)	**0.19**	40.39	80.82	40.39	53.86
MEEPs-SL ($\epsilon = 8$)	0.24	46.1	98.63	46.1	62.83
SBM	0.22	47.4	**100**	47.4	64.31

Table 4.12: Evaluation on Summer School Network. The best result for each of the evaluation measures is shown in bold.

is best for MϵEPs-SL and EEP from [1] for $\epsilon = 4$. This is primarily due to the more number of positions is both these partitions, which reduces the number of incorrect role annotations to other actors at same positions. For the *precision* metric, MϵEPs-CL for $\epsilon = 4$ is a clear winner, followed closely by EEP for $\epsilon = 4$ and SBM. The *recall* is high for SBM and MϵEPs-CL with $\epsilon = 8$, since both of them have fewer positions as compared to the others. MϵEPs-CL for $\epsilon = 4$ clearly emerges as a winner for the *F1 score* measure, followed by EEP for $\epsilon = 8$. This signifies that MϵEPs-CL with $\epsilon = 4$ balances both *precision* and *recall*, which is a desirable property. Overall, MϵEPs-CL with $\epsilon = 4$ is a clear winner, followed closely by EEP with $\epsilon = 8$ and SBM.

Qualitative Analysis of Positions found using MϵEPs for the Summer School Network

We present a qualitative analysis of the roles found with MϵEPs complete-link linkage for $\epsilon = 4$ on the SSN. Figure 4.8 shows the actor-actor distance matrix of summer school network from MϵEPs-CL with $\epsilon = 4$. The 73 nodes of the distance matrix are rearranged using the HAC complete-link linkage combination distance. The red line on the dendrogram depicts the best clustering level as determined by Algorithm 7. The red squares depict the 12 non-singleton clusters found at this level of the dendrogram tree hierarchy. We interpret these clusters and show how they correspond to the different roles of people that attended the event. The interpretation of the clusters starting from the top left corner of the Figure 4.8 is as follows:

(i) The first cluster having 4 people mostly comprising "attendee" *Visitors* of the summer school, with an exception of a *Local* "attendee". All members of this cluster have moderate degrees. The dissimilarity of the *Local* with the *Visitors* is evident in the Figure 4.8, the local corresponds to the left most element in the plot.

(ii) The second cluster having 2 people who are "attendee" *Visitors*. Both have a moderately low degree.

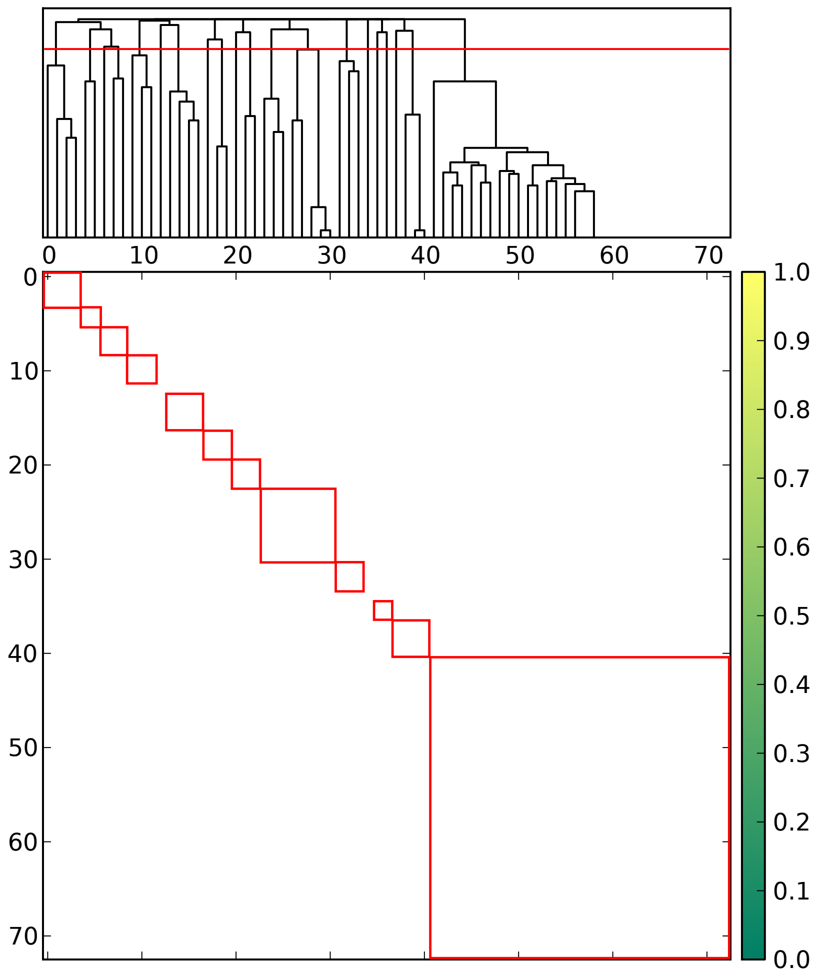


Figure 4.8: Heatmap of actor-actor distance matrix of Summer School Network from MϵEPs-CL with $\epsilon = 4$. The 73 nodes of the distance matrix are rearranged using the HAC with complete-link combination distance. The corresponding dendrogram is shown at the top of the figure. The red line on the dendrogram depicts the best clustering level as determined by Algorithm 7. The red squares depict the 12 non-singleton clusters found at this level of the dendrogram tree hierarchy. We present the qualitative analysis of these 12 positions.

(iii) The third cluster having 3 members, two "attendee" *Visitors* and one "attendee" *Local*. All members have moderate degrees. The local didn't attend all sessions actively, hence the connection pattern is more similar to visitors who responded. The local is the left most element in the plot.

(iv) The fourth cluster having 3 members, two "attendee" *Visitors* and one "attendee" *Speaker* (*i.e.*, visiting speaker). All members have moderate degree of connections.

(v) The fifth cluster having 4 members, all of them being "attendee" *Visitors*. The similarity among all the four members is visually evident in the plot.

(vi) The sixth cluster having 3 members, two of them are *Senior* "organizers" and one of them is "attendee" *Speaker*. All members have high degree of connections, consisting of people who interacted with most of the people attending the summer school.

(vii) The seventh cluster having 3 members, one *Senior* "organizer", one *Local* "organizer" and one "attendee" *Visitor*. The members have moderately high degrees. This implies that the senior organizer didn't interact as much with other people, as the other senior organizers did. The visitor interacted more as compared to other visitors of the summer school. The dissimilarity between the connection pattern of the senior organizer (left most in the cluster) is evident in the plot.

(viii) The eighth cluster having 8 people. It has a mix of people in role of *Local* "organizers" and "attendee" *Visitors*. The organizers were the "quiet" ones, *i.e.*, the people who didn't respond to the summer school survey, but interacted with most of the people. Hence they have moderate degree. The visitors in this block were the people who also have moderate degree of connections. The similarity among the locals is evident from the right most members of the cluster in the figure.

(ix) The ninth cluster having 3 people. This block has two “attendee” *Visitors* and one “attendee” *Speaker*. All of them were non-respondents.

(x) The tenth block having 2 people. These are the moderate degree organizers similar to the seventh cluster, one of them being *Senior* and the other one being *Local*. Dissimilarity in their role pattern is evident from the plot.

(xi) The eleventh cluster having 4 people. These are the *Local* “organizers” with an exception of a *Senior* “organizer”. They have moderately high degree of connections. The senior organizer has relatively less connections than other people in the same role.

(xii) The twelfth block having 29 low degree nodes. This block has a mix of roles, but predominantly having *Visitors* or *Speakers* who didn’t interact with other people. This block also has 2 *Senior Organizers* who were also *Speakers*.

In the *stochastic blockmodel* [69] of the SSN, the authors identified 7 blocks. We get a partition similarity score of 80% between the positions of this SBM and the positions identified by our approach (MϵEPs-CL, $\epsilon = 4$). We get more blocks primarily because, an *epsilon* value of 4 doesn’t combine blocks having moderately-low and moderate degrees. Same applies for blocks having high degrees and moderately-high degrees. The advantage with MϵEPs is that, we can tune *epsilon* to achieve granularity as required in the analysis.

Results of Dynamic Analysis

Results of Partition Similarity Score We perform the dynamic analysis as discussed in the previous sections on the JMLR Co-Authorship & Co-Citation networks and DBLP Co-Authorship network.

The tables from Table 4.13 to Table 4.18 tabulate the *partition similarity score* (Chapter 3, Equation 3.1) for each of the JMLR Co-citation network from year 2006 to 2011, for varying values of $\epsilon = 2, 4, 6$ found using MϵEPs with complete-link and single-link clustering. The source network at time t is depicted in the row of the table. The column corresponds to the evolved network at time $t + \delta t$. MϵEPs with single-link linkage consistently performs better than complete-link linkage. Partitioning with higher values of ϵ correspond to higher partition similarity scores, as evident from Tables 4.13, 4.14. This attributed due to fewer number of positions, which increases the likelihood of overlap amongst positions. Partitioning with a small value of $\epsilon = 2$ as depicted in Tables 4.17, 4.18 gives partition similarity of at least 65% for networks separated by an year. We also get a partition overlap of ˜50% even when the networks are separated by 5 years, as evident from Table 4.18. A smaller ϵ corresponds to more number of positions in the partition, hence we get less number of overlapping positions. In summary, MϵEPs is a useful approach for studying evolution of positions across time, we got a partition similarity as high as 96% for the Co-Citation network separated by an year in time.

The comparison of various techniques of positional analysis for the partition similarity score is depicted in Figure 4.9. The figure shows the partition similarity score of year 2006 co-citation network with networks from years 2007 $\rightarrow$ 2011. MϵEPs-SL is a clear winner followed closely by SBM [69], MϵEPs-CL and ϵEP [1].

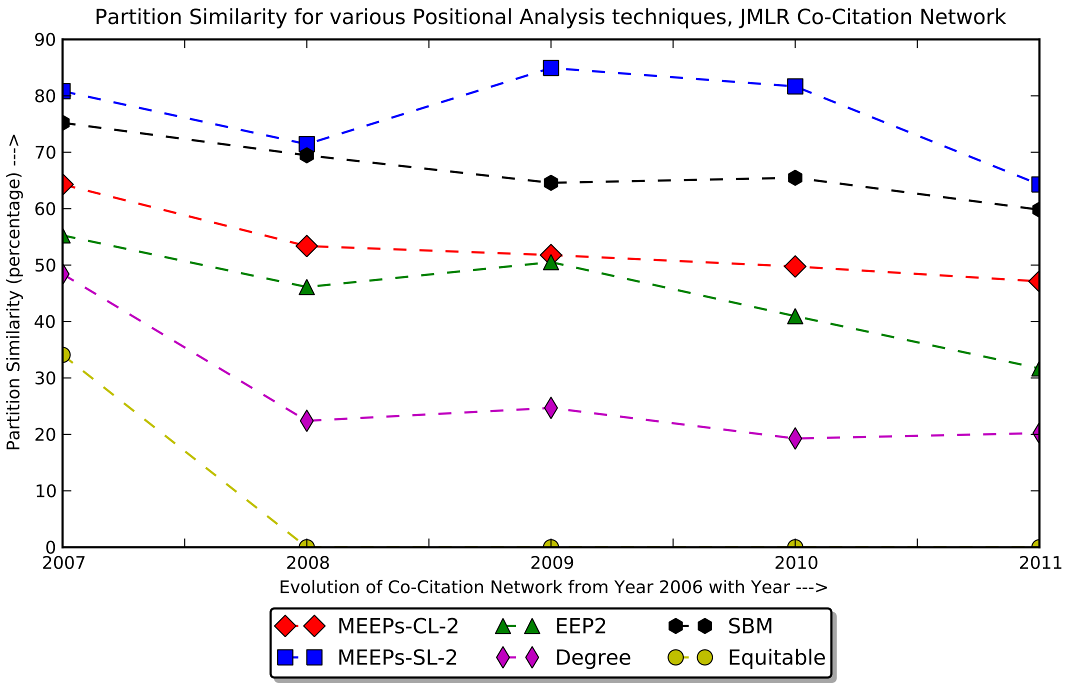


Figure 4.9: Comparison of Partition Similarity Score for JMLR Co-Citation Network using various Positional Analysis methods. Source network is year 2006 Co-Citation network, compared with networks from years 2007 → 2011.

DP and EP perform badly as the number of years start increasing, with EP having 0% partition overlap after year 2007.

Source Network	2007	2008	2009	2010	2011
2006	92.27	87.17	84.86	84.46	88.09
2007		93.31	90.8	88.13	91.75
2008			93.1	90.39	92.47
2009				92.7	91.29
2010					94.48

Table 4.13: Evolution of a JMLR-CoCitation Network with MEEPs SL Epsilon=6

Source Network	2007	2008	2009	2010	2011
2006	77.48	68.78	65.7	67.24	62.27
2007		78.52	74.4	73.24	69.65
2008			80.61	78.52	75.46
2009				82.33	76.64
2010					83.34

Table 4.14: Evolution of a JMLR-CoCitation Network with MEEPs CL Epsilon=6

Source Network	2007	2008	2009	2010	2011
2006	76.75	78.93	88.48	87.21	73.19
2007		85.93	91.68	91.13	79.86
2008			95.7	95.56	92.76
2009				97.61	95.54
2010					96.32

Table 4.15: Evolution of a JMLR-CoCitation Network with MEEPs SL Epsilon=4

Source Network	2007	2008	2009	2010	2011
2006	74.48	66.97	69.58	71.75	61.51
2007		71.44	68.72	71.37	66.15
2008			77.08	70.93	68.38
2009				77.32	75
2010					79.9

Table 4.16: Evolution of a JMLR-CoCitation Network with MEEPs CL Epsilon=4

Source Network	2007	2008	2009	2010	2011
2006	80.82	71.43	84.93	81.67	64.29
2007		86.77	90.78	87.23	77.45
2008			93.45	90.14	85.31
2009				96.7	87.41
2010					89.82

Table 4.17: Evolution of a JMLR-CoCitation Network with MEEPs SL Epsilon=2

Source Network	2007	2008	2009	2010	2011
2006	64.29	53.37	51.78	49.75	47.12
2007		68.18	59.57	53.13	57.94
2008			73.64	65.5	64.43
2009				74.42	69.63
2010					77.95

Table 4.18: Evolution of a JMLR-CoCitation Network with MEEPs CL Epsilon=2

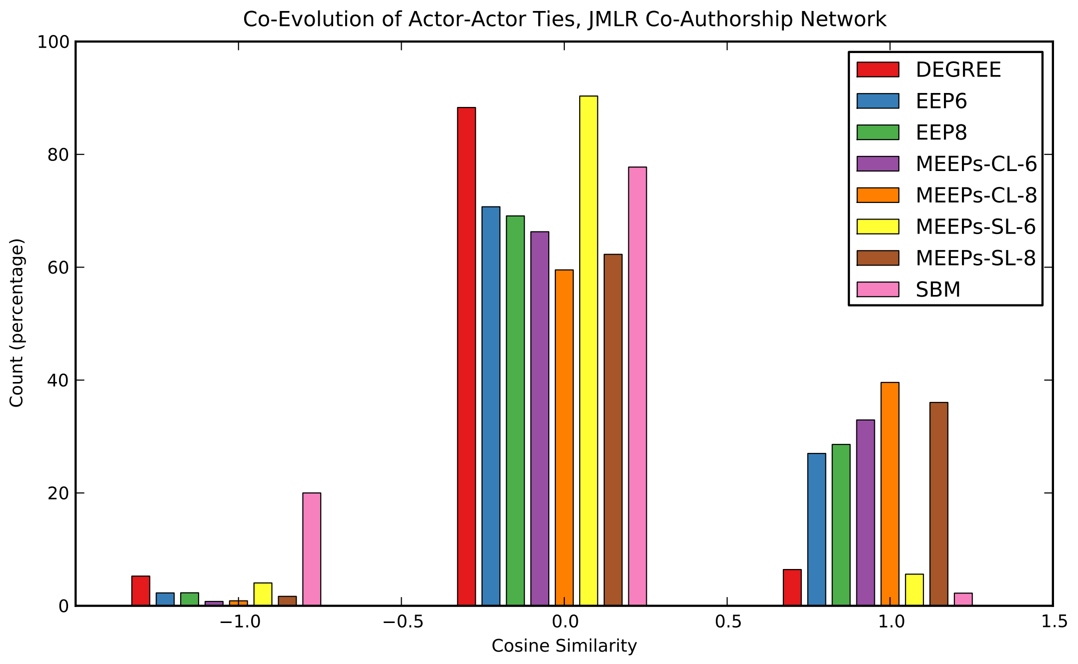


Figure 4.10: Co-Evolution of Actor-Actor Ties for JMLR Co-Authorship Network from year 2010 to 2011. Cosine similarity value close to 1 signifies high degree of similarity.

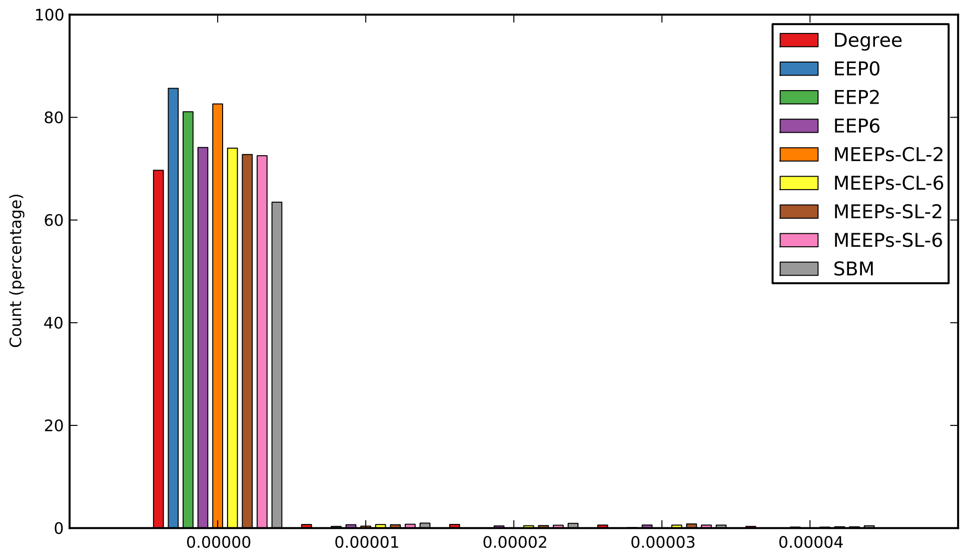
Results of Evolution of Actor-Actor Ties

The results of actor-actor *tie evolution* are depicted in Figure 4.10. The plot shows the percentage of Co-evolving Actors versus their Cosine Similarity between the actor-actor difference degree vectors from time t to $t + \delta t$ as discussed in Section 4.6.2. Cosine similarity value close to 1 signifies high degree of similarity. We compare MϵEPs CL and SL with degree partition, SBM [69] and the ϵ-equitable partitioning from [1] for $\epsilon = 6$ and $\epsilon = 8$. Equitable partition of the network doesn't appear in the study since all components of the *difference degree vector* of the time t network are *zero*. This happens because actor-actor pairs which occupy same position in EP, have exactly same number of links to all the other positions. Hence, their difference DV is 0 and therefore, the *cosine similarity* (Eq. 4.16) for tie-evolution vectors under equitable partition is undefined.

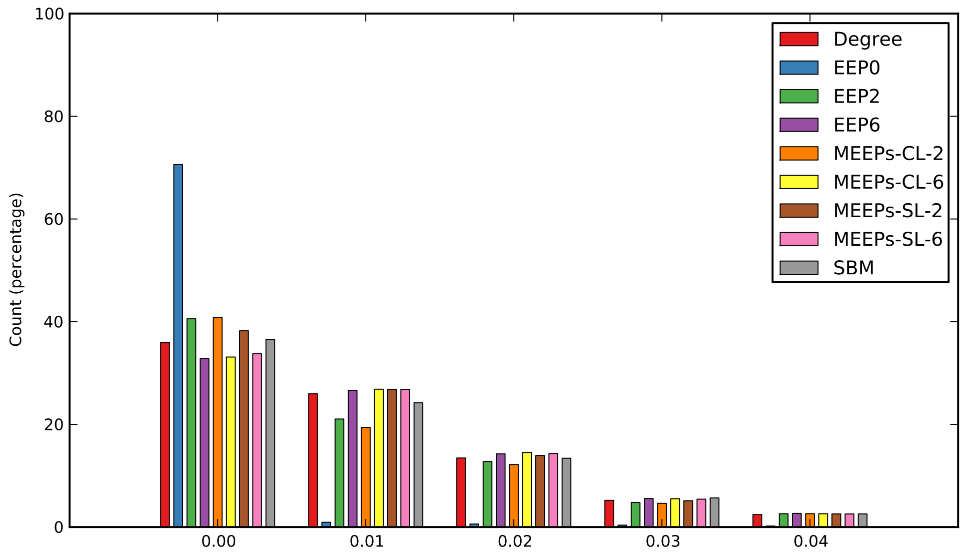
As evident from Figure 4.10, close to 40% actor-pairs follow their interaction patterns with same set of positions in the evolved network in MϵEPs. This signifies that a good number of actor-pairs, who add new collaboration links with time, mostly add them to similar social positions. The co-evolving actor-actor pairs found using ϵ-equitable partition based approaches show tie evolution properties. On the other hand, the co-evolving actors found using DP and SBM have tie evolution difference degree vectors either independent or dissimilar to each other as evident from the plot. To conclude, MϵEPs performed better than all the other methods and successfully captured the co-evolution of node ties/links to other positions. The significance of tie evolution characteristics of our method can be easily used in link recommendation systems.

Results on Study of Network Centric properties for Co-Evolving Actor Pairs

We study the evolution of various *graph theoretic network centric properties* for co-evolving actor-pairs of the DBLP Co-Authorship network. The evaluation methodology is same as discussed in Chapter 3, Section 3.4.3. Figure 4.11 shows the results. The *x-axis* corresponds to the bins containing the difference of a network centric property. The *y-axis* corresponds to the frequency of node pairs that belong to a particular bin, as a percentage of the total number of node pairs that occupy the same position in the partition. EP outperforms all the other methods, followed closely by MϵEPs-CL clustering for $\epsilon = 2$. SBM is the worst performer of all the methods for betweenness centrality and number of triangles (Figure 4.11 (a) and (c)). The percentage counts of the closeness centrality (Figure 4.11 (b)) are more spread out across initial few bins. This implies that there is more variation in

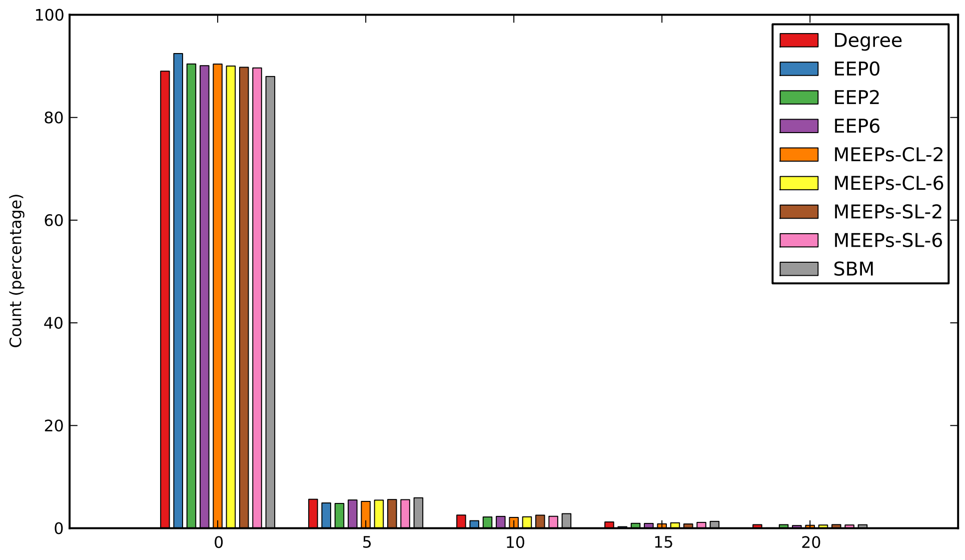


(a) Difference of Betweenness Centrality



(b) Difference of Closeness Centrality

Figure 4.11: Co-evolving node pairs for DBLP Co-Authorship graph from year 2008 $\rightarrow$ 2013. (a) Difference of Betweenness Centrality. (b) Difference of Closeness Centrality.

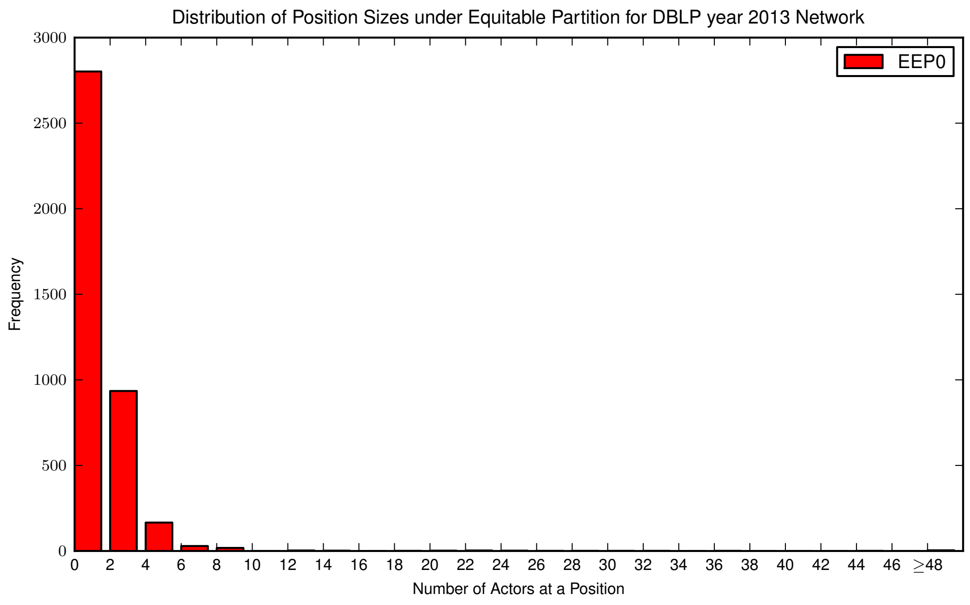


(c) Difference of Triangles

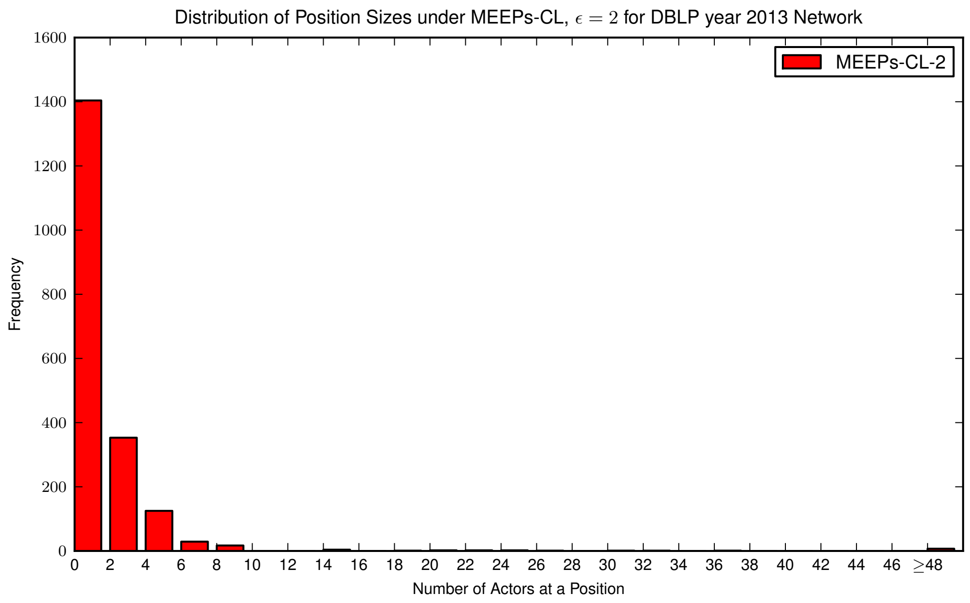
Figure 4.11: Co-evolving node pairs for DBLP Co-Authorship graph from year 2008 $\rightarrow$ 2013. (c) Difference of Triangles. A low value of difference signifies that for a co-evolving node pair (a, b) at time t, the network centric property of node a and b at time $t + \delta t$ have also evolved similarly.

the values of closeness centrality for actor-pairs in the evolved network. The ϵEP based approaches with lower values of ϵ perform better due to their closeness to equitable partition.

Though EP performs the best, they have many singleton positions. On the other hand, SBM and DP have too few positions, most of them having large number of nodes. The distribution of *position sizes* and their respective counts for each of these methods is shown in Figure 4.12. Epsilon equitable partition based approaches maintain a balance between these two extremes, by having a fairly balanced distribution of non-singleton positions. The number of non-trivial positions increase for higher values ϵ, though for very large values of ϵ, the distribution would be similar to that of DP or SBM. Therefore, MϵEPs is a consistent performer, both from the perspective of actor co-evolution characteristics and number of positions it gives.

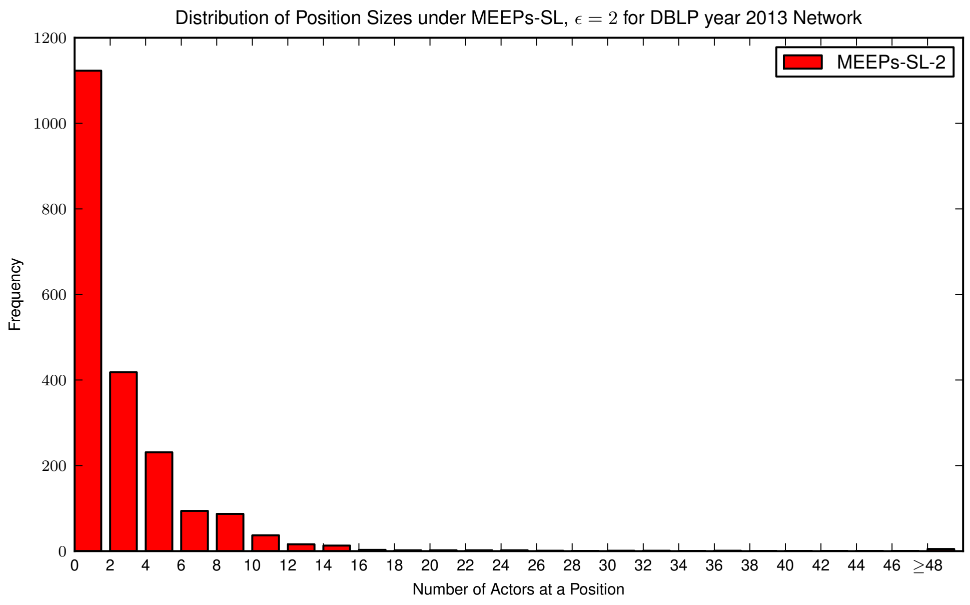


(a) Position Size Distribution for Equitable Partition

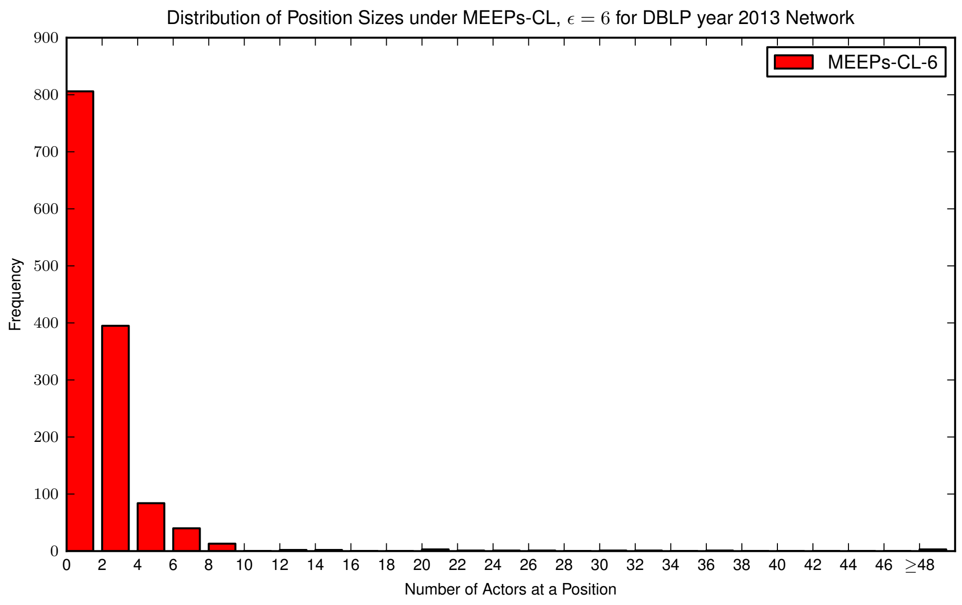


(b) Position Size Distribution for MϵEPs-CL, $\epsilon = 2$

Figure 4.12: Position Size Distribution for DBLP Co-Authorship graph for year 2013. (a) Equitable Partition. (b) MϵEPs complete-link, $\epsilon = 2$. EP mostly gives trivial positions. The number of non-singleton positions given by MϵEPs for $\epsilon = 2$ is quite less.

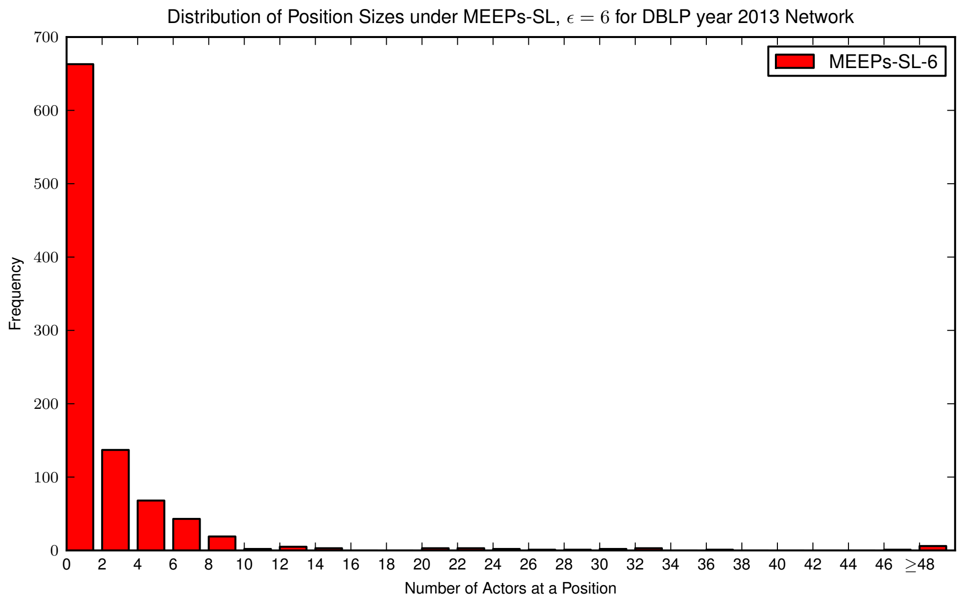


(c) Position Size Distribution for MϵEPs-SL, ϵ = 2

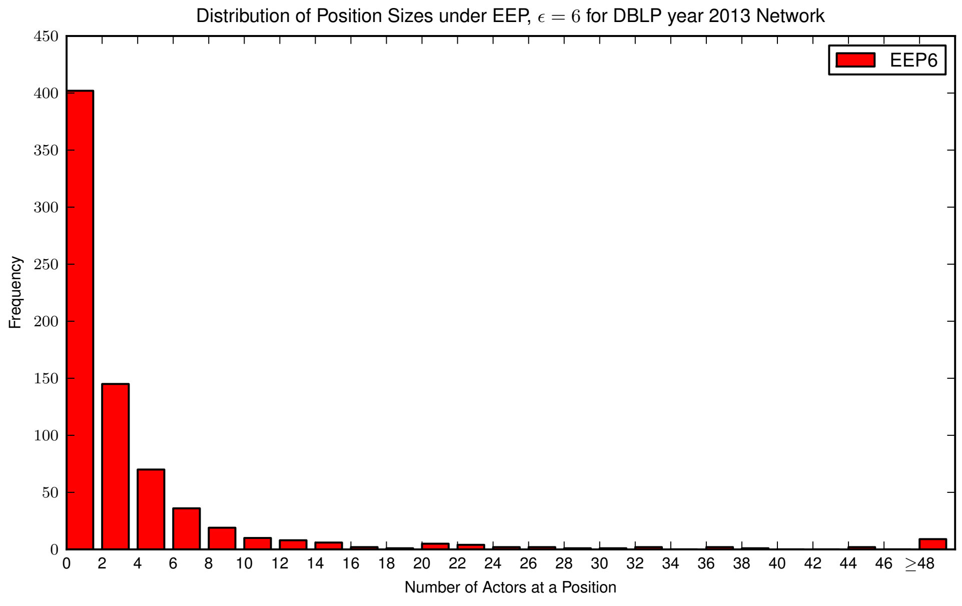


(d) Position Size Distribution for MϵEPs-CL, ϵ = 6

Figure 4.12: Position Size Distribution for DBLP Co-Authorship graph for year 2013. (c) MϵEPs single-link, ϵ = 2. (d) MϵEPs complete-link, ϵ = 6.

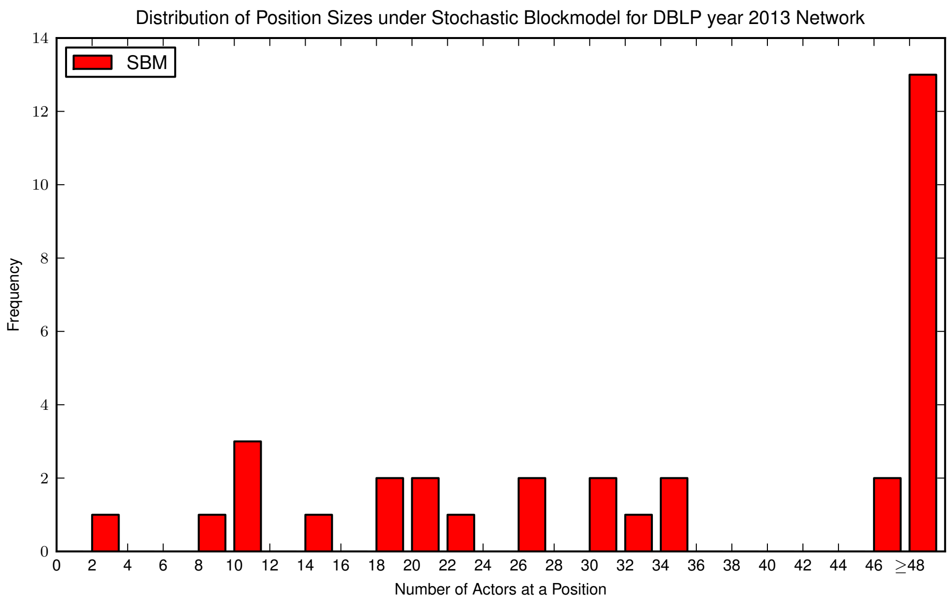


(e) Position Size Distribution for MϵEPs-SL, ϵ = 6

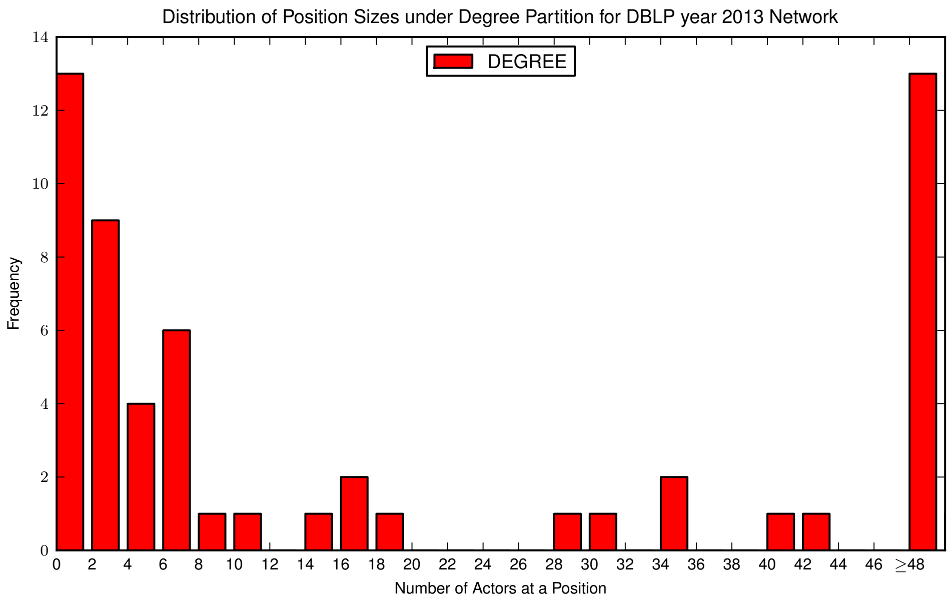


(f) Position Size Distribution for ϵ-Equitable Partition

Figure 4.12: Position Size Distribution for DBLP Co-Authorship graph for year 2013. (e) MϵEPs single-link, ϵ = 6. (f) EEP, ϵ = 6. Increasing the *epsilon* value, reduces the number of non-trivial positions that we get using MϵEPs, there is also a gradual increase in positions having lot of nodes, as evident from the last bin.



(g) Position Size Distribution for Stochastic Blockmodel



(h) Position Size Distribution for Degree Partition

Figure 4.12: Position Size Distribution for DBLP Co-Authorship graph for year 2013. (g) Stochastic Blockmodel. (h) Degree Partition. SBM and DP give us too few positions, both having positions with large number of nodes. On the other hand, MϵEPs gives us the ability to *tune* the number of positions by varying the ϵ according to the level of abstraction required in the study.

4.7 Conclusions and Discussion

We proposed a new notion of equivalence for discovering positions performing multiple roles from a structural equivalence approach. The in-depth evaluation of our proposed approach on real world ground-truth networks shows promising results. Further, the results of our approach show that MϵEPs is a promising tool for studying the evolution of nodes and their ties in dynamic networks.

Discussion MϵEPs closely resembles *mixed membership stochastic blockmodels* (MMSB) [45] in spirit. In both these methods, an actor is allowed to occupy *multiple positions* while allowing a bounded deviation from perfect equivalence. The primary difference between these two methods is that our notion determines equivalences purely from a structural equivalence aspect, where as MMSB address the same using probabilistic models.

The authors in [76] propose the notion of *Role eXtraction (RolX)*. *RolX* automatically determines the underlying roles in a network based on its structural features. *RolX* is closely related to our work; the assignment of a node to roles is mixed-membership. The authors demonstrate the advantage of their role discovery approach in various mining tasks including transfer learning and finding structural similarity.

CHAPTER 5

Conclusion and Future Work

5.1 Conclusions

In this thesis, we proposed ϵ-equitable partition based approaches (*i*) for scalable positional analysis, and (*ii*) for discovering positions performing multiple roles. We summarize our work as follows:

1. To the best of our knowledge, this is the first attempt at doing positional analysis on a large scale online social network dataset. We have been able to compute ϵEP for a significantly large component of the `Flickr` social graph using our Parallel ϵEP Algorithm.

2. We proposed a new notion of equivalence for discovering positions performing multiple roles from a structural equivalence approach. The evaluation of our proposed MϵEPs approach on real world multi-role ground truth networks show promising results.

3. The results of both our proposed approaches show that ϵEP and MϵEPs are promising tools for studying the evolution of nodes and their ties in time evolving networks.

We also presented **efficient implementation** for both the proposed methods. The summary is as follows:

1. For the scalable ϵ-equitable partition algorithm we implemented a Lightweight MapReduce framework using open source tools, which gave us *millisecond* guarantees across *iterative* MapReduce steps. Further, this implementation exploits *data locality* by intelligently *partitioning* the graph data across computing nodes.

2. For the multiple ϵ-equitable partitions algorithm, we achieved *parallelism* in computing these multiple ϵEPs by using a common shared instance of *vertex degree vectors* of the graph and cell mapping files. This implementation significantly reduced (*i*) the memory footprint, due to use of shared objects and (*ii*) execution time, since re-computation of degree vectors was no longer needed for the computation of the next ϵ-equitable partition.

5.2 Future Scope of Work

5.2.1 Structural Partitioning of Weighted Graphs

The definition ϵ-equitable partition applies to undirected simple graphs. Since real world networks can be directed, weighted, and multi-relational, it would be interesting to extend our definition to these classes of graphs.

The notion of *edge-weight* in a social network graph can be used to represent the *strength* of social tie between two people. For example, an edge connecting user a and user b may carry more weight than the edge connecting user a and user c, since

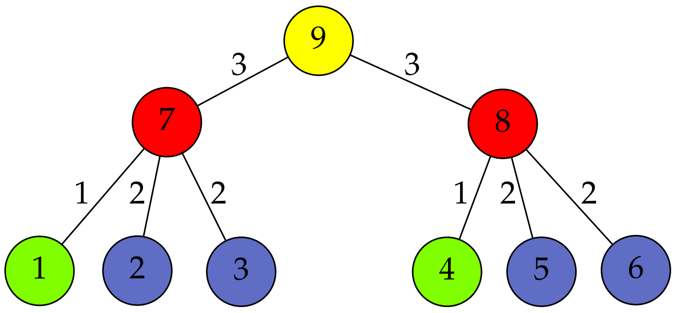


Figure 5.1: Example edge-weighted graph. The corresponding *weighted equitable partition* is [{1,4},{2,3,5,6},{7,8},{9}]

a and b interact daily on a social network as opposed to one or two interactions a month for the latter case. In this section, we present research directions on the notion of *equitable partition* and ϵ*-equitable partition* for **weighted graphs**. We define them as follows:

Definition 5.1. *(weighted equitable partition)* A partition $\pi = \{c_1, c_2, ..., c_n\}$ on *edge-weighted* graph $G \equiv \langle V, E \rangle$, where V is the vertex set and E is the edge set is said to be *weighted equitable* if,

$$\text{for all } 1 \leq i, j \leq n,\ strength(u, c_j) = strength(v, c_j) \text{ for all } u, v \in c_i \tag{5.1}$$

where,

$$strength(v_i, c_j) = \{\Sigma w(v_i, v_k) \mid (v_i, v_k) \in E \text{ and } v_k \in c_j\} \tag{5.2}$$

where, $w(v_i, v_k)$ denotes the edge-weight of the edge $(v_i, v_k) \in E$. The term $strength(v_i, c_j)$ denotes the sum of edge-weights of vertices in cell c_j adjacent to the vertex v_i. Here, cell c_j denotes a position and therefore $strength(v_i, c_j)$ means the *strength* actor v_i has to the position c_j. Example *weighted equitable partition* is shown in Figure 5.1.

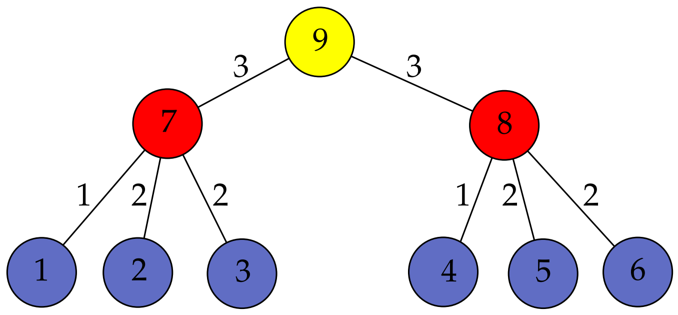


Figure 5.2: Example edge-weighted graph. The corresponding *weighted ϵ-equitable partition* is [{1,2,3,4,5,6},{7,8},{9}]

Definition 5.2. *(weighted ϵ-equitable partition)* A partition $\pi = \{c_1, c_2, ..., c_n\}$ on *edge-weighted* graph $G \equiv \langle V, E \rangle$, where V is the vertex set and E is the edge set is said to be *weighted ϵ-equitable* if,

$$\text{for all } 1 \leq i, j \leq n,\ |strength(u, c_j) - strength(v, c_j)| \ \leq\ \epsilon, \text{ for all } u, v \in c_i \tag{5.3}$$

The above definition proposes a relaxation to the strict partitioning condition of weighted equitable partition, an error of ϵ in the number of connections of an actor is allowed for it to be equivalent to an actor at another position.

Computation of Weighted Equitable and Weighted ϵ-Equitable Partition: We compute these notions by modifying the EP Algorithm 1 and ϵEP Algorithm 4 respectively. We change the way in which the SPLIT procedure "*splits*" the partition for each iteration. This is achieved by changing the function f, Equation 2.3. The modified function f is defined as follows:

$$\begin{aligned} &f : V \rightarrow \mathcal{N} \\ &f(u) = strength(u, c_a),\ \forall u \in V \end{aligned} \tag{5.4}$$

The function f, maps every vertex $u \in V$ to its *strength* (Equation 5.2) to a subset $c_a \subseteq V$ of the vertex set. c_a is the vertex set of the current *active* cell of the partition

π. Few preliminary experimental results on the weighted ϵ-equitable partition (WϵEP) on the JMLR Co-Citation Network are presented in Tables 5.1 and 5.2. The number of times two papers are *co-cited* together represents the *edge-weight*. The WϵEP gives a partition similarity score of as high as 91% for the co-citation network an year apart (Table 5.2). An interesting observation from WϵEP is that, higher ϵ value doesn't necessarily increase the partition similarity score. This implies that, the relaxation of ϵ in *strength* of a node to other positions has an effect of altering node's position in time evolved graph. Inferring the meaning of change in node positions and its qualitative comparison to the positions given by other positional analysis techniques is beyond the purview of this thesis. We intend to study the notion of weighted ϵ-equitable partitioning in more depth and on different datasets.

Method	**2008**	**2009**	**2010**	**2011**
MϵEPs-CL-2	68.17	59.57	53.12	57.94
MϵEPs-SL-2	86.77	90.77	87.22	77.45
WϵEP-2	64.28	57.14	40.00	41.67
WϵEP-6	62.62	48.88	43.21	43.75

Table 5.1: Comparison of Weighted ϵ-Equitable Partition with MϵEPs using the Partition Similarity score (Equation 3.1) for the JMLR Co-Citation Network of year 2007, with years from 2008 $\rightarrow$ 2011.

Method	**WϵEP-1**	**WϵEP-2**	**WϵEP-6**
Partition Similarity	91.17	87.5	75.52

Method	**MϵEPs-SL-2**	**MϵEPs-CL-2**	**MϵEPs-SL-6**	**MϵEPs-CL-6**
Partition Similarity	89.82	77.95	94.48	83.34

Table 5.2: Comparison of Weighted ϵ-Equitable Partition with MϵEPs using the Partition Similarity score (Equation 3.1) for the JMLR Co-Citation Network of year 2010 with year 2011.

5.2.2 Scalable Equitable Partitioning

In future, it would be interesting to explore the implied advantage of our Parallel ϵEP Algorithm to find the *coarsest equitable partition* of very large graphs for an $\epsilon = 0$. Finding the equitable partition of a graph forms an important intermediate stage in all the practical graph automorphism finding softwares [38, 39]. Another possible research direction is to explore algorithms for positional analysis of very large graphs using vertex-centric computation paradigms such as Pregel and GraphChi [77, 78].

APPENDIX A

Partition Similarity Score

In this appendix, we give a detailed note on the partition similarity score (Equation 3.1). We have used this as an evaluation measure to compare two partitions.

A.1 Mathematical Preliminaries

This section briefs out few mathematical preliminaries, which form the basis for our partition similarity score.

Given, graph G ≡ ⟨V, E⟩, V is the vertex set, E is the edge set and $\pi = \{c_1, c_2, ..., c_K\}$ is a partition of V. We define the following for any two partitions of a graph G ≡ ⟨V, E⟩:

(i) Two *partitions* π_1 and π_2 are **equal**, *iff* they both partition the vertex set V of G exactly in the same way of each other.

Example,

$$let,\ \pi_1 = \{\{v_1, v_2, v_3, v_4\}, \{v_5, v_6\}, \{v_7\}, \{v_8, v_9, v_{10}\}\}$$

$$\pi_2 = \{\{v_6, v_5\}, \{v_3, v_2, v_4, v_1\}, \{v_9, v_8, v_{10}\}, \{v_7\}\}.$$

$$then,\ \pi_1 = \pi_2$$

i.e. the order of cells in partition and the order of vertices inside a cell is not important.

(ii) We define the **intersection** of two *partitions* π_1 and π_2, as a partition containing the cells obtained from the *set intersection* operator applied *cell-wise* to member cells of π_{ϵ_1} and π_{ϵ_2} (discarding the *empty* sets).

Example,

$$let,\ \pi_1 = \{\{v_1, v_2, v_3\}, \{v_4, v_5\}, \{v_6, v_7, v_8\}\} \text{ and}$$

$$\pi_2 = \{\{v_1, v_2\}, \{v_3, v_4, v_5\}, \{v_6, v_7\}, \{v_8\}\}.$$

$$then,\ \pi_1 \cap \pi_2 = \{\{v_1, v_2\}, \{v_3\}, \{v_4, v_5\}, \{v_6, v_7\}, \{v_8\}\}$$

(iii) Two *partitions* π_1 and π_2 are **dissimilar**, *iff* their intersection leads to a *discrete* partition. A discrete partition is a one with only *singleton* cells.

Example,

$$let,\ \pi_1 = \{\{v_1, v_2, v_3\}, \{v_4, v_5\}\} \text{ and}$$

$$\pi_2 = \{\{v_1, v_4\}, \{v_3, v_5\}, \{v_2\}\}.$$

$$then,\ \pi_1 \cap \pi_2 = \{\{v_1\}, \{v_2\}, \{v_3\}, \{v_4\}, \{v_5\}\}$$

Here, $\pi_1 \cap \pi_2$ gives a *discrete* partition.

A.2 Simplified Representation of the Partition Similarity Score

Equation 3.1 can be represented in a simplified form as follows:

$$
\begin{aligned}
sim(\pi_1, \pi_2) \\
&= \frac{1}{2}\left[\left(\frac{N - |\pi_1 \cap \pi_2|}{N - |\pi_1|}\right) + \left(\frac{N - |\pi_1 \cap \pi_2|}{N - |\pi_2|}\right)\right] \\
&= \frac{1}{2}\left(1 - \frac{|\pi_1 \cap \pi_2|}{N}\right)\left[\left(\frac{1}{1 - \frac{|\pi_1|}{N}}\right) + \left(\frac{1}{1 - \frac{|\pi_2|}{N}}\right)\right] \\
&= \frac{1}{2}C(\pi_1 \cap \pi_2)\left[\frac{1}{C(\pi_1)} + \frac{1}{C(\pi_2)}\right] \\
&= \frac{C(\pi_1 \cap \pi_2)}{H(C(\pi_1), C(\pi_2))}
\end{aligned}
\tag{A.1}
$$

where,

$C(\pi) = \left(1 - \frac{|\pi|}{N}\right)$,

$|\pi|$ = cardinality of π,

N = cardinality of the *discrete* partition of π,

$H(x, y)$ = *harmonic mean* of x and y.

The authors in [79] survey and compare several notions of distance indices between partitions on the same set, which are available in the literature.

A.3 MapReduce Algorithm to Compute the Partition Similarity Score

The partition similarity score of Equation 3.1 requires the cardinality of the intersection set of the two partitions π_1 and π_2. Finding the intersection of two partitions as per the definition of *intersection* from (*ii*), Appendix A.1 is $O(n^2)$ operation, where n being the total number of vertices in the partition. Computing this for very large graphs becomes intractable. To counter this problem, we provide an algorithm based on the MapReduce paradigm [10] to compute the size of the *intersection set* of π_1 and π_2 (*i.e.*, $|\pi_1 \cap \pi_2|$). The algorithm is presented in Algorithm box 8. The algorithm initializes by *enumerating* the indices of π_2 for each cell index of partition π_1. For each key from this tuple, the MAP operation checks if these two cells *intersect* or not. The MAP emits a *value* of 1 corresponding to a constant *key*. The REDUCE operations computes the *sum* of these individual 1*s*. This *sum* corresponds to $|\pi_1 \cap \pi_2|$, which is used to compute the partition similarity score from Equation 3.1.

A note on Algorithm 8: The INITIALIZE method of Algorithm 8 (*line* 3), primarily involves replicating/enumerating the cell indices of π_2 to all the cell indices of π_1. Since *cross* operations are computationally very costly, the tractability of the Algorithm is inherently dependant on ability to generate the *cross product* set of the cell index tuples of the two input partitions.

Algorithm 8 MapReduce Partitions Intersection Set Cardinality

Input: Partitions π_1 and π_2. Let π_1={$cell_1$:[v_1, v_2], $cell_2$:[v_3, v_4, v_5], ..., $cell_K$:[v_{n-2}, v_{n-1}, v_n]} **and** π_2={$cell_1$:[v_1, v_2, v_3], $cell_2$:[v_4, v_5], ..., $cell_L$:[v_{n-1}, v_n]}
Output: Partitions intersection set cardinality $|\pi_1 \cap \pi_2|$

```
1: class Mapper
2:   tupleList enumCells=[ ]

3:   method initialize()
4:     for each cell_index i of $\pi_1$ (i.e. $1 \rightarrow K$) enumerate the cell_index j of $\pi_2$ (i.e. $1 \rightarrow L$) do
5:       add tuple(i, j) them to enumCells

6:   method map(id t, tuple (i, j))
7:     intersect ← {$\pi_1(i) \cap \pi_2(j)$}                          ▷ Appendix A.1, (ii)
8:     if intersect $\neq \phi$ then
9:       emit(id intersect, 1)          ▷ If the two cells have a overlap, emit value 1 corresponding to a constant key "intersect"
```

```
1: class Reducer
2:   method reduce(id key, values)
3:     sum = 0
4:     for value in values
5:       sum = sum + value
6:     emit(key, sum)                                              ▷ $|\pi_1 \cap \pi_2|$
```

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LIST OF PAPERS BASED ON THESIS

1. Gupte, P.V., Ravindran, B., "Multiple Epsilon Equitable Partitions - Roles and Positional Analysis for Real World Networks," *At the XXXII Meeting of the International Network for Social Network Analysis, Redondo Beach, USA, March 2012. (SUNBELT 2012).*

2. Gupte, P.V., Ravindran, B., "Scalable Positional Analysis for Studying Evolution of Nodes in Networks," *In SIAM Data Mining 2014 Workshop on Mining Networks and Graphs: A Big Data Analytic Challenge, Philadelphia, USA, April 2014. (SDM MNG 2014).*

3. Gupte, P.V., Ravindran, B., "Discovering Multiple Roles in Social Networks," *Under Preparation*.