# Robust Ensemble Clustering Using Probability Trajectories

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Abstract—Although many successful ensemble clustering approaches have been developed in recent years, there are still two limitations to most of the existing approaches. First, they mostly overlook the issue of uncertain links, which may mislead the overall consensus process. Second, they generally lack the ability to incorporate global information to refine the local links. To address these two limitations, in this paper, we propose a novel ensemble clustering approach based on sparse graph representation and probability trajectory analysis. In particular, we present the elite neighbor selection strategy to identify the uncertain links by locally adaptive thresholds and build a sparse graph with a small number of probably reliable links. We argue that a small number of probably reliable links can lead to significantly better consensus results than using all graph links regardless of their reliability. The random walk process driven by a new transition probability matrix is utilized to explore the global information in the graph. We derive a novel and dense similarity measure from the sparse graph by analyzing the probability trajectories of the random walkers, based on which two consensus functions are further proposed. Experimental results on multiple real-world datasets demonstrate the effectiveness and efficiency of our approach. The MATLAB source code of this work is available at: https://www.researchgate.net/publication/284259332.

Index Terms—Ensemble clustering, consensus clustering, uncertain links, random walk, probability trajectory

### 1 INTRODUCTION

The ensemble clustering technique has recently been drawing increasing attention due to its ability to combine multiple clusterings to achieve a probably better and more robust clustering [1], [2], [3], [4], [5], [6], [7], [8]. Despite the fact that many ensemble clustering approaches have been developed in recent years, there are still two limitations to most of the existing approaches.

First, the existing approaches mostly overlook the problem of uncertain links (or unreliable links) in the ensemble, which may mislead the overall consensus process. In the general formulation of the ensemble clustering problem [1], [4], [6], [7], we have no access to the original data features, as only the different types of relational information are available. The most basic relational information are the links between objects which reflect how objects are grouped in the same cluster or different clusters in the ensemble [1]. Based on the object-object links, coarser grains of links can be defined, e.g., the links between objects and clusters, the links between clusters, the links between base clusterings, etc. The links of one type or different types can be further

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used to form the similarity matrix [1], [3], [4], construct the graph model [9], [10], [11], or define the optimization problem [2], [12], [13].

A link between two data objects denotes that they appear in the same cluster in one or more base clusterings. The links between objects are typically represented by the coassociation (CA) matrix [1], [3], [14]. In the similarity graph induced by the CA matrix, each node corresponds to a data object and the weight of each link corresponds to an entry in the CA matrix. However, previous approaches generally overlook the different reliability of the links (or the entries in the CA matrix) and may suffer from the collective influence of the unreliable links. As an example, we construct an ensemble of 10 base clusterings for the MNIST dataset (see Section 5.2 for more details). Figure 1 illustrates the distribution of the link weights in the similarity graph induced by the CA matrix, and Table 1 shows the percentages of the links with different weights that make correct decisions. Note that a "link" with zero-weight does not count as a link here. If there is a link between objects  $x_i$  and  $x_j$  in the graph AND  $x_i$  and  $x_j$  are in the same class in the groundtruth, then we say the link between  $x_i$  and  $x_j$  makes a correct decision. As shown in Table 1, the links with greater weights are much more likely to make correct decisions and generally more reliable than the small-weight links. But unfortunately, the small-weight links, which are probably unreliable (or uncertain), make up the majority of the graph links (see Fig. 1). As pointed out in [7], when the number of the uncertain links is large, the collective influence of them may mislead the ensemble clustering process or even lead to deteriorative clustering results. It remains an open problem how to effectively and efficiently deal with the uncertain links (or probably unreliable links) and thereby enhance the robustness and accuracy of the consensus results.

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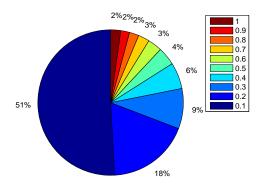


Fig. 1. The distribution of the link weights for the similarity graph induced by the CA matrix for the MNIST dataset

TABLE 1
The distribution of the links with different weights and the proportion of them making correct decisions for the MNIST dataset

Weight	#Links with the weight #All (non-zero) Links	$\left  \begin{array}{c} \underline{\# Links \ with \ the \ weight \ that \ make \ correct \ decisions}} \\ \underline{\# Links \ with \ the \ weight} \end{array} \right $
1	2%	83%
0.9	2%	73%
0.8	2%	65%
0.7	3%	58%
0.6	3%	50%
0.5	4%	43%
0.4	6%	35%
0.3	9%	27%
0.2	18%	18%
0.1	51%	9%

Second, the existing ensemble clustering approaches mostly lack the ability to utilize global structure information to refine the local links. In the classical evidence accumulation clustering [1] and some of its extensions [3], [14], the CA matrix reflects the local (or *direct*) relationship, i.e., the co-occurrence relationship, between objects, yet generally neglects the *indirect* relationship inherent in the ensemble. Let  $x_i$  and  $x_j$  be two nodes in the graph. If there is a (nonzero) link between  $x_i$  and  $x_j$ , then we say that there is a *direct* relationship between them. If there exist  $\xi$  nodes (with  $\xi \geq 1$ ), say,  $x'_1, \dots, x'_{\xi}$ , such that there are links between  $x_i$ and  $x'_1$ , between  $x'_{\xi}$  and  $x_i$ , and between  $x'_k$  and  $x'_{k+1}$  for any  $1 \le k < \xi$ , then  $x_i$  and  $x_j$  are indirectly connected by the  $\xi$  nodes. Here we say there is a  $\xi$ -step *indirect* relationship between  $x_i$  and  $x_j$ . We refer to the entirety of the direct relationships and the different steps of indirect relationships as the *global structure information*. Three sample graphs are illustrated in Fig. 2(a), Fig. 2(b), and Fig. 2(c), respectively. Although the direct link weights between  $x_1$ and  $x_2$  and between  $x_2$  and  $x_3$  remain unchanged across the three sample graphs in Fig. 2, the global structures of the three graphs are very different. The local links may be affected by the noise and the inherent complexity of the realworld datasets, while the global structure information is more robust to the potential local errors and can provide an alternative way to explore the relationship between objects. As pointed out in [4], the relationship between objects lies not only in the direct connections, but also in the indirect connections. The key problem here is how to exploit the global structure information in the ensemble effectively and

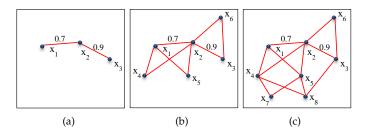


Fig. 2. How are the relationships between  $x_1$  and  $x_2$  and between  $x_2$  and  $x_3$  in the context of (a) a graph with three nodes, (b) a graph with six nodes, and (c) a graph with eight nodes?

efficiently and thereby improve the final clustering results.

Aiming to tackle the aforementioned two limitations, in this paper, we propose an ensemble clustering approach based on sparse graph representation and probability trajectory analysis.

We introduce the concept of microclusters as a compact representation for the ensemble data, which is able to greatly reduce the problem size and facilitate the computation. To deal with the uncertain links, we propose a k-nearestneighbor-like strategy termed elite neighbor selection (ENS) to identify the uncertain links and build a sparse graph termed K-elite neighbor graph (K-ENG) that preserves only a small number of probably reliable links. Two microclusters are elite neighbors if the link between them has a large weight (see Definition 6). We argue that the use of a small number of probably reliable links is capable of reflecting the overall structure of the graph and may lead to much better and more robust clustering results than using all graph links without considering their reliability. According to our experimental analysis, we find that only preserving several percent or even less than one percent of the links via the ENS strategy can result in significant improvements to the final consensus results compared to using all links in the original graph.

Having constructed the K-ENG graph, we proceed to exploit the global structure information to refine local links by means of random walks. The random walk technique has proved to be a powerful tool for finding community structures (or cluster structures) in the field of community discovery [15], [16], [17], [18]. The random walks are performed on the sparse graph K-ENG and each node in K-ENG is treated as a start node for a random walker. We propose a new transition probability matrix that simultaneously considers the link weights and the node sizes. By analyzing the probability trajectories of the random walkers starting from different initial nodes, we derive a novel and dense similarity measure termed probability trajectory based similarity (PTS) from the sparse graph. The PTS explores the pair-wise relationships by capturing the global structure information in the sparse graph via random walk trajectories. Based on PTS, two consensus functions are further proposed, namely, probability trajectory accumulation (PTA) and probability trajectory based graph partitioning (PTGP).

The overall process of our approach is illustrated in Fig. 3. Given the ensemble of base clusterings, we first map the data objects to a set of microclusters and compute the microcluster based co-association (MCA) matrix. With each

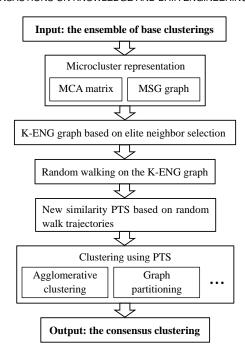


Fig. 3. Flow diagram of the proposed approach.

microcluster treated as a node, we construct the microcluster similarity graph (MSG) according to the MCA matrix. Then, the ENS strategy is performed on the MSG and the sparse graph K-ENG is constructed by preserving a small number of probably reliable links. The random walks are conducted on the K-ENG graph and the PTS similarity is obtained by comparing random walk trajectories. Having computed the new similarity matrix, any pair-wise similarity based clustering methods can be used to achieve the consensus clustering. Typically, we propose two novel consensus functions, termed PTA and PTGP, respectively. Note that PTA is based on agglomerative clustering, while PTGP is based on graph partitioning. Figure 4 summarizes the average performances (over nine real-world datasets) of the proposed PTA and PTGP methods and four existing methods, i.e., MCLA [9], GP-MGLA [19], EAC [1], and WEAC [19], with varying ensemble sizes. Each method is run 20 times on each dataset and their average NMI scores are shown in Fig. 4. By dealing with the uncertain links and the global structure information, the proposed PTA and PTGP methods exhibit a significant advantage in clustering robustness (to various datasets and ensemble sizes) over the baseline methods. Please see Section 5 for more extensive details of our experimental evaluation.

The main contributions of our approach are summarized as follows:

 Our approach addresses the issue of uncertain links in an effective and efficient manner. We propose to identify the uncertain links by the ENS strategy and build a sparse graph with a small number of probably reliable links. Our empirical study shows the advantage of using only a small number of probably reliable links rather than all graph links regardless of their reliability.

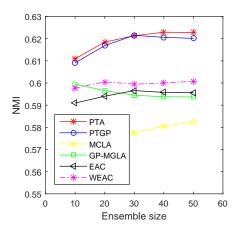


Fig. 4. Average performances (in terms of NMI) of different approaches over nine different real-world datasets with varying ensemble size  ${\cal M}$ .

- 2) Our approach is able to incorporate global information to construct more accurate local links by exploiting the random walk trajectories. The random walkers driven by a new probability transition matrix are utilized to explore the graph structure. A dense similarity measure is further derived from the sparse graph *K*-ENG using probability trajectories of the random walkers.
- 3) Extensive experiments are conducted on a variety of real-world datasets. The experimental results show that our approach yields significantly better performance than the state-of-the-art approaches w.r.t. both clustering accuracy and efficiency.

The rest of this paper is organized as follows. The related work is introduced in Section 2. The formulation of the ensemble clustering problem is provided in Section 3. The proposed ensemble clustering approach is described in Section 4. The experimental results are reported in Section 5. Section 6 concludes the paper.

### 2 RELATED WORK

There is a large amount of literature on ensemble clustering in the past few decades [20]. The existing ensemble clustering approaches can be categorized into three main classes, that is, (i) the pair-wise similarity based approaches [1], [3], [14], [21], (ii) the median partition based approaches [12], [13], and (iii) the graph partitioning based approaches [8], [9], [10], [22].

The pair-wise similarity based approaches represent the ensemble information by some pair-wise similarity measure [1], [3], [14], [21]. The evidence accumulation clustering (EAC) proposed by Fred and Jain [1] is probably the best-known pair-wise similarity based approach. In EAC, a co-association (CA) matrix is constructed by counting how many times two objects occur in the same cluster in the ensemble of multiple base clusterings. By treating the CA matrix as a new similarity matrix, clustering algorithms, such as the agglomerative clustering methods, can be further utilized to obtain the consensus clustering. Li et al. [21] proposed a hierarchical clustering algorithm to construct the consensus clustering using the CA matrix. The concept

of normalized edges is introduced in [21] to measure the similarity between clusters. Wang et al. [14] extended the EAC method by taking the cluster sizes into consideration and proposed the probability accumulation method.

The median partition based approaches aim to find a clustering (or partition) that maximizes the similarity between this clustering and all of the base clusterings, which can be viewed as finding the median point of the base clusterings [12], [13]. Due to the huge space of all possible clusterings, it is generally infeasible to find the optimal solution for the median partition problem. In fact, the median partition problem is NP-complete [13]. Cristofor and Simovici [12] proposed to find an approximative solution for the ensemble clustering problem by exploiting the genetic algorithm, in which clusterings are represented as chromosomes. Topchy et al. [13] proposed to formulate the median partition problem into a maximum likelihood problem and solved it by the EM algorithm.

The graph partitioning based approaches are another main category of ensemble clustering [8], [9], [10]. Strehl and Ghosh [9] formulated the ensemble clustering problem into a graph partitioning problem and proposed three ensemble clustering approaches: cluster-based similarity partitioning algorithm (CSPA), hypergraph partitioning algorithm (HG-PA), and meta-clustering algorithm (MCLA). Fern and Brodley [10] formulated the clustering ensemble into a bipartite graph by treating both clusters and objects as graph nodes and obtained the consensus clustering by partitioning the bipartite graph. Ren et al. [8] proposed to assign weights to data objects with regard to how difficult it is to cluster them and presented three graph partitioning algorithms based on the weighted-object scheme, that is, weightedobject meta clustering (WOMC), weighted-object similarity partition (WOSP) clustering, and weighted-object hybrid bipartite (WOHB) graph partition clustering.

Despite the significant success, there are still two limitations to most of the existing ensemble clustering approaches. First, the existing approaches mostly overlook the problem of uncertain links which may mislead the consensus process. Second, most of them lack the ability to incorporate global structure information to refine local links accurately and efficiently. Recently, some efforts have been made to address these two limitations. To deal with the uncertain links, Yi et al. [7] proposed an ensemble clustering approach based on global thresholding and matrix completion. However, using global thresholds may lead to isolated nodes, i.e., all of the links connected to a node may be cut out, due to the lack of local adaptivity. Moreover, in the approach of [7], a parameter C is used to scale the noise term in the objective function (see [7] for more details) and plays a sensitive and crucial role for yielding a good consensus clustering. Without knowing the ground-truth in advance, tuning the parameter C for [7] is very difficult and computationally expensive. To exploit the indirect relationships in the ensemble, Iam-On et al. [4], [6] proposed to refine the CA matrix by considering the shared neighbors between clusters. The approaches in [4] and [6] utilize the common neighborhood information, i.e., the 1-step indirect relationships, and have not gone beyond the 1-step indirect relationships to explore the more comprehensive structure information in the ensemble. To utilize multi-step indirect structure information, in the work

of [23], Iam-on et al. proposed to refine pair-wise links by the SimRank similarity (SRS), which, however, suffers from its high computational complexity and is not feasible for large datasets (see Fig. 11). Different from [7] and [23], in this paper, we propose to tackle these two limitations in a unified and efficient manner. We present the elite neighbor selection strategy to identify the uncertain links by locally adaptive thresholds and build a sparse graph with a small number of probably reliable links, which has shown its advantage compared to using the whole original graph without considering the reliability of the links (see Section 5). To explore the global structure information of the graph, we exploit the random walk process with a new transition probability matrix. By analyzing the probability trajectories of random walkers, a novel and dense similarity measure termed PTS is derived from the sparse graph. Specifically, based on the PTS, two ensemble clustering algorithms are further proposed, termed PTA and PTGP, respectively.

### 3 PROBLEM FORMULATION

In Table 2, we summarize the notations that are used throughout the paper. Let  $\mathcal{X}=\{x_1,\cdots,x_N\}$  be a dataset of N objects. Given M partitions of  $\mathcal{X}$ , each treated as a base clustering, the goal is to find a consensus clustering  $\pi^*$  that summarizes the information of the ensemble. The ensemble is denoted as  $\Pi=\{\pi^1,\cdots,\pi^M\}$ , where  $\pi^k=\{C_1^k,\cdots,C_{n^k}^k\}$  is the k-th base clustering. Let  $Cls^k(x_i)$  be the cluster in  $\pi^k$  that contains object  $x_i$ . If  $x_i\in C_j^k$ , then  $Cls^k(x_i)=C_j^k$ . Let  $\mathcal{C}=\{C_1,\cdots,C_{N_c}\}$  be the set of clusters in all of the M base clusterings. Obviously,  $N_c=\sum_{k=1}^M n^k$ .

With regard to the difference in the input information, there are two formulations of the ensemble clustering problem. In the first formulation, the ensemble clustering system takes both the clustering ensemble  $\Pi$  and the data features of  $\mathcal X$  as inputs [24], [25]. In the other formulation, the ensemble clustering system takes only the clustering ensemble  $\Pi$  as input and has no access to the original feature vectors of the dataset [1], [4], [6], [7]. In this paper, we comply with the latter formulation of the ensemble clustering problem, which is also the common practice for most of the existing ensemble clustering algorithms [20]. That is, in our formulation, the *input* of the ensemble clustering system is the ensemble  $\Pi$ , and the *output* is the consensus clustering  $\pi^*$ .

## 4 ENSEMBLE CLUSTERING USING PROBABILITY TRAJECTORIES

In this section, we describe the proposed ensemble clustering approach based on sparse graph representation and probability trajectory analysis.

The overall process of the proposed approach is illustrated in Fig. 3. The microclusters are used as a compact representation for the clustering ensemble. The microcluster based co-association (MCA) matrix for the ensemble is computed and a microcluster similarity graph (MSG) is constructed from the MCA matrix with the microclusters treated as graph nodes. In order to deal with the uncertain links, we propose a *k*-nearest-neighbor-like pruning strategy termed elite neighbor selection (ENS), which is able to identify the uncertain links by locally adaptive thresholds.

TABLE 2 Summary of notations

N	Number of data objects in a dataset
$x_i$	Data object
$\mathcal{X}_{h}$	Dataset of N objects, $\mathcal{X} = \{x_1, \dots, x_N\}$
$n^k$	Number of clusters in the $k$ -th base clustering
$C_{j}^{k}$	The $j$ -th cluster in the $k$ -th base clustering
$\pi^{\not k}$	The $k$ -th base clustering, $\pi^k = \{C_1^k, \cdots, C_{n^k}^k\}$
M	Number of base clusterings
П	Ensemble of $M$ base clusterings, $\Pi = \{\pi^1, \cdots, \pi^M\}$
$\pi^*$	Consensus clustering
$N_c$	Total number of clusters in Π
$C_i$	The <i>i</i> -th cluster in $\Pi$
$\mathcal{C} \  ilde{N}$	Set of clusters in $\Pi$ , $\mathcal{C} = \{C_1, \cdots, C_{N_c}\}$
	Number of microclusters
$\overset{y_i}{\mathcal{Y}}$	The <i>i</i> -th microcluster Set of microclusters, $\mathcal{Y} = \{y_1, \cdots, y_{\tilde{N}}\}$
$ ilde{n}_i$	Number of data objects in $y_i$
$b_{ij}$	Number of times $x_i$ and $x_j$ occur in the same cluster in $\Pi$
$a_{ij}$	Entry of co-association (CA) matrix
$\overset{ij}{A}$	CA matrix, $A = \{a_{ij}\}_{N \times N}$
$ ilde{b}_{ij}$	Number of times $y_i$ and $y_j$ occur in the same cluster in $\Pi$
$\tilde{a}_{ij}$	Entry of microcluster based co-association (MCA) matrix
$ ilde{ ilde{A}}_{ij}$	MCA matrix, $\tilde{A} = \{\tilde{a}_{ij}\}_{\tilde{N} \times \tilde{N}}$
$egin{array}{c}  ilde{G} \  ilde{V} \end{array}$	Microcluster similarity graph (MSG)
$ ilde{V}$	Node set of $\tilde{G}$ . Note that $\tilde{V} = \mathcal{Y}$
$ ilde{L}$	Link set of $ ilde{G}$
$ ilde{w}_{\underline{i}j}$	Weight between two nodes in $ ilde{G}$
$\bar{G}$	K-elite neighbor graph ( $K$ -ENG)
$ar{V}$	Node set of $\bar{G}$ . Note that $\tilde{V} = \mathcal{Y}$
$ar{L}$	Link set of $\bar{G}$
$ar{w}_{ij}$	Weight between two nodes in <i>G</i>
$p_{ij}$	(1-step) transition probability from $y_i$ to $y_j$
$P_{T}$	(1-step) transition probability matrix, $P = \{p_{ij}\}_{\tilde{N} \times \tilde{N}}$
$P^{T}_{ij} \ P^{T}$	$T$ -step transition probability from $y_i$ to $y_j$
	$T$ -step transition probability matrix, $P^T = \{p_{ij}^T\}_{\tilde{N} \times \tilde{N}}$
$p_{i:}^T \\ PT_i^T$	The <i>i</i> -th row of $P^T$ , $p_{i:}^T = \{p_{i1}^T, \cdots, p_{i\tilde{N}}^T\}$
$PT_i^T$	Probability trajectory of a random walker starting from
DEC	node $y_i$ with length $T$
$PTS_{ij}$	Probability trajectory based similarity between $y_i$ and $y_j$
$\mathcal{R}^{(0)}$	Set of the initial regions for PTA,
	$\mathcal{R}^{(0)} = \{R_1^{(0)}, \cdots, R_{ \mathcal{R}^{(0)} }^{(0)}\}$
$S^{(0)}$	Initial similarity matrix for PTA,
	$S^{(0)} = \{s_{ij}^{(0)}\}_{ \mathcal{R}^{(0)}  \times  \mathcal{R}^{(0)} }$
$\mathcal{R}^{(t)}$	Set of the <i>t</i> -step regions for PTA,
, 0	$\mathcal{R}^{(t)} = \{R_1^{(t)}, \cdots, R_{ \mathcal{R}^{(t)} }^{(t)}\}$
-:(4)	$\mathcal{R}^{(t)} = \{n_1^{-}, \cdots, n_{ \mathcal{R}^{(t)} }\}$
$S^{(t)}$	The <i>t</i> -step similarity matrix for PTA,
	$S^{(t)} = \{s_{ij}^{(t)}\}_{ \mathcal{R}^{(t)}  \times  \mathcal{R}^{(t)} }$
$\ddot{G}$	Microcluster-cluster bipartite graph (MCBG)
$\ddot{N}$	Number of nodes in $\ddot{G}$
$egin{array}{c} \ddot{G} \ \ddot{N} \ \ddot{V} \ \ddot{L} \end{array}$	Node set of $\ddot{G}$
$\ddot{L}$	Link set of $\ddot{G}$
$\ddot{w}_{ij}$	Weight between two nodes in $\ddot{G}$

A sparse graph termed K-elite neighbor graph (K-ENG) is then constructed with only a small number of probably reliable links. The ENS strategy is a crucial step in our approach. We argue that using a small number of probably reliable links may lead to significantly better consensus results than using all graph links regardless of their reliability. The random walk process driven by a new transition probability matrix is performed on the K-ENG to explore the global structure information. From the sparse graph K-ENG, a dense similarity measure termed PTS is derived by exploiting the probability trajectories of the random walk-

TABLE 3
An example of the microcluster representation

Data objects	Cluste	r labels	- Microcluster labels
Butu objects	$\pi^1$	$\pi^2$	
$x_1$	$C_1^1$	$C_1^2$	$y_1$
$x_2$	$C_1^1$	$C_{1}^{2}$	$y_1$
$x_3$	$C_1^1$	$C_{1}^{2}$	$y_1$
$x_4$	$C_1^1$	$C_{2}^{2}$	$y_2$
$x_5$	$C_2^1$	$C_{2}^{2}$	$y_3$
$x_6$	$C_{2}^{1}$	$C_{2}^{2}$	$y_3$
$x_7$	$C_{2}^{1}$	$C_{3}^{2}$	$y_4$
$x_8$	$C_{2}^{1}$	$C_{3}^{2}$	$y_4$

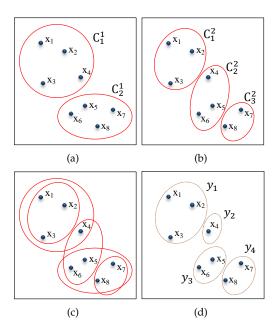


Fig. 5. Illustration of the example in Table 3. (a) The base clustering  $\pi^1$ . (b) The base clustering  $\pi^2$ . (c) The intersection of  $\pi^1$  and  $\pi^2$ . (d) The microcluster representation for the ensemble of  $\pi^1$  and  $\pi^2$ .

ers. Two novel consensus functions are further proposed, termed PTA and PTGP, respectively. In the following, we describe each step of our framework in detail.

### 4.1 Microcluster Based Representation

In this paper, we propose to discover the object relationship by analyzing the probability trajectories of the random walkers. One hurdle in conducting random walks is the computational complexity. In a graph of N nodes, it takes  $O(TN^2)$  operations to calculate T steps of random walks, which limits its application in large datasets. A practical strategy is to use a larger granularity than the original objects to reduce the number of graph nodes. In the field of image segmentation, superpixels are often adopted as the primitive objects [26]. However, with neither the spatial constraints of the image data nor access to the original data features, the conventional superpixel segmentation methods [26] are not applicable for generating the primitive segments for the ensemble clustering problem. In this paper,

we introduce the concept of microclusters as a compact representation for the ensemble. The objects  $x_i$  and  $x_j$  are defined to be in the same microcluster if and only if they occur in the same cluster for *all* of the M base clusterings, i.e., for  $k = 1, \dots, M$ ,  $Cls^k(x_i) = Cls^k(x_j)$ .

**Definition 1.** Let y be a set of objects. The set y is a microcluster if and only if (i)  $\forall x_i, x_j \in y$  and  $k \in \mathbb{Z}$  s.t.  $1 \leq k \leq M$ ,  $Cls^k(x_i) = Cls^k(x_j)$ , and (ii)  $\forall x_i \in y$  and  $x_j \notin y$ ,  $\exists k \in \mathbb{Z}$  s.t.  $1 \leq k \leq M$ ,  $Cls^k(x_i) \neq Cls^k(x_j)$ .

Given the clustering ensemble, we can produce a set of  $\tilde{N}$  non-overlapping microclusters, denoted as

$$\mathcal{Y} = \{y_1, \cdots, y_{\tilde{N}}\}. \tag{1}$$

Intuitively, the set of microclusters is produced by intersecting the M base clusterings. As it is defined, there are no clues to distinguish the objects in the same microcluster given the information of the ensemble  $\Pi$ . In our work, the microclusters are utilized as the primitive objects. For any microcluster  $y_i \in \mathcal{Y}$  and cluster  $C_j^k \in \pi^k$ , it holds that either every object in  $y_i$  is in  $C_j^k$  or no object in  $y_i$  is in  $C_j^k$ . Because the microclusters are treated as primitive objects, in the following, if all objects in  $y_i$  are in  $C_j^k$ , we write it as  $y_i \in C_j^k$  rather than  $y_i \subseteq C_j^k$ ; otherwise, we write it as  $y_i \notin C_j^k$  rather than  $y_i \subseteq C_j^k$ . Let  $Cls^k(y_i)$  denote the cluster in  $\pi^k$  that contains the microcluster  $y_i$ . If  $y_i \in C_j^k$ , then  $Cls^k(y_i) = C_i^k$ .

In Table 3 and Fig. 5, we show an example of a dataset with eight objects to describe the construction of the microclusters. There are two base clusterings in the example, namely,  $\pi^1$  and  $\pi^2$ , which consist of two and three clusters, respectively. With regard to Definition 1, four microclusters can be produced using  $\pi^1$  and  $\pi^2$ , which correspond to the intersection of  $\pi^1$  and  $\pi^2$  (as illustrated in Fig. 5(c) and 5(d)).

**Definition 2.** The co-association (CA) matrix of the clustering ensemble  $\Pi$  is defined as

$$A = \{a_{ij}\}_{N \times N},\tag{2}$$

where

$$a_{ij} = \frac{b_{ij}}{M} \tag{3}$$

and  $b_{ij}$  denotes how many times the objects  $x_i$  and  $x_j$  occur in the same cluster among the M base clusterings.

**Definition 3.** The microcluster based co-association (MCA) matrix of the clustering ensemble  $\Pi$  is defined as

$$\tilde{A} = \{\tilde{a}_{ij}\}_{\tilde{N} \times \tilde{N}},\tag{4}$$

where

$$\tilde{a}_{ij} = \frac{\tilde{b}_{ij}}{M} \tag{5}$$

and  $\tilde{b}_{ij}$  denotes how many times the microclusters  $y_i$  and  $y_j$  occur in the same cluster among the M base clusterings.

**Theorem 1.** For all  $x_i, x_j \in \mathcal{X}, y_k, y_l \in \mathcal{Y}$  such that  $x_i \in y_k$  and  $x_j \in y_l$ , it holds that  $a_{ij} = \tilde{a}_{kl}$ .

*Proof.* Given  $x_i, x_j \in \mathcal{X}, y_k, y_l \in \mathcal{Y}$ , we have  $a_{ij} = b_{ij}/M$  and  $\tilde{a}_{kl} = \tilde{b}_{kl}/M$  according to Definitions 2 and 3. To prove  $a_{ij} = \tilde{a}_{kl}$ , we need to prove  $b_{ij} = \tilde{b}_{kl}$ . Given  $x_i \in y_k$  and

 $x_j \in y_l$ , for any base clustering  $\pi^m \in \Pi$ , if  $y_k$  and  $y_l$  are in the same cluster in  $\pi^m$ , then  $x_i$  and  $x_j$  are in the same cluster in  $\pi^m$ . Thus we have  $b_{ij} \geq \tilde{b}_{kl}$ . If  $y_k$  and  $y_l$  are in different clusters in  $\pi^m$ , then  $x_i$  and  $x_j$  are in different clusters. Thus we have  $b_{ij} \leq \tilde{b}_{kl}$ . Because  $b_{ij} \geq \tilde{b}_{kl}$  and  $b_{ij} \leq \tilde{b}_{kl}$ , we have  $b_{ij} = \tilde{b}_{kl}$ , which leads to  $a_{ij} = \tilde{a}_{kl}$ .

Similar to the conventional CA matrix [1] (see Definition 2), the microcluster based co-association (MCA) matrix is computed by considering how many times two microclusters occur in the same cluster in  $\Pi$ . Then the microcluster similarity graph (MSG) is constructed based on the MCA matrix (see Definition 4). By using the microclusters, the size of the similarity graph is reduced from N to  $\tilde{N}$ .

**Definition 4.** The microcluster similarity graph (MSG) is defined as

$$\tilde{G} = (\tilde{V}, \tilde{L}), \tag{6}$$

where  $\tilde{V} = \mathcal{Y}$  is the node set and  $\tilde{L}$  is the link set. The weight of the link between the nodes  $y_i$  and  $y_j$  is defined as

$$\tilde{w}_{ij} = \tilde{a}_{ij}. \tag{7}$$

### 4.2 Elite Neighbor Selection

In this section, we introduce the elite neighbor selection (ENS) strategy to deal with the problem of uncertain links. The uncertain links are the connections in the similarity graph that are of low confidence (typically with small weights). One key issue here is how to decide a proper threshold to classify low-confidence and high-confidence and thereby identify the uncertain links in the graph. Yi et al. [7] proposed to use global thresholds to identify the uncertain entries in the similarity matrix, which, however, has several drawbacks in practical applications. First, it neglects the local structure of the similarity graph and may lead to isolated nodes. Second, it is also a difficult task to find a proper global threshold for different clustering ensembles due to the inherent complexity of real-world datasets. Instead of using global thresholds, in this paper, we propose a k-nearest-neighbor-like strategy, termed ENS, to identify the uncertain links by locally adaptive thresholds.

**Definition 5.** The K-elite neighbor threshold for a node  $y_i$  in the MSG is defined as the value of the K-th largest link weight connected to  $y_i$ , which is denoted as  $Thres_K(y_i)$ .

Having constructed the MSG graph (see Definition 4), we define the K-elite neighbor threshold, denoted as  $Thres_K(y_i)$ , for each node  $y_i$  in the graph (see Definition 5). Given two node  $y_i$  and  $y_j$  in the MSG graph, if  $y_i$  is one of the top-K neighbors of  $y_j$  OR  $y_j$  is one of the top-K neighbors of  $y_i$ , then  $y_i$  and  $y_j$  are referred to as the K-elite neighbors for each other. Formally, the definition of the K-elite neighbor relationship is symmetric, i.e.,  $y_i \in K$ -EN( $y_j$ ) is equivalent to  $y_j \in K$ -EN( $y_i$ ) (see Theorem 2).

**Definition 6.** Given two nodes  $y_i$  and  $y_j$  in the MSG graph,  $y_i$  is a K-elite neighbor (K-EN) of  $y_j$  if and only if  $\tilde{w}_{ij} \geq Thres_K(y_i)$  or  $\tilde{w}_{ij} \geq Thres_K(y_j)$ . The set of the K-elite neighbors (K-ENs) of  $y_i$  is denoted as K-EN $(y_i)$ .

**Theorem 2.** The K-elite neighbor relationship is symmetric, i.e., for all  $y_i, y_j \in \mathcal{Y}$ ,  $y_i$  is a K-elite neighbor of  $y_j$  if and only if  $y_j$  is a K-elite neighbor of  $y_i$ .

*Proof.* Given  $y_i \in K\text{-EN}(y_j)$ , it holds that  $\tilde{w}_{ij} \geq Thres_K(y_i)$  or  $\tilde{w}_{ij} \geq Thres_K(y_j)$ . Thus we have  $y_j \in K\text{-EN}(y_i)$  according to Definition 6. Given  $y_i \notin K\text{-EN}(y_j)$ , it holds that  $\tilde{w}_{ij} < Thres_K(y_i)$  and  $\tilde{w}_{ij} < Thres_K(y_j)$ . Thus we have  $y_j \notin K\text{-EN}(y_i)$ .

**Definition 7.** The K-elite neighbor graph (K-ENG) is defined as

$$\bar{G} = (\bar{V}, \bar{L}), \tag{8}$$

where  $\bar{V} = \mathcal{Y}$  is the node set and  $\bar{L}$  is the link set. The weight of the link between the nodes  $y_i$  and  $y_j$  is defined as

$$\bar{w}_{ij} = \begin{cases} \tilde{w}_{ij}, & \text{if } y_i \in K\text{-EN}(y_j), \\ 0, & \text{otherwise.} \end{cases}$$
 (9)

The K-elite neighbor graph (K-ENG) is constructed by preserving a certain number of probably reliable links in the MSG. The link between two nodes, say,  $y_i$  and  $y_j$ , is preserved if and only if  $y_i$  is a K-elite neighbor of  $y_j$ , i.e.,  $y_i \in K$ -EN( $y_j$ ). In our experimental study, we have shown that setting K to a small value, e.g., in the interval of [5,20], which preserves only several percent or even less than one percent of the links in the MSG, can lead to much better and more robust clustering results than preserving a great portion or even all of the links. In the following steps, the small number of probably reliable links are exploited by the random walk process and a dense pair-wise measure is derived from the sparse graph K-ENG.

### 4.3 From Sparse Graph to Dense Similarity

To discover the cluster structure from the sparse graph K-ENG, we use the random walks to explore the graph and propose to derive a dense pair-wise similarity measure based on the probability trajectories of random walkers. A random walker is a dynamic process that randomly transits from one node to one of its neighbors with a certain transition probability. The random walk technique has been widely used in the field of community discovery [15], [16], [17], [18] due to its ability of finding community structures, or cluster structures, in a graph. As pointed out in [17], the random walkers that start from the same cluster are more likely to have similar patterns when visiting the graph. In other words, the random walkers that start from the same cluster are more likely to have similar trajectories when they randomly walk on the graph than the random walkers that start from different clusters. Based on the random walk technique, in this paper, we propose to discover the latent relationships between graph nodes by analyzing the probability trajectories of the random walkers that start from different nodes.

The nodes in the K-ENG are microclusters, each of which consists of a certain number of original objects. Here, we refer to the number of objects in a microcluster as the size of the microcluster. In a link-weighted graph, the transition probability from a node to one of its neighbors is generally proportional to the weight of the link between them [15], [16], [17]. In the graph model of [15], [16], and [17], all of the

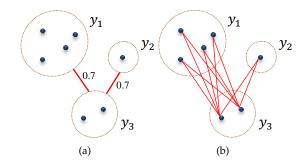


Fig. 6. Illustration of a graph with three microclusters as nodes. (a) The microcluster-microcluster links. (b) The (hidden) object-object links.

nodes are identical, which is different from the K-ENG in that the nodes in K-ENG may be of different sizes or even significantly different sizes. There is a need to distinguish the nodes of different sizes when deciding the transition probabilities.

In Fig. 6(a), we illustrate a graph with three nodes, each being a microcluster. The nodes  $y_1$ ,  $y_2$ , and  $y_3$  consist of four, one, and two objects, respectively. There are two (microcluster-microcluster) links in this graph which are equally weighted at 0.7. When treating the three nodes equally, the transition probabilities from  $y_3$  to  $y_1$  and from  $y_3$ to  $y_2$  are equally 0.5, i.e.,  $p_{31} = p_{32} = 0.7/(0.7 + 0.7) = 0.5$ . However, the microcluster-microcluster links are representative of a certain number of hidden object-object links. With respect to the object-object relationships, there are  $4 \times 2 = 8$ and  $1 \times 2 = 2$  hidden object-object links between  $y_1$  and  $y_3$  and between  $y_2$  and  $y_3$ , respectively (see Fig. 6(b)). The weights of the object-object links correspond to the entries of the CA matrix (see Definition 2), whereas the weights of the microcluster-microcluster links correspond to the entries of the MCA matrix (see Definition 3). According to Theorem 1, the weight of every object-object link between  $y_1$  and  $y_3$ (or between  $y_2$  and  $y_3$ ) is equal to that of the microclustermicrocluster link between  $y_1$  and  $y_3$  (or between  $y_2$  and  $y_3$ ), that is to say, the weight of every object-object link in the graph illustrated in Fig. 6(b) is equal to 0.7. If we perform random walks on the object granularity rather than the microcluster granularity, the probability of walking from one of the objects in  $y_3$  to one of the objects in  $y_1$  would be four times as great as the probability of walking from one of the objects in  $y_3$  to one of the objects in  $y_2$ .

To reflect the hidden object-object connections in a microcluster based graph, the construction of the transition probability matrix needs to take into consideration the sizes of the microclusters. Specifically, the transition probability from a microcluster node, say,  $y_i$ , to one of its neighbors should be proportional to the size of this neighbor if the weights of the links between  $y_i$  and all of its neighbors are equal. In our scenario, both the weights between  $y_i$  and its neighbors and the sizes of its neighbors may be different. Let  $\tilde{n}_i$  be the size of a microcluster  $y_i$ . The transition probability from  $y_i$  to one of its neighbors, say,  $y_j$ , is defined to be proportional to the sum of the weights of all hidden object-object links between  $y_i$  and  $y_j$ , i.e.,  $\tilde{n}_i \cdot \tilde{n}_j \cdot \bar{w}_{ij}$ . Because  $\tilde{n}_i$  is a constant given the node  $y_i$ , the probability of walking from  $y_i$  to one of its neighbors  $y_j$  therefore should be proportional to  $\tilde{n}_j \cdot \bar{w}_{ij}$ .

Formally, the definition of the transition probability matrix on the K-ENG is given in Definition 8.

**Definition 8.** Let  $P = \{p_{ij}\}_{\tilde{N} \times \tilde{N}}$  be the transition probability matrix of the random walk on the K-ENG. The transition probability from node  $y_i$  to node  $y_j$  is defined as

$$p_{ij} = \frac{\tilde{n}_j \cdot \bar{w}_{ij}}{\sum_{k \neq i} \tilde{n}_k \cdot \bar{w}_{ik}},\tag{10}$$

where  $\tilde{n}_j$  is the number of objects in  $y_j$ .

The random walk process is driven by the transition probability matrix P. Let  $P^T = \{p_{ij}^T\}_{\tilde{N} \times \tilde{N}}$  be the T-step transition probability matrix, i.e., probability distribution at step T, where  $p_{ij}^T$  is the probability that a random walker starting from node  $y_i$  arrives at node  $y_j$  at step T. The probability distribution at step 1 is obviously the transition probability matrix, i.e.,  $P^1 = P$ . The probability distribution at step T is computed as  $P^T = P \cdot P^{T-1}$ , for  $T \geq 2$ .

Let  $p_{i:}^T = \{p_{i1}^T, \cdots, p_{i\tilde{N}}^T\}$  denote the probability distribution of node  $y_i$  at step T, which is the i-th row of  $P^T$ and represents the probability of going from node  $y_i$  to each node in the graph by the random walk process at step T. The relationship between node  $y_i$  and node  $y_j$  can be studied by comparing their probability distributions at a certain step [16]. However, the probability distributions at different steps reflect different scales of information for the graph structure. Using a single step of probability distribution as the feature of a node overlooks the properties of this node at different scales. In order to take advantage of multi-scale information in the graph, we propose to exploit the probability trajectory for describing the random walk process starting from each node, which considers the probability distributions from step 1 to step T rather than a single step. The formal definition of the probability trajectory is given in Definition 9.

**Definition 9.** The probability trajectory of a random walker starting from node  $y_i$  with length T is defined as a  $T\tilde{N}$ -tuple:

$$PT_i^T = \{p_{i:}^1, p_{i:}^2, \cdots, p_{i:}^T\},$$
 (11)

where  $p_{i:}^{T}$  is the probability distribution of node  $y_i$  at step T.

The probability trajectory of a random walker starting from a given node is a TN-tuple and can be viewed as a feature vector for the node. We further define a pairwise similarity measure based on the probability trajectory representation.

**Definition 10.** The probability trajectory based similarity (PTS) between node  $y_i$  and node  $y_j$  is defined as

$$PTS_{ij} = Sim(PT_i^T, PT_i^T), \tag{12}$$

where Sim(u, v) is a similarity measure between two vectors u and v.

In fact, any similarity measure can be used in Eq. (12). In our work, we use the cosine similarity as the similarity measure, which effectively captures the relationship between the random walk trajectories. The cosine similarity between two vectors u and v is computed as follows:

$$Sim_{cos}(u,v) = \frac{\langle u,v \rangle}{\sqrt{\langle u,u \rangle \cdot \langle v,v \rangle}},$$
(13)

where  $\langle u, v \rangle$  is the inner product of u and v.

Therefore we obtain the new similarity measure PTS using the probability trajectory of the random walker starting from each node. Specifically, the random walks are performed on the sparse graph K-ENG which preserves only a small number of probably reliable links by the ENS strategy. The probability trajectories on the K-ENG are used as the feature vectors for the graph nodes, which incorporates multi-scale graph information into a  $T\tilde{N}$ -tuple by the different steps of the random walks. Theoretically, it is possible that the K-ENG may consist of more than one connected component, in which case we can perform the random walk on each connected component of the graph separately and then map the random walk trajectories at each component back to the whole graph to facilitate the computation.

For clarity, the algorithm of computing PTS is given in Algorithm 1.

## Algorithm 1 (Computation of Probability Trajectory Based Similarity)

Input:  $\Pi$ , k.

- 1: Obtain the set of microclusters  $\mathcal{Y}$  from  $\Pi$ .
- 2: Compute the MCA matrix by Eq. (4).
- 3: Build the graph MSG using the MCA matrix.
- 4: Construct the sparse graph *K*-ENG by the ENS strategy.
- 5: Perform random walks on *K*-ENG with the transition probability matrix given in Eq. (10).
- 6: Compute the new similarity PTS by Eq. (12).

Output:  $\mathcal{Y}$ ,  $\{PTS_{ij}\}_{\tilde{N}\times\tilde{N}}$ .

### 4.4 Consensus Functions

Having generated the new similarity measure PTS, the next step is to obtain the consensus clustering. Here, any clustering algorithm based on pair-wise similarity can be applied to the PTS measure to obtain the final clustering. Typically, we propose two different types of consensus functions based on PTS, termed probability trajectory accumulation (PTA) and probability trajectory based graph partitioning (PTGP), respectively.

### 4.4.1 Probability Trajectory Accumulation (PTA)

In this section, we introduce the consensus function termed PTA, which is based on hierarchical agglomerative clustering.

To perform hierarchical clustering, the set of microclusters are treated as the initial regions and the PTS is used as the similarity measure to guide the region merging process. Let  $\mathcal{R}^{(0)} = \{R_1^{(0)}, \cdots, R_{|\mathcal{R}^{(0)}|}^{(0)}\}$  denote the set of initial regions, where  $R_j^{(0)} = y_j$  and  $|\mathcal{R}^{(0)}| = \tilde{N}$ . Let  $S^{(0)} = \{s_{ij}^{(0)}\}_{|\mathcal{R}^{(0)}| \times |\mathcal{R}^{(0)}|}$  be the initial similarity matrix, where  $s_{ij}^{(0)} = PTS_{ij}$ .

In each step, the two regions with the highest similarity are merged into a new and bigger region and thus the number of regions decrements by one. Then the similarity matrix for the new set of regions will be computed w.r.t. average-link (AL), complete-link (CL), or single-link (SL). Let  $\mathcal{R}^{(t)} = \{R_1^{(t)}, \cdots, R_{|\mathcal{R}^{(t)}|}^{(t)}\}$  be the set of generated regions in the t-step, for  $t=1,2,\cdots,\tilde{N}-1$ , where  $|\mathcal{R}^{(t)}|$  is the number of regions in  $\mathcal{R}^{(t)}$ . Note that each region contains

one or more microclusters. We write it as  $y_i \in R_j^{(t)}$  if microcluster  $y_i$  is in region  $R_j^{(t)}$ . Let  $S^{(t)} = \{s_{ij}^{(t)}\}_{|\mathcal{R}^{(t)}| \times |\mathcal{R}^{(t)}|}$  be the similarity matrix for  $\mathcal{R}^{(t)}$ , which can be computed w.r.t. AL, CL, or SL. That is

$$s_{ij}^{(t)} = \begin{cases} \frac{1}{|R_i^{(t)}| \cdot |R_j^{(t)}|} \sum_{y_k \in R_i^{(t)}, y_l \in R_j^{(t)}} PTS_{kl}, & \text{If Method=AL,} \\ \sum_{y_k \in R_i^{(t)}, y_l \in R_j^{(t)}} PTS_{kl}, & \text{If Method=CL,} \\ \max_{y_k \in R_i^{(t)}, y_l \in R_j^{(t)}} PTS_{kl}, & \text{If Method=SL,} \end{cases}$$

where  $|R_i^{(t)}|$  is the number of microclusters in  $R_i^{(t)}$ .

The region merging process is performed iteratively and the number of regions decrements by one in each step. Obviously, after the  $(\tilde{N}-1)$ -step, there will be one region left, which contains the entire set of the microclusters. Then we have a dendrogram, i.e., a hierarchical representation of clusterings. Each level in the dendrogram represents a clustering with a certain number of clusters (or regions). The final clustering is obtained by specifying a level for the dendrogram.

An advantage of agglomerative clustering is that it can efficiently generate a hierarchy of clusterings where each level represents a clustering with a certain number of clusters. However, the region merging process is inherently local and greedy. A mistaken merging may lead to increasing errors in the following merging steps. The similarity measure determines the region merging order and plays a crucial role in agglomerative clustering. In our work, the PTS measure is able to deal with the uncertain links and incorporate the global structure information in the ensemble, which is beneficial for improving the accuracy and robustness of the agglomerative clustering. The experimental results also show the advantage of the PTA method (base on PTS) compared to other pair-wise similarity based methods [1], [4], [7], [19], [23] (see Section 5.5 and Table 9).

For clarity, the PTA algorithm is summarized in Algorithm 2.

## Algorithm 2 (Probability Trajectory Accumulation) Input: $\Pi$ , k.

- 1: Compute the microclusters and the PTS measure according to Algorithm 1.
- 2: Initialize the set of regions  $\mathcal{R}^{(0)}$ .
- 3: Construct the dendrogram iteratively:

for 
$$t = 1, 2, \dots, \tilde{N} - 1$$

Merge the most similar two regions in  $\mathcal{R}^{(t-1)}$  w.r.t.  $S^{(t-1)}$ . Obtain the new set of regions  $\mathcal{R}^{(t)}$ .

Compute the new similarity matrix  $S^{(t)}$ .

### end for

- 4: Find the clustering with k clusters in the dendrogram.
- 5: Obtain the final clustering by mapping microclusters back to objects.

**Output:** the consensus clustering  $\pi^*$ .

## 4.4.2 Probability Trajectory Based Graph Partitioning (PT-GP)

In this section, we introduce the consensus function termed PTGP, which is based on bipartite graph formulation.

A bipartite graph is constructed by treating both clusters and microclusters as nodes. As illustrated in Fig. 7, there are

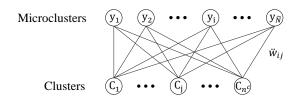


Fig. 7. The microcluster-cluster bipartite graph (MCBG)

no links between two clusters or between two microclusters. A link between two nodes exists if and only if one of the nodes is a cluster and the other is a microcluster. The weight of the link between a microcluster and a cluster is decided by the similarity between them. Here, we define the similarity between a microcluster  $y_i$  and a cluster  $C_j$  as the average PTS measure between  $y_i$  and the microclusters in  $C_j$ . The formal definition is given as follows.

**Definition 11.** The similarity between a microcluster  $y_i$  and a cluster  $C_j$  is defined as

$$Sim_{mc}(y_i, C_j) = Sim_{mc}(C_j, y_i)$$

$$= \frac{1}{|C_j|} \sum_{y_k \in C_i} PTS_{ik},$$
(15)

where  $|C_i|$  is the number of microclusters in  $C_i$ .

**Definition 12.** *The microcluster-cluster bipartite graph (MCBG) is defined as* 

$$\ddot{G} = (\ddot{V}, \ddot{L}),\tag{16}$$

where  $\ddot{V} = \mathcal{Y} \bigcup \mathcal{C} = \{\ddot{v}_1, \dots, \ddot{v}_{\ddot{N}}\}$  is the node set,  $\ddot{N} = \tilde{N} + N_c$  is the number of nodes and  $\ddot{L}$  is the link set. The weight of the link between nodes  $\ddot{v}_i$  and  $\ddot{v}_j$  is defined as

$$\ddot{w}_{ij} = \begin{cases} Sim_{mc}(\ddot{v}_i, \ddot{v}_j), & \text{if } \ddot{v}_i \in \mathcal{Y}, \ddot{v}_j \in \mathcal{C} \\ & \text{or } \ddot{v}_i \in \mathcal{C}, \ddot{v}_j \in \mathcal{Y}, \\ 0, & \text{otherwise.} \end{cases}$$
(17)

By treating both clusters and microclusters as nodes, the microcluster-cluster bipartite graph (MCBG) is constructed according to Definition 12. With regard to the bipartite structure of the MCBG, the efficient graph partitioning method Tcut [26] can be used to partition the graph into a certain number of disjoint sets of nodes. The microcluster nodes in the same segment are treated as a cluster and thus the final consensus clustering can be obtained by mapping the microclusters back to the data objects.

For clarity, we summarize the PTGP algorithm in Algorithm 3

# Algorithm 3 (Probability Trajectory Based Graph Partitioning) Input: $\Pi$ , k.

- 1: Compute the microclusters and the PTS measure according to Algorithm 1.
- 2: Compute the microcluster-cluster similarity by Eq. (15).
- 3: Build the bipartite graph MCBG.
- 4: Partition the MCBG into k clusters using Tcut.
- Obtain the final clustering by mapping microclusters back to objects.

**Output:** the consensus clustering  $\pi^*$ .

TABLE 4
Description of the benchmark datasets

Dataset	#Object	#Attribute	#Class
MF	2,000	649	10
IS	2,310	19	7
MNIST	5,000	784	10
ODR	5,620	64	10
LS	6,435	36	6
PD	10,992	16	10
USPS	11,000	256	10
FC	11,340	54	7
KDD99-10P	49,402	41	23
KDD99	494,020	41	23

### 5 EXPERIMENTS

In this section, we conduct experiments using ten real-world datasets. All of the experiments are conducted in Matlab R2014a 64-bit on a workstation (Windows Server 2008 R2 64-bit, 8 Intel 2.40 GHz processors, 96 GB of RAM).

### 5.1 Datasets and Evaluation Method

In our experiments, we use ten real-world datasets, namely, *Multiple Features (MF), Image Segmentation (IS), MNIST, Optical Digit Recognition (ODR), Landsat Satellite (LS), Pen Digits (PD), USPS, Forest Covertype (FC), KDD99-10P and KDD99.* The *MNIST* dataset and the *USPS* dataset are from [27] and [28], respectively. The *KDD99* dataset is from the UCI KDD Archive [29], whereas *KDD99-10P* is a 10% subset of *KDD99*. The other six datasets are from the UCI machine learning repository [30]. The details of the benchmark datasets are given in Table 4.

We use the normalized mutual information (NMI) [9] to evaluate the quality of the consensus clusterings, which provides a sound indication of the shared information between two clusterings. Note that a higher NMI indicates a better test clustering.

### 5.2 Construction of Ensembles

To evaluate the effectiveness of the proposed approach over various combinations of base clusterings, we construct a pool of a large number of base clusterings. In our experiments, we use the k-means algorithm and the rival penalized competitive learning (RPCL) [31] algorithm to construct the base clustering pool. The k-means and RPCL algorithms are performed repeatedly with random initializations and parameters. The numbers of initial clusters for k-means and RPCL are randomly chosen in the interval of [2, ub], where  $ub = \min\{\sqrt{N}/2, 50\}$  is the upper bound of the number of clusters and N is the number of objects in the dataset. By running k-means and RPCL 100 times respectively, a pool of 200 base clusterings is obtained for each benchmark dataset.

For each run of the proposed methods and the baseline ensemble clustering methods, we generate the ensemble by randomly drawing M base clusterings from the base clustering pool. Unless specially mentioned, the ensemble size M=10 is used in this paper. To rule out the factor of getting lucky occasionally, the average performances of the proposed methods and the baseline methods are evaluated and compared over a large number of runs.

### 5.3 Parameter Analysis

In this paper, we propose two ensemble clustering methods, termed PTA and PTGP, respectively. There are two parameters, namely, K and T, in the proposed methods. The parameter K specifies how many neighbors of a node will be treated as elite neighbors and preserved. The smaller the parameter K is, the sparser the K-ENG will be. The parameter T is the length of the probability trajectories.

We first test the influence of parameter K on the proportion of preserved links in the K-ENG. The average information of the MSG over 20 runs on each dataset is shown in Table 5. Because the microclusters are generated by intersecting multiple base clusterings, the number of microclusters is affected by the total number of objects as well as the shapes of cluster boundaries. For the KDD99-10P and KDD99 datasets, the number of microclusters is less than 1% of the number of the original objects. For the other datasets, the number of microclusters is averagely about 10% to 20% of the number of the original objects, i.e., using microclusters as nodes reduces the graph size by about 80%to 90%. The number of links in the MSG is also given in Table 5. Note that a link between two nodes exists if and only if the weight between them is non-zero, i.e., a "link" with zero-weight does not count as a link here. By cutting out the probably unreliable links in the MSG via the ENS strategy, the sparse graph K-ENG is constructed. The ratio of preserved links (RatioPL) is defined as

RatioPL = 
$$\frac{\text{\#Links in } K\text{-ENG}}{\text{\#Links in MSG}}$$
. (18)

For each parameter setting of K and T, we run the proposed methods 20 times with the ensemble of base clusterings randomly drawn from the base clustering pool (see Section 5.2) at each time. The RatioPL with respect to different values of K is shown in Table 6. When K=ALL, all links in MSG are preserved. The average NMI scores of PTA and PTGP with varying K and T are reported in Tables 7 and 8, respectively. The performances of PTA and PTGP are consistently good when K is set in the interval of [5,20] on the benchmark datasets and significantly better than setting K=ALL. As can be seen in Tables 6, 7 and 8, preserving a small proportion of the links via the ENS strategy can lead to significantly better performance than using all graph links by setting K=ALL.

As shown in Tables 7 and 8, the performances of the proposed PTA and PTGP methods are robust over various parameter settings. Setting K and T to moderate values, e.g., both in the interval of [5,20], leads to consistently good performances on the benchmark datasets. Empirically, it is suggested that the parameters K and T be set in the interval of  $[\sqrt{\tilde{N}}/5,\sqrt{\tilde{N}}]$ , where  $\tilde{N}$  is the number of the graph nodes in the K-ENG. In the following of this paper, we set both K and T to the floor of  $\sqrt{\tilde{N}}/2$  in all experiments on the benchmark datasets.

### 5.4 Comparison against Base Clusterings

The purpose of ensemble clustering is to combine multiple base clusterings into a probably better and more robust clustering. In this section, we compare the proposed PTA (associated with average-link) and PTGP methods against

TABLE 5
Average information of the MSG graph over 20 runs.

Dataset	MF	IS	MNIST	ODR	LS	PD	USPS	FC	KDD99-10P	KDD99
#Node (i.e., $\tilde{N}$ )	242	297	1,438	899	1,064	1,095	2,975	1,837	230	301
#Link	12,978	19,778	468, 453	153, 949	219, 753	208, 146	1,825,938	583, 369	19, 260	34, 509

TABLE 6 Average RatioPL over 20 runs with varying parameter K.

	K	1	2	4	8	16	32	64	ALL
	MF	2.4%	3.4%	6.6%	11.4%	21.1%	43.5%	82.1%	100.0%
	IS	2.0%	3.2%	5.9%	10.5%	19.4%	37.9%	70.1%	100.0%
	MNIST	0.6%	0.9%	1.7%	2.9%	5.0%	8.7%	16.2%	100.0%
RatioPL	ODR	1.0%	1.6%	3.0%	4.9%	8.5%	15.0%	31.0%	100.0%
Ratioi L	LS	0.8%	1.1%	2.3%	3.8%	6.9%	12.4%	23.9%	100.0%
	PD	0.9%	1.2%	2.4%	4.0%	7.1%	13.5%	28.1%	100.0%
	USPS	0.3%	0.5%	1.0%	1.7%	2.9%	5.0%	8.7%	100.0%
	FC	0.5%	0.7%	1.5%	2.4%	4.4%	8.0%	15.2%	100.0%
	KDD99-10P	1.7%	2.1%	4.2%	9.2%	23.9%	53.4%	90.0%	100.0%
	KDD99	1.6%	1.9%	3.6%	7.2%	14.3%	34.0%	68.9%	100.0%

TABLE 7 Average performance (in terms of NMI) of PTA over 20 runs with varying parameters K and T.

K	1	2	4	8	16	32	64	ALL				10	)			
T				10	)				1	2	4	8	16	32	64	128
MF	0.585	0.597	0.630	0.627	0.605	0.560	0.538	0.535	0.613	0.617	0.619	0.620	0.620	0.620	0.619	0.615
IS	0.574	0.612	0.632	0.615	0.595	0.592	0.610	0.609	0.613	0.616	0.611	0.612	0.611	0.612	0.611	0.612
MNIST	0.556	0.575	0.585	0.584	0.589	0.574	0.538	0.486	0.567	0.585	0.582	0.591	0.593	0.591	0.592	0.592
ODR	0.770	0.792	0.819	0.820	0.813	0.798	0.757	0.713	0.790	0.816	0.813	0.817	0.816	0.817	0.812	0.810
LS	0.599	0.595	0.615	0.618	0.621	0.612	0.586	0.539	0.600	0.613	0.618	0.620	0.620	0.627	0.632	0.637
PD	0.714	0.715	0.757	0.765	0.761	0.735	0.698	0.678	0.722	0.759	0.768	0.765	0.762	0.762	0.761	0.760
USPS	0.560	0.565	0.585	0.590	0.591	0.579	0.570	0.442	0.574	0.587	0.588	0.592	0.595	0.594	0.594	0.587
FC	0.235	0.237	0.247	0.254	0.250	0.237	0.221	0.199	0.246	0.245	0.257	0.255	0.254	0.250	0.250	0.250
KDD99-10P	0.565	0.599	0.624	0.659	0.664	0.592	0.562	0.561	0.677	0.681	0.686	0.677	0.671	0.668	0.676	0.670
KDD99	0.538	0.560	0.613	0.682	0.700	0.644	0.570	0.562	0.687	0.693	0.698	0.700	0.691	0.689	0.694	0.693

TABLE 8 Average performance (in terms of NMI) of PTGP over 20 runs with varying parameters K and T.

K	1	2	4	8	16	32	64	ALL				10	)			
T				10	)				1	2	4	8	16	32	64	128
MF	0.609	0.610	0.627	0.621	0.596	0.536	0.499	0.495	0.619	0.617	0.619	0.616	0.610	0.607	0.599	0.597
IS	0.610	0.615	0.623	0.616	0.589	0.582	0.603	0.594	0.615	0.618	0.614	0.611	0.613	0.611	0.608	0.616
MNIST	0.575	0.577	0.585	0.587	0.587	0.576	0.533	0.471	0.581	0.583	0.585	0.586	0.588	0.589	0.589	0.587
ODR	0.809	0.815	0.822	0.830	0.821	0.799	0.745	0.679	0.812	0.817	0.824	0.824	0.824	0.821	0.818	0.814
LS	0.604	0.607	0.615	0.623	0.623	0.621	0.586	0.505	0.615	0.616	0.616	0.615	0.626	0.629	0.631	0.631
PD	0.746	0.747	0.759	0.762	0.756	0.727	0.696	0.649	0.749	0.751	0.759	0.765	0.766	0.761	0.760	0.758
USPS	0.575	0.570	0.578	0.586	0.582	0.572	0.556	0.404	0.566	0.570	0.576	0.580	0.580	0.588	0.584	0.574
FC	0.224	0.227	0.235	0.238	0.237	0.234	0.218	0.195	0.229	0.231	0.232	0.236	0.237	0.237	0.236	0.234
KDD99-10P	0.618	0.620	0.627	0.643	0.646	0.591	0.524	0.521	0.673	0.675	0.665	0.659	0.655	0.656	0.664	0.662
KDD99	0.620	0.622	0.624	0.686	0.701	0.653	0.571	0.567	0.709	0.713	0.720	0.722	0.721	0.698	0.696	0.704

the base clusterings. Figure 8 illustrates the average NMI scores and the variances of the proposed methods and the base clusterings over 100 runs. As shown in Fig. 8, for the benchmark datasets, the proposed PTA and PTGP algorithms produce overall more accurate clusterings than the base clusterings. Especially, for the *ODR*, *LS*, *PD*, *KDD99-10P*, and *KDD99* datasets, the proposed methods achieve significant improvements in terms of NMI compared to the base clusterings.

## 5.5 Comparison against Other Ensemble Clustering Approaches

In this section, we evaluate the effectiveness and robustness of the proposed PTA and PTGP methods by comparing them against ten ensemble clustering methods, namely, cluster-based similarity partitioning algorithm (CSPA) [9], hypergraph partitioning algorithm (HGPA) [9], meta-clustering algorithm (MCLA) [9], seeded random walk (SRW) [22], graph partitioning with multi-granularity link analysis (GP-MGLA) [19], evidence accumulation clustering (EAC)

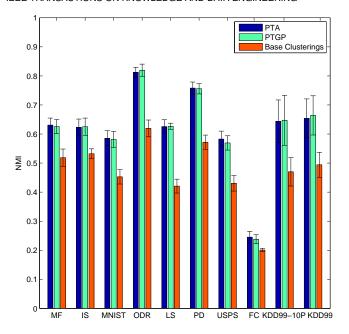


Fig. 8. Average performances in terms of NMI of our methods and the base clusterings over  $100\ {\rm runs}.$ 

[1], SimRank similarity based method (SRS) [23], weighted connected-triple method (WCT) [4], ensemble clustering by matrix completion (ECMC) [7], and weighted evidence accumulation clustering (WEAC) [19].

Of the ten baseline ensemble clustering methods, CSPA, HGPA, MCLA, SRW, and GP-MGLA are graph partitioning based methods, while EAC, SRS, WCT, ECMC, and WEAC are pair-wise similarity based methods. The pair-wise similarity based methods construct a similarity matrix based on the ensemble information. For each of the pair-wise similarity based methods and the proposed PTA method, we use three agglomerative clustering methods to obtain the final clusterings, namely, average-link (AL), complete-link (CL), and single-link (SL). Thus, each pair-wise similarity based method is associated with three sub-methods. For the other baseline methods, we use the parameter settings as suggested by the authors in the their papers [1], [4], [9], [19], [22], [23].

We run the proposed PTA and PTGP methods and the baseline methods 100 times on each dataset. If a method is computationally infeasible to be performed on a dataset, the corresponding NMI score will be labeled as "N/A". For each run, the ensemble of base clusterings is randomly drawn from the base clustering pool (see Section 5.2). As the number of clusters of the consensus clustering needs to be pre-specified for the baseline methods and the proposed methods, to compare their clustering results in a fair way, we use two criteria to choose cluster numbers in the experiments, namely, best-k and true-k. In the best-k criterion, the cluster number that leads to the best performance is specified for each method. In the true-k criterion, the true number of classes of the dataset is specified for each method.

The average performances of the proposed PTA and PTGP methods and the baseline methods over 100 runs are reported in Table 9. Each pair-wise similarity based method is associated with one of the three agglomerative clustering

methods, namely, AL, CL, and SL. As shown in Table 9, PTA-AL achieves the highest NMI scores for the MF, MNIST, and USPS w.r.t. both best-k and true-k and almost the highest NMI scores for the ODR, LS, PD, FC, KDD99-10P, and KDD99 datasets. The proposed PTGP method achieves the highest scores for the ODR and LS datasets w.r.t. both best-k and true-k and almost the highest scores for the MF, IS, PD, USPS, FC, KDD99-10P, and KDD99 datasets. To compare the performance of the test methods in a clearer way, Fig. 9 shows the number of times of each method being ranked in the top 3 (in terms of NMI) in Table 9. Out of the 20 columns in Table 9, PTGP and PTA-AL are ranked in the top 3 (among the 24 test methods) 19 times and 18 times, respectively, while the best baseline method is ranked in the top 3 only 4 times (see Fig. 9). As can be seen in Table 9 and Fig. 9, the proposed PTA and PTGP methods achieve the overall best performance in clustering accuracy and robustness compared to the baseline methods across a variety of datasets.

It is worth mentioning that the PTGP method significantly outperforms the other five graph partitioning based methods, namely, CSPA, HGPA, MCLA, SRW, and GP-MGLA. Specifically, the PTGP method yields higher, or even significantly higher, NMI scores than the other graph partitioning based methods on all of the benchmark datasets (see Table 9). Also, we compare the PTA method to the other five pair-wise similarity based methods, namely, EAC, SRS, WCT, ECMC, and WEAC, w.r.t. the same agglomerative clustering method. As shown in Table 9, the PTA-AL method achieves the best performance among the pairwise similarity based methods (all associated with AL) on all of the benchmark datasets. When considering CL or SL, the advantages of PTA become even greater. The PTA-CL method significantly outperforms the other pair-wise similarity based methods associated with CL on all benchmark datasets except IS. The PTA-SL method achieves far better consensus results than the other pair-wise similarity based methods associated with SL on all of the benchmark datasets. With the ability of handling uncertain links and incorporating global information to construct more accurate local links, the proposed PTA and PTGP methods perform significantly better than the baseline ensemble clustering methods on the benchmark datasets.

### 5.6 Robustness to Ensemble Size M

In this section, we further evaluate the robustness of the proposed methods with varying ensemble sizes M. For each ensemble size M, we run the PTA and PTGP methods and the baseline methods 20 times and report their average performances in Fig. 10. Here, all pair-wise similarity based methods are associated with AL. The PTA and PTGP methods produce consistently good results with different ensemble sizes. As shown in Fig. 10, the PTA and PTGP methods yield the best or nearly the best performance with varying M for the benchmark datasets. Especially, for the MF, IS, PD, FC, KDD99-10P, and KDD99 datasets, the PTA and PTGP methods exhibit significant advantages in the robustness to varying ensemble sizes over the baseline methods. Further, we illustrate the average performances of different approaches over nine datasets, KDD99 not

TABLE 9

Average performances (in terms of NMI) over 100 runs by different ensemble clustering methods (The three highest scores in each column are highlighted in bold, while the highest one indicated with brackets.)

	λ	1F	I	S	MN	IIST	Ol	OR .	I	S
Method	Best-k	True-k	Best-k	True-k	Best-k	True-k	Best-k	True-k	Best-k	True-k
PTA-AL	0.631	0.614	0.623	0.607	0.585	0.578	0.813	0.804	0.626	0.622
PTA-CL	0.629	0.611	0.620	0.609	0.582	0.577	0.805	0.793	0.595	0.584
PTA-SL	0.612	0.522	0.616	0.521	0.523	0.103	0.760	0.533	0.552	0.114
PTGP	0.626	0.613	0.625	0.611	0.581	0.576	0.819	0.813	0.627	0.625
CSPA	0.597	0.591	0.605	0.605	0.493	0.486	0.726	0.723	0.511	0.475
HGPA	0.485	0.231	0.500	0.457	0.423	0.120	0.643	0.353	0.406	0.324
MCLA	0.617	0.596	0.623	0.609	0.536	0.518	0.785	0.770	0.550	0.518
SRW	0.468	0.197	0.509	0.175	0.393	0.126	0.514	0.135	0.434	0.124
GP-MGLA	0.618	0.604	0.613	0.608	0.569	0.557	0.807	0.798	0.615	0.607
EAC-AL	0.603	0.578	0.612	0.605	0.570	0.555	0.792	0.772	0.596	0.569
EAC-CL	0.572	0.508	0.622	0.442	0.460	0.203	0.651	0.389	0.459	0.282
EAC-SL	0.531	0.173	0.542	0.413	0.021	0.002	0.257	0.099	0.079	0.002
SRS-AL	0.613	0.584	0.614	0.603	0.575	0.557	0.794	0.772	0.603	0.583
SRS-CL	0.587	0.547	0.625	0.585	0.554	0.534	0.771	0.744	0.536	0.453
SRS-SL	0.484	0.189	0.579	0.358	0.017	0.002	0.130	0.003	0.065	0.001
WCT-AL	0.605	0.579	0.617	0.606	0.585	0.562	0.800	0.774	0.617	0.603
WCT-CL	0.579	0.546	0.634	0.612	0.561	0.529	0.774	0.741	0.540	0.459
WCT-SL	0.596	0.247	0.599	0.415	0.028	0.002	0.318	0.132	0.213	0.002
ECMC-AL	0.588	0.333	0.593	0.277	0.554	0.132	0.780	0.328	0.584	0.018
ECMC-CL	0.591	0.520	0.560	0.411	0.446	0.276	0.617	0.454	0.402	0.204
ECMC-SL	0.416	0.166	0.560	0.200	0.041	0.015	0.350	0.177	0.071	0.001
WEAC-AL	0.606	0.583	0.610	0.605	0.577	0.569	0.799	0.785	0.608	0.596
WEAC-CL	0.581	0.520	0.618	0.431	0.463	0.194	0.643	0.371	0.456	0.235
WEAC-SL	0.602	0.268	0.605	0.417	0.039	0.002	0.348	0.126	0.228	0.002
Method	P	D'D	US	SPS	F	C		99-10P		D99
Method	Best-k	True-k	US Best-k	SPS True-k	Best-k	C True-k	Best-k	99-10P True- <i>k</i>	Best-k	True-k
Method PTA-AL	Best- <i>k</i> 0.757	True- <i>k</i>	US Best- <i>k</i> <b>0.583</b>	True-k 0.565	Best- <i>k</i> 0.243	True-k 0.232	Best- <i>k</i> <b>0.644</b>	99-10P True-k <b>0.525</b>	Best- <i>k</i> <b>0.654</b>	True-k <b>0.510</b>
Method PTA-AL PTA-CL	P Best-k 0.757 0.749	True-k 0.732 0.733	US Best-k <b>0.583</b> 0.552	True- <i>k</i> 0.565 0.530	Best- <i>k</i> 0.243 0.230	7rue-k 0.232 0.214	Best- <i>k</i> 0.644  0.659	99-10P True-k <b>0.525</b> 0.509	Best-k 0.654 0.683	True-k  0.510 0.489
Method PTA-AL PTA-CL PTA-SL	P Best-k  0.757 0.749 0.700	True-k  0.732 0.733 0.445	US Best-k 0.583 0.552 0.499	True-k  0.565 0.530 0.051	Best-k  0.243 0.230 0.247	True-k  0.232 0.214 0.011	0.644 0.659 0.636	99-10P True-k 0.525 0.509 0.545	Best-k  0.654  0.683  0.635	7rue-k 0.510 0.489 0.545
Method  PTA-AL PTA-CL PTA-SL PTGP	Best-k 0.757 0.749 0.700 0.755	True-k  0.732 0.733 0.445 0.738	US Best-k  0.583 0.552 0.499 0.568	True-k  0.565 0.530 0.051 0.551	Best-k 0.243 0.230 0.247 0.239	True-k  0.232 0.214 0.011 0.220	Best-k  0.644  0.659  0.636  0.647	09-10P True-k 0.525 0.509 0.545 0.527	Best-k  0.654  0.683  0.635  0.664	True-k  0.510 0.489 0.545 0.535
Method  PTA-AL PTA-CL PTA-SL PTGP CSPA	P Best-k 0.757 0.749 0.700 0.755 0.669	True-k 0.732 0.733 0.445 0.738 0.661	US Best-k  0.583 0.552 0.499 0.568  0.481	True-k  0.565 0.530 0.051 0.551 0.469	Best-k 0.243 0.230 0.247 0.239 0.213	True-k  0.232 0.214 0.011 0.220 0.199	Best-k  0.644  0.659  0.636  0.647  N/A	09-10P True-k 0.525 0.509 0.545 0.527 N/A	Best-k  0.654  0.683  0.635  0.664  N/A	True-k  0.510 0.489 0.545 0.535 N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA	P Best-k 0.757 0.749 0.700 0.755 0.669 0.584	True-k 0.732 0.733 0.445 0.738 0.661 0.193	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407	True-k  0.565 0.530 0.051 0.551  0.469 0.017	Best-k 0.243 0.230 0.247 0.239 0.213 0.167	True-k  0.232 0.214 0.011 0.220  0.199 0.103	Best-k  0.644  0.659  0.636  0.647  N/A  0.311	09-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155	Best-k  0.654  0.683  0.635  0.664  N/A  N/A	True-k  0.510 0.489 0.545 0.535  N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699	True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676	US Best-k 0.583 0.552 0.499 0.568 0.481 0.407 0.519	True-k  0.565 0.530 0.051  0.551  0.469 0.017 0.488	Best-k 0.243 0.230 0.247 0.239 0.213 0.167 0.229	C True-k 0.232 0.214 0.011 0.220 0.199 0.103 0.204	Best-k  0.644  0.659  0.636  0.647  N/A  0.311  0.622	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305	Best-k  0.654  0.683  0.635  0.664  N/A  N/A  0.621	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW	P Best-k 0.757 0.749 0.700 0.755 0.669 0.584 0.699 0.469	True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467	True-k  0.565 0.530 0.051 0.551  0.469 0.017 0.488 0.112	F Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198	True-k 0.232 0.214 0.011 0.220 0.199 0.103 0.204 0.047	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622 N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A	Best-k  0.654  0.683  0.635  0.664  N/A  N/A  0.621  N/A	7.510 0.510 0.489 0.545 0.535 N/A N/A 0.044 N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA	P Best-k 0.757 0.749 0.700 0.755 0.669 0.584 0.699 0.469 0.754	True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560	7FS True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547	F Best-k 0.243 0.230 0.247 0.239 0.213 0.167 0.229 0.198 0.227	C True-k 0.232 0.214 0.011 0.220 0.199 0.103 0.204 0.047 0.189	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631	0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503	Best-k  0.654  0.683  0.635  0.664  N/A  N/A  0.621  N/A  0.623	7 True-k 0.510 0.489 0.545 0.535 0.535 0.644 0.044 0.462
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA EAC-AL	P Best-k 0.757 0.749 0.700 0.755 0.669 0.584 0.699 0.469 0.754	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560 0.550	7FS True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526	F Best-k 0.243 0.230 0.247 0.239 0.213 0.167 0.229 0.198 0.227	C True-k 0.232 0.214 0.011 0.220 0.199 0.103 0.204 0.047 0.189 0.194	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631 0.629	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510	Best-k  0.654  0.683  0.635  0.664  N/A  N/A  0.621  N/A  0.623  N/A	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044 N/A 0.462 N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA EAC-AL EAC-CL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615	True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424	True-k  0.565 0.530 0.051 0.551  0.469 0.017 0.488 0.112 0.547  0.526 0.169	F Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601	9-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A 0.623  N/A N/A	0.510 0.489 0.545 0.535 N/A N/A 0.044 N/A 0.462 N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA EAC-AL EAC-CL EAC-SL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367	70 True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011	True-k  0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001	F Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525	9-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A 0.623  N/A N/A N/A	0.510 0.489 0.545 0.535 N/A N/A 0.044 N/A 0.462 N/A N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A	778 True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A	F Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A	C True-k  0.232 0.214 0.011 0.220 0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A	9-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621  N/A 0.623  N/A N/A N/A N/A	0.510 0.489 0.545 0.535 N/A N/A 0.044 N/A 0.462 N/A N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A N/A	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A	PS True-k  0.565 0.530 0.051 0.551  0.469 0.017 0.488 0.112 0.547  0.526 0.169 0.001 N/A N/A	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A 0.623  N/A N/A N/A N/A N/A	0.510 0.489 0.545 0.535 N/A N/A 0.044 N/A 0.462 N/A N/A N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A N/A N/A	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A	US Best-k 0.583 0.552 0.499 0.568 0.481 0.407 0.519 0.467 0.560 0.424 0.011 N/A N/A	PS True-k  0.565 0.530 0.051 0.551  0.469 0.017 0.488 0.112 0.547  0.526 0.169 0.001 N/A N/A N/A	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A N/A	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621  N/A 0.623  N/A N/A N/A N/A N/A	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044  N/A 0.462  N/A N/A N/A N/A N/A N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA EAC-AL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.754  0.740 0.615 0.367 N/A N/A N/A 0.752	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695	US Best-k 0.583 0.552 0.499 0.568 0.481 0.407 0.519 0.467 0.560 0.424 0.011 N/A N/A N/A 0.563	PS True-k  0.565 0.530 0.051 0.551  0.469 0.017 0.488 0.112 0.547  0.526 0.169 0.001 N/A N/A N/A N/A 0.533	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A N/A 0.229	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A 0.623  N/A N/A N/A N/A N/A N/A N/A	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044  N/A 0.462  N/A N/A N/A N/A N/A N/A N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL WCT-CL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A N/A N/A 0.752 0.694	70 True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A N/A 0.563 0.516	True-k  0.565 0.530 0.051 0.551  0.469 0.017 0.488 0.112 0.547  0.526 0.169 0.001 N/A N/A N/A 0.533 0.476	Best-k 0.243 0.230 0.247 0.239 0.213 0.167 0.229 0.198 0.227 0.221 0.207 0.032 N/A N/A N/A 0.229 0.217	C True-k  0.232 0.214 0.011  0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199 0.189	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A	Best-k  0.654  0.683  0.635  0.664  N/A  N/A  0.621  N/A  0.623  N/A  N/A  N/A  N/A  N/A  N/A  N/A  N/	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044 N/A 0.462  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL SRS-AL SRS-SL WCT-AL WCT-SL	P Best-k 0.757 0.749 0.700 0.755 0.669 0.584 0.699 0.469 0.754 0.615 0.367 N/A N/A N/A 0.752 0.694 0.575	70 True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621 0.015	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011  N/A N/A N/A 0.563 0.516 0.011	7 True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A N/A N/A 0.533 0.476 0.001	Best-k 0.243 0.230 0.247 0.239 0.213 0.167 0.229 0.198 0.227 0.221 0.207 0.032 N/A N/A N/A 0.229 0.217 0.033	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199 0.189 0.001	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A	Best-k  0.654  0.683  0.635  0.664  N/A  N/A  0.621  N/A  N/A  N/A  N/A  N/A  N/A  N/A  N/	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044 N/A 0.462  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL WCT-CL WCT-SL ECMC-AL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A N/A N/A 0.752 0.694 0.575 N/A	70 True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621 0.015 N/A	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A 0.563 0.516 0.011 N/A	7PS True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A N/A N/A 0.533 0.476 0.001 N/A	Best-k 0.243 0.230 0.247 0.239 0.213 0.167 0.229 0.198 0.227 0.221 0.207 0.032 N/A N/A N/A 0.229 0.217 0.033 N/A	C True-k  0.232 0.214 0.011  0.220  0.199 0.103 0.204  0.047 0.189  0.194 0.073 0.002  N/A N/A N/A 0.199 0.189 0.001 N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A N/A N/A	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A 0.623  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044 N/A 0.462  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL WCT-AL WCT-SL ECMC-AL ECMC-CL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A N/A N/A 0.752 0.694 0.575 N/A N/A N/A	70 True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621 0.015 N/A N/A	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A 0.563 0.516 0.011 N/A N/A	778 True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A N/A 0.533 0.476 0.001 N/A N/A N/A	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A N/A 0.229 0.217 0.033 N/A N/A N/A	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199 0.189 0.001 N/A N/A N/A N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/	99-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A	N/A
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL WCT-CL WCT-SL ECMC-AL ECMC-CL ECMC-SL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367  N/A N/A N/A 0.752 0.694 0.575 N/A N/A N/A N/A N/A	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621 0.015 N/A N/A N/A	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A 0.563 0.516 0.011 N/A N/A N/A N/A N/A	7PS True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A N/A 0.533 0.476 0.001 N/A N/A N/A N/A N/A N/A N/A N/A N/A	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A N/A 0.229 0.217 0.033 N/A N/A N/A N/A N/A N/A	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199 0.199 0.109 0.194 0.194 0.073 0.002 N/A N/A N/A N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/	9-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044 N/A 0.462  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-AL EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL WCT-CL WCT-SL ECMC-AL ECMC-SL WEAC-AL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367 N/A N/A N/A 0.752 0.694 0.575 N/A N/A N/A N/A N/A N/A N/A 0.751	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621 0.015 N/A N/A N/A N/A N/A N/A 0.716	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A N/A 0.563 0.516 0.011 N/A N/A N/A N/A N/A N/A N/A N/A O.561	778 True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A N/A 0.533 0.476 0.001 N/A	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A N/A 0.229 0.217 0.033 N/A N/A N/A N/A N/A N/A N/A 0.229	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199 0.189 0.001 N/A N/A N/A N/A N/A N/A 0.199	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/	9-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A N/A N/A N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A 0.623  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044  N/A 0.462  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/
Method  PTA-AL PTA-CL PTA-SL PTGP  CSPA HGPA MCLA SRW GP-MGLA  EAC-CL EAC-SL SRS-AL SRS-CL SRS-SL WCT-AL WCT-CL WCT-SL ECMC-AL ECMC-SL	P Best-k  0.757 0.749 0.700 0.755  0.669 0.584 0.699 0.469 0.754  0.740 0.615 0.367  N/A N/A N/A 0.752 0.694 0.575 N/A N/A N/A N/A N/A	7D True-k 0.732 0.733 0.445 0.738 0.661 0.193 0.676 0.109 0.731 0.699 0.382 0.013 N/A N/A N/A 0.695 0.621 0.015 N/A N/A N/A	US Best-k  0.583 0.552 0.499 0.568  0.481 0.407 0.519 0.467 0.560  0.550 0.424 0.011 N/A N/A 0.563 0.516 0.011 N/A N/A N/A N/A N/A	7PS True-k 0.565 0.530 0.051 0.551 0.469 0.017 0.488 0.112 0.547 0.526 0.169 0.001 N/A N/A 0.533 0.476 0.001 N/A N/A N/A N/A N/A N/A N/A N/A N/A	Best-k  0.243 0.230 0.247 0.239  0.213 0.167 0.229 0.198 0.227  0.221 0.207 0.032 N/A N/A N/A 0.229 0.217 0.033 N/A N/A N/A N/A N/A N/A	C True-k  0.232 0.214 0.011 0.220  0.199 0.103 0.204 0.047 0.189  0.194 0.073 0.002 N/A N/A N/A 0.199 0.199 0.109 0.194 0.194 0.073 0.002 N/A N/A N/A N/A	Best-k  0.644 0.659 0.636 0.647  N/A 0.311 0.622  N/A 0.631  0.629 0.601 0.525  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/	9-10P True-k 0.525 0.509 0.545 0.527 N/A 0.155 0.305 N/A 0.503 0.510 0.504 0.218 N/A N/A N/A N/A N/A N/A	Best-k  0.654 0.683 0.635 0.664  N/A N/A 0.621 N/A	True-k  0.510 0.489 0.545 0.535  N/A N/A 0.044 N/A 0.462  N/A N/A N/A N/A N/A N/A N/A N/A N/A N/

included, in Fig. 4, which is in fact the average of the first nine sub-figures in Fig. 10, i.e., the sub-figures from Fig. 10(a) to Fig. 10(i). Figure 4 provides an average view to compare our methods and the baseline methods across datasets, which demonstrates the advantage of our methods in the robustness to various datasets and ensemble sizes. In particular, the advantage of the proposed methods becomes even greater when the ensemble size gets larger, e.g., when the ensemble size goes beyond 20 (see Fig. 4).

### 5.7 Execution Time

In this section, we evaluate the time performances of the proposed PTA and PTGP methods and the baseline methods

with varying data sizes. The experiments are conducted on varying subsets of the *KDD99* dataset. The sizes of the subsets range from 0 to the full size 494,020. The execution times of the proposed methods and the baseline methods w.r.t. varying data sizes are illustrated in Fig. 11. Note that the time lines of PTA and PTGP almost overlap with each other due to their very similar time performances. Besides that, the time lines of EAC and WEAC also nearly overlap with each other. As shown in Fig. 11, the proposed PTA and PTGP methods exhibit a significant advantage in efficiency over the baseline methods. Especially, the proposed PTGP and PTA methods consume 3.22 seconds and 3.70 seconds, respectively, to process the entire dataset of KDD99 which

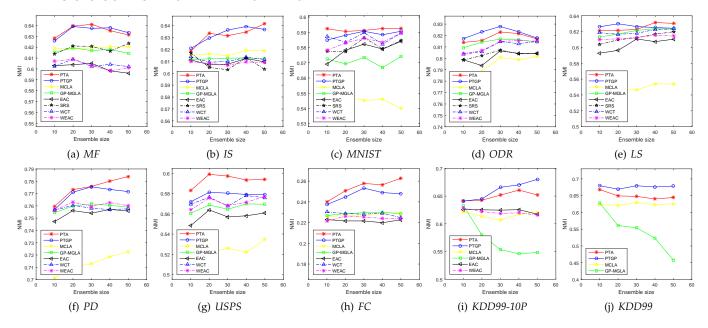


Fig. 10. The average performances over 20 runs by different approaches with varying ensemble sizes M.

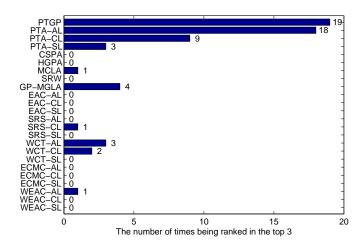


Fig. 9. The number of times of each method to be ranked in the top 3 (in terms of NMI) across the 20 columns in Table 9.

consists of nearly half a million objects, whereas eight out of the ten baseline methods are not even computationally feasible to process such large-scale datasets.

### 6 CONCLUSION

In this paper, we propose a novel ensemble clustering approach based on sparse graph representation and probability trajectory analysis. The microclusters are exploited as primitive objects to speedup the computation. We present the ENS strategy to identify uncertain links in a locally adaptive manner and construct a sparse graph with a small number of probably reliable links. It has been shown that the use of a small number of probably reliable links can lead to significantly better clusterings than using all graph links regardless of their reliability. To explore the global structure information in the ensemble, we utilize the random walks driven by a new transition probability matrix that considers

the link weights and the node sizes simultaneously. A novel and dense similarity measure termed PTS is derived from the sparse graph *K*-ENG by analyzing the probability trajectories of the random walkers. Based on PTS, we further propose two consensus functions, termed PTA and PTGP, respectively. Extensive experiments have been conducted on ten real-world datasets. The experimental results show that our approach significantly outperforms the state-of-the-art approaches in both clustering accuracy and efficiency.

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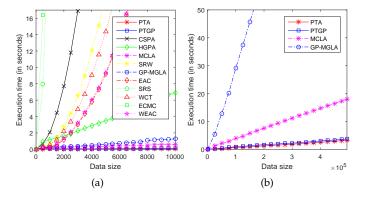


Fig. 11. Execution time of different ensemble clustering approaches as the data size varies (a) from 0 to 10,000 and (b) from 0 to 494,020.

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