Merging error analysis of name disambiguation based on author similarity
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Abstract
Falsely identifying different authors as one is called merging error in the name disambiguation of coauthorship networks. Research on the measurement and distribution of merging errors helps to collect high quality coauthorship networks. In the aspect of measurement, we provide a Bayesian model to measure the errors through author similarity. We illustratively use the model and coauthor similarity to measure the errors caused by initial-based name disambiguation methods. The empirical result on large-scale coauthorship networks shows that using coauthor similarity cannot increase the accuracy of disambiguation through surname and the initial of the first given name. In the aspect of distribution, expressing coauthorship data as hypergraphs and supposing the merging error rate is proper to hyperdegree with an exponent, we find that hypergraphs with a range of network properties highly similar to those of low merging error hypergraphs can be constructed from high merging error hypergraphs. It implies that focusing on the error correction of high hyperdegree nodes is a labor- and time-saving approach of improving the data quality for coauthorship network analysis.

Introduction
Modern sciences increasingly involve collaborative research [1–3], which contributes not only to the breakthrough achievement unattainable by individual [4, 5], but also to the transmission and combination of knowledge [6]. Coauthorship in scientific papers, as a valid proxy of the collaborations [13], can be expressed graphically by the name of coauthorship networks, where nodes and edges represent authors
and coauthorship respectively. Studies of large-scale coauthorship networks provide a bird-eye view of collaboration patterns in diverse fields, and have become an important topic of social sciences [8].

There exist ambiguities in collection of coauthorship networks, known as the author name disambiguation, which manifest themselves in two ways: one individual is identified as two or more authors (splitting error), or two or more individuals may be identified as one author (merging error). Here the term “individual” refers to a person in reality, and the term “author” refers to an entity obtained through name disambiguation methods [9][11]. Current name disambiguation methods can be classified into two classes: the methods using only the information of provided names (e. g. initial based methods), and the methods requiring additional information (e. g. email address) [12]. The difficulty of collecting additional information lead to the frequent usage of initial-based methods [13][15]. Some works use the provided names on papers directly to identify authors, which produces few merging errors in specific data [16][18].

Actually, all network data would contain systematic errors and observation errors, and those errors could have deleterious effects on estimations of the topological properties and statistical metrics of networks [19][22]. There has been extensive research, especially in social sciences, on sources of the errors, measuring and minimizing the errors [23]. The research has generally focused on missing and spurious interactions [24][26], which is the umbrella name disambiguation fall under [27]. Distortive effects of initial-based name disambiguation are mostly caused by merging author identities [28], which deflates the number of nodes, average shortest paths, global clustering coefficient, etc., which inflates average number of papers per author, average number of collaborators per author, giant component size, etc. Those distortions can reach a substantial level for large-scale coauthorship networks.

Based on the important models of Butts and Newman on general networks [27][29], we take a Bayesian model to give a general framework to measure merging errors through author similarity. To test the model effectiveness, we use two datasets formed by the papers from Proceedings of the National Academy of Sciences (PNAS) and Physical Review E (PRE) respectively. Those papers are published over 2007-2015. The data are aggregated from ISI Web of Science [http://www.webofscience.com]. Based on coauthor similarity and those data, we demonstratively utilize the model to measure the merging errors produced by using specific disambiguation methods, for instance, initial based methods. The outputs verify the well-known result that using surname and the initial of the first given name can produce numerous merging errors in large-scale networks. Moreover, in this case, the outputs show the coauthor similarity carries negative information on merging errors, which means using coauthor similarity cannot help to
increase the accuracy of this method. The carried information is positive in case of using surname and initials of all given names, and that of using provided names.

Coauthorship networks, in essential, are hypergraphs, where nodes represent authors, and the authors of a paper form a hyperedge. For authors, their hyperdegree refers to the number of papers they published, and degree refers to the number of their collaborators. The model outputs show that the merging errors measured through coauthor similarity do not distribute uniformly, where nodes with a high hyperdegree suffer substantial merging errors. We conjecture the merging error rate is proper to hyperdegree with an exponent. Following the conjecture, we can construct hypergraphs from high merging error hypergraphs (which are obtained by using surname and the initial of the first given name). The constructed hypergraphs have a range of statistical properties (e.g., degree distribution) highly similar to those of the hypergraphs obtained by using the provided names on papers (which suffer few merging errors). Those high similarities imply it is reasonable to regard the conjectured distribution as a possible one of merging errors. Knowing error distribution helps to find labor- and time-saving approaches to collecting high quality coauthorship networks.

This report is organized as follows: Section 2 and Section 3 introduce name disambiguation methods and a Bayesian model for measuring the merging errors of those methods respectively; Sections 4 and 5 are concerned with estimation and distribution of the errors respectively; The conclusion is drawn in Section 6.

**Name disambiguation**

The mostly adopted name disambiguation approach is using surname and the initial of the first given name (SIF hereafter): individuals sharing a surname and the initial of the first given name are regarded to be the same author. This approach produces substantial merging errors, but no splitting error unless authors misspelled their name. The other frequently used method relies on surname and the initials of all given names (SIA hereafter). This method is also prone to the merging errors, the risk of which is smaller than that of SIF. However, the method suffers splitting errors, because some authors do not provide their given names consistently. Taking names with surname “Newman” in PNAS 2007-2015 as examples (Table 1), we can see SIF generates substantial merging errors, and SIA few, but some splitting errors (Table 2). We check manually and find that “Mark Newman” and “M. E. J. Newman” refer to
the same author, so do “Charles M. Newman” and “C. M. Newman”.

Table 1. The provided names with the surname “Newman” in PNAS 2007-2015.

| Newman K. | Newman John C. | Newman Thomas C. | Newman Barbara A. |
|-----------|----------------|------------------|-------------------|
| Eric A.   | Lee S. Newman  | David J. Newman  | Lee A. Newman      |
| Ruchi M.  | Melissa C. Newman | Mari-Anne Newman | Robert A. Newman  |
| M. E. J.  | Jeffrey Newman | Ian Newman       | Aaron J. Newman    |
| C. M.     | George E. Newman | Andrew J. Newman | Amy H. Newman      |
| Karyn L.  | Scott M. Newman | James P. Newman  | Craig S. Newman    |
| Bryan     | Timothy K. Newman | John W. Newman | Sally J. Newman   |
| Miles     | Adam G. Newman | John R. S. Newman | Scott H. Newman   |
| Richmond  | Mark Newman    | Jack D. Newman   | Charles M. Newman  |

Table 2. Examples of merging errors produced by using SIF and SIA respectively.

| Method | Entity | Provided given names |
|--------|--------|----------------------|
| Newman L | Lee S. | Lee A. | M. E. J. | Miles | Mark |
| Newman M | Melissa C. | Mari Anne | John W. | John R. S. | Jack D. |
| Newman J | John C. | Jeffrey | James P. | |
| Newman D | Dianne K. | David J. | |
| Newman B | Barbara A. | Bryan | |
| Newman C | C. M. | Craig S. | Charles M. | |
| Newman A | Aaron J. | Andrew J. | Amy H. | Adam G. |
| Newman T | Thomas C. | Timothy K. | | |
| Newman R | Ruchi M. | Robert A. | Richmond S. | |
| Newman S | Scott M. | Sally J. | Scott H. | |
| Newman CM | C. M. | Charles M. | |
| Newman M | Miles | Mark | |
| Newman AJ | Aaron J. | Andrew J. | |

Except the bolded cases, all cases are wrong.

As Kim et al points out [28], the misidentification caused by initial-based methods is mainly through merging errors, which make those methods unsuitable for analyzing the most productive authors, the size of giant components, etc. Using the similarity of individuals helps to increase the accuracy of those methods. Features of author, such as the provided name (PN hereafter), names of coauthors, affiliation information, and email address can be utilized to produce a similarity profile of individual pairs. These features have proved to be effective in name disambiguation of specific cases [30–35]. An appropriate definition of the similarity profile is still a challenge and needs further research.

Bayesian model

Based on information of author similarity, we want to measure the probability that author (node) pairs identified as one individual are actually one (which is expressed by connecting the two nodes through an edge). Those measurements are assumed to be independent identically distributed random variables, conditioned on the ground-truth relationship valued as \( A_{ij} \) for all node pair \((i, j)\), where \( A_{ij} = 1 \) means
the node pair are actually one individual, and $A_{ij} = 0$ means not. That is, the probability of measuring
the edge between nodes $i$ and $j$ depends only on $A_{ij}$. This dependence can be parameterized by two
quantities: the false negative rate $e^-$ that is the probability of an absent edge where one truly exists
(spitting error), and the false positive rate $e^+$ that is the probability of observing an edge where none
exists (merging error).

Consider $N_l$ nodes with the same entity $l$. The entity is obtained through a name disambiguation
method, which is simply called “entity” hereafter. Within those nodes, we specify a real value $N_{ij}$ for
the observed features of node pair $(i, j)$, and a real value $E_{ij}$ for the similarity of those features. The
probability of observing $E_{ij}$ and $N_{ij}$ conditional on ground-truth $A_{ij}$ and errors is the following Bernoulli
mixture

$$p(E_{ij}, N_{ij}|A_{ij}, e^+, e^-) = B(E_{ij}, N_{ij}|1 - e^-)^{A_{ij}} 	imes B(E_{ij}, N_{ij}|e^+)^{(1-A_{ij})},$$

where $B(E_{ij}, N_{ij}|\alpha) \propto \alpha^{E_{ij}} (1 - \alpha)^{N_{ij} - E_{ij}}$ is the Beta density.

We assume that $A_{ij}$, $e^+$ and $e^-$ are uncertain, therefore, priors are assigned to them. The prior
distribution of $A_{ij}$ is determined via a hyperparameter $\phi_{ij}$, the specific form of which adopted here is
$A_{ij} \sim \phi_{ij}^{A_{ij}} (1 - \phi_{ij})^{1 - A_{ij}}$. Choice of the values of $\phi_{ij}$ reflects the prior knowledge regarding the structure of
the criterion data. One possibility is to chose $\phi_{ij} = \sum_{l,k} E_{lk} / \sum_{l,k} N_{lk}$, which is the median density of the
observed network [27]. Hereafter the density is denoted by $\rho$. We suppose the error probabilities $e^+$ and
$e^-$ are drawn independently from two Beta distributions, namely $e^+ \sim \text{Beta}(\alpha^+, \beta^+)$, $e^- \sim \text{Beta}(\alpha^-, \beta^-)$.
In practice, we specify $\alpha^+ = \beta^- = N_l \rho$ and $\alpha^- = \beta^+ = N_l (1 - \rho)$.

Given the above, we can identify the posterior to within a normalizing constant by using the Bayes’
theorem. The unnormalized posterior of $A_{ij}$ given $N_{ij}, E_{ij}$ and error rates is

$$p(A_{ij}|E_{ij}, N_{ij}, e^+, e^-) \propto p(E_{ij}, N_{ij}|A_{ij}, e^+, e^-)p(A_{ij})$$

$$= B(E_{ij}, N_{ij}|1 - e^-)^{A_{ij}} \times B(E_{ij}, N_{ij}|e^+)^{(1-A_{ij})} \times \phi_{ij}^{A_{ij}} (1 - \phi_{ij})^{1 - A_{ij}}$$

Eq. (2) is recognizable as the unnormalized form of a Beta distribution. Maximization with respect to
$A_{ij}$ will give us the maximum-likelihood value

$$\hat{A}_{ij} = \frac{\phi_{ij}(1 - e^-)^{E_{ij}}e^{-N_{ij} - E_{ij}}}{\phi_{ij}(1 - e^-)^{E_{ij}}e^{-N_{ij} - E_{ij}} + (1 - \phi_{ij})e^{+E_{ij}}(1 - e^+)^{N_{ij} - E_{ij}}}.$$  \hfill (3)

The same logic can be utilized for the false positive probability, namely

$$p(e^+|E, N, A, e^-) \propto p(E, N|A, e^+, e^-)p(e^+) = \prod_{i<j} p(E_{ij}, N_{ij}|A_{ij}, e^+, e^-)p(e^+)$$

$$= \prod_{i<j} B(E_{ij}, N_{ij}|1 - e^-)^{A_{ij}} \times B(E_{ij}, N_{ij}|e^+)^{1-A_{ij}}\text{Beta}(\alpha^+, \beta^+)$$

$$= e^+\sum_{i<j} E_{ij}A_{ij} + \alpha^+ - 1 \sum_{i<j} (N_{ij} - E_{ij})A_{ij} + \beta^+ - 1,$$

where $A = (A_{ij})$, $E = (E_{ij})$ and $N = (N_{ij})$ are $N_l \times N_l$ matrixes. Maximizing with respect to $e^+$ and performing the same calculation for $e^-$, we obtain

$$\hat{e}^+ = \frac{\sum_{i<j} E_{ij}A_{ij} + \alpha^+}{\sum_{i<j} N_{ij}A_{ij} + \alpha^+ + \beta^+},$$

$$\hat{e}^- = 1 - \frac{\sum_{i<j} E_{ij}(1 - A_{ij}) + \alpha^-}{\sum_{i<j} N_{ij}(1 - A_{ij}) + \alpha^- + \beta^-}.$$  \hfill (5)

The following provides an illustration (Fig. 1) and an implementation of the model (Table 3).

**Table 3. The process of the Bayesian model.**

| Input: Observed $N_l \times N_l$ matrixes $E$ and $N$ for entity $l$. |
| --- |
| Calculate $\rho = \sum_{i,j} E_{ij}/\sum_{i,j} N_{ij}$; |
| Specify $\alpha^+ = \beta^- = N_l\rho$ and $\alpha^- = \beta^+ = N_l(1 - \rho)$; |
| Initialize $e^+ = \rho$, $e^- = 1 - \rho$ and $\phi_{ij} = \rho$ for all $i, j$; |
| Repeat: |
| Calculate $A_{ij}$ through Eq. (3); |
| Submit $A_{ij}$ into Eqs. (4) to calculate $e^+$ and $e^-$; |
| Break if convergence or maximum number of iterations is reached. |
| Output: Matrix $A$, errors $e^+$ and $e^-$. |

The values of errors help to evaluate the information of adopted similarity weight. Error rates $e^+ \rightarrow \alpha^+/(\alpha^+ + \beta^+)$ and $e^- \rightarrow \alpha^-/(\alpha^- + \beta^-)$ imply that the weighted similarity carries no information. More broadly, the information based on observations is related to $1 - (e^+ + e^-)$, with increasingly positive/negative values indicating increasing/decreasing information in the direction of observations [29].
Error estimation

One cannot address the evaluation of the merging errors or specific network properties (e.g., the number of individuals) without specifying the weight of similarity information. The weight reflects our prior information regarding the criterion data. Taking coauthor similarity as an example, we could select the weight of common coauthors depending on the relative problems in existing literatures. The reasonability of using coauthor information is that if the merged authors are different individuals, their coauthors do not probably collaborate, or are wrongly merged simultaneously.

Suppose we have quantified the information of similarity for each entity, and know specific prior information of hyperparameters. Then we could adopt the Bayesian model to estimate the number of individuals. For each entity $l$, the evaluated edge density is $\rho_l = \sum_{i<j} \hat{A}_{ij}/N_l(N_l-1)/2$. Therefore, the evaluated number of individuals with entity $l$ is $\hat{N}_l = (1 - \rho_l)N_l + \rho_l$, and the evaluated number of individuals is $\hat{N} = \sum_{l=1}^{L} \hat{N}_l$.

We use the credible information of the number of individuals in PNAS 2012 (which is provided in Reference [28], which has little difference between the information we obtained) to find a weight for coauthor similarity. Then we use the weight to predict the number of individuals in PNAS 2007-
2015 (Table 4). The high error values of SIF imply the unreliability of this method for large-scale networks. The low error values of PN are due to the relatively complete name information provided by authors, and to the relatively low proportion of Chinese names (Table 5). In the data, there are 96.1% percent of authors providing the full information of the first given name. However, using provided names can still produce errors by merging, when the authors provide exactly the same name. Asian names, especially Chinese names, were found to account for those merging errors [28]. We count the number and appearance frequency of entities that have a given name shorter than six characters and a surname among major 100 Chinese surnames. Note that people with those surnames account for 84.7% of the total Chinese population, where the data come from Wikipedia. The low proportion of such authors in the data (3.8%), especially the low proportion of those authors conditional on publishing more than one paper (1.5%), makes us feel confident that the effect of name repetition is limited.

**Table 4. Specific statistical indicators of the empirical data.**

| Parameters | Years     | Method | $N$    | $\hat{N}$ | $\bar{e}^+$ | $\bar{e}^-$ |
|------------|-----------|--------|--------|-----------|-------------|-------------|
| $a = 0.75, b = 0.00, c = 1.00$ | 2012      | SIF    | 23,050 | 25,691    | 0.701       | 0.145       |
|           | 2007-2015 |        | 115,463| 135,806   | 0.648       | 0.211       |
| $a = 1.00, b = 0.50, c = 1.00$ | 2012      | SIA    | 24,767 | 26,029    | 0.247       | 0.246       |
|           | 2007-2015 |        | 136,322| 15,5506   | 0.231       | 0.226       |
| $a = 1.00, b = 0.60, c = 1.00$ | 2012      | PN     | 26,825 | 26,825    | 0.134       | 0.131       |
|           | 2007-2015 |        | 161,780| 161,795   | 0.145       | 0.132       |

Indicator $N$ is the numbers of authors identified by a given name disambiguation method, e.g., SFI. For all node pair $i, j$, parameter $a$ is the weight $E_{ij}$ conditional on the node pair having common coauthors (identified by SIF), and $b$ is that having no. Parameter $c$ is the weight $N_{ij}$. Indicator $\hat{N}$ is the estimated number of nodes, $\bar{e}^+$ and $\bar{e}^-$ are average merging and splitting errors of all entities respectively.

**Table 5. Specific statistical indicators of the empirical data.**

| Data   | $a$   | $b$  | $c$   | $d$  |
|--------|-------|------|-------|------|
| PNAS   | 3.12% | 1.30%| 3.86% | 0.62%|
| PRE    | 3.85% | 1.58%| 33.6% | 11.9%|

Indicators $a$ and $b$ are the percent of authors who have a surname among major 100 Chinese surnames and only one given name shorter than six characters, and the percent of those authors further conditioned on publishing more than one papers respectively. Indicators $c$ and $d$ are the percent of authors who use surname and the initial of the first given name, and the percent of those authors further conditioned on publishing more than one papers respectively.

We also use three other settings to weight coauthor similarity (Table 6). The large difference between
the number of nodes identified by NP and the estimated number shows that without knowing a reasonable weight of observation information, we have no way of evaluating the reliability and accuracy of name disambiguation methods.

**Table 6.** Specific statistical indicators of the empirical data.

| Parameters | Data | Method | $N$     | $\hat{N}$ | $\hat{e}^+$ | $\hat{e}^-$ |
|------------|------|--------|---------|-----------|------------|------------|
| $a = 0.50$ | SIF  | PNAS   | 115,463 | 145634    | 0.765      | 0.269      |
| $b = 0.00$ | SIA  | PN     | 136,322 | 166,131   | 0.731      | 0.306      |
|            |      |        | 161,780 | 190,211   | 0.681      | 0.357      |
| $c = 1.00$ | SIF  | PRE    | 27,925  | 36,137    | 0.723      | 0.311      |
|            | SIA  | PN     | 30,552  | 38,983    | 0.707      | 0.328      |
|            |      |        | 36,915  | 45,861    | 0.677      | 0.360      |
| $a = 0.75$ | PNAS | SIF    | 115,463 | 129,826   | 0.515      | 0.494      |
| $b = 0.25$ | SIA  | PN     | 136,322 | 146312    | 0.481      | 0.469      |
|            |      |        | 161,780 | 165,435   | 0.431      | 0.426      |
| $c = 1.00$ | SIF  | PRE    | 27,925  | 32,680    | 0.473      | 0.456      |
|            | SIA  | PN     | 30,552  | 34,564    | 0.457      | 0.444      |
|            |      |        | 36,915  | 39,549    | 0.427      | 0.417      |
| $a = 1.00$ | PNAS | SIF    | 115,463 | 144,638   | 0.265      | 0.261      |
| $b = 0.50$ | SIA  | PN     | 136,322 | 155506    | 0.231      | 0.226      |
|            |      |        | 161,780 | 169,515   | 0.181      | 0.175      |
| $c = 1.00$ | SIF  | PRE    | 27,925  | 33,600    | 0.223      | 0.214      |
|            | SIA  | PN     | 30,552  | 34,924    | 0.207      | 0.197      |
|            |      |        | 36,915  | 39,503    | 0.177      | 0.167      |

The meanings of indicators and parameters are the same as those in Table 2.

**Error distribution**

Without knowing how and where merging errors happen and distribute, we cannot predict which entities will be most heavily compromised. The hypergraph obtained through SIF (SIF hypergraph hereafter) can be constructed from that through PN (PN hypergraph hereafter) by aggregating some pairs of provided names with the same surname and the same initial of the first given name. For example, “Thomas C. Newman” and “Timothy K. Newman” are merged as “T. Newman”. Hence large-scale SIF hypergraph would suffer more merging errors than PN hypergraph. Aggregating a pair of node $i$ and $j$ is implemented by removing $j$, and reattaching all of $j$’s hyperedges to $i$.

Supposing the merging error rate is the same for each pair, the errors would more probably happen on
the entities with a high hyperdegree, especially on those high to an irrational extent. In fact, averaging
the estimation $\hat{N}_l$ for all of the entities $l$ with $k$-hyperdegree, we can see that this average estimate of
SIA increases with the growth of hyperdegree (Fig. 2). It implies the merging errors measured by using
the model and coauthor similarity do not distribute uniformly, where the nodes with a high hyperdegree
suffer more merging errors. Why we only consider SIA, because the high value of $\hat{e}^+$ for SIF makes the
estimation $\hat{N}_l$ has no value of reference, and using the model and coauthor similarity does not detect
obvious merging errors in PN hypergraph (Table 5).

Figure 2. The relationship between hyperdegrees and merging errors. The errors are
measured through the Bayesian model and based on coauthor similarity. The value on vertical axis is
the average $\hat{N}_l$ of entities $l$ that have hyperdegree $k$. The parameters and inputs of the model are listed
in Table 1.

Knowing SIF hypergraph can be aggregated from PN hypergraph, we address the reverse process: Re-
construct a hypergraph from FI hypergraph through disaggregation, and demand that the main network
properties of the reconstructed one are highly similar to those of PN hypergraph. Since PN hypergraph
suffers low merging errors (at least according to the error measured through the model and based on
colleague similarity), we could regard a distribution is a possible one of merging errors, if following the
distribution to select nodes to disaggregate can obtain such hypergraph from SIF hypergraph.

From the experiments on the empirical data, we find that the reconstruction mission can be well
completed by selecting nodes according to a probability proper to their hyperdegree with a given exponent
(Figs. 3 4). The detail reconstruction process is described in Table 7. Note that we try to select nodes
according to the rank of hyperdegree and to the probability proper to hyperdegree, and find that using
those selections cannot complete the reconstruction mission.

To test the rationality of the hypothesis of merging error distribution, we compare specific structural
Figure 3. The distribution of collaborators per author and that of papers per author. The description of network data are listed in Table 8. The data are binned on abscissa axes to extract the trends hiding in noise tails.

characteristics and statistical properties of PN hypergraph and those of the reconstructed one, such as degree distribution, hyperdegree distribution, clustering coefficient, assortative coefficient, etc.

The substantial low-degree/hyperdegree nodes and the small merging error rate in the total individuals result the robustness of the hook part of degree/hyperdegree distribution under merging errors (Fig. 3). Note that a small error rate in a large-scale network will give substantial errors. Meanwhile, merging high-degree/hyperdegree nodes inflates their degree/hyperdegree dramatically, which results the greater changes in the tail of degree/hyperdegree distribution (Fig. 3). However, distribution type of degree and that of hyperdegree are more resistant to merging error, namely keeping a hook head and a fat tail.

Considering the two nodes in Fig. 5a, merging them will reduce their local clustering coefficient from 1 to 1/3. When merging high-degree nodes, the local clustering coefficients of the merged nodes will reduce significantly (Fig. 5b). In reality, the coauthors of falsely merged individuals are not wrongly merged simultaneously, or do not probably collaborate. Hence merging errors will generate many connected
node triples that do not form triangles, and so deflates the local clustering coefficients of the falsely merged nodes (especially that of the high degree nodes, Figs. 4a-b) and the global clustering coefficients of networks (the fraction of connected triples of nodes which also form triangles).

The same logic could be used to analyze the effect of merging errors on assortativity coefficient [15]. Considering the merged nodes in Fig. 5a, merging will increase the difference between node degree and average degree of node neighbors. The difference is significant if merging happens between high-degree nodes (Fig. 5b, Figs. 4c-d). Hence under the reasonable supposition of using coauthor similarity, merging errors will inflate the difference, therefore deflates the Pearson correlation coefficient of degrees between pairs of collaborated authors, which is just the definition of assortativity coefficient (Table 8).

The behaviors of clustering and assortativity differ from the authors with a low degree to those with a high degree, which appears as the slop transition in the functions: the average local clustering coefficient and average neighbor degree of $k$-degree nodes [16]. As Fig. 4 shows, those transitions are kept under
Table 7. Node disaggregation of hypergraph.

| Input: Hypergraph $H$, the number of nodes needed to be splitted $n$. |
| Fit the distribution of papers per author of PN hypergraph, and denote by $P(k)$; |
| For $t$ from 1 to $n$: |
| Select a node $i$ (without replacement) according to the probability proper to its hyperdegree with a given exponent $\mu$; |
| Divide the hyperedges of $i$ into $l$ subsets, the sizes of which are draw from $P(k)$; |
| Append $l$ new nodes, and attach each new node to a subset; |
| Delete $i$. |

Output: Reconstructed hypergraph $H'$. The parameters $(n, \mu)$ are $(3, 381, 0.8)$ for PRE 2007-2015, and $(32, 568, 0.667)$ for PNAS 2007-2015.

Table 8. Specific statistical indicators of the analyzed networks.

| Network  | NN    | NE    | GCC  | AC   | AP   | PG   |
|----------|-------|-------|------|------|------|------|
| PNAS-SIF | 115,462 | 1,049,253 | 0.832 | 0.064 | 4.176 | 0.968 |
| PNAS-PN  | 161,780 | 1,074,836 | 0.896 | 0.554 | 6.599 | 0.848 |
| PNAS-RC  | 161,674 | 1,160,682 | 0.856 | 0.547 | 5.660 | 0.943 |
| PRE-SIF  | 27,925  | 86,648  | 0.773 | 0.237 | 6.148 | 0.814 |
| PRE-PN   | 37,528  | 90,711  | 0.838 | 0.394 | 9.254 | 0.583 |
| PRE-RC   | 37,110  | 99,549  | 0.775 | 0.242 | 7.379 | 0.796 |

The networks are obtained from the papers of PNAS and PRE over 2007-2015 through SIF and PN respectively, and from the hypergraphs reconstructed from SIF hypergraphs. The indicators are the number of nodes (NN), the number of edges (NE), global clustering coefficient (GCC), assortativity coefficient (AC), average shortest path length (AP) and the node proportion of the giant component (PG). The values of AP of the first three networks are calculated by sampling 15,000 pairs of nodes.

Discussion and conclusion

We have discussed three basic problems with respect to dealing with merging error, the principal error of name disambiguation in coauthorship networks: measuring merging error; evaluating the influence of merging error on the statistical and structural properties of networks; discussing approaches to collecting high quality data.

Firstly, based on author similarity, we provide a Bayesian model to measure merging errors. We illustratively use coauthor similarity to test the effectiveness of three typical name disambiguation methods.
The empirical results on large-scale coauthorship networks show the coauthor similarity cannot help to improve the accuracy of using surname and the initial of the first name.

Secondly, we comparably analyze a range of network properties of hypergraphs with high merging errors and those of hypergraphs with low merging errors. The theoretical analysis and empirical results show that the effects are relatively small/large on specific statistical properties (such as average local clustering coefficient, degree distribution) of nodes with low/high degree.

Lastly, based on the supposition that the merging error rate is proper to node hyperdegree with an exponent, we show how to reconstruct hypergraphs from high merging error hypergraphs, which have a range of network properties considerably similar to those of low merging error hypergraphs. It implies that gathering more complete information for the entities with high hyperdegree, especially with irrationally high hyperdegree, than collecting complete information for all entities is an efficient strategy in obtaining high quality coauthorship networks.
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