Project 4 - Group 6

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\ ### Setup: assign Knitr root directory and load dependencies We set the `knitr` root.dir to the project directory (`projDir`) and load/install the necessary packages to run our `main.Rmd` script. [Code omitted]

Section I: Paper 3

"Name Disambiguation in Author Citations using a K-way Spectral Clustering Method"

As discussed in `Section 3.1` of the paper, authors Han, Zha, and Giles use **three** citation attributes to design features for name disambiguation. Those attributes are:

- co-author names
- paper titles
- publication venue titles

Together these attributes are called a 'citation vector.' For a dataset with m features, each citation is representated as an m-dimensional vector given by $M = (\alpha_1, \ldots, \alpha_m)$, where α_i is the weight assigned to feature i. Two types of feature weights assignments are profiled: (i) TFIDF and (ii) normalized TF ("NTF").

We demonstrate how we create the citation vector from our clean data sources in the `output` library in the chunks below:

Step 1: Load text file

We parse raw data from the `data` folder into the appropriate format using the `Data_Cleaning.R` script contained in the `lib` folder. THe parsed datasets are stored in the `output` folder.

```
source(file.path(projDir,"lib","feature_extraction.R"))
exFile <- file.path(projDir,"output","Agupta.csv")
exText <- readTextFile(exFile)
exText %>%
  tbl_df() %>%
  select(QuestAuthor, Coauthor, Paper, Journal) %>%
  head() %>%
  kable(format = "markdown")
```

QuestAuthor	Coauthor	Paper	Journal
A Gupta	NA	Stanford DASH Multiprocessor: The Hardware and Software Approach	PARLE Parallel Architectures and Languages Europe
A Gupta	A Acero; Y Rui	Automatically extracting highlights for TV Baseball programs	ACM Multimedia
A Gupta	A Acharya; M Tambe	Implementation of Production Systems on Message-Passing Computers	IEEE Trans Parallel Distrib Syst
A Gupta	A Agarwal	Memory-Reference Characteristics of Multiprocessor Applications under MACH	SIGMETRICS Measurement and Modeling of Computer Systems
A Gupta	A Agrawal; N Chaddha; T Meng	Variable Compression Using JPEG	ICMCS International Conference Multimedia Computing and Systems
A Gupta	A Balachandran; E Sanocki; G Jancke; J Grudin; J Cadiz	Distance learning through distributed collaborative video viewing	CSCW Conference Computer Supported Cooperative Work

Step 2: Prep the co-author and journal terms to be included in the document term matrix

We want the individual co-author names and journal names to be considered as single 'terms' in our corpus. Therefore, we collapse the spaces separating the unique letters in someone's name, so that it appears to be a term. For example, "C L Zhang" would become "clzhang". Likewise, with journal names, we combine them into a single string without spaces so that each journal is a unique term in our Document Term Matrix.

```
as_tibble(exText) %>%
    mutate(x = str_replace_all(Coauthor, " ", "")) %>%
    mutate(x = str_replace_all(x, ";", " ")) %>%
    mutate(y = str_replace_all(Journal, " ", "")) %>%
    mutate(term_col = tolower(paste(x, y, Paper))) %>%
    select(term_col) %>%
    head() %>%
    kable(format = 'markdown')
```

term_col
na parleparallelarchitecturesandlanguageseurope stanford dash multiprocessor: the hardware and software approach
aacero yrui acmmultimedia automatically extracting highlights for tv baseball programs
aacharya mtambe ieeetransparalleldistribsyst implementation of production systems on message-passing computers
aagarwal sigmetricsmeasurementandmodelingofcomputersystems memory-reference characteristics of multiprocessor applications under mach
aagrawal nchaddha tmeng icmcsinternationalconferencemultimediacomputingandsystems variable compression using jpeg
abalachandran esanocki gjancke jgrudin jcadiz cscwconferencecomputersupportedcooperativework distance learning through distributed collaborative video viewing

Step 3: Run our spectral clustering method on the example dataset

We use the `tm` package to construct citation vectors in the manner described above. We then use the `matching_matrix` and `performance_statistics` functions in the `lib/evaluation_metrics.R` file to benchmark our results. Below we describe the details of our spectral clustering implementation. Our spectral clustering implementation is contained in `lib/SpectralClustering.R` and includes the following key methods:

- **affinity** : creates an affinity matrix
- **simFunction** : similarity function
- **similarity** : creates a similarity matrix from a similarity kernel
- **specClusteringKM** : method for assigning clusters using k-means
- **specClusteringQR** : method for assigning clusters based on cosine similarities using QR decomposition with pivoting

Details of Gaussian-similarity-kernel and k-means clustering implementation

First, we compute the simmilarity between citations from the TF-IDF or NTF matrix of citations. We use a Gaussian kernel as a measure of similarity. Then, we create an undirected graph based on the similarities to extract some manifold in the data, we thereby obtain A, the affinity matrix. After, we calculate the degree matrix D (diagonal) where each diagonal value is the degree of the respective vertex (*e.g.* sum of rows).

We compute the unnormalized graph Laplacian: $U = D - A$. Then, assuming that we want k clusters, we find the k smallest eigenvectors of U. This represents the points in a new k-dimensional space with low-variance. Finally, in this transformed space, it becomes easy for a standard k-means clustering to find the appropriate clusters.

Gram Matrix

From the TF-IDF or NTF matrix of citations, we compute the cosine similarity between each citation vectors as follows:

$$similarity = cos(\theta) = \frac{a \cdot b}{\|a\| \, \|b\|} = \frac{\sum_{i=1}^{n} a_i b_i}{\sqrt{\sum_{i=1}^{n} a_i^2} \sqrt{\sum_{i=1}^{n} b_i^2}}$$

This matrix is called the **Gram matrix** A. In the first step of the algorithm, we determine the k largest eigenvectors of A: X_k, a n-by-k matrix. Each row of X_k corresponds to a citation vector. Then, we compute the **QR decomposition with column pivoting** applied to ${X_k}^T$, *e.g.* we find the matrices P (permutation matrix, n-by-n), Q (orthogonal, k-by-k) and R (left-upper-triangular, k-by-n), so that:

$${X_k}^T P = QR = Q[R_{11}, R_{12}]$$

R_{11} will be the k-by-k upper-triangular matrix. We then compute the matrix $\hat{R}$:

$$\hat{R} = R_{11}^{-1} R P^T = R_{11}^{-1}[R_{11}, R_{12}]P^T = [I_k, R_{11}^{-1} R_{12}]P^T$$

Finally, the cluster membership of each citation vector is determined by the row index of the largest element in absolute value of the corresponding column of $\hat{R}$.

Example study using methods in our `lib/SpectralClustering.R` script

For reproducability, we avoid computing k-means in this `Rmd` file because of running time. We run this study on the Normalized Term Frequencies (NTF) and the TF-IDF objects we extract in the `lib/feature_extraction.R` script.

```
source(file.path(projDir,"lib","SpectralClustering.R"))
source(file.path(projDir,"lib","evaluation_measures.R"))

# estimated time 6 sec
start.time <- Sys.time()

num_authors <- length(unique(exText$AuthorID))
author_id <- exText$AuthorID
exDTM <- createCitationMatrix(exText)

exTFIDF <- weightTfIdf(exDTM, normalize = FALSE)
exNTF <- weightTf(exDTM)

exResultsTFIDF <- runSpectralClusteringQR(exTFIDF, num_authors)
exResultsNTF <- runSpectralClusteringQR(exNTF, num_authors)

m0 <- matching_matrix(author_id,exResultsTFIDF)
m1 <- matching_matrix(author_id,exResultsNTF)

p0 <- performance_statistics(m0)
p1 <- performance_statistics(m1)

end.time <- Sys.time()
study.time <- end.time - start.time

kable(data.frame(study_time = study.time), format = "markdown")
```

study_time
4.742489 secs

Step 4: View results from sample study

We examine some results from our sample methods to confirm our methodology is producing reasonable results.

```
ex_df <- data.frame(
    study=rep("Agupta", 2),
    method=c("QR Spectral Clustering - TFIDF",
             "QR Spectral Clustering - NTF"),
    precision=c(p0$precision, p1$precision),
    recall=c(p0$recall, p1$recall),
    f1=c(p0$f1, p1$f1),
    accuracy=c(p0$accuracy, p1$accuracy),
    mcc=c(p0$mcc, p1$mcc)
    )

kable(ex_df, format = "markdown", digits = 2)
```

study	method	precision	recall	f1	accuracy	mcc
Agupta	QR Spectral Clustering - TFIDF	0.13	0.25	0.17	0.76	0.05
Agupta	QR Spectral Clustering - NTF	0.11	0.28	0.16	0.70	0.02

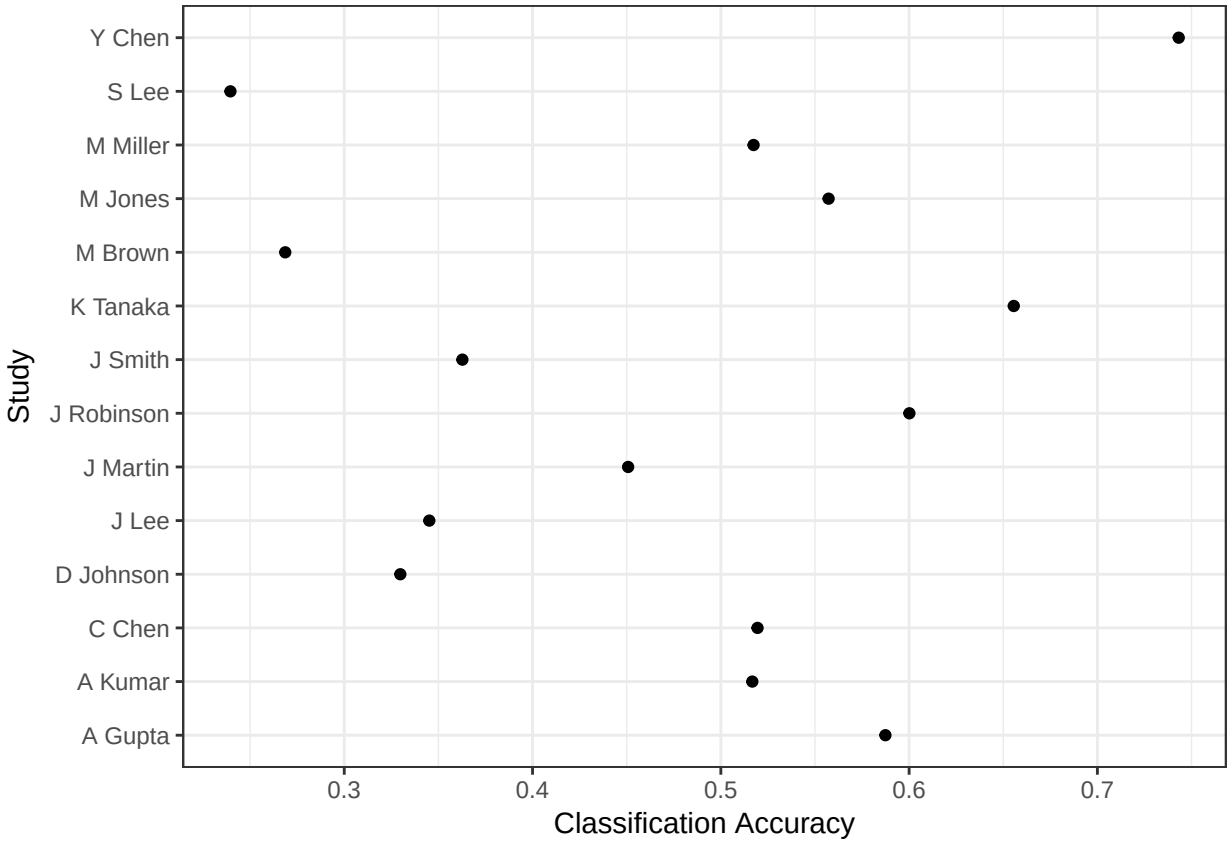
NOTE: Notice the f1 score. The F1 score can be interpreted as a weighted average of the precision and recall (with both weighted equally), where an F1 score reaches its best value at 1 and worst at 0. It is given by:

$$F_\beta = \frac{(1+\beta^2)\cdot \text{true positive}}{(1+\beta^2)\cdot \text{true positive} + \beta^2 \cdot \text{false negative} + \text{false positive}}$$

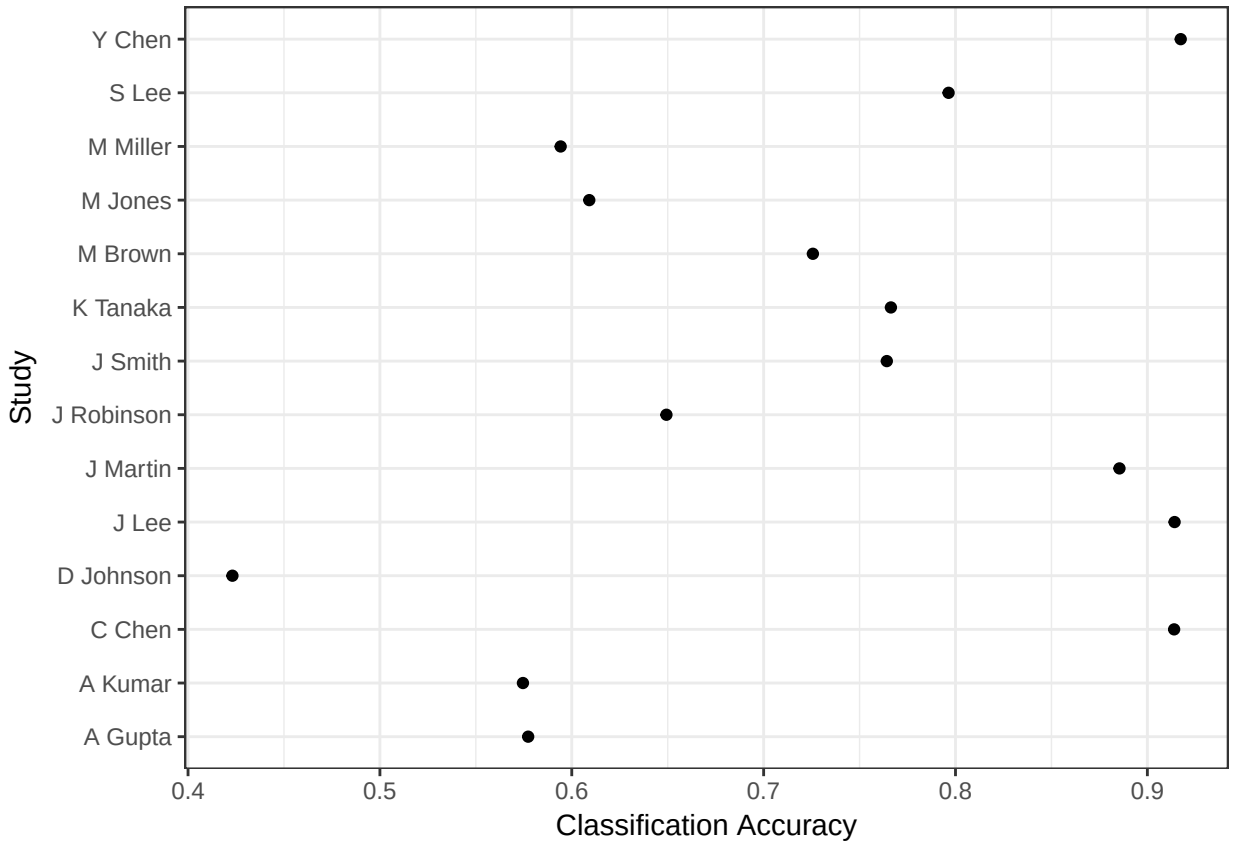
Step 5: Load results from all studies

Separately, we have run our spectral clustering methods on all of our cleaned and labeled datasets in `output` and saved the results in `output/studies`. We plot the results of our studies below.

```
load(file.path(projDir,"output/processed_data/prelimResults.RData"))
tb %>%
  transform(accuracy  = as.numeric(accuracy)) %>%
  arrange(desc(accuracy)) %>%
  ggplot(aes(x=accuracy, y=study)) +
  geom_point() +
  theme_bw() +
  xlab('Classification Accuracy') +
  ylab('Study')
```



```
tb_teacher%>%
  transform(accuracy  = as.numeric(accuracy)) %>%
  arrange(desc(accuracy)) %>%
  ggplot(aes(x=accuracy, y=study)) +
  geom_point() +
  theme_bw() +
  xlab('Classification Accuracy') +
  ylab('Study')
```




```
# needs implementation
```

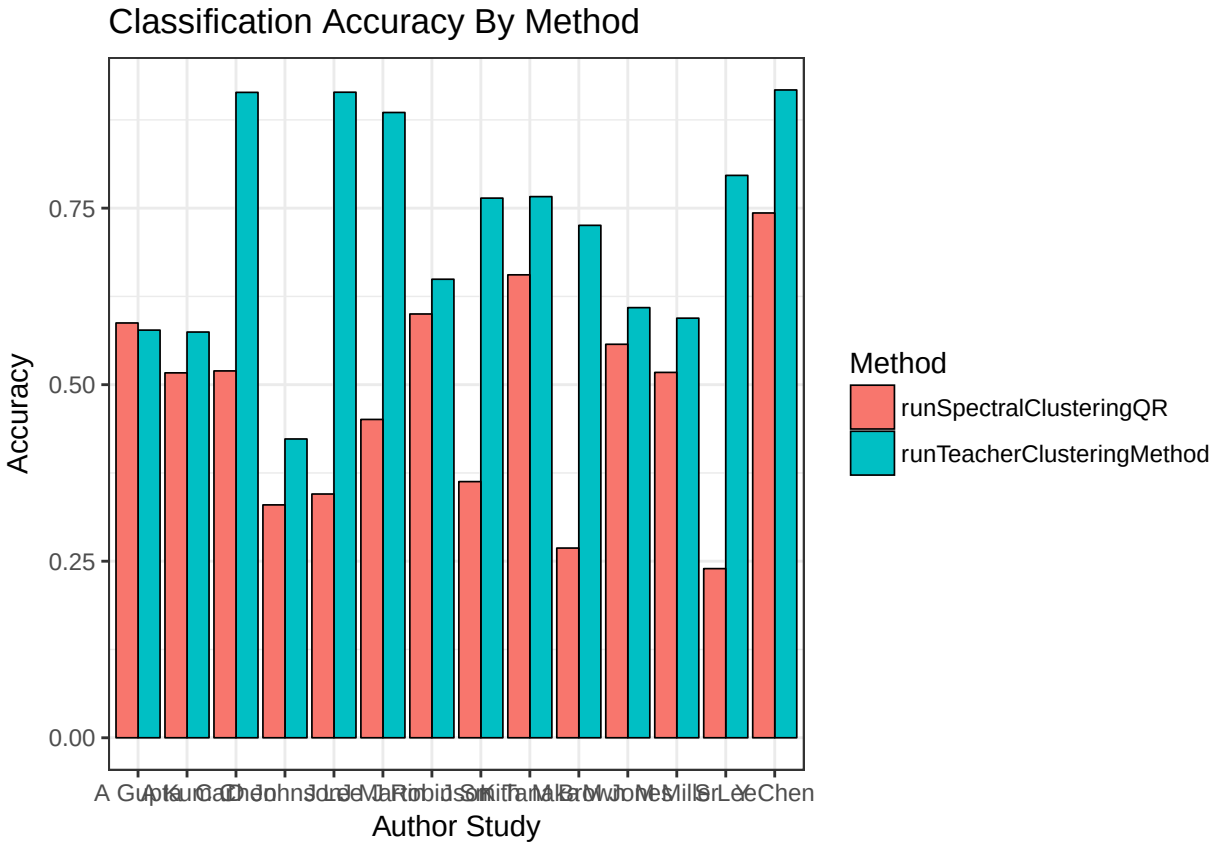
Alternate implementation of the plot

```
fj <- full_join(tb,tb_teacher) %>%
  mutate(accuracy = as.numeric(accuracy))
```

```
## Joining, by = c("study", "method", "precision", "recall", "f1", "accuracy", "mcc", "time")
```

plot

```
ggplot(data=fj, aes(x=study, y=accuracy, fill=method)) +
    geom_bar(colour="black", stat="identity",
             position=position_dodge(),
             size=.3) +                         # Thinner lines
    scale_fill_hue(name="Method") +      # Set legend title
    xlab("Author Study") + ylab("Accuracy") + # Set axis labels
    ggtitle("Classification Accuracy By Method") +     # Set title
    theme_bw()
```



General Notes on Spectral Clustering vs K-Means using Term Frequency:

Why TF-IDF? Term frequency counts the number of times a word from a corpus apprears in a particular document. Some words appear frequently in all documents (i.e. they are common locally). Other words appear rarely in the corpus (i.e. they are rare globally). Inverse document frequency weights words that appear rarely more heavily, implying that rare words are more important for determining the cluster assignment of a particular document than words that are common to all documents in a corpus. Importantly, TF-IDF can be used with

Distance measures

Scaled Euclidean Distance:

$$d(x_i, x_q) = \sqrt{a_1(x_i[1] - x_q[1])^2 + \ldots + a_d(x_i[d] - x_q[d])^2}$$

Cosine Similarity:

$$\frac{x_i^T x_q}{\|x_i\| \, \|x_q\|} = cos(\theta)$$

K-means algorithm

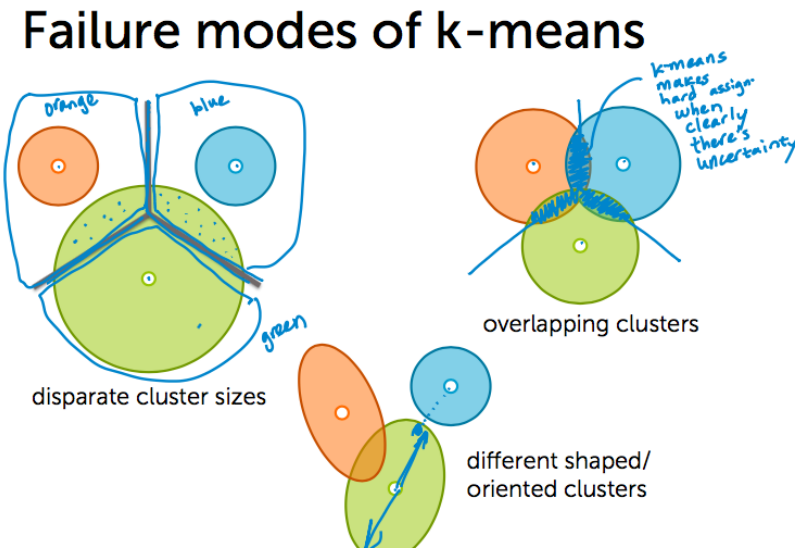
1. Initialize cluster centers
2. Assign observations to closest cluster center
3. Revise cluster centers as mean of assigned observations
4. Repeat steps 1 & 2 until convergence

Complexity of brute-force search

Given a query point, $O(N)$ distance computations per 1-NN query. By extension, $O(N \log k)$ distance computations per k-NN query.

Failure modes of k-means

- disparate cluster sizes
- overlapping clusters
- different shaped / oriented clusters



In the most basic implementation, k-means tries to make cluster assignments of documents using euclidean distances based on distances from cluster centers:

$$z_i \leftarrow \arg\min \left\| u_j - \mathbf{x}_i \right\|_2^2$$

This method is problematic because only the center of the cluster matters. In other words, this method assumes that clusters are spherically symmetric. Although weighted Euclidean distances could be used, we would need to know which weights were appropriate, and even with weights, the clusters would still have the same axis-aligned ellipses.

In the author disambiguation problem, we are faced with a conundrum, namely that kmeans generally fails to give good results when the distance metric used produces 'overlapping' clusters. Since authors that share names may work in related fields, this type of disambiguation problem calls for a more probabalistic approach. This is the motivation for using 'mixture models,' which enables clustering based on **learned weightings** of features when computing cluster assignments.

Section II: Paper 6

"A Constraint-Based Probabilistic Framework for Name Disambiguation"

In this paper, Zhang, Tang, Li, and Wang propose a mixture model using the expectations maximization algorithm to perform name disambiguation. They propose a 'semi-supervised' framework to "combine the advantages of supervised and unsupervised methods." What does this mean in practice? Essentially, we are trying to figure out the

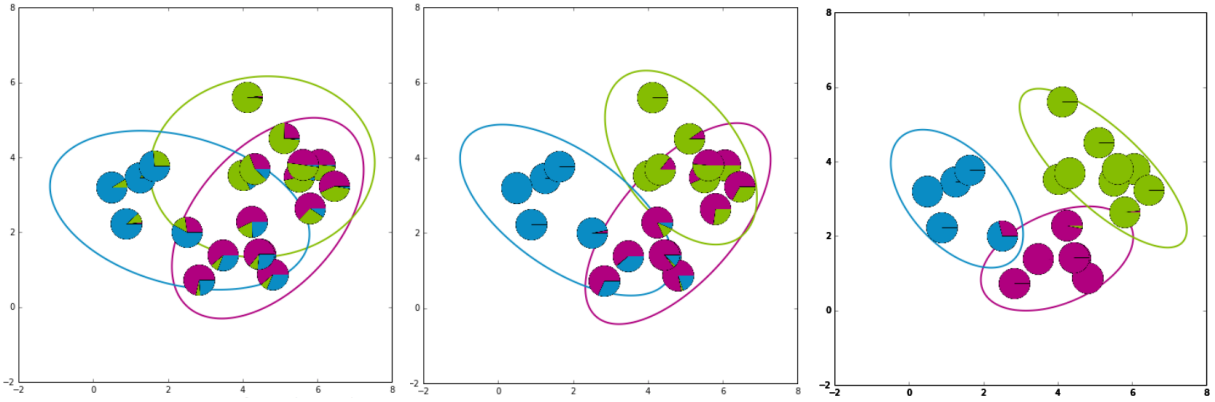


Table 2 contstraints:

c_2 for any two papers, if they share a co-author, c_2 is 1, otherwise is 0 c_6 if co-authors of any two papers are are also

Minimize the objective function by using EM algorithm:

Objective Function:

$$\max p(Y|X) \propto \min f_{obj} = \sum_i \sum_j \{D(x_i, x_j) I(l_i \neq l_j) \sum_{c_k \in C} [w_k c_k(p_i, p_j)]\} + \sum_{x_i \in X} D(x_i, y_{l_i}) + \log Z$$

where,

$$D(x_i, y_{l_i})$$

is the distance between paper i and researcher y_{l_i} w_k is the weight of for c_k Z is the normalization factor

Constraints: The constraint function is a Boolean-valued function and is defined as follow:

$$c(p_i, p_j) = \begin{cases} 1, & \text{if } p_i \text{ and } p_j \text{ satisfy the constraint } c_l \\ 0, & \text{otherwise} \end{cases}$$

We define six types of constraints and formalize them in the framework. We propose employing EM algorithm to learn different distance metric for different persons.

The rest of the paper is organized as follows. In Section 2, we review related work. In Section 3, we formalize the disambigua- tion problem. In Section 4, we explain our approach to the prob- lem and in Section 5, we give the experimental results. We con- clude the paper in Section 6.

Our method is based on a unified probabilistic model using Hid- den Markov Random Fields (HMRF). This model incorporates constraints and a parameterized-distance measure. The disam- biguation problem is cast as assigning a tag to each paper with each tag representing an actual researcher yi.

a-posteriori probability as the objective function

We aims at finding the maximum of the objective

Six types of constraints are incorporated into the objec- tive function, where constraints are considered as a form of su- pervision. If one paper's label assignment violates a constraint, it will be penalized in some sense, which in turn affects the result.

The EM process can be summarized as follows: in the E-step, given the current researcher representatives (the set of assigned papers), every paper is re-assigned to the researcher by maximiz- ing p(Y|X). In the M-step, the researcher representative yh is re- estimated from the assignments to maximize p(Y|X) again, and the distance measure is updated to increase the objective function.

In the E-step, assignments of data points to researchers are up- dated to maximize the $p(Y\|X)$. A greedy algorithm is used to se- quentially update the assignment of each paper

Three tasks are executed by the Expectation Maximization (EM) method: learning parameters of the distance measure, re- assignment of paper to researchers, and update of researcher rep- resentatives yk. We define our distance function $D(x_i, x_j)$ as follows:

$$D(x_i, x_j) = 1 - \frac{x_i^T \mathbf{A} x_j}{\|x_i\|_A \|x_j\|_A}$$

, where

$$\|x_i\|_A = \sqrt{x_i^T \mathbf{A} x_j}$$

Each paper xi is assigned to yh that minimizes the function:

$$f(y_h, x_i) = \sum_i D(x_i, y_h) + \sum_{i,j \neq i} \{D(x_i, x_j) \sum_{c_k \notin C} [w_k c_k(x_i, x_j)]\}$$

In the M-step, each researcher representative is updated by the arithmetic mean of its points:

$$y_h = \frac{\sum_{i:l_i=h} x_i}{\left\| \sum_{i:l_i=h} x_i \right\|_A}$$

Step 1: Load and process the data

```
AKumar <- read.csv(file.path(projDir,"output","AKumar.csv"))
AGupta <- read.csv(file.path(projDir,"output","Agupta.csv"))
CChen <- read.csv(file.path(projDir,"output","CChen.csv"))
DJohnson <- read.csv(file.path(projDir,"output","DJohnson.csv"))
JLee <- read.csv(file.path(projDir,"output","JLee.csv"))
JMartin <- read.csv(file.path(projDir,"output","JMartin.csv"))
JRobinson <- read.csv(file.path(projDir,"output","JRobinson.csv"))
JSmith <- read.csv(file.path(projDir,"output","JSmith.csv"))
KTanaka <- read.csv(file.path(projDir,"output","KTanaka.csv"))
YChen <- read.csv(file.path(projDir,"output","YChen.csv"))
SLee <- read.csv(file.path(projDir,"output","SLee.csv"))
MMiller <- read.csv(file.path(projDir,"output","MMiller.csv"))
MJones <- read.csv(file.path(projDir,"output","MJones.csv"))
MBrown <- read.csv(file.path(projDir,"output","MBrown.csv"))
```

```
# Write a function to calcuate the DTM for paper
dtm_paper <- function(df) {
  it_train <- itoken(as.character(df$Paper),
                     preprocessor = tolower,
                     tokenizer = word_tokenizer,
                     ids = nrow(df),
                     # turn off progressbar because it won't look nice in rmd
                     progressbar = FALSE)
  vocab <- create_vocabulary(it_train, stopwords = c("a", "an", "the", "in","on","at", "of", "above", "
  # Now that we have a vocabulary list, we can construct a document-term matrix.
  vectorizer <- vocab_vectorizer(vocab)
  dtm_train <- create_dtm(it_train, vectorizer)

  return(dtm_train)
}

# Write a function to calcuate the DTM for coauthor
dtm_coauthor <- function(df) {
  it_train <- itoken(as.character(df$Coauthor),
                     preprocessor = tolower,
                     tokenizer = word_tokenizer,
                     ids = nrow(df),
                     # turn off progressbar because it won't look nice in rmd
                     progressbar = FALSE)
  vocab <- create_vocabulary(it_train)
  # Now that we have a vocabulary list, we can construct a document-term matrix.
  vectorizer <- vocab_vectorizer(vocab)
  dtm_train <- create_dtm(it_train, vectorizer)

  return(dtm_train)
}

# Write a function to calcuate the DTM for Journal
dtm_journal <- function(df) {
  it_train <- itoken(as.character(df$Journal),
                     preprocessor = tolower,
                     tokenizer = word_tokenizer,
                     ids = nrow(df),
                     # turn off progressbar because it won't look nice in rmd
                     progressbar = FALSE)
  vocab <- create_vocabulary(it_train)
  # Now that we have a vocabulary list, we can construct a document-term matrix.
  vectorizer <- vocab_vectorizer(vocab)
  dtm_train <- create_dtm(it_train, vectorizer)

  return(dtm_train)
}
```

Then, we want to use DTM to compute TF-IDF transformation on DTM.

```
dtm_paper_tfidf <- function(df) {
  tfidf <- TfIdf$new()
  return(fit_transform(dtm_paper(df), tfidf))
}
```

```
dtm_coauthor_tfidf <- function(df) {
  tfidf <- TfIdf$new()
  return(fit_transform(dtm_coauthor(df), tfidf))
}

dtm_journal_tfidf <- function(df) {
  tfidf <- TfIdf$new()
  return(fit_transform(dtm_journal(df), tfidf))
}

# We want to combine the three citations together
dtm_tfidf <- function(df) {
  total <- cbind(dtm_paper_tfidf(df), dtm_coauthor_tfidf(df), dtm_journal_tfidf(df))
  return(total)
}

# pap <- dtm_paper_tfidf(AGupta)
# coa <- dtm_coauthor_tfidf(AGupta)
# jor <- dtm_journal_tfidf(AGupta)

## compute cosine similarities matrix (Gram Matrix)
docsdissim <- function(df) {
  cosSparse(t(dtm_tfidf(df)))
}
```

Step 3: Clustering

Following suggestion in the paper 6, we carry out hierarchical clustering method under the cosine distance as the baseline method. The number of clsters is assumed known as stated in the paper.

```
basemodel <- function(df) {
  cossim <- docsdissim(df)
  rownames(cossim) <- c(1:nrow(dtm_tfidf(df)))
  colnames(cossim) <- c(1:nrow(dtm_tfidf(df)))

  h <- hclust(as.dist(cossim), method = "ward.D") #
  result_hclust <- cutree(h,length(unique(df$AuthorID))) # {stats} package
  return(result_hclust)
}

basemodel_AGupta <- basemodel(AGupta)
basemodel_AKumar <- basemodel(AKumar)
# start.time <- Sys.time()
# cossim <- docsdissim(AGupta)
# rownames(cossim) <- c(1:nrow(dtm_tfidf(AGupta)))
# colnames(cossim) <- c(1:nrow(dtm_tfidf(AGupta)))
#compute pairwise cosine similarities using cosSparse function in package qlcMatrix
# h <- hclust(as.dist(cossim), method = "ward.D")
# result_hclust <- cutree(h,length(unique(AGupta$AuthorID)))
# end.time <- Sys.time()
# time_hclust <- end.time - start.time
# table(result_hclust)
```

```
matching_matrix_hclust_AGupta <- matching_matrix(AGupta$AuthorID,basemodel_AGupta)
performance_hclust_AGupta <- performance_statistics(matching_matrix_hclust_AGupta)

matching_matrix_hclust_AKumar <- matching_matrix(AKumar$AuthorID,basemodel_AKumar)
performance_hclust_AKumar <- performance_statistics(matching_matrix_hclust_AKumar)

compare_df <- data.frame(author=c("AGupta","AKumar"),
                         precision=c(performance_hclust_AGupta$precision, performance_hclust_AKumar$pre
                         recall=c(performance_hclust_AGupta$recall, performance_hclust_AKumar$recall),
                         f1=c(performance_hclust_AGupta$f1, performance_hclust_AKumar$f1),
                         accuracy=c(performance_hclust_AGupta$accuracy, performance_hclust_AKumar$accura

kable(compare_df, format = "markdown", caption="Comparision of performance for two clustering methods",
```

author	precision	recall	f1	accuracy
AGupta	0.08	0.04	0.05	0.86
AKumar	0.19	0.07	0.10	0.74