Project 4 - Example Main Script

Team 11 3/22/2017

Summary:

In this project, we implemented, evaluated and compared the algorithms in paper 1: Information Processing and Management (Kang 2009), and paper 5: Author Disambiguation using Error-driven Machine Learning with a Ranking Loss Function(Culotta 2007) for Entity Resolution. We created an author disambiguation system that divides the same-name author occurrences in citation data into different clusters, each of which are expected to correspond to a real individual. Paper 1 suggested a single-link agglomerative clusering algorithm and each name occurrence is represented by a set of his/her coauthor names. Specifically, we set the number of overlapping coauthors to 1. We also used hierarchical clustering. In addition, we implemented Cluster Scoring Function, Error-driven Online Training, and Ranking MIRA. After comparing these two methods,

Step 0: Load the packages, specify directories

```
if (!require("pacman")) install.packages("pacman")

## Loading required package: pacman

pacman::p_load(text2vec, plyr,qlcMatrix, kernlab, knitr)
setwd("~/Spr2017-proj4-team-11/doc")
```

Step 1: Load and process the data

For each record in the dataset, there are some information we want to extract and store them in a regular form: canonical author id, coauthors, paper title, publication venue title.

After generated a list of 14 elements using Professor Zheng's code, we reorganizes it into a list of 14 dataframes for easier access and processing.

```
source("../lib/dataclean.R")
```

Step 2: Feature design

Feature design

Paper 1 : Following the section 5.2, that each name occurrence is represented by a set of his/her coauthor names.

Paper 5: We want to use coauthors, paper titles and journey titles to design features for citations. We count the same-coauthor occurrences, and used bigram, trigram, TF-IDF, edit distance... to extract features from paper title and journey title.

```
# source("../lib/coauthormatrix.R")
load("../data/sim_matrix.RData")
```

Step 3: Clustering

We used a hierarchical clustering method for both paper 1 and paper 5. The algorithm also follows section 5.2 in paper 1.

Algorithm 2

Agglomerative Clustering for Same-name Author Occurrences

```
Input:
                                           a_1, \ldots, a_n; same-name author occurrences
                                           a_i = \{v_{i1}, \dots, v_{im}\}; each name occurrence a_i has a set of m (m \ge 0) his/her coauthor names
                                           \theta; a cluster-merging threshold
Initialize:
                                           c_i = \{a_i\}; consider each name occurrence a_i as an element of cluster c_i
Loop:
                                           DO
                                                For each cluster-pair (c_i, c_i), calculate CSim(c_i, c_i)
3
                                                   CSim(c_i,c_j) = max(ASim(a_x, a_y)), \forall a_x \in c_i, \forall a_y \in c_j
                                                   ASim(a_x,a_y) = |a_x \cap a_y|
5
                                                Find the most similar cluster-pair (c_u, c_v)
                                                   (c_u, c_v) = \operatorname{argmax} CSim(c_i, c_j)
                                                c_{u\_v} = c_u \cup c_v; merge c_u and c_v into a new larger cluster c_{u\_v} ENDIF
                                                IF CSim(c_u, c_v) \ge \theta THEN
10
                                           WHILE (CSim(c_u, c_v) \geqslant \theta)
Output:
                                           Clusters of author occurrences: \{c_k\}
```

For paper 1, we considered two scenarios : we combine all the single-element cluster; or we don't combine them.

```
source("../lib/singlelink.R")
start.time <- Sys.time()
# cluster_temp.list <- NULL
# cluster_temp.list <- llply(simmatrix.list,singlecluster,theta=1)
load("../doc/cluster_temp_1.RData")
cluster.combined <- NULL
cluster.combined <- llply(cluster_temp.list,comninecluster)
cluster.notcombined <- NULL
cluster.notcombined <- llply(cluster_temp.list,splitcluster)
end.time <- Sys.time()
time_scluter <- end.time - start.time
# combind cluster table for AGupta
table(cluster.combined[[1]])</pre>
```

##																		
##	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
##	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54
##	1 55	1 56	1 57	1 58	1 59	1 60	1 61	1 62	1 63	1 64	1 65	1 66	1 67	1 68	1 69	1 70	1 71	1 72
##	55 1	1	1	50 1	59 1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	91	92	93	94	95	96	97	98	99	100	101	_	103	_	105	106	107	108
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	145	146	147	148	149		151			154			157		159	160	161	162
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	163	164	165	166	167		169	170		172					177	178	179	180
##	1	1	1	1	1	1	1	1	1	1 190	1	1	1	1	1 195	1	1	1
##	181 1	182 1	183	184 1	185 1	186 1	187 1	188 1	189 1	190	191	192 1	193	194 1	195	196 1	197 1	198 1
##	199	200	201			204				208			211		213	214	215	216
##	1	1	1	1	1	1	200	1	1	1	1	1	1	1	1	1	1	1
##	217	218	219	220	221	222		224		_	227		229	230	231	232	233	234
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	271	272	273	274	275	276	277	278				282			285	286	287	288
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	289	290 1	291 1	292 1	293 1	294 1	295 1	296 1	297 1	298 1	299	300	301	302 1	303	304	305	306
##	307				_	312		314				318			321	322	323	324
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	_	_	_	_		_	_	_	_	_				_	_	_	_	342
##				1													1	1
##	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
##	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
##	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378
##					1	1	1	1	1	1	1			1	1	1	1	1
				382														
##						1		1		1	1		1		1	1	1	1
				400														
##						1				1					1	1	1	1
##			417	418 1		420	421	422	423	424	425		427		429	430	431	432
																		450
##	±33	+04	+30	430	±31	430	±33	440	441	442	443	444	440	440	441	440	443	400

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```

Here, I only showed the cluster result of a subset of the data, "AGupta.txt" to further illustrate the difference of these two scenarios.

Evlatuion

Step 4: Evaluation

To evaluate the performance of the method, it is required to calculate the degree of agreement between a set of system-output partitions and a set of true partitions. In general, the agreement between two partitions is measured for a pair of entities within partitions. The basic unit for which pair-wise agreement is assessed is a pair of entities (authors in our case) which belongs to one of the four cells in the following table (Kang et at.(2009)):

Matching matrix for the agreement between two sets of clusters

	Gold standard clusters (G)			
		Match	Mismatch	
Machine-generated clusters (M)	Match Mismatch	a c	b d	

Let M be the set of machine-generated clusters, and G the set of gold standard clusters. Then, in the table, for example, a is the number of pairs of entities that are assigned to the same cluster in each of M and G. Hence, a and d are interpreted as agreements, and b and c disagreements. When the table is considered as a confusion matrix for a two-class prediction problem, the standard "Precision", "Recall", "F1", and "Accuracy" are defined as follows.

$$\begin{aligned} & \text{Precision} = \frac{a}{a+b} \\ & \text{Recall} = \frac{a}{a+c} \\ & \text{F1} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \\ & \text{Accuracy} = \frac{a+d}{a+b+c+d} \end{aligned}$$

```
source("../lib/evaluation_measures.R")
#### paper 1
matching_matrix_single <- NULL
matching_matrix_combined <- NULL</pre>
for (i in 1:14){
  matching_matrix_single[[i]] <- matching_matrix(data[[i]],cluster.notcombined[[i]])</pre>
  matching matrix combined[[i]] <- matching matrix(data[[i]],cluster.combined[[i]])</pre>
}
f1.list.single <- NULL
accuracy.list.single <- NULL
f1.list.combined <- NULL
accuracy.list.combined <- NULL
clustering_errors_single <- NULL</pre>
clustering_errors_combined <- NULL</pre>
for (i in 1:14){
  f1.list.single[i] <- performance_statistics(matching_matrix_single[[i]])$f1
  f1.list.combined[i] <- performance_statistics(matching_matrix_combined[[i]])$f1</pre>
  accuracy.list.single[i] <- performance_statistics(matching_matrix_single[[i]]) $accuracy
  accuracy.list.combined[i] <- performance_statistics(matching_matrix_combined[[i]]) $accuracy
}
```

Step 3: Clustering

Following suggestion in the paper, we carry out spectral clustering on the Gram matrix of the citation vectors by using R function specc() in *kernlab*. The number of clusters is assumed known as stated in the paper.

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