

FINAL PROJECT REPORT

SEARCH RETRIEVAL SYSTEM

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CSC 575: INTELLIGENT INFORMATION RETRIEVAL

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Introduction:

Many clinical trials require patients for the studies that are to be conducted for the trials in the medical research, but due to the high rate of insufficient patients recruitment, there's a possibility that the study or trial may need to be terminated permanently.

The TREC clinical trials track has concluded to perform the trials in a way such that a patient who has similar disease or who has the similar symptoms related to a particular study, all their medical history and records are needed to be updated on the clinicaltrials.gov website so that the different doctor/researcher can refer to the previous trial that has already been performed. The data set is broken down into eligible and non-relevant queries to distinguish between patients who have sufficient information from people who have insufficient information about the disease or trial being conducted.

The structured data is helpful for clinical trials as the description of the patient that is mentioned in the data set is only limited to his or her disease topics. The TREC clinical trials provides a platform for doctors or researchers a platform, for evaluating patients matching symptoms for clinical trial requirements, for example if a researcher comes all the way to the middle of the research and then something bad happens to the patient and then after some time a person researcher gets a similar patient from the point where the previous research was held he can continue from there instead of starting the whole research from the beginning which can be more effective and save time in the field of medical research.

About Dataset:

In the dataset of 2021 Clinical Trials Track, we have data of several different patient's cases that are created by people who have received medical training.

The information of patients is recorded in an .xml file, where we have:

- 1. Task: which is "2021 TREC Clinical Trials"
- 2. Number: patient case number recorded.
- 3. Description: in the form of corpus, where we have detailed description of patient, like how old he/she is, their gender, which department dealt with their case, and what disease or symptoms they had, and the detailed medical report of what all things have been identified by the practitioner.

Functions and Implementation:

Since we have five zip files we are combining into a single zip:

- 1. ClinicalTrials.2021-04-27.part1.zip
- 2. ClinicalTrials.2021-04-27.part2.zip
- 3. ClinicalTrials.2021-04-27.part3.zip
- 4. ClinicalTrials.2021-04-27.part4.zip
- 5. ClinicalTrials.2021-04-27.part5.zip

This will give us Final_combined_ClinicalTrials.zip.

Each of the zip file contains 500+ .xml files. Looping through each xml and extracting only useful tags and converting it into a Data Frame.

Important Columns in the clinical trials dataset:

['org_study_id', 'nct_id', 'brief_title', 'sponsor_agency', 'brief_summary', 'detailed_description', 'condition', 'eligibility_condition', 'eligibility_gender', 'eligibility_minage', 'eligibility_maxage']

df	df_clinical_trial.head()													
	org_study_id	nct_id	brief_title	sponsor_agency	brief_summary	detailed_description	condition	eligibility_condition	eligibility_gender	eligibility				
0	NCRR- M01RR01070- 0506	D000102	Congenital Adrenal Hyperplasia: Calcium Channe	National Center for Research Resources (NCRR)	This study will test the ability of extended r	This protocol is designed to assess both acute	Congenital Adrenal Hyperplasia	Inclusion Criteria: - diagnosed	All					
1	NCRR- M01RR00400- 0587	D000104	Does Lead Burden Alter Neuropsychological Deve	National Center for Research Resources (NCRR)	Inner city children are at an increased risk f		Lead Poisoning	Inclusion Criteria: - Pregnant m	Female					
2	2002LS032	D000105	Vaccination With Tetanus and KLH to Assess Imm	Masonic Cancer Center, University of Minnesota	The purpose of this study is to learn how the	Patients will receive each vaccine once only c	Cancer	Inclusion Criteria: - Patients m	All					
3	NCRR- M01RR03186- 9943	D000106	41.8 Degree Centigrade Whole Body Hyperthermia	National Center for Research Resources (NCRR)	Recently a non- toxic system for whole body hyp		Rheumatic Diseases	Inclusion Criteria: - Patients a	All					

1. Corpus

Converting of pd.DataFrame to a dictionary where 'nct_id' is our index, 'brief_summary', 'detailed_description', 'condition', 'eligibility_condition' and 'brief_title' and these columns are combined to form our document data for each document ID.

2. Queries

Fetching the data from the URL 'https://www.trec-cds.org/topics2021.xml' and converting it into pd.DataFrame for queries.

3. Pre-Processing of Corpus:

First, we have removed punctuations, then we converted our string to lower case and then split it into a list, and used a nltk package to fetch the stop words and performing stemming. This removed the stop words and do the stemming for the whole corpus dataset.

```
preprocessing_documents()

{'D000102': ['protocol',
    'design',
    'assess',
    'acut',
    'chronic',
    'effect',
    'calcium',
    'channel',
    'antagonist',
    'nifedipin',
    'hypothalamicpituitaryadren',
    'axi'.
```

Counting the occurrences of each word in the document with document id and frequency, we get the output as below.

Output:

```
Word
          Total Fred
                                                    Posting(Doc-ID, Count)
                               Document Freq
aa 18 11 [('D000451', 1), ('D000640', 3), ('D000655', 2), ('D000715', 2), ('D000717', 2), ('D000722', 2), ('D000724', 2), ('D000781', 1), ('D000863', 1), ('D000881', 1), ('D001013', 1)]
                                                          [('D001103', 1), ('D001117', 1)]
[('D001103', 2)]
aactg
                                       2
aactgsponsor
                   2
                                       1
                                                           [('D000478', 1)]
[('D000864', 2), ('D000885', 1), ('D000903', 1), ('D000912', 1), ('D000919', 1),
aand
abacavir
                                       10
('D000922', 1), ('D000940', 1), ('D001086', 2), ('D001118', 2), ('D001119', 1)]
abandon
                                                           [('D000126', 1), ('D000586', 2)]
[('D000604', 1)]
                                      2
abat
                                                          [('D000679', 1), ('D000704', 1), ('D000718', 1), ('D000735', 1), ('D001009', 1)]
[('D000468', 1), ('D001097', 1)]
[('D000864', 10), ('D000872', 1), ('D000885', 11), ('D000912', 4), ('D000919',
abbott
abbrevi
                   48
ahc
4), ('D000922', 2), ('D000940', 2), ('D001086', 11), ('D001119', 3)] abdomen 2 2 [('D000571', 1), ('D001118', 1)]
abdomin
                   9
                                                           [('D000410', 1), ('D000502', 1), ('D000619', 2), ('D000668', 2), ('D000742', 1),
('D000927', 1), ('D001054', 1)]
                                                           [('D000394', 1)]
abductor
                                                           [('D000938', 1), ('D001101', 1)]
```

4. Calculating IDF

Writing a function to compute the IDF values of the terms present in the documents, we are creating a idf_dict which holds the IDF values for all the words.

```
def compute_tfidf(term, doc_id):
    tf = sorted_dict[term][doc_id]
    idf = math.log2(N / len(sorted_dict[term]))
    idf_dict[term]=math.log2(N / len(sorted_dict[term]))
    return tf * idf
```

Output:

```
idf dict
{'aa': 6.50635266602479,
  aactg': 8.965784284662087,
 'aactgsponsor': 9.965784284662087,
  aand: 9.965784284662087,
 'abacavir': 6.643856189774724,
 'abandon': 8.965784284662087,
 'abat': 9.965784284662087,
 'abbott': 7.643856189774724
 'abbrevi': 8.965784284662087,
 'abc': 6.795859283219775,
 'abdomen': 8.965784284662087,
 'abdomin': 7.158429362604483.
 'abductor': 9.965784284662087,
  aberr': 8.965784284662087,
  abg': 8.965784284662087,
 'abi': 9.965784284662087,
 'abil': 3.0350469470992008,
 'abl': 3.3658714424749596,
 'ablat': 7.380821783940931,
```

5. Synonyms for Query Expansion and Vector Representation of Query.

Our Original Query

```
q=queries_topics()['Queries'].loc[1]
q
```

'48 M with a h/o HTN hyperlipidemia, bicuspid aortic valve, and tobacco abuse who presented to his cardiologist on [**2148-10-1 **] with progressive SOB and LE edema. TTE revealed severe aortic stenosis with worsening LV function. EF was 25%. RV pressure was 41 and had biatrial enlargement. Noted to have 2+ aortic insufficiency with mild MR. He was sent home from cardiology clinic with Lasix and BB (which he did not tolerate), continued to have worsening SOB and LE edema and finally presented here for evaluation. NnDuring this admission repeat echo confirmed critical aortic stenosis showing left ventricular hypertrophy with cavit y dilation and severe global hypokinesis, severe aortic valve stenosis with underlying bicuspid aortic valve, dilated ascending aorta, mild pulmonary artery systolic hypertension. The patient underwent a preop workup for valvular replacement with preop che est CT scan and carotid US (showing moderate heterogeneous plaque with bilateral 1-39% ICA stenosis). He also underwent a cardiac cath with right heart cath to evaluate his pulm art pressures which showed no angiographically apparent flow-limiting coronary vartery disease.'

We have used this word2vec model and used to find different words/synonyms for our query expansion.

After synonym expansion

word2vec_model = gensim/.models.KeyedVectors.load_word2vec_format(r'GoogleNews-vectors-negative300.bin', binary=True)

After expanding the query, I have used the same pre-processing steps for queries as we have used for corpus main dataset by removing punctuations, stop words and stemming of each query.

We get the doclength, queries length, which helps us in getting the inverted index values.

To calculate the document length, we are taking the sum of the squares of document weights and multiplying them with their respective IDF values of their term. To calculate the cosine similarity, we are taking the square root of the tf_idf, and similarly to calculate dice and jaccard similarity, we take the sum of the tf_idf values.

To calculate the queries length, we take the sum of square of their respective weights.

To store the documents with their respective similarity score we create a hashmap.

To get the similar documents for the query we create a new hash map with zero scores and using the respective similarity we find the score for each document which is then run iteratively to find the term weights for the whole query and document ID.

```
doclength('Cosine')
 {88: 52.34522400686566
  391: 68.8333182632571
  827: 36.479099045668626,
  860: 51.48244626564064,
  1031: 123.85800401823795.
  594: 72.43232056054718,
  187: 88.29420531833908,
  451: 56.43759276363038
  1027: 59,42673819874818,
  75: 101.07253823659555,
  676: 64.32699841183141.
  247: 62.275927178992696.
  415: 76.11012066446108,
Queries Length
 querieslength(q, "Cosine")
```

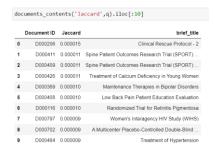
85.96852949851773

This gives us the output"

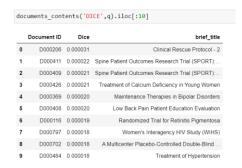
Cosine similarity values for our documents:



Jaccard similarity values for our documents:



Dice similarity values for our documents:



From our original corpus data, we have selected the title information and the similarity to show with respective to the document id.

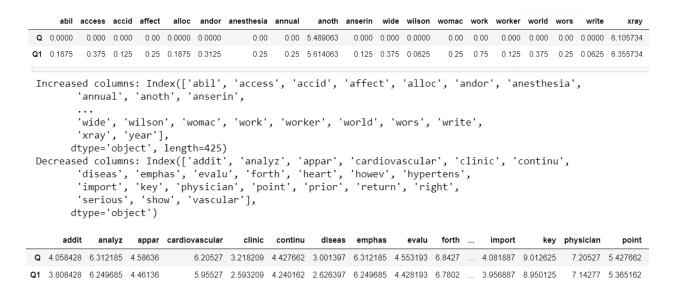
Query Expansion and Relevance Feedback:

Sometimes when a user enters a query, the terms may be not in his dictionary, so this is where rocchhio relevance feedback comes which ask the user about relevant and non-relevant documents and gives the new query.

This new query may have few added terms and may have few terms disregarded when compared to the original query.

By default, we have used alpha =0.5 and beta=0.25 to calculate the modified guery.

Output



Similarly, we have also found the cosine similarity of the old and new query with the documents.

Output:

sim_documents																
	D000451	D000640	D000655	D000715	D000717	D000722	D000724	D000781	D000863	D000881		D000804	D000195	D000201	D000248	D000267
Q	0.030363	0.042787	0.062930	0.034433	0.053253	0.030803	0.037903	0.052951	0.043168	0.046173		0.015526	0.000000	0.000000	0.012360	0.012360
Q1	0.049905	0.062739	0.077363	0.052517	0.070795	0.042710	0.058867	0.063837	0.057259	0.062395		0.028502	0.004361	0.008367	0.021112	0.017589

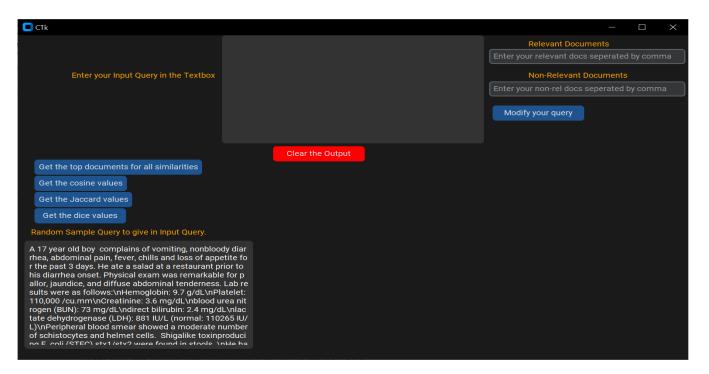
GUI APPLICATION:

We have created an interactive implementation of our search retrieval system using Tkinter module, where we enter the query and it gives us the combined results of the cosine similarity, jaccard similarity and dice similarity.

We also ask the user about the relevant and non-relevant documents and shows the suggested vocabulary terms which can be helpful in retrieving the desired sets of documents.

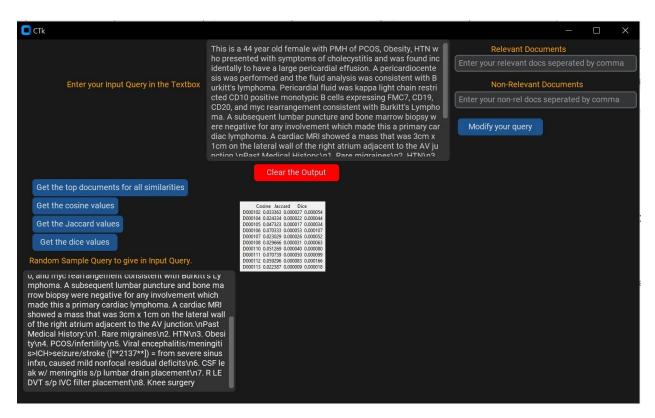
Since the queries are large, we have also created a random generator of query which is given to the user to select and see the result.

Output:

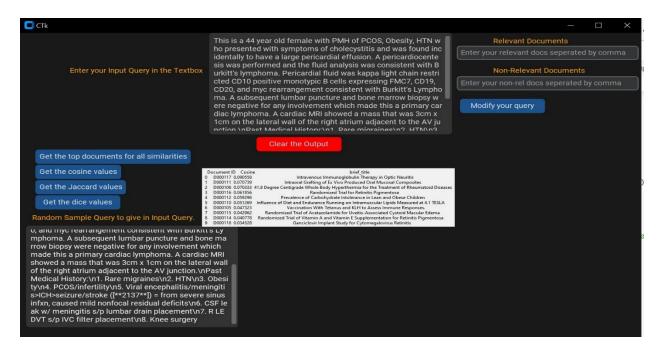


Entering the query:

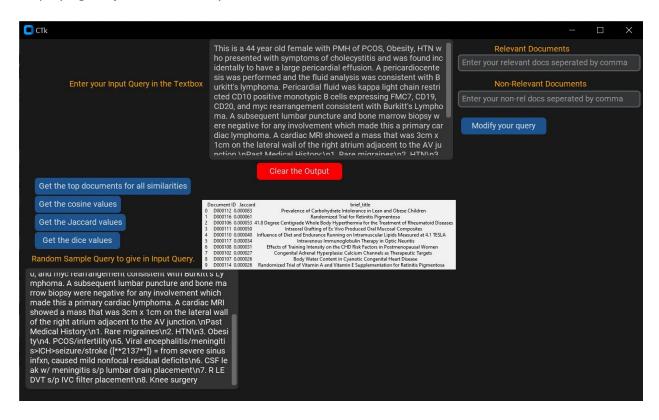
Getting all the similarity scores, with respect to the top 10 similar documents.



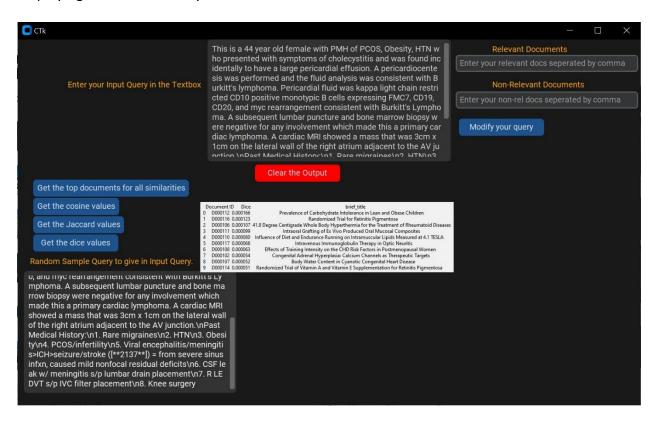
Displaying the cosine similarity scores:



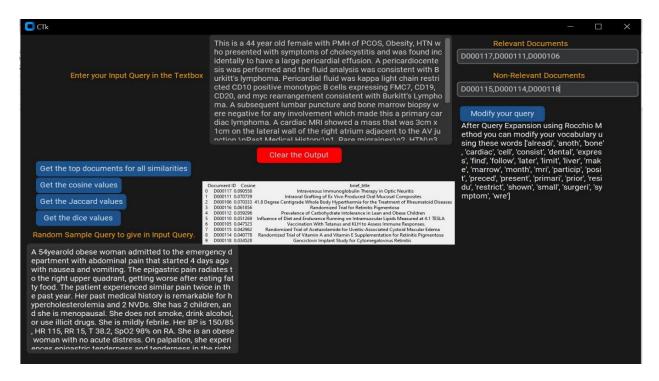
Displaying the jaccard similarity scores:



Displaying the dice similarity scores:



Giving the relevant and non-relevant documents it gives us the words that we can use in our vocabulary.



Evaluation:

The dataset used to evaluate our search/retrieval system is Medline dataset from the University of Glasgow.

The dataset can be obtained on http://ir.dcs.gla.ac.uk/resources/test collections/medl/

We have performed same pre-processing steps, term-weighting and inverted index as we have performed above and we got an precision of 0.6 and recall of 0.25.

From the above precision and recall values, we can say that our search/retrieval system works fairly well.

Appendices:

Here is the Jupyter Notebook and the HTML file for the search engine retrieval.





YouTube Link:

https://youtu.be/Kz1P5lzgqic