

Project Name	Medical Information Retrieval and Management		
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Prepared by	Group 11		

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# Workflow

### **Action Items**

Task or Deliverable	Task Owner
Identifying the dataset	Nikhil
Analyzing the dataset	Koushik
Loading and cleaning the dataset	Poojitha
Constructing Inverted Index	Koushik
Calculating TF-IDF	Poojitha
Calculation of Cosine similarity	Koushik
Implementing Document Summarization	Poojitha
Evaluation of Document Summarization	Nikhil
Final Report Creation	Poojitha,Nikhil,Koushi k
Frontend Implementation	Koushik

## **Abstract**

A critical component of healthcare systems is the management and retrieval of medical information. Managing and retrieving information has become a difficult undertaking as a result of the quick expansion of medical information. Medical personnel can access and recover patient information more quickly and conveniently with the use of a dependable medical information management and retrieval system, improving patient care. The purpose of this paper is to provide an overview of the idea of managing and retrieving medical information, the significance of doing so for healthcare, and the numerous approaches and technologies that can be used to do so. Healthcare professionals can more easily and rapidly access the relevant data by retrieving and summarizing medical reports, which will improve patient care.

Searching for and obtaining pertinent medical information from a variety of sources, including medical databases, electronic health records, and medical literature, is known as medical information retrieval. Finding medical records can take a while, especially when there is a lot of information involved. Medical information retrieval systems utilize machine learning and natural language processing to help healthcare providers find and quickly retrieve pertinent medical information.

Medical report summarizing is the creation of brief, intelligible summaries from medical records. Because medical reports are sometimes lengthy and filled with technical jargon, it can be challenging for healthcare professionals to immediately identify the pertinent information. Medical report summarizing systems collect the most crucial information from medical reports and condense it using machine learning algorithms and methods of natural language processing.

## **Project Design**

**Information Retrieval (IR):** IR is a design technique used to look for pertinent data in huge datasets. It is employed in medical information retrieval to extract pertinent patient data from clinical trial datasets, medical literature databases, and electronic health record systems.

**Natural Language Processing (NLP)**: NLP is a branch of artificial intelligence that focuses on processing and analyzing human language. It is a fundamental technology used in medical information retrieval and summarization of reports.

#### **Document search**

To retrieve the medical records from corpus we are using TF-IDF method to effectively retrieve a record based on user query. The acronym "Term Frequency – Inverse Document Frequency" stands for this. This method counts the number of words in a collection of documents. Each word is typically given a score to indicate how important it is to the document and corpus. Information retrieval and text mining applications frequently use this method.

Any computer language can more easily comprehend textual data when it is presented as a numerical value. Therefore, in order to better represent the text, we must vectorize all of it. We may further carry out numerous activities, such as locating the pertinent papers, rating, clustering, etc. by vectorizing the documents. When you conduct a google search, this specific method is employed.

TF-IDF = Term Frequency (TF) \* Inverse Document Frequency (IDF)

- t term (token)
- d document (set of tokens)
- N count of documents
- corpus the entire set of documents

### **Term Frequency**

The frequency of a word in a document depends on the length of the document and the generality of the word. To normalize the frequency value, we divide the frequency with the total number of words in the document.

tf(t,d) = count of t in d / number of words in d

### **Document Frequency**

The most important details are that TF is the frequency counter for a term in document d, while DF is the count of occurrences of term t in the document set N.

df(t) = occurrence of t in N documents

#### **Inverse Document Frequency**

IDF is the inverse of document frequency, which measures the informativeness of a term. It is low for the most frequent words, such as stop words, as they are present in almost all of the documents. This gives a relative weightage to the word.

$$tf-idf(t, d) = tf(t, d) * log(N/(df + 1))$$

### **Implementation**

#### **Dataset Analysis**

Analyzing the data is the first step in any machine learning activity. The dataset comprises of two folders containing English papers with various names. Different alignment patterns can be used to distinguish the title, however the majority are center aligned. Each folder contains an index.html file that may be used to browse the dataset. This file lists all the document names and their titles. In other words, the titles are provided to the user without being fully extracted from each document.

#### Loading and cleaning the dataset

Here we load text files into database for further searching the documents. Before any processing is done the data needs to be cleaned. Data Cleaning process helps to eliminate inconsistencies in the dataset. We remove things like special characters ,headings, newline characters, convert the text to lower case etc. We use UTF-8 encoding while reading the data from files to make sure consistency is maintained across all the documents.

#### **Constructing Inverted Index**

In this step we create an inverted index. An inverted index is a data structure used to search and efficiently retrieve information based on keywords. It works by mapping each unique word or term in a set of documents to the documents that contain it. Here are the steps to construct an inverted index.

**Tokenization:** Break each document into a sequence of words or terms. This process involves removing punctuation, converting all characters to lowercase, and removing stop words (common words like "and," "the," "a," etc. that do not provide meaningful information).

**Create a dictionary**: Create a dictionary that maps each unique word or term to an empty list. This dictionary will serve as the inverted index.

**Posting:** For each term in a document, add the document to the list of documents associated with that term in the dictionary. This process is known as posting.

**Sort the dictionary**: Sort the inverted index (dictionary) by the terms in alphabetical order.

#### **Calculating TF-IDF values**

Using the above formula we calculate the tf-idf value for each token in the query. We use the inverted index created to easily obtain the count of documents in which the token is present

#### **Ranking using Cosine Similarity**

The simplest way to determine how similar two documents are is to use the matching score, which adds the tf\_idf values of the tokens that are in the query for each document. For instance, we must determine whether a word is included in each document, and if it is, the tf\_idf value is added to the matching score of that specific doc\_id. The top k documents will be selected after sorting.

When we provide lengthy queries, Matching Score fails miserably because it cannot properly score the pages it provides as relevant. Cosine similarly measures the similarity in cosine space (the angle between the vectors) by marking all the documents as vectors of tf-idf tokens. Cosine similarity is the best way to determine relevance when the query length is modest but it may be strongly related to the document.

#### **Analyzing the results**

Here we view the resultant documents that are retrieved by the model. We are displaying the top 10 highly matching documents.

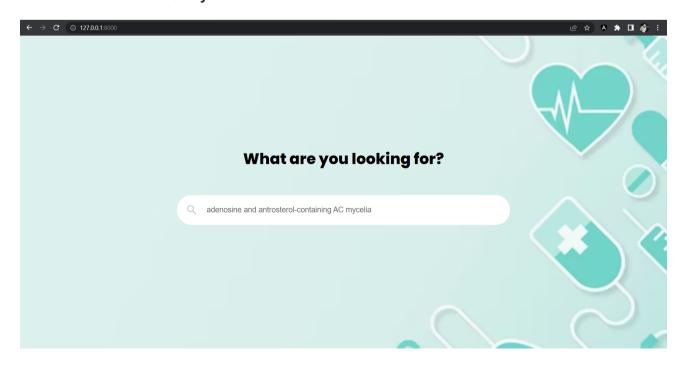
#### 1. Run the Django Server

```
Rint: See above for details.

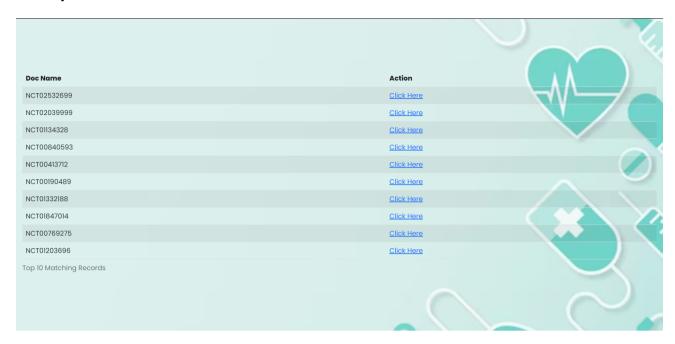
C:\Users\91949\OneDrive\Documents\Courses\Information Retrieval\Project\searchapp>python .\manage.py runserver
Watching for file changes with StatReloader
Performing system checks...

System check identified no issues (0 silenced).
April 20, 2023 - 20:00:50
Django version 4.2, using settings 'searchapp.settings'
Starting development server at http://127.0.0.1:8090/
Quit the server with CTRL-BREAK.
```

#### 2. Enter the Search Query



#### 3. Top 10 Documents



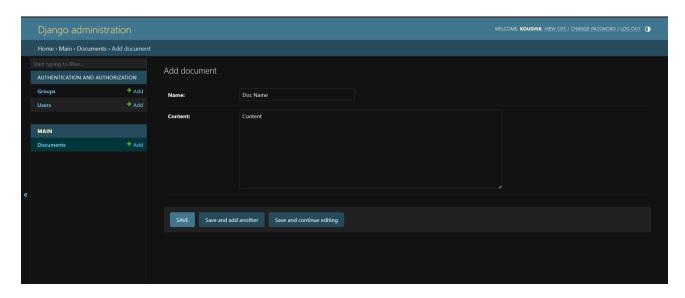
#### 4 View the contents of Documents

#### Document: NCT02532699

#### Content:

TITLE: Anti-hypertensive Effect of Mycelia of Antrodia Cinnamomea SUMMARY: This the first report undertaken to assess the effect of supplementation with oral gamma-aminobutyric acid GABA, adenosine and antrosterol-containing AC mycelia on blood pressure among people with mild hypertension. Overall, AC mycelia consumption for 8 weeks could successfully reduce mean diastolic and systolic BP through the suppression of PRA that is linked to downstream suppression of angiotensin || formation, which further decreases the sympathetic outflow that leads to hypertension. In addition to blood pressure lowering properties, AC mycelia also has beneficial effect in reducing oxidative stress, significantly. No adverse events were noted, suggesting that AC mycelia deserve its consideration as a candidate for safe alternative treatment to conventional anti-hypertensive medications. DETAILED DESCRIPTION: This the first report undertaken to assess the effect of supplementation with oral gamma-aminobutyric acid GABA, adenosine and antrosterol-containing AC mycelia on blood pressure among people with mild hypertension. Forty-one subjects with systolic blood pressure SBP between 130 and 179 mm Hg and/or diastolic blood pressure DBP between 85 and 109 mm Hg were randomized to receive either AC mycelia or starch placebo for 8 weeks, and had follow-up observation for an additional 2 weeks. SBP in the subjects given GABA, adenosine and antrosterol-rich AC mycelia significantly decreased compared to those who received the placebo p<0.05. DBP also decreased after the intake of AC mycelia. Compared to the placebo, AC mycelia significantly reduced plasma renin activity by a maximum of 25 % and 36 % on week 8. This suppression suggested that AC mycelia is a potent inhibitor of renin, and its bioavailability is sufficient to produce BP reduction after a short term of oral administration. Neither adverse events nor abnormal laboratory findings were noted throughout the study period, suggesting that GABA. adenosine and antrosterol-rich AC mycelia significantly decreased borderline hypertension, which may support its consideration as a safe alternative treatment compared to conventional anti-hypertensive medications. ELIGIBILITY CRITERIA: Inclusion Criteria: - Eligible subjects were untreated hypertensive men or women aged between 20 and 80 years old with SBP between 130 and 179 mmHg and/or DBP between 85 and 109 mmHg as measured in a sitting position Exclusion Criteria: - Subjects were excluded if they had a history of major cardiovascular disease, severe liver dysfunction, insulin-dependent diabetes mellitus or stroke. They were also excluded if they routinely consumed alcohol, were pregnant or unable to comprehend study instructions.

#### 5. Add new Documents



#### 6. View Data in Database

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SQL 1	,	〈 1 / 10 <b>〉</b> 1 - 50 of <b>498</b>
id	name	
539	NCT00000408	TITLE: Low Back Pain Patient Education Evaluation SUMMARY: Back pain is one of the most common of
540	NCT00000492	TITLE: Beta-Blocker Heart Attack Trial BHAT SUMMARY: To determine whether the regular administrat
541	NCT00000501	TITLE: Hypertension Prevention Trial HPT Feasibility Study SUMMARY: To test the feasibility and
542	NCT00001252	TITLE: Human Movement Database SUMMARY: This study will collect information on the different way:
543	NCT00001552	TITLE: Characteristics of Idiopathic Familial Voice Disorders SUMMARY: The purpose the study is
544	NCT00001853	TITLE: Diabetes and Heart Disease Risk in Blacks SUMMARY: It is unknown if obesity contributes to
545	NCT00001986	TITLE: 1-Octanol to Treat Essential Tremor SUMMARY: This study will evaluate the safety and effec
546	NCT00003702	TITLE: Methotrexate Compared With Dactinomycin in Treating Patients With Gestational Trophoblastic Neo
547	NCT00004727	TITLE: Antiplatelet Therapy to Prevent Stroke in African Americans SUMMARY: The African-American
548	NCT00005127	TITLE: Muscatine Heart Study SUMMARY: To conduct longitudinal and cross-sectional studies of risk
549	NCT00005485	TITLE: Environmental and Genetic Factors That Influence Cardiovascular Disease in African Americans SU
550	NCT00005757	TITLE: Racial Variation in ACEGenetic and Physiologic Bases SUMMARY: To determine whether diffe
551	NCT00006196	TITLE: The Relationship Between Vitamin D, Fingernail Thickness and Bone Density SUMMARY: Vitamin
552	NCT00011102	TITLE: Prevention of Weight Gain SUMMARY: The purpose of this study is to test methods for preven
553	NCT00043277	TITLE: Study Of Angiomax In Infants Under Six Months With Thrombosis SUMMARY: The goals of this
554	NCT00044876	TITLE: Treatment of Uterine Fibroids With CDB-2914, an Experimental Selective Progesterone Receptor And
555	NCT00061139	TITLE: Constraint-Based Therapy to Improve Motor Function in Children With Cerebral Palsy SUMMARY:
556	NCT00067691	TITLE: Acupuncture for Shortness of Breath in Cancer Patients SUMMARY: The purpose of this study
557	NCT00077948	TITLE: Enoximone Plus Extended-Release Metoprolol Succinate in Subjects With Advanced Chronic Heart Fa
558	NCT00080366	TITLE: Octanol to Treat Essential Tremor SUMMARY: This study will evaluate the effectiveness of

#### 7. Inverted Index



#### 8. Document Summarization

Here to summarize the large medical documents we are using the GENSIM summarizer. Gensim stands for "Generate Similar" is a popular open source natural language processing (NLP) library used for unsupervised topic modeling. It uses top academic models and modern statistical machine learning to perform various complex. Gensim is implemented in Python is designed to handle large text collections using data streaming as well as incremental online

algorithms. This makes it different from those machine learning software packages that target only in-memory processing.

#### Cleaning the data set

```
| Import re | Import options | Import sys | Import sys
```

#### Installing gensim using pip

```
Pipi install gensim=-3.6.0

Looking in indexes: https://pypi.org/simple, https://us-python.pkg.dev/colab-wheels/public/simple/
Collecting gensim=-3.6.0

Downloading gensim=-3.6.0 ab. tan-gz (23.1 MB)

Preparing metadata (setup.py) ... done
Requirement already satisfied: scipy>=0.11.3 in /usr/local/lib/python3.9/dist-packages (from gensim=-3.6.0) (1.22.4)
Requirement already satisfied: scipy>=0.18.1 in /usr/local/lib/python3.9/dist-packages (from gensim=-3.6.0) (1.10.1)
Requirement already satisfied: six>-1.5.0 in /usr/local/lib/python3.9/dist-packages (from gensim=-3.6.0) (1.10.1)
Requirement already satisfied: six>-1.5.0 in /usr/local/lib/python3.9/dist-packages (from gensim=-3.6.0) (1.6.0)
Requirement already satisfied: smart open>-1.2.1 in /usr/local/lib/python3.9/dist-packages (from gensim=-3.6.0) (6.3.0)
Building wheels for collected packages: gensim
Building wheel for gensim (setup.py) ... done
Created wheel for gensim (setup.py) ... done
Created wheel for gensim (setup.py) ... done
Created wheel for gensim (setup.py) ... done
Stored in directory: /root/.cache/pip/wheels/61/12/f2/84de20fba5e870553796b834d11109992f06ddc28aaead086

Successfully built gensim
Installing collected packages: gensim
Attempting uninstall: gensim
Found existing installation: gensim 4.3.1
Uninstalling gensim=4.3.1:
Successfully uninstalled gensim=4.3.1
Successfully uninstalled gensim=4.3.1
```

#### Summarized documents

```
[4] from gensim.summarization import summarize

#Here we are using gensim summarize to summarize the text in the document

print(summarize(DOCUMENT, ratio-0.2, split-False))

This study will develop and evaluate an approach to low back pain that allows subjects to talk with each other and with health professionals via an Internet discussion group.

This study will develop and evaluate in a randomized trial a low back pain intervention that allows subjects to talk with each other and with health professionals via an Internet discussion group.

[5] print(summarize(DOCUMENT, word_count-50, split-False))

This study will develop and evaluate an approach to low back pain that allows subjects to talk with each other and with health professionals via an Internet discussion group.

This study will develop and evaluate in a randomized trial a low back pain intervention that allows subjects to talk with each other and with health professionals via an Internet discussion group.

This study will develop and evaluate in a randomized trial a low back pain intervention that allows subjects to talk with each other and with health professionals via an Internet discussion group.
```

## **Project Milestones**

The following are the milestones of this project.

- **1. Data Collection:** Collect data from various sources such as medical literature databases, clinical trial datasets, and other relevant sources.
- **2. Data Preprocessing:** The collected data to remove noise, normalize the data, and convert it into a structured format that can be analyzed and features are extracted.
- **3. Frontend Development :** The UI part of the project is developed using HTML, CSS, Bootstrap enable end users to search for medical information and to show relevant information.
- 4. **Backend Development:** The supporting backend is developed for the system we used Django, Python, SQLite database.
- **5. Information Retrieval Model Development:** Here we developed an information retrieval model using TF-IDF model that can search for relevant information in large datasets
- **6. Text Summarization Model Development:** Here we developed a text summarization model that can summarize relevant information from unstructured data, such as clinical notes or medical literature. We used the GENSIM model to summarize the medical information.
- **7. Evaluation:** The eighth milestone is to evaluate the models and the models are evaluated using different evaluation metrics.

### **Evaluation Results**

To evaluate the model we are using using cosine similarity we are ranking the order of the medical documents. We are using rouge metric to evaluate the summarizer and calculate the Precision, recall and F1 score. Recall-Oriented Understudy for Gisting Evaluation (ROUGE) is a widely used metric to evaluate the quality of automatic summarization systems. It measures the overlap between the generated summary and the reference summary in terms of n-gram overlap, sentence similarity, and other measures. Gensim provides a ROUGE implementation, which can be used to calculate ROUGE scores.

#### **Evaluation of Summarizer**

```
Summary = summarize(DOCDERT, word_count-50, split-false)
print(summary)

D. His study will develop and evaluate an approach to low back pain that allows subjects to talk with each other and with health professionals via an intermet discussion group.
This study will develop and evaluate in a randomized trial a low back pain intervention that allows subjects to talk with each other and with health professionals via an intermet discussion group.

[18] |pip install rouge

| Develop |
```

#### **Latent Semantic analysis**

```
[14] # remove singular values below threshold
sy threshold = 0.5
min_sigma_value = max(singular_values) * cy_threshold
singular_values(singular_values) * cy_threshold
sp_singular_values(singular_values) * cy_threshold
sp_singular_values(singular_values
```

#### **Results of TF-IDF Model**

```
| Code |
```

### References

He, Y., Jiang, M., Wang, J., & Huang, X. (2018). Medical text mining and its applications in academic medicine. Journal of Healthcare Engineering, 2018, 2710652. doi: 10.1155/2018/2710652

Sarker, A., & Gonzalez, G. (2015). Portable automatic text summarization for medical articles: A multi-document summarization approach. Journal of Biomedical Informatics, 53, 314-329. doi: 10.1016/j.jbi.2014.12.004

Roberts, K., Rodriguez, L., Shojaee, A., & Demner-Fushman, D. (2018). A comparative study of different summarization algorithms on a clinical corpus. Journal of Biomedical Informatics, 86, 76-86. doi: 10.1016/j.jbi.2018.07.009

Luo, Y., Uzuner, O., Szolovits, P., & Starren, J. (2014). Segment convolutional neural networks (Seg-CNNs) for classifying relations in clinical notes. Journal of the American Medical Informatics Association, 22(2), 253-265. doi: 10.1136/amiajnl-2013-002091

https://radimrehurek.com/gensim/intro.html#:~:text=Gensim%20is%20a%20free%20open,u sing%20unsupervised%20machine%20learning%20algorithms.

https://en.wikipedia.org/wiki/Tf%E2%80%93idf

https://scikit-learn.org/stable/modules/metrics.html#cosine-similarity

# **Project Code**

### **Text Summarization**

```
import math
from collections import Counter
import operator
import numpy as np
import re
import optparse
import os
import glob
import sys
#Reading the documents
files = glob.glob(os.path.join(", '*'))
#print(files)
doc_numbers = list()
text = list()
title=list()
# Cleaning the documents
for file in files:
  # Open the file
 try:
   with open(file, 'r', encoding='utf-8') as f:
      # Read the contents of the file
      content = f.read()
     t=content.split('\n')
     st =t[1]
      st=st.replace(' ', '')
     title.append(st)
      stripped_content = content.replace('\n', '')
      stripped_content = stripped_content.replace(' ', '')
```

```
stripped_content = stripped_content.replace('TITLE:','')
     stripped_content = stripped_content.replace('SUMMARY:','')
     stripped_content = stripped_content.replace('DETAILED DESCRIPTION:','')
     stripped_content = stripped_content.replace('ELIGIBILITY CRITERIA:','')
     stripped_content = stripped_content.replace('Inclusion Criteria:','')
     stripped_content = stripped_content.replace('Exclusion Criteria:','')
     doc_numbers.append(file)
     text.append(stripped_content)
     DOCUMENT = stripped_content
     break
  except:
   continue
import re
DOCUMENT = re.sub(r'\n|\r', '', DOCUMENT)
DOCUMENT = re.sub(r' +', '', DOCUMENT)
DOCUMENT = DOCUMENT.strip()
!pip install gensim==3.6.0
from gensim.summarization import summarize
#Using the Gensim Summarizer
print(summarize(DOCUMENT, ratio=0.2, split=False))
summary = summarize(DOCUMENT, word_count=50, split=False)
print(summary)
!pip install rouge
from rouge import Rouge
rouge = Rouge()
reference_summary = "This study will develop and evaluate an approach to low back pain that allows subjects
to talk with each other and with health professionals via an Internet discussion group. Outcome measures
include health behaviors, health status, and health care use. Must have access to a computer with e-mail, be 18
years old, and have seen a doctor for back pain at least once in the past year. Back pain or sciatica can lead to
severe limitations, legal proceedings, bladder/bowel control issues, and numbness in the crotch."
scores = rouge.get_scores(summary, reference_summary)
print("ROUGE-1 Precision:", scores[0]['rouge-1']['p'])
print("ROUGE-1 Recall:", scores[0]['rouge-1']['r'])
print("ROUGE-1 F1-score:", scores[0]['rouge-1']['f'])
print("ROUGE-2 Precision:", scores[0]['rouge-2']['p'])
print("ROUGE-2 Recall:", scores[0]['rouge-2']['r'])
```

```
print("ROUGE-2 F1-score:", scores[0]['rouge-2']['f'])
print("ROUGE-L Precision:", scores[0]['rouge-l']['p'])
print("ROUGE-L Recall:", scores[0]['rouge-l']['r'])
print("ROUGE-L F1-score:", scores[0]['rouge-l']['f'])
from scipy.sparse.linalg import svds
def low_rank_svd(matrix, singular_count=2):
 u, s, vt = svds(matrix, k=singular_count)
 return u, s, vt
num_sentences = 8
num_topics = 3
u, s, vt = low_rank_svd(td_matrix, singular_count=num_topics)
print(u.shape, s.shape, vt.shape)
term_topic_mat, singular_values, topic_document_mat = u, s, vt
sv_{threshold} = 0.5
min_sigma_value = max(singular_values) * sv_threshold
singular_values[singular_values < min_sigma_value] = 0
salience_scores = np.sqrt(np.dot(np.square(singular_values), np.square(topic_document_mat)))
salience_scores
top_sentence_indices = (-salience_scores).argsort()[:num_sentences]
top_sentence_indices.sort()
print('\n'.join(np.array(sentences)[top_sentence_indices]))
similarity_matrix = np.matmul(dt_matrix, dt_matrix.T)
print(similarity_matrix.shape)
np.round(similarity_matrix, 3)
TF-IDF
from bs4 import BeautifulSoup
from nltk.tokenize import RegexpTokenizer
import math
from collections import Counter
import operator
import numpy as np
import re
import optparse
```

```
import os
import glob
import sys
class IRModel:
  invertedIndex ={}
  def __init__(self, path2docs):
   self.docno, self.raw_documents = self.extract_text(path2docs)
   self.documents = self.preprocess(self.raw_documents)
   self.vocab = self.get_vocab(self.documents)
   self.N = len(self.documents) # total number of documents
   self.invertedIndex = self.generate_inverted_index(self.docno,self.documents)
  def extract_text(self, path2docs):
   files = glob.glob(os.path.join(path2docs, '*'))
   #print(files)
   doc_numbers = list()
   text = list()
   for file in files:
     raw=[]
     try:
       with open(file, 'r', encoding='utf-8') as f:
         content = f.read()
         #Retrieving file name
         fname=file.split('\\')
         fname=fname[-1]
         doc_numbers.append(fname)
         stripped_content = content.replace('\n', '')
         stripped_content = stripped_content .replace('TITLE:','')
         stripped_content = stripped_content .replace('SUMMARY:','')
         stripped_content = stripped_content .replace('DETAILED DESCRIPTION:','')
         stripped_content = stripped_content .replace('ELIGIBILITY CRITERIA:','')
         stripped_content = stripped_content .replace('Inclusion Criteria:','')
         stripped_content = stripped_content .replace('Exclusion Criteria:','')
         raw.append(content)
         text.append(stripped_content)
```

```
except:
   continue
 text.pop()
 raw.pop()
 doc_numbers.pop()
 return doc_numbers, text
def preprocess(self, text):
 tokenizer = RegexpTokenizer(r'\w+')
 preprocessed = list()
 for t in text:
   t = t.lower()
    preprocessed.append(tokenizer.tokenize(t))
 return preprocessed
def preprocess_str(self, sentence):
 tokenizer = RegexpTokenizer(r'\w+')
 sentence = tokenizer.tokenize(sentence.lower())
 return sentence
def get_vocab(self, text):
 vocab = list()
 for doc in text:
    vocab.extend(doc)
 set(vocab)
 return set(vocab)
def generate_inverted_index(self,docno,documents):
 for idx,doc in enumerate(documents):
    for token in doc:
     if token in self.invertedIndex:
       self.invertedIndex[token].add(docno[idx])
     else:
       self.invertedIndex[token] = {docno[idx]}
  #print(self.invertedIndex)
 with open('InvertedIndex.txt', 'w', encoding='utf-8') as f:
   for key, value in self.invertedIndex.items():
     f.write(key+':'+str(value)+'\n')
```

```
return self.invertedIndex
 defidf(self, term):
   n_term = len(self.invertedIndex[term])
   if n_{term} = 0:
     return 0
   else:
     return math.log(self.N / n_term)
 def tf(self, term, doc):
   terms_in_doc = Counter(doc)
   max_term = max(terms_in_doc.values())
   return terms_in_doc[term] / max_term
 def get_vector(self, terms, document, idf_scores):
   vector = list()
   for term, idf in zip(terms, idf_scores):
     tf_idf = self.tf(term, document) * idf
     vector.append(tf_idf)
   return vector
 def similarity_scores(self, query):
   query = self.preprocess_str(query)
   idf_scores = [self.idf(term) for term in query]
   query_vec = self.get_vector(query, query, idf_scores)
   print(idf_scores)
   print(query_vec)
   # Get similarity scores for each document
   similarity_socres = dict()
   for doc, no in zip(self.documents, self.docno):
     doc_vec = self.get_vector(query, doc, idf_scores)
     # caculate the cosine similarity
     if np.dot(query_vec, doc_vec)!=0:
       cosine_sim = np.dot(query_vec, doc_vec) / (np.sqrt(np.sqm(np.square(query_vec))) *
np.sqrt(np.sum(np.square(doc_vec))))
     else: cosine_sim = 0
     similarity_scores[no] = cosine_sim
   # Sorting
```

```
similarity_scores = sorted(similarity_scores.items(), key=operator.itemgetter(1), reverse=True)
        return similarity_scores
def start(query):
    sys.stdout.reconfigure(encoding='utf-8')
    folder\_path = \text{'C:}\Users\91949\OneDrive\Documents\Courses\Information\ Retrieval\Project\Medical\Normation\ Retrieval\Project\Medical\Normation\ Retrieval\Project\Medical\Normation\ Retrieval\Project\Medical\Normation\ Retrieval\Normation\ Retrieval\ Retrieval\ Retrieval\ Retri
Information Retrieval\\docs\\'
    path2docs = folder_path
    articles = IRModel(path2docs)
    queries = [query]
    # Rank total documents with the cosine similarity and tf-idf
    res=[]
    for a in queries:
        print(q)
        sim_scores = articles.similarity_scores(q)
        docno = [no for no, score in sim_scores]
        top_10_docs= docno[:10]
        res=top_10_docs
        print("Top 10 Documents")
        print(top_10_docs)
        print('Documents and similarity score')
        print(sim_scores[:10])
    return res
search_doc.html
<html>
  <head>
    <meta http-equiv="Content-Type" content="text/html; charset=UTF-8" />
    <meta name="viewport" content="width=device-width, initial-scale=1" />
    <meta http-equiv="X-UA-Compatible" content="IE=edge" />
    <meta name="author" content="colorlib.com">
    k ref="https://fonts.googleapis.com/css?family=Poppins:400,800" rel="stylesheet" />
    link rel="stylesheet" href="https://cdn.jsdelivr.net/npm/bootstrap@5.2.3/dist/css/bootstrap.min.css"
integrity="sha384-rbsA2VBKQhqqwzxH7pPCaAqO46MqnOM80zW1RWuH61DGLwZJEdK2Kadq2F9CUG65"
crossorigin="anonymous">
    <script src="https://cdn.jsdelivr.net/npm/bootstrap@5.2.3/dist/js/bootstrap.min.js" integrity="sha384-</p>
```

cuYeSxntonz0PPNlHhBs68uyIAVpIIOZZ5JqeqvYYIcEL727kskC66kF92t6Xl2V" crossorigin="anonymous"></script>

```
<script src="https://cdn.jsdelivr.net/npm/bootstrap@5.2.3/dist/js/bootstrap.bundle.min.js"</pre>
integrity="sha384-kenU1KFdBle4zVF0s0G1M5b4hcpxyD9F7jL+jjXkk+Q2h455rYXK/7HAuoJl+0I4"
crossorigin="anonymous"></script>
</head>
<body>
 <div class="s006">
   <caption>Top 10 Matching Records</caption>
    <thead>
     Doc Name
      Action
     </thead>
    {% for doc in docList %}
     {{doc}}
      <a href="doc/{{doc}}">Click Here</a>
     {% endfor %}
    </div>
</body>
</html>
index.html
<html>
<head>
 <meta http-equiv="Content-Type" content="text/html; charset=UTF-8" />
 <meta name="viewport" content="width=device-width, initial-scale=1" />
 <meta http-equiv="X-UA-Compatible" content="IE=edge" />
 <meta name="author" content="colorlib.com">
```

k href="https://fonts.googleapis.com/css?family=Poppins:400,800" rel="stylesheet" />

```
integrity="sha384-rbsA2VBKQhqqwzxH7pPCaAqO46MgnOM80zW1RWuH61DGLwZJEdK2Kadq2F9CUG65"
crossorigin="anonymous">
 <script src="https://cdn.isdelivr.net/npm/bootstrap@5.2.3/dist/js/bootstrap.min.js" integrity="sha384-</pre>
cuYeSxntonz0PPNlHhBs68uyIAVpIIOZZ5JqeqvYYIcEL727kskC66kF92t6Xl2V" crossorigin="anonymous"></script>
  <script src="https://cdn.jsdelivr.net/npm/bootstrap@5.2.3/dist/js/bootstrap.bundle.min.js"</p>
integrity="sha384-kenU1KFdBle4zVF0s0G1M5b4hcpxyD9F7jL+jjXkk+Q2h455rYXK/7HAuoJl+0I4"
crossorigin="anonymous"></script>
</head>
 <body>
<div class="s006">
  <form method="POST" action="{% url 'search_doc' %}" name="searched">
   {% csrf_token %}
   <fieldset>
    <legend>What are you looking for?</legend>
    <div class="inner-form">
     <div class="input-field">
      <button class="btn-search" type="button">
       <svg xmlns="http://www.w3.org/2000/svg" width="24" height="24" viewBox="0 0 24 24">
       <path d="M15.5 14h-.79l-.28-.27C15.41 12.59 16 11.11 16 9.5 16 5.91 13.09 3 9.5 3S3 5.91 3 9.5 5.91 16 9.5</p>
16c1.61 0 3.09-.59 4.23-1.57l.27.28v.79l5 4.99L20.49 19l-4.99-5zm-6 0C7.01 14 5 11.99 5 9.5S7.01 5 9.5 5 14 7.01
14 9.5 11.99 14 9.5 14z"></path>
      </svq>
      </button>
      <input id="search" name="query" type="text" placeholder="Enter your search query" value="" />
     </div>
    </div>
   </fieldset>
  </form>
 </div>
 </body>
</html>
doc_details.html
<html>
 <head>
 <meta http-equiv="Content-Type" content="text/html; charset=UTF-8" />
 <meta name="viewport" content="width=device-width, initial-scale=1" />
```

```
<meta http-equiv="X-UA-Compatible" content="IE=edge" />
 <meta name="author" content="colorlib.com">
 <link href="https://fonts.googleapis.com/css?family=Poppins:400,800" rel="stylesheet" />
 integrity="sha384-rbsA2VBKQhggwzxH7pPCaAqO46MgnOM80zW1RWuH61DGLwZJEdK2Kadq2F9CUG65"
crossorigin="anonymous">
 <script src="https://cdn.jsdelivr.net/npm/bootstrap@5.2.3/dist/js/bootstrap.min.js" integrity="sha384-</p>
cuYeSxntonz0PPNlHhBs68uyIAVpIIOZZ5JqeqvYYIcEL727kskC66kF92t6Xl2V" crossoriqin="anonymous"></script>
 <script src="https://cdn.jsdelivr.net/npm/bootstrap@5.2.3/dist/js/bootstrap.bundle.min.js"</p>
integrity="sha384-kenU1KFdBle4zVF0s0G1M5b4hcpxyD9F7jL+jjXkk+Q2h455rYXK/7HAuoJl+0I4"
crossorigin="anonymous"></script>
 </head>
 <style>
   .s006 {
  min-height: 100vh;
  display: -ms-flexbox;
  -ms-flex-pack: center;
   justify-content: center;
  -ms-flex-align: center;
    align-items: center;
  font-family: 'Poppins', sans-serif;
  background: url("https://img.freepik.com/free-vector/clean-medical-background_53876-116875.jpg");
  background-size: cover;
  background-position: center center;
  padding: 15px;
 </style>
<body>
 <div class="s006" >
   <h1>Document: {{doc.name}}</h1>
   <br/>
   <div>
   <h2>Content: </h2>
   </div>
   </br>
   {{doc.content}}
```

```
</div>
 </body>
</html>
views.py
from django.shortcuts import render
from django.http import HttpResponse
from . import tfidf
# Create your views here.
from .models import Document
defindex(request):
 return render(request,'index.html')
def doc_by_id(request,doc):
 doc1 = Document.objects.get(name=doc)
 if(doc1):
   return render(request,'doc_details.html',{'doc':doc1})
 else:
   return render(request,'doc_details.html',{})
def search_doc(request):
 if(request.method=="POST"):
   query = request.POST.get("query", "")
   li = tfidf.start(query)
   # res=""
   # for doc in li:
      res+= doc
   return render(request,'search_doc.html',{'query':query,'docList':li})
  else:
   return render(request,'search_doc.html',{})
models.py
from django.db import models
# Create your models here.
```

```
class Document(models.Model):
    name = models.CharField(max_length=200)
    content = models.TextField()

urls.py
from django.urls import path
from . import views

urlpatterns = [
    path("",views.index,name="index"),
    path("doc/<str:doc>",views.doc_by_id,name='doc_by_id'),
    path("search_doc",views.search_doc,name='search_doc')
    ]
```