	Report - COVID19 papers (CORD-19)  # Itamar Fradkin - 312531064
	# Ron Boxer - 321219008  first you need to download the files from Here  Note- After downloading the zip file -  Unzip - metadata.csv & pdf_json folder (Keep the sturcted folder((document_parses)).
,	Insert this files into 'data' folder & create new folder named- 'minidataset' in 'document_parses' folder  We created several utilits which can be found in 'utils' folder.  let`s load and take a look on the metadata.
[2]:	<pre>import json import os import cotools import shutil</pre>
[3]:	<pre>import pandas as pd import numpy as np  DATASET_PATH = 'data/'</pre>
[4]:	<pre>METADATA_PATH = 'data/metadata.csv' MINI_DATASET_JSON_PATH = 'data/document_parses/minidataset'  import utils.dataset as ut df = ut.load_metadata()</pre>
[5]:	C:\Users\ronbo\anaconda3\lib\site-packages\IPython\core\interactiveshell.py:3338: DtypeWarning: Columns (1,4,5,6,13,14,15,16) have mixed types.Specify dtype option on import or set low_memory=False. if (await self.run_code(code, result, async_=asy)):
t[5]:	cord_uid source_x title doi pmcid pubmed_id license abstract publish_time authors journal mag_id who_covidence_id arxiv_id pdf
	d7ea1370848eac2a4e421c20fc30a69dfa69566e 9w762whh
	e4494dc889fcaadde2f5c0fcf401e7e8a3d96a63 6ltgimq0 Medline; immunosensor PMC; for rapid and WHO hig  Eisevier, Electrochemical Mohammad; electrochemical 2022-04-01 Gumus, Z. Talanta NaN NaN NaN document_parses/pdf_json/e4494dc889fca approa  Soylak  Krishnan
	12bc48af0b3196eef7e887807130b8553e8d7190 vmsyu6w7 Medline; Interventions PMC; for crisis WHO manag  12bc48af0b3196eef7e887807130b8553e8d7190 vmsyu6w7 Medline; Interventions PMC; for crisis manag  10.1016/j.ijdrr.2022.102830 PMC8865137 3.5229e+07 no-cc both the negative an
	fea63a0a7eb45059214491c2cb894f7a98b5f65c tx49s7f8  Medline; PMC; WHO COVID-19's Impact  A Qualitative Examination of COVID-19's Impact  A Qualitative Examination of COVID-19's Impact  PMC WHO COVID-19's Impact  Purpose To Marwah, A.; International
	631cf2b3762bf36ecfe686765b08cbc34351fbd9 aagrsfeh
	cbd8c8f742fb5a032e1b041da900a8a51623cc79 htwp70hc  Medline; PMC; WHO  PMC; WHO  Comparison of chest CT severity scoring system  PMC; WHO  Regarding the  Comparison of chest CT severity scoring system  PMC compare the diagnostic performance  10.1007/s00330-021-08432-5  PMC876013 3.50318e+07 no-cc  PMC876013 3.50318e+07 no-cc  PMC90SE: To compare the diagnostic performance  Ali H.; Mounir, Ahmad M.; Ramadan,  Curley, Pachadia  Curley, Pachadia  PMC90SE: To compare the diagnostic performance  PMC curley, Pachadia  PMC curley, PMC curley, Pachadia  PMC curley, PMC
	5bacfca63b11318e9788197ca3005a1135138956 4jqclOny PMC articles on home spirometry  Missed Modiling approximation of the properties of the
	637abda16edb7c7245861431108ff8f25aeea80f 7221cj12 Mediffe, Opportunities to PMC identify cryptococcosi  10.1177/20499361211066363 PMC8771738 3.50703e+07 nc both innate and adapti  This study investigates  Chen, Ping-
	49ae4f05cc3d5dadcd9ee8d7df2a6cbe6afcb8fb 33c5rxm2
:	a4bb5b7bfd9cf309d443cf439d29502ccd30e1a5 tbhb2lhc Mediffe, Chailenges and 10.1016/j.aquaculture.2021.737348 PMC8414286 3.44939e+07 no-cc disease 2022-01-15 Taposhi Aquaculture NaN NaN NaN document_parses/pdf_json/a4bb5b7bfd9rdsease 2022-01-15 Taposhi NaN NaN NaN NaN NaN NaN NaN NaN NaN Na
[6]:	As we only need some of the data, we move a small cohort into an entirely separate folder. (It will take a while :))  ut.move_files(df)
[7]:	Now we will use outsource package - 'cord-19-tools' to help us load the papers effitiantly.  pip install cord-19-tools  Requirement already satisfied: cord-19-tools in c:\users\ronbo\anaconda3\lib\site-packages (0.3.3)  Requirement already satisfied: ymltodict in c:\users\ronbo\anaconda3\lib\site-packages (from cord-19-tools) (0.12.0)
	Requirement already satisfied: xmltodict in c:\users\ronbo\anaconda3\lib\site-packages (from cord-19-tools) (0.12.0)  Note: you may need to restart the kernel to use updated packages.  # Load papers import cotools data = cotools.Paperset(MINI_DATASET_JSON_PATH)
[9]:	<pre>covid_df = ut.load_papers_into_df(data, size=20000) covid_df.head()</pre>
	title paper_id abstract body_text  Recruitment methods and yield rates in a clini 000e6f401f0f46b240cc81f2c9ef41914bfb9e06 Background: Although the prevalence of hyperten The prevalence of hypertension is increasing w  Impact of the COVID-19 Pandemic on Daily Life 0012308e8c02792b907c31935868f1afbff2c59b Using a mixed methods design, this study aimed travel restrictions. These measures aimed to p  Colchicine Against SARS-CoV-2 Infection: What 0015cecc298c3bdb9bda0e0b84b38ebdcca716f Coronavirus disease 2019 caused by the severe Systemic inflammation is the hallmark of coron
	3 Use and misuse of prescription stimulants by u 001716d1b1c1e9d9c1c8b3751e620371f2ddf2d4 Background: Misuse of prescription stimulants Global Drug Survey, an increase of neuroenhanc 4 A Neural Phillips Curve and a Deep Output Gap 001746ab8ab396aa3a7bc6b45ba75f26ec860fa9 Many problems plague the estimation of Phillip Few equations are as central to modern macroec
	Part A - Paper Similarity using gzip as our compresing method on text data only  Normalized compression distance (NCD) is a way of measuring the similarity between two objects, be it two documents, two letters, two emails, two music scores, two languages, two programs, two pictures, two systems, two genomes, to name a few. Such a measurement should not application dependent or arbitrary. A reasonable definition for the similarity between two objects is how difficult it is to transform them into each other. Further information can be found on this blog post
	If two objects compress better together than separately, it means they share common patterns and are similar!! here is the formula-  NCD Formula
[10]:	Let's take a paper as an example. Calculate the NCD distance to all other papers and take the 10 closest papers.  import utils.model as model  paper_id = '88b80f02e54d2ed8c9f05f422b45f4810a6a405b' # Example  k = 10
[10]:	similarity_df = model.k_similar_papers(paper_id, k, covid_df,txt_to_encode='abstract') similarity_df  title paper_id abstract body_text ncd_distance
	Explainable machine learning to predict long-t 88b80f02e54d2ed8c9f05f422b45f4810a6a405b Background: Machine learning (ML) model is inc The long-term outcome is currently an emerging 0.037691  Comparative analysis of explainable machine le 8710f527c4706f1ae42013a4d7688b1ec03f73aa Background: Machine learning (ML) holds the pr underlying structure of the data, while ML mod 0.777518  Prediction of 3-year risk of diabetic kidney d 18a795e30445a0f4ab3eb1be1198a805deb0e1fa Background: Established prediction models of D clinical decision-making. Understanding the ri 0.795195
	Predicting the necessity of oxygen therapy in 5d6ad19f8d11971024d1b7a4a23e6cd7378cd15b Medical oxygen is a critical element in the tr Since the spread of COVID-19 in December 2019, 0.805654  Article 852736 1 (2022) A Promising Preoperati 5b9d41960cd05dbc62122130019030e29f1b4ae2 Background: The non-invasive preoperative diag Hepatocellular carcinoma (HCC) is one of the m 0.807205  Mortality Predictive Value of APACHE II and SO 6621c2bde72488b15a577d92fb8613a7746126b Background. COVID-19 pandemic has become a glo In December 2019, severe acute respiratory syn 0.813725  Journal Pre-proofs Can we reliably automate cl 32d17d06540281827e8a013e51f98e953e7f114f Background: Building Machine Learning (ML) mod What was already known on the topic: Classic 0.818610
	Predicting ionized hypocalcemia: External vali 8dd1465054a2ef6c952fedf0ed9af361ea1a38ef Background: Ionized hypocalcemia is common in New York City was the epicenter of the COVID-1 0.824499  Early changes in laboratory tests predict live 959423993ae9a583d8f26edf1842128dc086ae06 Background: Most patients with coronavirus dis Studies have shown that COVID-19 can affect 0.828033  Comparing different machine learning technique 53d8d480246f79239ebc56e87c0384a8085ba514 Background: Coronavirus disease 2019 (COVID-19) Coronavirus disease 2019 (COVID-19) has been a 0.828685
	24656 Comparison of Regression and Machine Learning e997ad775d1eed1188a65bc0b60f50a87cf46851 Background: Depression is highly prevalent and Depression is the most common psychiatric diso 0.828889  In this example, we found some similar papers using the comparison method. our paper was in the field of machine learning From the results, we can see that we got papers in the field of machine learning are also represented.
	Part B - Clustering using Compression method from Part A  Our idea is to make several features based on the compression method. we saw in part A that actually, we can get some similar papers based on this method. so we decided to enrich the idea and create 3 features based on compression on the title, paper body text, and abstract text. think this logic will find clusters with similar papers.
[11]:	<pre>import gzip  def compress(x):     x = str(x).encode()     1_x = len(gzip.compress(x))</pre>
	return 1_x  # Apply Compression method from Part A train = covid_df.copy()
[12]:	<pre>train['comp_title'] = train['title'].apply(compress) train['comp_body'] = train['body_text'].apply(compress) train['comp_abstract'] = train['abstract'].apply(compress)  # Pre- prossece before clustering - Normalization</pre> # Pre- prossece before clustering - Normalization
	<pre>from sklearn.preprocessing import StandardScaler , MinMaxScaler  normalizer = MinMaxScaler() paper_ids = covid_df['paper_id'] train = train[['paper_id', 'comp_title', 'comp_body', 'comp_abstract']]</pre>
	<pre>train['comp_title'] = normalizer.fit_transform(train[['comp_title']]) train['comp_body'] = normalizer.fit_transform(train[['comp_body']]) train['comp_abstract'] = normalizer.fit_transform(train[['comp_abstract']]) train</pre>
[12]:	paper_id         comp_title         comp_body         comp_abstract           0         000e6f401f0f46b240cc81f2c9ef41914bfb9e06         0.135011         0.026254         0.075546           1         0012308e8c02792b907c31935868f1afbff2c59b         0.092677         0.050131         0.030028           2         0015cecc2298c3bdb9bda0e0b84b38ebdcca716f         0.069794         0.027313         0.050121
	3 001716d1b1c1e9d9c1c8b3751e620371f2ddf2d4 0.127002 0.036918 0.055819 4 001746ab8ab396aa3a7bc6b45ba75f26ec860fa9 0.050343 0.141596 0.166362
	26979         ffeb944868a31900fb661d78835ae1b22655fb22         0.137300         0.021210         0.072404           26980         ffeba2e1ac4c562c93da63f732f73cea26327793         0.081236         0.031219         0.047636           26986         fff951fc332133ecdffe8506d630494b552b126b         0.077803         0.049735         0.010156
	26988       fffacb29c594a89c2e2db9a844a496c540ad913c       0.148741       0.022383       0.000658         26990       fffed5cd958beb441f517c58f6d04990fe62c7c2       0.141876       0.019907       0.058815         17664 rows × 4 columns
[13]:	Choose optimal K - Elbow method  from sklearn import metrics from scipy.spatial.distance import cdist
	<pre>from sklearn.cluster import KMeans import matplotlib.pyplot as plt  # run kmeans with many different k distortions = []</pre>
	<pre>K = range(2, 17)  data = train[['comp_title','comp_body','comp_abstract']]  for k in K:</pre>
[14]:	<pre>k_means = KMeans(n_clusters=k, random_state=42).fit(data) k_means.fit(data) distortions.append(sum(np.min(cdist(data, k_means.cluster_centers_, 'euclidean'), axis=1)) / train.shape[0])  X_line = [K[0], K[-1]]</pre> <pre>X_line = [K[0], K[-1]]</pre>
*1*	<pre>Y_line = [distortions[0], distortions[-1]]  # Plot the elbow plt.plot(K, distortions, 'b-') plt.plot(X_line, Y_line, 'r')</pre>
	plt.xlabel('k') plt.ylabel('Distortion') plt.title('The Elbow Method showing the optimal k') plt.show()
	The Elbow Method showing the optimal k  0.036 - 0.034 - 0.032 - 0.033
	0.032 - 50 0.030 - 0.028 - 0.026 -
	0.024 -
[15]:	2 4 6 8 10 12 14 16  k  Final Clustering K= 5  kmeans = KMeans(n_clusters=5, random_state=0)
	<pre>#predict the labels of clusters. label = kmeans.fit_predict(train[['comp_title','comp_body','comp_abstract']])</pre>
[16]:	Visualizatoion  import matplotlib.pyplot as plt import numpy as np
	<pre>fig = plt.figure(1, figsize=(25, 6)) ax = plt.axes(projection = '3d') ax.scatter(data.iloc[:, 0], data.iloc[:, 1], data.iloc[:, 2], marker='.', c = label) plt.xlim([0, 0.3]) plt.ylim([0, 0.4])</pre>
	ax.set_zlim(0, 0.4);
	0.40 0.35 0.30 0.25
	0.20 0.15 0.10 0.05 0.00
	0.00 0.05 0.10 0.15 0.10 0.15
	Looks like a good separation
	Analysis In order to see if the clusters actually presenting similar papers we will take the example from part A and check if they are in the same cluster.  example_paper = '88b80f02e54d2ed8c9f05f422b45f4810a6a405b'  example_paper raw data = train[train['paper id'] = example_paper]
	<pre>example_paper_raw_data = train[train['paper_id'] == example_paper] predicted_cluster_example_paper = kmeans.predict(example_paper_raw_data[['comp_title','comp_body','comp_abstract']])[0] counter = 0  for similar_paper in similarity_df['paper_id'].values[1:]:</pre>
	<pre>paper_raw_data = train[train['paper_id'] == similar_paper] paper_raw_data = paper_raw_data[['comp_title','comp_body','comp_abstract']] paper_pridiction = kmeans.predict(paper_raw_data) if paper_pridiction == predicted_cluster_example_paper:     counter += 1</pre>
[17]:	counter  7  Wow! Seven out of ten were in the same cluster. In addition, we saw in Part A an example paper in the field of machine learning. therefore, This cluster seems to represent a good collection of papers in the field of machine learning.
	Furhter Work Based only on the compression method and using only text data in this work, we got pretty good results. For future work, we would like to add some more methods, such as word embedding (DOC2VEC), and create a model that incorporates both methods and more metadata feature Using this approach, we believe that we will achieve better performance and similarity.