COVID Literature Clustering

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COVID-19 Open Research Dataset Challenge (CORD-19)

An Al challenge with Al2, CZI, MSR, Georgetown, NIH & The White House

Allen Institute for AI in collaboration with 6 other organizations, released a dataset containing over 125 thousand literature articles about information on the COVID-19 pandemic

The main aim of our project is to perform clustering of our articles to better classify them based on the topics they cover. The literatures could contain research papers, blog articles, studies, etc based on a variety of topics like virus behaviour, symptoms, prevention, vaccination, etc.

Dataset

- -The dataset was originally in the form of .json files
- -We extracted the text corpus to get 128915 rows of data
- -Out of over 30 possible column values, we chose this as our final dataset:

	paper_id	title	authors	abstract	body_text
0	0000028b5cc154f68b8a269f6578f21e31f62977	"Multi-faceted" COVID-19: Russian experience	NaN	NaN	['According to current live statistics at the
1	0001418189999fea7f7cbe3e82703d71c85a6fe5	Absence of surface expression of feline infect	['E Cornelissen', 'H Dewerchin', 'E Hamme', 'H	['Feline infectious peritonitis virus (FIPV) p	['Feline infectious peritonitis (FIP) is a fat
2	00033d5a12240a8684cfe943954132b43434cf48	Detection of Severe Acute Respiratory Syndrome	['Petra Wandernoth', 'Katharina Kriegsmann', '	['Background: Amplification of viral ribonucle	['Severe acute respiratory syndrome coronaviru
3	0003793cf9e709bc2b9d0c8111186f78fb73fc04	Title: Rethinking high-risk groups in COVID-19	['Anastasia Vishnevetsky', 'Michael Levy']	NaN	["How do we protect our high-risk" patient po
4	000379d7a7f37a2ccb978862b9f2016bd03259ea	ScienceDirect ScienceDirect Effect of Nanomate	['Harish Devaraj', 'Rajiv Malhotra']	['approach. The NM shape in the conformal circ	['Integration of functional electronic devices

Data cleaning

There were quite a few NaN values in our dataset. Since all the values are string, we converted the NaN values to None so that we can use it for EDA and model fitting

Another problem was that our body had a lot of null strings. We also removed those rows too.

We also removed any papers where the number of authors > 30, since it is unlikely that a single paper have too many authors We performed our analysis on 20% of our data chosen randomly

paper_id	0		
title	14023		
authors	12465		
abstract	41063		
body text	0		

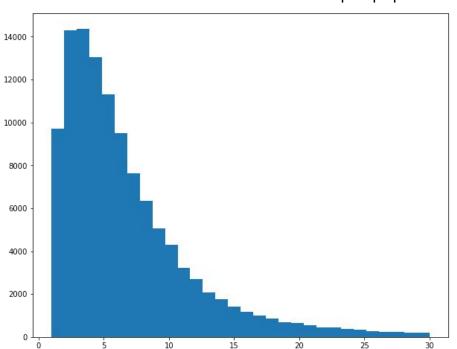
Natural Language Processing

Tokenization and stemming converts all words into their root word and removing word extensions (like -ing and -ers) in order to standardize the text corpus

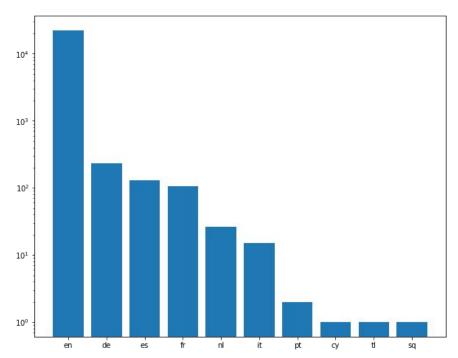
The TF-IDF Vectorizer is used for converting our text corpus to a vector representation of the words. It also removes all unnecessary stop words

Exploratory Data Analysis

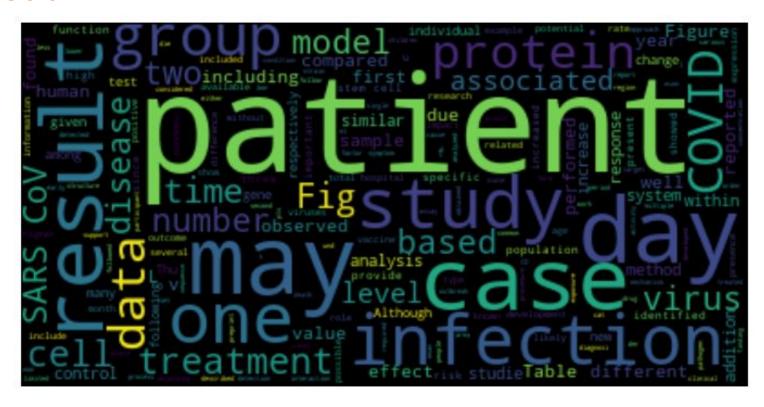
Distribution of number of authors per paper



Distribution of languages



Word Cloud

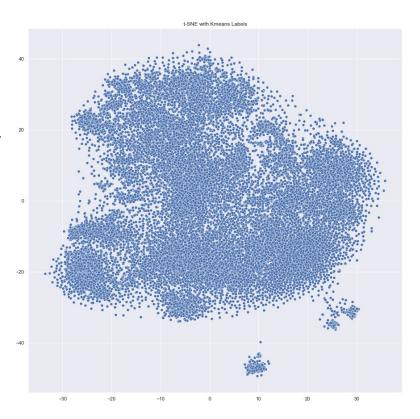


Dimensionality Reduction

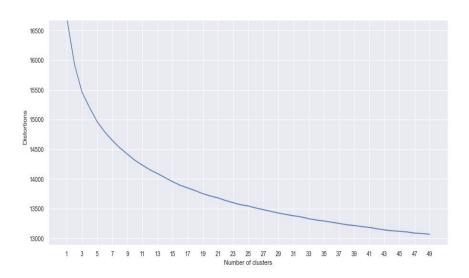
- PCA: Fit a PCA model to reduce dimensions while retaining 95% of the variance in our data. We got the number of principal components to be 644

shape after PCA: (25783, 644)

- TSNE: Fit a TSNE model to our data to reduce it to two dimensions with the resulting graph looking like:



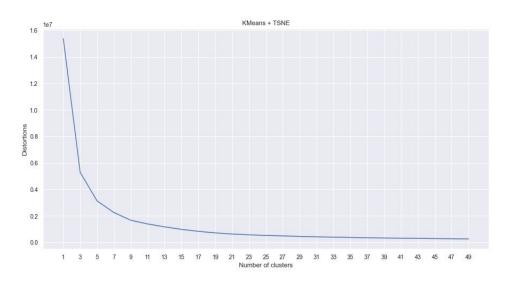
Clustering: KMeans + PCA



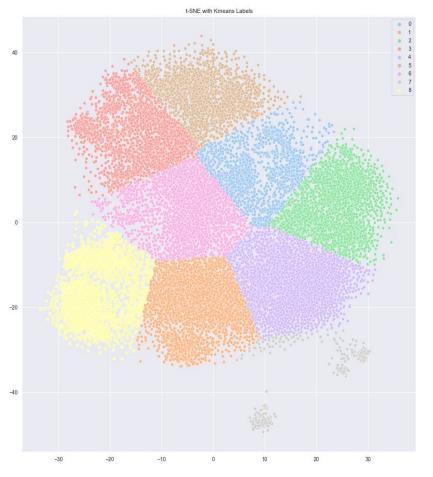
Optimal number of clusters = 15



Clustering: KMeans + TSNE



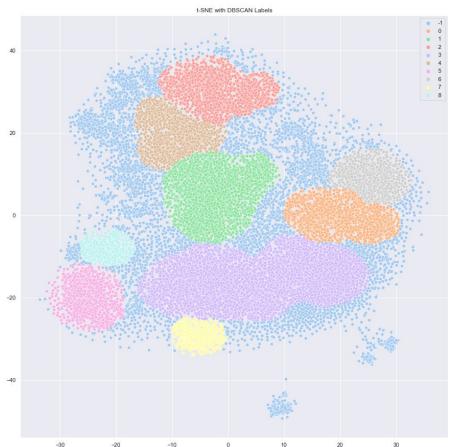
Optimal number of clusters = 9



Clustering: DBSCAN + TSNE

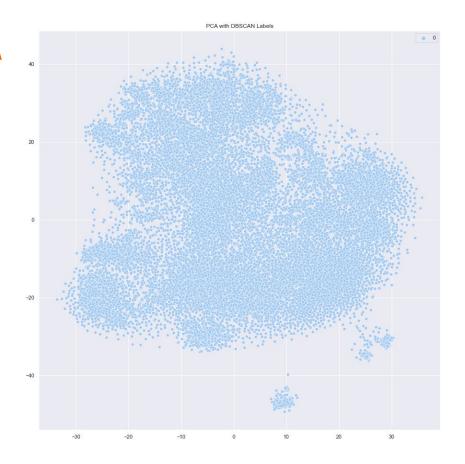
Chose value of eps and min_samples by trial and error

eps = 4; $min_samples = 500$



Clustering: DBSCAN + PCA

Due to computational limitations, we were unable to fit an appropriate DBSCAN on our PCA reduced data. This is the we got after using similar parameters as KMeans



Conclusions and future scope

For the text corpus that we chose,

- TSNE performed much better than PCA, however TSNE ends up losing a lot of the variance in the data. Therefore, PCA is a better dimensionality reduction technique to capture variance.
- KMeans fit better as we got a defined number of clusters, whereas there was a lot of trial and error involved in DBSCAN
- There are ways to tune the hyperparameters (eps, min_samples) of DBSCAN or use other options, like the OPTICS algorithm, to get the best possible values of DBSCAN, which are a part of the future scope of this project.

Thank you

Questions?