covid19

June 12, 2020

Covid19 Literature Clustering and Classification

This is a kaggle notebook solution to the kaggle problem: https://www.kaggle.com/allen-institute-for-ai/CORD-19-research-challenge

0.0.1 Dataset Description

In response to the COVID-19 pandemic, the White House and a coalition of leading research groups have prepared the COVID-19 Open Research Dataset (CORD-19). CORD-19 is a resource of over 100,000 scholarly articles, about COVID-19, SARS-CoV-2, and related coronaviruses.

By using `clustering` for labelling in combination with `dimensionality reduction` for visualization, the collection of literature can be represented by a scatter plot. On this plot, publications of highly similar topic will share a label and will be plotted near each other. In order, to find meaning in the clusters, topic modelling will be performed to find the keywords of each cluster.

The text is parsed from the body of each document using Natural Language Processing (NLP). Each document instance di is turned into a feature vector Xi using `Term Frequency-inverse Document Frequency (TF-IDF)`. Applying Dimensionality Reduction to each feature vector Xi using `t-Distributed Stochastic Neighbor Embedding (t-SNE)` similar research articles are clustered in the two dimensional plane X embedding Y1. Principal Component Analysis (PCA) is used to project down the dimensions of X to a number of dimensions that keep .95 variance while removing noise and outliers in embedding Y2. K-means clustering is applied on Y2, where k is 20, to label each cluster on Y1. Applying Topic Modeling on X using `Latent Dirichlet Allocation (LDA)` keywords are discovered from each cluster. The clusters are investigated visually on the plot, zooming down to specific articles as needed, and via classification using Stochastic Gradient Descent (SGD).

[1]:
```
# Loading libraries

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import glob
import json

import matplotlib.pyplot as plt
plt.style.use('ggplot')
```

[2]:
```python
# Loading meta data

root_path = '/kaggle/input/CORD-19-research-challenge/'
metadata_path = f'{root_path}/metadata.csv'
meta_df = pd.read_csv(metadata_path, dtype={'pubmed_id': str,
                                            'Microsoft Academic Paper ID': str,
                                            'doi': str
                                           })
meta_df.head()
```

```
/opt/conda/lib/python3.7/site-packages/IPython/core/interactiveshell.py:3063:
DtypeWarning: Columns (13,14) have mixed types.Specify dtype option on import or
set low_memory=False.
  interactivity=interactivity, compiler=compiler, result=result)
```

[2]:
```
   cord_uid                                       sha source_x  \
0  ug7v899j  d1aafb70c066a2068b02786f8929fd9c900897fb      PMC
1  02tnwd4m  6b0567729c2143a66d737eb0a2f63f2dce2e5a7d      PMC
2  ejv2xln0  06ced00a5fc04215949aa72528f2eeaae1d58927      PMC
3  2b73a28n  348055649b6b8cf2b9a376498df9bf41f7123605      PMC
4  9785vg6d  5f48792a5fa08bed9f56016f4981ae2ca6031b32      PMC

                                               title                    doi  \
0  Clinical features of culture-proven Mycoplasma…  10.1186/1471-2334-1-6
1  Nitric oxide: a pro-inflammatory mediator in l…           10.1186/rr14
2    Surfactant protein-D and pulmonary host defense           10.1186/rr19
3               Role of endothelin-1 in lung disease           10.1186/rr44
4  Gene expression in epithelial cells in respons…           10.1186/rr61

      pmcid pubmed_id license  \
0  PMC35282  11472636   no-cc
1  PMC59543  11667967   no-cc
2  PMC59549  11667972   no-cc
3  PMC59574  11686871   no-cc
4  PMC59580  11686888   no-cc

                                            abstract publish_time  \
0  OBJECTIVE: This retrospective chart review des…   2001-07-04
1  Inflammatory diseases of the respiratory tract…   2000-08-15
2  Surfactant protein-D (SP-D) participates in th…   2000-08-25
3  Endothelin-1 (ET-1) is a 21 amino acid peptide…   2001-02-22
4  Respiratory syncytial virus (RSV) and pneumoni…   2001-05-11

                                             authors         journal  mag_id  \
0              Madani, Tariq A; Al-Ghamdi, Aisha A  BMC Infect Dis     NaN
1  Vliet, Albert van der; Eiserich, Jason P; Cros…      Respir Res     NaN
2                                  Crouch, Erika C      Respir Res     NaN
```

```
3  Fagan, Karen A; McMurtry, Ivan F; Rodman, David M      Respir Res     NaN
4  Domachowske, Joseph B; Bonville, Cynthia A; Ro…      Respir Res     NaN

  who_covidence_id arxiv_id  \
0              NaN      NaN
1              NaN      NaN
2              NaN      NaN
3              NaN      NaN
4              NaN      NaN

                                   pdf_json_files  \
0  document_parses/pdf_json/d1aafb70c066a2068b027…
1  document_parses/pdf_json/6b0567729c2143a66d737…
2  document_parses/pdf_json/06ced00a5fc04215949aa…
3  document_parses/pdf_json/348055649b6b8cf2b9a37…
4  document_parses/pdf_json/5f48792a5fa08bed9f560…

                              pmc_json_files  \
0  document_parses/pmc_json/PMC35282.xml.json
1  document_parses/pmc_json/PMC59543.xml.json
2  document_parses/pmc_json/PMC59549.xml.json
3  document_parses/pmc_json/PMC59574.xml.json
4  document_parses/pmc_json/PMC59580.xml.json

                                                url  s2_id
0  https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3…    NaN
1  https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5…    NaN
2  https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5…    NaN
3  https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5…    NaN
4  https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5…    NaN
```

[3]:
```
meta_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 138794 entries, 0 to 138793
Data columns (total 19 columns):
 #   Column            Non-Null Count   Dtype
---  ------            --------------   -----
 0   cord_uid          138794 non-null  object
 1   sha               65379 non-null   object
 2   source_x          138794 non-null  object
 3   title             138753 non-null  object
 4   doi               114271 non-null  object
 5   pmcid             71391 non-null   object
 6   pubmed_id         101517 non-null  object
 7   license           138794 non-null  object
 8   abstract          107032 non-null  object
 9   publish_time      138780 non-null  object
 10  authors           133451 non-null  object
 11  journal           131249 non-null  object
 12  mag_id            0 non-null       float64
 13  who_covidence_id  26182 non-null   object
 14  arxiv_id          1727 non-null    object
 15  pdf_json_files    65379 non-null   object
 16  pmc_json_files    50818 non-null   object
 17  url               126725 non-null  object
 18  s2_id             113843 non-null  float64
dtypes: float64(2), object(17)
memory usage: 20.1+ MB
```

[4]:
```
# Get path to all JSON files:

all_json = glob.glob(f'{root_path}/**/*.json', recursive=True)
len(all_json)
```

[4]:
```
120464
```

[5]:
```
# File Reader Class


class FileReader:
    def __init__(self, file_path):
        with open(file_path) as file:
            content = json.load(file)
            self.paper_id = content['paper_id']
            self.abstract = []
            self.body_text = []
            # Abstract
            for entry in content['abstract']:
                self.abstract.append(entry['text'])
            # Body text
            for entry in content['body_text']:
                self.body_text.append(entry['text'])
            self.abstract = '\n'.join(self.abstract)
            self.body_text = '\n'.join(self.body_text)
    def __repr__(self):
        return f'{self.paper_id}: {self.abstract[:200]}... {self.body_text[:
 ↪200]}...'
first_row = FileReader(all_json[0])
print(first_row)
```

```
457ca409fb8641be73680f3697936d7a627f5442: … An adenovirus (AVI group-specific
latex agglutination test (LA) was assessed for its ability to detect AVs in
faeces and to confirm the isolation of AVs in cell culture. It detected all of
62 strains …
```

```
[6]: # adding break after every words when character length reach to certain amount.

def get_breaks(content, length):
    data = ""
    words = content.split(' ')
    total_chars = 0

    # add break every length characters
    for i in range(len(words)):
        total_chars += len(words[i])
        if total_chars > length:
            data = data + "<br>" + words[i]
            total_chars = 0
        else:
            data = data + " " + words[i]
    return data
```

0.0.2 Load the Data into DataFrame

```
[7]: dict_ = {'paper_id': [], 'doi':[], 'abstract': [], 'body_text': [], 'authors':␣
     ↪[], 'title': [], 'journal': [], 'abstract_summary': []}
for idx, entry in enumerate(all_json):
    if idx % (len(all_json) // 10) == 0:
        print(f'Processing index: {idx} of {len(all_json)}')

    try:
        content = FileReader(entry)
    except Exception as e:
        continue  # invalid paper format, skip

    # get metadata information
    meta_data = meta_df.loc[meta_df['sha'] == content.paper_id]
    # no metadata, skip this paper
    if len(meta_data) == 0:
        continue

    dict_['abstract'].append(content.abstract)
    dict_['paper_id'].append(content.paper_id)
    dict_['body_text'].append(content.body_text)

    # also create a column for the summary of abstract to be used in a plot
    if len(content.abstract) == 0:
        # no abstract provided
        dict_['abstract_summary'].append("Not provided.")
    elif len(content.abstract.split(' ')) > 100:
        # abstract provided is too long for plot, take first 100 words append␣
↪with ...
        info = content.abstract.split(' ')[:100]
        summary = get_breaks(' '.join(info), 40)
        dict_['abstract_summary'].append(summary + "...")
    else:
        # abstract is short enough
        summary = get_breaks(content.abstract, 40)
        dict_['abstract_summary'].append(summary)

    # get metadata information
    meta_data = meta_df.loc[meta_df['sha'] == content.paper_id]

    try:
        # if more than one author
        authors = meta_data['authors'].values[0].split(';')
        if len(authors) > 2:
            # if more than 2 authors, take them all with html tag breaks in␣
↪between
            dict_['authors'].append(get_breaks('. '.join(authors), 40))
        else:
            # authors will fit in plot
            dict_['authors'].append(". ".join(authors))
    except Exception as e:
        # if only one author - or Null valie
        dict_['authors'].append(meta_data['authors'].values[0])

    # add the title information, add breaks when needed
    try:
        title = get_breaks(meta_data['title'].values[0], 40)
        dict_['title'].append(title)
    # if title was not provided
    except Exception as e:
        dict_['title'].append(meta_data['title'].values[0])

    # add the journal information
    dict_['journal'].append(meta_data['journal'].values[0])

    # add doi
    dict_['doi'].append(meta_data['doi'].values[0])

df_covid = pd.DataFrame(dict_, columns=['paper_id', 'doi', 'abstract',␣
↪'body_text', 'authors', 'title', 'journal', 'abstract_summary'])
df_covid.head()
```

```
Processing index: 0 of 120464
Processing index: 12046 of 120464
Processing index: 24092 of 120464
Processing index: 36138 of 120464
Processing index: 48184 of 120464
Processing index: 60230 of 120464
Processing index: 72276 of 120464
Processing index: 84322 of 120464
Processing index: 96368 of 120464
Processing index: 108414 of 120464
Processing index: 120460 of 120464
```

[7]:

```
                                   paper_id                             doi  \
0  457ca409fb8641be73680f3697936d7a627f5442    10.1016/0888-0786(93)90032-u
1  7db22f7f81977109d493a0edf8ed75562648e839    10.1371/journal.pone.0103456
2  4a487430085a45904f4463e6e462a63f98adefad  10.1016/j.jemermed.2004.11.022
3  66b16f35496816d1091009e6df08945485e57ffc       10.1101/2020.05.13.093971
4  d95fb677837e1d2572cfdc7dd95a630d5f64930d   10.1016/j.outlook.2012.07.013

                                            abstract  \
0
1  Scorpine, a small cationic peptide from the ve…
2  e Abstract-To differentiate severe acute respi…
3  The recently emerged SARS-CoV-2 (Coronaviridae…
4  The increasing interconnectedness of the world…

                                           body_text  \
0  An adenovirus (AVI group-specific latex agglut…
1  The oldest known scorpions lived around 430 mi…
2  Severe acute respiratory syndrome (SARS) is a …
3  region. Phylogenetic analysis, natural selecti…
4  The increasing interconnectedness in the world…

                                             authors  \
0   Bryden, AS.  Ashley, CR.  Cotterill, H. <br>C…
1   Zhang, Chao.  He, Xinlong.  Gu, Yaping.  Zhou…
2   Chang, Shang-Miao.  Liu, Ching-Lung.  Kuo,<br…
3   Nour, Islam.  Alanazi, Ibrahim O..  Hanif, At…
4   Hunter, Anita.  Wilson, Lynda.  Stanhope,<br>…

                                               title  \
0   Detection of adenoviruses in faeces and the<b…
1   Recombinant Scorpine Produced Using SUMO<br>F…
2   Comparative study of patients with and withou…
3   Insights into molecular evolution<br>recombin…
4   Global health diplomacy: An integrative<br>re…

                                             journal  \
0  Serodiagnosis and Immunotherapy in Infectious …
```

```
1                                           PLoS One
2                    The Journal of Emergency Medicine
3                                            bioRxiv
4                                     Nursing Outlook

                                    abstract_summary
0                                      Not provided.
1   Scorpine, a small cationic peptide from the<b…
2   e Abstract-To differentiate severe acute<br>r…
3   The recently emerged SARS-CoV-2<br>(Coronavir…
4   The increasing interconnectedness of the<br>w…
```

[8]:
```python
# Adding word count columns for both abstract and body_text

df_covid['abstract_word_count'] = df_covid['abstract'].apply(lambda x: len(x.
 ↪strip().split()))  # word count in abstract
df_covid['body_word_count'] = df_covid['body_text'].apply(lambda x: len(x.
 ↪strip().split()))  # word count in body
df_covid['body_unique_words']=df_covid['body_text'].apply(lambda x:
 ↪len(set(str(x).split())))  # number of unique words in body
df_covid.head()
```

[8]:
```
                                   paper_id                             doi  \
0  457ca409fb8641be73680f3697936d7a627f5442    10.1016/0888-0786(93)90032-u
1  7db22f7f81977109d493a0edf8ed75562648e839    10.1371/journal.pone.0103456
2  4a487430085a45904f4463e6e462a63f98adefad  10.1016/j.jemermed.2004.11.022
3  66b16f35496816d1091009e6df08945485e57ffc       10.1101/2020.05.13.093971
4  d95fb677837e1d2572cfdc7dd95a630d5f64930d   10.1016/j.outlook.2012.07.013

                                            abstract  \
0
1  Scorpine, a small cationic peptide from the ve…
2  e Abstract-To differentiate severe acute respi…
3  The recently emerged SARS-CoV-2 (Coronaviridae…
4  The increasing interconnectedness of the world…

                                           body_text  \
0  An adenovirus (AVI group-specific latex agglut…
1  The oldest known scorpions lived around 430 mi…
2  Severe acute respiratory syndrome (SARS) is a …
3  region. Phylogenetic analysis, natural selecti…
4  The increasing interconnectedness in the world…

                                             authors  \
0   Bryden, AS.  Ashley, CR.  Cotterill, H. <br>C…
1   Zhang, Chao.  He, Xinlong.  Gu, Yaping.  Zhou…
2   Chang, Shang-Miao.  Liu, Ching-Lung.  Kuo,<br…
```

```
3   Nour, Islam.  Alanazi, Ibrahim O..  Hanif, At…
4   Hunter, Anita.  Wilson, Lynda.  Stanhope,<br>…

                                             title  \
0   Detection of adenoviruses in faeces and the<b…
1   Recombinant Scorpine Produced Using SUMO<br>F…
2   Comparative study of patients with and withou…
3   Insights into molecular evolution<br>recombin…
4   Global health diplomacy: An integrative<br>re…

                                           journal  \
0  Serodiagnosis and Immunotherapy in Infectious …
1                                         PLoS One
2                The Journal of Emergency Medicine
3                                          bioRxiv
4                                  Nursing Outlook

                                  abstract_summary  abstract_word_count  \
0                                    Not provided.                    0
1   Scorpine, a small cationic peptide from the<b…                 253
2   e Abstract-To differentiate severe acute<br>r…                 183
3   The recently emerged SARS-CoV-2<br>(Coronavir…                 174
4   The increasing interconnectedness of the<br>w…                 226

   body_word_count  body_unique_words
0             1616                643
1             3543               1332
2             3060               1086
3              461                267
4             4228               1437
```

[9]:
```
df_covid.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 61655 entries, 0 to 61654
Data columns (total 11 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   paper_id             61655 non-null  object
 1   doi                  59833 non-null  object
 2   abstract             61655 non-null  object
 3   body_text            61655 non-null  object
 4   authors              60366 non-null  object
 5   title                61654 non-null  object
 6   journal              56315 non-null  object
 7   abstract_summary     61655 non-null  object
 8   abstract_word_count  61655 non-null  int64
 9   body_word_count      61655 non-null  int64
 10  body_unique_words    61655 non-null  int64
dtypes: int64(3), object(8)
memory usage: 5.2+ MB
```

```
[10]: df_covid['abstract'].describe(include='all')
```

```
[10]: count     61655
      unique    42612
      top
      freq      18784
      Name: abstract, dtype: object
```

```
[11]: # Handling duplicates

      df_covid.drop_duplicates(['abstract', 'body_text'], inplace=True)
      df_covid['abstract'].describe(include='all')
```

```
[11]: count     61501
      unique    42612
      top
      freq      18686
      Name: abstract, dtype: object
```

```
[12]: df_covid['body_text'].describe(include='all')
```

```
[12]: count                                                 61501
      unique                                                61498
      top       The recent COVID-19 Coronavirus outbreak and t…
      freq                                                      2
      Name: body_text, dtype: object
```

0.1 Data Pre-processing

```
[13]: # In Kaggle we cannot handle the whole dataframe. So we limit the dataframe to␣
       ↪10,000 instances

      df = df_covid.sample(10000, random_state=42)
      del df_covid
```

```
[14]: df.dropna(inplace=True)
      df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 8869 entries, 29945 to 51559
Data columns (total 11 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   paper_id             8869 non-null   object
 1   doi                  8869 non-null   object
 2   abstract             8869 non-null   object
 3   body_text            8869 non-null   object
 4   authors              8869 non-null   object
 5   title                8869 non-null   object
 6   journal              8869 non-null   object
 7   abstract_summary     8869 non-null   object
 8   abstract_word_count  8869 non-null   int64
 9   body_word_count      8869 non-null   int64
 10  body_unique_words    8869 non-null   int64
dtypes: int64(3), object(8)
memory usage: 831.5+ KB
```

0.1.1 Handling multiple languages

[15]:
```
!pip install langdetect
```

```
Collecting langdetect
  Downloading langdetect-1.0.8.tar.gz (981 kB)
     |                 | 981 kB 4.5 MB/s eta 0:00:01
Requirement already satisfied: six in /opt/conda/lib/python3.7/site-
packages (from langdetect) (1.14.0)
Building wheels for collected packages: langdetect
  Building wheel for langdetect (setup.py) … done
  Created wheel for langdetect: filename=langdetect-1.0.8-py3-none-any.whl
size=993191
sha256=ad692989d4d33c3eef0e24c95309b1bab84be7bf630d6b6f0ed18ef92dd66fc0
  Stored in directory: /root/.cache/pip/wheels/59/f6/9d/85068904dba861c0b9af74e2
86265a08da438748ee5ae56067
Successfully built langdetect
Installing collected packages: langdetect
Successfully installed langdetect-1.0.8
WARNING: You are using pip version 20.1; however, version 20.1.1 is
available.
You should consider upgrading via the '/opt/conda/bin/python3.7 -m pip install
--upgrade pip' command.
```

[16]:
```
from tqdm import tqdm
from langdetect import detect
from langdetect import DetectorFactory

# set seed
```

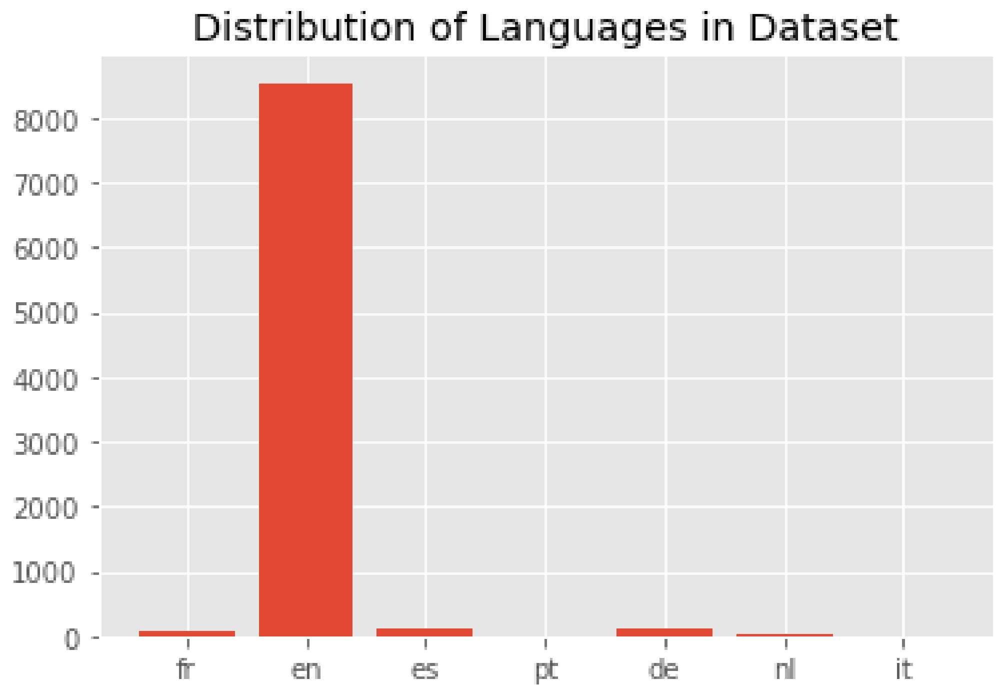
```python
DetectorFactory.seed = 0

# hold label - language
languages = []

# go through each text
for ii in tqdm(range(0,len(df))):
    # split by space into list, take the first x intex, join with space
    text = df.iloc[ii]['body_text'].split(" ")

    lang = "en"
    try:
        if len(text) > 50:
            lang = detect(" ".join(text[:50]))
        elif len(text) > 0:
            lang = detect(" ".join(text[:len(text)]))
    # ught... beginning of the document was not in a good format
    except Exception as e:
        all_words = set(text)
        try:
            lang = detect(" ".join(all_words))
        # what!! :( let's see if we can find any text in abstract...
        except Exception as e:

            try:
                # let's try to label it through the abstract then
                lang = detect(df.iloc[ii]['abstract_summary'])
            except Exception as e:
                lang = "unknown"
                pass

    # get the language
    languages.append(lang)
```

```
100%|          | 8869/8869 [01:48<00:00, 81.80it/s]
```

[17]:
```python
from pprint import pprint

languages_dict = {}
for lang in set(languages):
    languages_dict[lang] = languages.count(lang)

print("Total: {}\n".format(len(languages)))
pprint(languages_dict)
```

```
Total: 8869

{'de': 126, 'en': 8540, 'es': 95, 'fr': 71, 'it': 7, 'nl': 25, 'pt': 5}
```

[18]:
```
df['language'] = languages
plt.bar(range(len(languages_dict)), list(languages_dict.values()),␣
 ↪align='center')
plt.xticks(range(len(languages_dict)), list(languages_dict.keys()))
plt.title("Distribution of Languages in Dataset")
plt.show()
```



[19]:
```
df = df[df['language'] == 'en']
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 8540 entries, 29945 to 51559
Data columns (total 12 columns):
 #   Column              Non-Null Count  Dtype
---  ------              --------------  -----
 0   paper_id            8540 non-null   object
 1   doi                 8540 non-null   object
 2   abstract            8540 non-null   object
 3   body_text           8540 non-null   object
 4   authors             8540 non-null   object
 5   title               8540 non-null   object
 6   journal             8540 non-null   object
 7   abstract_summary    8540 non-null   object
 8   abstract_word_count 8540 non-null   int64
 9   body_word_count     8540 non-null   int64
 10  body_unique_words    8540 non-null   int64
 11  language             8540 non-null   object
dtypes: int64(3), object(9)
memory usage: 867.3+ KB
```

[20]:
```
# Download the spacy bio parser

from IPython.utils import io
with io.capture_output() as captured:
    !pip install https://s3-us-west-2.amazonaws.com/ai2-s2-scispacy/releases/v0.
 ↪2.4/en_core_sci_lg-0.2.4.tar.gz
```

[21]:
```
import spacy
from spacy.lang.en.stop_words import STOP_WORDS
import en_core_sci_lg  # model downloaded in previous step
```

[22]:
```
# finding and removing stopwords (common words that will act as noise in the␣
 ↪clustering step).

import string

punctuations = string.punctuation
stopwords = list(STOP_WORDS)
stopwords[:10]
```

[22]:
```
['anywhere',
 'to',
 'between',
 '’ve',
 'herself',
 'get',
 'might',
 "'ve",
 'fifty',
 'within']
```

[23]:
```
# Reference: https://www.kaggle.com/danielwolffram/
 ↪topic-modeling-finding-related-articles

custom_stop_words = [
    'doi', 'preprint', 'copyright', 'peer', 'reviewed', 'org', 'https', 'et',␣
 ↪'al', 'author', 'figure',
    'rights', 'reserved', 'permission', 'used', 'using', 'biorxiv', 'medrxiv',␣
 ↪'license', 'fig', 'fig.',
    'al.', 'Elsevier', 'PMC', 'CZI', 'www'
]
```

```
for w in custom_stop_words:
    if w not in stopwords:
        stopwords.append(w)
```

[24]:
```
# Parser
parser = en_core_sci_lg.load(disable=["tagger", "ner"])
parser.max_length = 7000000

def spacy_tokenizer(sentence):
    mytokens = parser(sentence)
    mytokens = [ word.lemma_.lower().strip() if word.lemma_ != "-PRON-" else␣
 ↪word.lower_ for word in mytokens ]
    mytokens = [ word for word in mytokens if word not in stopwords and word␣
 ↪not in punctuations ]
    mytokens = " ".join([i for i in mytokens])
    return mytokens
```

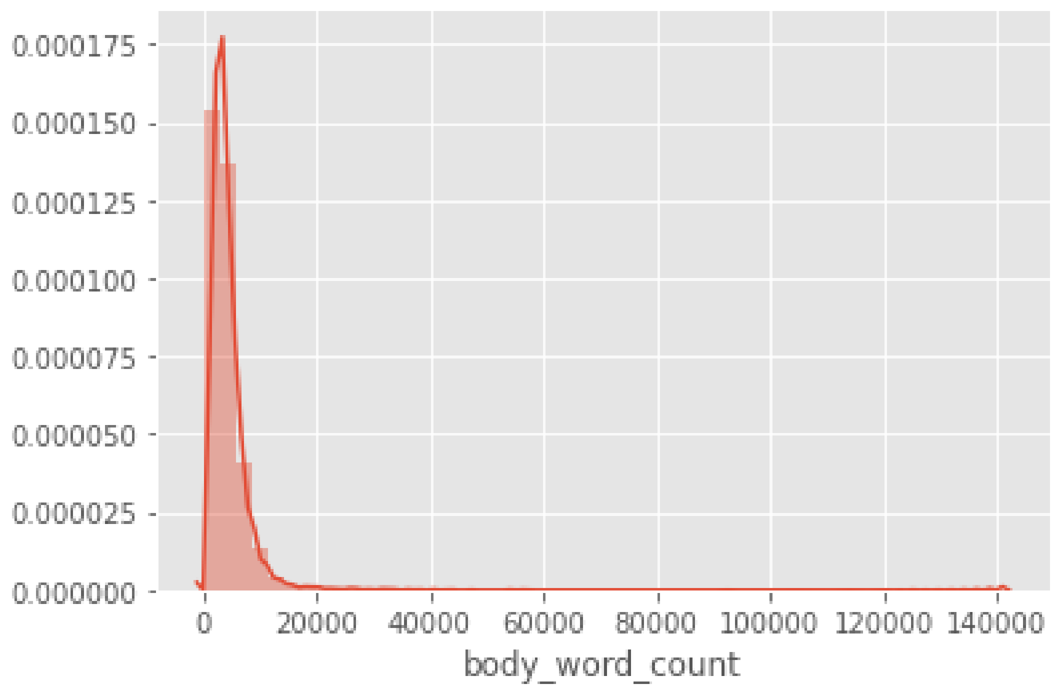
[25]:
```
tqdm.pandas()
df["processed_text"] = df["body_text"].progress_apply(spacy_tokenizer)
```

```
/opt/conda/lib/python3.7/site-packages/tqdm/std.py:666: FutureWarning: The Panel
class is removed from pandas. Accessing it from the top-level namespace will
also be removed in the next version
  from pandas import Panel
100%|      | 8540/8540 [52:32<00:00,  2.71it/s]
```

0.1.2 Word count in the papers

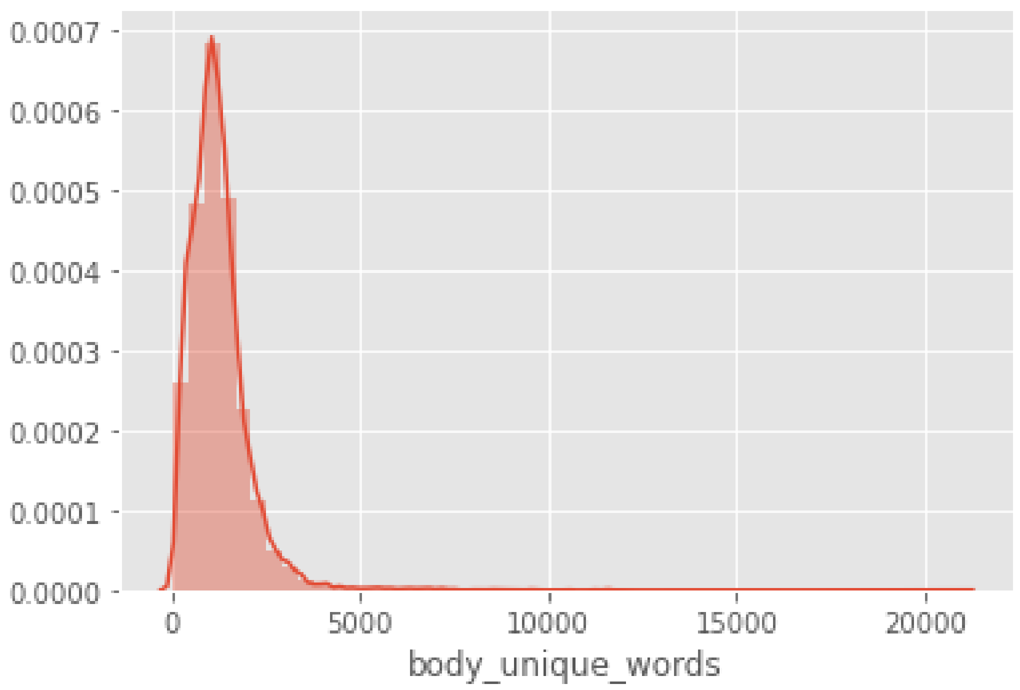
[26]:
```
import seaborn as sns
sns.distplot(df['body_word_count'])
df['body_word_count'].describe()
```

[26]:
```
count      8540.000000
mean       3903.383255
std        4290.373956
min          13.000000
25%        1720.750000
50%        3180.000000
75%        4912.500000
max      140853.000000
Name: body_word_count, dtype: float64
```



[27]:
```
sns.distplot(df['body_unique_words'])
df['body_unique_words'].describe()
```

[27]:
```
count     8540.000000
mean      1248.926932
std        894.493538
min         13.000000
25%        734.750000
50%       1123.000000
75%       1543.000000
max      20966.000000
Name: body_unique_words, dtype: float64
```



0.2 Vectorization

Converting the into a format that can be handled by our algorithms. For this purpose we will be using tf-idf. This will convert our string formatted data into a measure of how important each word is to the instance out of the literature as a whole.

[28]:
```
from sklearn.feature_extraction.text import TfidfVectorizer
def vectorize(text, maxx_features):

    vectorizer = TfidfVectorizer(max_features=maxx_features)
    X = vectorizer.fit_transform(text)
    return X
```

We will be clustering based on the content of the body text. The maximum number of features will be limited. Only the top 2 ** 12 features will be used, eseentially acting as a noise filter. Additionally, more features cause painfully long runtimes.

[29]:
```
text = df['processed_text'].values
X = vectorize(text, 2 ** 12)
X.shape
```

[29]:
```
(8540, 4096)
```

0.3 PCA & Clustering

Let's see how much we can reduce the dimensions while still keeping 95% variance. We will apply Principle Component Analysis (PCA) to our vectorized data. The reason for this is that by keeping a large number of dimensions with PCA, you don't destroy much of the information, but hopefully will remove some noise/outliers from the data, and make the clustering problem easier for k-means. Note that X_reduced will only be used for k-means, t-SNE will still use the original feature vector X that was generated through tf-idf on the NLP processed text.

[30]:
```
from sklearn.decomposition import PCA

pca = PCA(n_components=0.95, random_state=42)
X_reduced= pca.fit_transform(X.toarray())
X_reduced.shape
```

[30]:
```
(8540, 2218)
```

To separate the literature, k-means will be run on the vectorized text

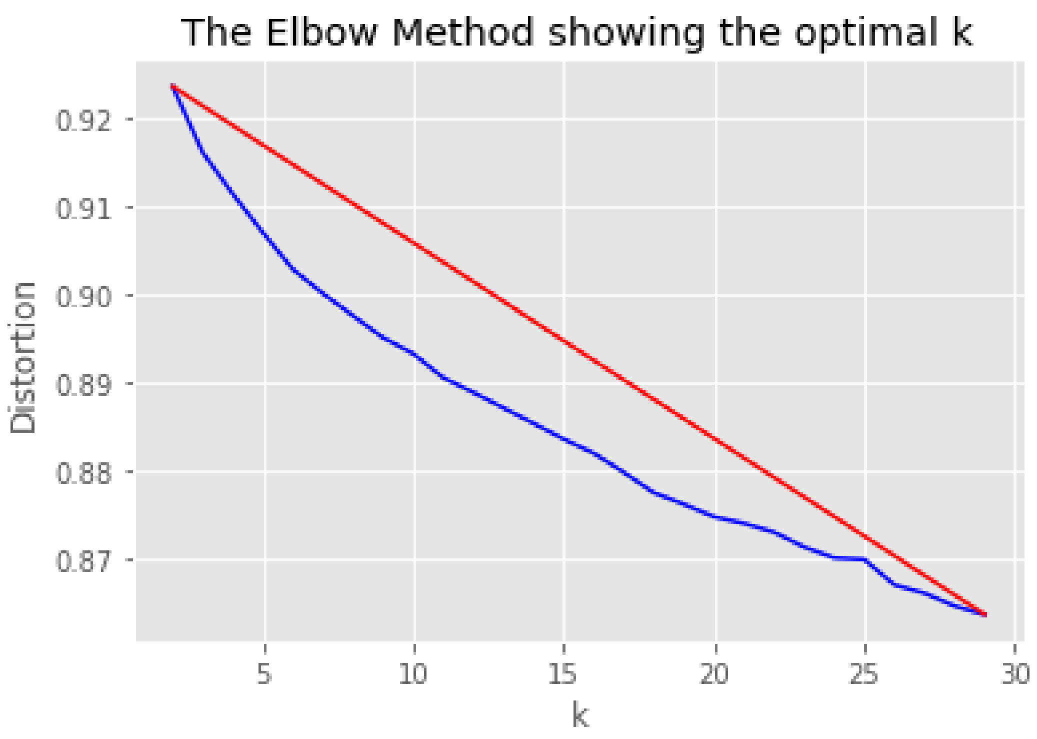
[31]:
```
from sklearn.cluster import KMeans
```

To find the best k value for k-means we'll look at the distortion at different k values. Distortion computes the sum of squared distances from each point to its assigned center. When distortion is plotted against k there will be a k value after which decreases in distortion are minimal. This is the desired number of clusters.

[32]:
```
from sklearn import metrics
from scipy.spatial.distance import cdist

# run kmeans with many different k
distortions = []
K = range(2, 30)
for k in K:
    k_means = KMeans(n_clusters=k, random_state=42).fit(X_reduced)
    k_means.fit(X_reduced)
    distortions.append(sum(np.min(cdist(X_reduced, k_means.cluster_centers_,␣
 ↪'euclidean'), axis=1)) / X.shape[0])
    print('Found distortion for {} clusters'.format(k))
```

```
Found distortion for 2 clusters
Found distortion for 3 clusters
Found distortion for 4 clusters
Found distortion for 5 clusters
Found distortion for 6 clusters
Found distortion for 7 clusters
Found distortion for 8 clusters
Found distortion for 9 clusters
Found distortion for 10 clusters
Found distortion for 11 clusters
Found distortion for 12 clusters
Found distortion for 13 clusters
Found distortion for 14 clusters
Found distortion for 15 clusters
Found distortion for 16 clusters
Found distortion for 17 clusters
Found distortion for 18 clusters
Found distortion for 19 clusters
Found distortion for 20 clusters
Found distortion for 21 clusters
Found distortion for 22 clusters
Found distortion for 23 clusters
Found distortion for 24 clusters
Found distortion for 25 clusters
Found distortion for 26 clusters
Found distortion for 27 clusters
Found distortion for 28 clusters
Found distortion for 29 clusters
```

[33]:
```
X_line = [K[0], K[-1]]
Y_line = [distortions[0], distortions[-1]]

# Plot the elbow
plt.plot(K, distortions, 'b-')
plt.plot(X_line, Y_line, 'r')
plt.xlabel('k')
plt.ylabel('Distortion')
plt.title('The Elbow Method showing the optimal k')
plt.show()
```



```
[34]: k = 20
      kmeans = KMeans(n_clusters=k, random_state=42)
      y_pred = kmeans.fit_predict(X_reduced)
      df['y'] = y_pred
```

0.4 Dimensionality Reduction with t-SNE

Using t-SNE we can reduce our high dimensional features vector to 2 dimensions. By using the 2 dimensions as x,y coordinates, the body_text can be plotted.

`t-Distributed Stochastic Neighbor Embedding (t-SNE)` reduces dimensionality while trying to keep similar instances close and dissimilar instances apart. It is mostly used for visualization, in particular to visualize clusters of instances in high-dimensional space

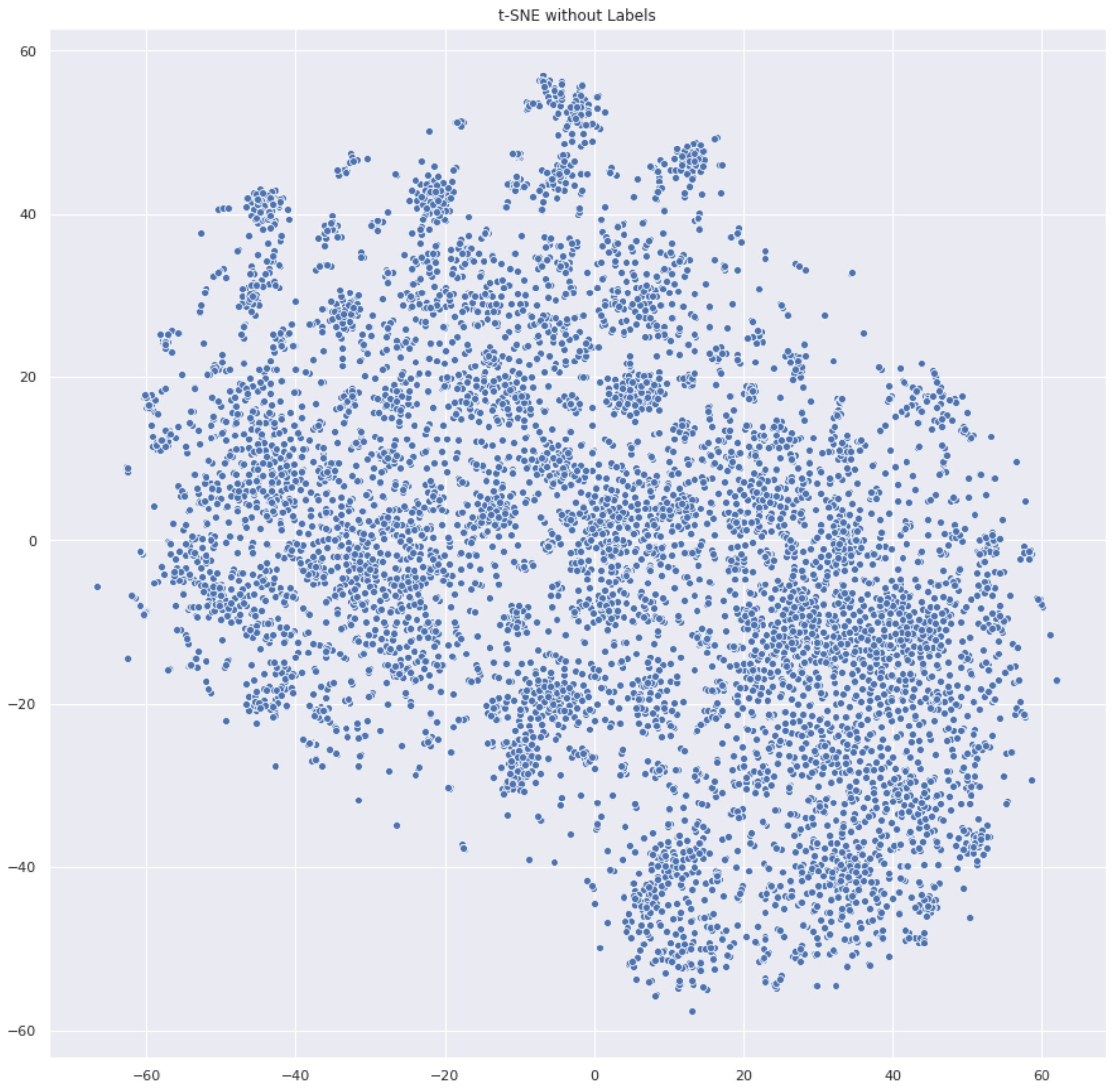
```
[35]: from sklearn.manifold import TSNE

      tsne = TSNE(verbose=1, perplexity=100, random_state=42)
      X_embedded = tsne.fit_transform(X.toarray())
```

```
[t-SNE] Computing 301 nearest neighbors…
[t-SNE] Indexed 8540 samples in 8.117s…
[t-SNE] Computed neighbors for 8540 samples in 791.041s…
[t-SNE] Computed conditional probabilities for sample 1000 / 8540
```

```
[t-SNE] Computed conditional probabilities for sample 2000 / 8540
[t-SNE] Computed conditional probabilities for sample 3000 / 8540
[t-SNE] Computed conditional probabilities for sample 4000 / 8540
[t-SNE] Computed conditional probabilities for sample 5000 / 8540
[t-SNE] Computed conditional probabilities for sample 6000 / 8540
[t-SNE] Computed conditional probabilities for sample 7000 / 8540
[t-SNE] Computed conditional probabilities for sample 8000 / 8540
[t-SNE] Computed conditional probabilities for sample 8540 / 8540
[t-SNE] Mean sigma: 0.359573
[t-SNE] KL divergence after 100 iterations with early exaggeration: 80.265076
[t-SNE] KL divergence after 1000 iterations: 1.896784
```

[36]:

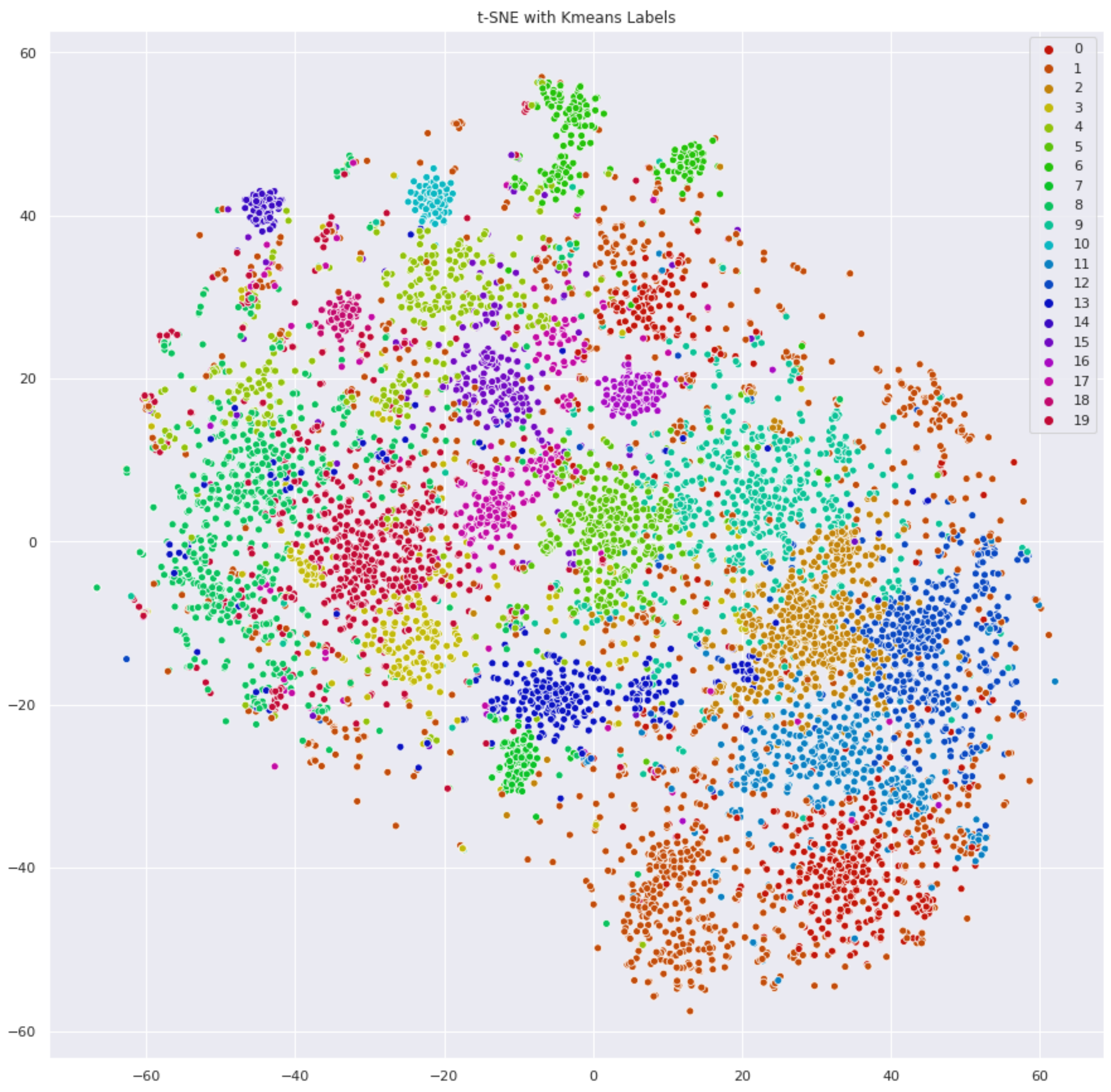
```
from matplotlib import pyplot as plt
import seaborn as sns

# sns settings
sns.set(rc={'figure.figsize':(15,15)})

# colors
palette = sns.color_palette("bright", 1)

# plot
sns.scatterplot(X_embedded[:,0], X_embedded[:,1], palette=palette)
plt.title('t-SNE without Labels')
plt.savefig("t-SNE_covid19.png")
plt.show()
```



There are some clusters we can immediately detect, but the many instances closer to the center are harder to separate. t-SNE did a good job at reducing the dimensionality, but now we need some labels. Let's use the clusters found by k-means as labels. This will help visually separate different concentrations of topics.

[37]:
```
%matplotlib inline
from matplotlib import pyplot as plt
import seaborn as sns

# sns settings
sns.set(rc={'figure.figsize':(15,15)})

# colors
palette = sns.hls_palette(20, l=.4, s=.9)
```

```
# plot
sns.scatterplot(X_embedded[:,0], X_embedded[:,1], hue=y_pred, legend='full',␣
 ↪palette=palette)
plt.title('t-SNE with Kmeans Labels')
plt.savefig("t-SNE_K-means_covid19.png")
plt.show()
```



The labeled plot gives better insight into how the papers are grouped. It is interesting that both k-means and t-SNE are able to agree on certain clusters even though they were ran independently. The location of each paper on the plot was determined by t-SNE while the label (color) was determined by k-means. If we look at a particular part of the plot where t-SNE has grouped many articles forming a cluster, it is likely that k-means is uniform in the labeling of this cluster (most of the cluster is the same color). This behavior shows that structure within the literature can be observed and measured to some extent.

Now there are other cases where the colored labels (k-means) are spread out on the plot (t-SNE). This is a result of t-SNE and k-means finding different connections in the higher dimensional data. The topics of these papers often intersect so it hard to cleanly separate them. This effect can be observed in the formation of subclusters on the plot. These subclusters are a conglomeration of different k-means labels but may share some connection determined by t-SNE.

This organization of the data does not act as a simple search engine. The clustering + dimensionality reduction is performed on the mathematical similarities of the publications. As an unsupervised approach, the algorithms may even find connections that were unnaparent to humans. This may highlight hidden shared information and advance further research.

0.5 Topic Modeling on Each Cluster

Now we will attempt to find the most significant words in each clusters. K-means clustered the articles but did not label the topics. Through topic modeling we will find out what the most important terms for each cluster are. This will add more meaning to the cluster by giving keywords to quickly identify the themes of the cluster.

For topic modeling, we will use `LDA (Latent Dirichlet Allocation)`. In LDA, each document can be described by a distribution of topics and each topic can be described by a distribution of words.

[38]:
```
from sklearn.decomposition import LatentDirichletAllocation
from sklearn.feature_extraction.text import CountVectorizer
```

[39]:
```
vectorizers = []

for ii in range(0, 20):
    # Creating a vectorizer
    vectorizers.append(CountVectorizer(min_df=5, max_df=0.9,␣
 ↪stop_words='english', lowercase=True,␣
 ↪token_pattern='[a-zA-Z\-][a-zA-Z\-]{2,}'))
```

[40]:
```
vectorizers[0]
```

[40]:
```
CountVectorizer(analyzer='word', binary=False, decode_error='strict',
                dtype=<class 'numpy.int64'>, encoding='utf-8', input='content',
                lowercase=True, max_df=0.9, max_features=None, min_df=5,
                ngram_range=(1, 1), preprocessor=None, stop_words='english',
                strip_accents=None, token_pattern='[a-zA-Z\\-][a-zA-Z\\-]{2,}',
                tokenizer=None, vocabulary=None)
```

[41]:
```
vectorized_data = []

for current_cluster, cvec in enumerate(vectorizers):
    try:
        vectorized_data.append(cvec.fit_transform(df.loc[df['y'] ==␣
↪current_cluster, 'processed_text']))
    except Exception as e:
        print("Not enough instances in cluster: " + str(current_cluster))
        vectorized_data.append(None)
```

[42]:
```
len(vectorized_data)
```

[42]:
```
20
```

[43]:
```
# number of topics per cluster
NUM_TOPICS_PER_CLUSTER = 20

lda_models = []
for ii in range(0, 20):
    # Latent Dirichlet Allocation Model
    lda = LatentDirichletAllocation(n_components=NUM_TOPICS_PER_CLUSTER,␣
↪max_iter=10, learning_method='online',verbose=False, random_state=42)
    lda_models.append(lda)

lda_models[0]
```

[43]:
```
LatentDirichletAllocation(batch_size=128, doc_topic_prior=None,
                          evaluate_every=-1, learning_decay=0.7,
                          learning_method='online', learning_offset=10.0,
                          max_doc_update_iter=100, max_iter=10,
                          mean_change_tol=0.001, n_components=20, n_jobs=None,
                          perp_tol=0.1, random_state=42, topic_word_prior=None,
                          total_samples=1000000.0, verbose=False)
```

For each cluster, we had created a correspoding LDA model in the previous step. We will now fit_transform all the LDA models on their respective cluster vectors

[44]:
```
clusters_lda_data = []

for current_cluster, lda in enumerate(lda_models):
    # print("Current Cluster: " + str(current_cluster))

    if vectorized_data[current_cluster] != None:
        clusters_lda_data.append((lda.
↪fit_transform(vectorized_data[current_cluster])))
```

0.5.1 Extracting the keywords from each cluster

[45]:
```
# Functions for printing keywords for each topic
def selected_topics(model, vectorizer, top_n=3):
    current_words = []
    keywords = []

    for idx, topic in enumerate(model.components_):
        words = [(vectorizer.get_feature_names()[i], topic[i]) for i in topic.
↪argsort()[:-top_n - 1:-1]]
        for word in words:
            if word[0] not in current_words:
                keywords.append(word)
                current_words.append(word[0])

    keywords.sort(key = lambda x: x[1])
    keywords.reverse()
    return_values = []
    for ii in keywords:
        return_values.append(ii[0])
    return return_values
```

[46]:
```
all_keywords = []
for current_vectorizer, lda in enumerate(lda_models):
    # print("Current Cluster: " + str(current_vectorizer))

    if vectorized_data[current_vectorizer] != None:
        all_keywords.append(selected_topics(lda,␣
↪vectorizers[current_vectorizer]))
```

[47]:
```
all_keywords[0][:10]
```

[47]:
```
['human',
 'research',
 'disease',
 'disaster',
 'animal',
 'study',
 'outbreak',
 'information',
 'development',
 'science']
```

[48]:
```
len(all_keywords)
```

[48]:
```
20
```

```
[49]: f=open('topics.txt','w')

      count = 0

      for ii in all_keywords:

          if vectorized_data[count] != None:
              f.write(', '.join(ii) + "\n")
          else:
              f.write("Not enough instances to be determined. \n")
              f.write(', '.join(ii) + "\n")
          count += 1

      f.close()
```

```
[50]: import pickle

      # save the COVID-19 DataFrame, too large for github
      pickle.dump(df, open("df_covid.p", "wb" ))

      # save the final t-SNE
      pickle.dump(X_embedded, open("X_embedded.p", "wb" ))

      # save the labels generate with k-means(20)
      pickle.dump(y_pred, open("y_pred.p", "wb" ))
```

0.6 Classification

```
[51]: # function to print out classification model report
      def classification_report(model_name, test, pred):
          from sklearn.metrics import precision_score, recall_score
          from sklearn.metrics import accuracy_score
          from sklearn.metrics import f1_score

          print(model_name, ":\n")
          print("Accuracy Score: ", '{:,.3f}'.format(float(accuracy_score(test,␣
       ↪pred)) * 100), "%")
          print("     Precision: ", '{:,.3f}'.format(float(precision_score(test,␣
       ↪pred, average='macro')) * 100), "%")
          print("        Recall: ", '{:,.3f}'.format(float(recall_score(test, pred,␣
       ↪average='macro')) * 100), "%")
          print("      F1 score: ", '{:,.3f}'.format(float(f1_score(test, pred,␣
       ↪average='macro')) * 100), "%")
```

[52]:
```python
from sklearn.model_selection import train_test_split

# test set size of 20% of the data and the random seed 42 <3
X_train, X_test, y_train, y_test = train_test_split(X.toarray(),y_pred,␣
↪test_size=0.2, random_state=42)

print("X_train size:", len(X_train))
print("X_test size:", len(X_test), "\n")
```

```
X_train size: 6832
X_test size: 1708
```

[53]:
```python
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import cross_val_predict
from sklearn.linear_model import SGDClassifier

# SGD instance
sgd_clf = SGDClassifier(max_iter=10000, tol=1e-3, random_state=42, n_jobs=4)
# train SGD
sgd_clf.fit(X_train, y_train)

# cross validation predictions
sgd_pred = cross_val_predict(sgd_clf, X_train, y_train, cv=3, n_jobs=4)

# print out the classification report
classification_report("Stochastic Gradient Descent Report (Training Set)",␣
↪y_train, sgd_pred)
```

```
Stochastic Gradient Descent Report (Training Set) :

Accuracy Score:  88.100 %
     Precision:  90.069 %
        Recall:  89.797 %
      F1 score:  89.879 %
```

To test for overfitting, let’s see how the model generalizes over the test set

[54]:
```python
# cross validation predictions
sgd_pred = cross_val_predict(sgd_clf, X_test, y_test, cv=3, n_jobs=4)

# print out the classification report
classification_report("Stochastic Gradient Descent Report (Training Set)",␣
↪y_test, sgd_pred)
```

```
Stochastic Gradient Descent Report (Training Set) :

Accuracy Score:  82.084 %
```

```
Precision:  87.492 %
   Recall:  81.240 %
 F1 score:  83.763 %
```

Now let's see how the model can generalize across the whole dataset.

```
[55]: sgd_cv_score = cross_val_score(sgd_clf, X.toarray(), y_pred, cv=10)
      print("Mean cv Score - SGD: {:,.3f}".format(float(sgd_cv_score.mean()) * 100),␣
       ↪"%")
```

```
Mean cv Score - SGD: 90.070 %
```