COVID-19 Literature Clustering

@inproceedings{COVID-19 Literature Clustering, author = {Eren, E. Maksim. Solovyev, Nick. Nicholas, Charles. Raff, Edward}, title = {COVID-19 Literature Clustering}, year = {2020}, month = {April}, location = {University of Maryland Baltimore County (UMBC), Baltimore, MD, USA}, note= {Malware Research Group}, url = {\url{https://github.com/MaksimEkin/COVID19-Literature-Clustering}} (https://github.com/MaksimEkin/COVID19-Literature-Clustering%7D%7D), howpublished = {TBA} }

Note: conda install -c conda-forge langdetect; conda install -c conda-forge spacy; conda install -c conda-forge spacy-model-en_core_web_lg

Data ¶

https://www.kaggle.com/allen-institute-for-ai/CORD-19-research-challenge/?select=metadata.csv (https://www.kaggle.com/allen-institute-for-ai/CORD-19-research-challenge/?select=metadata.csv)

In [1]:
```
import numpy as np
import pandas as pd
import glob
import json

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

In [2]:
```
pwd
```

Out[2]:
```
'/Users/admin/Desktop/python/covid19/covid19_nlp'
```

In [3]:
```
root_path = '/Users/admin/Desktop/python/covid19/covid19_nlp'
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/anaconda3/lib/python3.7/site-packages/IPython/core/interactiveshell.
py:3063: DtypeWarning: Columns (13,14) have mixed types.Specify dtype opt
ion on import or set low_memory=False.
  interactivity=interactivity, compiler=compiler, result=result)
```

Out[3]:

	cord_uid	sha	source_x	title	doi	
0	ug7v899j	d1aafb70c066a2068b02786f8929fd9c900897fb	PMC	Clinical features of culture-proven Mycoplasma...	10.1186/1471-2334-1-6	P
1	02tnwd4m	6b0567729c2143a66d737eb0a2f63f2dce2e5a7d	PMC	Nitric oxide: a pro-inflammatory mediator in l...	10.1186/rr14	P
2	ejv2xln0	06ced00a5fc04215949aa72528f2eeaae1d58927	PMC	Surfactant protein-D and pulmonary host defense	10.1186/rr19	P
3	2b73a28n	348055649b6b8cf2b9a376498df9bf41f7123605	PMC	Role of endothelin-1 in lung disease	10.1186/rr44	P
4	9785vg6d	5f48792a5fa08bed9f56016f4981ae2ca6031b32	PMC	Gene expression in epithelial cells in respons...	10.1186/rr61	P

In [4]:
```
meta_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 128492 entries, 0 to 128491
Data columns (total 19 columns):
 #   Column            Non-Null Count   Dtype  
---  ------            --------------   -----  
 0   cord_uid          128492 non-null  object 
 1   sha               55751 non-null   object 
 2   source_x          128492 non-null  object 
 3   title             128464 non-null  object 
 4   doi               100586 non-null  object 
 5   pmcid             60771 non-null   object 
 6   pubmed_id         99124 non-null   object 
 7   license           128492 non-null  object 
 8   abstract          101611 non-null  object 
 9   publish_time      128477 non-null  object 
 10  authors           123725 non-null  object 
 11  journal           122195 non-null  object 
 12  mag_id            0 non-null       float64
 13  who_covidence_id  17071 non-null   object 
 14  arxiv_id          1395 non-null    object 
 15  pdf_json_files    55751 non-null   object 
 16  pmc_json_files    43753 non-null   object 
 17  url               49173 non-null   object 
 18  s2_id             102980 non-null  float64
dtypes: float64(2), object(17)
memory usage: 18.6+ MB
```

Fetch All of JSON File Path¶

In [5]:
```
all_json = glob.glob(f'{root_path}/**/*.json', recursive=True)
len(all_json)
```

Out[5]: 103314

Helper Functions

In [ ]:
```
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[
first_row = FileReader(all_json[0])
print(first_row)
```

In [7]:
```
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
```

Load the Data into DataFrame¶

In [51]:
```
dict_ = {'paper_id': [], 'doi':[], 'abstract': [], 'body_text': [], 'author
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 appe
        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
            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', 'bod
df_covid.head()
```

```
Processing index: 0 of 103314
Processing index: 10331 of 103314
Processing index: 20662 of 103314
Processing index: 30993 of 103314
Processing index: 41324 of 103314
Processing index: 51655 of 103314
Processing index: 61986 of 103314
Processing index: 72317 of 103314
Processing index: 82648 of 103314
Processing index: 92979 of 103314
Processing index: 103310 of 103314
```

Out[51]:

	paper_id	doi	abstract	bo
0	4fcb95cc0c4ea6d1fa4137a4a087715ed6b68cea	10.1007/s00431-019-03543-0	Abnormal levels of end-tidal carbon dioxide (E...	Improv in n intensi
1	86d4262de73cf81b5ea6aafb91630853248bff5f	10.1016/j.bbamcr.2011.06.011	The endoplasmic reticulum (ER) is the biggest ...	endo reticulum a multi
2	b2f67d533f2749807f2537f3775b39da3b186051	10.1016/j.fsiml.2020.100013		Th dispropo nu inc
3	9ec0b1175992879d5b8d3351ef40a28bb48f18ce	10.1016/j.jhin.2019.07.001		Sir, Tes respirato infec
4	4ed70c27f14b7f9e6219fe605eae2b21a229f23c	10.1080/14787210.2017.1271712		The Mid res sy cor

Some feature engineering

In [52]:
```
df_covid['abstract_word_count'] = df_covid['abstract'].apply(lambda x: len(
df_covid['body_word_count'] = df_covid['body_text'].apply(lambda x: len(x.s
df_covid['body_unique_words']=df_covid['body_text'].apply(lambda x:len(set(
df_covid.head()
```

Out[52]:

	paper_id	doi	abstract	bo
0	4fcb95cc0c4ea6d1fa4137a4a087715ed6b68cea	10.1007/s00431-019-03543-0	Abnormal levels of end-tidal carbon dioxide (E...	Improv in n intensi
1	86d4262de73cf81b5ea6aafb91630853248bff5f	10.1016/j.bbamcr.2011.06.011	The endoplasmic reticulum (ER) is the biggest ...	endo reticulum a multi
2	b2f67d533f2749807f2537f3775b39da3b186051	10.1016/j.fsiml.2020.100013		Th dispropo nu inc
3	9ec0b1175992879d5b8d3351ef40a28bb48f18ce	10.1016/j.jhin.2019.07.001		Sir, Tes respirato infec
4	4ed70c27f14b7f9e6219fe605eae2b21a229f23c	10.1080/14787210.2017.1271712		The Mid res sy cor

In [53]:
```
df_covid.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 52471 entries, 0 to 52470
Data columns (total 11 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   paper_id             52471 non-null  object
 1   doi                  50995 non-null  object
 2   abstract             52471 non-null  object
 3   body_text            52471 non-null  object
 4   authors              51301 non-null  object
 5   title                52471 non-null  object
 6   journal              48182 non-null  object
 7   abstract_summary     52471 non-null  object
 8   abstract_word_count  52471 non-null  int64 
 9   body_word_count      52471 non-null  int64 
 10  body_unique_words    52471 non-null  int64 
dtypes: int64(3), object(8)
memory usage: 4.4+ MB
```

Handle Possible Duplicates

In [54]:
```
df_covid['abstract'].describe(include='all')
```

Out[54]:
```
count     52471
unique    37150
top
freq      15128
Name: abstract, dtype: object
```

In [55]:
```
df_covid.drop_duplicates(['abstract', 'body_text'], inplace=True)
df_covid['abstract'].describe(include='all')
```

Out[55]:
```
count     52339
unique    37150
top
freq      15034
Name: abstract, dtype: object
```

In [56]:
```
df_covid['body_text'].describe(include='all')
```

Out[56]:
```
count                                52339
unique                               52334
top       J o u r n a l P r e -p r o o f
freq                                     3
Name: body_text, dtype: object
```

Take a Look at the Data

In [57]:
```
df_covid.head()
```

Out[57]:

	paper_id	doi	abstract	bo
0	4fcb95cc0c4ea6d1fa4137a4a087715ed6b68cea	10.1007/s00431-019-03543-0	Abnormal levels of end-tidal carbon dioxide (E...	Improv in n intensi
1	86d4262de73cf81b5ea6aafb91630853248bff5f	10.1016/j.bbamcr.2011.06.011	The endoplasmic reticulum (ER) is the biggest ...	endo reticulum a multi
2	b2f67d533f2749807f2537f3775b39da3b186051	10.1016/j.fsiml.2020.100013		Th dispropo nu inc
3	9ec0b1175992879d5b8d3351ef40a28bb48f18ce	10.1016/j.jhin.2019.07.001		Sir, Tes respirato infec
4	4ed70c27f14b7f9e6219fe605eae2b21a229f23c	10.1080/14787210.2017.1271712		The Mid res sy cor

In [58]:
```
df_covid.describe()
```

Out[58]:

	abstract_word_count	body_word_count	body_unique_words
count	52339.000000	52339.000000	52339.000000
mean	157.998223	4769.102199	1409.134756
std	186.518579	9996.566795	1640.970446
min	0.000000	1.000000	1.000000
25%	0.000000	2008.000000	802.000000
50%	151.000000	3359.000000	1164.000000
75%	234.000000	5130.000000	1606.000000
max	7415.000000	279623.000000	38298.000000

Data Pre-processing

In [59]:
```
df = df_covid.sample(10000, random_state=42)
#del df_covid
```

In [60]:
```
df.dropna(inplace=True)
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 8908 entries, 39318 to 3570
Data columns (total 11 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   paper_id             8908 non-null   object
 1   doi                  8908 non-null   object
 2   abstract             8908 non-null   object
 3   body_text            8908 non-null   object
 4   authors              8908 non-null   object
 5   title                8908 non-null   object
 6   journal              8908 non-null   object
 7   abstract_summary     8908 non-null   object
 8   abstract_word_count  8908 non-null   int64 
 9   body_word_count      8908 non-null   int64 
 10  body_unique_words    8908 non-null   int64 
dtypes: int64(3), object(8)
memory usage: 835.1+ KB
```

In [61]:
```
df.dropna(inplace=True)
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 8908 entries, 39318 to 3570
Data columns (total 11 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   paper_id             8908 non-null   object
 1   doi                  8908 non-null   object
 2   abstract             8908 non-null   object
 3   body_text            8908 non-null   object
 4   authors              8908 non-null   object
 5   title                8908 non-null   object
 6   journal              8908 non-null   object
 7   abstract_summary     8908 non-null   object
 8   abstract_word_count  8908 non-null   int64 
 9   body_word_count      8908 non-null   int64 
 10  body_unique_words    8908 non-null   int64 
dtypes: int64(3), object(8)
memory usage: 835.1+ KB
```

Handling multiple languages

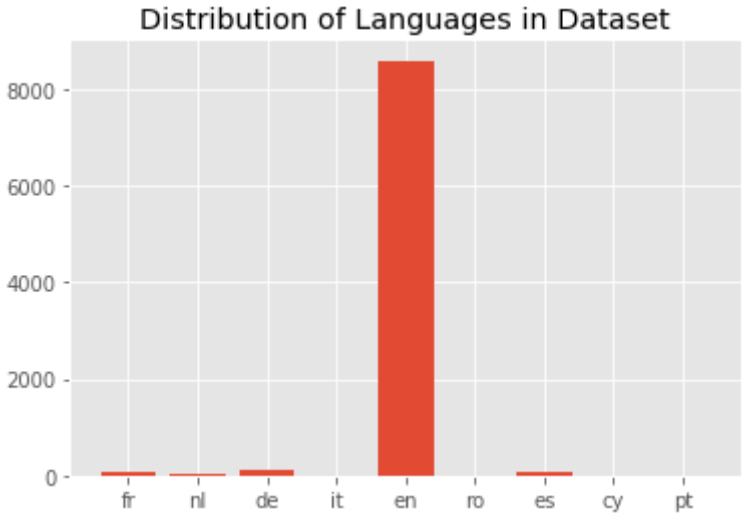
In [62]:
```
from tqdm import tqdm
from langdetect import detect
from langdetect import DetectorFactory

# set seed
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%|██████████| 8908/8908 [01:02<00:00, 142.79it/s]
```

In [63]:
```
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: 8908

{'cy': 1,
 'de': 132,
 'en': 8601,
 'es': 64,
 'fr': 90,
 'it': 5,
 'nl': 13,
 'pt': 1,
 'ro': 1}
```

In [64]:
```
df['language'] = languages
plt.bar(range(len(languages_dict)), list(languages_dict.values()), align='c
plt.xticks(range(len(languages_dict)), list(languages_dict.keys()))
plt.title("Distribution of Languages in Dataset")
plt.show()
```



In [65]:
```
df = df[df['language'] == 'en']
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 8601 entries, 39318 to 3570
Data columns (total 12 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   paper_id             8601 non-null   object
 1   doi                  8601 non-null   object
 2   abstract             8601 non-null   object
 3   body_text            8601 non-null   object
 4   authors              8601 non-null   object
 5   title                8601 non-null   object
 6   journal              8601 non-null   object
 7   abstract_summary     8601 non-null   object
 8   abstract_word_count  8601 non-null   int64 
 9   body_word_count      8601 non-null   int64 
 10  body_unique_words    8601 non-null   int64 
 11  language             8601 non-null   object
dtypes: int64(3), object(9)
memory usage: 873.5+ KB
```

In [66]:
```
# 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/release
```

In [69]:
```
#NLP
import spacy
from spacy.lang.en.stop_words import STOP_WORDS
import en_core_web_lg  # model downloaded in previous step
```

Stopwords

In [70]:
```
import string

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

Out[70]:
```
['all',
 'own',
 'already',
 'towards',
 'then',
 'whoever',
 'say',
 'which',
 'into',
 'take']
```

In [71]:
```
custom_stop_words = [
    'doi', 'preprint', 'copyright', 'peer', 'reviewed', 'org', 'https', 'et
    'rights', 'reserved', 'permission', 'used', 'using', 'biorxiv', 'medrxi
    'al.', 'Elsevier', 'PMC', 'CZI', 'www'
]

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

A function that will process the text data

In [72]:
```
# Parser
parser = en_core_web_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-" els
    mytokens = [ word for word in mytokens if word not in stopwords and wor
    mytokens = " ".join([i for i in mytokens])
    return mytokens
```

Applying the text-processing function on the body_text

In [73]:
```
tqdm.pandas()
df["processed_text"] = df["body_text"].progress_apply(spacy_tokenizer)
```

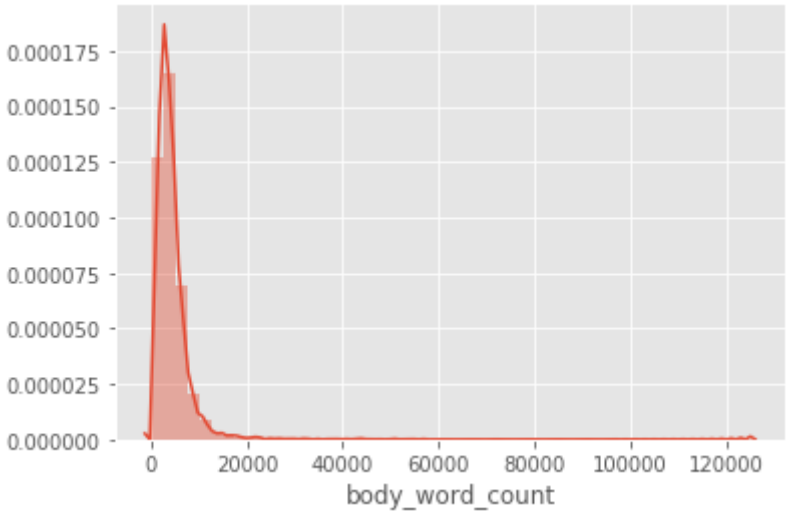
```
/opt/anaconda3/lib/python3.7/site-packages/tqdm/std.py:658: FutureWarnin
g: The Panel class is removed from pandas. Accessing it from the top-leve
l namespace will also be removed in the next version
  from pandas import Panel
100%|██████████| 8601/8601 [54:59<00:00,  2.61it/s]
```

Word count in the papers

In [74]:
```
import seaborn as sns
```

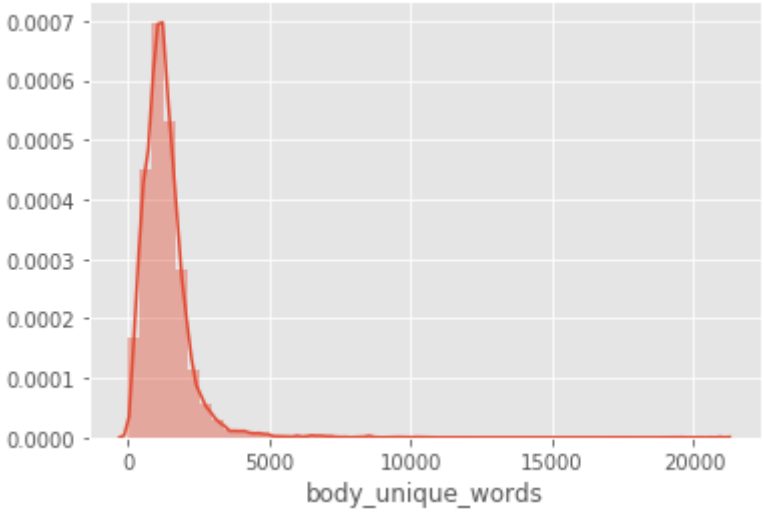
In [75]:
```
sns.distplot(df['body_word_count'])
df['body_word_count'].describe()
```

Out[75]:
```
count      8601.000000
mean       4210.114754
std        4191.947514
min           4.000000
25%        2069.000000
50%        3434.000000
75%        5180.000000
max      124703.000000
Name: body_word_count, dtype: float64
```



In [76]:
```
sns.distplot(df['body_unique_words'])
df['body_unique_words'].describe()
```

Out[76]:
```
count     8601.000000
mean      1326.235438
std        897.425493
min          4.000000
25%        826.000000
50%       1191.000000
75%       1617.000000
max      20966.000000
Name: body_unique_words, dtype: float64
```



Vectorization

In [77]:
```
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
```

In [78]:
```
text = df['processed_text'].values
X = vectorize(text, 2 ** 12)
X.shape
```

Out[78]:
```
(8601, 4096)
```

PCA & Clustering

In [79]:
```
from sklearn.decomposition import PCA

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

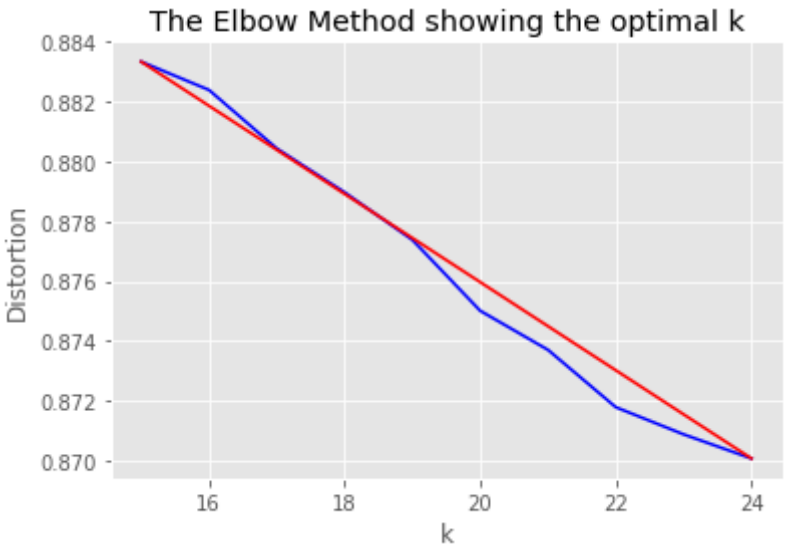
Out[79]: (8601, 2178)

In [80]:
```
from sklearn.cluster import KMeans
```

How many clusters?

In [85]:
```
from sklearn import metrics
from scipy.spatial.distance import cdist

# run kmeans with many different k
distortions = []
K = range(15, 25)
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_
    #print('Found distortion for {} clusters'.format(k))
```

In [86]:
```
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()
```



Run k-means

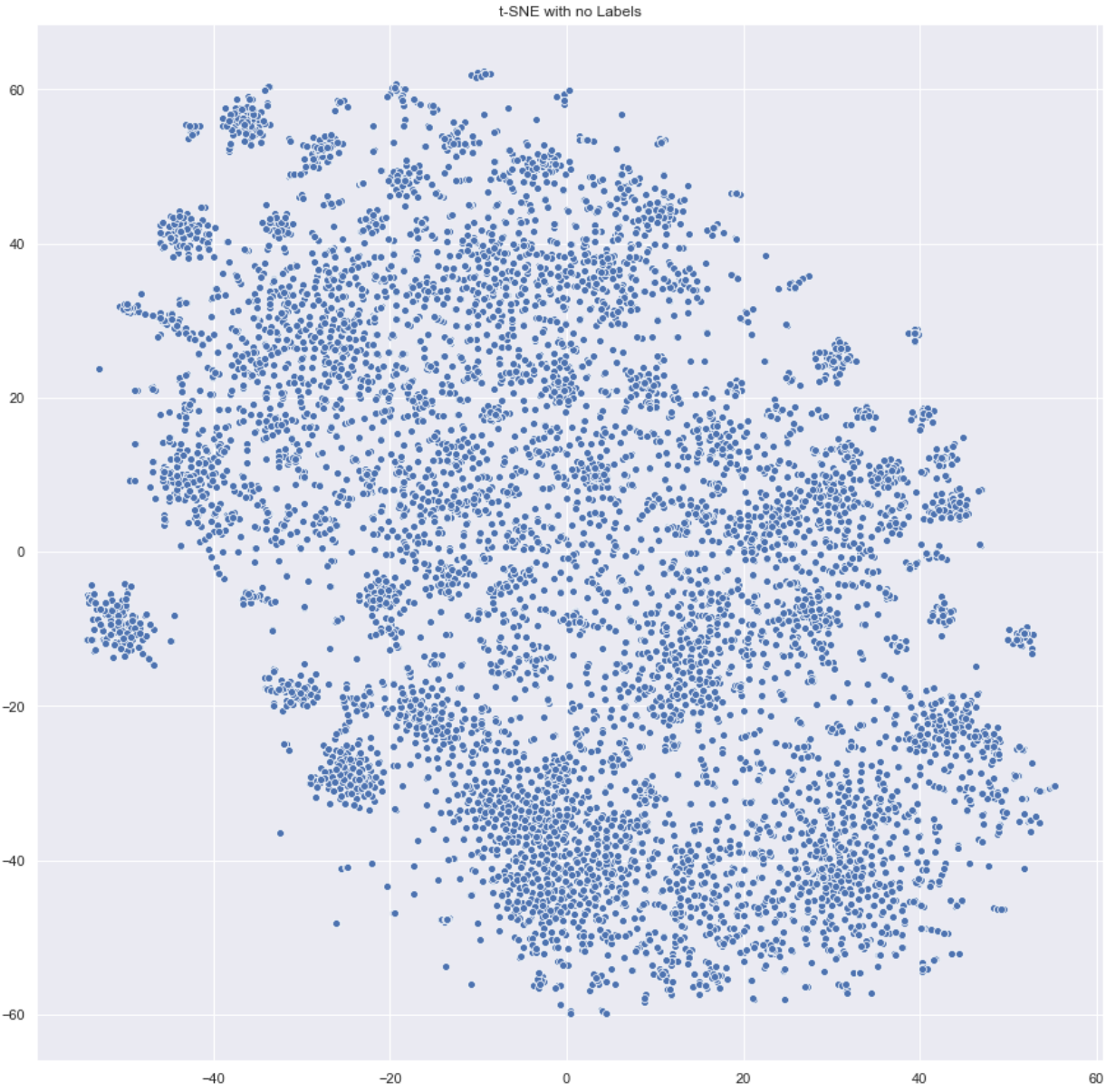
In [87]:
```
k = 20
kmeans = KMeans(n_clusters=k, random_state=42)
y_pred = kmeans.fit_predict(X_reduced)
df['y'] = y_pred
```

Dimensionality Reduction with t-SNE

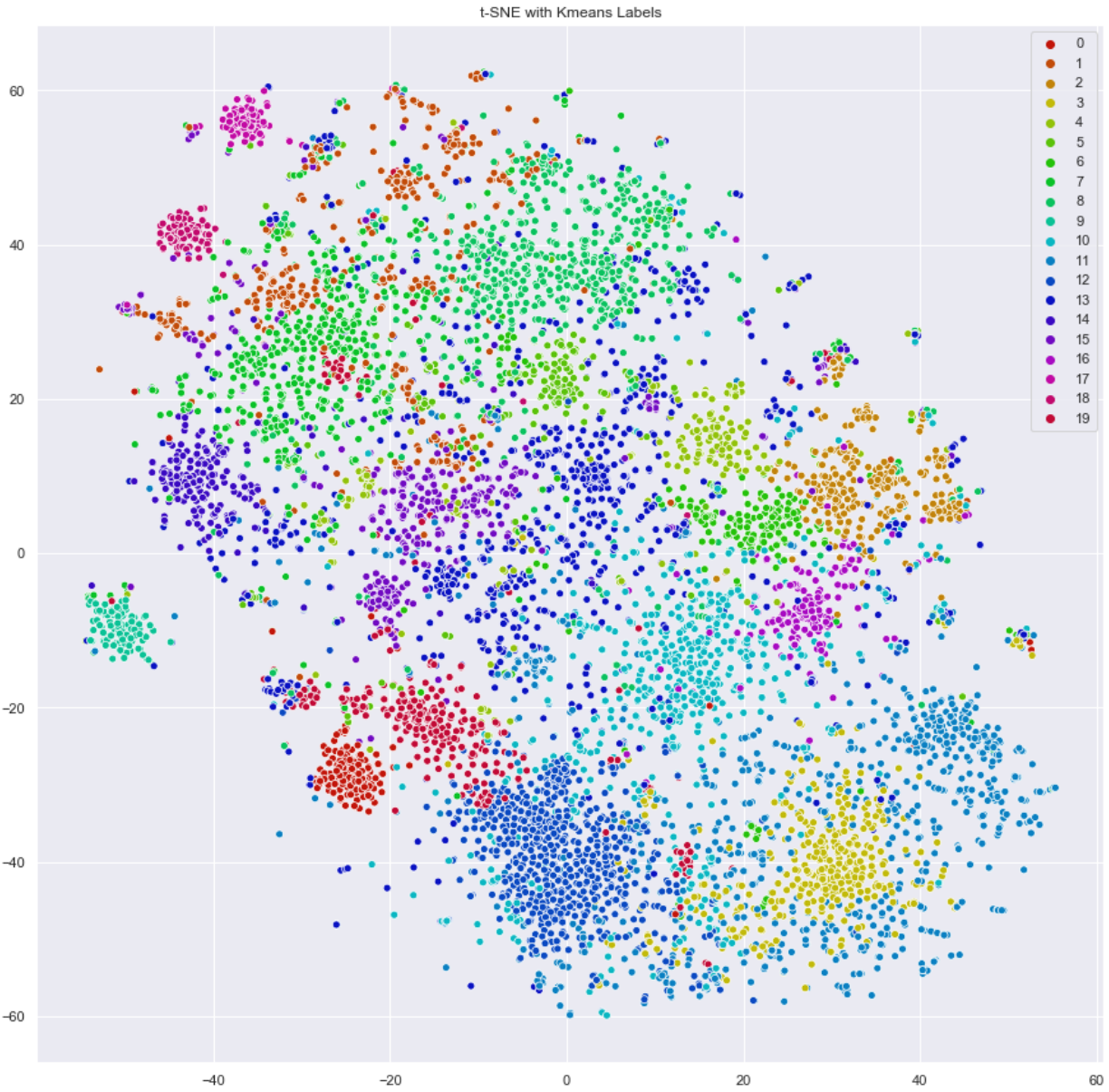
In [88]:
```
from sklearn.manifold import TSNE

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 8601 samples in 6.389s...
[t-SNE] Computed neighbors for 8601 samples in 542.246s...
[t-SNE] Computed conditional probabilities for sample 1000 / 8601
[t-SNE] Computed conditional probabilities for sample 2000 / 8601
[t-SNE] Computed conditional probabilities for sample 3000 / 8601
[t-SNE] Computed conditional probabilities for sample 4000 / 8601
[t-SNE] Computed conditional probabilities for sample 5000 / 8601
[t-SNE] Computed conditional probabilities for sample 6000 / 8601
[t-SNE] Computed conditional probabilities for sample 7000 / 8601
[t-SNE] Computed conditional probabilities for sample 8000 / 8601
[t-SNE] Computed conditional probabilities for sample 8601 / 8601
[t-SNE] Mean sigma: 0.367739
[t-SNE] KL divergence after 50 iterations with early exaggeration: 80.517
990
[t-SNE] KL divergence after 1000 iterations: 1.871137
```

In [89]:
```
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 with no Labels')
plt.savefig("t-sne_covid19.png")
plt.show()
```



In [91]:
```
%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'
plt.title('t-SNE with Kmeans Labels')
plt.savefig("improved_cluster_tsne.png")
plt.show()
```



Topic Modeling on Each Cluster

In [92]:
```
from sklearn.decomposition import LatentDirichletAllocation
from sklearn.feature_extraction.text import CountVectorizer
```

In [93]:
```
vectorizers = []

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

In [94]:
```
vectorizers[0]
```

Out[94]:
```
CountVectorizer(analyzer='word', binary=False, decode_error='strict',
                dtype=<class 'numpy.int64'>, encoding='utf-8', input='con
tent',
                lowercase=True, max_df=0.9, max_features=None, min_df=5,
                ngram_range=(1, 1), preprocessor=None, stop_words='englis
h',
                strip_accents=None, token_pattern='[a-zA-Z\\-][a-zA-Z\\-]
{2,}',
                tokenizer=None, vocabulary=None)
```

In [95]:
```
vectorized_data = []

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

In [96]:
```
len(vectorized_data)
```

Out[96]:
```
20
```

In [97]:
```
# 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, ma
    lda_models.append(lda)

lda_models[0]
```

Out[97]:
```
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)
```

In [98]:
```
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
```

In [99]:
```
# 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 top
        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
```

In [100]:
```
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_vector
```

In [104]:
```
all_keywords[0][:10]
```

Out[104]:
```
['mouse',
 'test',
 'camel',
 'vaccine',
 'pro',
 'sars',
 'residue',
 'package',
 'signal',
 'therapy']
```

In [102]:
```
len(all_keywords)
```

Out[102]:
```
20
```

Save current outputs to file

In [105]:
```
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()
```

In [106]:
```
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" ))
```

Classify

In [107]:
```
# 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, p
    print("     Precision: ", '{:,.3f}'.format(float(precision_score(test,
    print("        Recall: ", '{:,.3f}'.format(float(recall_score(test, pre
    print("      F1 score: ", '{:,.3f}'.format(float(f1_score(test, pred, a
```

Split the data into train/test sets

In [108]:
```
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, tes

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

```
X_train size: 6880
X_test size: 1721
```

In [109]:
```
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)",
```

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

Accuracy Score:  88.038 %
     Precision:  89.648 %
        Recall:  88.208 %
      F1 score:  88.851 %
```

Test for overfitting

In [110]:
```
# 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)",
```

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

Accuracy Score:  83.614 %
     Precision:  86.200 %
        Recall:  85.327 %
      F1 score:  85.504 %
```

In [111]:
```
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()) * 10
```

```
Mean cv Score - SGD: 89.629 %
```

Plotting the data

In [ ]:
```
import os

# change into lib directory to load plot python scripts
main_path = os.getcwd()
lib_path = '/kaggle/input/kaggle-resources'
os.chdir(lib_path)
```

In [120]:
```
from bokeh.models import CustomJS

# handle the currently selected article
def selected_code():
    code = """
            var titles = [];
            var authors = [];
            var journals = [];
            var links = [];
            cb_data.source.selected.indices.forEach(index => titles.push(so
            cb_data.source.selected.indices.forEach(index => authors.push(s
            cb_data.source.selected.indices.forEach(index => journals.push(
            cb_data.source.selected.indices.forEach(index => links.push(sou
            title = "<h4>" + titles[0].toString().replace(/<br>/g, ' ') + "
            authors = "<p1><b>Authors:</b> " + authors[0].toString().replac
            // journal = "<b>Journal</b>" + journals[0].toString() + "<br>"
            link = "<b>Link:</b> <a href='" + "http://doi.org/" + links[0].
            current_selection.text = title + authors + link
            current_selection.change.emit();
    """
    return code

# handle the keywords and search
def input_callback(plot, source, out_text, topics):

    # slider call back for cluster selection
    callback = CustomJS(args=dict(p=plot, source=source, out_text=out_text,
                var key = text.value;
                key = key.toLowerCase();
                var cluster = slider.value;
                var data = source.data;


                x = data['x'];
                y = data['y'];
                x_backup = data['x_backup'];
                y_backup = data['y_backup'];
                labels = data['desc'];
                abstract = data['abstract'];
                titles = data['titles'];
                authors = data['authors'];
                journal = data['journal'];
                if (cluster == '20') {
                    out_text.text = 'Keywords: Slide to specific cluster to
                    for (i = 0; i < x.length; i++) {
                        if(abstract[i].includes(key) ||
                        titles[i].includes(key) ||
                        authors[i].includes(key) ||
                        journal[i].includes(key)) {
                            x[i] = x_backup[i];
                            y[i] = y_backup[i];
                        } else {
                            x[i] = undefined;
                            y[i] = undefined;
                        }
                    }
```

```
                }
                else {
                    out_text.text = 'Keywords: ' + topics[Number(cluster)];
                    for (i = 0; i < x.length; i++) {
                        if(labels[i] == cluster) {
                            if(abstract[i].includes(key) ||
                            titles[i].includes(key) ||
                            authors[i].includes(key) ||
                            journal[i].includes(key)) {
                                x[i] = x_backup[i];
                                y[i] = y_backup[i];
                            } else {
                                x[i] = undefined;
                                y[i] = undefined;
                            }
                        } else {
                            x[i] = undefined;
                            y[i] = undefined;
                        }
                    }
                }
            source.change.emit();
            """)
    return callback
```

In [122]:
```
# required libraries for plot
#from call_backs import input_callback, selected_code  # file with customJS
                                                       # github.com/MaksimEk
import bokeh
from bokeh.models import ColumnDataSource, HoverTool, LinearColorMapper, Cu
from bokeh.palettes import Category20
from bokeh.transform import linear_cmap, transform
from bokeh.io import output_file, show, output_notebook
from bokeh.plotting import figure
from bokeh.models import RadioButtonGroup, TextInput, Div, Paragraph
from bokeh.layouts import column, widgetbox, row, layout
from bokeh.layouts import column
```

In [115]:
```
# go back
#os.chdir(main_path)
```

Load the Keywords per Cluster

In [117]:
```
import os

topic_path = 'topics.txt'
with open(topic_path) as f:
    topics = f.readlines()
```

Setup

In [118]:
```
# show on notebook
output_notebook()
# target labels
y_labels = y_pred

# data sources
source = ColumnDataSource(data=dict(
    x= X_embedded[:,0],
    y= X_embedded[:,1],
    x_backup = X_embedded[:,0],
    y_backup = X_embedded[:,1],
    desc= y_labels,
    titles= df['title'],
    authors = df['authors'],
    journal = df['journal'],
    abstract = df['abstract_summary'],
    labels = ["C-" + str(x) for x in y_labels],
    links = df['doi']
    ))

# hover over information
hover = HoverTool(tooltips=[
    ("Title", "@titles{safe}"),
    ("Author(s)", "@authors{safe}"),
    ("Journal", "@journal"),
    ("Abstract", "@abstract{safe}"),
    ("Link", "@links")
],
point_policy="follow_mouse")

# map colors
mapper = linear_cmap(field_name='desc',
                     palette=Category20[20],
                     low=min(y_labels) ,high=max(y_labels))

# prepare the figure
plot = figure(plot_width=1200, plot_height=850,
           tools=[hover, 'pan', 'wheel_zoom', 'box_zoom', 'reset', 'save',
           title="Clustering of the COVID-19 Literature with t-SNE and K-Me
           toolbar_location="above")

# plot settings
plot.scatter('x', 'y', size=5,
          source=source,
          fill_color=mapper,
          line_alpha=0.3,
          line_color="black",
          legend = 'labels')
plot.legend.background_fill_alpha = 0.6
```

(https://bokeh.org) Loading BokehJS ...

```
BokehDeprecationWarning: 'legend' keyword is deprecated, use explicit 'le
gend_label', 'legend_field', or 'legend_group' keywords instead
```

Widgets

In [123]:
```
# Keywords
text_banner = Paragraph(text= 'Keywords: Slide to specific cluster to see t
input_callback_1 = input_callback(plot, source, text_banner, topics)

# currently selected article
div_curr = Div(text="""Click on a plot to see the link to the article.""",h
callback_selected = CustomJS(args=dict(source=source, current_selection=div
taptool = plot.select(type=TapTool)
taptool.callback = callback_selected

# WIDGETS
slider = Slider(start=0, end=20, value=20, step=1, title="Cluster #", callb
keyword = TextInput(title="Search:", callback=input_callback_1)

# pass call back arguments
input_callback_1.args["text"] = keyword
input_callback_1.args["slider"] = slider
```

Style

In [124]:
```
# STYLE
slider.sizing_mode = "stretch_width"
slider.margin=15

keyword.sizing_mode = "scale_both"
keyword.margin=15

div_curr.style={'color': '#BF0A30', 'font-family': 'Helvetica Neue, Helveti
div_curr.sizing_mode = "scale_both"
div_curr.margin = 20

text_banner.style={'color': '#0269A4', 'font-family': 'Helvetica Neue, Helv
text_banner.sizing_mode = "scale_both"
text_banner.margin = 20

plot.sizing_mode = "scale_both"
plot.margin = 5

r = row(div_curr,text_banner)
r.sizing_mode = "stretch_width"
```

SHOW

In [125]:
```
# LAYOUT OF THE PAGE
l = layout([
    [slider, keyword],
    [text_banner],
    [div_curr],
    [plot],
])
l.sizing_mode = "scale_both"

# show
output_file('t-sne_covid-19_interactive.html')
show(l)
```