Assignment3_45921407_MohammedSadiqAbuwala_COMP8210

October 29, 2021

0.0.1 Importing / installing libraries

[1]:
```
#Use the following code to install any required libraries that are missing
#!pip install -U pip setuptools wheel
#!pip install -U spacy
#!python -m spacy download en_core_web_sm
#!pip install --upgrade gensim
#!pip install --user torch torchvision torchaudio
#!pip install --user transformer
#!pip install --user pyldavis
#!pip install --user wordcloud
#!pip install --user -U nltk
from pprint import pprint
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline
import torch
from transformers import BertTokenizer
import gensim.models.phrases as gen
from gensim.models.coherencemodel import CoherenceModel
from wordcloud import WordCloud
import seaborn as sns
import pyLDAvis
import pyLDAvis.sklearn
import re
from gensim import models,corpora
import nltk
nltk.download('stopwords')
import string
string.punctuation
stopwords = nltk.corpus.stopwords.words('english')
from sklearn.decomposition import PCA
from sklearn.cluster import MiniBatchKMeans
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.cluster import KMeans
from sklearn import metrics
from scipy.spatial.distance import cdist
```

```python
from sklearn.manifold import TSNE
from sklearn.decomposition import LatentDirichletAllocation
from nltk.tokenize import word_tokenize
from nltk.stem.snowball import SnowballStemmer
from sklearn.feature_extraction.text import TfidfVectorizer, CountVectorizer
from sklearn.feature_extraction.text import CountVectorizer, TfidfVectorizer
from tqdm._tqdm_notebook import tqdm_notebook,tnrange,tqdm
from collections import Counter,OrderedDict
from nltk.stem.wordnet import WordNetLemmatizer
lmtzr = WordNetLemmatizer()
import warnings
import pyLDAvis.gensim_models
import re, nltk, spacy, gensim
from sklearn.decomposition import LatentDirichletAllocation, TruncatedSVD
from sklearn.model_selection import GridSearchCV
import warnings
warnings.filterwarnings('ignore')
```

```
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:34: DeprecationWarning: `np.float`
is a deprecated alias for the builtin `float`. To silence this warning, use
`float` by itself. Doing this will not modify any behavior and is safe. If you
specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  method='lar', copy_X=True, eps=np.finfo(np.float).eps,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:164: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  method='lar', copy_X=True, eps=np.finfo(np.float).eps,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:281: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  eps=np.finfo(np.float).eps, copy_Gram=True, verbose=0,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:865: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
```

```
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  eps=np.finfo(np.float).eps, copy_X=True, fit_path=True,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:1121: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  eps=np.finfo(np.float).eps, copy_X=True, fit_path=True,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:1149: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  eps=np.finfo(np.float).eps, positive=False):
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:1379: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  max_n_alphas=1000, n_jobs=None, eps=np.finfo(np.float).eps,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:1621: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  max_n_alphas=1000, n_jobs=None, eps=np.finfo(np.float).eps,
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\linear_model\_least_angle.py:1755: DeprecationWarning:
`np.float` is a deprecated alias for the builtin `float`. To silence this
warning, use `float` by itself. Doing this will not modify any behavior and is
safe. If you specifically wanted the numpy scalar type, use `np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  eps=np.finfo(np.float).eps, copy_X=True, positive=False):
C:\Users\abuwa\anaconda3\lib\site-packages\sklearn\decomposition\_lda.py:28:
DeprecationWarning: `np.float` is a deprecated alias for the builtin `float`. To
silence this warning, use `float` by itself. Doing this will not modify any
behavior and is safe. If you specifically wanted the numpy scalar type, use
`np.float64` here.
Deprecated in NumPy 1.20; for more details and guidance:
```

```
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  EPS = np.finfo(np.float).eps
C:\Users\abuwa\anaconda3\lib\site-
packages\sklearn\feature_extraction\image.py:172: DeprecationWarning: `np.int`
is a deprecated alias for the builtin `int`. To silence this warning, use `int`
by itself. Doing this will not modify any behavior and is safe. When replacing
`np.int`, you may wish to use e.g. `np.int64` or `np.int32` to specify the
precision. If you wish to review your current use, check the release note link
for additional information.
Deprecated in NumPy 1.20; for more details and guidance:
https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  dtype=np.int):
[nltk_data] Downloading package stopwords to
[nltk_data]     C:\Users\abuwa\AppData\Roaming\nltk_data…
[nltk_data]   Package stopwords is already up-to-date!
<ipython-input-1-06ecb96179f3>:43: TqdmDeprecationWarning: This function will be
removed in tqdm==5.0.0
Please use `tqdm.notebook.*` instead of `tqdm._tqdm_notebook.*`
  from tqdm._tqdm_notebook import tqdm_notebook,tnrange,tqdm
```

0.1 Task 1 - What is the distribution of journals per source?

Due to large dataset, limited memory and performance availability, a portion of the dataset it used (220,000 rows). The 'nrows' value can be easily changed for a larger dataset if more memory and performance is available.

```
[2]: df = pd.read_csv("metadata.csv",nrows=220000)
```

Getting the journal count by source and visualizing the data via table.

```
[3]: new_df = df.value_counts(subset=['source_x', 'journal']).
      ↪reset_index(name="count")
     new_df.head(20)
```

```
[3]:    source_x                                     journal  count
     0   Medline                                         BMJ   2862
     1   Medline                          Journal of virology   2154
     2   BioRxiv                                      bioRxiv   2036
     3       PMC                             Reactions Weekly   1602
     4   Medline                                       Nature   1301
     5   Medline                                         JAMA   1041
     6       PMC                                     PLoS One   1004
     7   Medline                          Surgical endoscopy    974
     8   Medline                                      Science    789
     9   Medline          The New England journal of medicine    766
     10  Medline  Proceedings of the National Academy of Science…   665
     11  Medline              The Journal of general virology    607
     12      PMC                                      Sci Rep    572
     13  Medline         Journal of neurointerventional surgery    536
```

```
14   Medline           AJNR. American journal of neuroradiology    532
15   Medline                             The Veterinary record    527
16   Medline                                          BMJ open    512
17   Medline                                          PloS one    504
18   Medline      Advances in experimental medicine and biology    504
19       PMC  Computational Science and Its Applications - I…    500
```

Getting the top 10 most frequent journals that appear in the dataset.

```
[4]: df['journal'].value_counts()[:10]
```

```
[4]: BMJ                      3155
     Journal of virology      2154
     bioRxiv                  2043
     Reactions Weekly         1620
     Nature                   1608
     PLoS One                 1276
     JAMA                     1134
     Surgical endoscopy        974
     Science                   878
     Lancet                    875
     Name: journal, dtype: int64
```

Extracting the top 10 most frequent journals from the dataset

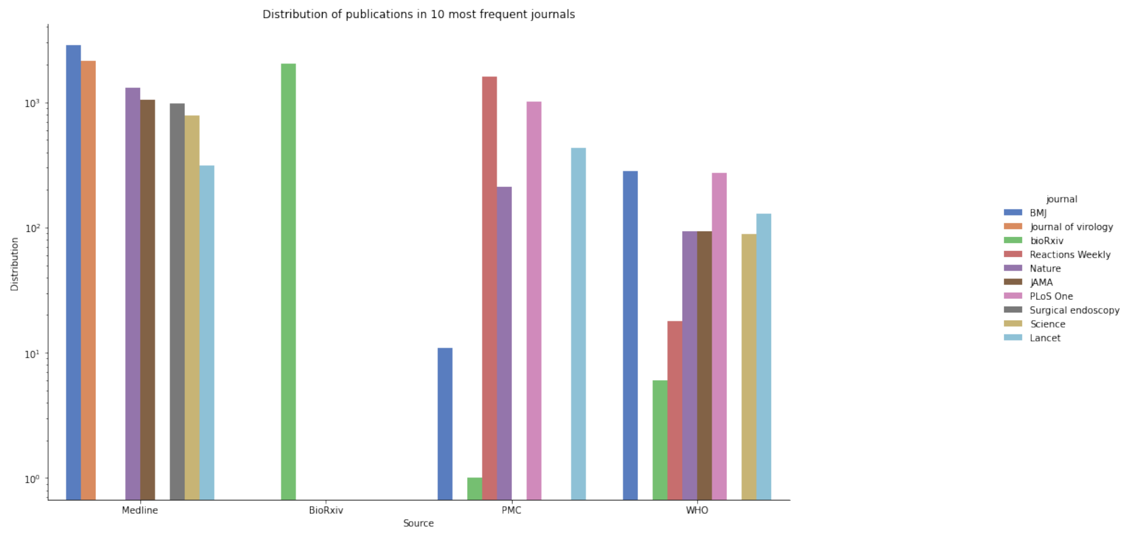
```
[5]: top_ten_journals = ['BMJ','Journal of virology','bioRxiv','Reactions␣
      ↪Weekly','Nature','PLoS One','JAMA','Surgical endoscopy','Science','Lancet' ]
```

Visualizing the dataset via a table after extracting top 10 most frequent journals

```
[6]: new_df = new_df[new_df.journal.isin(top_ten_journals)]
```

Distribution of journals by source via clustered column chart. Plotting is conducted using seaborn catplot.

```
[7]: # Visualization of a barplot
     g = sns.catplot(x="source_x", y=new_df['count'], hue="journal",
                         data=new_df, kind="bar",
                         height=5, palette="muted", legend=True, log=True)

     g.fig.set_figwidth(18)
     g.fig.set_figheight(8)
     plt.title('Distribution of publications in 10 most frequent journals')
     plt.xlabel('Source')
     plt.ylabel('Distribution')
     plt.show()
```



Outcome: Although 7 sources exist in total, the clustered column chart shows only 4 sources. This may be because the remaining sources do not have any journal distribution or they do not possess enough journals that could be appropriately visualized in the chart.

0.1.1 Task 2 - What are the main clusters?

```
[8]: df = pd.read_csv("metadata.csv",nrows=1500)
```

Due to limited memory and performance availability, a portion of the dataset will be used (1500 rows). The 'nrows' value can be easily changed for a larger dataset if more memory and performance is available. A larger dataset will always yield a more accurate representation of the entire dataset.

Dropping all empty rows in the abstract column and extract the column for further analysis.

```
[9]: df = df.dropna(subset=['abstract'])
     df['abstract'] = df['abstract'].astype(str)
     df = pd.DataFrame(df['abstract'])
     df
```

```
[9]:                                              abstract
     0     OBJECTIVE: This retrospective chart review des…
     1     Inflammatory diseases of the respiratory tract…
     2     Surfactant protein-D (SP-D) participates in th…
     3     Endothelin-1 (ET-1) is a 21 amino acid peptide…
     4     Respiratory syncytial virus (RSV) and pneumoni…
     …                                                 …
     1494  Glycyrrhizic acid (GA) is a triterpene glycosi…
```

```
1495   Background: Upper respiratory tract infections…
1496   BACKGROUND: Various pathways have been implica…
1497   INTRODUCTION: There is a hyperoxidative state …
1498   INTRODUCTION: The aim of this study was to inv…

[1435 rows x 1 columns]
```

Verifying that no null values exist in the abstract column.

```
[10]: df.isnull().sum()
```

```
[10]: abstract    0
      dtype: int64
```

Text preprocessing is conducted. We'll also add our own custom stopwords which include some common words used in research papers.

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

      stopwords.extend(custom_stop_words)

      # A function to prepare the text
      def clean(text):
          regex = re.compile('[' + re.escape(string.punctuation) + '0-9\\r\\t\\n]')
          text = regex.sub(" ", text.lower())
          words = text.split(" ")
          words = [re.sub('\S*@\S*\s?', '', sent) for sent in words]
          words = [re.sub('\s+', ' ', sent) for sent in words]
          words = [re.sub("\'", "", sent) for sent in words]
          words = [w for w in words if not len(w) < 2]
          words = [w for w in words if w not in stopwords]
          words = [lmtzr.lemmatize(w) for w in words]
          words = ' '.join([str(w) for w in words])
          return words
```

Applying above function to the abstract column.

```
[12]: df["clean_abstract"] = df["abstract"].apply(clean)
```

Tokenizing the text in abstract column with BertTokenizer

```
[13]: def sen_to_vec(sentence):
          tokenizer=BertTokenizer.from_pretrained('bert-base-uncased')
          tokens=tokenizer.tokenize(sentence)
          tokens = ['[CLS]'] + tokens + ['[SEP]']
```

```
    T=624
    padded_tokens=tokens +['[PAD]' for _ in range(T-len(tokens))]
    attn_mask=[ 1 if token != '[PAD]' else 0 for token in padded_tokens  ]
    seg_ids=[0 for _ in range(len(padded_tokens))]
    sent_ids=tokenizer.convert_tokens_to_ids(padded_tokens)
    return np.array(sent_ids)
```

After tokenizaton is completed, it is stored in a new data frame 'final_df' for further analysis.

[14]:
```
df["array"] = df["clean_abstract"].apply(sen_to_vec)
final_df = pd.DataFrame(df["array"])
final_df = final_df.pop('array').apply(pd.Series)
final_df = final_df.fillna(0)
final_df.head(3)
```

[14]:
```
     0      1      2      3      4      5      6      7     8      9  …  \
0  101   7863  15354   3673   3319   5577   4958   5178  4328   6779  …
1  101  20187   4295  16464  12859   4141   3378   8319  2537   9152  …
2  101  14175  18908   4630   5250  11867  17257  25605  3433  15938  …

   614  615  616  617  618  619  620  621  622  623
0    0    0    0    0    0    0    0    0    0    0
1    0    0    0    0    0    0    0    0    0    0
2    0    0    0    0    0    0    0    0    0    0

[3 rows x 624 columns]
```

Using PCA to reduce the dimensionality of tokenized array data to 2 so that it can be visualized efficiently.

[15]:
```
from sklearn.decomposition import PCA

pca = PCA(n_components = 2)
X_PCA=pca.fit_transform(final_df)

print(final_df.shape)
print(X_PCA.shape)
```

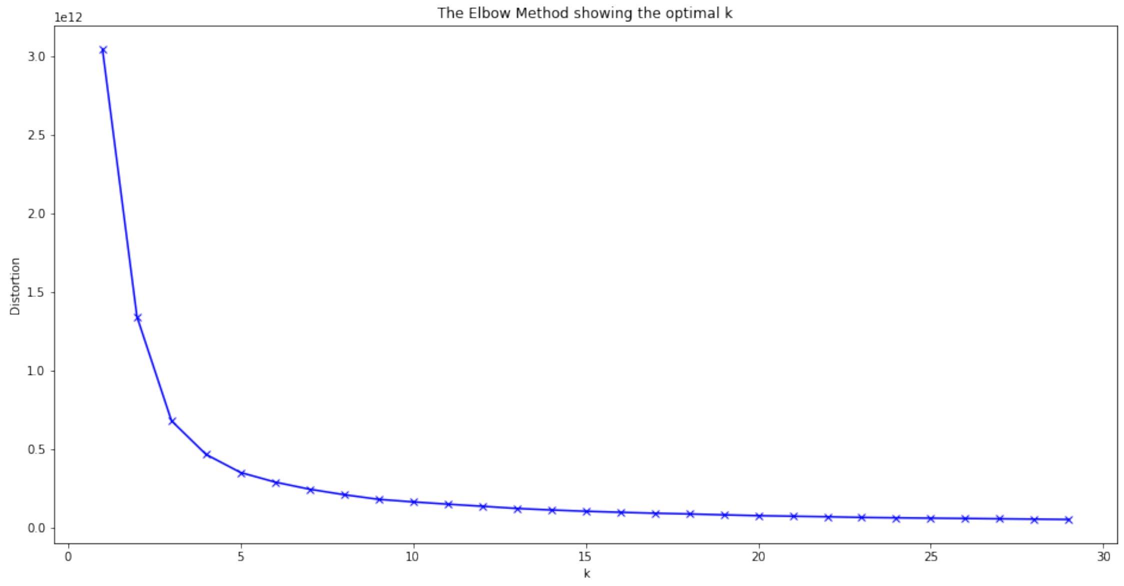
```
(1435, 624)
(1435, 2)
```

Finding the best K value for our Kmeans model.

[16]:
```
distortions = []
K = range(1,30)
for k in K:
    kmeanModel = KMeans(n_clusters=k)
    kmeanModel.fit(X_PCA)
    distortions.append(kmeanModel.inertia_)
```

Finding the best K value by using Elbow method visualization.

```
[17]: plt.figure(figsize=(16,8))
      plt.plot(K, distortions, 'bx-')
      plt.xlabel('k')
      plt.ylabel('Distortion')
      plt.title('The Elbow Method showing the optimal k')
      plt.show()
```



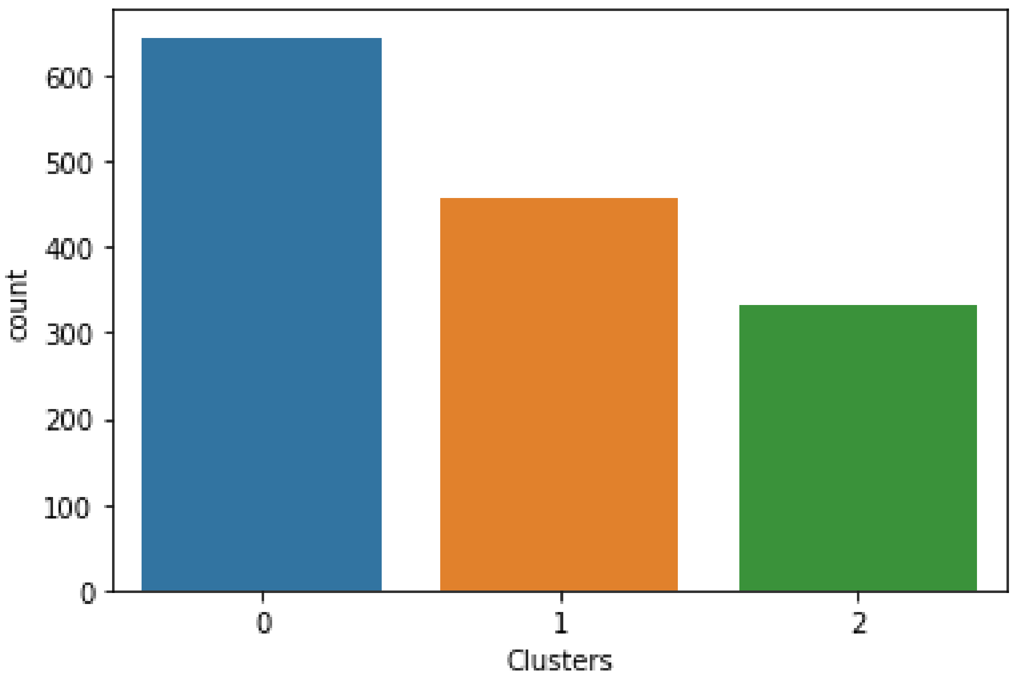
By analyzing above graph, we can deduce k = 3.

```
[18]: k = 3
      kmeans = KMeans(n_clusters=k, random_state=42)
      y_pred = kmeans.fit_predict(X_PCA)
      df['Clusters'] = y_pred
```

Vizualisation of clusters.

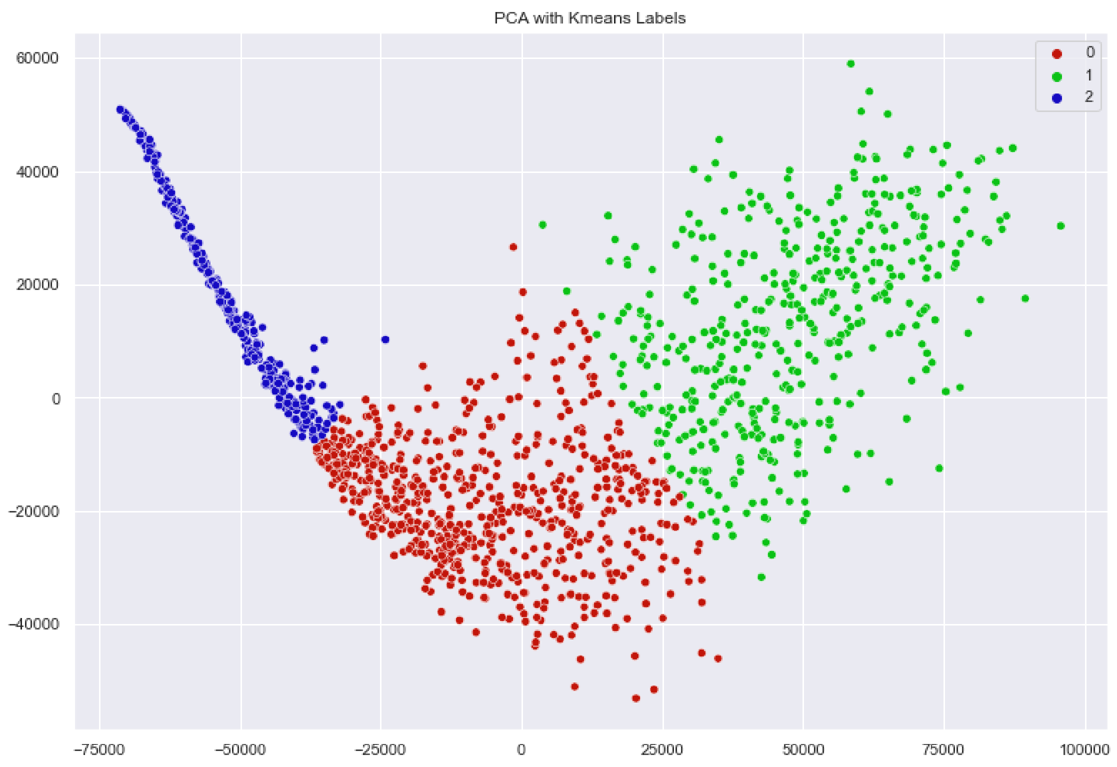
```
[19]: sns.countplot(df['Clusters'])
```

```
[19]: <AxesSubplot:xlabel='Clusters', ylabel='count'>
```



2D representation of each document in its corresponding clusters. The clustered are represented by its following colours.

[20]:
```
# sns settings
sns.set(rc={'figure.figsize':(13,9)})

# colors
palette = sns.hls_palette(3, l=.4, s=.9)

# plot
sns.scatterplot(X_PCA[:,0], X_PCA[:,1], hue=y_pred, legend='full',␣
 ↪palette=palette)
plt.title('PCA with Kmeans Labels')
plt.savefig("clusterRevised.png")
plt.show()
```



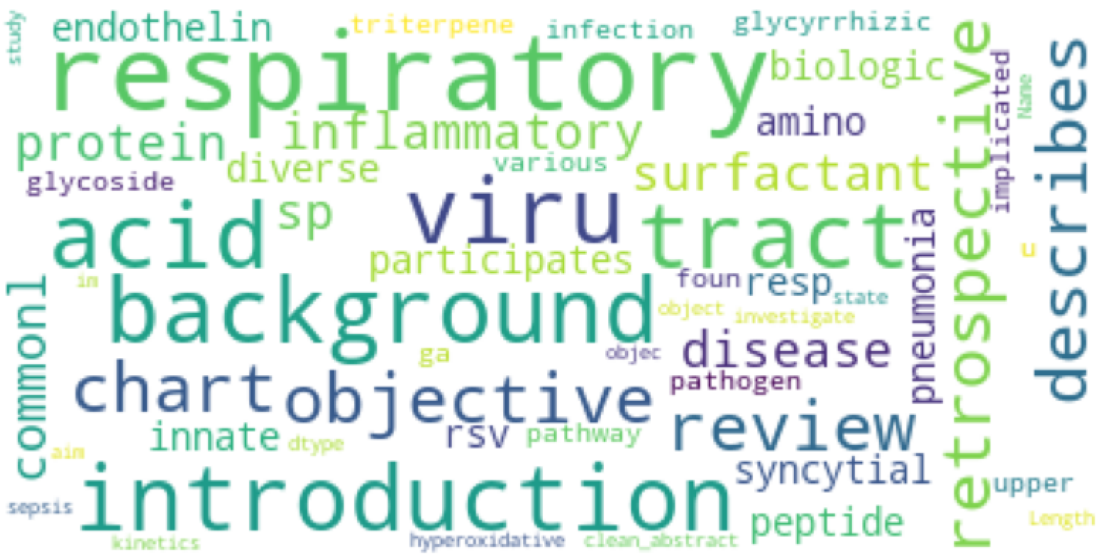
0.1.2 Task 3 - For each cluster, what are the most representative words?

We will use cleaned abstract data obtained earlier to produce the wordcloud.

[21]:
```
wordcloud =␣
↪WordCloud(background_color='white',stopwords=stopwords,max_words=200,max_font_size=40,rando
↪generate(str(df['clean_abstract']))
```

[22]:
```
print(wordcloud)
fig = plt.figure(1)
plt.imshow(wordcloud)
plt.axis('off')
plt.show()
fig.savefig("word1.png", dpi=900)
```

```
<wordcloud.wordcloud.WordCloud object at 0x000001905114BAF0>
```



Note: Upon analyzing the above Wordcloud, we can see that even more meaningful results can be obtained if more custom stopwords are added to our list such as "introduction", "background", "objective". This can easily be done by adding these words to our already created list above "custom_stop_words". However, as the program takes many hours to run for even small datasets, it was decided to not perform this operation again.

0.1.3 Task 4 - What are the most common topics?

Preprocessing of data using gensim.

[23]:
```
data = df.clean_abstract.values.tolist()
def sent_to_words(sentences):
    for sentence in sentences:
        yield(gensim.utils.simple_preprocess(str(sentence), deacc=True))  #␣
 ↪deacc=True removes punctuations
data_words = list(sent_to_words(data))
print(data_words[:1])
```

```
[['objective', 'retrospective', 'chart', 'review', 'describes', 'epidemiology',
'clinical', 'feature', 'patient', 'culture', 'proven', 'mycoplasma',
'pneumoniae', 'infection', 'king', 'abdulaziz', 'university', 'hospital',
'jeddah', 'saudi', 'arabia', 'method', 'patient', 'positive', 'pneumoniae',
'culture', 'respiratory', 'specimen', 'january', 'december', 'identified',
'microbiology', 'record', 'chart', 'patient', 'result', 'patient', 'identified',
'required', 'admission', 'infection', 'community', 'acquired', 'infection',
'affected', 'age', 'group', 'common', 'infant', 'pre', 'school', 'child',
'occurred', 'year', 'round', 'common', 'fall', 'spring', 'three', 'quarter',
'patient', 'comorbidities', 'twenty', 'four', 'isolates', 'associated',
'pneumonia', 'upper', 'respiratory', 'tract', 'infection', 'bronchiolitis',
'cough', 'fever', 'malaise', 'common', 'symptom', 'crepitation', 'wheeze',
'common', 'sign', 'patient', 'pneumonia', 'crepitation', 'bronchial',
'breathing', 'patient', 'likely', 'non', 'patient', 'present', 'pneumonia',
'versus', 'patient', 'pneumonia', 'uneventful', 'recovery', 'recovered',
'following', 'complication', 'died', 'pneumoniae', 'infection', 'died', 'due',
'underlying', 'comorbidities', 'patient', 'died', 'pneumoniae', 'pneumonia',
'comorbidities', 'conclusion', 'result', 'similar', 'published', 'data',
'except', 'finding', 'infection', 'common', 'infant', 'preschool', 'child',
'mortality', 'rate', 'pneumonia', 'patient', 'comorbidities', 'high']]
```

Lemmatization

[24]:
```
def lemmatization(texts, allowed_postags=['NOUN', 'ADJ', 'VERB', 'ADV']):␣
↪#'NOUN', 'ADJ', 'VERB', 'ADV'
    texts_out = []
    for sent in texts:
        doc = nlp(" ".join(sent))
        texts_out.append(" ".join([token.lemma_ if token.lemma_ not in␣
↪['-PRON-'] else '' for token in doc if token.pos_ in allowed_postags]))
    return texts_out
```

[25]:
```
# Initialize spacy ‘en’ model, keeping only tagger component (for efficiency)
# Run in terminal: python -m spacy download en
nlp = spacy.load("en_core_web_sm", disable=['parser', 'ner'])
# Do lemmatization keeping only Noun, Adj, Verb, Adverb
data_lemmatized = lemmatization(data_words, allowed_postags=['NOUN', 'ADJ',␣
↪'VERB', 'ADV']) #select noun and verb
print(data_lemmatized[:2])
```

```
['objective retrospective chart review describe epidemiology clinical feature
patient culture prove mycoplasma infection king method patient positive
pneumoniae culture respiratory speciman identify microbiology record chart
patient result patient identify require admission infection community acquire
infection affect age group common infant pre school child occur year round
common fall spring quarter patient comorbiditie isolate associate upper
respiratory tract cough fever malaise common symptom crepitation wheeze common
sign patient pneumonia bronchial breathing patient likely non patient present
pneumonia patient pneumonia uneventful recovery recover follow complication die
pneumoniae infection die due underlie comorbiditie patient die pneumonia
comorbiditie conclusion result similar publish datum find infection common
infant preschool child mortality rate pneumonia patient comorbiditie high',
'inflammatory disease respiratory tract commonly associate elevated production
nitric oxide increase index dependent oxidative stress know anti microbial anti
inflammatory anti oxidant property various line evidence support contribution
lung injury several disease model basis biochemical evidence often presume
dependent oxidation due formation oxidant peroxynitrite alternative mechanism
involve phagocyte derive heme protein myeloperoxidase peroxidase operative
condition inflammation overwhelm literature generation activity respiratory
tract scope commentary review area comprehensively instead focus recent evidence
concept presume contribution inflammatory disease lung']
```

Data is vectorized using CountVectorizer

```
[26]: vectorizer = CountVectorizer(analyzer='word',
                                   min_df=10,
      # minimum reqd occurences of a word
                                   stop_words='english',
      # remove stop words
                                   lowercase=True,
      # convert all words to lowercase
                                   token_pattern='[a-zA-Z0-9]{3,}')

      data_vectorized = vectorizer.fit_transform(data_lemmatized)
```

Buildng an LDA Model.

Since we had 3 clusters we will stick to 3 topics, to be able to make a comparison.

```
[27]: # Build LDA Model
      lda_model = LatentDirichletAllocation(n_components=3,              # Number of␣
       ↪topics
                                            max_iter=10,
      # Max learning iterations
                                            learning_method='online',
                                            random_state=100,
      # Random state
                                            batch_size=128,
      # n docs in each learning iter
                                            evaluate_every = -1,
      # compute perplexity every n iters, default: Don't
                                            n_jobs = -1,
      # Use all available CPUs
                                           )
      lda_output = lda_model.fit_transform(data_vectorized)
      print(lda_model)  # Model attributes
```

```
LatentDirichletAllocation(learning_method='online', n_components=3, n_jobs=-1,
                          random_state=100)
```

For each topic, get the top n keywords.

```
[29]: # Show top n keywords for each topic
      def show_topics(vectorizer=vectorizer, lda_model=lda_model, n_words=20):
          keywords = np.array(vectorizer.get_feature_names())
          topic_keywords = []
          for topic_weights in lda_model.components_:
              top_keyword_locs = (-topic_weights).argsort()[:n_words]
              topic_keywords.append(keywords.take(top_keyword_locs))
          return topic_keywords
```

```
topic_keywords = show_topics(vectorizer=vectorizer, lda_model=lda_model,␣
 ↪n_words=15)

# Topic - Keywords Dataframe
df_topic_keywords = pd.DataFrame(topic_keywords)
df_topic_keywords.columns = ['Word '+str(i) for i in range(df_topic_keywords.
 ↪shape[1])]
df_topic_keywords.index = ['Topic '+str(i) for i in range(df_topic_keywords.
 ↪shape[0])]
df_topic_keywords
```

[29]:
```
           Word 0     Word 1     Word 2     Word 3       Word 4    Word 5  \
Topic 0       use    disease  influenza     health        virus  sequence
Topic 1   patient  infection      study  influenza  respiratory  clinical
Topic 2      cell    protein      virus       gene    infection     viral

             Word 6 Word 7    Word 8  Word 9    Word 10   Word 11    Word 12  \
Topic 0      method  study    result   model      datum  pandemic   analysis
Topic 1        high    day    severe  result  treatment   disease  mortality
Topic 2  expression    use  activity   human      study    induce   response

              Word 13     Word 14
Topic 0  transmission  population
Topic 1         virus        case
Topic 2        result        host
```

Adding appropriate labels for the 3 topics.

[30]:
```
Topics = ["Research","Disease and Treatment","Virus Behaviour"]

df_topic_keywords["Topics"]=Topics
df_topic_keywords
```

[30]:
```
           Word 0     Word 1     Word 2     Word 3       Word 4    Word 5  \
Topic 0       use    disease  influenza     health        virus  sequence
Topic 1   patient  infection      study  influenza  respiratory  clinical
Topic 2      cell    protein      virus       gene    infection     viral

             Word 6 Word 7    Word 8  Word 9    Word 10   Word 11    Word 12  \
Topic 0      method  study    result   model      datum  pandemic   analysis
Topic 1        high    day    severe  result  treatment   disease  mortality
Topic 2  expression    use  activity   human      study    induce   response

              Word 13     Word 14                 Topics
Topic 0  transmission  population               Research
Topic 1         virus        case  Disease and Treatment
Topic 2        result        host        Virus Behaviour
```

Defining a function to predict topic for a given text document. Furthermore, as an example, topic is inferred for a given text. This can be seen in the result below.

```
[36]: nlp = spacy.load('en_core_web_sm', disable=['parser', 'ner'])
def predict_topic(text, nlp=nlp):
    global sent_to_words
    global lemmatization
# Step 1: Clean with simple_preprocess
    mytext_2 = list(sent_to_words(text))
# Step 2: Lemmatize
    mytext_3 = lemmatization(mytext_2, allowed_postags=['NOUN', 'ADJ', 'VERB',␣
 ↪'ADV'])
# Step 3: Vectorize transform
    mytext_4 = vectorizer.transform(mytext_3)
# Step 4: LDA Transform
    topic_probability_scores = lda_model.transform(mytext_4)
    topic = df_topic_keywords.iloc[np.argmax(topic_probability_scores), 1:14].
 ↪values.tolist()

    # Step 5: Infer Topic
    infer_topic = df_topic_keywords.iloc[np.argmax(topic_probability_scores),␣
 ↪-1]

    #topic_guess = df_topic_keywords.iloc[np.argmax(topic_probability_scores),␣
 ↪Topics]
    return infer_topic, topic, topic_probability_scores
# Predict the topic
mytext = ["initial coronavirus study promising we will now finish final␣
 ↪analysis"]
infer_topic, topic, prob_scores = predict_topic(text = mytext)

print(infer_topic)
```

```
Research
```

0.1.4 Task 5 - What are the most common topics in each cluster?

Information from the topics in task 4 is used to characterise the topics in each cluster and adding it to the dataframe.

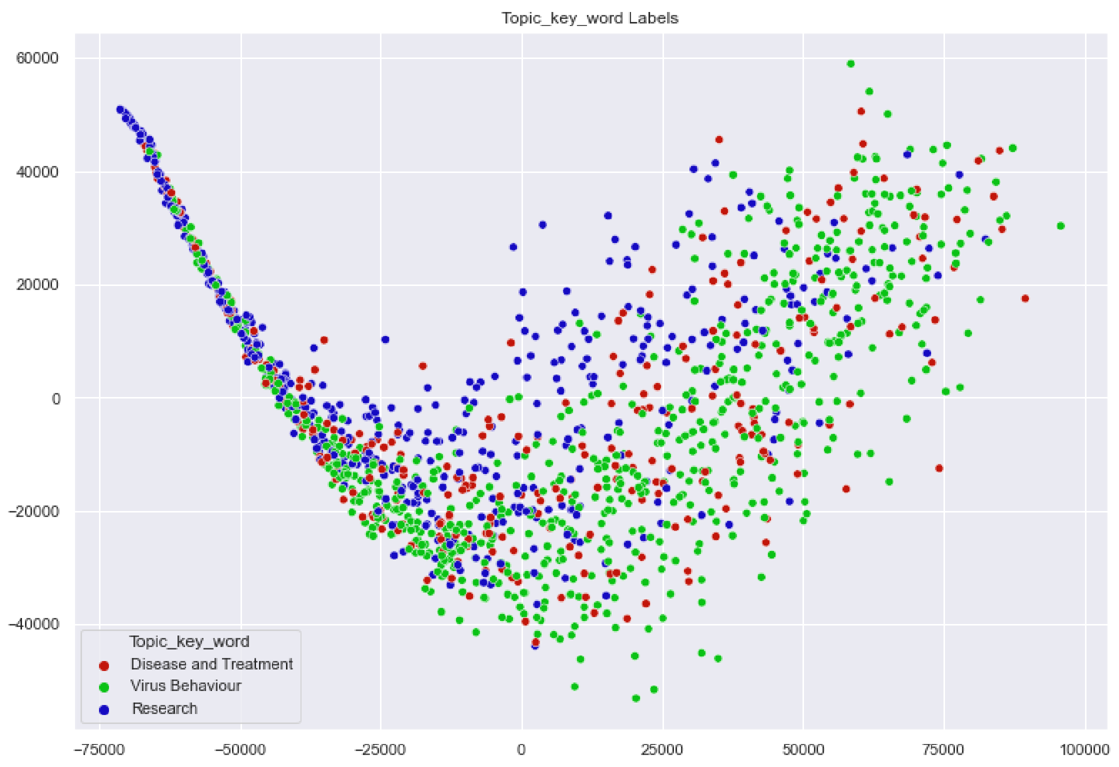
```
[37]: def apply_predict_topic(text):
 text = [text]
 infer_topic, topic, prob_scores = predict_topic(text = text)
 return(infer_topic)
df["Topic_key_word"]= df['abstract'].apply(apply_predict_topic)
df.head()
```

```
[37]:                                            abstract  \
0  OBJECTIVE: This retrospective chart review des…
```

```
1  Inflammatory diseases of the respiratory tract…
2  Surfactant protein-D (SP-D) participates in th…
3  Endothelin-1 (ET-1) is a 21 amino acid peptide…
4  Respiratory syncytial virus (RSV) and pneumoni…

                                      clean_abstract  \
0  objective retrospective chart review describes…
1  inflammatory disease respiratory tract commonl…
2  surfactant protein sp participates innate resp…
3  endothelin amino acid peptide diverse biologic…
4  respiratory syncytial virus rsv pneumonia viru…

                                               array  Clusters  \
0  [101, 7863, 15354, 3673, 3319, 5577, 4958, 517…         0
1  [101, 20187, 4295, 16464, 12859, 4141, 3378, 8…         2
2  [101, 14175, 18908, 4630, 5250, 11867, 17257, …         1
3  [101, 2203, 14573, 18809, 13096, 5648, 25117, …         2
4  [101, 16464, 26351, 22123, 4818, 7865, 12667, …         2

          Topic_key_word
0  Disease and Treatment
1        Virus Behaviour
2        Virus Behaviour
3        Virus Behaviour
4        Virus Behaviour
```

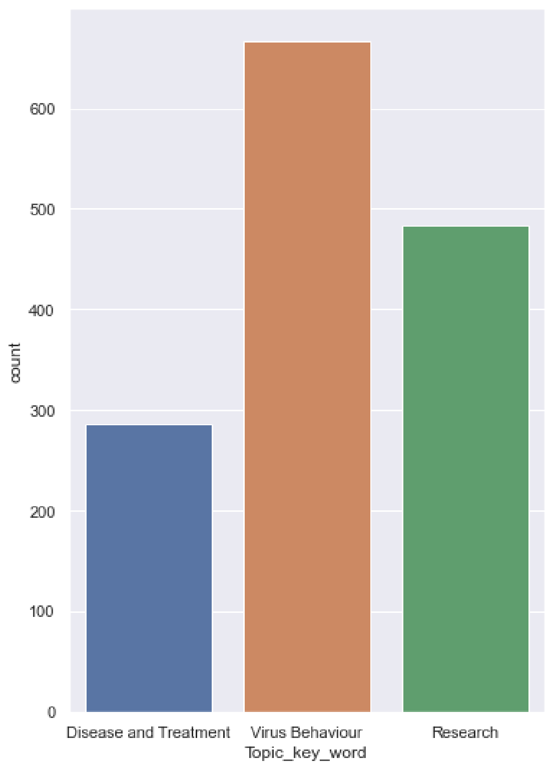
Visualization of top 3 common topics.

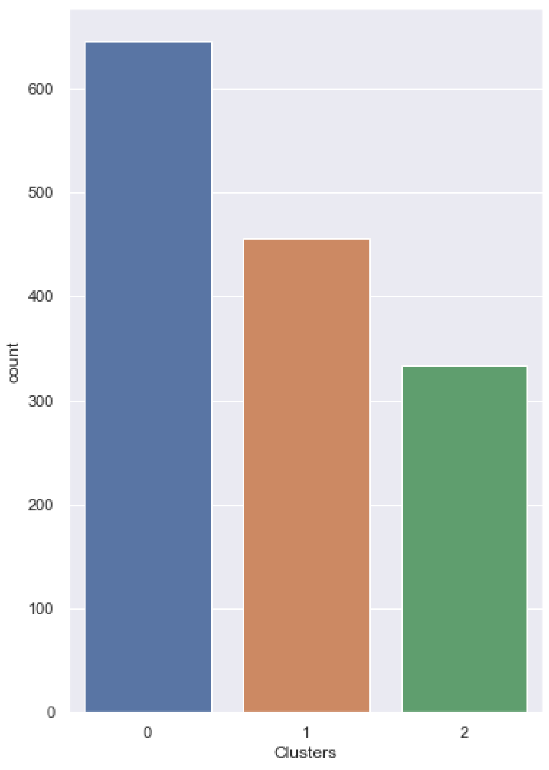
[38]:
```
# sns settings
sns.set(rc={'figure.figsize':(14,10)})

# colors
palette = sns.hls_palette(3, l=.4, s=.9)

# plot
sns.scatterplot(X_PCA[:,0], X_PCA[:,1], hue=df['Topic_key_word'],␣
 ↪legend='full', palette=palette)
plt.title('Topic_key_word Labels')
plt.savefig("clusterRevised.png")
plt.show()
```



Comparison of Kmeans clusters and Topics from Lda

[39]:
```
fig, ax =plt.subplots(1,2)
sns.countplot(df['Topic_key_word'], ax=ax[0])
sns.countplot(df['Clusters'], ax=ax[1])
fig.show()
```


count
0
100
200
300
400
500
600
Disease and Treatment
Virus Behaviour
Research
Topic_key_word


count
0
100
200
300
400
500
600
0
1
2
Clusters