In [2]:

```
# Importing modules
import gensim
from gensim.utils import simple_preprocess
from gensim.parsing.preprocessing import STOPWORDS
from nltk.stem import WordNetLemmatizer, SnowballStemmer
from nltk.stem.porter import *
import numpy as np
np.random.seed(2018)
import nltk
import pandas as pd
import os
import openai

os.chdir('../../..')

# Read data into papers. Please change directory to re-run
papers = pd.read_csv('C:/Users/PC/Downloads/lab_sessions/lab6/data_expanded.csv')

# Print head
papers.head()
```

Out[2]:

	NCT Number	Study Title	Brief Summary	Study Results	Conditions	Primary Outcome Measures	Se (M
0	NCT00080951	Irinotecan, Fluorouracil, Leucovorin, and Oxal...	RATIONALE: Drugs used in chemotherapy, such as...	NO	Colorectal Cancer	tumor response rate, Up to 5 years	progre yea
1	NCT02495051	Esophageal Atresia: Metaplasia, Barrett	The frequency of Barrett's esophagus (BE) has ...	NO	Gastroesophageal Reflux|Esophagus, Barrett	presence of gastric and / or intestinal metapl...	pr esop anoma
2	NCT00023751	Surgery With or Without Chemotherapy and Radia...	RATIONALE: Drugs used in chemotherapy use diff...	NO	Colorectal Cancer	disease-free survival, Up to 5 years	overal years|c
3	NCT00017212	DX-8951f in Treating Patients With Metastatic ...	RATIONALE: Drugs used in chemotherapy use diff...	NO	Esophageal Cancer|Gastric Cancer	NaN	
4	NCT01288612	Comparative Effectiveness of Endoscopic Assess...	The hypothesis of this study was that the comp...	YES	Barrett's Esophagus	Percentage of Subjects Who Agreed to Participa...	S Intuba rat

In [3]:

```
# Remove the columns
papers = papers.drop(columns=['Study Results','Other Outcome Measures'], axis=1)

# Print out the first rows of papers
papers.head()
```

Out[3]:

	NCT Number	Study Title	Brief Summary	Conditions	Primary Outcome Measures	Secondary Outcome Measures
0	NCT00080951	Irinotecan, Fluorouracil, Leucovorin, and Oxal...	RATIONALE: Drugs used in chemotherapy, such as...	Colorectal Cancer	tumor response rate, Up to 5 years	time to progression, Up to 5 years|overall sur...
1	NCT02495051	Esophageal Atresia: Metaplasia, Barrett	The frequency of Barrett's esophagus (BE) has ...	Gastroesophageal Reflux|Esophagus, Barrett	presence of gastric and / or intestinal metapl...	presence of esophagitis or anomalies at the an...
2	NCT00023751	Surgery With or Without Chemotherapy and Radia...	RATIONALE: Drugs used in chemotherapy use diff...	Colorectal Cancer	disease-free survival, Up to 5 years	overall survival, Up to 5 years|colostomy-free...
3	NCT00017212	DX-8951f in Treating Patients With Metastatic ...	RATIONALE: Drugs used in chemotherapy use diff...	Esophageal Cancer|Gastric Cancer	NaN	NaN
4	NCT01288612	Comparative Effectiveness of Endoscopic Assess...	The hypothesis of this study was that the comp...	Barrett's Esophagus	Percentage of Subjects Who Agreed to Participa...	Rate of Successful Intubation, The rate of suc...

In [4]:

```
papers2 = pd.DataFrame()
```

In [5]:

```
# Load the regular expression library this process is for data cleaning
import re

# Fill NA values and ensure all values are treated as strings
papers2['1st_Outcomes'] = papers['Primary Outcome Measures'].fillna('').astype(str)
papers2['2nd_Outcomes'] = papers['Secondary Outcome Measures'].fillna('').astype(str)
papers2['Condition'] = papers['Conditions'].fillna('').astype(str)
papers2['Summary'] = papers['Brief Summary'].fillna('').astype(str)
papers2['Titles'] = papers['Study Title'].fillna('').astype(str)

# Remove punctuation
papers2['1st_Outcomes'] = papers2['1st_Outcomes'].map(lambda x: re.sub('[,\.!?]', '', x)
papers2['2nd_Outcomes'] = papers2['2nd_Outcomes'].map(lambda x: re.sub('[,\.!?]', '', x)
papers2['Condition'] = papers2['Condition'].map(lambda x: re.sub('[,\.!?]', '', x))
papers2['Summary'] = papers2['Summary'].map(lambda x: re.sub('[,\.!?]', '', x))
papers2['Titles'] = papers2['Titles'].map(lambda x: re.sub('[,\.!?]', '', x))

# Convert the titles to lowercase
papers2['1st_Outcomes'] = papers2['1st_Outcomes'].map(lambda x: x.lower())
papers2['2nd_Outcomes'] = papers2['2nd_Outcomes'].map(lambda x: x.lower())
papers2['Condition'] = papers2['Condition'].map(lambda x: x.lower())
papers2['Summary'] = papers2['Summary'].map(lambda x: x.lower())
papers2['Titles'] = papers2['Titles'].map(lambda x: x.lower())
```

In [6]:

```
papers2.head()
```

Out[6]:

	1st_Outcomes	2nd_Outcomes	Condition	Summary	Titles
0	tumor response rate up to 5 years	time to progression up to 5 years|overall surv...	colorectal cancer	rationale: drugs used in chemotherapy such as ...	irinotecan fluorouracil leucovorin and oxalipl...
1	presence of gastric and / or intestinal metapl...	presence of esophagitis or anomalies at the an...	gastroesophageal reflux|esophagus barrett	the frequency of barrett's esophagus (be) has ...	esophageal atresia: metaplasia barrett
2	disease-free survival up to 5 years	overall survival up to 5 years|colostomy-free ...	colorectal cancer	rationale: drugs used in chemotherapy use diff...	surgery with or without chemotherapy and radia...
3			esophageal cancer|gastric cancer	rationale: drugs used in chemotherapy use diff...	dx-8951f in treating patients with metastatic ...
4	percentage of subjects who agreed to participa...	rate of successful intubation the rate of succ...	barrett's esophagus	the hypothesis of this study was that the comp...	comparative effectiveness of endoscopic assess...

In [7]:

```
len(papers2['Summary'])
```

Out[7]:

```
4763
```

In [8]:

```
# Initialize the WordNet Lemmatizer
lemmatizer = WordNetLemmatizer()

# Function to lemmatize a given text
def lemmatize_stemming(text):
    return lemmatizer.lemmatize(text)

# Function to preprocess a given text
def preprocess(text):
    result = []
    for token in gensim.utils.simple_preprocess(text):
        if token not in gensim.parsing.preprocessing.STOPWORDS and len(token) > 3:
            result.append(lemmatize_stemming(token))
    return result
```

In [9]:

```
doc_sample = papers2.loc[5, 'Summary']

print('original Summary: ')
words = []
for word in doc_sample.split(' '):
    words.append(word)
print(words)

print('\n\n tokenized and lemmatized Summary: ')
print(preprocess(doc_sample))
```

```
original Summary:
['the', 'purpose', 'of', 'this', 'study', 'is', 'to', 'evaluate', 'the',
'defecatory', 'function', 'when', 'nerve', 'fibers', 'around', 'the', 'inf
erior', 'mesenteric', 'artery(ima)', 'and', 'left', 'colic', 'artery(lc
a)', 'are', 'preserved(so', 'called', 'low', 'ligation', ')', 'or', 'not(h
igh', 'ligation)', 'in', 'the', 'rectosigmoid', 'and', 'rectal', 'cancer',
'surgery']


 tokenized and lemmatized Summary:
['purpose', 'study', 'evaluate', 'defecatory', 'function', 'nerve', 'fibe
r', 'inferior', 'mesenteric', 'artery', 'left', 'colic', 'artery', 'preser
ved', 'called', 'ligation', 'high', 'ligation', 'rectosigmoid', 'rectal',
'cancer', 'surgery']
```

In [10]:

```
#processes and cleans all data columns
processed_summary=papers2['Summary'].map(preprocess)
processed_1_outcome=papers2['1st_Outcomes'].map(preprocess)
processed_2_outcome=papers2['2nd_Outcomes'].map(preprocess)
processed_titles=papers2['Titles'].map(preprocess)
```

In [11]:

```
processed_summary
```

Out[11]:

```
0       [rationale, drug, chemotherapy, irinotecan, fl...
1       [frequency, barrett, esophagus, increased, adu...
2       [rationale, drug, chemotherapy, different, way...
3       [rationale, drug, chemotherapy, different, way...
4       [hypothesis, study, comparative, effectiveness...
                              ...
4758    [clinical, trial, hypothesize, microbiota, bac...
4759    [nonpolypoid, colorectal, neoplasm, crns, rela...
4760    [chemotherapy, given, standard, treat, cancer,...
4761    [single, study, ass, resection, rate, liver, m...
4762    [multicenter, phase, randomized, active, contr...
Name: Summary, Length: 4763, dtype: object
```

In [12]:

```
print('----Start of Dictionary for LDA ----')
# Create a dictionary from the processed_summary
dictionary_summary = gensim.corpora.Dictionary(processed_summary)

# Initialize a count variable
count = 0
# Filter the dictionary by removing extremes
dictionary_summary.filter_extremes(no_below=15, no_above=0.5, keep_n=100000)

# Iterate over the items in the dictionary
for k, v in dictionary_summary.iteritems():
    print(k, v)
    count += 1
    if count > 10:
        break
```

```
---- this is summaries----
0 cell
1 chemotherapy
2 colorectal
3 combination
4 combining
5 different
6 dividing
7 drug
8 effectiveness
9 fluorouracil
10 growing
```

In [13]:

```
# Create a Bag-of-Words (BoW) representation of the summary corpus
bow_corpus_summary = [dictionary_summary.doc2bow(doc) for doc in processed_summary]
```

In [14]:

```
# Select the Bag-of-Words representation for a specific document (index 5)
bow_doc = bow_corpus_summary[5]
# Iterate over each item in the Bag-of-Words representation
for i in range(len(bow_doc)):
    print("Word {} (\"{}\") appears {} time.".format(bow_doc[i][0],
                                                 dictionary_summary[bow_doc[i][0]],
bow_doc[i][1]))
```

```
Word 18 ("purpose") appears 1 time.
Word 72 ("high") appears 1 time.
Word 76 ("rectal") appears 1 time.
Word 79 ("surgery") appears 1 time.
Word 87 ("artery") appears 2 time.
Word 88 ("called") appears 1 time.
Word 89 ("evaluate") appears 1 time.
Word 90 ("function") appears 1 time.
Word 91 ("inferior") appears 1 time.
Word 92 ("left") appears 1 time.
Word 93 ("nerve") appears 1 time.
```

In [15]:

```
from gensim import corpora, models
# Create a TF-IDF model from the Bag-of-Words summary corpus
tfidf_summary = models.TfidfModel(bow_corpus_summary)

# Apply TF-IDF transformation to the entire summary corpus
corpus_tfidf_summary = tfidf_summary[bow_corpus_summary]

# Iterate over the transformed corpus and print the first document
from pprint import pprint
for doc in corpus_tfidf_summary:
    pprint(doc)
    break
```

```
[(0, 0.24574561295855715),
 (1, 0.21005222631406456),
 (2, 0.08230301124716685),
 (3, 0.1399743890823888),
 (4, 0.24529621077294597),
 (5, 0.15061463590661664),
 (6, 0.18791658243231862),
 (7, 0.2868533765348094),
 (8, 0.17126347178031678),
 (9, 0.21042996357535607),
 (10, 0.21447957819590424),
 (11, 0.20683884403617328),
 (12, 0.19656106276617302),
 (13, 0.24322877703853832),
 (14, 0.19211372927681555),
 (15, 0.12748362371199942),
 (16, 0.19526312422344508),
 (17, 0.10664363605677096),
 (18, 0.08943013297696623),
 (19, 0.15870067707792096),
 (20, 0.339754247664755),
 (21, 0.13249059890840834),
 (22, 0.15204299692560141),
 (23, 0.09481311337937268),
 (24, 0.2063853617337529),
 (25, 0.17843864820315505),
 (26, 0.18194302836847615)]
```

In [16]:

```python
# Train an LDA (Latent Dirichlet Allocation) model on the Bag-of-Words summary corpus
lda_model1 = gensim.models.LdaMulticore(bow_corpus_summary, num_topics=80, id2word=dicti

# Initialize an empty list to store the LDA topics
lda_list=[]


# Iterate over the topics in the LDA model and print them
for idx, topic in lda_model1.print_topics(-1):
    print('Topic: {} \nWords: {}'.format(idx, topic))
    topic1_string='Topic: {} \nWords: {}'.format(idx, topic)
    lda_list.append(topic1_string)
```

```
Topic: 0
Words: 0.032*"treatment" + 0.014*"gastric" + 0.012*"response" + 0.012
*"tumor" + 0.012*"chemotherapy" + 0.011*"clinical" + 0.010*"advanced" +
0.010*"colorectal" + 0.008*"combination" + 0.008*"primary"
Topic: 1
Words: 0.023*"surgery" + 0.019*"group" + 0.018*"treatment" + 0.014*"col
orectal" + 0.014*"respiratory" + 0.014*"pulmonary" + 0.014*"compare" +
0.013*"postoperative" + 0.012*"performed" + 0.012*"participant"
Topic: 2
Words: 0.018*"treatment" + 0.017*"gastric" + 0.015*"screening" + 0.014
*"disease" + 0.011*"immune" + 0.010*"objective" + 0.010*"tumor" + 0.010
*"related" + 0.009*"clinical" + 0.009*"great"
Topic: 3
Words: 0.052*"care" + 0.036*"palliative" + 0.029*"week" + 0.027*"treatm
ent" + 0.018*"placebo" + 0.015*"randomized" + 0.014*"receive" + 0.013
*"standard" + 0.012*"visit" + 0.011*"oral"
Topic: 4
Words: 0.036*"cell" + 0.035*"tumor" + 0.027*"stage" + 0.018*"treatment"
+ 0.018*"colorectal" + 0.010*"growth" + 0.010*"test" + 0.009*"associate
```

In [17]:

```
# Train an LDA (Latent Dirichlet Allocation) model on the TF-IDF summary corpus
lda_model_tfidf = gensim.models.LdaMulticore(corpus_tfidf_summary, num_topics=80, id2wor

# Initialize an empty list to store the LDA topics for the TF-IDF version
tfidf_list=[]

# Iterate over the topics in the LDA model and print them
for idx, topic in lda_model_tfidf.print_topics(-1):
    print('Topic: {} \nWords: {}'.format(idx, topic))
    topic_string='Topic: {} \nWords: {}'.format(idx, topic)
    tfidf_list.append(topic_string)
```

```
+ 0.012*"decision" + 0.011*"colonic"
Topic: 25
Words: 0.037*"dose" + 0.023*"tolerated" + 0.021*"maximum" + 0.019*"comb
ination" + 0.018*"determine" + 0.016*"irinotecan" + 0.015*"phase" + 0.0
15*"kras" + 0.014*"recommended" + 0.014*"concurrent"
Topic: 26
Words: 0.019*"fatigue" + 0.018*"mfolfox" + 0.015*"bleeding" + 0.014*"sy
mptom" + 0.012*"developing" + 0.012*"cancerous" + 0.010*"late" + 0.010
*"protect" + 0.009*"identified" + 0.009*"woman"
Topic: 27
Words: 0.024*"supportive" + 0.015*"swallowing" + 0.014*"depression" +
0.013*"best" + 0.012*"subject" + 0.011*"message" + 0.011*"care" + 0.011
*"quantitative" + 0.010*"consent" + 0.009*"screening"
Topic: 28
Words: 0.017*"water" + 0.014*"leak" + 0.012*"esophageal" + 0.011*"optio
n" + 0.010*"examination" + 0.010*"anastomotic" + 0.010*"carcinoma" + 0.
009*"treated" + 0.009*"histologically" + 0.009*"localized"
Topic: 29
Words: 0.039*"vitamin" + 0.030*"pemetrexed" + 0.025*"esophagus" + 0.020
*"barrett" + 0.020*"chemoprevention" + 0.015*"certain" + 0.014*"observ
```

In [43]:

```
# Iterate over the topics and for the first document in the summary corpus BOW model
for index, score in sorted(lda_model1[bow_corpus_summary[0]], key=lambda tup: -1*tup[1])
    print("\nTopic: {}".format( lda_model1.print_topic(index, 10)))
    break
```

```
Topic: 0.062*"chemotherapy" + 0.039*"tumor" + 0.033*"stop" + 0.033*"cell"
+ 0.028*"drug" + 0.025*"therapy" + 0.022*"radiation" + 0.020*"trial" + 0.0
20*"treating" + 0.020*"purpose"
```

In [44]:

```
# Iterate over the topics for the first document in the summary corpus TF-IDF model
for index, score in sorted(lda_model_tfidf[corpus_tfidf_summary[0]], key=lambda tup: -1*
    print("\nTopic: {}".format(lda_model1.print_topic(index, 10)))
```

```
Topic: 0.026*"colorectal" + 0.022*"combination" + 0.017*"advanced" + 0.016
*"tumor" + 0.015*"chemotherapy" + 0.014*"metastatic" + 0.013*"colonoscopy"
+ 0.013*"cell" + 0.012*"trial" + 0.012*"paclitaxel"
```

In [45]:

```
# Set the OpenAI API key make sure to use your own key, or the notebook will not work
openai.api_key = ################################
import requests
# Create an empty list to store the scores
list_of_scores=[]
# Iterate over the topics and scores for the first document in the summary corpus
for index, score in sorted(lda_model1[bow_corpus_summary[0]], key=lambda tup: -1*tup[1])
# Append the topic string to the list of scores
    list_of_scores.append(lda_model1.print_topic(index))
    break

# Define the user input query for the LLM
input1=' give all of the measurements found without scores for the topics below: '

# Define the URL for the OpenAI API
URL = "https://api.openai.com/v1/chat/completions"

# Construct the complete query by joining the list of scores
query=(input1 + ', '.join(list_of_scores))

# Construct the payload for the API request
payload = {
"model": "gpt-3.5-turbo-16k",
"messages": [{'role': 'system','content':'you are a translation system. Your role is to
            {"role": "user", "content": query}],
"temperature" : 0.8,
"top_p":0.87,
"n" : 1,
"stream": False,
"presence_penalty":0.03,
"frequency_penalty":0.5,
}

headers = {
"Content-Type": "application/json",
"Authorization": f"Bearer {openai.api_key}"
}
# Send a POST request to the OpenAI API
response = requests.post(URL, headers=headers, json=payload, stream=False)

# Parse the response JSON
response_json = response.json()

# Extract the chatbot response
chatbot_response = response_json['choices'][0]['message']['content']

# Split the chatbot response into a list of individual measurements
measurements_list = chatbot_response.strip().split('\n')

#Print the list of measurements
for measurement in measurements_list:
    print(measurement)
```

```
[measurement of chemotherapy effectiveness, measurement of tumor response,
measurement of cell response, measurement of drug efficacy, measurement of
therapy outcomes, measurement of radiation impact, measurement of trial ou
tcomes]
```

In [27]:

```
# Set the OpenAI API key make sure to use your own key, or the notebook will not work
openai.api_key = ################################
import requests

# Create empty lists to store the scores and measurements
list_of_scores_tfidf=[]
list_all_measurements_tfidf=[]


for z in tfidf_list:
    list_of_scores_tfidf=z
 # Define the user input query for TF-IDF
    input_tfidf=' give all of the measurements found without scores for the topics below
    URL_tfidf = "https://api.openai.com/v1/chat/completions"
    query_tfidf=(input_tfidf + ', '.join(list_of_scores_tfidf))
    payload_tfidf = {
    "model": "gpt-3.5-turbo-16k",
    "messages": [{'role': 'system','content':'you are a translation system. Your role is
                {"role": "user", "content": query_tfidf}],
    "temperature" : 0.8,
    "top_p":0.87,
    "n" : 1,
    "stream": False,
    "presence_penalty":0.03,
    "frequency_penalty":0.5,
    }

    headers_tfidf = {
    "Content-Type": "application/json",
    "Authorization": f"Bearer {openai.api_key}"
    }
    try:
         # Send a POST request to the OpenAI API for TF-IDF and get the response
        response_tfidf = requests.post(URL_tfidf, headers=headers_tfidf, json=payload_tf
        response_json_tfidf = response_tfidf.json()
        chatbot_response_tfidf = response_json_tfidf['choices'][0]['message']['content']
        # Split the chatbot response into a list of individual measurements
        measurements_list_tfidf = chatbot_response_tfidf.strip().split('\n')
        print(chatbot_response_tfidf.strip().split('\n'))
        list_all_measurements_tfidf.append((chatbot_response_tfidf.strip().split('\n')))
    except:
        continue
#Print the list of measurements
for measurement in measurements_list_tfidf:
    print(measurement)
```

```
['[measurement of laparoscopic surgery, measurement of gastric surgery,
measurement of comparing lymph recovery, measurement of versus node typ
e, measurement of anal recovery]']
['[measurement of safe use, measurement of gastric treatment, measureme
nt of docetaxel treatment, measurement of cisplatin treatment, measurem
ent of malignancy, measurement of oral treatment, measurement of causat
ion, measurement of small size, measurement of capecitabine treatment,
measurement of effectiveness]']
['measurement of familial adenomatous polyposis', 'measurement of monit
or', 'measurement of fluid', 'measurement of observed', 'measurement of
surgery', 'measurement of bevacizumab', 'measurement of giving', 'measu
rement of randomized']
['measurement of tumor growth, measurement of cell response, measuremen
t of drug efficacy, measurement of colorectal treatment, measurement of
screening effectiveness, measurement of bevacizumab impact, measurement
of chemotherapy effectiveness, measurement of therapy outcomes']
['measurement of tumor growth', 'measurement of cell response', 'measur
ement of drug efficacy', 'measurement of colorectal treatment', 'measur
ement of screening effectiveness', 'measurement of bevacizumab impact',
```

In [23]:

```
openai.api_key = ################################
import requests

list_of_scores_lda=[]
list_all_measurements_lda=[]

for x in lda_list:
    list_of_scores_lda=x

    input_lda=' give all of the measurements found without scores for the topics below:
    URL_lda = "https://api.openai.com/v1/chat/completions"
    query_lda=(input1 + ', '.join(list_of_scores_lda))
    payload_lda = {
    "model": "gpt-3.5-turbo-16k",
    "messages": [{'role': 'system','content':'you are a translation system. Your role is
            {"role": "user", "content": query_lda}],
    "temperature" : 0.8,
    "top_p":0.87,
    "n" : 1,
    "stream": False,
    "presence_penalty":0.03,
    "frequency_penalty":0.5,
    }

    headers_lda = {
    "Content-Type": "application/json",
    "Authorization": f"Bearer {openai.api_key}"
    }
    try:
        response_lda = requests.post(URL_lda, headers=headers_lda, json=payload_lda, str
        response_json_lda = response_lda.json()
        chatbot_response_lda = response_json_lda['choices'][0]['message']['content']
        # Split the chatbot response into a list of individual measurements
        measurements_list_lda = chatbot_response_lda.strip().split('\n')
        print(chatbot_response_lda.strip().split('\n'))
        list_all_measurements_lda.append((chatbot_response_lda.strip().split('\n'))),
    except:
        continue
#Print the list of measurements
for measurement in measurements_list_lda:
    print(measurement)
```

```
['[measurement of treatment, measurement of gastric, measurement of res
ponse, measurement of tumor, measurement of chemotherapy, measurement o
f clinical, measurement of advanced, measurement of colorectal, measure
ment of combination, measurement of primary]']
['measurement of surgery, measurement of group, measurement of treatmen
t, measurement of colorectal, measurement of respiratory, measurement o
f pulmonary, measurement of compare, measurement of postoperative, meas
urement of performed, measurement of participant']
['[measurement of treatment, measurement of gastric, measurement of scr
eening, measurement of disease, measurement of immune, measurement of o
bjective, measurement of tumor, measurement of related, measurement of
clinical, measurement of great]']
['measurement of tumor growth, measurement of palliative care, measurem
ent of weekly treatment, measurement of placebo, measurement of randomi
zed, measurement of receive, measurement of standard, measurement of vi
sit, measurement of oral']
['measurement of tumor growth', 'measurement of cell response', 'measur
ement of drug efficacy', 'measurement of colorectal treatment', 'measur
ement of screening effectiveness', 'measurement of growth', 'measuremen
```

In [28]:

```
import ast

def clean_item(item):
    # Remove square brackets, quotes, and extra white spaces
    item = item.replace('[', '').replace(']', '').replace('\'', '').strip()

    # If the item contains commas, it was actually a list in string format
    # Split it into a real list
    if ',' in item:
        item = item.split(', ')

    return item

# Flatten the list and clean the items
flat_list_lda = [clean_item(item) for sublist in list_all_measurements_lda for item in s
flat_list_tfidf=[clean_item(item) for sublist in list_all_measurements_tfidf for item in
# In case there are any sublists remaining (from the string lists), flatten again
flat_list_lda = [item for sublist in flat_list_lda for item in (sublist if isinstance(su
flat_list_tfidf = [item for sublist in flat_list_tfidf for item in (sublist if isinstanc
# Convert to set to remove duplicates, and back to list
unique_flat_list_lda = list(set(flat_list_lda))
unique_flat_list_tfidf = list(set(flat_list_tfidf))
print('this is lda/bow set for all gotten measruements also known as classes for our cas
print(unique_flat_list_lda)
print('this is tfidf set for all gotten measruements also known as classes for our case'
print(unique_flat_list_tfidf)
```

```
this is lda/bow set for all gotten measruements also known as classes f
or our case
['measurement of gastric diagnosis', 'measurement of effect', 'measurem
ent of pain', 'measurement of cost', 'measurement of colonic', 'measure
ment of symptom', 'advanced', 'measurement of rectal', 'measurement of
device', 'measurement of time', 'measurement of intervention outcomes',
'measurement of effective', 'measurement of regorafenib', 'measurement
of subject response', 'measurement of visit', 'measurement of western t
reatment', 'measurement of related', 'measurement of method', 'measurem
ent of life outcomes', 'measurement of tumor growth', 'measurement of o
ptical', 'measurement of capecitabine effectiveness', 'measurement of c
ell trial', 'measurement of colon size', 'measurement of safety', 'meas
urement of test', 'measurement of surgery rate', 'measurement of mcr',
'measurement of recommendation', 'measurement of treated', 'measurement
of gastric tumor growth', 'response', 'measurement of cohort', 'measure
ment of weekly treatment', 'measurement of progression', 'measurement o
f detection', 'measurement of laparoscopic', 'measurement of group', 'm
easurement of FOBt (fecal occult blood test)', 'measurement of pulmonar
y', 'measurement of purpose', 'measurement of preventing', 'measurement
```

In [29]:

```python
#every outputted class/measurement for the TF-IDF model
for elem in unique_flat_list_tfidf:
    print (elem)
```

```
measurement of develop
measurement of cost
measurement of colonic
measurement of relapsed
measurement of rectal
measurement of sequence
measurement of tolerated combination
measurement of blood response
measurement of white outcomes
measurement of participant safety
measurement of capecitabine effectiveness
measurement of optical
measurement of flow
measurement of histology
measurement of polypectomy
measurement of session
measurement of investigate
measurement of detecting half oncology
measurement of colorectal treatment
```

In [30]:

```python
#every outputted class/measurement for the BOW model
for elem in unique_flat_list_lda:
    print (elem)
```

```
measurement of gastric diagnosis
measurement of effect
measurement of pain
measurement of cost
measurement of colonic
measurement of symptom
advanced
measurement of rectal
measurement of device
measurement of time
measurement of intervention outcomes
measurement of effective
measurement of regorafenib
measurement of subject response
measurement of visit
measurement of western treatment
measurement of related
measurement of method
measurement of life outcomes
```

In [46]:

```python
#amount of classes
len(unique_flat_list_tfidf)
```

Out[46]:

```
477
```

In [47]:

```
len(unique_flat_list_lda)
```

Out[47]:

```
289
```

In [33]:

```
from owlready2 import *
onto_path=(r"C:\Users\PC\Downloads\lab_sessions\lab6\ontology.owl")
onto=get_ontology(onto_path).load()
# Access classes in the ontology
golden_ontology_measurements_list=[]
for cls in onto.classes():
    class_name = cls.label.first() if cls.label else cls.name
    golden_ontology_measurements_list.append(class_name)
```

In [34]:

```
golden_ontology_measurements_list
```

Out[34]:

```
['clinical measurement',
 'cardiovascular measurement',
 'blood pressure measurement',
 'calculated blood pressure',
 'whole body morphological measurement',
 'body morphological measurement',
 'body weight',
 'body length',
 'hip circumference',
 'body temperature',
 'proximal hind limb circumference',
 'hind limb morphological measurement',
 'waist to hip ratio (WHR)',
 'calculated body morphological measurement',
 'blood chemistry measurement',
 'blood measurement',
 'red blood cell count',
 'red blood cell morphological measurement',
```

In [35]:

```
# Create TF-IDF ontology from parsed classes
TFIDF_ontology = get_ontology("http://test.org/onto.owl")
TFIDF_list=[]
with TFIDF_ontology:
    # Define a list of classes
    for elem in unique_flat_list_tfidf:
        TFIDF_list.append(elem)

    # Loop through the list and create classes in the ontology
    for class_name in TFIDF_list:
        types.new_class(class_name, (Thing,))

#Please make sure to change the directory
directory = os.path.expanduser(r"C:\Users\PC\Downloads\lab_sessions\lab6")
file_path = os.path.join(directory, "TFIDF.owl")
# Save the ontology to a file
TFIDF_ontology.save(file = file_path, format = "rdfxml")
```

In [36]:

```
# Create BOW ontology from parsed classes
BOW_ontology = get_ontology("http://test1.org/onto1.owl")
Bow_list=[]
with BOW_ontology:
    # Define a list of classes
    for elem1 in unique_flat_list_lda:
        Bow_list.append(elem1)

    # Loop through the list and create classes in the ontology
    for class_name1 in Bow_list:
        types.new_class(class_name1, (Thing,))

#Please make sure to change the directory
directory = os.path.expanduser(r"C:\Users\PC\Downloads\lab_sessions\lab6")
file_path1 = os.path.join(directory, "BOW.owl")
# Save the ontology to a file
BOW_ontology.save(file = file_path1, format = "rdfxml")
```

In [37]:

```
def hash_list(lst):
    """Hash a list by creating a sorted tuple of its unique elements"""
    return tuple(sorted(set(lst)))

def count_matching_lists(list_of_lists1, list_of_lists2):
    hash_set1 = {hash_list(lst) for lst in list_of_lists1}
    hash_set2 = {hash_list(lst) for lst in list_of_lists2}

    matches = hash_set1.intersection(hash_set2)

    return len(matches)

count = count_matching_lists(unique_flat_list_tfidf, unique_flat_list_lda)

print(f"There are {count} matching elements in the two sets.")
```

```
There are 99 matching elements in the two sets.
```

In [38]:

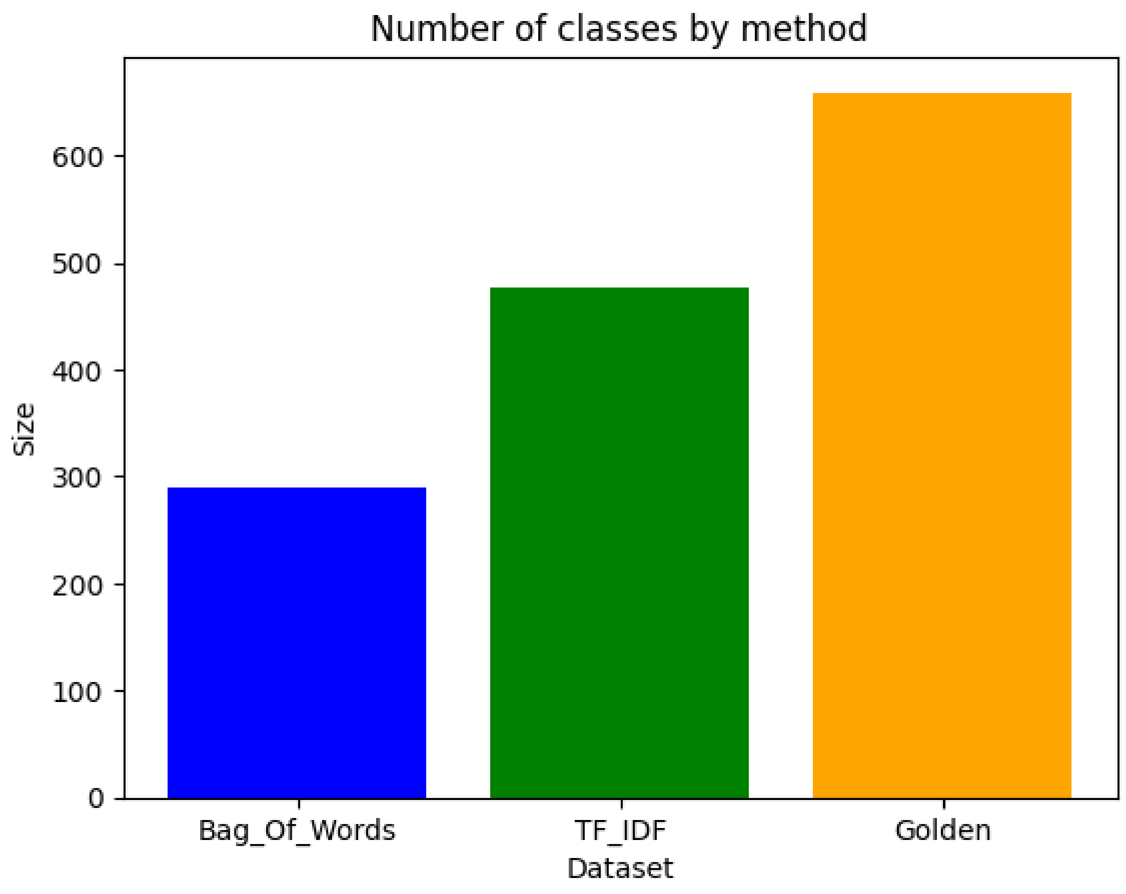
```
#number of classes in golden ontology
len(golden_ontology_measurements_list)
```

Out[38]:

```
659
```

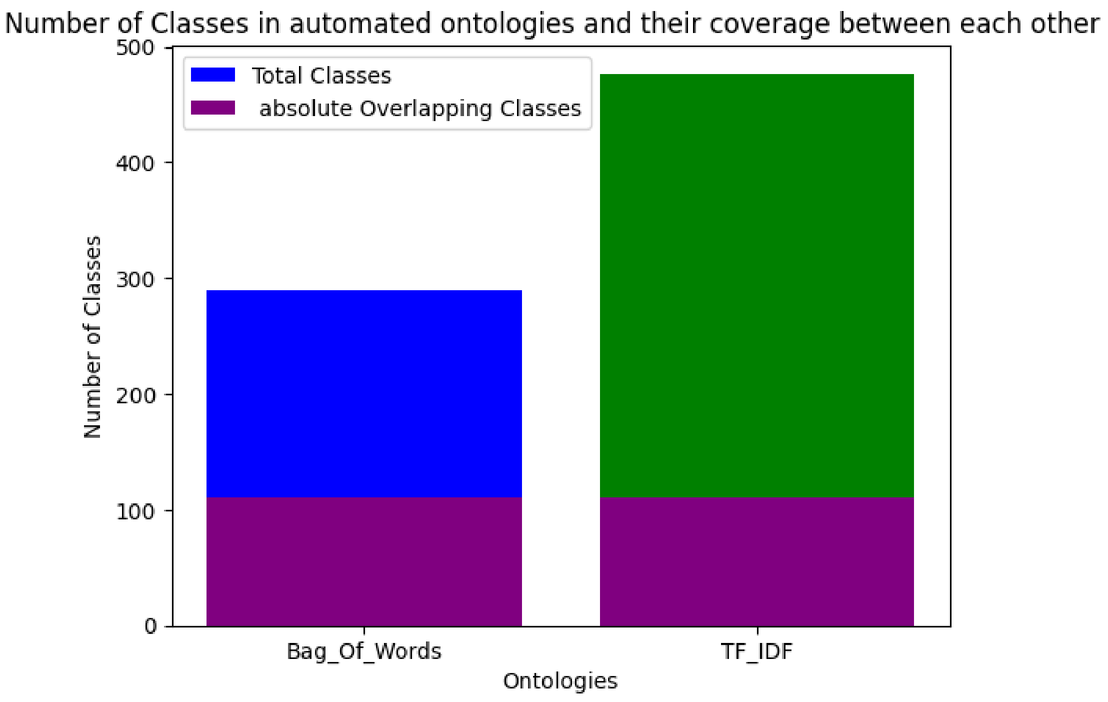
In [39]:

```
import matplotlib.pyplot as plt

# Dataset names and sizes
dataset_names = ['Bag_Of_Words', 'TF_IDF', 'Golden']
dataset_sizes = [len(unique_flat_list_lda), len(unique_flat_list_tfidf), len(golden_onto

# Define colors for each dataset
dataset_colors = ['blue', 'green', 'orange']

# Create bar chart
plt.bar(dataset_names, dataset_sizes, color=dataset_colors)

# Add labels and title
plt.xlabel('Dataset')
plt.ylabel('Size')
plt.title('Number of classes by method')

# Display the bar chart
plt.show()
```



In [40]:

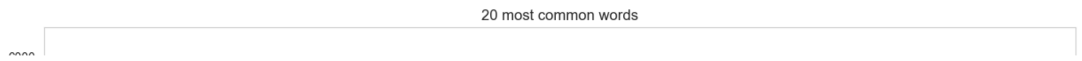
```
import matplotlib.pyplot as plt

# Total number of classes
total_classes = [len(unique_flat_list_lda),len(unique_flat_list_tfidf) ]

# Number of overlapping classes
overlapping_classes = [111,111]

# Dataset names
dataset_names = ['Bag_Of_Words', 'TF_IDF']


# Define colors for each dataset
dataset_colors = ['blue', 'green']

# Create bar chart for total classes
plt.bar(dataset_names, total_classes, color=dataset_colors, label='Total Classes')

# Create bar chart for overlapping classes
plt.bar(dataset_names, overlapping_classes, color='purple', label=' absolute Overlapping

# Add labels and title
plt.xlabel('Ontologies')
plt.ylabel('Number of Classes')
plt.title('Number of Classes in automated ontologies and their coverage between each oth



# Add legend
plt.legend()



# Display the bar chart
plt.show()
```



In [41]:

```python
# Load the library with the CountVectorizer method
from sklearn.feature_extraction.text import CountVectorizer
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns
sns.set_style('whitegrid')
%matplotlib inline

# Helper function
def plot_20_most_common_words(count_data, count_vectorizer):
    import matplotlib.pyplot as plt
    words = count_vectorizer.get_feature_names_out()
    total_counts = np.zeros(len(words))
    for t in count_data:
        total_counts+=t.toarray()[0]

    count_dict = (zip(words, total_counts))
    count_dict = sorted(count_dict, key=lambda x:x[1], reverse=True)[0:20]
    words = [w[0] for w in count_dict]
    counts = [w[1] for w in count_dict]
    x_pos = np.arange(len(words))

    plt.figure(2, figsize=(15, 15/1.6180))
    plt.subplot(title='20 most common words')
    sns.set_context("notebook", font_scale=1.25, rc={"lines.linewidth": 2.5})
    sns.barplot(x_pos, counts, palette='husl')
    plt.xticks(x_pos, words, rotation=90)
    plt.xlabel('words')
    plt.ylabel('counts')
    plt.show()

# Initialise the count vectorizer with the English stop words
count_vectorizer = CountVectorizer(stop_words='english')

# Fit and transform the processed titles
summary_data = count_vectorizer.fit_transform(papers2['Summary'])


# Visualise the 10 most common words
plot_20_most_common_words(summary_data, count_vectorizer)
```

```
C:\Users\PC\anaconda3\lib\site-packages\seaborn\_decorators.py:36: Futu
reWarning: Pass the following variables as keyword args: x, y. From ver
sion 0.12, the only valid positional argument will be `data`, and passi
ng other arguments without an explicit keyword will result in an error
or misinterpretation.
  warnings.warn(
```

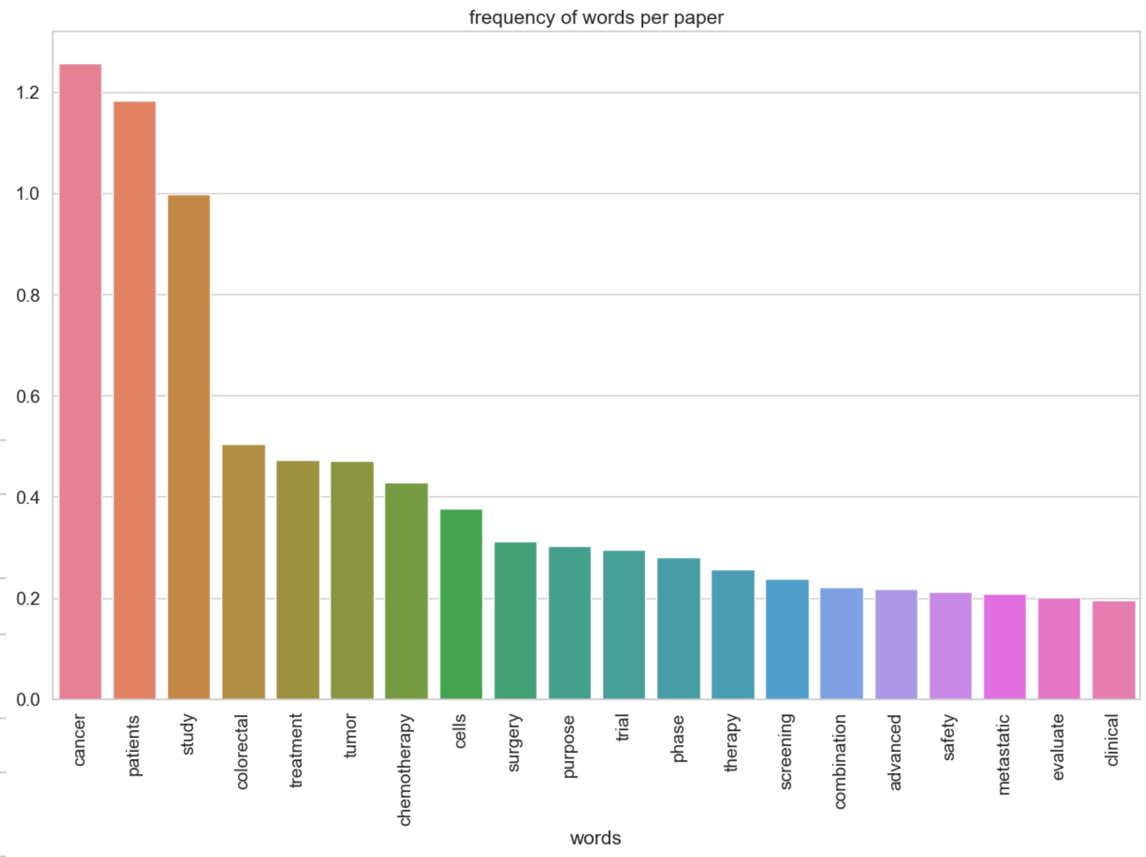


```
In [ ]:
```

In [42]:

```
def plot_20_most_common_words_avg2(count_data, count_vectorizer, total_papers):
    import matplotlib.pyplot as plt
    words = count_vectorizer.get_feature_names_out()
    total_counts = np.zeros(len(words))
    for t in count_data:
        total_counts+=t.toarray()[0]

    # calculate average counts
    avg_counts = total_counts/total_papers

    count_dict = (zip(words, avg_counts))
    count_dict = sorted(count_dict, key=lambda x:x[1], reverse=True)[0:20]
    words = [w[0] for w in count_dict]
    counts = [w[1] for w in count_dict]
    x_pos = np.arange(len(words))

    plt.figure(2, figsize=(15, 15/1.6180))
    plt.subplot(title='frequency of words per paper')
    sns.set_context("notebook", font_scale=1.25, rc={"lines.linewidth": 2.5})
    sns.barplot(x_pos, counts, palette='husl')
    plt.xticks(x_pos, words, rotation=90)
    plt.xlabel('words')
    #plt.ylabel('average counts per paper')
    plt.show()

# Initialise the count vectorizer with the English stop words
count_vectorizer = CountVectorizer(stop_words='english')

# Fit and transform the processed titles
summary_data = count_vectorizer.fit_transform(papers2['Summary'])

# Total number of papers
total_papers = 4763

# Visualise the 10 most common words
plot_20_most_common_words_avg2(summary_data, count_vectorizer, total_papers)
```

```
C:\Users\PC\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureW
arning: Pass the following variables as keyword args: x, y. From version
0.12, the only valid positional argument will be `data`, and passing other
arguments without an explicit keyword will result in an error or misinterp
retation.
  warnings.warn(
```


frequency of words per paper
1.2
1.0
0.8
0.6
0.4
0.2
0.0
cancer
patients
study
colorectal
treatment
tumor
chemotherapy
cells
surgery
purpose
trial
phase
therapy
screening
combination
advanced
safety
metastatic
evaluate
clinical
words