# Assignment_2_AmazonFineFood_EDA

October 3, 2018

## 1 Amazon Fine Food Analysis

## 2 1 Loading the data

In [1]:
```
%matplotlib inline
import warnings
warnings.filterwarnings("ignore")

import sqlite3
import pandas as pd
import numpy as np
import nltk
import string
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.feature_extraction.text import TfidfTransformer
from sklearn.feature_extraction.text import TfidfVectorizer

from sklearn.preprocessing import StandardScaler
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.metrics import confusion_matrix
from sklearn import metrics
from sklearn.metrics import roc_curve, auc
from nltk.stem.porter import PorterStemmer

import re
import string
from nltk.corpus import stopwords
from nltk.stem import PorterStemmer
from nltk.stem.wordnet import WordNetLemmatizer

from gensim.models import Word2Vec
from gensim.models import KeyedVectors
import pickle

con = sqlite3.connect('database.sqlite') #loading data
```

```
        #filtering only positive and negative reviews
        filtered_data = pd.read_sql_query(""" SELECT * FROM Reviews WHERE Score != 3 """, con)

        # renaming the score with less than 3 to negative and more than 3 to positive
        def partition(x):
            if x < 3:
                return 'negative'
            return 'positive'

        #changing reviews with score less than 3 to be positive and vice-versa
        actualScore = filtered_data['Score']
        positiveNegative = actualScore.map(partition)
        filtered_data['Score'] = positiveNegative

        print("number of attributes and size of the data is")
        print(filtered_data.shape) #number of attributes and size of the data
        filtered_data.head() # prints first few rows
```

```
C:\Users\tm00501760\AppData\Local\Continuum\anaconda3\lib\site-packages\gensim\utils.py:1212: U
  warnings.warn("detected Windows; aliasing chunkize to chunkize_serial")


number of attributes and size of the data is
(525814, 10)
```

Out[1]:

| | Id | ProductId | UserId | ProfileName | \ |
|---|---|---|---|---|---|
| 0 | 1 | B001E4KFG0 | A3SGXH7AUHU8GW | delmartian | |
| 1 | 2 | B00813GRG4 | A1D87F6ZCVE5NK | dll pa | |
| 2 | 3 | B000LQOCH0 | ABXLMWJIXXAIN | Natalia Corres "Natalia Corres" | |
| 3 | 4 | B000UA0QIQ | A395BORC6FGVXV | Karl | |
| 4 | 5 | B006K2ZZ7K | A1UQRSCLF8GW1T | Michael D. Bigham "M. Wassir" | |

| | HelpfulnessNumerator | HelpfulnessDenominator | Score | Time | \ |
|---|---|---|---|---|---|
| 0 | 1 | 1 | positive | 1303862400 | |
| 1 | 0 | 0 | negative | 1346976000 | |
| 2 | 1 | 1 | positive | 1219017600 | |
| 3 | 3 | 3 | negative | 1307923200 | |
| 4 | 0 | 0 | positive | 1350777600 | |

| | Summary | Text |
|---|---|---|
| 0 | Good Quality Dog Food | I have bought several of the Vitality canned d... |
| 1 | Not as Advertised | Product arrived labeled as Jumbo Salted Peanut... |
| 2 | "Delight" says it all | This is a confection that has been around a fe... |
| 3 | Cough Medicine | If you are looking for the secret ingredient i... |
| 4 | Great taffy | Great taffy at a great price. There was a wid... |

## 3 Observations:

Load the dataset for Amazon Food Reviews and segergate dataset based on positive and negative reviews i.e., reviews with ratings less than 3 is considered to be negative reviews and reviews with rating greater than 3 is considered to be positive review.

## 4 2 Data Cleaning

## 5 2.1 Deduplicating

```
In [2]: #Sorting data according to ProductId in ascending order
        sorted_data=filtered_data.sort_values('ProductId', axis=0, ascending=True, inplace=Fals
        print("Size of sorted data according to the product id:")
        print(sorted_data.shape)

        #removing the duplicate entries
        final=sorted_data.drop_duplicates(subset={"UserId","ProfileName","Time","Text"}, keep=
        final.shape

        final=final[final.HelpfulnessNumerator<=final.HelpfulnessDenominator]

        print("Size after removing the duplicate entries:")
        print(final.shape)

        #Number of positive and negative reviews present in sorted dataset:
        print("Number of positive and negative reviews present in sorted dataset:")
        final['Score'].value_counts()
```

```
Size of sorted data according to the product id:
(525814, 10)
Size after removing the duplicate entries:
(364171, 10)
Number of positive and negative reviews present in sorted dataset:
```

```
Out[2]: positive    307061
        negative     57110
        Name: Score, dtype: int64
```

## 6 Observation:

Resultant is the output after removing the duplicates based on unique product Id.

## 7 2.2 Stemming

```
In [3]: import nltk
        from nltk.stem import SnowballStemmer
```

```
import re
stop = set(stopwords.words('english')) #set of stopwords
sno = nltk.stem.SnowballStemmer('english') #initialising the snowball stemmer

#function to remove html tagged words
def removehtml(sentence):
    remove = re.compile('<.*?>')
    removetext = re.sub(remove, ' ', sentence)
    return removetext

#function to remove word of any pinctuation and special characters
def removepunct(sentence):
    removed = re.sub(r'[?|!|\'|"|#]',r'',sentence)
    removed = re.sub(r'[.|,|)|(|\|/]',r' ',removed)
    return  removed

print("Stop words found in the given dataset are:")
print(stop)
```

```
Stop words found in the given dataset are:
{"that'll", 'once', 'so', 'y', 'does', 'did', 'won', 'out', 'some', 'if', 'him', 'yours', 'the
```

In [4]:
```
#Code for implementing step-by-step the checks mentioned in the pre-processing phase
# this code takes a while to run as it needs to run on 500k sentences.
i=0
str1=' '
final_string=[]
all_positive_words=[] # store words from +ve reviews here
all_negative_words=[] # store words from -ve reviews here.
s=''
for sent in final['Text'].values:
    filtered_sentence=[]
    sent=removehtml(sent) # calling function to remove HTMl tags
    for w in sent.split():
        for cleaned_words in removepunct(w).split(): #calling the function to remove p
            if((cleaned_words.isalpha()) & (len(cleaned_words)>2)):
                if(cleaned_words.lower() not in stop):
                    s=(sno.stem(cleaned_words.lower())).encode('utf8')
                    filtered_sentence.append(s)
                    if (final['Score'].values)[i] == 'positive':
                        all_positive_words.append(s) #list of all words used to descri
                    if(final['Score'].values)[i] == 'negative':
                        all_negative_words.append(s) #list of all words used to descri
                else:
                    continue
                else:
                    continue
```

```
            str1 = b" ".join(filtered_sentence) #final string of cleaned words

            final_string.append(str1)
            i+=1
```

```
In [5]: final['CleanedText']=final_string #adding a column of CleanedText which displays the d
        final['CleanedText']=final['CleanedText'].str.decode("utf-8")
```

```
In [6]: final.head(3) #below the processed review can be seen in the CleanedText Column
```

```
        # store final table into an SQlLite table for future.
        conn = sqlite3.connect('final.sqlite')
        c=conn.cursor()
        conn.text_factory = str
        final.to_sql('Reviews', conn,  schema=None, if_exists='replace', index=True, index_labe
```

## 8 Observation:

Stemming is performed on the deduplicated data to remove stop words and special characters. And finally store the pre-processed dataset.

## 9 2.3 Considering 4000 samples from 364k dataset

```
In [7]: positive_reviews=final[final["Score"]=="positive"].sample(n=1000)
        negative_reviews=final[final["Score"]=="negative"].sample(n=1000)
        final_4k=pd.concat([positive_reviews,negative_reviews])
        print("Shape of 4k dataset")
        print(final_4k.shape)
        score_4k=final_4k["Score"]
        print("Shape of 4k scores only:")
        print(score_4k.shape)
```

```
Shape of 4k dataset
(2000, 11)
Shape of 4k scores only:
(2000,)
```

## 10 Observation:

Considering the randon 2000 data points i.e., 1000 data points of positive reviews and negative reviews from the preprocessed data to reduce time complexity.

## 11 3 t-SNE Representations:

## 12 3.1 BOW

In [17]:
```
count_vector=CountVectorizer(ngram_range=(1,2))
final_count=count_vector.fit_transform(final_4k['CleanedText'].values)
print("Type of final count:")
print(type(final_count))
print("Shape of final count:")
print(final_count.shape)
```

```
Type of final count:
<class 'scipy.sparse.csr.csr_matrix'>
Shape of final count:
(2000, 68387)
```

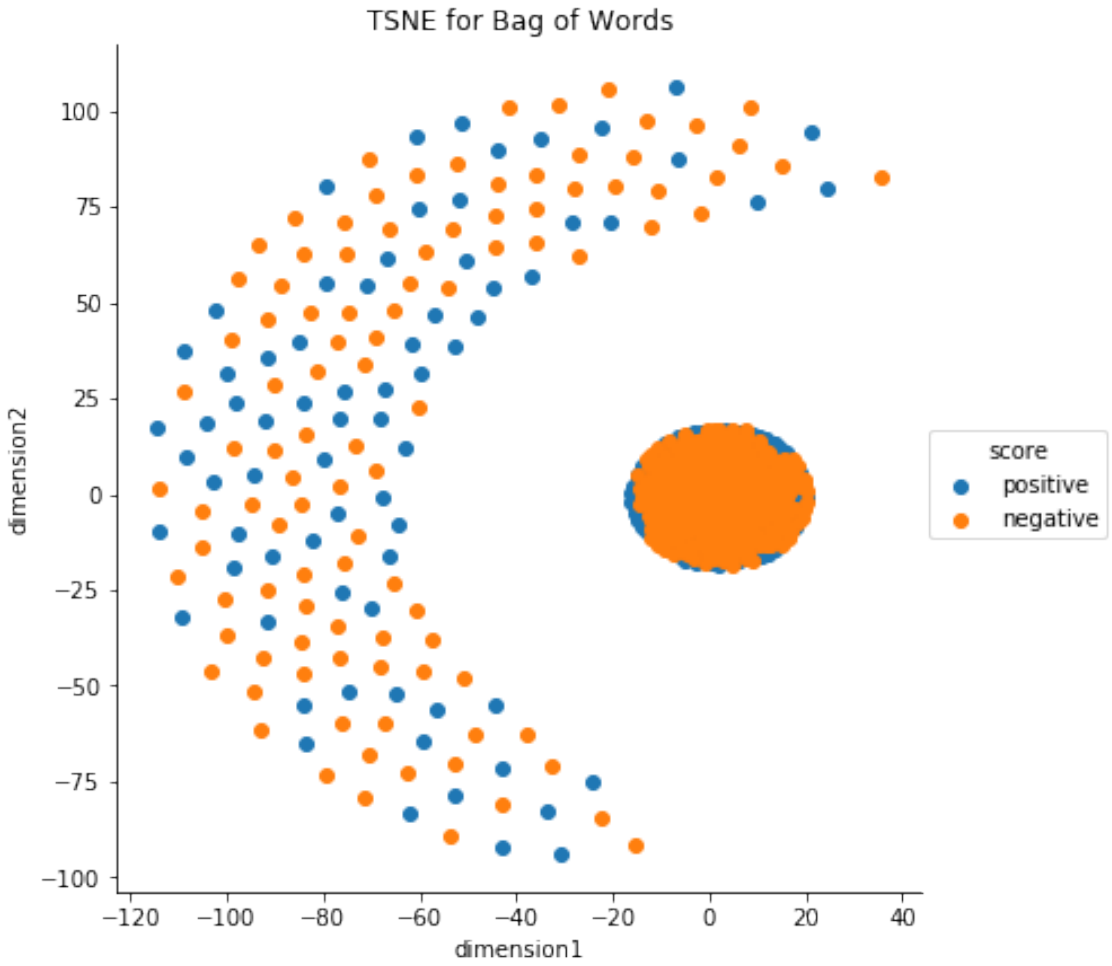
In [19]:
```
from sklearn.preprocessing import StandardScaler

standard_data = StandardScaler(with_mean = False).fit_transform(final_count)
standard_data = standard_data.todense()
print("Type of standard count:")
print(type(standard_data))
print("Shape of standard count:")
print(standard_data.shape)
```

```
Type of standard count:
<class 'numpy.matrixlib.defmatrix.matrix'>
Shape of standard count:
(2000, 68387)
```

```
C:\Users\tm00501760\AppData\Local\Continuum\anaconda3\lib\site-packages\sklearn\utils\validatio
  warnings.warn(msg, DataConversionWarning)
C:\Users\tm00501760\AppData\Local\Continuum\anaconda3\lib\site-packages\sklearn\utils\validatio
  warnings.warn(msg, DataConversionWarning)
```

In [20]:
```
from sklearn.manifold import TSNE
model = TSNE(n_components=2, random_state=0, perplexity = 30, n_iter = 5000)
tsne_data = model.fit_transform(standard_data)
tsne_data = np.vstack((tsne_data.T, score_4k)).T
tsne_df = pd.DataFrame(data=tsne_data, columns=("dimension1", "dimension2", "score"))
sns.FacetGrid(tsne_df, hue="score", size=6).map(plt.scatter, 'dimension1', 'dimension2
plt.title("TSNE for Bag of Words")
plt.show()
```




## 13 Observation:

From the above representation, there is large number of overlap and it is unable to seperate positive and negative reviews.

## 14 3.2 TF-IDF

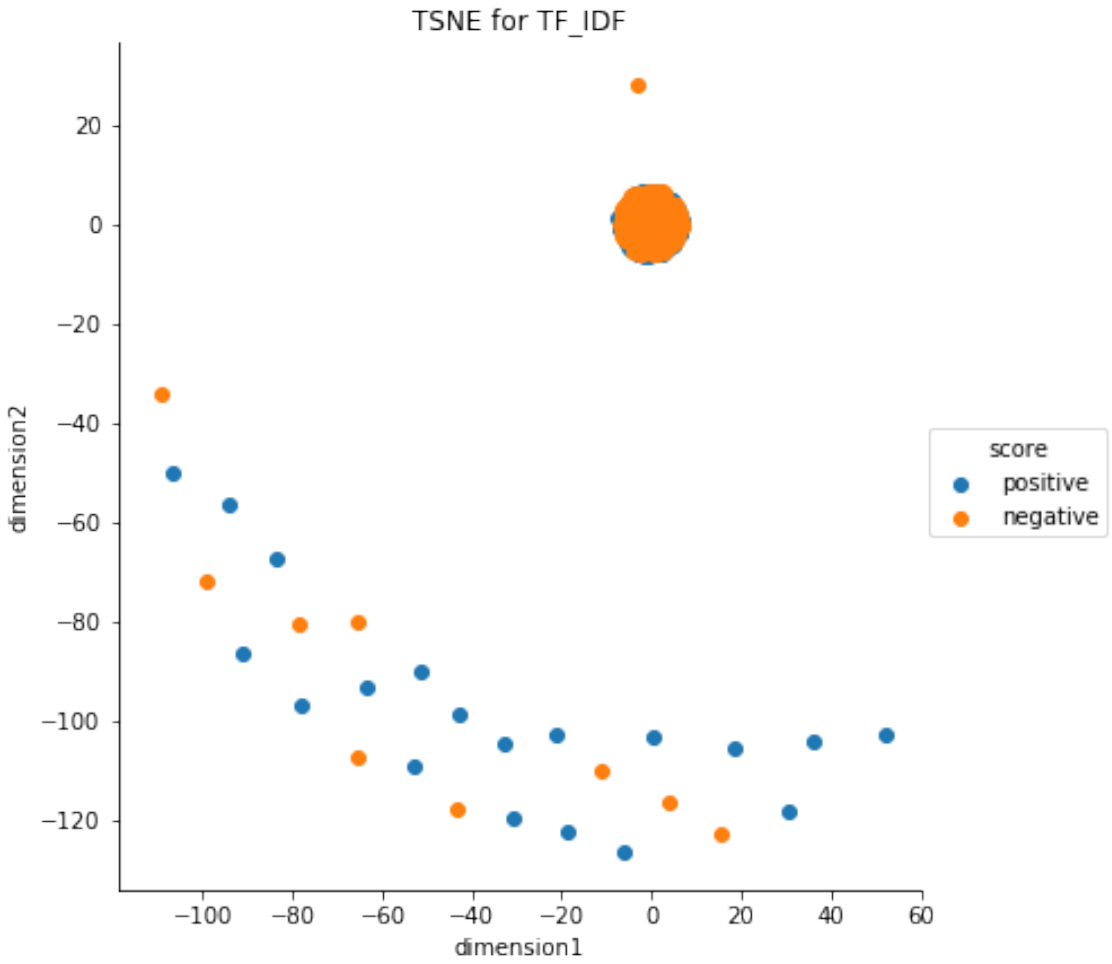
```
In [12]: tfidf_vector=TfidfVectorizer(ngram_range=(1,2))
         final_tfidf=tfidf_vector.fit_transform(final_4k['CleanedText'].values)
         print("Type of final_tfidf count:")
         print(type(final_tfidf))
         print("Shape of final_tfidf count:")
         print(final_tfidf.shape)

         standard_data = StandardScaler(with_mean = False).fit_transform(final_tfidf)
```

```
        standard_data = standard_data.todense()
        print("Type of standard ifidf:")
        print(type(standard_data))
        print("Shape of standard ifidf:")
        print(standard_data.shape)
```

```
Type of final_tfidf count:
<class 'scipy.sparse.csr.csr_matrix'>
Shape of final_tfidf count:
(2000, 66666)
Type of standard ifidf:
<class 'numpy.matrixlib.defmatrix.matrix'>
Shape of standard ifidf:
(2000, 66666)
```

```
In [12]: from sklearn.manifold import TSNE
         model = TSNE(n_components=2, perplexity = 30)
         tsne_data = model.fit_transform(standard_data)
         tsne_data = np.vstack((tsne_data.T, score_4k)).T
         tsne_df = pd.DataFrame(data=tsne_data, columns=("dimension1", "dimension2", "score"))
         sns.FacetGrid(tsne_df, hue="score", size=6).map(plt.scatter, 'dimension1', 'dimension2
         plt.title("TSNE for TF_IDF")
         plt.show()
```




## 15 Observation:

Seperation between the positive and negative reviews are difficult because of over-lapping.

## 16 3.3 Avg w2v

```
In [15]: import gensim
         list_of_sent = []
         for sent in final_4k['Text'].values:
             filtered_sentence = []
             sent=removehtml(sent)
             for w in sent.split():
                 for cleaned_words in removepunct(w).split():
                     if(cleaned_words.isalpha()):
                         filtered_sentence.append(cleaned_words.lower())
```

```
                    else:
                        continue
            list_of_sent.append(filtered_sentence)

        print(final_4k['Text'].values[0])
        print("**************************************************************")
        print(list_of_sent[0])
        print(final_4k.shape)
```

```
I have been suffering from chronic constipation my whole life. Four to nine days of misery was
**************************************************************
['i', 'have', 'been', 'suffering', 'from', 'chronic', 'constipation', 'my', 'whole', 'life', 'f
(2000, 11)
```

```
In [16]: w2v_model=gensim.models.Word2Vec(list_of_sent,min_count=5,size=50, workers=4)
         w2v = w2v_model[w2v_model.wv.vocab]
         w2v.shape
```

```
Out[16]: (2557, 50)
```

```
In [17]: words = list(w2v_model.wv.vocab)
         print(len(words))
```

```
2557
```

```
In [18]: w2v_model.wv.most_similar('tasty')
```

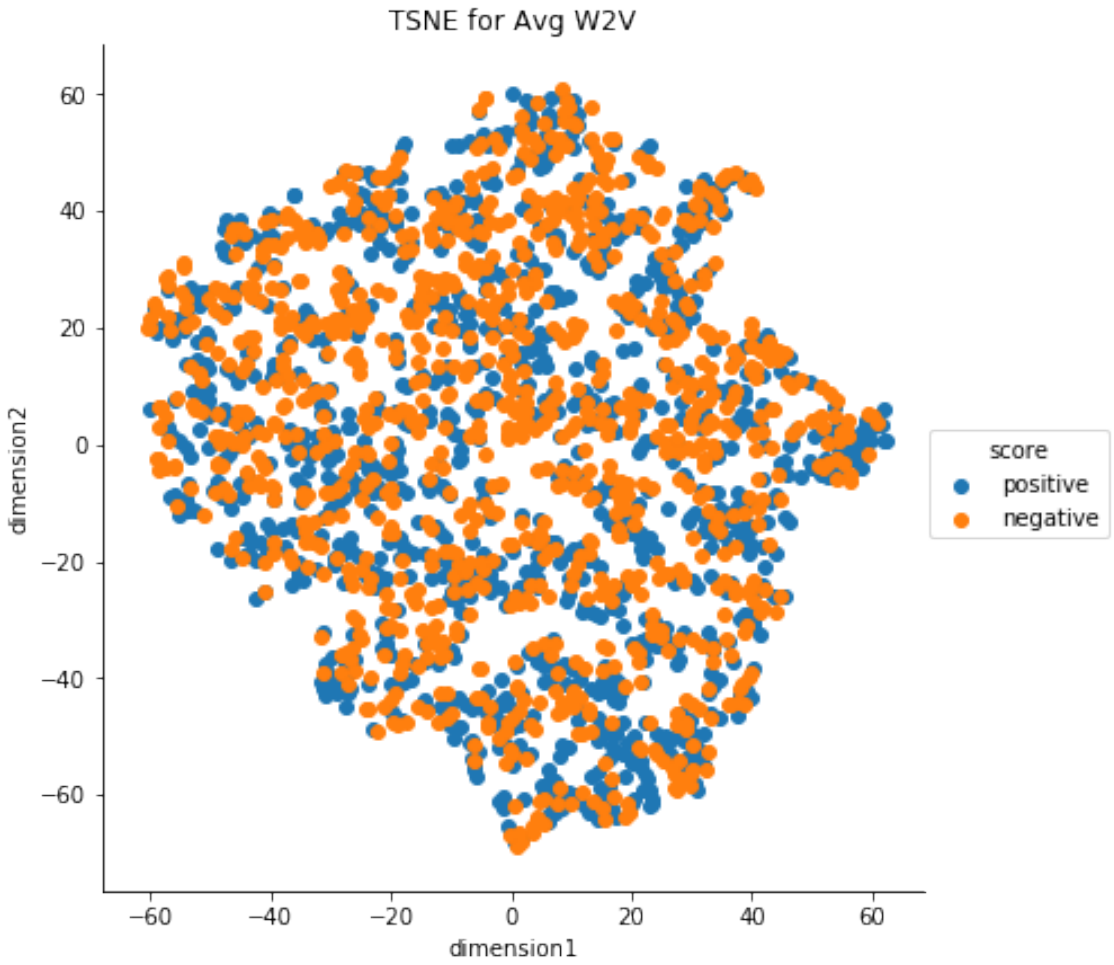
```
Out[18]: [('delicious', 0.9993318319320679),
          ('salty', 0.9992820024490356),
          ('pretty', 0.9992383718490601),
          ('healthy', 0.9992357492446899),
          ('bar', 0.9991680979728699),
          ('real', 0.9991409778594971),
          ('snack', 0.9991224408149719),
          ('also', 0.9990518093109131),
          ('rich', 0.9990414381027222),
          ('light', 0.9990360140800476)]
```

```
In [19]: sent_vectors = []; # the avg-w2v for each sentence/review is stored in this list
         for sent in list_of_sent: # for each review/sentence
             sent_vec = np.zeros(50) # as word vectors are of zero length
             cnt_words =0; # num of words with a valid vector in the sentence/review
             for word in sent: # for each word in a review/sentence
                 try:
                     vec = w2v_model.wv[word]
                     sent_vec += vec
                     cnt_words += 1
```

```
            except:
                pass
        sent_vec /= cnt_words
        sent_vectors.append(sent_vec)
    print(len(sent_vectors))
    print(len(sent_vectors[0]))
```

```
2000
50
```

In [18]:
```
from sklearn.manifold import TSNE
model = TSNE(n_components=2, random_state=0, perplexity = 30, n_iter = 5000)
tsne_data = model.fit_transform(sent_vectors)
tsne_data = np.vstack((tsne_data.T, score_4k)).T
tsne_df = pd.DataFrame(data=tsne_data, columns=("dimension1", "dimension2", "score"))
sns.FacetGrid(tsne_df, hue="score", size=6).map(plt.scatter, 'dimension1', 'dimension2
plt.title("TSNE for Avg W2V")
plt.show()
```



## 17 3.4 Avg ifidf

In [21]:
```
tfidf_feat = tfidf_vector.get_feature_names() # tfidf words/col-names
# final_tf_idf is the sparse matrix with row= sentence, col=word and cell_val = tfidf

tfidf_sent_vectors = []; # the tfidf-w2v for each sentence/review is stored in this l
row=0;
for sent in list_of_sent: # for each review/sentence
    sent_vec = np.zeros(50) # as word vectors are of zero length
    weight_sum =0; # num of words with a valid vector in the sentence/review
    for word in sent: # for each word in a review/sentence
        try:
            vec = w2v_model.wv[word]
            # obtain the tf_idfidf of a word in a sentence/review
            tf_idf = final_tfidf[row, tfidf_feat.index(word)]
            sent_vec += (vec * tf_idf)
            weight_sum += tf_idf
        except:
            pass

    sent_vec /= weight_sum
    tfidf_sent_vectors.append(sent_vec)
    row += 1
```

In [22]:
```
len(tfidf_sent_vectors)
```

Out[22]: 2000

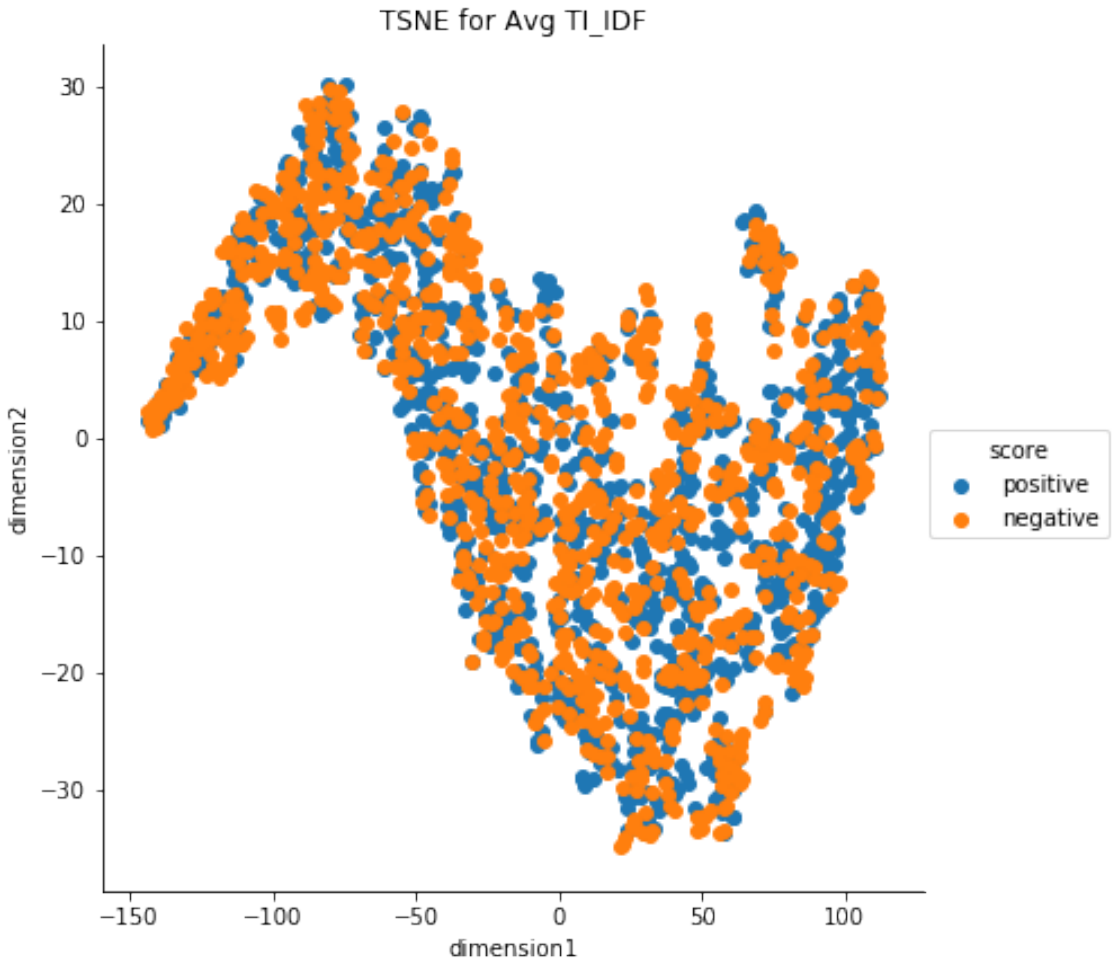
In [23]:
```
np.isnan(tfidf_sent_vectors)
```

Out[23]:
```
array([[False, False, False, ..., False, False, False],
       [False, False, False, ..., False, False, False],
       [False, False, False, ..., False, False, False],
       ...,
       [False, False, False, ..., False, False, False],
       [False, False, False, ..., False, False, False],
       [False, False, False, ..., False, False, False]])
```

In [24]:
```
tfidf_sent_vectors = np.nan_to_num(tfidf_sent_vectors)
```

In [25]:
```
from sklearn.manifold import TSNE
model = TSNE(n_components=2, random_state=0, perplexity = 30, n_iter = 5000)
tsne_data = model.fit_transform(tfidf_sent_vectors)
tsne_data = np.vstack((tsne_data.T, score_4k)).T
tsne_df = pd.DataFrame(data=tsne_data, columns=("dimension1", "dimension2", "score"))
```

```
sns.FacetGrid(tsne_df, hue="score", size=6).map(plt.scatter, 'dimension1', 'dimension2
plt.title("TSNE for Avg TI_IDF")
plt.show()
```




## 18 Conclusion:

1. From the above representations, non of the t-SNE plots gives the seperation between positive and negative reviews.
2. Above plots may vary based on attributes like no. of data points considered, iterations, perplexity etc.