# Multi-label Disease Classification from Medline Articles

A huge number of journal articles are published each year focusing on various kinds of diseases. The number of articles is further increased due to the overlapping of scope of various subjects; for instance, articles on medicine and journals on chemistry may both focus on autoimmune diseases.

We'll use this notebook to develop a model which will take in MEDLINE articles and will classify it into one or more disease categories (or even none of the categories) based on the abstract of the article.

#### Import basic packages & set seed for reproducibility

In [1]:
```
import numpy as np
import pandas as pd
import os
import sys
import datetime
import matplotlib.pyplot as plt

np.random.seed(7)
```

#### Load packages specific to MEDLINE

Use "Medline" package from "biopython" to parse the MEDLINE file(s)

*Details of the package are found in:*

- *http://biopython.org/ (http://biopython.org/)*
- *http://biopython.org/DIST/docs/api/Bio-module.html (http://biopython.org/DIST/docs/api/Bio-module.html)*
- *http://biopython.org/DIST/docs/api/Bio.Medline-module.html (http://biopython.org/DIST/docs/api/Bio.Medline-module.html)*

In [2]:
```
from collections import defaultdict
from Bio import Medline
```

## Vectorization of Words (Word Embedding)

Natural language processing (NLP) systems traditionally treat words as discrete atomic symbols. For example, ‘tiger’ may be represented as “W1” and 'cat' as “W2”. These encodings are arbitrary and provide no useful information regarding the relationships that may exist between the individual symbols. Representing words as unique, discrete symbols furthermore leads to data sparsity, and usually means that we may need more data in order to successfully train statistical models. Using vector representations can overcome some of these obstacles.

We want these vectors to be created in such a way that they somehow represent the word and its context, meaning, and semantics. For example, we’d like the vectors for the words ‘tiger’ and ‘cat’ to reside in relatively the same area in the vector space when compared to ‘car’ since they’re both animals of the same family of species (viz., ‘Felidae’). The vector representation of a word is also known as a word embedding.

To create these “word embedding” (i.e. vector representation of words), we will use the famous “Word2Vec” model instead of reinventing the wheel. The Word2Vec model is created by Google – one of the biggest players in the ML game and was trained on a massive Google News dataset that contained over 100 billion different words.

In [3]:
```
import gensim

# Load pre-trained Word2Vec model
modelWord2Vec = gensim.models.KeyedVectors.load_word2vec_format('../utils/PubMed-and-PMC-w2v.bin', binary=True)
vocab_size = len(modelWord2Vec.wv.vocab)

print('Loaded the word vectors!')
print('Total number of words:', vocab_size)
print('Most common words:', modelWord2Vec.wv.index2word[0], modelWord2Vec.wv.index2word[1], modelWord2Vec.wv.index2word[2])
print('Least common words:', modelWord2Vec.wv.index2word[vocab_size-1], modelWord2Vec.wv.index2word[vocab_size-2], modelWord2Vec.wv.index2word[vocab_size-3])
```

```
Loaded the word vectors!
Total number of words: 4087446
Most common words: </s> the ,
Least common words: Fl-NC(11-55) MAA-mediated balsalazide-treated
```

```
/home/sxd24/anaconda3/lib/python3.6/site-packages/ipykernel_launcher.py:5: DeprecationWarning: Call to deprecated `wv` (Attribute will be removed in 4.0.0, use self instead).
  """
/home/sxd24/anaconda3/lib/python3.6/site-packages/ipykernel_launcher.py:9: DeprecationWarning: Call to deprecated `wv` (Attribute will be removed in 4.0.0, use self instead).
  if __name__ == '__main__':
/home/sxd24/anaconda3/lib/python3.6/site-packages/ipykernel_launcher.py:10: DeprecationWarning: Call to deprecated `wv` (Attribute will be removed in 4.0.0, use self instead).
  # Remove the CWD from sys.path while we load stuff.
```

***Demonstration - Word Embedding***

Let us demonstrate the word embedding by searching our word list for a word like "malignancy" and then access its corresponding vector through the embedding matrix and find out the terms which are close by.

In [4]:
```
print('Most similar word to \"malignancy\":')
print(modelWord2Vec.most_similar(positive="malignancy", topn=3))
```

```
Most similar word to "malignancy":
[('neoplasm', 0.7846177816390991), ('neoplasms', 0.7320481538772583), ('malignancies', 0.7179752588272095)]
```

**Vectorize our Vocabulary**

Set maximum size of the Vocabulary: In an ideal scenario, we would like to use the entire list of words. But due to limited memory availability we'll limit our vocabulary

In [5]:
```
maxVocab = 100000
wordsList = list(modelWord2Vec.vocab.keys())[:maxVocab]
```

Create an array to hold the vector representation of all our vocabulary

*Note: In case a given word is not present in our vocabulary, assign a random value*

In [6]:
```
wordVectors = np.zeros((maxVocab, modelWord2Vec.vector_size), dtype='float32')
idx = 0
for word in wordsList:
    if word in modelWord2Vec:
        wordVectors[idx] = modelWord2Vec[word]
    else:
        wordVectors[idx] = np.random.uniform(low=-1, high=1, size=(200, ))
    idx = idx+1
```

# Import a "test record"

Import a test record to test the functions until the main dataset is loaded. Being a single record, it'll also save time & memory during the sanity checks

In [7]:
```
with open("../data/medline_abstracts/medline_27253005.txt") as handle:
    testRecord = Medline.read(handle)
    print("PubMed ID:", testRecord['PMID'])
    print("Title of the article:", testRecord['TI'])
    print("Abstract:", testRecord['AB'])
```

```
PubMed ID: 27253005
Title of the article: Childhood Vascular Tumors Treatment (PDQ(R)): Patient V
ersion
Abstract: This PDQ cancer information summary has current information about t
he treatment of childhood vascular tumors. It is meant to inform and help pat
ients, families, and caregivers. It does not give formal guidelines or recomm
endations for making decisions about health care. Editorial Boards write the
PDQ cancer information summaries and keep them up to date. These Boards are m
ade up of experts in cancer treatment and other specialties related to cance
r. The summaries are reviewed regularly and changes are made when there is ne
w information. The date on each summary ("Date Last Modified") is the date of
the most recent change. The information in this patient summary was taken fro
m the health professional version, which is reviewed regularly and updated as
needed, by the PDQ Pediatric Treatment Editorial Board.
```

# Define Utility Functions & Values

Define the functions and set the values which will be used throughout the script

#### Import packages required for data cleansing

In [8]:
```
import re
import nltk

nltk.download('stopwords')
nltk.download('punkt')
nltk.download('wordnet')

from nltk.corpus import stopwords
from nltk.util import ngrams
from nltk.tokenize import word_tokenize
from nltk.stem.wordnet import WordNetLemmatizer
from string import punctuation
```

```
[nltk_data] Downloading package stopwords to /home/sxd24/nltk_data...
[nltk_data]   Package stopwords is already up-to-date!
[nltk_data] Downloading package punkt to /home/sxd24/nltk_data...
[nltk_data]   Package punkt is already up-to-date!
[nltk_data] Downloading package wordnet to /home/sxd24/nltk_data...
[nltk_data]   Package wordnet is already up-to-date!
```

#### Define the Disease Category List

Define a list with the category of diseases which we're trying to classify

In [9]:
```
categoryList = defaultdict(list)
categoryLabel = ["hemic-and-lymphatic-diseases", "immune-system-diseases", "mu
sculoskeletal-diseases", "neoplasms", "other"]
```

### fnGetLabels - Function to return an array corresponding to a label

Define a function which will convert a given category of disease into a corresponding encoded array

In [10]:
```
def fnGetLabels(recIdx):
    encodedLabel = np.zeros(len(categoryLabel), dtype='int32')
    idx = 0
    rec = whitelistedArticles[recIdx]
    for label in categoryLabel:
        if rec['diseaseCategory'] in label:
            encodedLabel[idx] = 1
        else:
            encodedLabel[idx] = 0
        idx = idx + 1
    return encodedLabel
```

### Define text cleansing categories

Define and set values for the text cleansing categories

In [11]:
```
blacklistStopWords = ['over', 'only', 'very', 'not', 'no']
additionalStopWords = ['background', 'objective']
customStopWords = set(stopwords.words('english') + additionalStopWords) - set(
blacklistStopWords)

print("Custom StopWords:\n", customStopWords)

greekLetters = [
    (r'α', 'alpha'),
    (r'β', 'beta'),
    (r'γ', 'gamma'),
    (r'δ', 'delta')
]

negContractions = [
    (r'aren\'t', 'are not'),
    (r'can\'t', 'can not'),
    (r'couldn\'t', 'could not'),
    (r'daren\'t', 'dare not'),
    (r'didn\'t', 'did not'),
    (r'doesn\'t', 'does not'),
    (r'don\'t', 'do not'),
    (r'isn\'t', 'is not'),
    (r'hasn\'t', 'has not'),
    (r'haven\'t', 'have not'),
    (r'hadn\'t', 'had not'),
    (r'mayn\'t', 'may not'),
    (r'mightn\'t', 'might not'),
    (r'mustn\'t', 'must not'),
    (r'needn\'t', 'need not'),
    (r'oughtn\'t', 'ought not'),
    (r'shan\'t', 'shall not'),
    (r'shouldn\'t', 'should not'),
    (r'wasn\'t', 'was not'),
    (r'weren\'t', 'were not'),
    (r'won\'t', 'will not'),
    (r'wouldn\'t', 'would not'),
    (r'ain\'t', 'am not')
]

otherContractions = {
    "'m": 'am',
    "'ll": 'will',
    "'s": 'has',
    "'d": 'had'
}

stripSpecialChars = re.compile("[^A-Za-z0-9]+")
stripNA = re.compile("^ NA$")
lmtzr = WordNetLemmatizer()
```

```
Custom StopWords:
 {'been', 'to', 'than', 'd', 'from', 'ma', 'why', 'then', 'again', "you'll",
"won't", 'such', 'those', 'o', "couldn't", 'myself', 'same', 'being', 'when',
'have', 'a', 'won', 'they', 'as', 'background', 'y', 'all', 'most', 'so', "ha
ven't", 'll', "you've", 'of', "weren't", "shan't", 'by', "should've", 'aren',
'wasn', 'with', 'were', 'ourselves', 'herself', "hasn't", 'couldn', 'i', 'jus
t', "shouldn't", 'mightn', 'my', 'few', 'each', 'haven', "aren't", 'where',
'on', 'isn', 'own', 'or', 'out', 'don', 'do', 'be', "that'll", 'that', 'now',
'weren', 'her', 'mustn', 'these', 'during', 'some', 've', 'them', 'its', 'the
mselves', 'she', 'shan', "you'd", 'the', 'while', 'yourselves', 're', 'm', 'h
adn', 'if', 'this', 'objective', "you're", "isn't", 'into', 'himself', 'an',
's', 'hasn', 'your', 'did', 'doesn', 'above', 'is', 'doing', 'was', 'more',
'what', 'under', 'too', 'but', 'whom', 'once', 'about', 't', 'his', 'in', 'it
self', 'here', 'yours', 'ours', 'it', 'me', 'for', 'after', 'yourself', 'he',
'had', 'can', "didn't", 'down', 'their', 'you', "wasn't", 'will', 'which', 'a
re', 'through', 'who', "don't", 'we', 'having', 'how', 'at', 'wouldn', "might
n't", 'until', 'between', 'before', 'hers', 'needn', 'our', 'further', "need
n't", 'am', 'has', "mustn't", "it's", "doesn't", 'because', 'against', 'belo
w', 'does', 'theirs', "she's", 'any', 'other', 'shouldn', "hadn't", 'didn',
'him', 'and', 'both', 'should', 'off', "wouldn't", 'up', 'nor', 'ain', 'ther
e'}
```

### Define max word length

Even though we'd like to use the entire abstract for prediction, due to hardware limitations we'll set the max word we'll consider per abstract. Similarly, for each sentence we'll set the max word length as 30 words.

In [12]:
```
maxFVWordLength = 300
maxSentenceWordLength = 30
```

### fnCleanSentence - Function to cleanse the input text

Define a function to clean a given sentence

In [13]:
```
def fnCleanSentence(text):
    text = re.sub(stripNA, "", text)
    text = text.replace("<br />", " ")
    return text
```

### fnComputeNGrams - Function to pre-process a given text

Define a function to process a given text, like transformation, stemming, removing stop-words, etc.

In [14]:
```
def fnComputeNGrams(text, n, removeStopwords=True, stemWords=True):
    text = text.strip()
    text = text.lower()
    text = re.sub(r"[^A-Za-z0-9^,!.\/'+-=]", " ", text)
    sents = nltk.sent_tokenize(text)
    allTokens = []

    for doc in sents:

        #--- Transform Negative Contractions ---#
        for t in negContractions:
            doc = re.sub(t[0], t[1], doc)

        #--- Transform Greek symbols ---#
        for t in greekLetters:
            doc = re.sub(t[0], t[1], doc)

        #--- Convert to lower case ---#
        doc = doc.lower()

        #--- Tokenize the words ---#
        tokens = word_tokenize(doc)

        #--- If removal of stop words is requested, do the needful ---#
        if removeStopwords:
            #--- Transform other contractions ---#
            tokens = [otherContractions[token] if otherContractions.get(toke
n) else token for token in tokens]

            #--- Remove punctuations ---#
            r = r'[a-zA-Z]+'
            tokens = [word for word in tokens if re.search(r, word)]

            #--- Remove irrelevant stopwords ---#
            tokens = [token for token in tokens if token not in customStopWo
rds]

        #--- If stemmer is requested, perform stemming ---#
        if stemWords:
            #--- Lemmatize ---#
            tokens = [lmtzr.lemmatize(token) for token in tokens]

        allTokens.extend(tokens)

    #--- If n = 1, then return the list of words (as if n=1, then n-grams =
 tokens), else compute n-grams ---#
    if n == 1:
        return allTokens
    else:
        return ngrams(allTokens, n)
```

Check the data cleansing functions (as defined above) with a test record

In [15]:
```
print("Original Text:\n", testRecord['AB'])
print("\nCleaned Text:\n", fnCleanSentence(testRecord['AB']))
print("\nn-Gram computed from Text:\n", fnComputeNGrams(testRecord['AB'], 1, True, True))
```

```
Original Text:
 This PDQ cancer information summary has current information about the treatm
ent of childhood vascular tumors. It is meant to inform and help patients, fa
milies, and caregivers. It does not give formal guidelines or recommendations
for making decisions about health care. Editorial Boards write the PDQ cancer
information summaries and keep them up to date. These Boards are made up of e
xperts in cancer treatment and other specialties related to cancer. The summa
ries are reviewed regularly and changes are made when there is new informatio
n. The date on each summary ("Date Last Modified") is the date of the most re
cent change. The information in this patient summary was taken from the healt
h professional version, which is reviewed regularly and updated as needed, by
the PDQ Pediatric Treatment Editorial Board.

Cleaned Text:
 This PDQ cancer information summary has current information about the treatm
ent of childhood vascular tumors. It is meant to inform and help patients, fa
milies, and caregivers. It does not give formal guidelines or recommendations
for making decisions about health care. Editorial Boards write the PDQ cancer
information summaries and keep them up to date. These Boards are made up of e
xperts in cancer treatment and other specialties related to cancer. The summa
ries are reviewed regularly and changes are made when there is new informatio
n. The date on each summary ("Date Last Modified") is the date of the most re
cent change. The information in this patient summary was taken from the healt
h professional version, which is reviewed regularly and updated as needed, by
the PDQ Pediatric Treatment Editorial Board.

n-Gram computed from Text:
 ['pdq', 'cancer', 'information', 'summary', 'current', 'information', 'treat
ment', 'childhood', 'vascular', 'tumor', 'meant', 'inform', 'help', 'patien
t', 'family', 'caregiver', 'not', 'give', 'formal', 'guideline', 'recommendat
ion', 'making', 'decision', 'health', 'care', 'editorial', 'board', 'write',
'pdq', 'cancer', 'information', 'summary', 'keep', 'date', 'board', 'made',
'expert', 'cancer', 'treatment', 'specialty', 'related', 'cancer', 'summary',
'reviewed', 'regularly', 'change', 'made', 'new', 'information', 'date', 'sum
mary', 'date', 'last', 'modified', 'date', 'recent', 'change', 'information',
'patient', 'summary', 'taken', 'health', 'professional', 'version', 'reviewe
d', 'regularly', 'updated', 'needed', 'pdq', 'pediatric', 'treatment', 'edito
rial', 'board']
```

**fnGetArray - Function to convert a text into numerical array**

Define a function to convert a text into numerical array for feeding it into the LSTM model

In [16]:
```
def fnGetArray(articleRec):

    #--- Define the empty array ---#
    equivArray = np.zeros((maxFVWordLength), dtype='int32')

    idxCnt = 0
    print("Abstracts:", articleRec['AB'])
    cleanedAbstract = fnCleanSentence(articleRec['AB'])
    split = fnComputeNGrams(cleanedAbstract, 1, True, True)
    for word in split:
        if idxCnt >= maxFVWordLength:
            break
        try:
            equivArray[idxCnt] = wordsList.index(word)
        except ValueError:
            equivArray[idxCnt] = maxVocab - 1 #conflate all unknown words to t
his one
        idxCnt = idxCnt + 1
    return equivArray
```

Check the function fnGetArray to check if the conversion of text to numeric array is working

In [17]:
```
print("Original Text:\n", testRecord['AB'])
print("\nCorresponding Array:\n", fnGetArray(testRecord))
```

```
Original Text:
 This PDQ cancer information summary has current information about the treatm
ent of childhood vascular tumors. It is meant to inform and help patients, fa
milies, and caregivers. It does not give formal guidelines or recommendations
for making decisions about health care. Editorial Boards write the PDQ cancer
information summaries and keep them up to date. These Boards are made up of e
xperts in cancer treatment and other specialties related to cancer. The summa
ries are reviewed regularly and changes are made when there is new informatio
n. The date on each summary ("Date Last Modified") is the date of the most re
cent change. The information in this patient summary was taken from the healt
h professional version, which is reviewed regularly and updated as needed, by
the PDQ Pediatric Treatment Editorial Board.
Abstracts: This PDQ cancer information summary has current information about
the treatment of childhood vascular tumors. It is meant to inform and help pa
tients, families, and caregivers. It does not give formal guidelines or recom
mendations for making decisions about health care. Editorial Boards write the
PDQ cancer information summaries and keep them up to date. These Boards are m
ade up of experts in cancer treatment and other specialties related to cance
r. The summaries are reviewed regularly and changes are made when there is ne
w information. The date on each summary ("Date Last Modified") is the date of
the most recent change. The information in this patient summary was taken fro
m the health professional version, which is reviewed regularly and updated as
needed, by the PDQ Pediatric Treatment Editorial Board.

Corresponding Array:
 [99999   120   248  2450   382   248    58  2033   667   209 11781  7003
  1142   145   405  9904    29  1978  5248  6885  7805  1768  2012   166
   207 17560  7153 14280 99999   120   248  2450  5839  1747  7153   490
  5186   120    58  8617   241   120  2450  1173  6165   316   490   183
   248  1747  2450  1747  1030  1015  1747   555   316   248   145  2450
   862   166  2929  1621  1173  6165  7165   905 99999  2071    58 17560
  7153     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0]
```

### Set the disease categories

Set the disease categories

In [18]:
```
diseaseCategories = []

diseaseCategoryRec = {'diseaseType': 'hemic-and-lymphatic-diseases', 'fileNa
me': '../data/medline_abstracts/hemic-and-lymphatic-diseases.medline.txt'}
diseaseCategories.append(diseaseCategoryRec)

diseaseCategoryRec = {'diseaseType': 'immune-system-diseases', 'fileName':
'../data/medline_abstracts/immune-system-diseases.medline.txt'}
diseaseCategories.append(diseaseCategoryRec)

diseaseCategoryRec = {'diseaseType': 'musculoskeletal-diseases', 'fileName':
 '../data/medline_abstracts/musculoskeletal-diseases.medline.txt'}
diseaseCategories.append(diseaseCategoryRec)

diseaseCategoryRec = {'diseaseType': 'neoplasms', 'fileName': '../data/medli
ne_abstracts/neoplasms.medline.txt'}
diseaseCategories.append(diseaseCategoryRec)

diseaseCategoryRec = {'diseaseType': 'other', 'fileName': '../data/medline_a
bstracts/none-of-the-above.medline.txt'}
diseaseCategories.append(diseaseCategoryRec)

print("diseaseCategories:\n", diseaseCategories)
```

```
diseaseCategories:
 [{'diseaseType': 'hemic-and-lymphatic-diseases', 'fileName': '../data/medlin
e_abstracts/hemic-and-lymphatic-diseases.medline.txt'}, {'diseaseType': 'immu
ne-system-diseases', 'fileName': '../data/medline_abstracts/immune-system-dis
eases.medline.txt'}, {'diseaseType': 'musculoskeletal-diseases', 'fileName':
'../data/medline_abstracts/musculoskeletal-diseases.medline.txt'}, {'diseaseT
ype': 'neoplasms', 'fileName': '../data/medline_abstracts/neoplasms.medline.t
xt'}, {'diseaseType': 'other', 'fileName': '../data/medline_abstracts/none-of
-the-above.medline.txt'}]
```

# Load and Prepare the Data

#### Define the datasets for holding the data

In [19]:
```
quarantineArticles = []
whitelistedArticles = []
```

#### Load the MEDLINE data (MEDLINE format)

Set the baseline for minumum number of words in each abstract for the abstract to be qualified for processing. If it does not meet the criteria, discard the article

In [20]:
```
minAbstractLength = 25

for medlineCategory in diseaseCategories:
    print("\nCategory:", medlineCategory['diseaseType'])
    print("File Name:", medlineCategory['fileName'])

    numQuarantinedRec = 0
    numWhitelistedRec = 0

    with open(medlineCategory['fileName'], "r", encoding='utf-8') as f:
        recArticle = Medline.parse(f)
        for rec in recArticle:
            lenAbstract = len(rec['AB'])
            lenFeatureVector = len(rec['TI']) + len(rec['AB'])
            articleRec = {'PMID': rec['PMID'], 'diseaseCategory': medlineCateg
ory['diseaseType'], 'FV': rec['TI']+rec['AB'], 'numWords': lenFeatureVector}
            if lenAbstract < minAbstractLength:
                quarantineArticles.append(articleRec)
                numQuarantinedRec = numQuarantinedRec + 1
            else:
                whitelistedArticles.append(articleRec)
                numWhitelistedRec = numWhitelistedRec + 1

    print("For category,", medlineCategory['diseaseType'], "number of discarde
d articles = ", numQuarantinedRec)
    print("For category,", medlineCategory['diseaseType'], "number of white-li
sted articles = ", numWhitelistedRec)

#--- Print the final numbers ---#
print("\nFor categories, total number of discarded articles = ", len(quarantin
eArticles))
print("For all categories, total number of white-listed articles = ", len(whit
elistedArticles))
```

```
Category: hemic-and-lymphatic-diseases
File Name: ../data/medline_abstracts/hemic-and-lymphatic-diseases.medline.txt
For category, hemic-and-lymphatic-diseases number of discarded articles =  1
For category, hemic-and-lymphatic-diseases number of white-listed articles =
12242

Category: immune-system-diseases
File Name: ../data/medline_abstracts/immune-system-diseases.medline.txt
For category, immune-system-diseases number of discarded articles =  2
For category, immune-system-diseases number of white-listed articles =  23963

Category: musculoskeletal-diseases
File Name: ../data/medline_abstracts/musculoskeletal-diseases.medline.txt
For category, musculoskeletal-diseases number of discarded articles =  4
For category, musculoskeletal-diseases number of white-listed articles =  179
23

Category: neoplasms
File Name: ../data/medline_abstracts/neoplasms.medline.txt
For category, neoplasms number of discarded articles =  7
For category, neoplasms number of white-listed articles =  30559

Category: other
File Name: ../data/medline_abstracts/none-of-the-above.medline.txt
For category, other number of discarded articles =  2
For category, other number of white-listed articles =  12247

For categories, total number of discarded articles =  16
For all categories, total number of white-listed articles =  96934
```

Check the discarded records for assurity

In [21]:
```
print ("Discarded records:\n")
for rec in quarantineArticles:
    print(rec['PMID'], rec['numWords'], rec['diseaseCategory'], rec['FV'])
```

```
Discarded records:

29033247 113 hemic-and-lymphatic-diseases Progressive reticulate skin pigment
ation and anonychia in a patient with bone marrow failure.KEY TEACHING POINT
S.
28536734 102 immune-system-diseases Livedo Reticularis on the Lower Limbs in
a Patient with Lupus Erythematosus: A Quiz.is missing (Quiz).
28251232 87 immune-system-diseases Oral diseases associated with fixed prosth
odontic restorations.[No Abstract Available].
29076861 103 musculoskeletal-diseases Nondrug Interventions Reduce Pain and O
pioid Use After Total Knee Arthroplasty.According to this study.
29033247 113 musculoskeletal-diseases Progressive reticulate skin pigmentatio
n and anonychia in a patient with bone marrow failure.KEY TEACHING POINTS.
28440364 91 musculoskeletal-diseases Diagnosis of an actively bleeding rectus
sheath hematoma by Contrast- Enhanced ultrasound..
28440363 97 musculoskeletal-diseases Ultrasound Imaging for Posterior Knee Pa
in: Tibial Nerve Schwannoma Not Popliteus Muscle Strain..
29076862 106 neoplasms Similar Mortality Rates After Surgery or Observation o
f Localized Prostate Cancer.According to this study.
28686217 93 neoplasms Meta-Analysis on Dietary Patterns and Pancreatic Cancer
Risk: Methodological Limitations.n/a.
28686193 88 neoplasms Reply to Alizadeh's Letter to the Editor Re: Lu, P.Y. e
t al., Nutrients 2017, 9, 38.n/a.
28629197 243 neoplasms Reply to the Letter to the Editor by C. Nicolazzo et a
l.: "Circulating Cell-Free DNA and Circulating Tumor Cells as Prognostic and
Predictive Biomarkers in Advanced Non-Small Cell Lung Cancer Patients Treated
with First-Line Chemotherapy".n/a.
28629196 207 neoplasms Letter to the Editor: "Circulating Cell-Free DNA and C
irculating Tumor Cells as Prognostic and Predictive Biomarkers in Advanced No
n-Small Cell Lung Cancer Patients Treated with First-Line Chemotherapy".n/a.
28578450 150 neoplasms Serologic evidence of Toxoplasma gondii infection amon
g cancer patients. A prospective study from Qassim region, Saudi Arabia.[No A
bstract Available].
28561877 79 neoplasms Subcutaneous Nodule on the Right Palm of a Young Boy: A
Quiz.is missing (Quiz).
28000494 42 other Twiddler's syndrome.No abstract available.
27444081 88 other Early-onset stroke, polyarteritis nodosa (PAN), and livedo
racemosa.KEY TEACHING POINTS.
```

**Shuffle the data to achieve randomness**

Shuffle the "whitelist" dataset multiple times so that we get a random order and records are not ordered by disease

In [22]:
```
np.random.shuffle(whitelistedArticles)
np.random.shuffle(whitelistedArticles)
```

***Persist the data for reloadability***

Save the data onto disk as numpy arrays for easier reloads

In [23]:
```
np.save('../data/medline_abstracts/npQuarantineArticles_CloselyAssociatedDisea
ses', quarantineArticles)
np.save('../data/medline_abstracts/npWhiteListArticles_CloselyAssociatedDiseas
es', whitelistedArticles)
```

**Data Profiling**

Perform data profiling and also re-confirm the validity of the hypothesis made before

In [24]:
```
numQuarantined = len(quarantineArticles)
numWhiteListArticles = len(whitelistedArticles)

print("Number of articles discarded due to smaller than threshold abstracts
 =", numQuarantined)
print("Number of articles that will be processed =", numWhiteListArticles)
```

```
Number of articles discarded due to smaller than threshold abstracts = 16
Number of articles that will be processed = 96934
```

**Calculate the Metrices**

Calculate the following metrices:

- Number of words per abstract
- Number of sentences per abstract
- Number of words per sentence per abstract

In [25]:
```
wordCntPerSentence = []
wordCntPerFV = []
sentenceCntPerFV = []

print("Convert whitelistedArticles into dataframe")
dfWhiteListArticles = pd.DataFrame(whitelistedArticles, columns=['PMID', 'dise
aseCategory', 'FV', 'numWords'])
print(dfWhiteListArticles.head(5))

for fv in dfWhiteListArticles['FV']:
    words = fv.split(' ')
    wordCntPerFV.append(len(words))

    sentences = fv.split('.')
    sentenceCntPerFV.append(len(sentences))

    for sentence in sentences:
        words = sentence.split(' ')
        wordCntPerSentence.append(len(words))
```

```
Convert whitelistedArticles into dataframe
       PMID           diseaseCategory  \
0  28363295  musculoskeletal-diseases
1  28188909  musculoskeletal-diseases
2  28636109  musculoskeletal-diseases
3  28704329                neoplasms
4  28813639                neoplasms

                                                FV  numWords
0  Biological Principles of Scar and Contracture....       700
1  Extensive preclinical evaluation of an inflixi...      1255
2  Xq26.1-26.3 duplication including MOSPD1 and G...      1316
3  Long-Term Oncological Outcome After Convention...      1996
4  Exploitation of Gene Expression and Cancer Bio...      1794
```

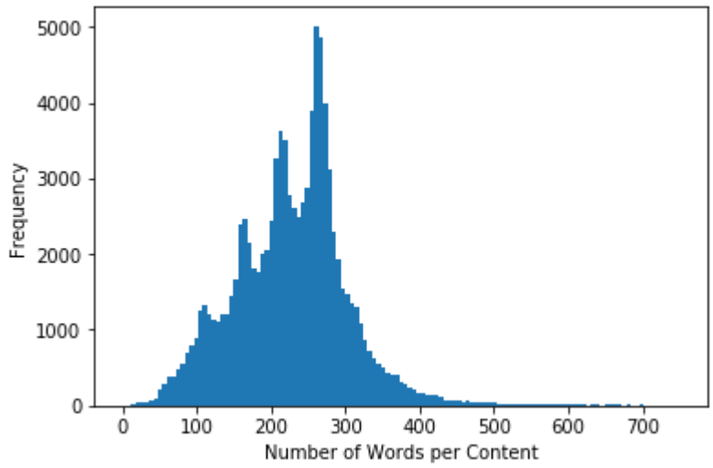
Print the number of words per content for 50 articles to eyeball the count

In [26]:
```
print(wordCntPerFV[1:50])
```

```
[160, 186, 271, 257, 214, 93, 272, 118, 180, 240, 51, 90, 165, 110, 369, 200,
148, 171, 284, 404, 132, 164, 159, 221, 218, 266, 278, 150, 224, 299, 266, 21
0, 164, 166, 268, 238, 392, 390, 711, 239, 331, 281, 139, 268, 184, 167, 98,
144, 165]
```

Plot the data to visualize the distribution of words by content

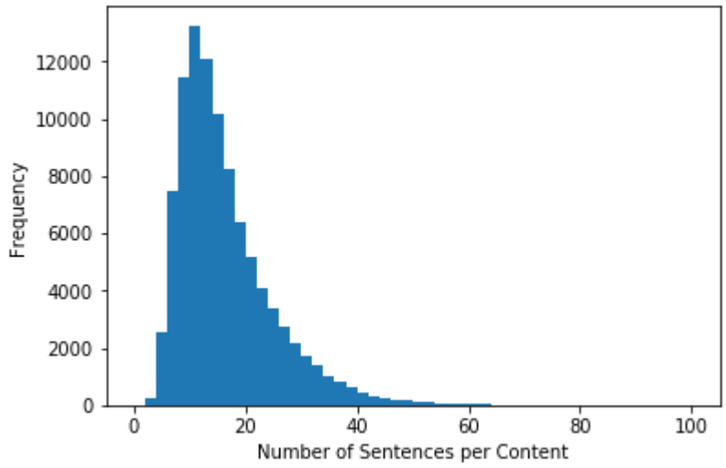
In [27]:
```
%matplotlib inline
plt.hist(wordCntPerFV, bins=125, range=(0, 750))
plt.xlabel('Number of Words per Content')
plt.ylabel('Frequency')
plt.show()

print("Median of the number of words per content =", np.median(wordCntPerFV))
```




```
Median of the number of words per content = 231.0
```

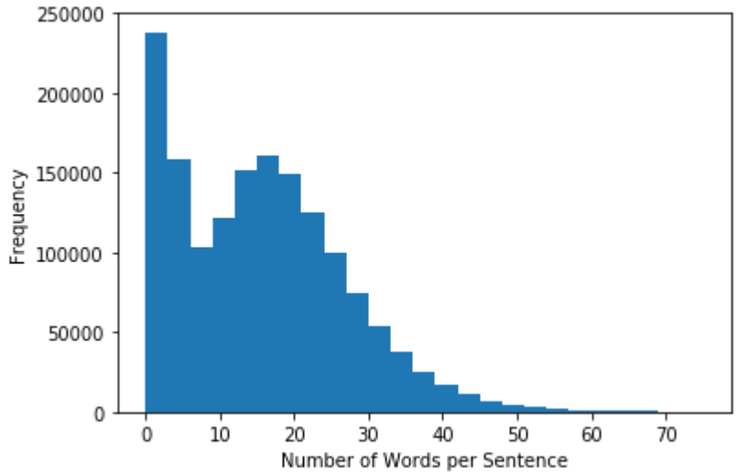
Based on the above histogram we can say that our hypothesis of setting the maxFVWordLength to the value we've chosen earlier holds good!

In [28]:
```
%matplotlib inline
plt.hist(sentenceCntPerFV, bins=50, range=(0, 100))
plt.xlabel('Number of Sentences per Content')
plt.ylabel('Frequency')
plt.show()

print("Median of the number of sentences per content =", np.median(sentenceCnt
PerFV))
```




```
Median of the number of sentences per content = 14.0
```

In [29]:
```
%matplotlib inline
plt.hist(wordCntPerSentence, bins=25, range=(0, 75))
plt.xlabel('Number of Words per Sentence')
plt.ylabel('Frequency')
plt.show()

print("Median of the number of words per sentences =", np.median(wordCntPerSen
tence))
```




```
Median of the number of words per sentences = 15.0
```

Based on the above histogram we can say that our hypothesis of setting the maxSentenceWordLength to the value we've chosen earlier holds good!

In [30]:
```
print("Total number of articles =", numWhiteListArticles)
print("Median of the number of sentences per content =", np.median(sentenceCnt
PerFV))
print("Median of the number of words per content =", np.median(wordCntPerFV))
print("Median of the number of words per sentences of articles =", np.median(w
ordCntPerSentence))
```

```
Total number of articles = 96934
Median of the number of sentences per content = 14.0
Median of the number of words per content = 231.0
Median of the number of words per sentences of articles = 15.0
```

**Vectorize the data - Encode all the Labels & Content**

Convert all articles into categorized labels and all the contents into vectors

In [31]:
```
print("Starting data encoding @", datetime.datetime.now().strftime("%Y-%m-%d
 %H:%M:%S"))

#--- Shuffle the dataset for one last time before encoding ---#
np.random.shuffle(whitelistedArticles)

articleIdx = 0
articleToID = {}
encodedLabels = np.zeros((numWhiteListArticles, len(categoryLabel)), dtype=
'int32')
encodedFV = np.zeros((numWhiteListArticles, maxFVWordLength), dtype='int32')

articleToIDChkPoint = "../data/medline_abstracts/checkpoints/articleToID.che
ckpoint-"
encodedLabelChkPoint = "../data/medline_abstracts/checkpoints/encodedLabel.c
heckpoint-"
encodedFVChkPoint = "../data/medline_abstracts/checkpoints/encodedFV.checkpo
int-"

#--- Loop through all white-listed articles in the dataset and convert them
 into vector ---#
for articleRec in whitelistedArticles:

    #--- Convert the articles into IDs ---#
    articlePMID = articleRec['PMID']
    articleToID[articlePMID] = articleIdx

    #--- Encode the labels ---#
    encodedLabels[articleIdx] = fnGetLabels(articleIdx)

    #--- Encode the feature vectors ---#
    wordCounter = 0
    cleanedFV = fnCleanSentence(articleRec['FV'])
    split = fnComputeNGrams(cleanedFV, 1, True, True)

    for word in split:
        try:
            encodedFV[articleIdx][wordCounter] = wordsList.index(word)
        except:
            #--- Assign all unknown words to the maximum value possible ---#
            encodedFV[articleIdx][wordCounter] = maxVocab - 1
        #--- Increment the wordCounter ---#
        wordCounter = wordCounter + 1
        if wordCounter >= maxFVWordLength:
            break

    #--- Increment the articleIdx ---#
    articleIdx = articleIdx + 1

    #--- Checkpoint ---#
    if articleIdx % 10000 == 0:
        numChkPoint = int(articleIdx / 10000)
        print("\nCheckpoint", numChkPoint, "@", datetime.datetime.now().strf
time("%Y-%m-%d %H:%M:%S"), "::", articleIdx, "articles processed")
        np.save(articleToIDChkPoint+str(numChkPoint), articleToID)
        np.save(encodedLabelChkPoint+str(numChkPoint), encodedLabels)
        np.save(encodedFVChkPoint+str(numChkPoint), encodedFV)

#--- Persist the final encoded dataset ---#
np.save('../data/medline_abstracts/articleToID', articleToID)
np.save('../data/medline_abstracts/encodedLabels', encodedLabels)
np.save('../data/medline_abstracts/encodedFV', encodedFV)

print("Completed data encoding @", datetime.datetime.now().strftime("%Y-%m-%
d %H:%M:%S"))
```

```
Starting data encoding @ 2018-04-08 20:34:14

Checkpoint 1 @ 2018-04-08 20:40:41 :: 10000 articles processed

Checkpoint 2 @ 2018-04-08 20:47:14 :: 20000 articles processed

Checkpoint 3 @ 2018-04-08 20:53:45 :: 30000 articles processed

Checkpoint 4 @ 2018-04-08 21:00:12 :: 40000 articles processed

Checkpoint 5 @ 2018-04-08 21:06:43 :: 50000 articles processed

Checkpoint 6 @ 2018-04-08 21:13:12 :: 60000 articles processed

Checkpoint 7 @ 2018-04-08 21:19:39 :: 70000 articles processed

Checkpoint 8 @ 2018-04-08 21:25:50 :: 80000 articles processed

Checkpoint 9 @ 2018-04-08 21:32:08 :: 90000 articles processed
Completed data encoding @ 2018-04-08 21:36:26
```

***Remove the checkpoint files***

In [32]:
```
os.system('rm -f ../data/medline_abstracts/checkpoints/*.checkpoint-*.npy')
```

Out[32]:
```
0
```

Eye ball the encoding, as done above

In [33]:
```
print("articleToID for PMID = 29538200\n", articleToID['29538200'])
print("Disease Label for PMID = 29538200\n", encodedLabels[articleToID['29538200']])
print("Encoded Abstract for PMID = 29538200\n", encodedFV[articleToID['29538200']])
```

```
articleToID for PMID = 29538200
 41012
Disease Label for PMID = 29538200
 [1 0 0 0 0]
Encoded Abstract for PMID = 29538200
 [99999  7314  1010   516   429   603  4104  5125   925   195   327   414
 99999 50722   424  2467  1010    87   677 61403 16363  1680   709   566
  1065  1400 15560   505   331  6484   505  6756   314   505 10691   505
  3097  4279  9315    48   416 27016  1906   287 99999  7314   145  3062
   327   195 29136  2075  1026 14671  9604  4824   263   145  1656   429
   603  4104  5125   925   566 99999   111  4086   959  1812 14688  2140
 29141  1207  1123   404  3749 17698 99999  7172  4347   203 99999  7314
   740   333  1418  7114  1410   303 99999  1242    93   236 12393 17481
    48   522   145  3526   133  9262 24048 28179  2467  1010    87   532
 73066   429   566  1065 61403   759 99999  7314  4109   947  1553    89
   456   253   454    58    87   599   745    37   905  7466   641  7188
  3075  1038  1881    93   182   172  1063 12426    92 99999  7314   807
   145   522     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0]
```

#### fnLoadData - Function to split the dataset and make it ready for LSTM

Develop a function which will take the dataset and split it and return a LSTM ready dataset

In [34]:
```
def fnLoadData(splitRatio):
    print("Starting the data wrangling @", datetime.datetime.now().strftime("%
Y-%m-%d %H:%M:%S"))

    numTestSet = int(numWhiteListArticles*splitRatio)
    numTrainingSet = numWhiteListArticles - numTestSet
    print("Size of Test Set =", numTestSet)
    print("Size of Training Set =", numTrainingSet)

    x_train = encodedFV[0:numTrainingSet, ]
    y_train = encodedLabels[0:numTrainingSet, ]

    x_test = encodedFV[numTrainingSet:numWhiteListArticles, ]
    y_test = encodedLabels[numTrainingSet:numWhiteListArticles, ]

    return (x_train, y_train), (x_test, y_test)
```

# Create Training and Validation Datasets

#### Split the dataset into training & test data

Split the entire dataset into training data and test data. As of now, we'll keep 80% of the data for training and 20% for testing

In [35]:
```
(x_train, y_train), (x_test, y_test) = fnLoadData(0.2)
```

```
Starting the data wrangling @ 2018-04-08 21:38:41
Size of Test Set = 19386
Size of Training Set = 77548
```

Check the dimensions of the training and test data sets

In [36]:
```
[x_train.shape, y_train.shape, x_test.shape, y_test.shape]
```

Out[36]:
```
[(77548, 300), (77548, 5), (19386, 300), (19386, 5)]
```

# ANN Architecture: Fully Connected Deep Learning Neural Network

#### Load Dependencies

Load the packages that will be required

In [37]:
```
import keras
from keras import regularizers
from keras.models import Sequential
from keras.layers import Dense, Flatten, Dropout, Embedding
from keras.layers.normalization import BatchNormalization
from keras.optimizers import adam
```

```
/home/sxd24/anaconda3/lib/python3.6/site-packages/h5py/__init__.py:36: Future
Warning: Conversion of the second argument of issubdtype from `float` to `np.
floating` is deprecated. In future, it will be treated as `np.float64 == np.d
type(float).type`.
  from ._conv import register_converters as _register_converters
Using TensorFlow backend.
```

### Set the hyper parameters

Set the hyper-parameters which will be used in subsequent model generation

In [38]:
```
#--- Training ---#
epochs = 10
batch_size = 128

#--- Vector-Space Embedding ---#
n_dim = modelWord2Vec.vector_size
n_unique_words = maxVocab
# n_words_to_skip = 5
max_review_length = maxFVWordLength

#--- Dense Layer Architecture ---#
n_dense = 128
dropout_ratio = 0.35

#--- Print the hyper-parameters which are set from other variables ---#
print("n_dim =", n_dim)
print("n_unique_words =", n_unique_words)
print("max_review_length =", max_review_length)
```

```
n_dim = 200
n_unique_words = 100000
max_review_length = 300
```

### Design the ANN architecture

In [39]:
```
modelFCDL = Sequential()
modelFCDL.add(Embedding(n_unique_words, n_dim, input_length=max_review_length
))
# model.add(LSTM(units=200, activation='softsign'))
modelFCDL.add(Dense(n_dense, activation='relu', input_dim=n_dim))
modelFCDL.add(Dropout(dropout_ratio))
modelFCDL.add(Dense(n_dense, activation='relu'))
modelFCDL.add(Dropout(dropout_ratio))
modelFCDL.add(Dense(n_dense, activation='relu'))
modelFCDL.add(Dropout(dropout_ratio))
modelFCDL.add(Dense(n_dense, activation='relu'))
modelFCDL.add(Dropout(dropout_ratio))
modelFCDL.add(Dense(n_dense, activation='relu'))
modelFCDL.add(Dropout(dropout_ratio))
modelFCDL.add(Dense(n_dense, activation='relu'))
modelFCDL.add(Flatten())
modelFCDL.add(Dense(5, activation='sigmoid')) # mathematically equivalent to s
oftmax with 5 classes

#--- Display the architecture of the generated model ---#
modelFCDL.summary()
```

```
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
embedding_1 (Embedding)      (None, 300, 200)          20000000
_________________________________________________________________
dense_1 (Dense)              (None, 300, 128)          25728
_________________________________________________________________
dropout_1 (Dropout)          (None, 300, 128)          0
_________________________________________________________________
dense_2 (Dense)              (None, 300, 128)          16512
_________________________________________________________________
dropout_2 (Dropout)          (None, 300, 128)          0
_________________________________________________________________
dense_3 (Dense)              (None, 300, 128)          16512
_________________________________________________________________
dropout_3 (Dropout)          (None, 300, 128)          0
_________________________________________________________________
dense_4 (Dense)              (None, 300, 128)          16512
_________________________________________________________________
dropout_4 (Dropout)          (None, 300, 128)          0
_________________________________________________________________
dense_5 (Dense)              (None, 300, 128)          16512
_________________________________________________________________
dropout_5 (Dropout)          (None, 300, 128)          0
_________________________________________________________________
dense_6 (Dense)              (None, 300, 128)          16512
_________________________________________________________________
flatten_1 (Flatten)          (None, 38400)             0
_________________________________________________________________
dense_7 (Dense)              (None, 5)                 192005
=================================================================
Total params: 20,300,293
Trainable params: 20,300,293
Non-trainable params: 0
_________________________________________________________________
```

### Configure Model

In [40]:
```
modelFCDL.compile(loss='categorical_crossentropy', optimizer='adam', metrics=[
'accuracy'])
# tensorboard = keras.callbacks.TensorBoard(log_dir="../logs", write_graph=Tru
e, write_images=True, histogram_freq=1)
```

### Train the Model

In [41]:
```
print("Starting the model training @", datetime.datetime.now().strftime("%Y-%m-%d %H:%M:%S"), "...")
modelFCDL.fit(x_train, y_train,
          batch_size=batch_size,
          epochs=epochs,
          verbose=1,
          validation_data=(x_test, y_test),
          shuffle=False)
print("Completed the model training @", datetime.datetime.now().strftime("%Y-%m-%d %H:%M:%S"))
```

```
Starting the model training @ 2018-04-08 21:39:19 ...
Train on 77548 samples, validate on 19386 samples
Epoch 1/10
77548/77548 [==============================] - 554s 7ms/step - loss: 1.1746 - acc: 0.5178 - val_loss: 1.0632 - val_acc: 0.5880
Epoch 2/10
77548/77548 [==============================] - 553s 7ms/step - loss: 0.8528 - acc: 0.6674 - val_loss: 0.9168 - val_acc: 0.6479
Epoch 3/10
77548/77548 [==============================] - 553s 7ms/step - loss: 0.7423 - acc: 0.7111 - val_loss: 0.8397 - val_acc: 0.6934
Epoch 4/10
77548/77548 [==============================] - 550s 7ms/step - loss: 0.6301 - acc: 0.7535 - val_loss: 0.7581 - val_acc: 0.7193
Epoch 5/10
77548/77548 [==============================] - 551s 7ms/step - loss: 0.5692 - acc: 0.7687 - val_loss: 0.7634 - val_acc: 0.7284
Epoch 6/10
77548/77548 [==============================] - 553s 7ms/step - loss: 0.5328 - acc: 0.7780 - val_loss: 0.7759 - val_acc: 0.7266
Epoch 7/10
77548/77548 [==============================] - 554s 7ms/step - loss: 0.5133 - acc: 0.7801 - val_loss: 0.8014 - val_acc: 0.7265
Epoch 8/10
77548/77548 [==============================] - 550s 7ms/step - loss: 0.4942 - acc: 0.7849 - val_loss: 0.7866 - val_acc: 0.7271
Epoch 9/10
77548/77548 [==============================] - 552s 7ms/step - loss: 0.4774 - acc: 0.7888 - val_loss: 0.8272 - val_acc: 0.7182
Epoch 10/10
77548/77548 [==============================] - 557s 7ms/step - loss: 0.4626 - acc: 0.7895 - val_loss: 0.8288 - val_acc: 0.7202
Completed the model training @ 2018-04-08 23:11:26
```

# Extra Code - Do not execute, but for reuse

## ANN Architecture - Multi-ConvNet Deep Learning Neural Network

In [ ]:
```
import keras
from keras import regularizers
from keras.models import Model
from keras.layers import Dense, Dropout, Embedding, Input, concatenate, SpatialDropout1D, Conv1D, GlobalMaxPooling1D
from keras.layers.normalization import BatchNormalization
from keras.optimizers import adam
```

#### Set the hyper parameters

Set the hyper-parameters which will be used in subsequent model generation

In [ ]:
```
#--- Training ---#
epochs = 6
batch_size = 128

#--- Vector-Space Embedding ---#
n_dim = modelWord2Vec.vector_size
n_unique_words = maxVocab
# n_words_to_skip = 5
max_review_length = maxFVWordLength
dropout_ratio_embed = 0.2

#--- Convolutional Layer Architecture:
n_conv_1 = n_conv_2 = n_conv_3 = 128
k_conv_1 = 3
k_conv_2 = 2
k_conv_3 = 4

#--- Dense Layer Architecture ---#
n_dense = 128
dropout_ratio = 0.4

#--- Print the hyper-parameters which are set from other variables ---#
print("n_dim =", n_dim)
print("n_unique_words =", n_unique_words)
print("max_review_length =", max_review_length)
```

**Design the ConvNet Architecture**

ANN architecture with ConvNets

In [ ]:
```
input_layer = Input(shape=(max_review_length,), dtype='int16', name='input') #
 supports integers +/- 32.7k
embedding_layer = Embedding(n_unique_words, n_dim, input_length=max_review_len
gth, name='embedding')(input_layer)
drop_embed_layer = SpatialDropout1D(dropout_ratio_embed, name='drop_embed')(em
bedding_layer)

conv_1 = Conv1D(n_conv_1, k_conv_1, activation='relu', name='conv_1')(drop_emb
ed_layer)
maxp_1 = GlobalMaxPooling1D(name='maxp_1')(conv_1)

conv_2 = Conv1D(n_conv_2, k_conv_2, activation='relu', name='conv_2')(drop_emb
ed_layer)
maxp_2 = GlobalMaxPooling1D(name='maxp_2')(conv_2)

conv_3 = Conv1D(n_conv_3, k_conv_3, activation='relu', name='conv_3')(drop_emb
ed_layer)
maxp_3 = GlobalMaxPooling1D(name='maxp_3')(conv_3)

concat = concatenate([maxp_1, maxp_2, maxp_3])

dense_layer = Dense(n_dense, activation='relu', name='dense')(concat)
drop_dense_layer = Dropout(dropout_ratio, name='drop_dense_01')(dense_layer)
dense_2 = Dense(128, activation='relu', name='dense_2')(drop_dense_layer)
dropout_2 = Dropout(dropout_ratio, name='drop_dense_2')(dense_2)

predictions = Dense(5, activation='sigmoid', name='output')(dropout_2)

modelCNN = Model(input_layer, predictions)

#--- Display the architecture of the generated model ---#
modelCNN.summary()
```

**Configure Model**

In [ ]:
```
modelCNN.compile(loss='categorical_crossentropy', optimizer='adam', metrics=[
'accuracy'])
# tensorboard = keras.callbacks.TensorBoard(log_dir="../logs", write_graph=Tru
e, write_images=True, histogram_freq=1)
```

**Train the Model**

In [ ]:
```
print("Starting the model training @", datetime.datetime.now().strftime("%Y-%m
-%d %H:%M:%S"), "...")
modelCNN.fit(x_train, y_train,
          batch_size=batch_size,
          epochs=epochs,
          verbose=1,
          validation_data=(x_test, y_test),
          shuffle=False)
print("Completed the model training @", datetime.datetime.now().strftime("%Y-%
m-%d %H:%M:%S"))
```

In [ ]:
```
import psutil
psutil.virtual_memory()
```

In [ ]:
```
#--- Create model checkpoint ---#
modelOutputDir = '../model-output/ann'
modelcheckpoint = ModelCheckpoint(filepath=output_dir+"/weights.{epoch:02d}.hd
f5")
if not os.path.exists(output_dir):
    os.makedirs(output_dir)
```

Check the function fnGetLabels() with some test data

In [ ]:
```
print("Encoded label for article with index = 0:\n", fnGetLabels(32000))
```

***Load the data if datasets are empty***

Load data from the *.npy if the datasets are empty

In [ ]:
```
if len(quarantineArticles) == 0:
    print("quarantineArticles is empty! Reloading the data from quarantineArti
cles.npy ...")
    QuarantineArticles = np.load('../data/medline_abstracts/npQuarantineArticl
es.npy')
else:
    print("quarantineArticles already contain data!")

if len(whitelistedArticles) == 0:
    print("whitelistedArticles is empty! Reloading the data from whitelistedAr
ticles.npy ...")
    whitelistedArticles = np.load('../data/medline_abstracts/npWhiteListArticl
es.npy')
else:
    print("whitelistedArticles already contain data!")
```

In [ ]:
```
print(whitelistedArticles)
```