Preprocess Required for Generating Train Data

```
import urllib.request
import time
import sys
import getopt
import pandas as pd
import numpy as np
import pickle

%run ../utils.ipynb

embSize = 200
ftrain='../data/SNP_train_data.txt'
ftest = "../data/SNP_test_data.txt"
# Replace with path of word embdding file
wefile = "../support/PubMed-and-PMC-w2v.bin"
random_seed=1331
```

Read Train Data

```
samples= pd.read_csv(ftrain,sep='\t')
Tr_sent_contents, Tr_entity1_list, Tr_entity2_list, Tr_sent_lables,_ = dataRead_snp(ftrain)
Tr_word_list, Tr_d1_list, Tr_d2_list = get_wordList_and_distances_snp(Tr_sent_contents)
print ("train_size", len(Tr_word_list))

Input File Reading
    train_size 935
```

Read Test Data

```
Te_sent_contents, Te_entity1_list, Te_entity2_list, Te_sent_lables,_ = dataRead_snp(ftest)
Te_word_list, Te_d1_list, Te_d2_list = get_wordList_and_distances_snp(Te_sent_contents)
print ("test_size", len(Te_word_list))

    Input File Reading
    test_size 365
```

Prepare Lable Matrix

Generate Word and Position Embedding Vectors

Word Embedding

```
sent_list = sum([Tr_word_list, Te_word_list], [])
word_dict, word_to_id, id_to_word = word_mapping(sent_list)
print( "word dictonary length", len(word_dict))
# Word Embedding
word_vectors = readWordEmb(word_dict,id_to_word,word_to_id, wefile, embSize,limit=2000000)
W_train = mapWordToId(Tr_word_list, word_to_id)
Found 2775 unique words (45627 in total)
     word dictonary length 2775
     Reading word vectors
     Loaded 2000000 pretrained embeddings.
     number of unknown word in word embedding 475
W_test = mapWordToId(Te_word_list, word_to_id)
   Position Embedding
d1_dict = makeDistanceList([Tr_d1_list, Te_d1_list])
d2_dict = makeDistanceList([Tr_d2_list, Te_d2_list])
d1_train = mapWordToId_list(Tr_d1_list, d1_dict)
d2_train = mapWordToId_list(Tr_d2_list, d2_dict)
d1_test = mapWordToId_list(Te_d1_list, d1_dict)
d2_test = mapWordToId_list(Te_d2_list, d2_dict)
  Pad Embdding Vectors
train_sent_lengths, test_sent_lengths = findSentLengths([Tr_word_list, Te_word_list])
sentMax = max(train_sent_lengths + test_sent_lengths)
#padding
W_train, d1_train, d2_train = paddData([W_train, d1_train, d2_train], sentMax)
type (W_test)
→ list
#padding
W_test, d1_test, d2_test = paddData([W_test, d1_test, d2_test ], sentMax)
type (W_test)
→ numpy.ndarray
```

Save Training data as a Pickle file

```
#with open('train_and_test_data_sentences_snp_2classWiki.pickle', 'wb') as handle:
with open('../data/pickles/train_and_test_data_sentences_snp_2class.pickle', 'wb') as handle:
    pickle.dump(W_train, handle)
    pickle.dump(d1_train, handle)
    pickle.dump(d2_train, handle)
    pickle.dump(Y_train, handle)
    pickle.dump(Tr_word_list, handle)
```

```
pickle.dump(W_test, handle)
pickle.dump(d1_test, handle)
pickle.dump(d2_test, handle)
pickle.dump(Y_test, handle)
pickle.dump(Te_word_list, handle)
pickle.dump(word_vectors, handle)
pickle.dump(word_dict, handle)
pickle.dump(d1_dict, handle)
pickle.dump(d2_dict, handle)
pickle.dump(label_dict, handle)
pickle.dump(sentMax, handle)
```

test data statistics

```
disease_list=np.array(Te_entity2_list)
disease_list=disease_list[:,0]
len(np.unique(disease_list))
labels=np.array(Te_sent_lables)
len(np.unique(disease_list[labels[:]=='negative']))
len(np.unique(disease_list[labels[:]=='neutral']))
len(np.unique(disease_list[labels[:]=='positive']))
gene_list=np.array(Te_entity1_list)
gene_list=gene_list[:,0]
len(np.unique(gene_list))
len(np.unique(gene_list[labels[:]=='negative']))
len(np.unique(gene_list[labels[:]=='neutral']))
len(np.unique(gene list[labels[:]=='positive']))
len(labels[labels[:]=='negative'])
len(labels[labels[:]=='positive'])
len(labels[labels[:]=='neutral'])
→ 166
```

train data statistics

```
disease_list=np.array(Tr_entity2_list)
disease_list=disease_list[:,0]
len(np.unique(disease_list))
labels=np.array(Tr_sent_lables)
len(np.unique(disease_list[labels[:]=='negative']))
len(np.unique(disease_list[labels[:]=='neutral']))
len(np.unique(disease_list[labels[:]=='positive']))
gene_list=np.array(Tr_entity1_list)
gene_list=gene_list[:,0]
len(np.unique(gene_list))
len(np.unique(gene list[labels[:]=='negative']))
len(np.unique(gene_list[labels[:]=='neutral']))
len(np.unique(gene_list[labels[:]=='positive']))
len(labels[labels[:]=='negative'])
len(labels[labels[:]=='positive'])
len(labels[labels[:]=='neutral'])
→▼ 142
Start coding or generate with AI.
Start coding or generate with AI.
```