pre_process

September 18, 2024

1 Preprocess Required for Generating Train Data

```
[1]: import urllib.request
   import time
   import sys
   import getopt
   import numpy as np
   import numpy as np
   import pickle

[2]: %run ../utils.ipynb

[24]: 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
```

2 Read Train Data

Input File Reading
train_size 935

3 Read Test Data

```
[19]: Te_sent_contents, Te_entity1_list, Te_entity2_list, Te_sent_lables,_ =_u 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

3.1 Prepare Lable Matrix

4 Generate Word and Position Embedding Vectors

4.0.1 Word Embedding

```
[25]: 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,u_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

[26]: W_test = mapWordToId(Te_word_list, word_to_id)
```

4.0.2 Position Embedding

```
[27]: 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)
[28]: d1_test = mapWordToId_list(Te_d1_list, d1_dict)
      d2_test = mapWordToId_list(Te_d2_list, d2_dict)
     4.0.3 Pad Embdding Vectors
[29]: 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)
[30]: type (W_test)
[30]: list
[31]: #padding
      W_test, d1_test, d2_test = paddData([W_test, d1_test, d2_test], sentMax)
```

[32]: type (W_test)

[32]: numpy.ndarray

5 Save Training data as a Pickle file

```
[33]: #with open('train_and_test_data_sentences_snp_2classWiki.pickle', 'wb') as⊔

shandle:

with open('.../data/pickles/train_and_test_data_sentences_snp_2class.pickle', u)

s'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(d1_test, handle)

pickle.dump(d2_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)
```

6 test data statistics

```
[34]: 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'])
```

[34]: 166

7 train data statistics

```
[35]: 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'])

[35]: 142
[]:
```