Tutorial_Toy_Example

January 25, 2019

In [1]: import os

```
import pandas as pd
        from MulticoreTSNE import MulticoreTSNE as TSNE
        %pylab inline
Populating the interactive namespace from numpy and matplotlib
In [2]: !mkdir -p sandbox #let's put all stuff in the sandbox
        os.chdir("sandbox")
0.0.1 Download a toy dataset which is describled in
"Detection of low-abundance bacterial strains in metagenomic datasets by eigengenome partitionin
Nature biotechnology 33.10 (2015): 1053.
In [3]: if not os.path.exists('lsaTestData.tar.gz'):
            !wget https://github.com/brian-cleary/LatentStrainAnalysis/raw/master/testData.tar.g
--2019-01-24 20:18:43-- https://github.com/brian-cleary/LatentStrainAnalysis/raw/master/testDat
Resolving github.com (github.com)... 192.30.253.112, 192.30.253.113
Connecting to github.com (github.com) | 192.30.253.112 | :443... connected.
HTTP request sent, awaiting response... 302 Found
Location: https://raw.githubusercontent.com/brian-cleary/LatentStrainAnalysis/master/testData.ta
--2019-01-24 20:18:43-- https://raw.githubusercontent.com/brian-cleary/LatentStrainAnalysis/mas
Resolving raw.githubusercontent.com (raw.githubusercontent.com)... 151.101.48.133
Connecting to raw.githubusercontent.com (raw.githubusercontent.com)|151.101.48.133|:443... connecting to raw.githubusercontent.com
HTTP request sent, awaiting response... 200 OK
Length: 17790844 (17M) [application/octet-stream]
Saving to: lsaTestData.tar.gz
lsaTestData.tar.gz 100%[==========] 16.97M 5.37MB/s
2019-01-24 20:18:47 (5.00 MB/s) - lsaTestData.tar.gz saved [17790844/17790844]
In [5]: !tar xf lsaTestData.tar.gz > /dev/null 2>&1
        !cat original_reads/SRR*.fastq > data.fastq
```

0.0.2 convert fastq file to a seq file

```
In [6]: !python ../../scripts/fastseq/fastqToSeq.py -i data.fastq -o data.seq
```

0.0.3 encode reads

```
In [3]: !python ../../scripts/fastseq/hashSeq.py -i data.seq --hash lsh -o data.hash -k 15
2019-01-24 20:21:47,114 - hashSeq - INFO - start converting...
2019-01-24 20:21:47,114 - hashSeq - INFO - parameters: {'out_file': 'data.hash', 'f': <function
2019-01-24 20:21:47,114 - hashSeq - INFO - creating hash ...
100%|| 660/660 [00:01<00:00, 407.13it/s]
2019-01-24 20:21:48,778 - hashSeq - INFO - finish creating hash ...
100%|| 100000/100000 [01:29<00:00, 1120.10it/s]
2019-01-24 20:23:23,446 - hashSeq - INFO - written 100000 lines
100%|| 100000/100000 [01:34<00:00, 1057.42it/s]
2019-01-24 20:25:03,310 - hashSeq - INFO - written 200000 lines
100%|| 374/374 [00:00<00:00, 430.20it/s]
2019-01-24 20:25:04,314 - hashSeq - INFO - written 200374 lines
2019-01-24 20:25:04,314 - hashSeq - INFO - finish converting...</pre>
```

0.0.4 train a model

```
In [4]: !../../fastseq skipgram -input data.hash -output model
```

```
Read 16M words
Number of words: 417165
Number of labels: 0
```

Progress: 100.0% words/sec/thread: 36280 lr: 0.000000 loss: 1.594164 ETA: 0h 0m% words/sec

0.0.5 Now the model is trained. To visualize it, first get vectors of reads

```
In [11]: def read_embedding(fname):
    with open(fname) as fin:
        lines=list(fin)
    assert len(lines)>1
    first_line=lines[0]
    num_word, dim_vec = [int(u) for u in first_line.split(" ")]
    assert len(lines)==num_word+1
    ret ={}
    for line in lines[1:]:
        lst = line.strip().split(" ")
        assert len(lst)==dim_vec+1, line
        if lst[0]=='</s>': continue
        word = int(lst[0])
        vec = np.array([float(u) for u in lst[1:]])
        ret[word]=vec
```

```
return ret,dim_vec
         embedding,dim_vec = read_embedding("model.vec")
         sequectors = []
         with open("data.hash") as fin:
             lines = list(fin)
         for i, line in enumerate(lines):
             words = [int(u) for u in line.strip().split(" ")]
             vec = [embedding[u] for u in words if u in embedding]
             sequectors.append(np.mean(vec,0) if len(vec)>0 else None) #np.zeros([dim_vec], dtype=
             #if i>10: break
0.0.6 Next get the labels
In [16]: seqs = pd.read_csv("data.seq",sep='\t', header=None, usecols=[0,1],index_col=0)
         seqs.columns=['id']
         seqs['is_spike'] = seqs['id'].map(lambda u: u.startswith("Spike"))
         seqs['vec']=seqvectors
         seqs.drop('id',axis=1,inplace=True)
         seqs=seqs[~seqs['vec'].isnull()]
         seqs[seqs['is_spike']].head()
Out[16]:
                is_spike
                                                                         vec
                    True [0.20901083720930236, 0.15879133023255815, -0...
         10001
                    True [-0.13977729186046522, -0.20089517674418603, 0...
         10002
         10003
                    True [0.11275851511627906, -0.12522697674418604, -0...
         10004
                    True [0.2775530279069768, -0.1323303697674418, -0.1...
                    True [0.10739388720930242, -0.0324119953488372, -0...
         10005
0.0.7 Now train TSNE
In [21]: seqs=seqs.sample(10000,replace=False) #to speed up
In [24]: tsne = TSNE(n_components=2, perplexity=100, n_jobs=8)
         X=np.array(list(seqs['vec'].values))
         X.shape
Out [24]: (10000, 100)
In [25]: %time Y = tsne.fit_transform(X)
CPU times: user 3min 39s, sys: 304 ms, total: 3min 39s
Wall time: 60 s
0.0.8 visualization
In [36]: labels=seqs['is_spike'].values
         plt.scatter(Y[labels][:,0],Y[labels][:,1],alpha=1,s=1)
```

```
plt.scatter(Y[~labels][:,0],Y[~labels][:,1],alpha=0.5,s=1)
plt.legend(['spike','non-spike'])
```

Out[36]: <matplotlib.legend.Legend at 0x7f2a8b8b1790>

