

# Python implementation of eigengenes computation

```
In [196]: import warnings
warnings.filterwarnings('ignore')
```

```
In [197]: import pandas as pd
import numpy as np
from sklearn.preprocessing import scale
import scipy.stats as ss
import matplotlib.pyplot as plt
```

```
In [198]: true_values = np.array([-1.0102, -0.9091, -0.8081, 0.8081, 0.9091, 1.0102])
```

```
In [199]: data = pd.read_table('Data/D1_C1.tsv', header=0, index_col=0)
data.head()
```

Out[199]:

	t1	t2	t3	t4	t5	t6
<b>Gene</b>						
<b>g007</b>	-1.1524	-1.1564	-0.0469	0.6112	1.3399	0.4046
<b>g019</b>	-0.6571	-1.2902	-0.2012	0.9135	-0.1780	1.4131
<b>g030</b>	-1.3393	-0.6260	-0.5066	0.2431	1.2010	1.0278
<b>g036</b>	-1.5168	-0.9040	1.0602	0.1920	0.7228	0.4458
<b>g045</b>	-0.4442	-1.1227	-0.8390	1.5532	0.6027	0.2500

Rows should be scaled so that the expression of each gene is centered and the standard deviation is 1:

```
In [200]: scaled_data = scale(data, axis=1)
```

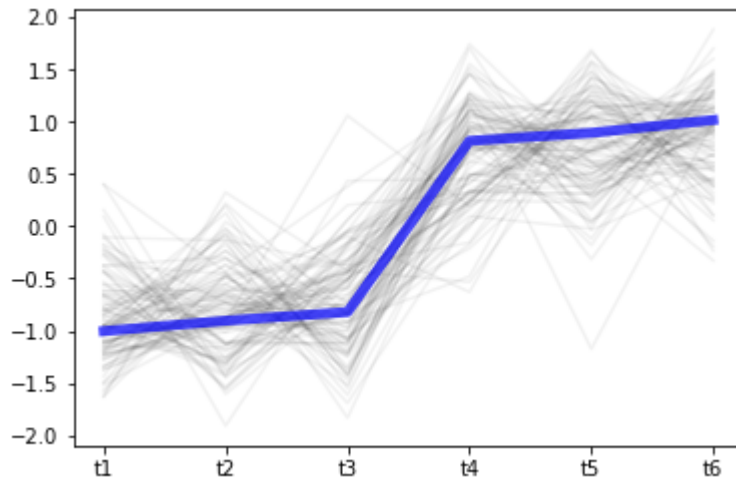
```
In [201]: svd = np.linalg.svd(scaled_data)
eigengenes = -svd[2][0]*(scaled_data.shape[1]-1)**0.5
eigengenes
```

```
Out[201]: array([-1.00365771, -0.90395277, -0.82081109,  0.81724356,  0.8938557 ,
                1.01732232])
```

```
In [202]: np.sum(np.abs(true_values - eigengenes))
```

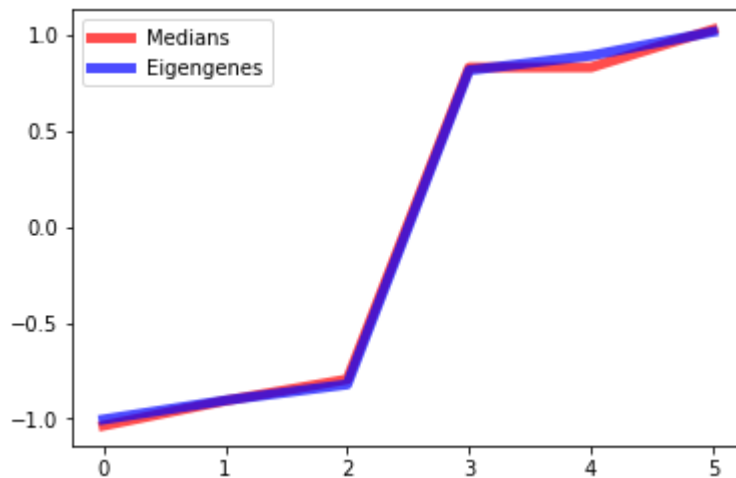
```
Out[202]: 0.055910791294392026
```

```
In [203]: plt.plot(data.transpose(), color='k', alpha=0.05)
plt.plot(eigengenes, lw=5, color='b', alpha=0.7);
```



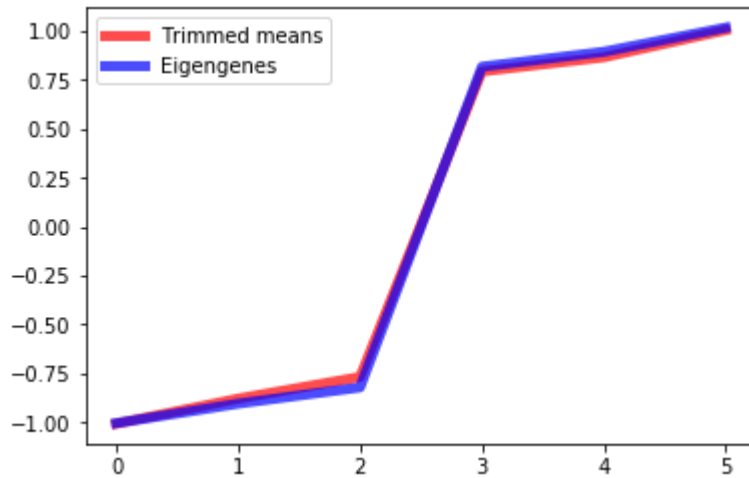
## Eigengenes vs. medians:

```
In [204]: plt.plot(np.median(scaled_data, axis=0), lw=5, color='r', alpha=0.7, label='Medians')
plt.plot(eigengenes, lw=5, color='b', alpha=0.7, label='Eigengenes')
plt.legend();
```



## Eigengenes vs. trimmed means:

```
In [205]: plt.plot(ss.trim_mean(scaled_data, 0.25, axis=0), lw=5, color='r', alp
ha=0.7, label='Trimmed means')
plt.plot(eigengenes, lw=5, color='b', alpha=0.7, label='Eigengenes')
plt.legend();
```



## Eigengenes vs. means:

```
In [206]: plt.plot(np.mean(scaled_data, axis=0), lw=5, color='r', alpha=0.7, lab
el='means')
plt.plot(eigengenes, lw=5, color='b', alpha=0.7, label='Eigengenes')
plt.legend();
```

