Perform Network Analysis

- Create a cinemanet table
- Perform correlation analysis and threshold filter with Research Matrix Theory
- Analyze properties of the network

Questions to answer with alpha and beta diversity analysis:

- How do the will Kate Kate Ben 1 or 2?
- Kate Ben 1 or 2 Kate Ben 1 or 2?
- How does Eli compare to Ali, Ali compare to Mel
- How does Kate compare to Ali

```
import sqlite3 as lite
import pandas as pd
import numpy as np
cnx = lite.connect('movies.db')
```

Import Data

```
df = pd.read_sql_table('movies', cnx)
df.dropna(inplace=True,axis=1,thresh=200)
df.groupby(['actor_1', 'actor_2'])['movieid'].count.sort_values(ascending)
```

```
actor_1  actor_2
Ali      Ali       1.000000
         Ben       0.500000
         Kate      0.333333
Ben      Ben       1.000000
         Kate      0.666667
Kate     Kate      1.000000
Mel      Mel       1.000000
Name: movieid, dtype: float64
```

```
df.pivot(index='actor_1', columns='actor_2', values='movieid')
df.groupby(['actor_1', 'actor_2'])['movieid'].count.unstack()
```

```
actor_2  Ali  Ben  Kate  Mel
actor_1
Ali      1.0  0.5  0.33  NaN
Ben      NaN  1.0  0.67  NaN
Kate     NaN  NaN  1.00  NaN
Mel      NaN  NaN   NaN  1.0
```

```
df.groupby(['actor_1', 'actor_2'])['movieid'].count.unstack().fillna(0)
```

```
actor_2  Ali  Ben  Kate  Mel
actor_1
Ali      1.0  0.5  0.33  0.0
Ben      0.0  1.0  0.67  0.0
Kate     0.0  0.0  1.00  0.0
Mel      0.0  0.0  0.00  1.0
```

```
df.groupby(['actor_1', 'actor_2'])['movieid'].count.unstack().fillna(0).T
```

```
actor_1  Ali  Ben  Kate  Mel
actor_2
Ali      1.0  0.0  0.0   0.0
Ben      0.5  1.0  0.0   0.0
Kate     0.33 0.67 1.00  0.0
Mel      0.0  0.0  0.0   1.0
```

```
df.groupby(['actor_1', 'actor_2'])['movieid'].count.unstack().fillna(0).T.dot(df.groupby(['actor_1', 'actor_2'])['movieid'].count.unstack().fillna(0))
```

```
actor_1  Ali   Ben   Kate  Mel
actor_1
Ali      1.00  0.50  0.33  0.0
Ben      0.50  1.25  0.67  0.0
Kate     0.33  0.67  1.11  0.0
Mel      0.0   0.0   0.0   1.0
```

Split Samples Into Groups

```
group = df.groupby('movieid')['actor_1']
group.head()
```

```
0    Ali
1    Ben
2    Ben
3    Ben
4    Ben
Name: actor_1, dtype: object
```

```
df['actor_1'].dropna(inplace=True)
df['actor_2'].dropna(inplace=True)
df['actor_1'].fillna('Ali',inplace=True)
df['actor_2'].fillna('Ali',inplace=True)
```

```
movieid  actor_1  actor_2  actorfacebooklikes_1  actorfacebooklikes_2  contentrating  director  directorfacebooklikes  duration  gross  id  imdbscore  language  numcritic  numuser  numvoted  plotkeywords  titleyear
0        Ali      Ali      1000                  1000                  PG             NaN       NaN                    NaN       NaN    NaN 7.1        NaN       NaN        NaN      NaN       NaN           NaN
1        Ben      Ben      1000                  1000                  PG             NaN       NaN                    NaN       NaN    NaN 7.1        NaN       NaN        NaN      NaN       NaN           NaN
2        Ben      Ben      1000                  1000                  PG             NaN       NaN                    NaN       NaN    NaN 7.1        NaN       NaN        NaN      NaN       NaN           NaN
3        Ben      Ben      1000                  1000                  PG             NaN       NaN                    NaN       NaN    NaN 7.1        NaN       NaN        NaN      NaN       NaN           NaN
4        Ben      Ben      1000                  1000                  PG             NaN       NaN                    NaN       NaN    NaN 7.1        NaN       NaN        NaN      NaN       NaN           NaN
```

Standardize Data For Correlation Analysis

Standardize relative attendance counts for PTA by subtracting the mean across all samples and dividing by variance across all samples. Use the relative attendance counts to calculate correlation between samples.

Source Timing Trial

```
df.groupby(['actor_1', 'actor_2'])['actorfacebooklikes_1'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['actorfacebooklikes_2'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['contentrating'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['director'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['directorfacebooklikes'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['duration'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['gross'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['id'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['imdbscore'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['language'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['numcritic'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['numuser'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['numvoted'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['plotkeywords'].count.sort_values(ascending)
df.groupby(['actor_1', 'actor_2'])['titleyear'].count.sort_values(ascending)
```

```
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: actorfacebooklikes_1, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: actorfacebooklikes_2, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: contentrating, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: director, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: directorfacebooklikes, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: duration, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: gross, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: id, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: imdbscore, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: language, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: numcritic, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: numuser, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: numvoted, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: plotkeywords, dtype: int64
actor_1  actor_2
Ali      Ali       1000
         Ben       1000
         Kate      1000
Ben      Ben       1000
         Kate      1000
Kate     Kate      1000
Mel      Mel       1000
Name: titleyear, dtype: int64
```

```
df.groupby(['actor_1', 'actor_2'])['actorfacebooklikes_1'].count.unstack
df.groupby(['actor_1', 'actor_2'])['actorfacebooklikes_2'].count.unstack
df.groupby(['actor_1', 'actor_2'])['contentrating'].count.unstack
df.groupby(['actor_1', 'actor_2'])['director'].count.unstack
df.groupby(['actor_1', 'actor_2'])['directorfacebooklikes'].count.unstack
df.groupby(['actor_1', 'actor_2'])['duration'].count.unstack
df.groupby(['actor_1', 'actor_2'])['gross'].count.unstack
df.groupby(['actor_1', 'actor_2'])['id'].count.unstack
df.groupby(['actor_1', 'actor_2'])['imdbscore'].count.unstack
df.groupby(['actor_1', 'actor_2'])['language'].count.unstack
df.groupby(['actor_1', 'actor_2'])['numcritic'].count.unstack
df.groupby(['actor_1', 'actor_2'])['numuser'].count.unstack
df.groupby(['actor_1', 'actor_2'])['numvoted'].count.unstack
df.groupby(['actor_1', 'actor_2'])['plotkeywords'].count.unstack
df.groupby(['actor_1', 'actor_2'])['titleyear'].count.unstack
```

```
<bmethod_DataFrameGroupBy.unstack of                  actorfacebooklikes_1
actor_1 actor_2 actor_3 actor_4 actor_5 actor_6 actor_7 actor_8 actor_9 actor_10 actor_11 actor_12 actor_13 actor_14 actor_15 actor_16 actor_17 actor_18 actor_19 actor_20 actor_21 actor_22 actor_23 actor_24 actor_25 actor_26 actor_27 actor_28 actor_29 actor_30 actor_31 actor_32 actor_33 actor_34 actor_35 actor_36 actor_37 actor_38 actor_39 actor_40
```

Try Circular Layout

```
> for (i in 1:20) {
+   plot.igraph(V(net)[module.colors[[i]]], layout=layout.circle)
+ }
```

Eigengene Analysis

```
> MEs = moduleEigenvalues(datExpr, colors)$eigenvectors
> head(MEs)
  ME1 ME2 ME3 ME4 ME5 ME6 ME7 ME8 ME9 ME10
1 0.0000 0.0000 0.0000 -0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
2 0.0000 0.0000 0.0000 -0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
3 0.0000 0.0000 0.0000 -0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
4 0.0000 0.0000 0.0000 -0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
5 0.0000 0.0000 0.0000 -0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
6 0.0000 0.0000 0.0000 -0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
  ME11 ME12 ME13 ME14 ME15 ME16 ME17 ME18 ME19 ME20
1 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
2 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
3 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
4 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
5 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
6 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
  ME21
1 0.0000
2 0.0000
3 0.0000
4 0.0000
5 0.0000
6 0.0000
> dim(MEs)[1]; dim(MEs)[2]; dim(MEs)[3]; length(MEs[,1])
[1] 20000
[1] 20000
[1] 21
[1] 20000
```

Visualize Eigengenes

Plots and the dendrogram of modules across samples

```
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("1: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("2: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("3: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("4: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("5: Module Eigengenes"))
```

```
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("6: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("7: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("8: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("9: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("10: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("11: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("12: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("13: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("14: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("15: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("16: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("17: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("18: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("19: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("20: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("21: Module Eigengenes"))
```

```
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("22: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("23: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("24: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("25: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("26: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("27: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("28: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("29: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("30: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("31: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("32: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("33: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("34: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("35: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("36: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("37: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("38: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("39: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("40: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("41: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("42: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("43: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("44: Module Eigengenes"))
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> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("47: Module Eigengenes"))
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> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("48: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("49: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("50: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("51: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("52: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("53: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("54: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("55: Module Eigengenes"))
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> sizeGrWindow(8,9); par(cex=0.9)
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> sizeGrWindow(8,9); par(cex=0.9)
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> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("59: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("60: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("61: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("62: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("63: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("64: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("65: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("66: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("67: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("68: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("69: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("70: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("71: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("72: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("73: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("74: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("75: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("76: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("77: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
> plotEigenvalues(MEs,colnames=T,marginal=FALSE,main=paste("78: Module Eigengenes"))
> sizeGrWindow(8,9); par(cex=0.9)
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