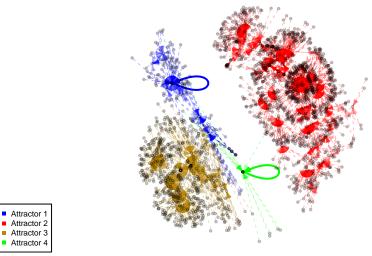
## Analyzing a hematopoietic genetic network

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```
attr <- getAttractors(HSC)
plotStateGraph(attr)</pre>
```



```
print(attr)
```

```
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
##
## Attractor 2 is a simple attractor consisting of 1 state(s) and has a basin of 16 state(s):
##
   |--<----|
##
##
##
   00010000100
##
   V
    |-->----|
##
##
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
  Attractor 3 is a simple attractor consisting of 2 state(s) and has a basin of 1258 state(s):
##
##
    |--<----|
##
   V
   00101111110
##
   11100110111
##
   |-->----|
##
##
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
## Attractor 4 is a simple attractor consisting of 2 state(s) and has a basin of 640 state(s):
##
   |--<----|
##
##
   V
##
   00101110110
##
   11100111111
##
##
##
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
Attractor 4 is the one that is closest to the experimental HSPC expression profile 11101111111 -
111001111111(Attractor 4)
attr <- getAttractors(HSC, type="asynchronous",</pre>
method="random", startStates=500)
print(attr)
## Attractor 1 is a simple attractor consisting of 1 state(s):
   |--<----|
##
##
##
  00010000100
##
   V
   |-->----|
##
##
```

```
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
## Attractor 2 is a simple attractor consisting of 1 state(s):
##
   |--<----|
##
##
  0000000000
##
   V
   |-->----|
##
##
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
## Attractor 3 is a complex/loose attractor consisting of 32 state(s) and 112 transition(s):
## 11101111111 => 11101110111
## 11101111111 => 11100111111
## 11101111111 => 01101111111
## 01101111111 => 01101110111
## 01101111111 => 01100111111
## 10101111111 => 10101110111
## 10101111111 => 10100111111
## 10101111111 => 11101111111
## 00101111111 => 00101110111
## 00101111111 => 00100111111
## 00101111111 => 01101111111
## 00101111111 => 10101111111
## 11100111111 => 11100111110
## 11100111111 => 11100110111
## 11100111111 => 11101111111
## 11100111111 => 10100111111
## 11100111111 => 01100111111
## 01100111111 => 01100111110
## 01100111111 => 01100110111
## 01100111111 => 01101111111
## 01100111111 => 00100111111
## 10100111111 => 10100111110
## 10100111111 => 10100110111
## 10100111111 => 10101111111
## 00100111111 => 00100111110
## 00100111111 => 00100110111
## 00100111111 => 00101111111
## 00100111111 => 10100111111
## 11101110111 => 11101111111
## 11101110111 => 11100110111
## 11101110111 => 01101110111
## 01101110111 => 01101111111
## 01101110111 => 01100110111
## 10101110111 => 10101111111
## 10101110111 => 10100110111
## 10101110111 => 11101110111
## 00101110111 => 00101111111
## 00101110111 => 00100110111
```

```
## 00101110111 => 01101110111
## 00101110111 => 10101110111
## 11100110111 => 11100110110
## 11100110111 => 11100111111
## 11100110111 => 11101110111
## 11100110111 => 10100110111
## 11100110111 => 01100110111
## 01100110111 => 01100110110
## 01100110111 => 01100111111
## 01100110111 => 01101110111
## 01100110111 => 00100110111
## 10100110111 => 10100110110
## 10100110111 => 10100111111
## 10100110111 => 10101110111
## 00100110111 => 00100110110
## 00100110111 => 00100111111
## 00100110111 => 00101110111
## 00100110111 => 10100110111
## 11101111110 => 11101111111
## 11101111110 => 11101110110
## 11101111110 => 11100111110
## 11101111110 => 01101111110
## 01101111110 => 01101111111
## 01101111110 => 01101110110
## 01101111110 => 01100111110
## 10101111110 => 10101111111
## 10101111110 => 10101110110
## 10101111110 => 10100111110
## 10101111110 => 11101111110
## 001011111110 => 00101111111
## 001011111110 => 00101110110
## 00101111110 => 00100111110
## 00101111110 => 01101111110
## 00101111110 => 10101111110
## 11100111110 => 11100110110
## 11100111110 => 11101111110
## 11100111110 => 10100111110
## 11100111110 => 01100111110
## 01100111110 => 01100110110
## 01100111110 => 01101111110
## 01100111110 => 00100111110
## 10100111110 => 10100110110
## 10100111110 => 10101111110
## 00100111110 => 00100110110
## 00100111110 => 00101111110
## 00100111110 => 10100111110
## 11101110110 => 11101110111
## 11101110110 => 11101111110
## 11101110110 => 11100110110
## 11101110110 => 01101110110
## 01101110110 => 01101110111
## 01101110110 => 01101111110
## 01101110110 => 01100110110
## 10101110110 => 10101110111
```

```
## 10101110110 => 11101110110
## 00101110110 => 00101110111
## 00101110110 => 001011111110
## 00101110110 => 00100110110
## 00101110110 => 01101110110
## 00101110110 => 10101110110
## 11100110110 => 11100111110
## 11100110110 => 11101110110
## 11100110110 => 10100110110
## 11100110110 => 01100110110
## 01100110110 => 01100111110
## 01100110110 => 01101110110
## 01100110110 => 00100110110
## 10100110110 => 10100111110
## 10100110110 => 10101110110
## 00100110110 => 00100111110
## 00100110110 => 00101110110
## 00100110110 => 10100110110
##
## Genes are encoded in the following order: Erg Eto2 Fli1 Gata1 Gata2 Hhex Pu1 Runx1 Scl Smad6 Zfpm1
Task 2: Attractor 3 appears to be an assynchronous attractor because it is a complex/loose attractor
Task 3: The average expression per gene for the 12 individual cells is:
Eto2: 0.33
Fli1: 0.25
Gata1: 0.00
Gata2: 0.04
Hhex: 0.50
```

and the avg activity per gene across the 32 states IS : Erg : 0.5

and the avg activity per gene ac Eto2: 0.5 Fli1: 1 Gata1: 0 Gata2: 0.5 Hhex: 1 Pu.1: 1 Runx1: 0.5 Scl: 1 Smad6: 1 Zfpm1: 0.5

Pu.1: 0.33 Runx1: 0.08 Scl: 0.67 Smad6: 0.13 Zfpm1: 0.42

## 10101110110 => 10101111110 ## 10101110110 => 10100110110

We concluded that the avg activities per gene were not similar except for the Gata1.

```
pdf("RBNs.pdf")
for(i in 1:10){  #initiating a loop
net<-generateRandomNKNetwork(n=10, k=i) # generating random networks with n=10 genes and each gene havi
plotNetworkWiring(net, main=i) #Plotting the network with title i</pre>
```

```
attr <- getAttractors(net) # getting the number of attractors and attributing it to the variable attr
plotStateGraph(attr, main=i) #plotting the attractors with i being the title
dev.off("RBNs.pdf") # closes the pdf directly when it opens
## Warning in dev.off("RBNs.pdf"): NAs introduced by coercion
## pdf
##
    3
pdf("Pertubations.pdf")
data(cellcycle)
attr <- getAttractors(cellcycle)</pre>
plotStateGraph(attr, main="Unperturbed network")
for(i in 1:5){
perturbedNet <- perturbNetwork(cellcycle, perturb="functions", method="bitflip")</pre>
attr <- getAttractors(perturbedNet)</pre>
plotStateGraph(attr, main=i)
dev.off("Perturbations.pdf")
## Warning in dev.off("Perturbations.pdf"): NAs introduced by coercion
## pdf
##
    4
```