

Arabidopsis Thaliana Network

Example for GeneNet 1.2.7 (June 2013) or later

This note reproduces the “Arabidopsis thaliana” network example from R. Opgen-Rhein and K. Strimmer. 2007. *From correlation to causation networks: a simple approximate learning algorithm and its application to high-dimensional plant gene expression data*. BMC Syst. Biol. **1**: 37. (<http://dx.doi.org/10.1186/1752-0509-1-37>)

The original source of the data is Smith et al. 2004. *Diurnal changes in the transcriptom encoding enzymes of starch metabolism provide evidence for both transcriptional and posttranscriptional regulation of starch metabolism in Arabidopsis leaves*. Plant Physiol. **136**: 2687-2699.

This example was suggested by Papapit Ingkasuwan, Division of Biotechnology, School of Bioresources and Technology, King Mongkut’s University of Technology Thonburi, Bangkok, Thailand.

Inspect Data

```
library("GeneNet")
```

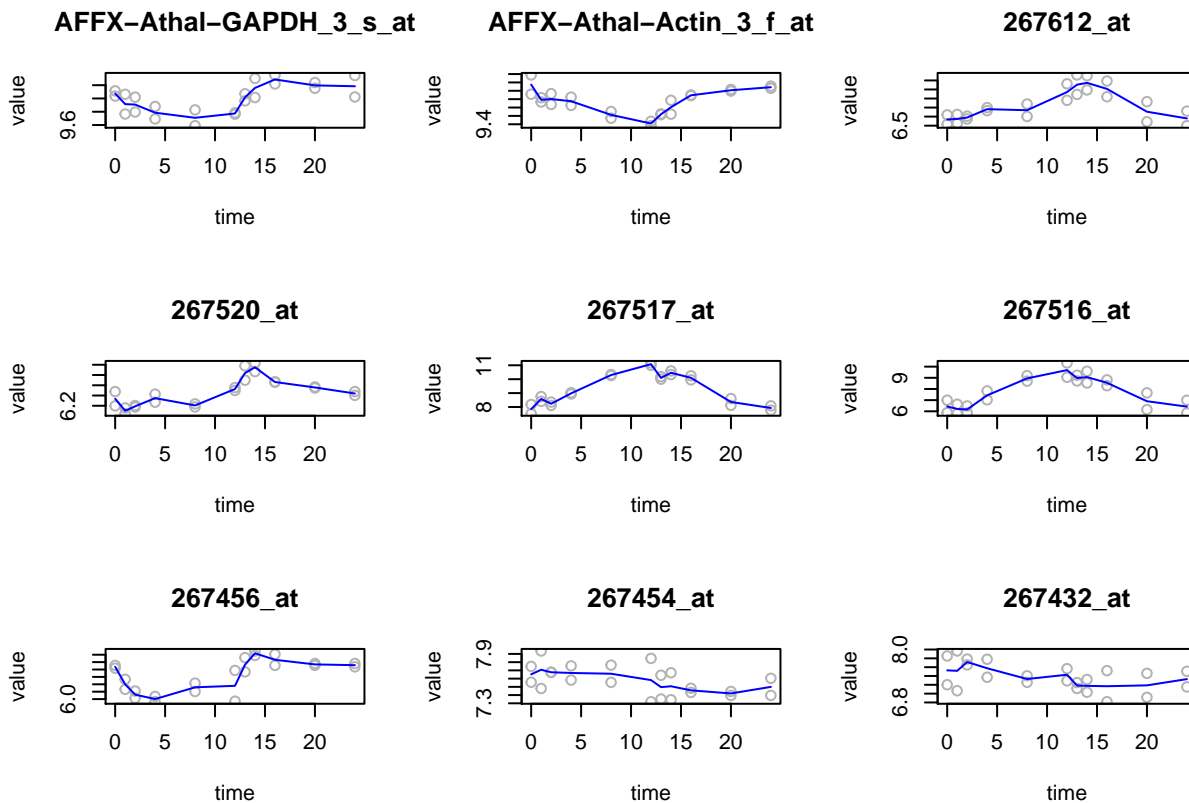
```
## Loading required package: corpcor
## Loading required package: longitudinal
## Loading required package: fdrtool
## Loading required package: igraph
```

```
data("arth800")
summary(arth800.expr)
```

```
## Longitudinal data:
## 800 variables measured at 11 different time points
## Total number of measurements per variable: 22
## Repeated measurements: yes
##
## To obtain the measurement design call 'get.time.repeats()'.
```

Plot time series:

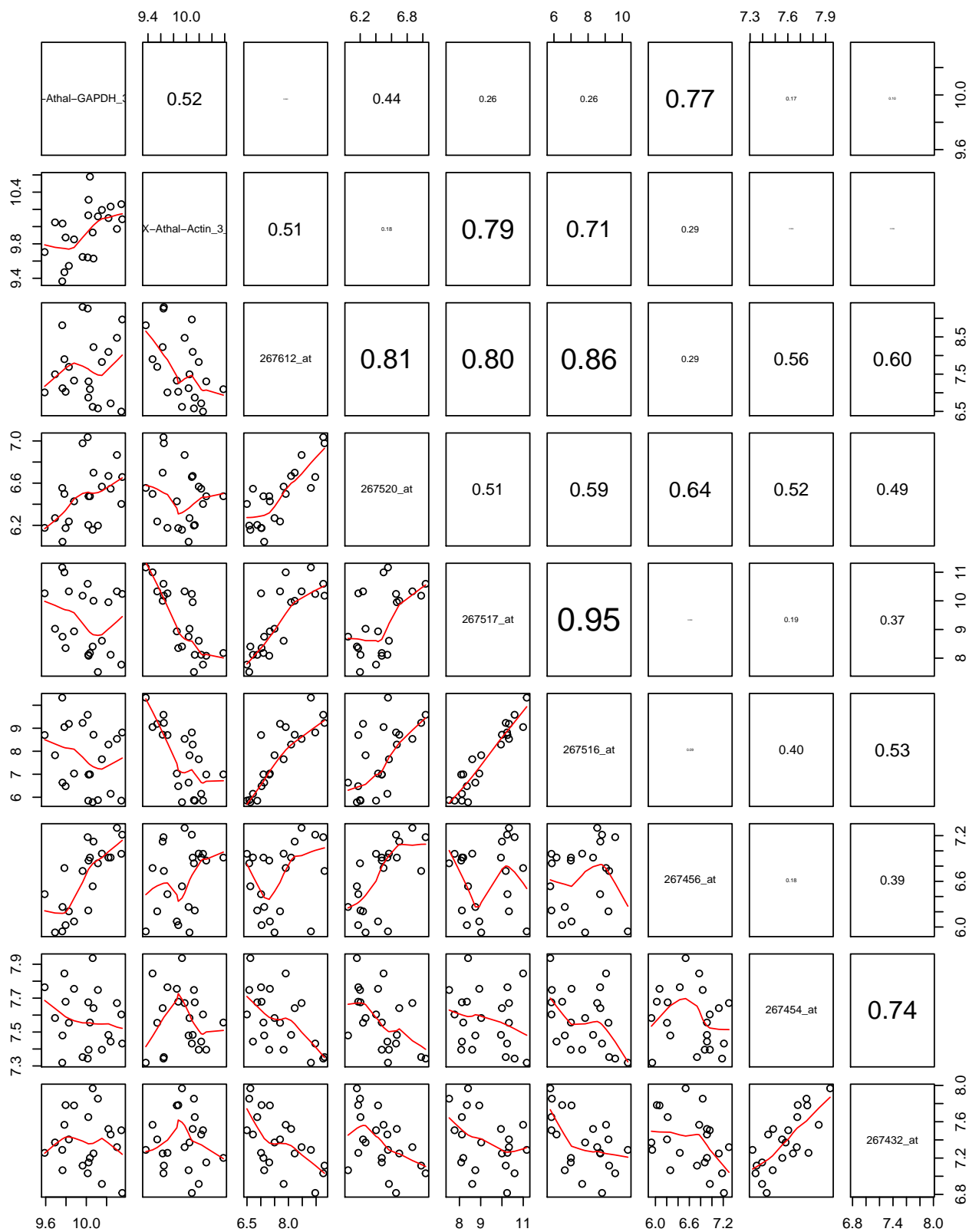
```
plot(arth800.expr, 1:9)
```



Inspect pairwise scatter plots:

```
panel.cor = function(x, y, digits=2, prefix="", cex.cor)
{
  usr = par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r = abs(cor(x, y))
  txt = format(c(r, 0.123456789), digits=digits)[1]
  txt = paste(prefix, txt, sep="")
  if(missing(cex.cor)) cex = 0.8/strwidth(txt)
  text(0.5, 0.5, txt, cex = cex * r)
}
```

```
pairs(arth800.expr[,1:9], lower.panel=panel.smooth, upper.panel=panel.cor)
```



Compute Partial correlations and Construct Graph

```
pcor.dyn = ggm.estimate.pcor(arth800.expr, method = "dynamic")

## Estimating optimal shrinkage intensity lambda (correlation matrix): 0.185

arth.edges = network.test.edges(pcor.dyn,direct=TRUE)

## Estimate (local) false discovery rates (partial correlations):
## Step 1... determine cutoff point
## Step 2... estimate parameters of null distribution and eta0
## Step 3... compute p-values and estimate empirical PDF/CDF
## Step 4... compute q-values and local fdr
## Step 5... prepare for plotting

##
## Estimate (local) false discovery rates (log ratio of spvars):
## Step 1... determine cutoff point
## Step 2... estimate parameters of null distribution and eta0
## Step 3... compute p-values and estimate empirical PDF/CDF
## Step 4... compute q-values and local fdr
## Step 5... prepare for plotting

dim(arth.edges)

## [1] 319600      10
```

We use the strongest 150 edges:

```
arth.net = extract.network(arth.edges, method.ggm="number", cutoff.ggm=150)

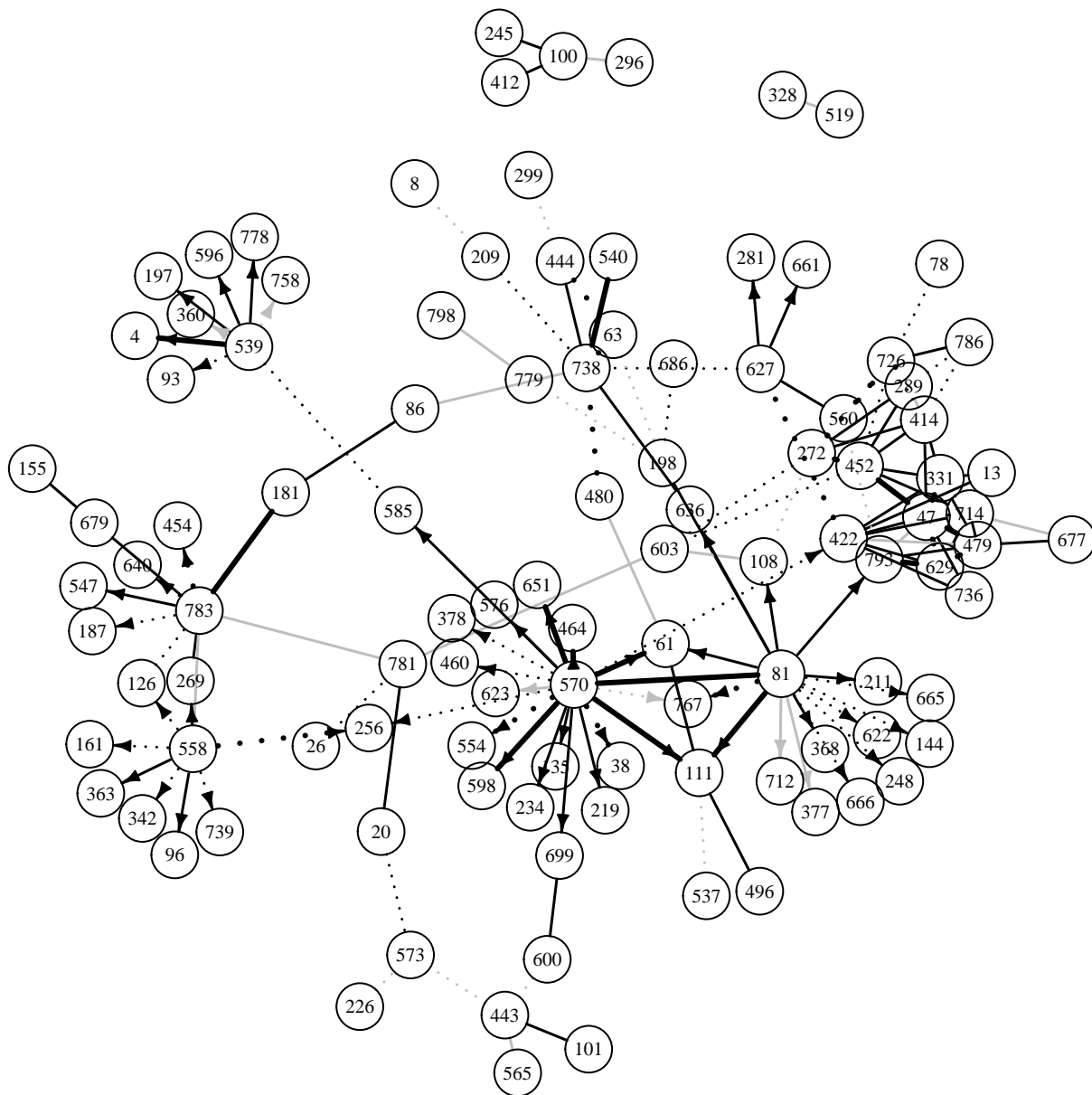
##
## Significant edges: 150
## Corresponding to 0.05 % of possible edges
##
## Significant directions: 10516
## Corresponding to 3.29 % of possible directions
## Significant directions in the network: 55
## Corresponding to 36.67 % of possible directions in the network
```

Plot Network

```
node.labels = as.character(1:ncol(arth800.expr))
igr = network.make.igraph(arth.net, node.labels)
```

```
plot(igr, main="Arabdiopsis Network", layout=layout.fruchterman.reingold,
     edge.arrow.size=0.5, vertex.size=9, vertex.label.cex=0.7)
```

Arabdiopsis Network



Further Analysis

Some of the discovered hubs:

```
sort(degree(igr), decreasing=TRUE)[1:10]
```

```
## 570  81 783  47 558 422 539 452 738 272
##  20  17  10   9   9   9   8   8   8   7
```

```
arth800.descr[570]
```

```
## [1] "AP2 transcription factor - like protein"
```

```
arth800.descr[81]
```

```
## [1] "ATRPAC43; DNA binding / DNA-directed RNA polymerase; DNA-directed RNA polymerase, putative, identical to ATRPAC43"
```

```
arth800.descr[558]
```

```
## [1] "structural constituent of ribosome; 60S ribosomal protein L35 (RPL35C), various ribosomal L35 proteins"
```

```
arth800.descr[539]
```

```
## [1] "DNA binding / transcription factor; basic helix-loop-helix (bHLH) family protein, contains Pfam domain PF00016"
```

```
arth800.descr[783]
```

```
## [1] "RNA binding / RNA methyltransferase; tRNA/rRNA methyltransferase (SpoU) family protein, similar to SpoU"
```