

# Uncovering gene regulatory relationships using networkBMA

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This document illustrates the use of the **networkBMA** R package (Fraley et al. 2012) to uncover regulatory relationships in yeast (*Saccharomyces cerevisiae*) from microarray data measuring time-dependent gene-expression levels in 95 genotyped yeast segregants subjected to a drug (rapamycin) perturbation.

## 1 Data

The expression data for this vignette is provided in the **networkBMA** package in the **vignette** database, which consists of three R objects:

**timeSeries:** A 582 by 102 data frame in which the first two columns are factors identifying the replicate and time (in minutes) after drug perturbation, and the remaining 100 columns are the expression measurements for a subset of 100 genes from the yeast-rapamycin experiment described in Yeung et al. (2011). There are  $582/6 = 97$  replicates (the 95 segregants plus two parental strains of the segregants), each with measurements at 6 time points. The complete time series data is available from Array Express (Parkinson et al. 2007) with accession number E-MTAB-412 (<http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-412>).

**reg.known:** A 18 by 3 data frame giving known regulatory relationships among this subset of 100 genes. The first two columns give the regulator and target gene, respectively, while the third encodes the source of the regulatory information ('YPD' for Yeast Proteome Database (Hodges et al. 1999) and 'SCPD' for The Promoter Database of *Saccharomyces cerevisiae* (Zhu and Zhang 1999). In this example, we constrained **reg.known** to high-confidence experimental results obtained from biochemical (non-high-throughput) experiments.

**reg.prob:** A 100 by 100 matrix, giving probability estimates for regulatory relationships in which the  $(i, j)$  entry gives the estimated probability that gene  $i$  regulates gene  $j$ . These were computed using the supervised framework integrating multiple data sources of Lo et al. (2011).

**referencePairs:** A 2-column data frame giving 287 regulator-gene pairs among the selected set of 100 genes reported from the literature. In this yeast example, the reference network was extracted from the documented evidence from the YEASTRACT database (Teixeira et al. 2006), which includes curated regulatory relationships from the literature inferred from high-throughput experiments.

**brem.data:** An 85 by 111 subset of the data used for network inference in yeast (Brem et al. 2002, Brem and Kruglyak 2005). The rows correspond to genes and the columns to experiments. Provided courtesy of Rachel Brem.

```

> library(networkBMA)
> data(vignette)
> dim(timeSeries)

[1] 582 102

> dim(reg.prob)

[1] 100 100

> dim(brem.data)

[1] 85 111

> reg.known

  Regulator TargetGene source
1   YDR216W   YKR009C   YPD
2   YER040W   YPL111W   YPD
3   YER040W   YKL015W   YPD
4   YER040W   YOR348C   YPD
5   YJR094C   YDR523C   YPD
6   YKL062W   YMR169C   YPD
7   YKL062W   YPL061W   YPD
8   YKL062W   YAL062W   YPD
9   YKL062W   YIL155C   YPD
10  YKL062W   YFL014W   YPD
11  YKL062W   YCR021C   YPD
12  YKL062W   YDR258C   YPD
13  YKL062W   YJR094C   YPD
14  YKL062W   YER150W   YPD
15  YKL062W   YNL194C   YPD
16  YBL103C   YNL037C   YPD
17  YKL112W   YCL064C   SCPD
18  YKL112W   YHR051W   SCPD

```

## 2 Network Modeling

Given the yeast expression data from the Rapamycin experiments, the `networkBMA` function can be invoked to estimate the probabilities of regulatory relationships using iterative Bayesian Model Averaging (Yeung et al. 2005, 2011):

```

> edges <- networkBMA(data = timeSeries[,-(1:2)],
+                      nTimePoints = length(unique(timeSeries$time)),
+                      prior.prob = reg.prob, known = reg.known,
+                      nvar = 50, ordering = "bic1+prior")
> edges[1:9,]

```

	Regulator	TargetGene	PostProb
1	YBL103C	YBL103C	1.0000000
2	YNR053C	YBL103C	1.0000000
3	YOR206W	YBL103C	1.0000000
4	YKL112W	YKL112W	1.0000000
5	YMR229C	YKL112W	1.0000000
6	YNR053C	YKL112W	0.8878645
7	YLL011W	YKL112W	0.1121355
8	YDR216W	YDR216W	1.0000000
9	YDL170W	YDR216W	1.0000000

For each gene  $g$ , the observed gene expression of genes at time  $t - 1$  serve as linear predictors for modeling the observed expression of gene  $g$  at time  $t$ . BMA modeling results in a weighted average of models consisting of relatively small numbers of predictors. The probability of gene  $h$  being a linear predictor in the model for gene  $g$  is taken as the probability that gene  $h$  regulates gene  $g$  in the network.

There are options for including known regulatory relationships and prior probabilities in the modeling (see Lo et al. 2011), as well as for ordering the variables, and for specifying the number of ordered variables to be included in the modeling.

### 3 Assessment of Network Models

Although, except for synthetic data, the true underlying network is unknown, the results can be assessed using a set of regulator-target gene network edges reported in the literature. The comparison is done as follows:

- Let  $E$  be the set of regulator-target gene edges resulting from **networkBMA**, possibly reduced using a probability threshold. In the context of the example in Section 2,  $E$  corresponds to the set of edges represented in the object **edges**.
- Let  $K$  be the set of known regulator-target gene edges hardcoded in the modeling. In the example in Section 2,  $K$  corresponds to **reg.known**.
- Let  $L$  be the set regulator-target gene edges reported in the literature. In the example in Section 2,  $L$  corresponds to **referencePairs**.
- Let  $E \setminus K$  and  $L \setminus K$  be the set of pairs in  $E$  and  $L$ , respectively, with any hardcoded edges removed. In the example of Section 2,  $E$  represented by **edges** contains 483 pairs, and  $L$  represented by **referencePairs** contains 287 pairs. Both  $E$  and  $L$  include all 18 of the known hardcoded edges  $K$  represented by **reg.known**. Hence  $E \setminus K$  contains 465 pairs, and  $L \setminus K$  contains 269 pairs.
- Let  $U$  be the set of all directed pairs  $r$ - $g$  such that  $r$  is a regulator in  $L \setminus K$  and  $g$  is a target gene in  $L \setminus K$ . For the example of Section 2,  $L \setminus K$  has 11 unique regulator genes and 99 unique target genes. So there are  $11 \times 99$  or 1089 pairs in  $U$ . Assume further that the linked pairs in  $U$  are precisely those pairs in  $L \setminus K$ , and that all other pairs are unlinked.

- Let  $U \setminus K$  be the set of pairs in  $U$  with any hardcoded edges removed (hardcoded edges may resurface in the unlinked pairs). For the example of Section 2, 17 of the 18 pairs in  $K$  occur in  $U$ , so there are  $1089 - 17 = 1072$  edges in  $U \setminus K$ .

The assessment is done using the contingency table of  $(E \setminus K) \cap (U \setminus K)$  relative to  $U \setminus K$ . For the example of Section 2, the assessment would be done with the 57 of the 465 pairs in  $E \setminus K$  that also belong to  $U \setminus K$ .

A function called `contabs.netBMA` is provided to produce contingency tables from a reference network according the procedure described above. Here we compare the edges produced in Section 2 by `networkBMA` modeling on the yeast data with the reference network `referencePairs` made up of results reported in the literature:

```
> ctables <- contabs.netwBMA( edges, referencePairs, reg.known,
+                               thresh=c(.5,.75,.9))
> ctables
```

	TP	FN	FP	TN
0.0402434734464825	23	246	33	770
0.0454930593677872	23	246	33	770
0.0547610726848114	23	246	32	771
0.0621177818036108	22	247	31	772
0.120313556351554	22	247	31	772
0.121759397028104	22	247	30	773
0.166119151754663	22	247	28	775
0.193411367909935	22	247	28	775
0.264308050711243	21	248	28	775
0.267765506855866	21	248	26	777
0.439806592523595	21	248	25	778
0.460479253259967	21	248	25	778
0.529176356437926	21	248	24	779
0.618320042575671	21	248	23	780
0.78955796127144	20	249	22	781
0.808602928008677	19	250	22	781
0.815135804441225	19	250	21	782
0.833880848245337	19	250	21	782
0.894277522630439	19	250	20	783
0.933660013920575	19	250	18	785
0.937882218196389	19	250	18	785
1	18	251	15	788

Another function called ‘`contabs`’ is provided for computing contingency tables when the true underlying network is known. The `scores` function can be used to obtain common assessment statistics from the contingency tables, including sensitivity, specificity, precision, recall, and false discovery rate among other measures.

```
> scores( ctables, what = c("FDR", "precision", "recall"))
```

	FDR	precision	recall
0.0402434734464825	0.5892857	0.4107143	0.08550186
0.0454930593677872	0.5892857	0.4107143	0.08550186
0.0547610726848114	0.5818182	0.4181818	0.08550186
0.0621177818036108	0.5849057	0.4150943	0.08178439
0.120313556351554	0.5849057	0.4150943	0.08178439
0.121759397028104	0.5769231	0.4230769	0.08178439
0.166119151754663	0.5600000	0.4400000	0.08178439
0.193411367909935	0.5600000	0.4400000	0.08178439
0.264308050711243	0.5714286	0.4285714	0.07806691
0.267765506855866	0.5531915	0.4468085	0.07806691
0.439806592523595	0.5434783	0.4565217	0.07806691
0.460479253259967	0.5434783	0.4565217	0.07806691
0.529176356437926	0.5333333	0.4666667	0.07806691
0.618320042575671	0.5227273	0.4772727	0.07806691
0.78955796127144	0.5238095	0.4761905	0.07434944
0.808602928008677	0.5365854	0.4634146	0.07063197
0.815135804441225	0.5250000	0.4750000	0.07063197
0.833880848245337	0.5250000	0.4750000	0.07063197
0.894277522630439	0.5128205	0.4871795	0.07063197
0.933660013920575	0.4864865	0.5135135	0.07063197
0.937882218196389	0.4864865	0.5135135	0.07063197
1	0.4545455	0.5454545	0.06691450

Areas under the ROC and Precision-Recall curves covered by contingency tables can also be estimated using functions `roc` and `prc`, with the option to plot the associated curves. The following gives the ROC and Precision-Recall curves associated with the default contingency tables, in which the thresholds are all values for posterior probabilities that appear in `edges`.

```
> roc( contabs.netwBMA( edges, referencePairs), plotit = TRUE)

      area      sector      width
0.552955098 0.002765027 0.021087680

> title("ROC")
> prc( contabs.netwBMA( edges, referencePairs), plotit = TRUE)

      area      sector      width
0.27665213 0.02082793 0.03484321

> title("Precision-Recall")
```

The resulting plots are shown in Figure 1. The output components are as follows:

- **area:** The estimated area under the curve for the horizontal sector ranging from 0 to 1. This should be used with caution when the sector in which the data falls is small.
- **sector:** The estimated area under the horizontal sector covered by the contingency tables.
- **width:** The width of the horizontal sector covered by the contingency tables.

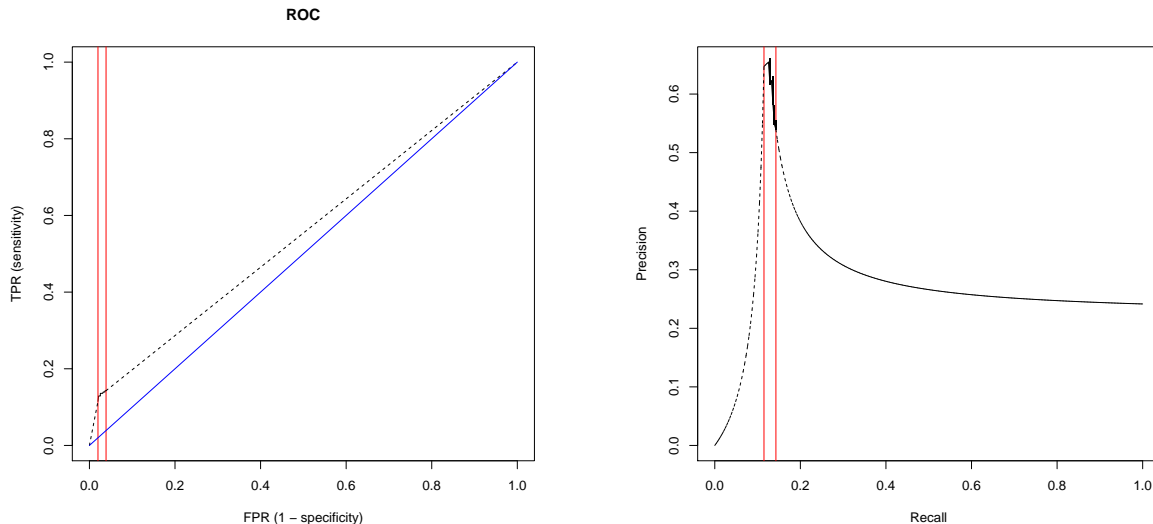


Figure 1: ROC and Precision-Recall curve sectors for a **networkBMA** model of the yeast-rapamycin test data. The black lines delineate the estimated curves. The vertical red lines delineate the range of horizontal values covered by the contingency tables. The dotted black lines are linear interpolants outside this range. The diagonal blue line on the ROC plot indicates the line between (0,0) and (1,1).

## 4 Linear Modeling for Static Gene Expression Data

**networkBMA** relies on sparse linear modeling via iterative Bayesian model averaging (BMA). BMA addresses uncertainty in model selection, and builds a weighted-average model from plausible models. The resulting model has better overall predictive ability than constituent models, and tends to use few variables from among a larger set. BMA has been iteratively extended to data with more variables than observations (Yeung et al. 2005, 2009, 2011). The **networkBMA** package includes a function, `iterateBMAlm`, for linear modeling via iterative BMA. We illustrate its use on a static gene expression dataset (without any time points), **brem.data**, to infer the regulators of a particular gene by regressing it on the expression levels of the other genes. Function `iterateBMAlm` can be applied to each gene so as to infer all edges in the network. For one gene, the procedure is as follows:

```
> gene <- "YNL037C"
> variables <- which(rownames(brem.data) != gene)
> control <- iBMAcontrolLM(OR = 50, nbest = 20, thresProbne0 = 5)
> iBMAmodel.YNL037C <- iterateBMAlm( x = t(brem.data[variables,]),
+                                   y = unlist(brem.data[gene,]), control = control)
```

Function `iBMAcontrolLM` facilitates input of BMA control parameters, including `nbest` for specifying the number of best models of each size to be initially retained, `OR` for defining the width of ‘Occam’s window’ for model exclusion, and `thresProbne0` for determining the cutoff for probability (in percent) of a variable being included in the modeling (Raftery et al.

2005). See the R help documentation for `iBMAcontrolLM` for a detailed description of these parameters, and Hoeting et al. (1999) for a tutorial on the underlying BMA paradigm. The estimated posterior probabilities (in percent) for genes that regulate YBL103C can be seen as follows:

```
> iBMAmodel.YNL037C$probne0[iBMAmodel.YNL037C$probne0 > 0]
```

YDL170W	YHR051W	YPR002W	YML123C	YIL136W	YAL062W	YJR148W
36.178933	75.032631	100.000000	7.010839	100.000000	32.299339	32.299339
YNL036W	YFR022W	YPL265W	YOR348C	YCL064C	YFL014W	YOR388C
63.821067	100.000000	100.000000	100.000000	74.315241	15.737407	7.281450
YDR380W	YGR183C	YJL153C				
67.700661	24.967369	32.299339				

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