

# Inferring mutual information networks using the *minet* package

Patrick E. Meyer, Frédéric Lafitte, Gianluca Bontempi

January 5, 2009

## 1 Introduction

The *minet* package provides a set of functions to infer mutual information networks from a dataset [10]. If fed with microarray data, the package returns a network where nodes denote genes and edges model statistical dependencies between genes. The weight of an edge provides evidence about the existence of a specific (e.g transcriptional) gene to gene interaction.

The inference proceeds in two steps. First, the Mutual Information Matrix (*MIM*) is computed, a square matrix whose  $MIM_{ij}$  term is the mutual information between gene  $X_i$  and  $X_j$ . Secondly, an inference algorithm takes the *MIM* matrix as input and attributes a score to each edge connecting a pair of nodes. Different entropy estimators are implemented in this package as well as different inference methods, namely `aracne`, `clr` and `mrnet` [1, 6, 9]. Also, the package integrates accuracy assessment tools, like PR-curves and ROC-curves, to compare the inferred network with a reference one.

This vignette guides the package user in :

1. Estimating the mutual information matrix and discretizing data if needed.
2. Inferring a network modeling the interactions between the dataset's variables.
3. Comparing the inferred network to a network of known interactions in order to compute  $F_\beta$  - scores.
4. Plotting precision-recall and receiver operating characteristic curves.
5. Plotting the inferred network using the *Rgraphviz* package.

The data used in the following examples was generated using the *SynTReN* simulator [4]. This data generator uses a known network of interacting genes in order to generate gene expression levels for all the genes included in the network. Once the network is inferred from the generated data, it can be compared to the true underlying network in order to validate the inference algorithm.

## 2 Mutual Information Estimation

Mutual information networks are a subcategory of network inference methods. These methods set a link between two nodes if it exhibits a high score based on the mutual information between the nodes.

Mutual information networks rely on the computation of the mutual information matrix (MIM), a square matrix whose element

$$MIM_{ij} = I(X_i; X_j) = \sum_{x_i \in \mathcal{X}_i} \sum_{x_j \in \mathcal{X}_j} p(x_i, x_j) \log p(x_i)p(x_j)$$

is the mutual information between  $X_i$  and  $X_j$ , where  $X_i \in \mathcal{X}, i = 1, \dots, n$ , is a discrete random variable denoting the expression level of the  $i$ th gene.

### 2.1 Obtaining The Mutual Information Matrix

```
> library(minet)
> data(syn.data)
> estimator = "mi.empirical"
> mim <- build.mim(discretize(syn.data), estimator)
> mim[1:5, 1:5]
```

|           | CDC11     | SWI4      | CDC10     | SPT16     | SWI4_SWI6 |
|-----------|-----------|-----------|-----------|-----------|-----------|
| CDC11     | 0.0000000 | 2.3025851 | 2.3025851 | 0.7784304 | 1.8996102 |
| SWI4      | 2.3025851 | 0.0000000 | 2.3025851 | 0.7784304 | 1.8996102 |
| CDC10     | 2.3025851 | 2.3025851 | 0.0000000 | 0.7784304 | 1.8996102 |
| SPT16     | 0.7784304 | 0.7784304 | 0.7784304 | 0.0000000 | 0.7375337 |
| SWI4_SWI6 | 1.8996102 | 1.8996102 | 1.8996102 | 0.7375337 | 0.0000000 |

In the above code, the mutual information matrix is built using the function `build.mim`. This function takes the dataset and one of the mutual information estimator explained in this section as input. All the estimators require discrete data values. The `discretize` function allows the user to choose between two binning algorithms.

### 2.2 Supervized Discretization

All the mutual information estimators described in this section require discrete data values. If the random variable  $X$  is continuous and can take values comprised between  $a$  and  $b$ , it is always possible to divide the interval  $[a, b]$  into  $|\mathcal{X}|$  subintervals in view of using the discrete estimators. The package provides a function that discretizes data using the equal frequency or equal width binning algorithm [5].

### 2.2.1 Equal Width Binning

The principle of the equal width discretization is to divide  $[a, b]$  into  $|\mathcal{X}|$  subintervals all having the same size:

$$\left[ a, a + \frac{b-a}{\mathcal{X}} \right[, \left[ a + \frac{b-a}{\mathcal{X}}, a + 2\frac{b-a}{\mathcal{X}} \right[, \dots, \left[ a + (|\mathcal{X}| - 1)\frac{b-a}{\mathcal{X}}, b + \epsilon \right[$$

Note that an  $\epsilon$  is added in the last interval in order to include the maximal value in one of the  $|\mathcal{X}|$  bins. This discretization scheme can be done in  $O(m)$ .

```
> library(minet)
> data(syn.data)
> disc <- "equalwidth"
> nbins <- sqrt(nrow(syn.data))
> ew.data <- discretize(syn.data, disc, nbins)
> syn.data[1:5, 1:5]

      CDC11      SWI4      CDC10      SPT16 SWI4_SWI6
1 0.4916395 0.2687357 0.5736381 0.2119972 0.2599864
2 0.8342323 0.6566324 0.8750186 0.2810182 0.6977198
3 0.8208405 0.6351676 0.8643861 0.4749119 0.6726126
4 0.9841594 0.9593638 0.9885627 0.9474643 0.9674964
5 0.9879920 0.9690066 0.9913392 0.9999866 0.9764548

> ew.data[1:5, 1:5]

      CDC11 SWI4 CDC10 SPT16 SWI4_SWI6
1      2     1      2      2          0
2      7     6      7      2          6
3      7     5      7      4          6
4      9     9      9      9          9
5      9     9      9      9          9
```

### 2.2.2 Equal Frequencies Binning

The equal frequency discretization scheme consist in dividing the interval  $[a, b]$  into  $|\mathcal{X}|$  intervals, each having the same number of data points (i.e.,  $\frac{m}{|\mathcal{X}|}$  points). As a result, the size of each interval can be different. Note that if the  $|\mathcal{X}|$  intervals have equal frequencies, the computation of entropy is straightforward since it is  $\log \frac{1}{|\mathcal{X}|}$ . However, there can be more than  $\frac{m}{|\mathcal{X}|}$  identical values in a vector of measurements. In the latter case, one of the bins will have more points than the others and the entropy will be different from  $\frac{1}{|\mathcal{X}|}$ .

```
> disc <- "equalfreq"
> ef.data <- discretize(syn.data, disc, nbins)
> ef.data[1:5, 1:5]
```

|   | CDC11 | SWI4 | CDC10 | SPT16 | SWI4_SWI6 |
|---|-------|------|-------|-------|-----------|
| 1 | 0     | 0    | 0     | 1     | 0         |
| 2 | 4     | 4    | 4     | 1     | 4         |
| 3 | 3     | 3    | 3     | 4     | 3         |
| 4 | 9     | 9    | 9     | 9     | 9         |
| 5 | 9     | 9    | 9     | 9     | 9         |

## 2.3 Mutual Information Estimators

The package implements four estimators, called "mi.empirical", "mi.mm", "mi.sg" and "mi.shrink".

### 2.3.1 Empirical Estimation

The estimation of mutual information relies on the estimation of entropy as suggested by the following formula:

$$I(X; Y) = H(X) + H(Y) - H(X, Y)$$

where

$$H(X) = - \sum_{x \in \mathcal{X}} p(x) \log(p(x))$$

is the entropy of the discrete variable  $X$ . The empirical estimator (also called "plug-in", "maximum likelihood" or "naive", see [29]) is simply the entropy of the empirical distribution:

$$\hat{H}^{emp}(p(X)) = - \sum_{i \in \mathcal{X}} \frac{nb(x_i)}{m} \log \frac{nb(x_i)}{m}$$

where  $nb(x_i)$  is the counting of data points in bin  $x_i$ .

### 2.3.2 Miller-Madow Estimation

The Miller-Madow estimation is given by the following formula which is the empirical entropy corrected by the asymptotic bias:

$$\hat{H}^{mm}(p(X)) = \hat{H}^{emp}(p(X)) + \frac{|\mathcal{X}| - 1}{2m}$$

where  $|\mathcal{X}|$  is the number of bins with non-zero probability.

### 2.3.3 Schurmann-Grassberger Estimation

The Dirichlet distribution is the multivariate generalization of the beta distribution. It is also the conjugate prior of the multinomial distribution in Bayesian statistics. More precisely, the density of a Dirichlet distribution takes the following form

$$f(X; \beta) = \frac{\prod_{i \in \mathcal{X}} \Gamma(\beta_i)}{\Gamma(\sum_{i \in \mathcal{X}} \beta_i)} \prod_{i \in \mathcal{X}} x_i^{\beta_i - 1}$$

where  $\beta_i$  is the prior probability of an event  $x_i$  and  $\Gamma(\cdot)$  is the gamma function, (see [8, 11] for more details).

In front of no apriori knowledge, the  $\beta_i$  are all set to equality ( $\beta_i = N$ ,  $i \in \mathcal{X}$ ) so as no event becomes more probable than another.

The entropy of a Dirichlet distribution can be computed directly with the following equation:

$$\hat{H}^{dir}(X) = \frac{1}{m + |\mathcal{X}|N} \sum_{i \in \mathcal{X}} (nb(x_i) + N)(\psi(m + |\mathcal{X}|N + 1) - \psi(nb(x_i) + N + 1))$$

where  $\psi(z) = \frac{d \ln \Gamma(z)}{dz}$  is the digamma function.

Various choice of prior parameters has been proposed in the literature. The Schurmann-Grassberger sets  $N = \frac{1}{|\mathcal{X}|}$ .

### 2.3.4 Shrinkage Entropy Estimation

The shrinkage estimation of the entropy [8] proposes to assign to an event  $x_i$  a mixture of two probability estimators:

$$\hat{p}(x_i) = \lambda \frac{1}{|\mathcal{X}|} + (1 - \lambda) \frac{nb(x_i)}{m}$$

The first one,  $\frac{1}{|\mathcal{X}|}$ , that has a zero variance but a large bias and the second one, the empirical one  $\frac{nb(x_i)}{m}$ , that has a larger variance but is unbiased. The advantage of shrinking the second one towards the first one is that, the resulting estimator outperform both individual estimates [14]. As the value of  $\lambda$  tends to one, the estimated entropy is moved toward the maximal entropy (uniform probability) whereas when  $\lambda$  is zero the estimated entropy tends to the value of the empirical one.

The parameter  $\lambda$  has to be chosen in order to minimize a risk function  $R(\lambda)$ .

$$R(\lambda) = E[\sum_{i \in \mathcal{X}} (\hat{p}(x_i) - p(x_i))^2]$$

In [14] the analytical value of  $\lambda$  that minimize the risk is expressed in generic terms. Applied to the problem of estimating bin probabilities [8], it gives

$$\lambda^* = \frac{|\mathcal{X}|(m^2 - \sum_{i \in \mathcal{X}} nb(x_i)^2)}{(m-1)(|\mathcal{X}| \sum_{i \in \mathcal{X}} nb(x_i)^2 - m^2)}$$

The entropy can then be computed using

$$\hat{H}^{shrink} = H(\hat{p}(X)) = - \sum_{i \in \mathcal{X}} \hat{p}(x_i) \log \hat{p}(x_i)$$

### 3 Network Inference

Three network inference methods are available in the package : `aracne`, `clr` and `mrnet`. These receive as input the mutual information matrix and return the weighted adjacency matrix of the network. The network can be directly inferred from the dataset by using the `minet` function. This function takes as input the dataset, the name of the estimator and the name of the discretization method to be used as well as the number of bins to be used.

#### 3.1 Obtaining The Network

In the following code, the `mrnet` algorithm is applied to the mutual information matrix estimated in the previous section:

```
> net <- mrnet(mim)
> net[1:5, 1:5]
```

|           | CDC11     | SWI4     | CDC10     | SPT16     | SWI4_SWI6 |
|-----------|-----------|----------|-----------|-----------|-----------|
| CDC11     | 0.0000000 | 2.302585 | 0.0000000 | 0.0000000 | 0.2905191 |
| SWI4      | 2.3025851 | 0.000000 | 2.3025851 | 0.0000000 | 1.8996101 |
| CDC10     | 0.0000000 | 2.302585 | 0.0000000 | 0.0000000 | 0.5064978 |
| SPT16     | 0.0000000 | 0.000000 | 0.0000000 | 0.0000000 | 0.0226205 |
| SWI4_SWI6 | 0.2905191 | 1.899610 | 0.5064979 | 0.0226205 | 0.0000000 |

The returned value is the weighted adjacency matrix of the network.

#### 3.2 MRNET

The MRNET approach [9] consists in repeating a MRMR feature selection procedure for each variable of the dataset. The MRMR method [13] starts by selecting the variable  $X_i$  having the highest mutual information with the target  $Y$ . In the following steps, given a set  $\mathcal{S}$  of selected variables, the criterion updates  $\mathcal{S}$  by choosing the variable  $X_k$  that maximizes  $I(X_k; Y) - \frac{1}{|\mathcal{S}|} \sum_{X_i \in \mathcal{S}} I(X_k; X_i)$ . The weight of each pair  $X_i, X_j$  will be the maximum score between the one computed when  $X_i$  is the target and the one computed when  $X_j$  is the target.

#### 3.3 CLR

The CLR algorithm [6] considers the MIM as the weighted adjacency matrix of the network but instead of using the information  $I(X_i; X_j)$  as the weight of the link between features  $X_i$  and  $X_j$ , it takes into account the score  $\sqrt{z_i^2 + z_j^2}$ , where

$$z_i = \max \left\{ 0, \frac{I(X_i; X_j) - \mu_i}{\sigma_i} \right\}$$

and  $\mu_i$  and  $\sigma_i$  are, respectively, the mean and the standard deviation of the empirical distribution of the mutual information values  $I(X_i; X_k)$ ,  $k = 1, \dots, n$ .

### 3.4 ARACNE

The ARACNE algorithm [1] is based on the Data Processing Inequality . This inequality states that, if gene  $X_1$  interacts with gene  $X_3$  through gene  $X_2$ , then

$$I(X_1; X_3) \leq \min(I(X_1; X_2), I(X_2; X_3))$$

The ARACNE procedure starts by assigning to each pair of nodes a weight equal to the mutual information. Then the weakest edge of each triplet is interpreted as an indirect interaction and is removed if the difference between the two lowest weights is above a threshold  $W_0$ . The function `aracne` has an extra argument `eps` which is the numerical value of  $W_0$ .

### 3.5 The minet function

The `minet` function infers directly the mutual information network from the input dataset. Besides the dataset, this function's arguments are the mutual information estimator, the inference method, the binning algorithm and the number of bins to be used. All the instructions used until now can then be summarized with the following call to `minet`:

```
> library(minet)
> data(syn.data)
> net <- minet(syn.data, method = "mrnet", estimator = "mi.empirical",
+   disc = "equalwidth", nbins = sqrt(nrow(syn.data)))
> net[1:5, 1:5]
```

|           | CDC11      | SWI4       | CDC10      | SPT16      | SWI4_SWI6  |
|-----------|------------|------------|------------|------------|------------|
| CDC11     | 0.00000000 | 0.07783305 | 0.12427277 | 0.00000000 | 0.03847938 |
| SWI4      | 0.07783305 | 0.00000000 | 0.68443641 | 0.03522452 | 0.73285129 |
| CDC10     | 0.12427277 | 0.68443641 | 0.00000000 | 0.01238448 | 0.19752001 |
| SPT16     | 0.00000000 | 0.03522452 | 0.01238448 | 0.00000000 | 0.01008181 |
| SWI4_SWI6 | 0.03847938 | 0.73285129 | 0.19752001 | 0.01008181 | 0.00000000 |

Note that in this case the returned object is the *normalized* weighted adjacency matrix of the network (i.e. the values range from 0 to 1).

## 4 Validation

### 4.1 Obtaining Confusion Matrices

The networks inferred using this package are weighted but many low weighted edges can be removed by using a threshold value. By setting to 0 all edges whose weight are lower than the threshold and to 1 the other edges weight, the network inference problem can be seen as a binary decision problem. The decision made by the algorithm can be summarized by a confusion matrix (see table 4.1).

In our case, the threshold value can be seen as the minimal edge weight required for the edge to be inferred : edges whose weight are strictly below the

| EDGE          | Infered | Not Infered |
|---------------|---------|-------------|
| Exists        | TP      | FN          |
| Doesn't Exist | FP      | TN          |

Table 1: Confusion matrix

threshold are removed from the network. Then, a different confusion matrix is obtained for each different threshold. The table returned by the `validate` function contains all the confusion matrices obtained with `steps` thresholds ranging from the lowest to the highest value of the edges weight.

```
> library(minet)
> data(syn.data)
> data(syn.net)
> net <- minet(syn.data)
> table <- validate(net, syn.net, steps = 20)
> table[1:10, ]
```

```
      thrsh  tp  fp  tn  fn
1  0.00 130 2370   0   0
2  0.05  74  202 2168  56
3  0.10  60  142 2228  70
4  0.15  60  110 2260  70
5  0.20  56   84 2286  74
6  0.25  56   62 2308  74
7  0.30  52   60 2310  78
8  0.35  48   40 2330  82
9  0.40  42   24 2346  88
10 0.45  42   22 2348  88
```

In the above code, the `validate` function compares the inferred network `net` to `syn.net`, the network underlying `syn.data`. Note that the true underlying network has to be a matrix containing values 1 (presence of the edge) or 0 (absence of the edge).

Each line of the returned table contains the threshold used and the confusion matrix obtained by comparing `syn.net` to the inferred network.

Note that the `validate` function distinguishes the following cases:

- Both networks are oriented
- Both networks are unoriented
- One of the network is oriented and the other unoriented

In the third case, the oriented network will be considered unoriented.



## 4.2 Using the Confusion Matrices

The confusion matrix summarizes the decisions made by the algorithm. Thus in order to compare inference algorithms, we compare their confusion matrix, more precisely, we compare several criteras that are derived from that matrix [3]:

- Precision:  $p = \frac{TP}{TP+FP}$
- Recall:  $r = \frac{TP}{TP+FN}$
- True Positive Rate:  $tpr = \frac{TP}{TP+TN}$
- False Positive Rate:  $fpr = \frac{FP}{FP+FN}$
- $F_\beta$ -score:  $F_\beta = (1 + \beta) \frac{pr}{\beta p + r}$

These scores are returned by the functions `rates`, `pr` and `fscores`. The functions `show.pr` and `show.roc` can be used to visualize precision-recall curves and receiver operating characteristic curves respectively. The `show.pr` function uses the precisions and recalls computed by the function `pr` and the `show.roc` relies on the rates returned by the `rates` function in order to plot receiver operating characteristic curves. All these functions take as input the data.frame returned by the `validate` function:

```
> library(minet)
> data(syn.data)
> data(syn.net)
> net1 <- minet(syn.data, method = "mrnet")
> net2 <- minet(syn.data, method = "clr")
> table1 <- validate(net1, syn.net, steps = 50)
> table2 <- validate(net2, syn.net, steps = 50)
```

Once the data.frames `table1` and `table2` are computed, we can use the function

- `pr(table)` to obtain precisions and recalls.
- `rates(table)` to obtain true positive rates and false positive rates.
- `fscores(table,beta)` to obtain  $F_\beta$  - scores.

Both functions `show.pr` and `show.roc` return the device associated to the plotting window used. This allows the user to plot several curves on the same figure. The following code generates the curves in figure 1.

```
> dev <- show.pr(table1, pch = 2, type = "b", col = "green")
> show.pr(table2, device = dev, pch = 1, type = "b", col = "blue")
```

pdf  
2

```
> dev <- show.roc(table1, type = "b", col = "green")
> show.roc(table2, device = dev, type = "b", col = "blue")
```

pdf  
3

### 4.3 Plotting the inferred network with *Rgraphviz*

In order to plot the inferred network, we suggest using the *Rgraphviz* package with the following code:

```
> library(minet)
> data(syn.data)
> net <- minet(dataset = syn.data, method = "aracne", estimator = "mi.mm")
> n <- list(fillcolor = "lightgreen", fontsize = 20, fontcolor = "red",
+   height = 0.4, width = 0.4, fixedsize = F)
```

The above code generates the graph in figure 2.

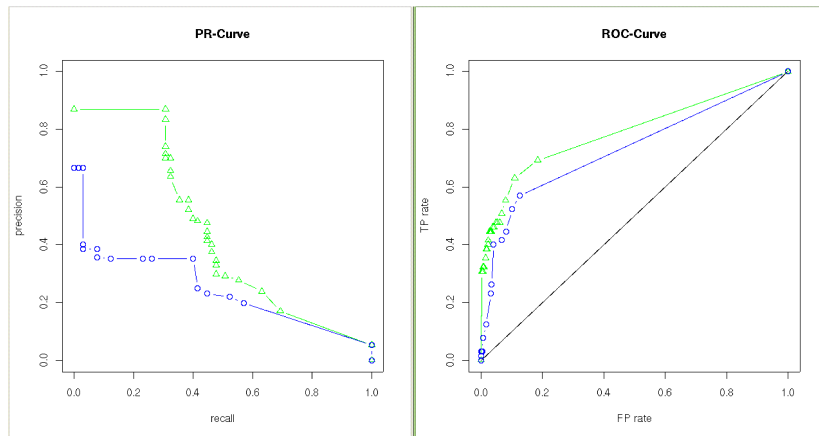
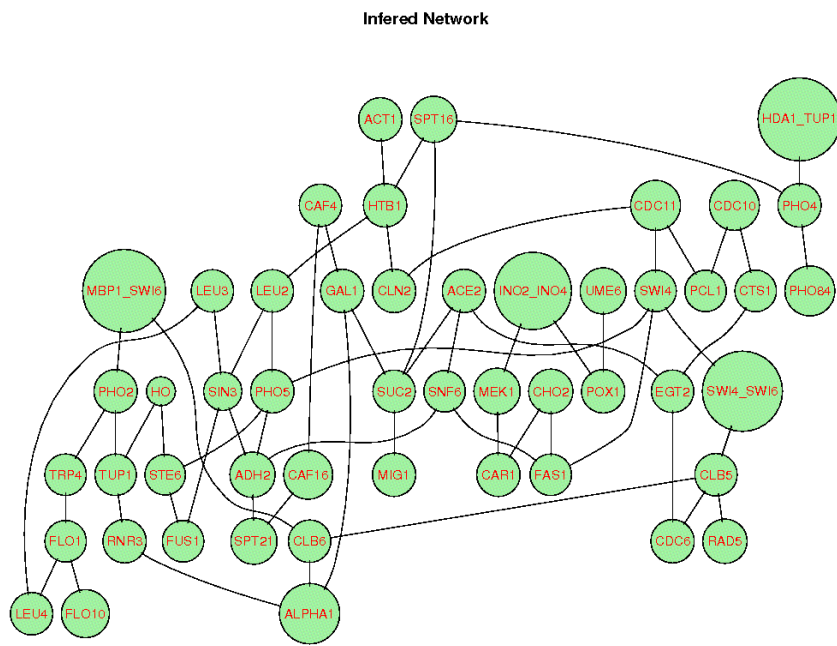


Figure 1: Precision-Recall curve (left) and Receiver Operating Characteristic curve (right), for both inference algorithms `mrnet` (green) and `clr` (blue).

Figure 2: Inferred network plotted using *Rgraphviz*



## References

- [1] Katia Basso, Adam Margolin, Gustavo Stolovitzky, Ulf Klein, Riccardo Dalla-Favera, and Andrea Califano. Reverse engineering of regulatory networks in human b cells. *Nature Genetics*, 37, 2005.
- [2] A. J. Butte and I.S. Kohane. Mutual information relevance networks: Functional genomic clustering using pairwise entropy measurements. *Pacific Symposium on Biocomputing*, 5:415–426, 2000.
- [3] J. Davis and M. Goadrich. The relationship between precision-recall and roc curves. *In Proceedings of the 23rd international conference on Machine learning*, 2006.
- [4] T. Van den Bulcke, K. Van Leemput, B. Naudts, P. van Remortel, H. Ma, A. Verschoren, B. De Moor, and K. Marchal. Syntren: a generator of synthetic gene expression data for design and analysis of structure learning algorithms. *BMC Bioinformatics*, 7(1):43, 2006.
- [5] J. Dougherty, R. Kohavi, and M. Sahami. Supervised and unsupervised discretization of continuous features. *In International Conference on Machine Learning*, pages pages 194–202, 1995.
- [6] J.J. Faith, B. Hayete, J.T. Thaden, I. Mogno, J. Wierzbowski, G. Cottarel, S. Kasif, J.J. Collins, and T.S. Gardner. Large-scale mapping and validation of escherichia coli transcriptional regulation from a compendium of expression profiles. *PLoS Biology*, 5, 2007.
- [7] T. S. Gardner and J. Faith. Reverse-engineering transcription control networks. *Physics of Life Reviews* 2, 2005.
- [8] J.Hausser. Improving entropy estimation and inferring genetic regulatory networks. *Master thesis of the National Institute of Applied Sciences Lyon*, 2006.
- [9] P. E. Meyer, K. Kontos, F. Lafitte, and G. Bontempi. Information-theoretic inference of large transcriptional regulatory networks. *EURASIP Journal on Bioinformatics and Systems Biology*, 2007.
- [10] P. E. Meyer, F. Lafitte, and G. Bontempi. minet: A R/Bioconductor Package for Inferring Large Transcriptional Networks Using Mutual Information. *BMC Bioinformatics*, 9:461, 2008.
- [11] I. Nemenman, W. Bialek, and R. de Ruyter van Steveninck. Entropy and information in neural spike trains: Progress on the sampling problem. *Physical Review Letters*, 69, 2004.
- [12] L. Paninski. Estimation of entropy and mutual information. *Neural Computation*, 15(6):1191–1253, 2003.

- [13] H. Peng, F. Long, and C. Ding. Feature selection based on mutual information: criteria of max-dependency, max-relevance, and min-redundancy. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 27(8), 2005.
- [14] J. Schafer and K. Strimmer. A shrinkage approach to large-scale covariance matrix estimation and implications for functional genomics. *Statistical Applications in Genetics and Molecular Biology*, 4(32), 2005.
- [15] T. Schurmann and P. Grassberger. Entropy estimation of symbol sequences. *Chaos*, 1996.
- [16] E. P. van Someren, L. F. A. Wessels, E. Backer, and M. J. T. Reinders. Genetic network modeling. *Pharmacogenomics*, 3(4):507–525, 2002.