## T-61.5110 Modeling of Biological Networks

Lähdesmäki, Khan, Nousiainen (Autumn 2013) Problem session, 28<sup>th</sup> Nov, 2013 https://noppa.aalto.fi/noppa/kurssi/t-61.5110/

# **Exercise Session 7**

**Submission**: If you *cannot attend* the exercise session then you are required to submit a report *before the start of exercise session on Thursday* (28<sup>th</sup> Nov 2013).

**Lectures Covered**: Bayesian networks

### 1. Bayesian network structure

- a. Install package Bnlearn. See what it contains.
- b. b. Learn Bayesian network structure for "learning.test" data using a score based method Hill-climbing. Discuss the network and how it is produced.
- c. Use the Grow-shrink algorithm which is a constraint based method to learn alternative structure for the data. Compare two networks. Discuss the possible the differences and highlight them in a plot.
- d. You have expert knowledge about the links in the network. Say, links in the network obtained using the Hill-climbing method Include your information as a constraint when relearning the structure using Grow-shrink algorithm. Verify that the new structure is equivalent to the structure learned using the Hill-climbing method

(Hint: You may want to check script learn bn.r.)

#### 2. More Bayesian networks

Load Sach data. Discretize the data using Bnlearn package. Create networks 500 random networks and use the Hill-climbing method to learn Bayesian networks. Measure the strength of the probabilistic relationships expressed by the arcs of the Bayesian networks and use model averaging to build a network containing only the significant arcs. Do similar analysis using bootstrapping with 500 replicates. Compare the averaged networks. Discuss your findings and the methods.

(Hint: See script Sachs.R.)

#### **References:**

- 1. Marco Scutari: Learning Bayesian Networks with the bnlearn R Package *Journal of Statistical Software:* July 2010, Volume 35, Issue 3. <a href="http://www.jstatsoft.org/">http://www.jstatsoft.org/</a>
- 2. http://www.bnlearn.com/book-useR/
- 3. Sachs K et al. (2005). Causal Protein-Signaling Networks Derived from Multiparameter Single-Cell Data. *Science*, 308(5721), pages 523-529.