Bioinformatics III

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Winter Semester 2019/2020

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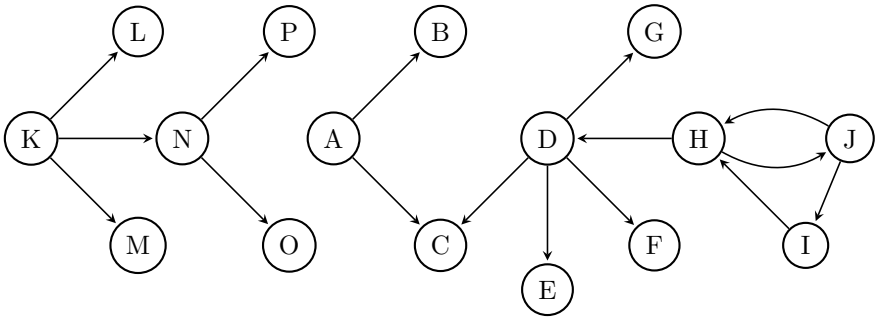
Exercise Sheet 7

Due: Dec 12, 2019 14:15

Submit your solutions on paper, hand-written or printed at the *beginning* of the lecture. Alternatively, you can send an email with a single PDF attachment to andreas.denger@bioinformatik.uni-saarland.de. Your submission should include code listings for programming exercises. Additionally, hand in a .zip file with your source code via email.

Co-expression Correlation and Master Regulatory Genes

Exercise 7.1: Identification of master-regulatory genes (40 points)



(a) Which *dominating sets* exist in the network shown above?

(b) What is the *minimum dominating set* (MDS) of this network?

(c) List the following sets of nodes and their sizes:

- Largest connected component in the directed graph
- Largest strongly connected component in the directed graph
- Largest connected component in the underlying undirected graph

Find the *minimum connected dominating set* (MCDS) for each of the three sets.

(d) Compare the MDS and MCDS in terms of size and write a short conclusion.

Exercise 7.2: Co-expression based on Correlation and Mutual Information (60 points)

Mutual information (I) and *Pearson correlation coefficient* ($Corr$) between two random variables are defined as:

$$I(X,Y) = \sum_{x \in X} \sum_{y \in Y} p(x,y) \times log\left(\frac{p(x,y)}{p(x) \times p(y)}\right)$$

$$Corr(X,Y) = \frac{\sum_{i=1}^{n}(x_i - \mu_X) \times (y_i - \mu_Y)}{\sqrt{\sum_{i=1}^{n}(x_i - \mu_X)^2} \times \sqrt{\sum_{i=1}^{n}(y_i - \mu_Y)^2}}$$

, where $p(x,y)$ is the *joint probability distribution* of expression levels x and y, $p(x)$ is the *marginal probability* of expression value x, and μ_X is the (arithmetic) mean expression for gene X.

(a) Calculate the Pearson correlation coefficient and mutual information for the data given below. Here, the data is comprised of two genes whose expression were measured over 6 time series. An expressed gene is denoted by value 1. Solve this task by hand.

Gene	t1	t2	t3	t4	t5	t6
gene1	0	0	1	1	1	0
gene2	0	1	0	0	1	1

(b) Explain the main difference between mutual information and Pearson correlation.

(c) What is the advantage of using rank-based correlation coefficients?

(d) Write a program that reads the time-series gene expression data given in the supplement and calculates the Pearson correlation coefficients for all pairs of genes.

(e) Plot the distribution of correlation coefficients between pairs of *distinct* genes (e.g. by using the distplot function from the Python package *seaborn*).

Interpret the shape of the plot and include it in your submission.

(f) Take a look at the correlation scores between the gene *MCTS1* and the other genes. Write a function that finds the gene with the:

- Highest correlation to *MCTS1*
- Lowest correlation to *MCTS1*
- Correlation to *MCTS1* that is closest to zero

Next, for each of these three genes, create a scatter plot with a linear regression model fit between its expression values and those of *MCTS1* (e.g. with the regplot function from the Python package *seaborn*).

Include the three plots in your submission and describe what you see.