

Bioinformatics III

Prof. Dr. Volkhard Helms
Maryam Nazarieh, Duy Nguyen, Thorsten Will
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Saarland University
Chair for Computational Biology

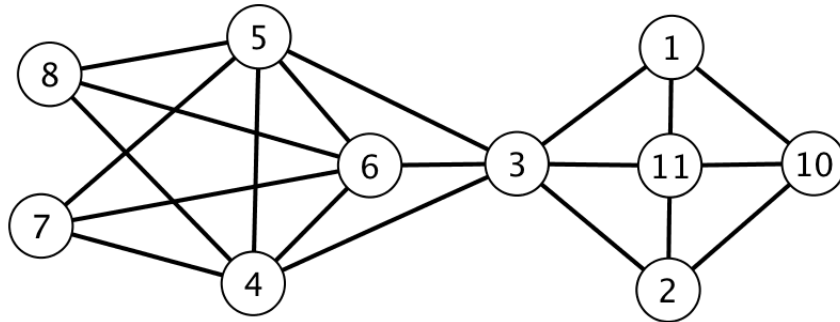
Exercise Sheet 4

Due: November 25, 2016 13:15

Submit your solutions on paper, hand-written or printed at the *beginning* of the lecture or in building E2 1, Room 3.09.

Exercise 4.1: Graph Modular Decomposition (50pts)

A module of a graph $G = (V, E)$ is a set $X \subseteq V$ of vertices where all vertices in X have the same neighbors in $V \setminus X$.



- Every single vertex of V satisfies the definition of a module is a trivial module. List the trivial modules in the graph given above.
- A module is called series if all included nodes are direct neighbors of each other. List all nodes which make series modules in the given graph and specify the series modules.
- A module is called parallel if all included nodes are non-neighbors. List all nodes which make a parallel module and specify the parallel module.
- A module is called prime if it does not fulfill the conditions either of a series or of a parallel module. List all nodes which make a prime module and specify the prime module.
- Draw a modular decomposition tree of this graph formed by prime, series and parallel modules.

Exercise 4.2: Gene Expression Prediction (50pts)

Decision tree is a classification method in which each internal node represents a test on a feature, each branch represents the outcome of the test and each leaf represents a class.

In this problem, we have a set of genes in the test data which are needed to be categorized into two groups of expressed and not expressed genes.

- Use the training data given in the table below to train the decision tree. The binary valued features (0,1) are DNA-methylation and histone modifications (H3K27me3, H3K27ac).

| Gene | DNA methylation | H3K27ac | H3K27me3 | class |
|--------|-----------------|---------|----------|---------------|
| gene1 | 1 | 1 | 1 | not-expressed |
| gene2 | 0 | 0 | 0 | not expressed |
| gene3 | 0 | 1 | 0 | expressed |
| gene 4 | 0 | 1 | 1 | not expressed |

- Determine for each feature, the best split by minimizing $\frac{N_L}{N} I(N_L) + \frac{N_R}{N} I(N_R)$, where $I(N)$ stands for node impurity of node N, $I(N) = 1 - \max p_N(k)$ where $p_N(k)$ is the fraction of training points at node N of class k and $k = 1, \dots, K$.
- Grow the tree until each leaf is maximal pure.
- Describe the path(s) from the root to the leaf which ends to gene expression.
- Label the class of the test data given below using the trained decision tree.

| Gene | DNA methylation | H3K27ac | H3K27me3 |
|--------|-----------------|---------|----------|
| gene5 | 1 | 0 | 0 |
| gene 6 | 0 | 0 | 1 |

Good Luck!