# Homework 2016
# Deadline 20 December 2016

**Exercise 1.** Write an algorithm that lists all the permutations on $n$ elements. Analyse the complexity of your algorithm in terms of input and output.

**Exercise 2.** We have seen in class the definition of two distances for comparing phylogenetic binary trees, the Robinson-Foulds distance ($RF$) and the maximum agreement subtree ($MAST$). Given two phylogenetic binary trees on the same set of $n$ leaves, $T_1, T2$, we recall the definition of these distances below :

1. $d_{RF}(T_1, T_2) = |BP(T_1)\Delta BP(T_2)|/2$ where $BP(T)$ is the set of the bipartitions of $T_1$ induced by each one of the edges.
2. $d_{MAST}(T_1, T_2) = n - MAST(T_1, T_2)$ where $MAST(T_1, T_2)$ is the largest cardinality of a set of leaves for which the subtrees induced in $T_1$ and $T_2$ are homeomorphic (*i.e.* all degree 2 nodes except of the root are contracted).

What is the maximum and the minimum value that the RF and the MAST distance can have ? Provide an example of two phylogenetic binary trees reaching these extreme cases.

**Exercise 3.** In a cophylogeny context we saw in class the event-based model for reconciling two phylogenetic binary trees. This models allows the identification of four type of events : (i) cospeciation, (ii) duplication, (iii) host-switch, (iv) loss. Given two phylogenetic binary trees is it always possible to find a reconciliation without host-switches ? Without duplications ?