Exercises – Phylogenetics

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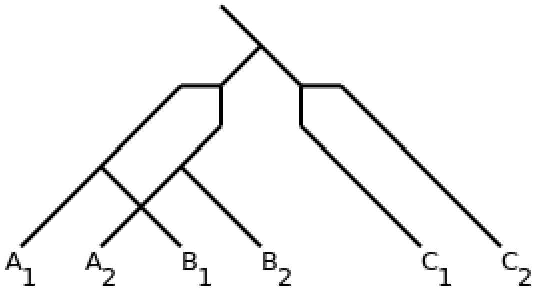
http://wiki.techfak.uni-bielefeld.de/gi/Teaching/2015winter/Phylogenetik

Exercise List 2 — 27.10.2015

Due to: 03.11.2015

Exercise 1 Gene and species trees. (2 Points)

(a) Write down all pairs of paralog and ortholog genes.



(b) Find out what *in-paralog* and *out-paralog* means. Explain the main difference.

Exercise 2 Gene tree / species tree reconciliation. (3 Points)

Consider the gene tree G and the species tree S in Newick notation.

$$\begin{aligned} G &= (g_4, ((g_6, g_7)g_3, g_5)g_2)g_1; \\ S &= (A, (B, C)n_2)n_1; \end{aligned}$$

Let both g_4 and g_5 be present in species A. Gene g_6 is in B and gene g_7 is found in C.

(a) Draw G and S. Label the internal nodes and leaves. Furthermore label the leaves of G with the corresponding names of the species.

(b) Calculate $\gamma(g_1)$, $\gamma(g_2)$ und $\gamma(g_3)$. Calculate the $M(.)$ for every node (including the leaves) in G and draw the matching arrows from G to S. Decide for every internal node if it's a duplication or speciation.

(c) Draw the received scenario from the species tree (similar to the picture in the lecture. Figure 2.5) **Hint** The scenario includes a deletion.

Exercise 3 Last common ancestor. (2 Points)

Consider the rooted tree $G = (V, E)$. How can you find the *last common ancestor* (LCA) for to given nodes u and v? Write an algorithm in *pseudo code* that can determine *LCA(u,v)*. What is the *worst case* run-time of your algorithm?

Hint: You can find examples for pseudo code in the lecture notes (page 13, 22, 23, 28, etc.)

Don't get confused! *lowest* and *last common ancestor* are basically the same. In phylogenetics the term *last common ancestor* is more common, since we're looking at the evolutionary time of events. However, if you think about vertices and trees in graph theory, the term *lowest common ancestor* is used, since there is no time involved in the analysis. Luckily the abbreviations of the words are the same.