

# Layout of Phylogenetic Networks and Multi-Labeled Trees

Poornima Venugopal, Sergey Bereg

<sup>1</sup>Department of Computer Science, University of Texas-Dallas

Recently, Multi-Labeled (MUL) trees have been used in polyploid studies to construct Phylogenetic networks [1]. We present a novel method to improve the layout of the Phylogenetic networks constructed from MUL trees. The idea is to rearrange the MUL tree to bring identical subtrees closer. We introduce a new metric *MIS-Distance* to quantify closeness of identical subtrees of MUL trees.

## Algorithm: *MUL-Arrange*

1. Identify the *maximal inextendible subtrees*[1] of an MUL tree  $T$
2. Swap the left and right subtrees of the root and compute the *MIS-Distance*. Retain the tree with minimal *MIS-Distance*.
3. Recursively apply the swap operation to the root nodes of the left and right subtrees retaining the MUL tree with the least *MIS-Distance* at each stage.
4. Repeat Steps 1 through 3 until the *MIS-Distance* output by consecutive iterations is the same.

**Illustration:** MUL Tree and Phylogenetic Network of part of tree appearing in [2] on plant taxa *Silene ajanensis* (S.a), *Silene sorenensis* (S.s), *Silene ostenfeldii* (S.o), *Silene involucrata* (S.i), and *Silene uralensis* (S.u).

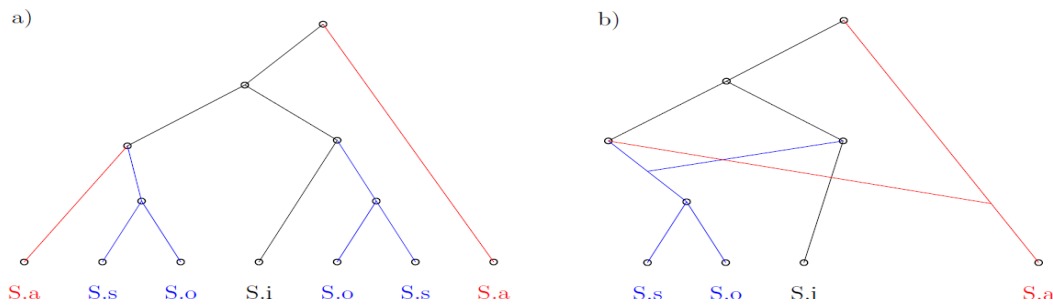


Figure 1: (a) Original MUL Tree (b) Phylogenetic Network

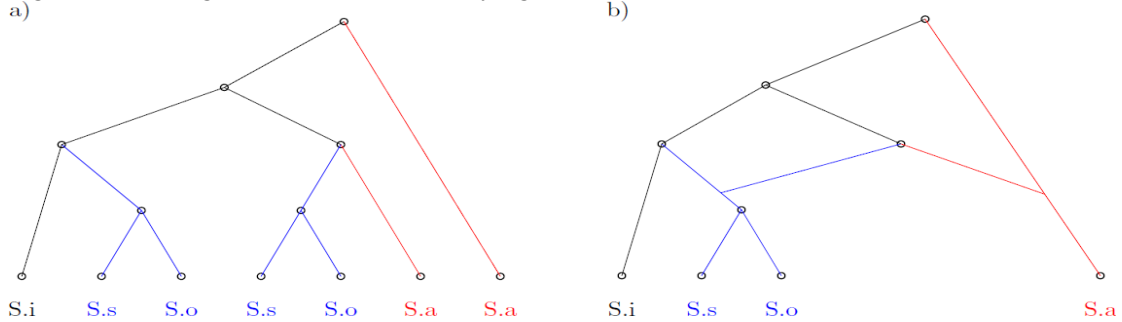


Figure 2: (a) Rearranged MUL Tree (b) Phylogenetic Network

## References:

1. K. T. Huber, B. Oxelman, M. Lott, V. Moulton, "Reconstructing the evolutionary history of polyploids from MultiLabeled trees", *Mol.Biol. Evol.* 23(9):1784-1791, 2006
2. Popp M, Oxelman B, "Origin and evolution North American Polyploid *Silene*", *Syst Bot* 30:302-13, 2005.