

# Neighbour-joining trees of distances between consensus

Blaise Li

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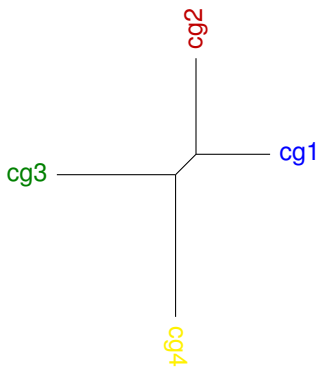
## Description of the supplementary material

For each analytical strategy, the tree was obtained by running the neighbour-joining algorithm implemented in the neighbor program from the phylip package, on the Robinson-Foulds symmetric difference distances calculated between the consensus trees obtained by applying the analytical strategy on the four datasets cg1 to cg4.

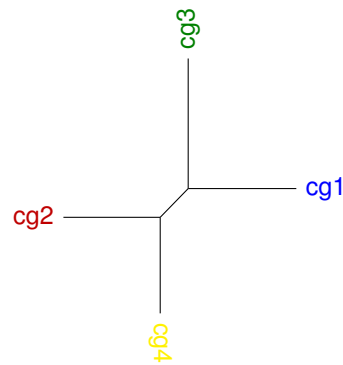
The branch lengths are represented at the same scale for all trees, and the analytical strategies are sorted in increasing order of average distance between consensus. Longer branch lengths are therefore observed at the end of this document.

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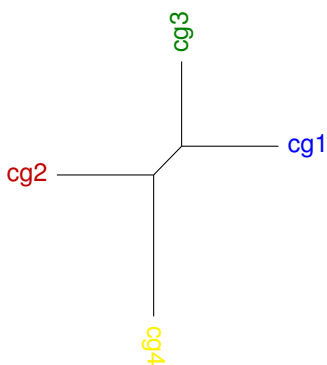
**degenS3**



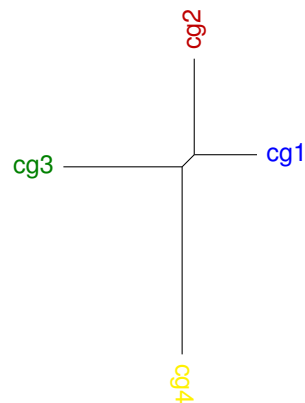
**translated**



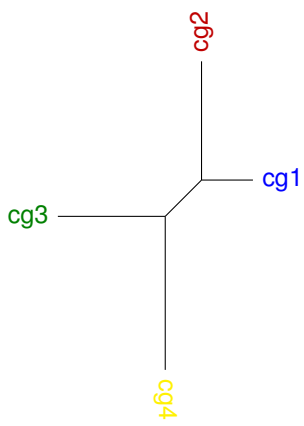
**degenLRS3**



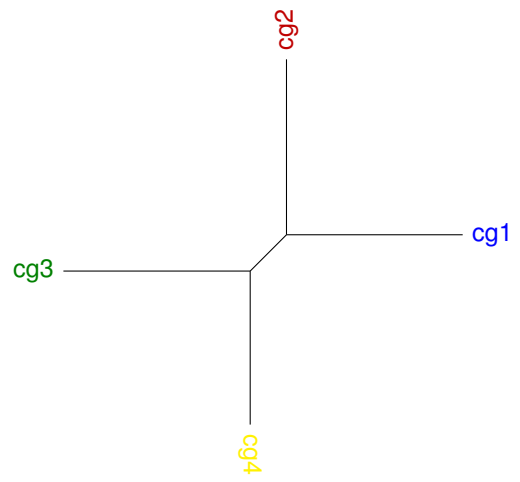
**degenLR3**



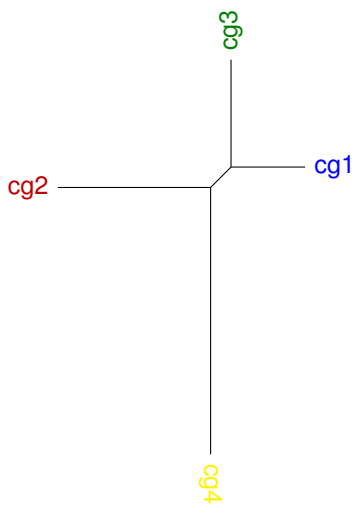
**degen3**



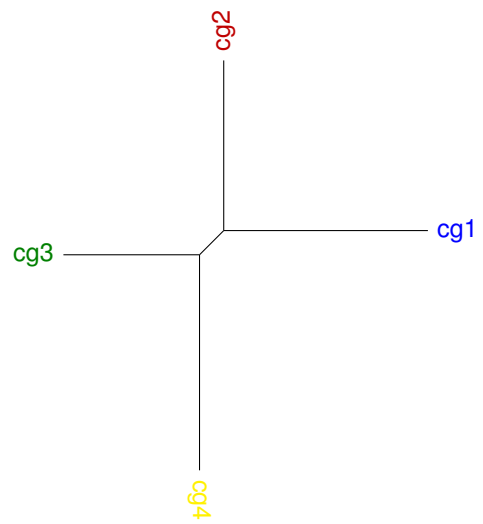
**degen12S**



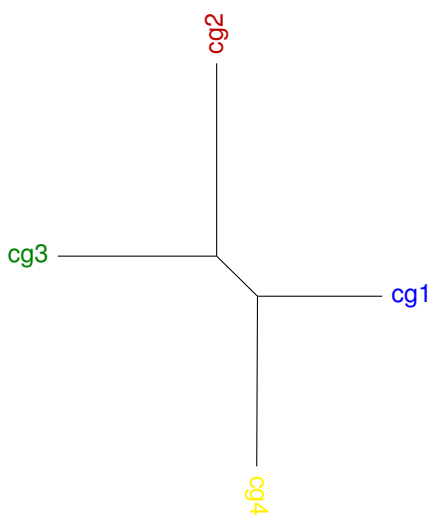
**NDCH**



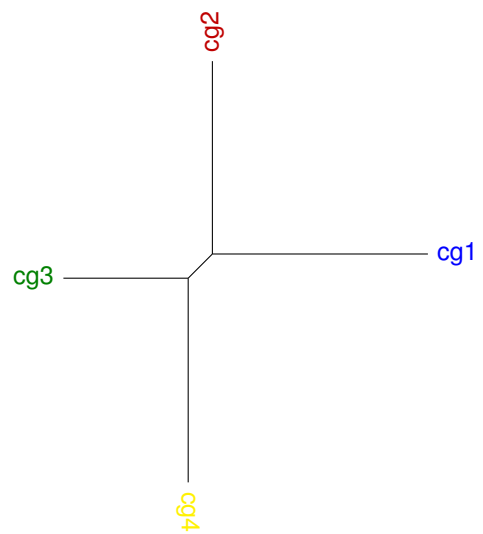
**degen1LR**



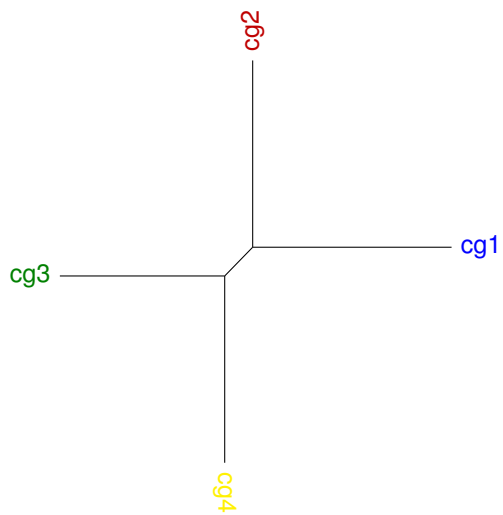
**unrecoded\_p**



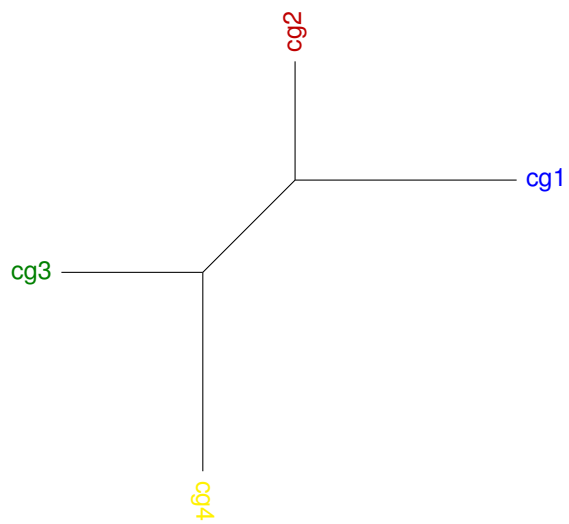
**degen12LRS**



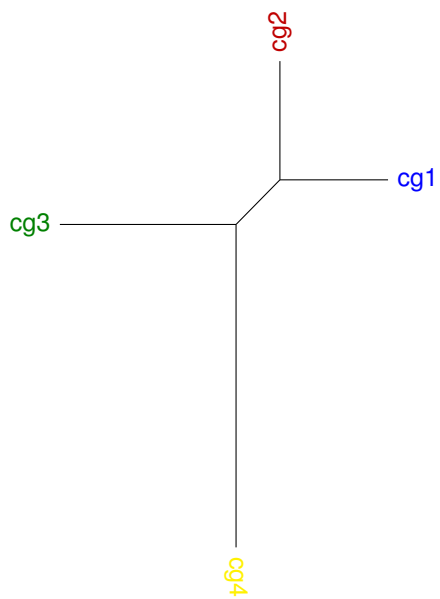
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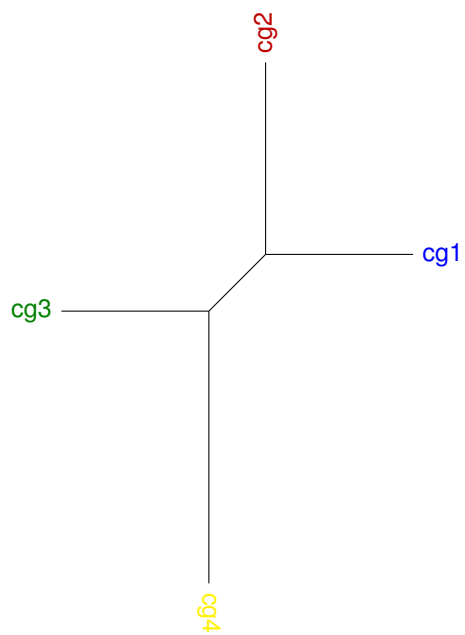
CAT



JCdist



logdet



**pars**

