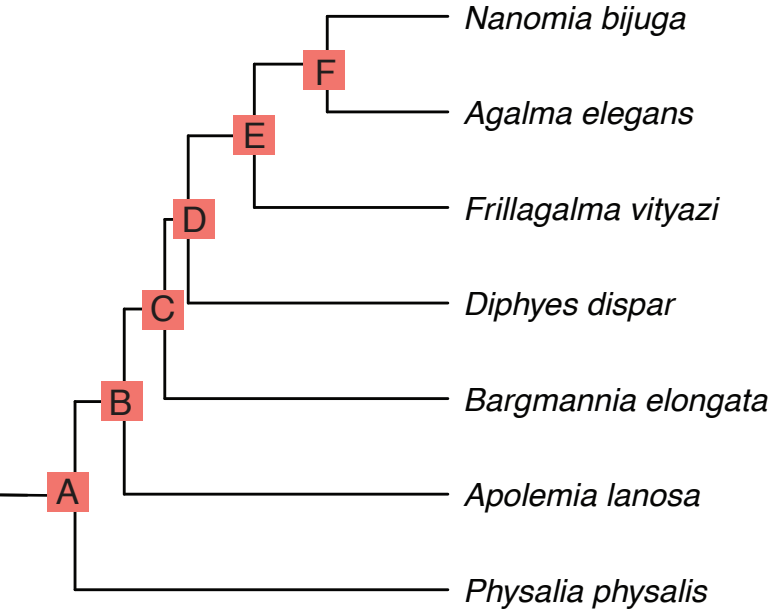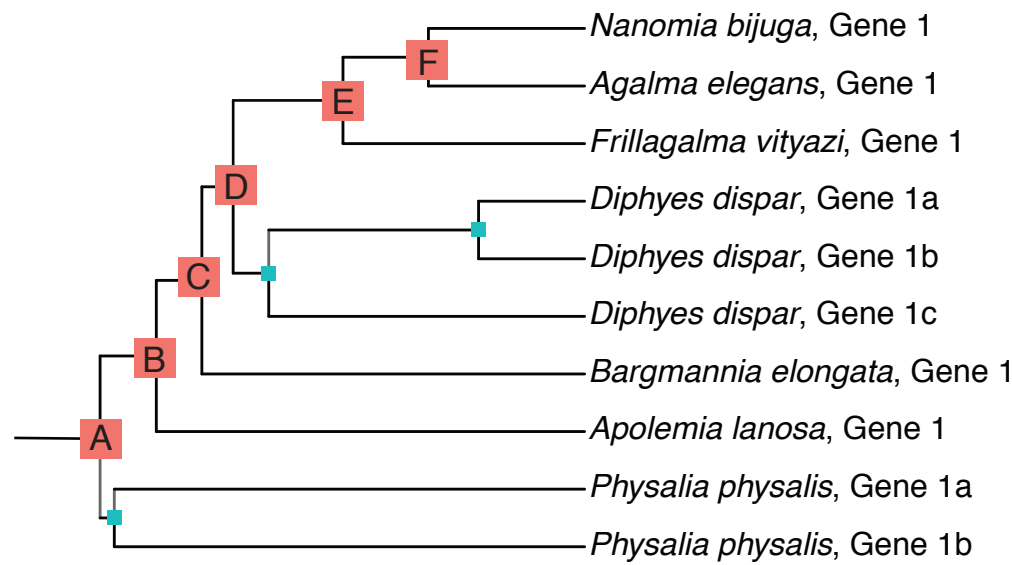**① Identify speciation and duplication nodes in the gene tree**

Siphonophore phylogeny
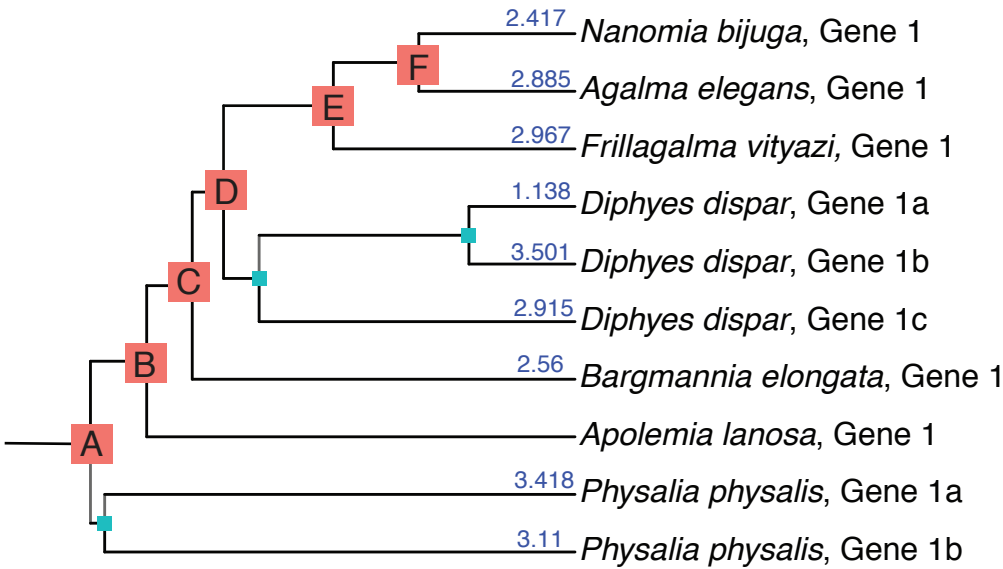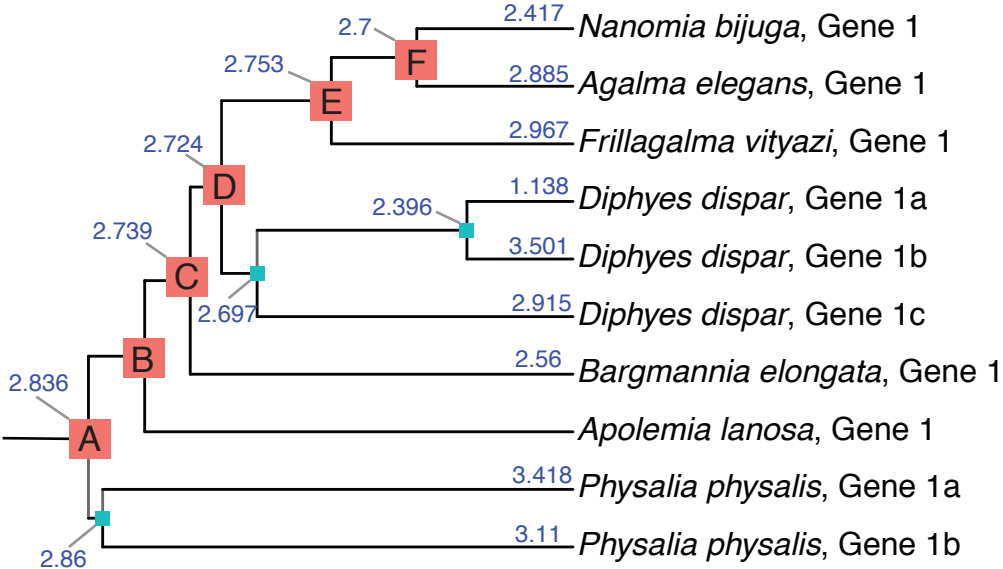
An exemplar gene tree

■ Speciation event   ■ Duplication event
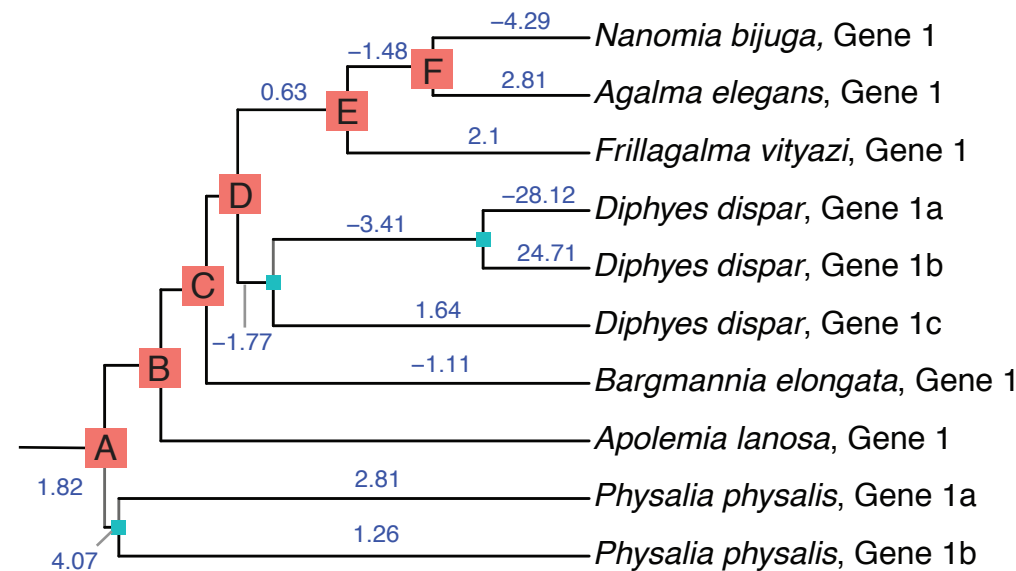
② Map expression values to tips of gene tree

③ Reconstruct ancenstral expression values at nodes

④ Calculate scaled change across branches

$$\text{Scaled change} = \frac{\text{Child node} - \text{parent node}}{\text{Calibrated branch length}}$$

⑤ Isolate corresponding branches across all gene trees

Species phylogeny

— Focal branch

Gene tree 1

Gene tree 2

...n gene trees