

Choose an outgroup species O from the set of three possible outgroups: *P. gerardiana*, *P. bungeana*, and *P. squamata*

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Dataset D

Dataset $D_{\rho,0}$

Dataset D_{ρ}

Dataset D_s

Dataset $D_{s,0}$

For each gene, construct **NJ** tree and root the tree using outgroup O

Create 1000 bootstrap sets of gene trees by randomly choosing with replacement $L_{\rho,0}$ gene trees

Estimate the species tree using either **STAR**, **STEAC**, **RTC**, or **MDC** for each of the 1000 bootstrap sets of gene trees

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Create 1000 bootstrap average p -distance matrices by randomly choosing with replacement L genes and calculating the distance as $\mathbf{P}^{all}$

Estimate the species tree using **NJ** for each of the 1000 bootstrap distance matrices and root each tree with outgroup O

Estimate the species tree using **SMRT with NJ** for each of the 1000 bootstrap distance matrices and root each tree with outgroup O

Create 1000 bootstrap concatenated alignments by randomly choosing with replacement L genes to concatenate

Estimate the species tree using either **ML**, **MP**, or **NJ** for each of the 1000 bootstrap concatenated alignments and root each tree with outgroup O

3

Estimate the species tree using **SMRT** with either **ML**, **MP**, or **NJ** for each of the 1000 bootstrap concatenated alignments and root each tree with outgroup O

3

For each gene, construct **ML**, **MP**, or **NJ** tree and root the tree using outgroup O

3

Create 1000 bootstrap sets of gene trees by randomly choosing with replacement $L_{s,0}$ gene trees

Estimate the species tree using either **STAR**, **STEAC**, **RTC**, or **MDC** for each of the 1000 bootstrap sets of gene trees

4

$3 \times 4 + 3 + 3 + 3 \times 3 + 3 \times 3 + 3 \times 3 \times 4 = 72$ phylogenetic inference strategies