

Reliability Assessment in Evolutionary Trees Using Grids

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Introduction: Phylogenetic Reconstruction

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...CTCGG CTTAC TTCTC TTCCT TCTCT...
...CTTGG CTTAT TCCCTT TTCCCT CCTTA...
...TTAGG GGCCC TCTTA CTAAT TCTAG...
...TGAAA CATTG GAGTA CTTCT ACTGT...
...TGAAA TATTG GTGTG ATCCT CCTAT...
...TGAAA CATCG GAGTA GTCCCT GTTCT...
...TGAAT GTCTG GTTTA ACAAT TTATT...
...TGATT AATTG GAGTA ATTAT TTTAT...
```

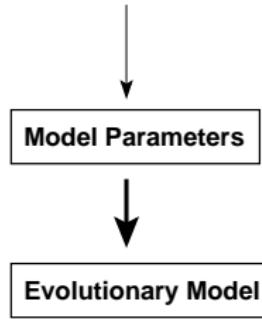
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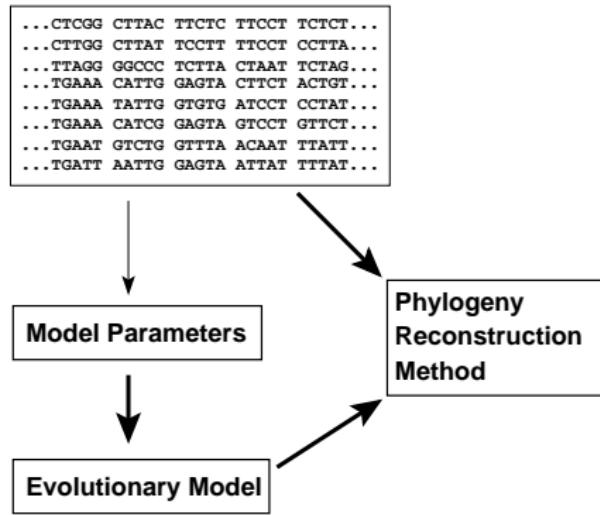
Evolutionary Model

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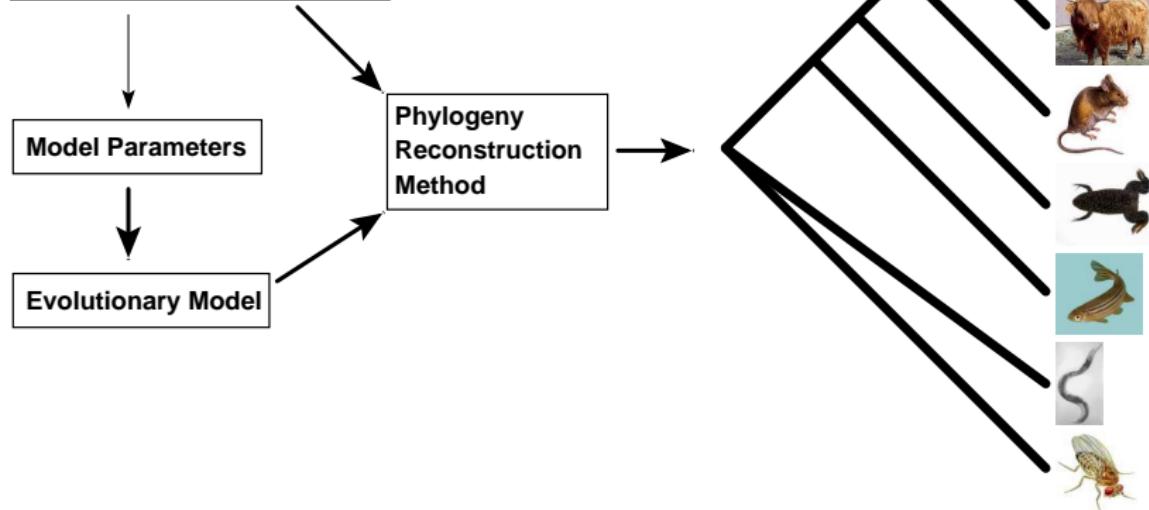


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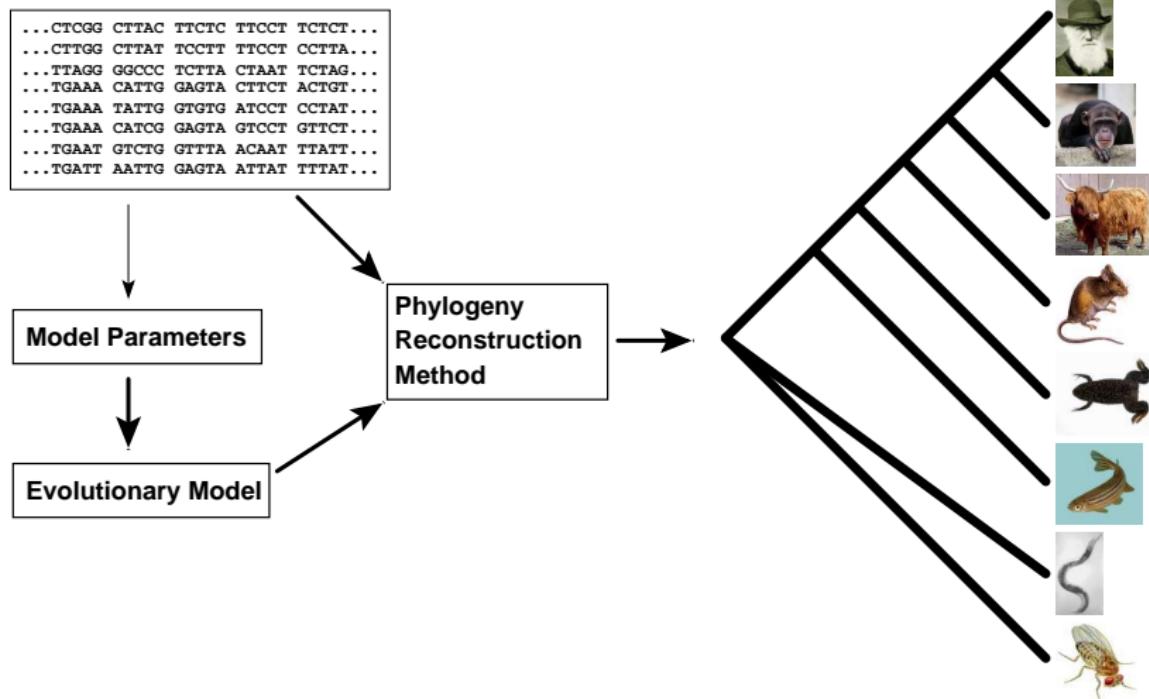


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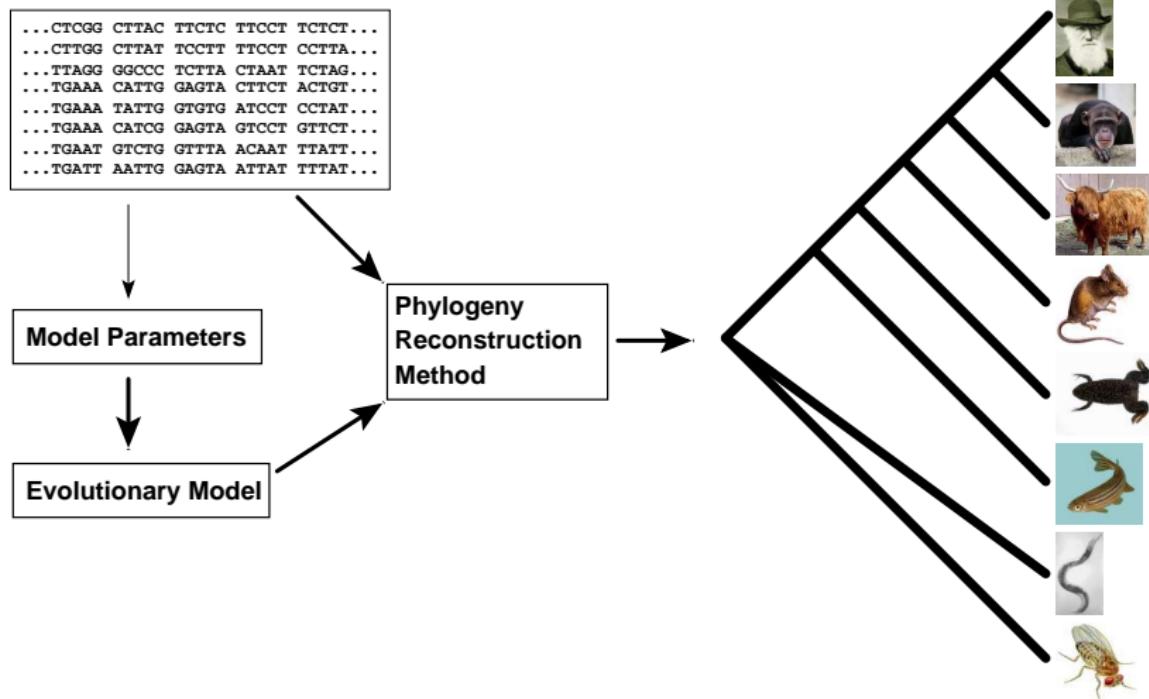


Introduction: Phylogenetic Reconstruction



Problem: Usually we get a tree without any measure of certainty for the reconstructed subtrees.

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Problem: Usually we get a tree without any measure of certainty for the reconstructed subtrees. Common solution: Bootstrapping.