

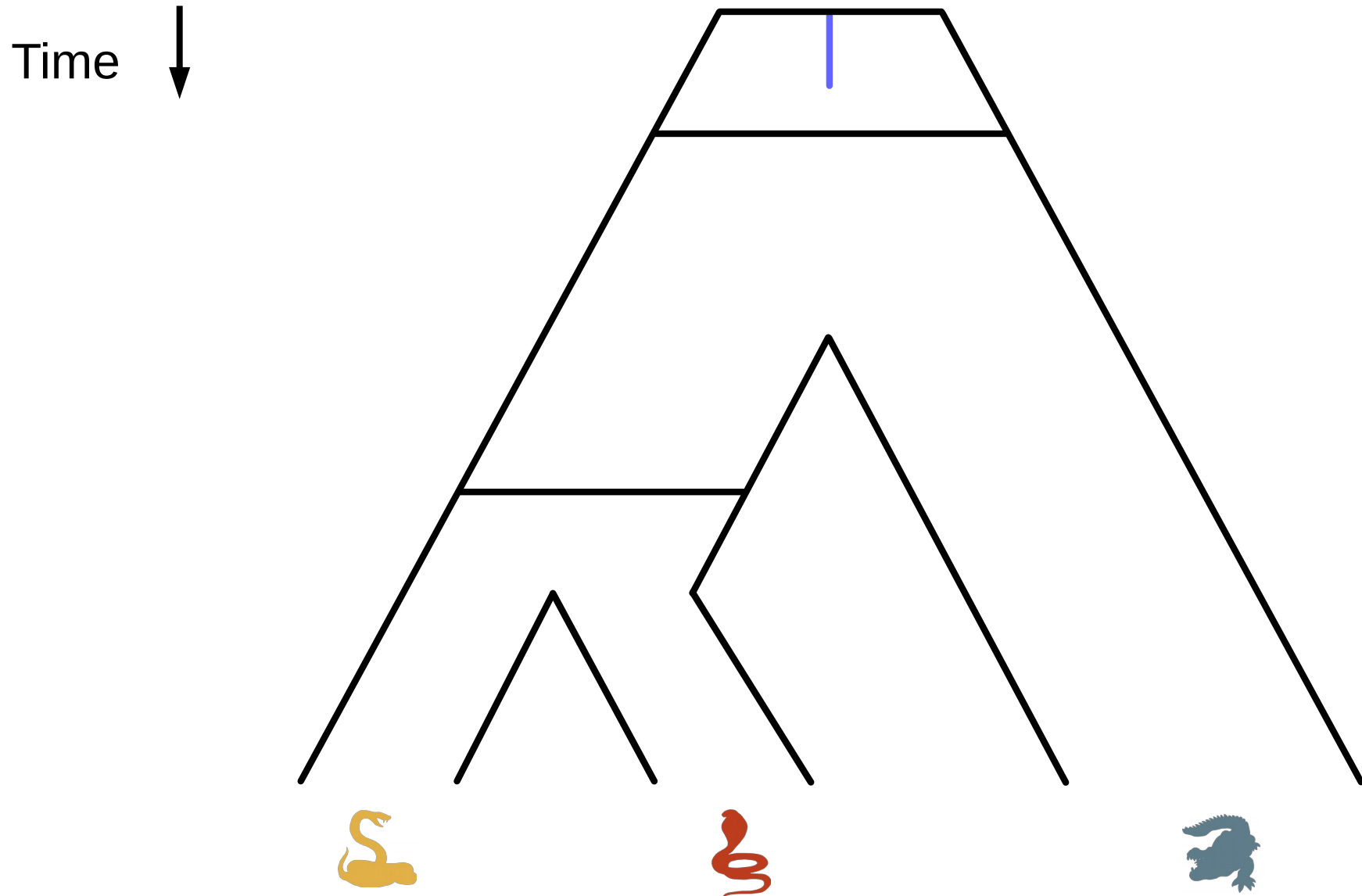
Introduction to GeneRax



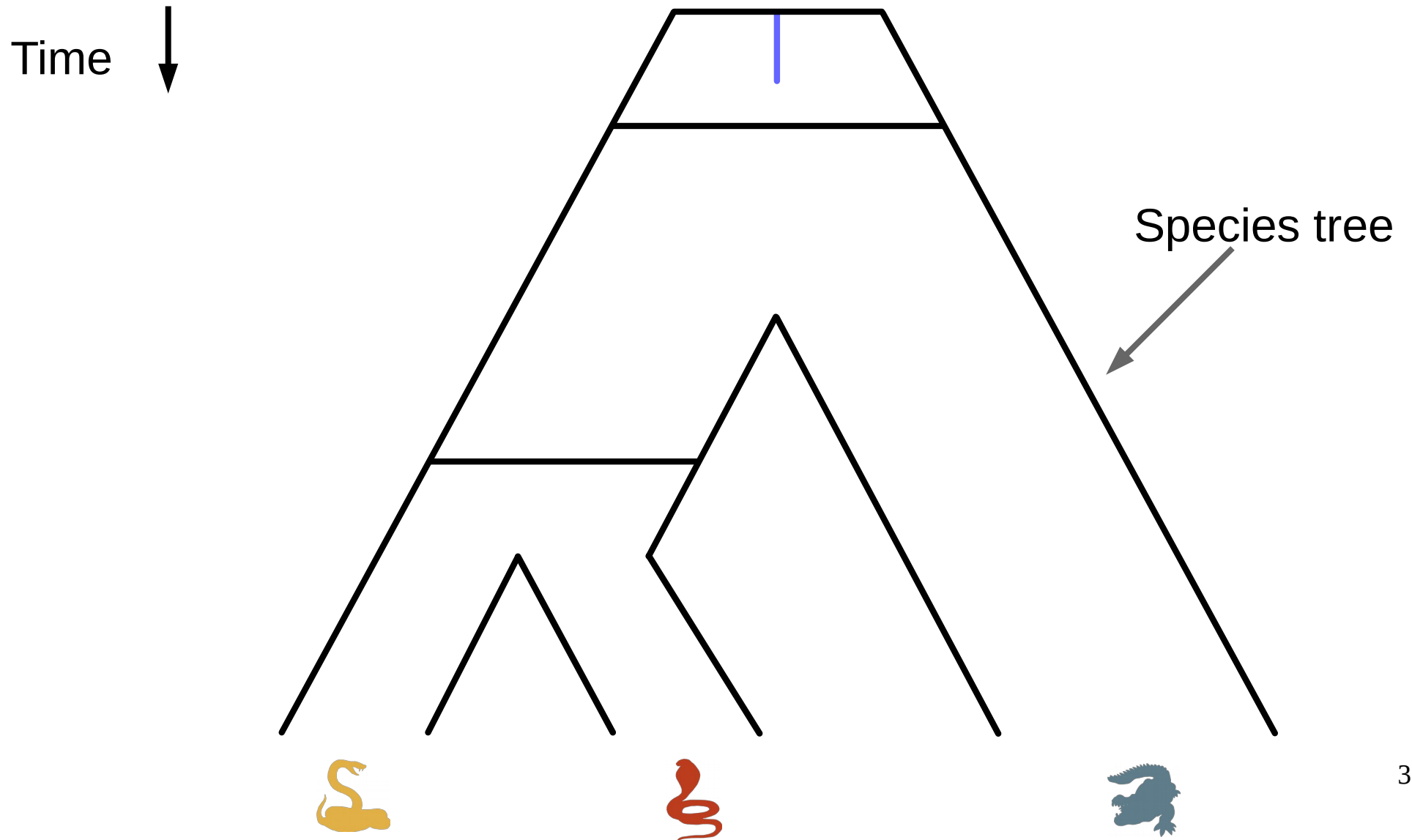
Benoit Morel



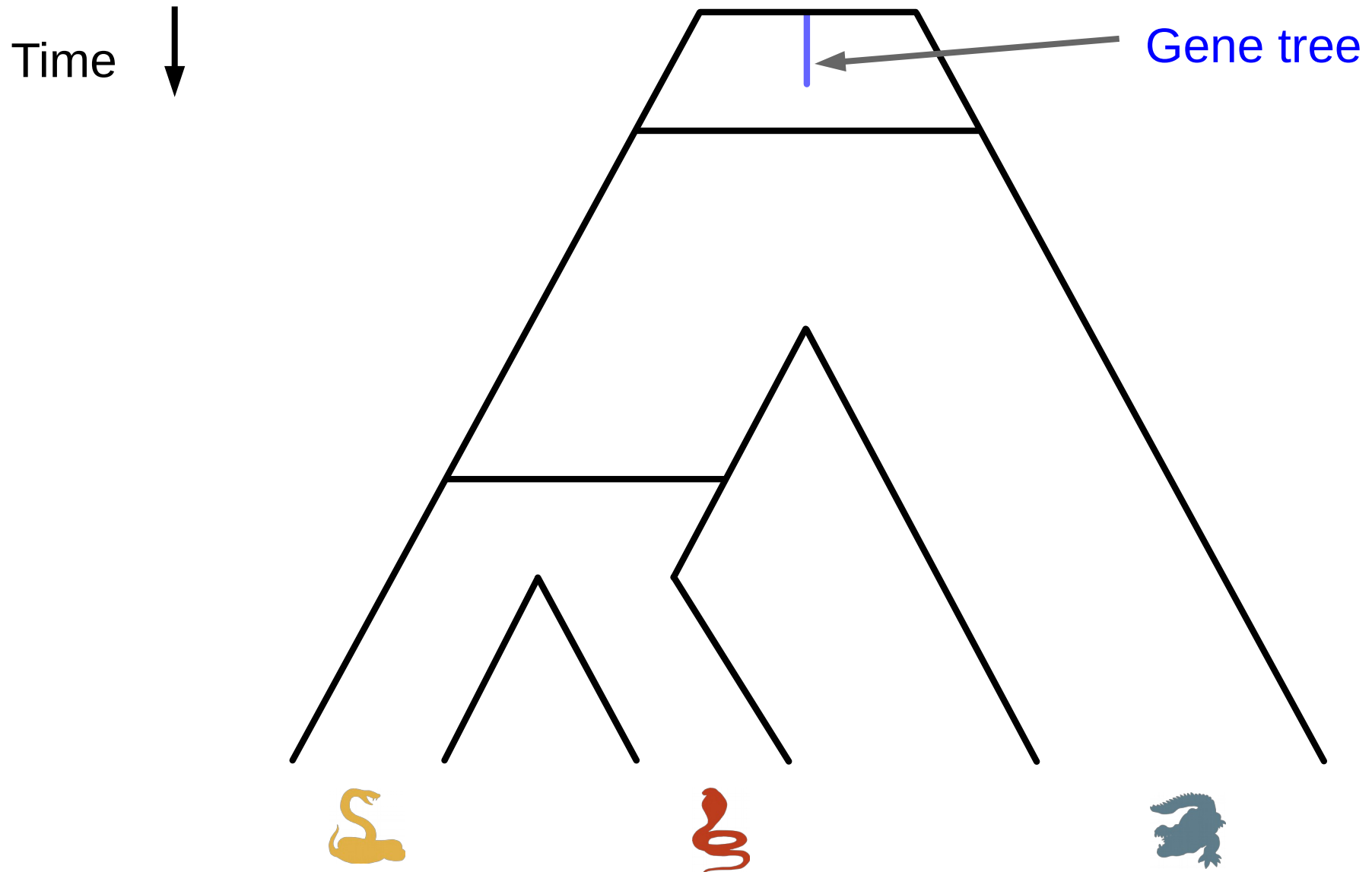
Gene evolution



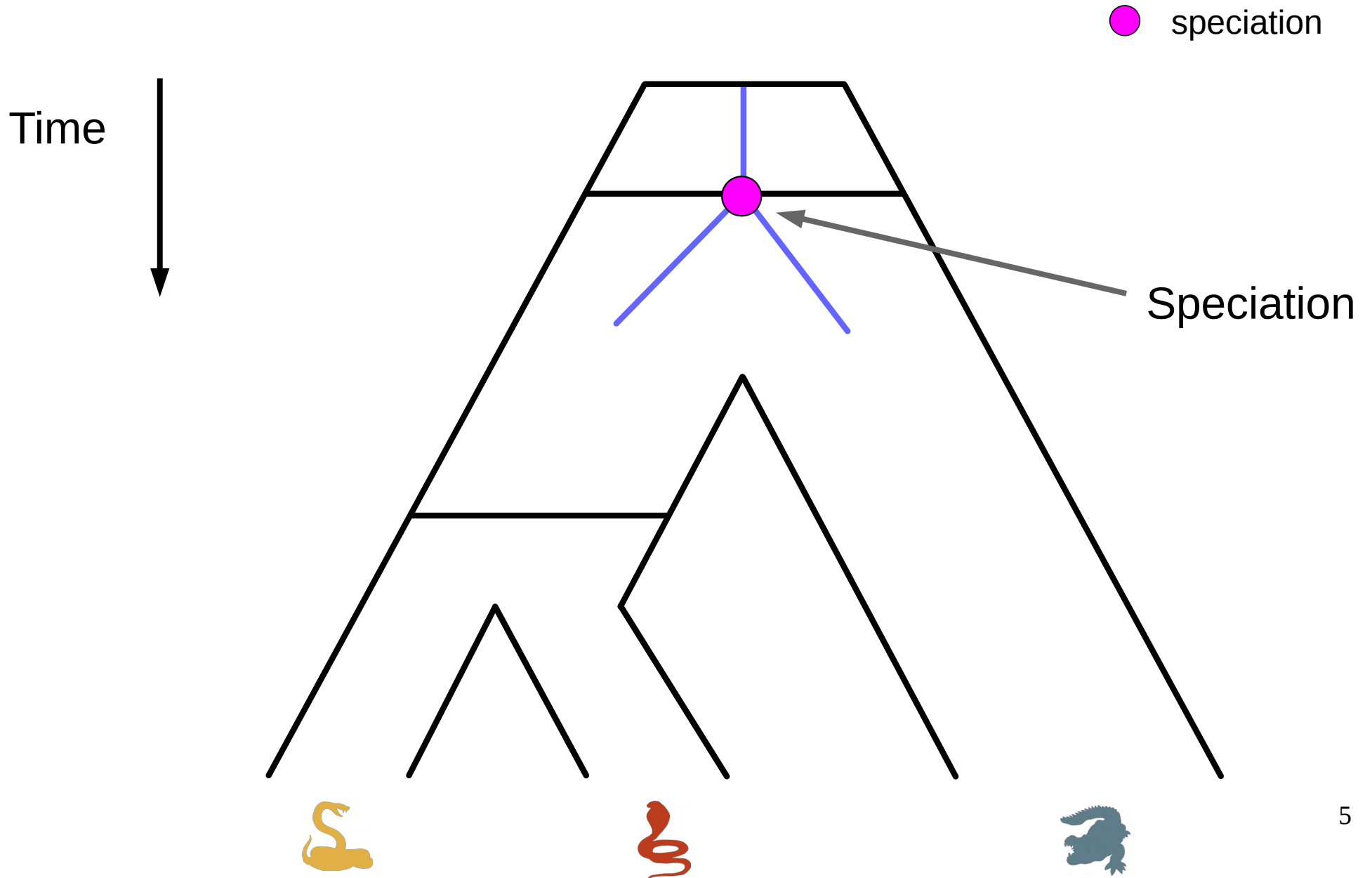
Gene evolution



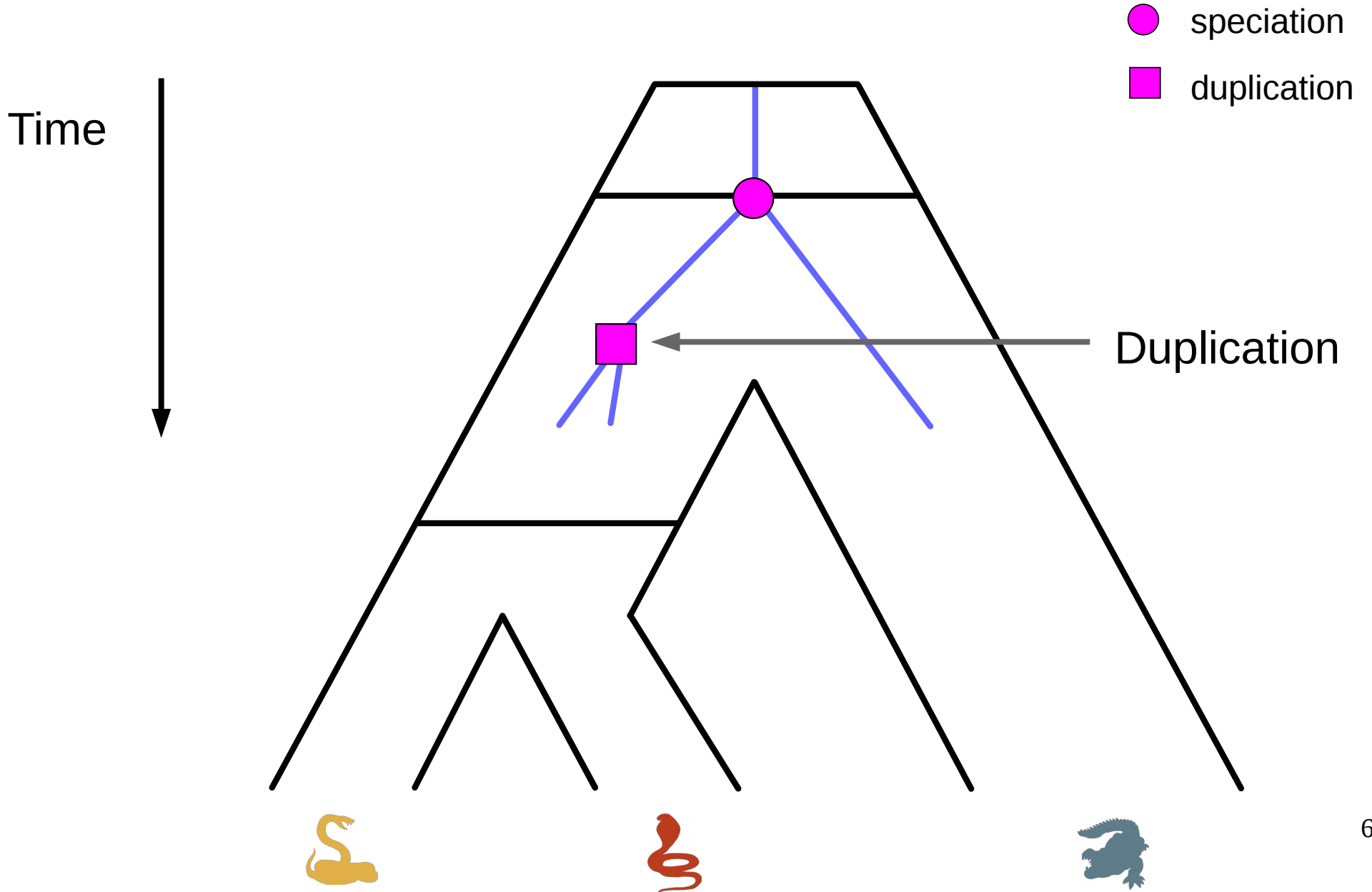
Gene evolution



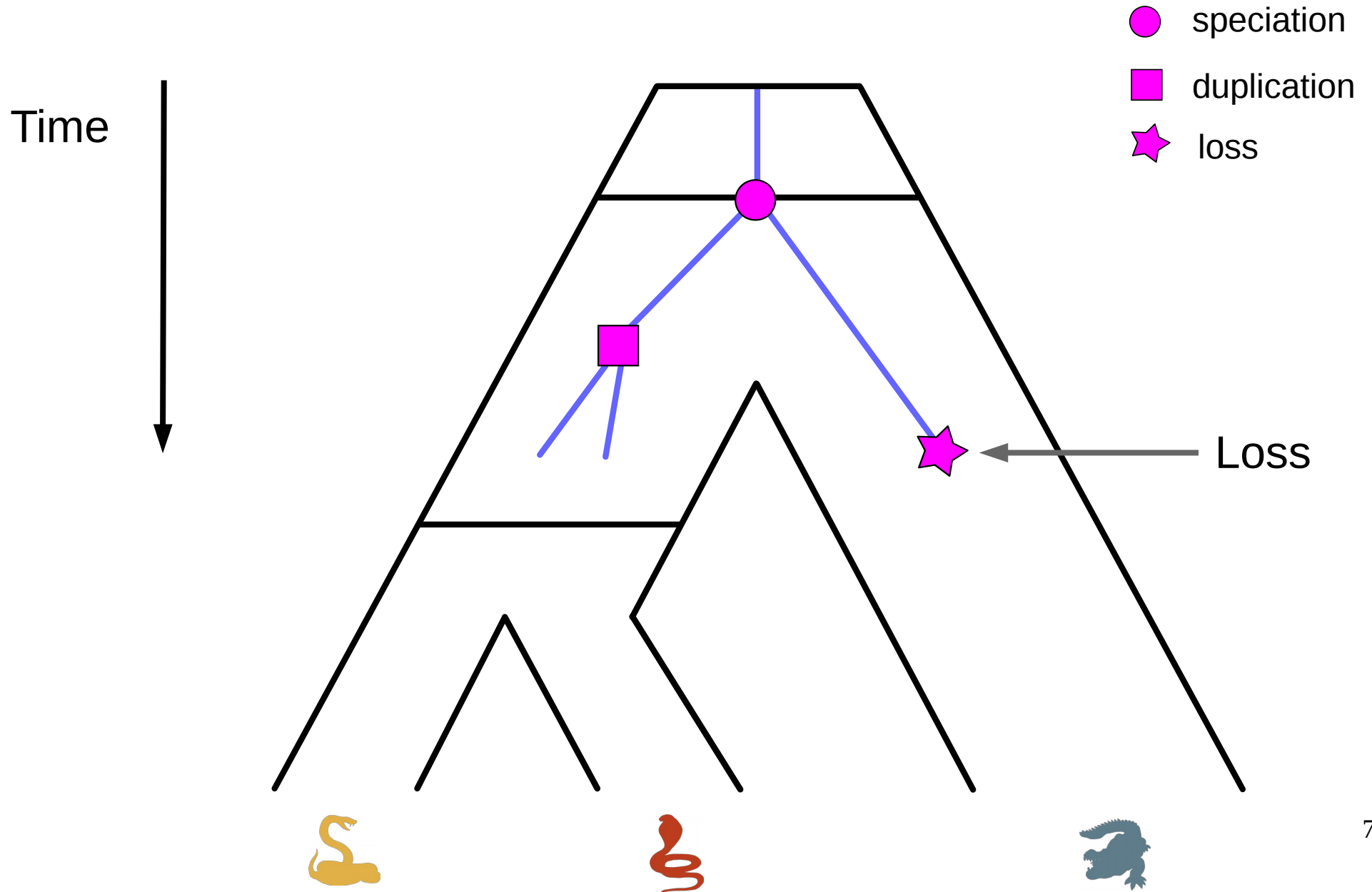
Gene evolution



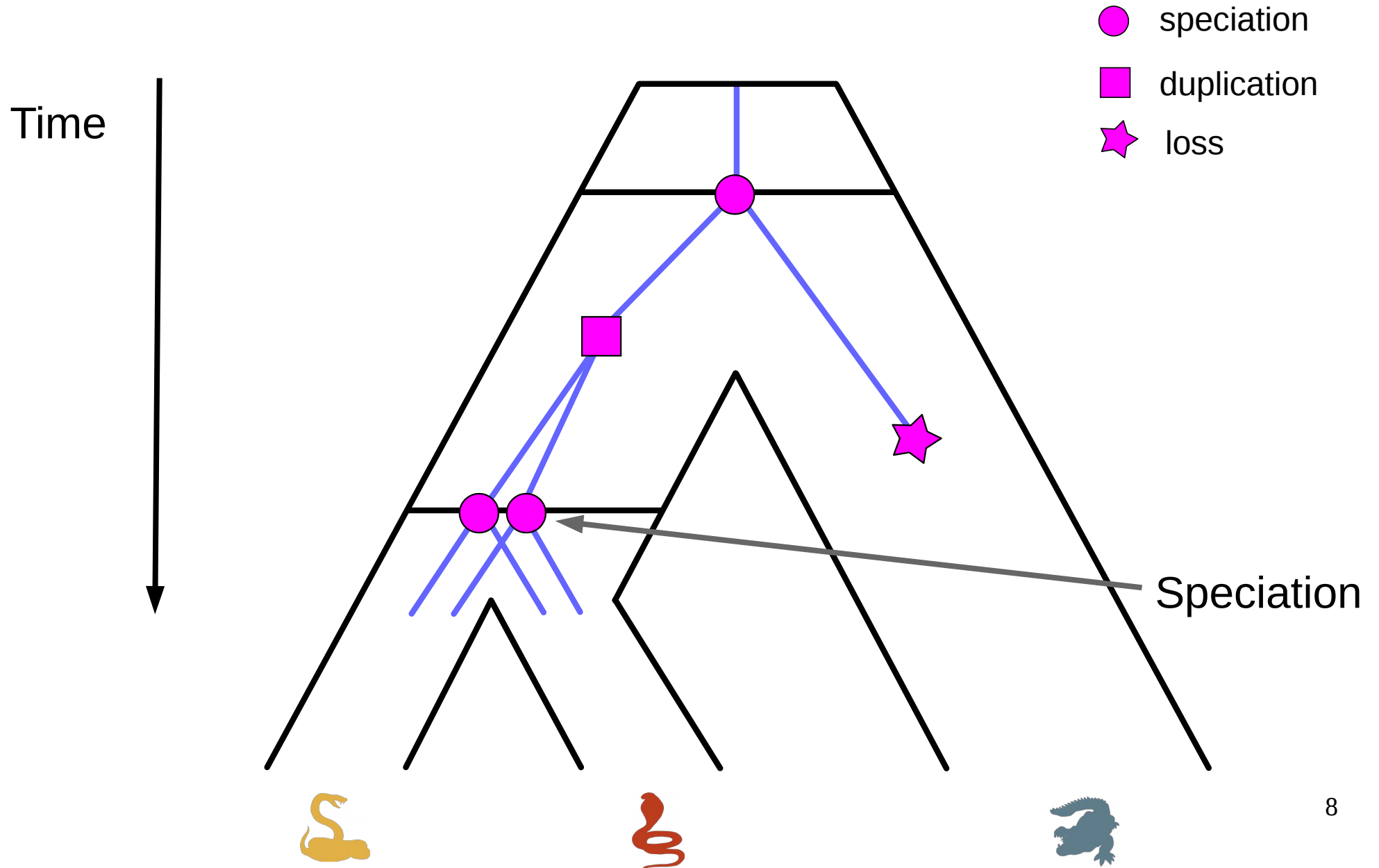
Gene evolution



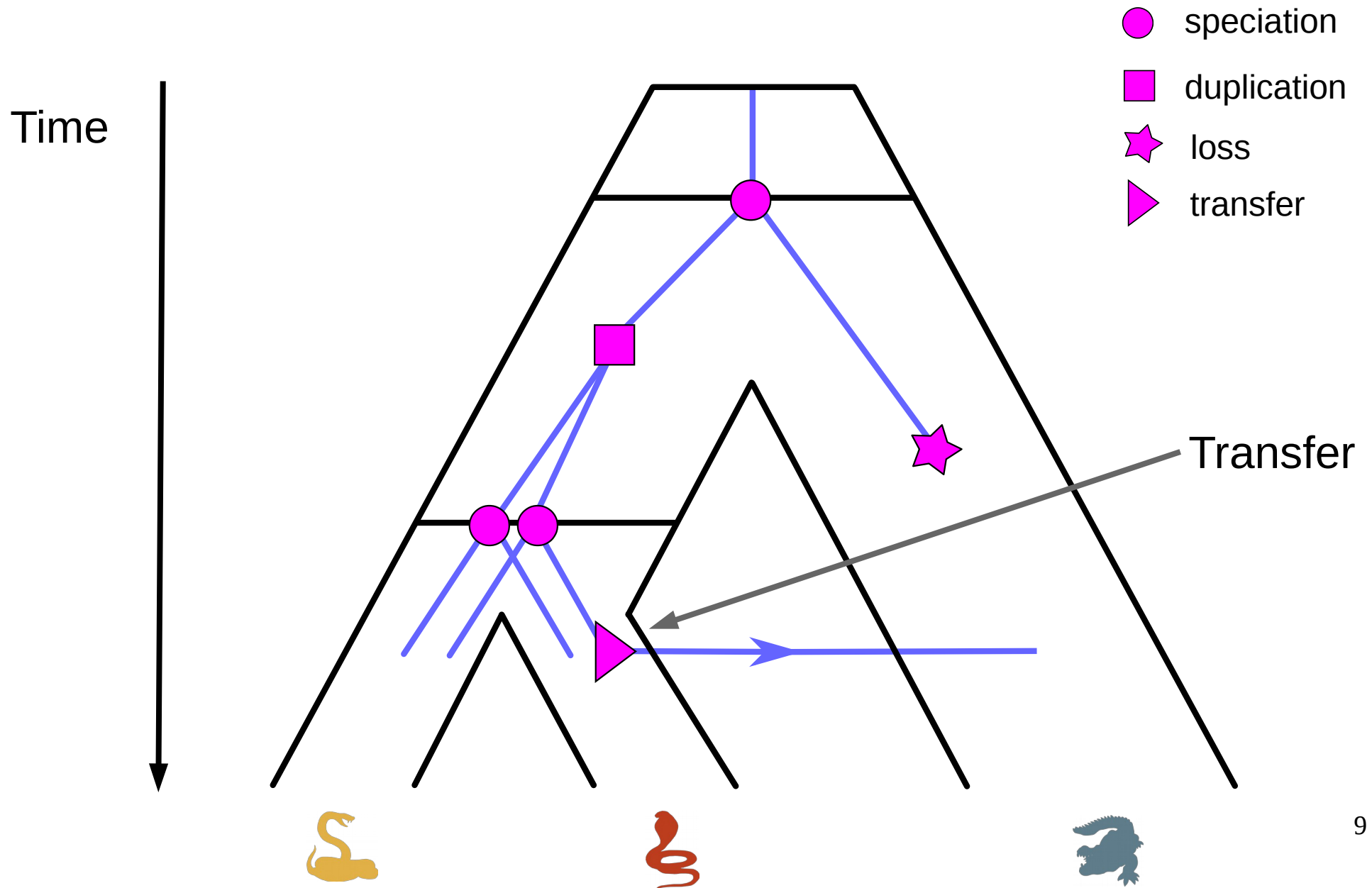
Gene evolution



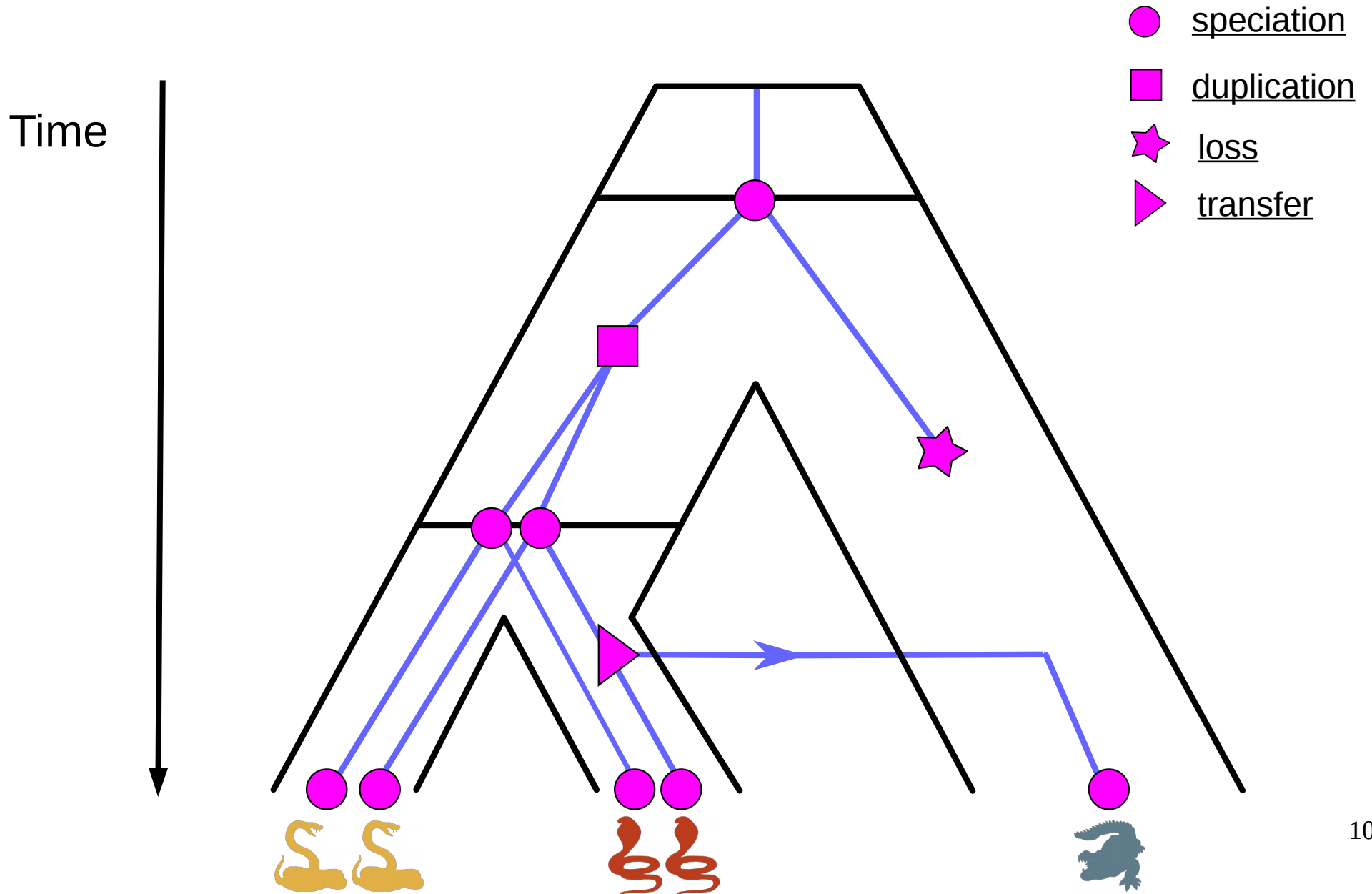
Gene evolution



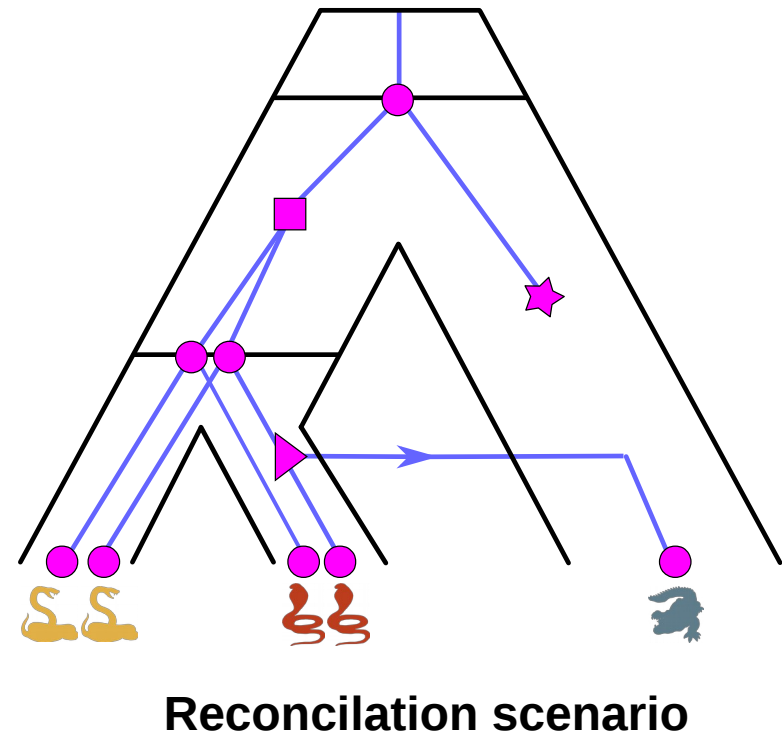
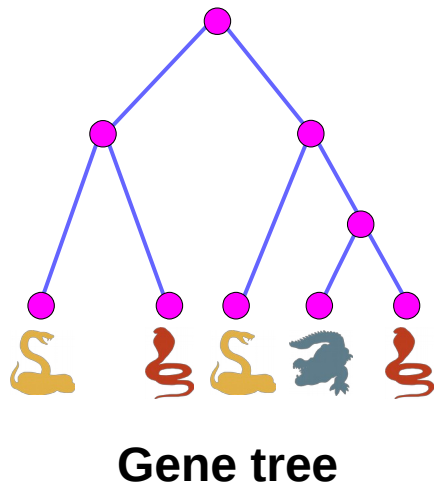
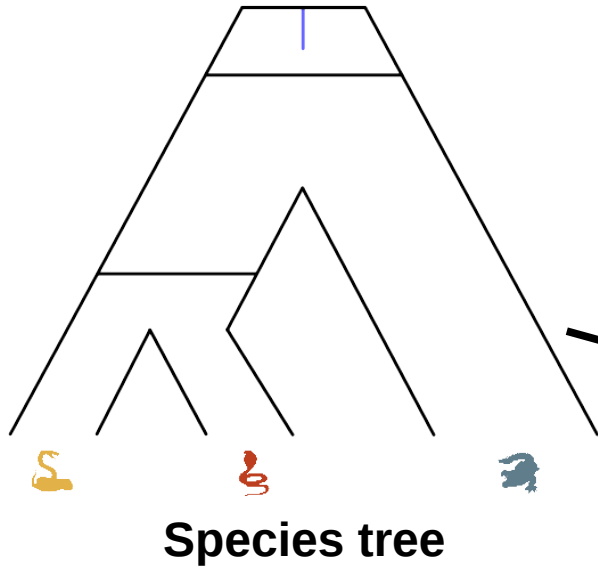
Gene evolution



Gene evolution



Reconciliation

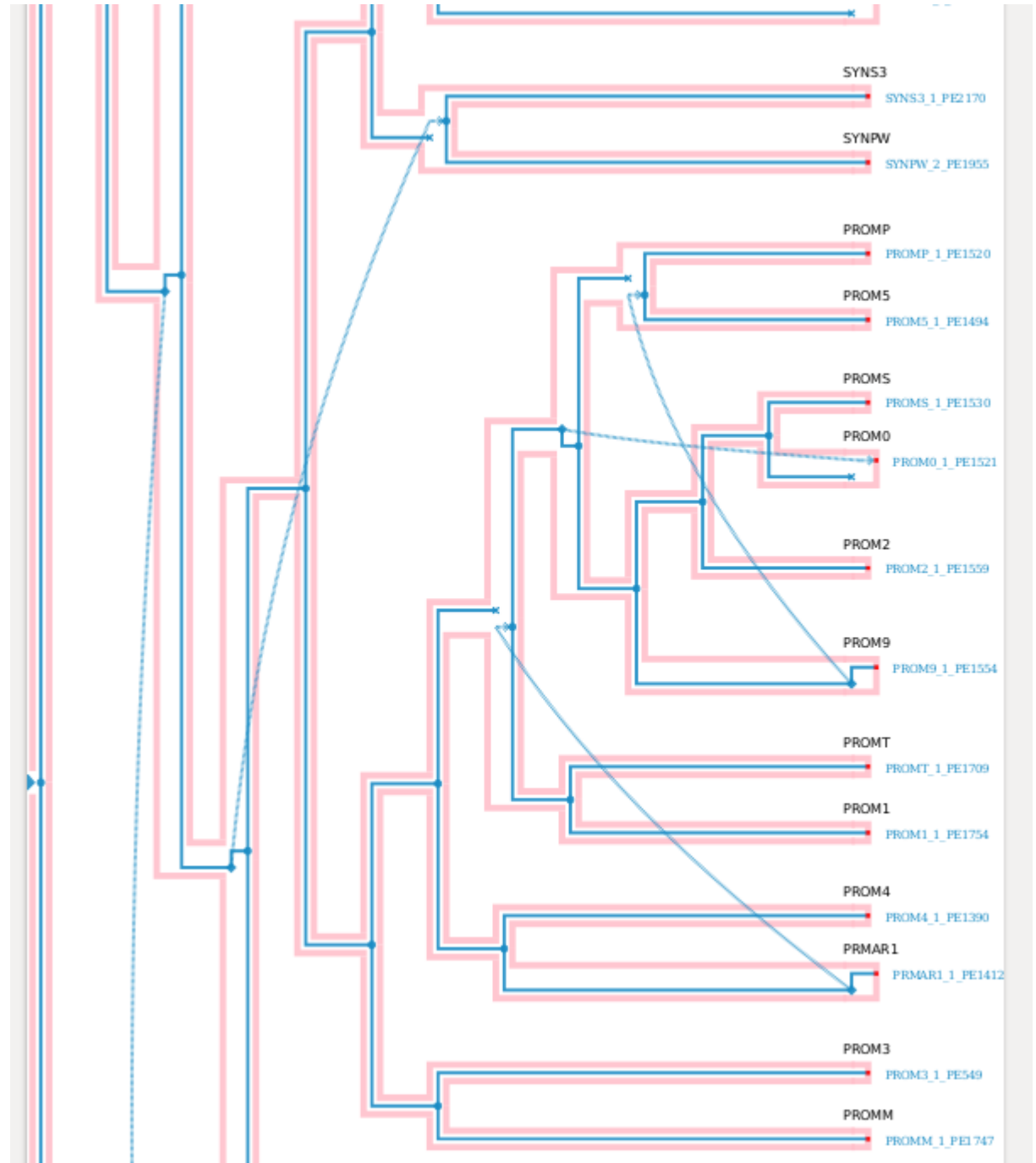


Obstacle to reconciliation

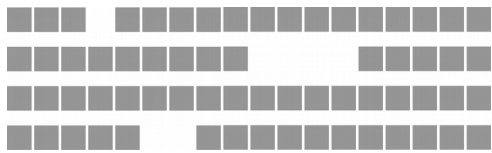
Gene trees inferred from the sequences only are often **inaccurate**



Overestimation of the
number of HGTs
because of gene tree
reconstruction error



RAxML-NG, IQTree etc.

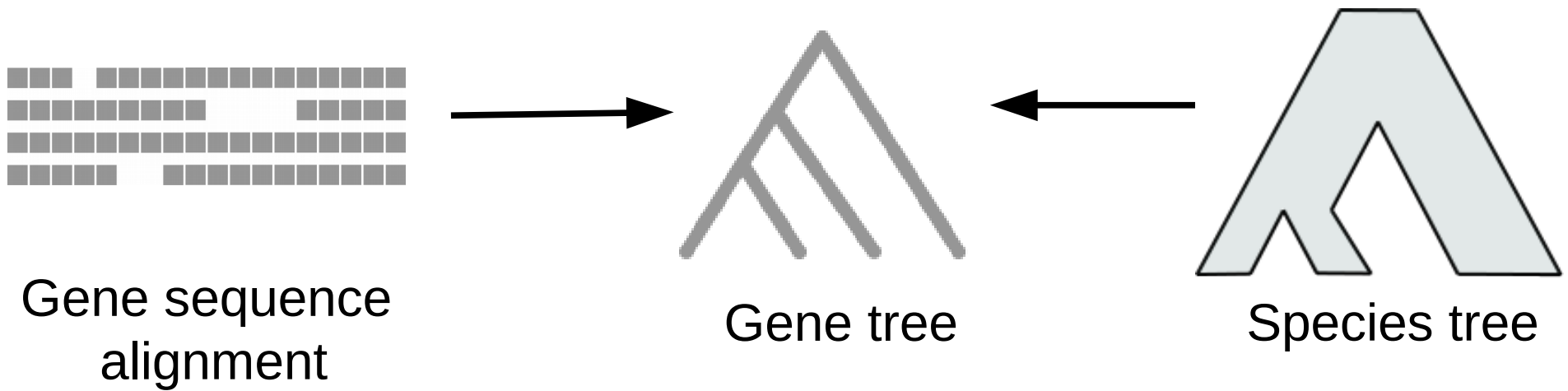


Gene sequence
alignment



Gene tree

Gene tree correction



RAxML-NG, IQTree etc.

Find the gene tree that maximizes the likelihood:

$$P(\text{alignment} | \text{tree})$$

GeneRax

Find the gene tree that maximizes the joint likelihood:

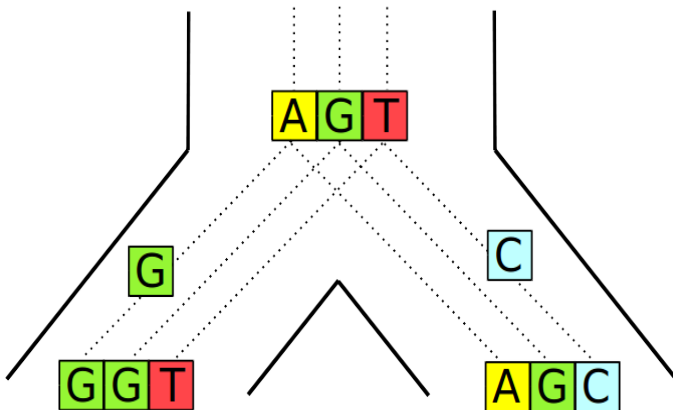
$$P(\text{[Genomic Map]} | \text{[Gene Tree]}) P(\text{[Gene Tree] | \text{[Phylogenetic Tree]}})$$

GeneRax

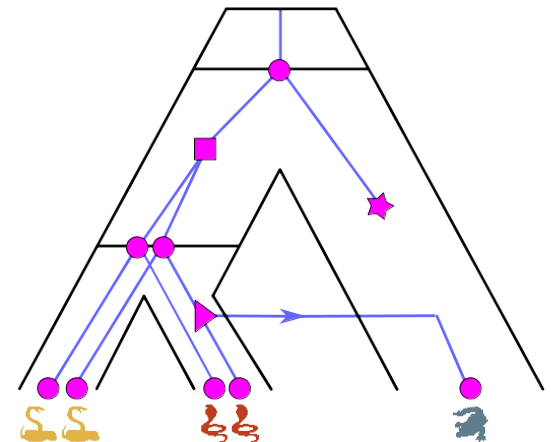
Find the gene tree that maximizes the joint likelihood:

$$P(\text{Sequences} | \text{Gene Tree}) \cdot P(\text{Gene Tree} | \text{Species Tree})$$

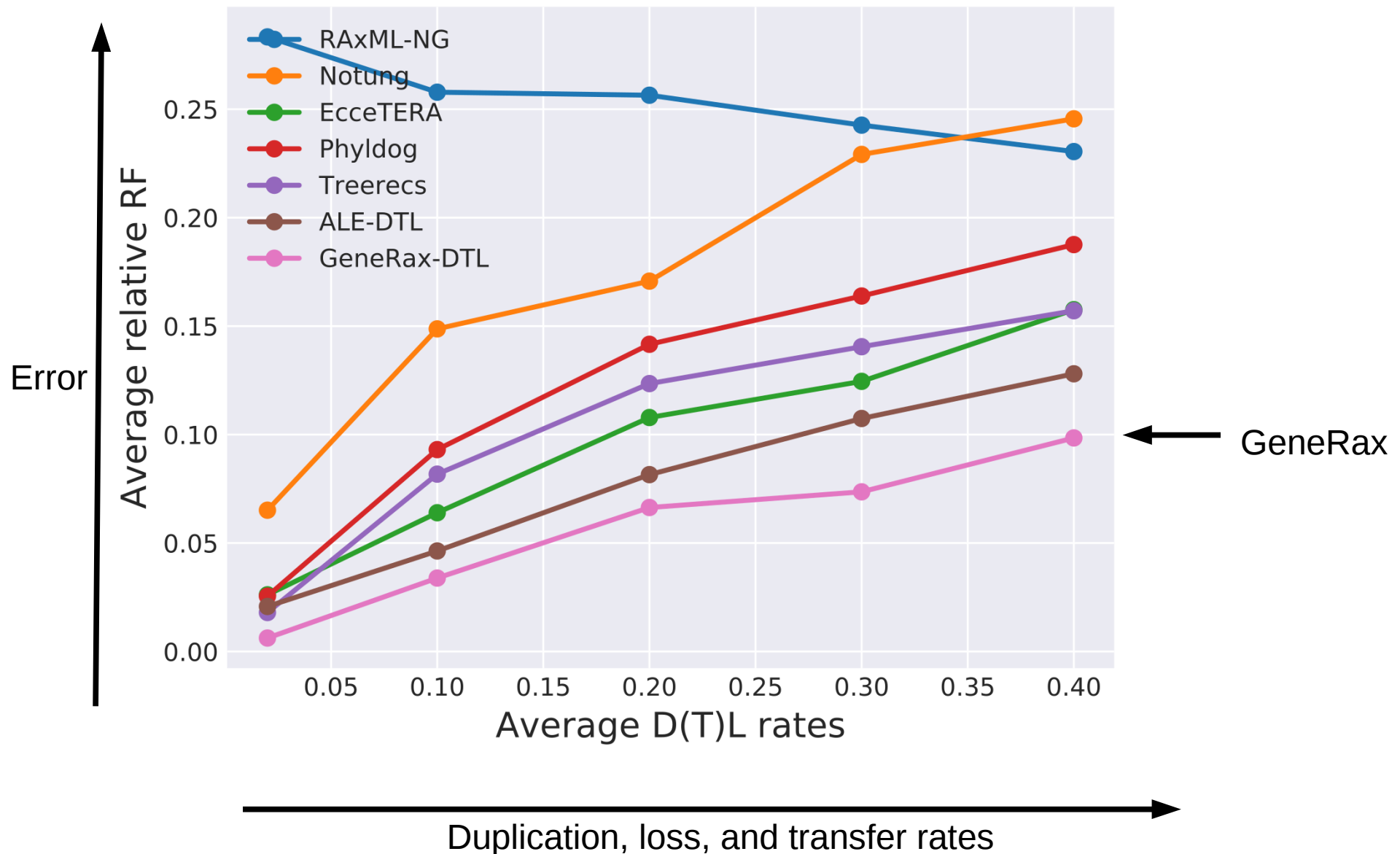
Phylogenetic likelihood

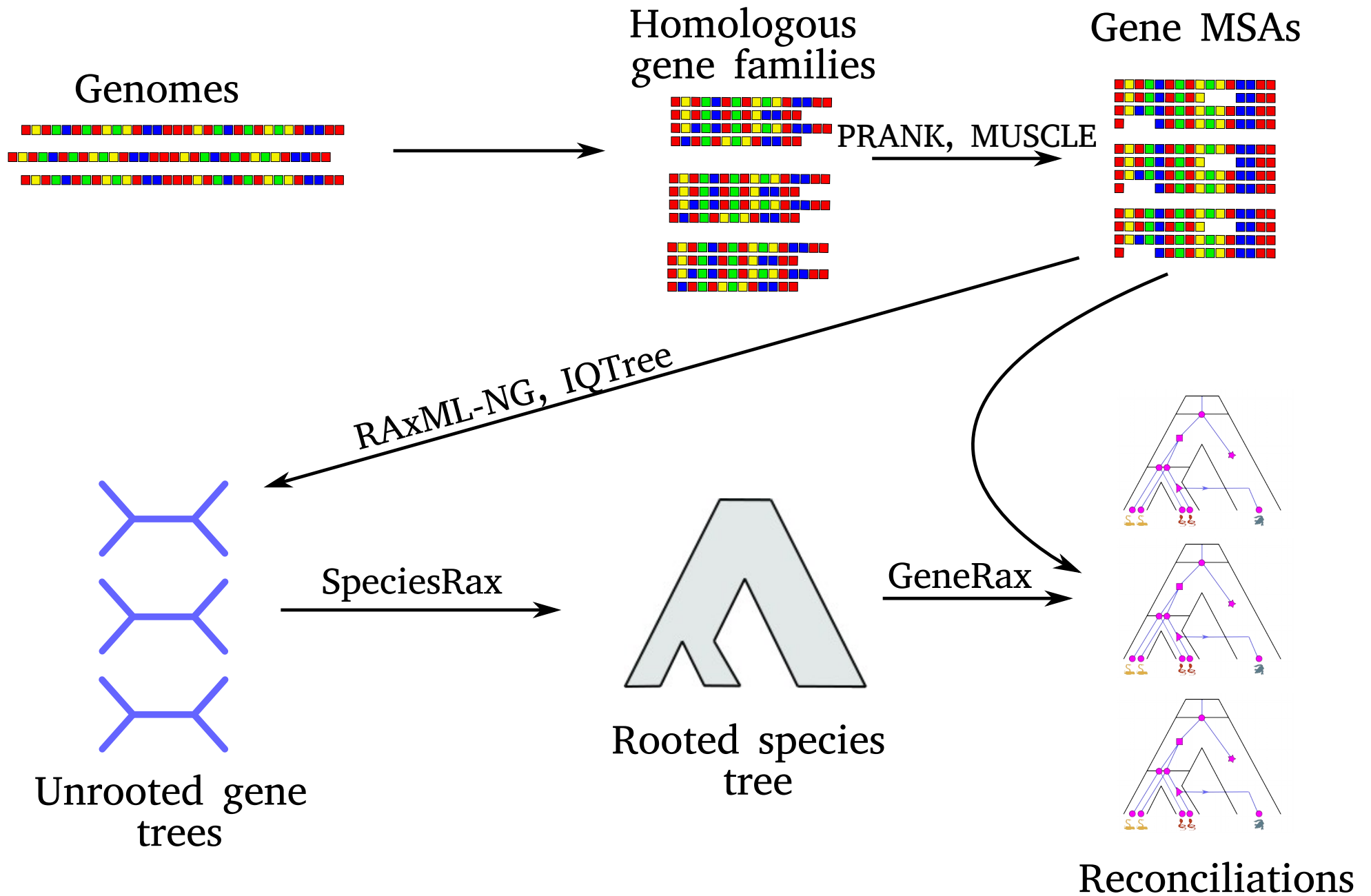


Reconciliation likelihood



Accuracy on simulations

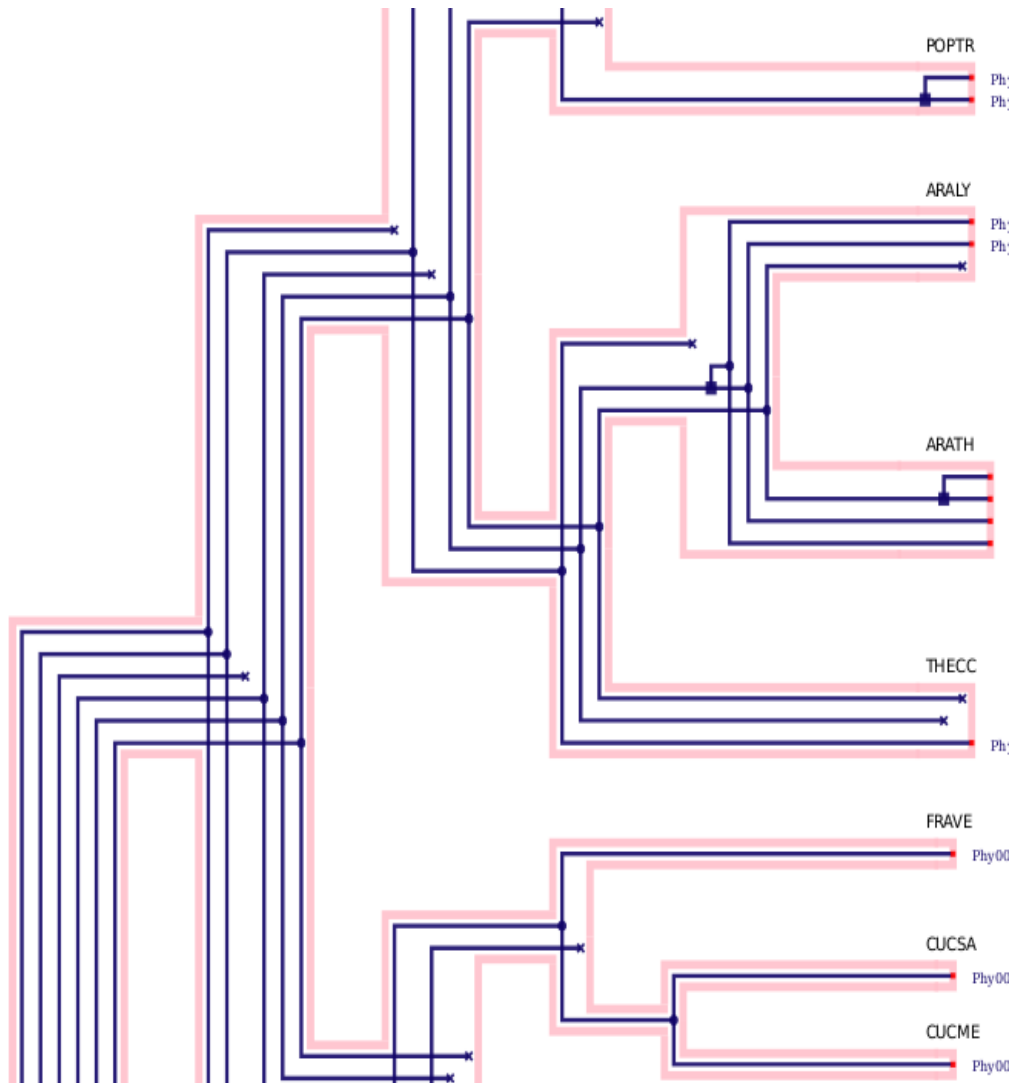




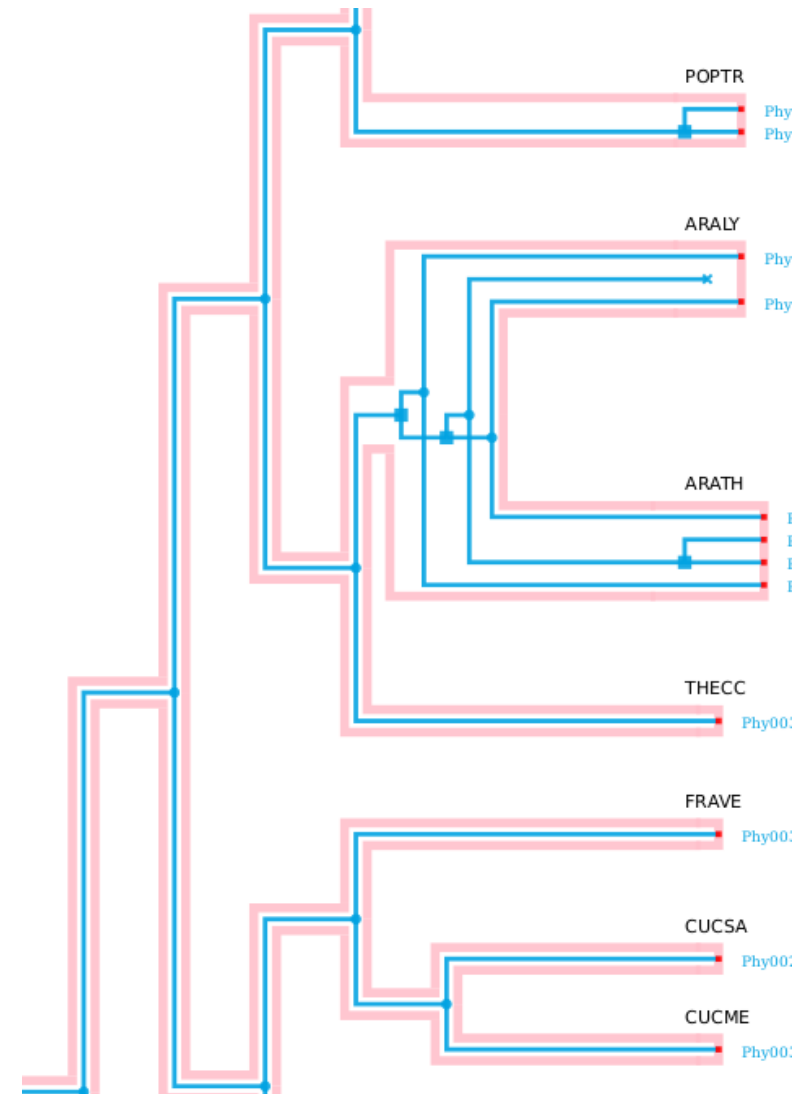
Short tutorial

- Reconciliation without correction
- Reconciliation with correction (GeneRax)
- Reconciliation with correction (Treerecs)
- And visualize those reconciliations! (Thirdkind)

Conclusion



No correction



With correction

The undatedDTL model

For a given gene copy at a given location in the species tree:

- $pS = P(\text{next event is a speciation})$
- $pD = P(\text{next event is a duplication})$
- $pL = P(\text{next event is a loss})$
- $pT = P(\text{next event is a transfer})$

$$pS + pD + pL + pT = 1.0$$

