

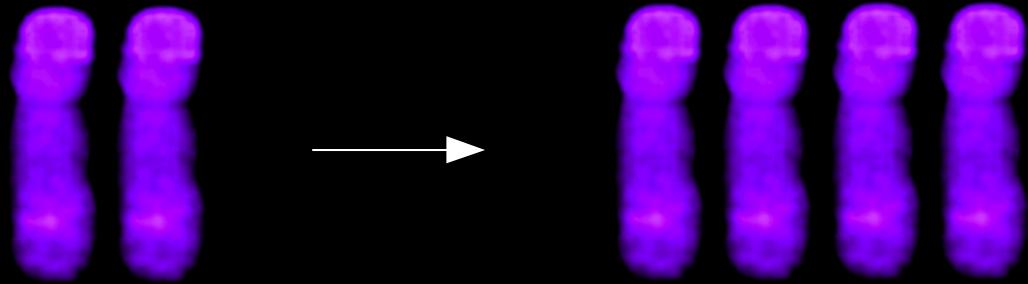
Correlating chromosome and climate evolution



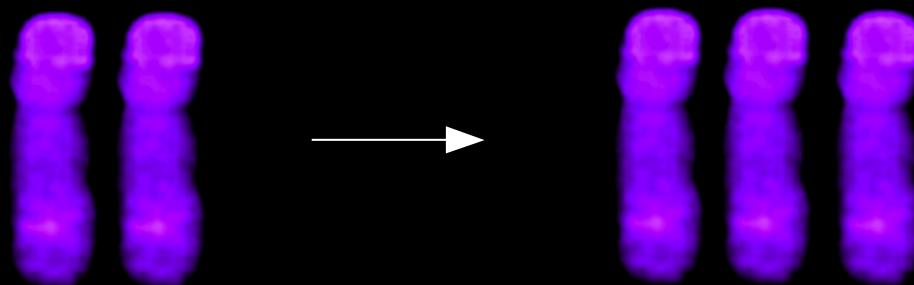
Jonathan Spoelhof



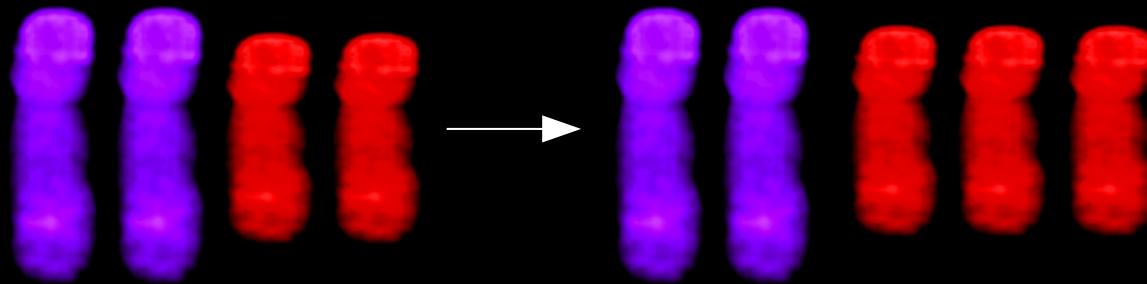
Chromosome number evolution



duplication



demi-
duplication



aneuploidy

Physiology

Altered vascular structure
(Bomblies, 2020, *Proceedings of the Royal Society B*)

Photosynthesis
(Coate & Doyle, 2013, 'Polyplloid and hybrid genomics')

Plant size
(Segraves, 2017, *New phytologist*)

Hybridization

Homoeolog expression anomalies

(Buggs et al., 2010, *Current Biology*)

Transgressive phenotypes

(McCarthy et al., 2017, *American Journal of Botany*)

Complex genotypes

Regulatory complexity
(Van de Peer et al., 2021, *The Plant Cell*)

Allelic diversity
(Schmickl & Yant, 2021, *New Phytologist*)

Are chromosomal
changes generally
correlated with shifts in
climatic evolution?

Steps

1. Reconstruct chromosomal evolution
2. Reconstruct climatic evolution
3. Compare the reconstructions

ChromEvol: Assessing the Pattern of Chromosome Number Evolution and the Inference of Polyploidy along a Phylogeny ③

Lior Glick, Itay Mayrose ✉ Author Notes

Molecular Biology and Evolution, Volume 31, Issue 7, July 2014, Pages 1914–1922,
<https://doi.org/10.1093/molbev/msu122>

Published: 07 April 2014

$$[Q]_{ij} = \begin{cases} \lambda + \lambda_l \times (i - 1) & j = i + 1 \text{ (ascending dysploidy)} \\ \delta + \delta_l \times (i - 1) & j = i - 1 \text{ (descending dysploidy)} \\ \rho & j = 2i \quad (\text{WGD}) \\ \mu & j = 1.5i \text{ (demi-polyploidy)} \\ 0 & \text{otherwise} \end{cases}$$

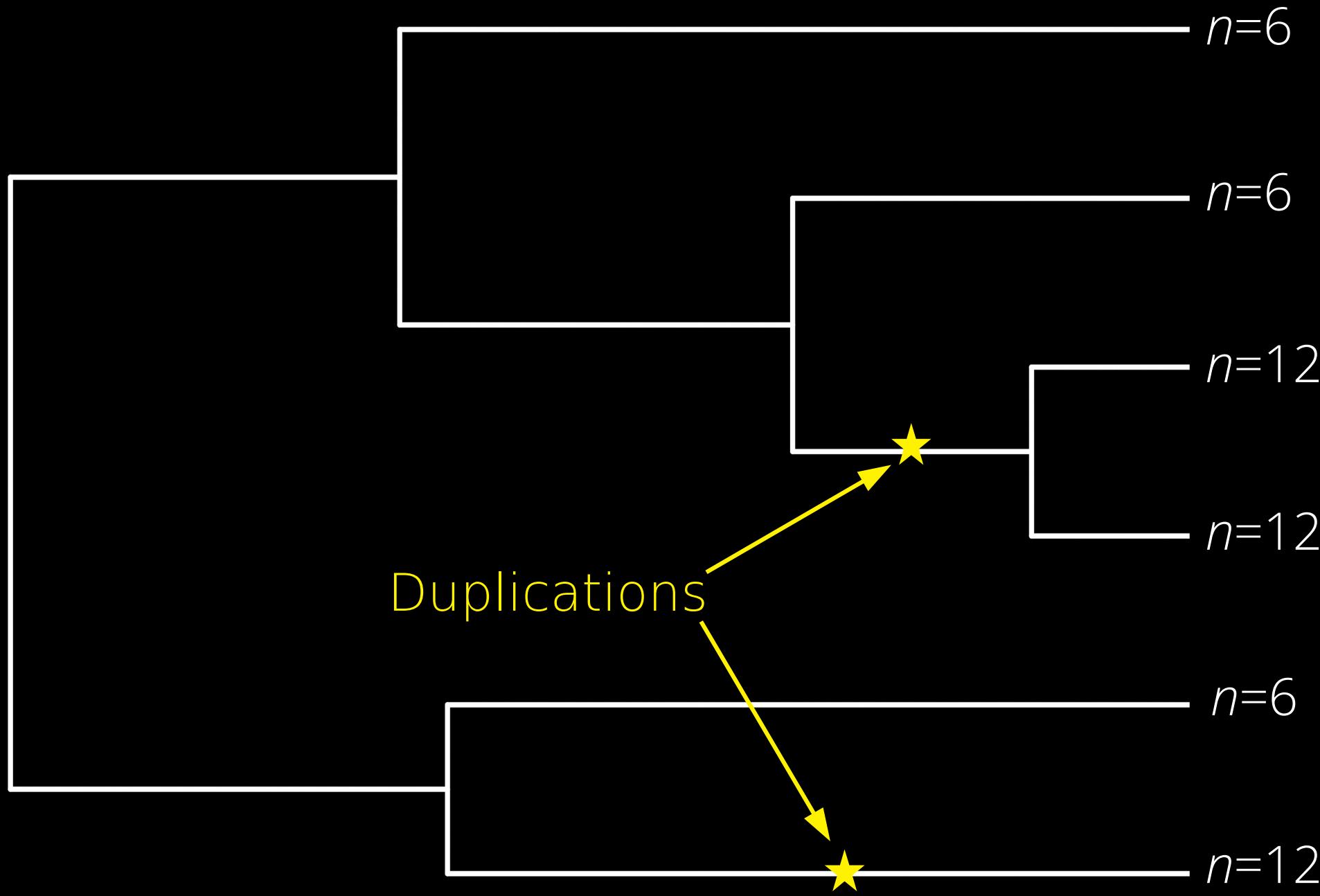
Evolutionary rate heterogeneity in chromosome count evolution: an application of the 'hidden-rates model'

Session: Macroevolution III

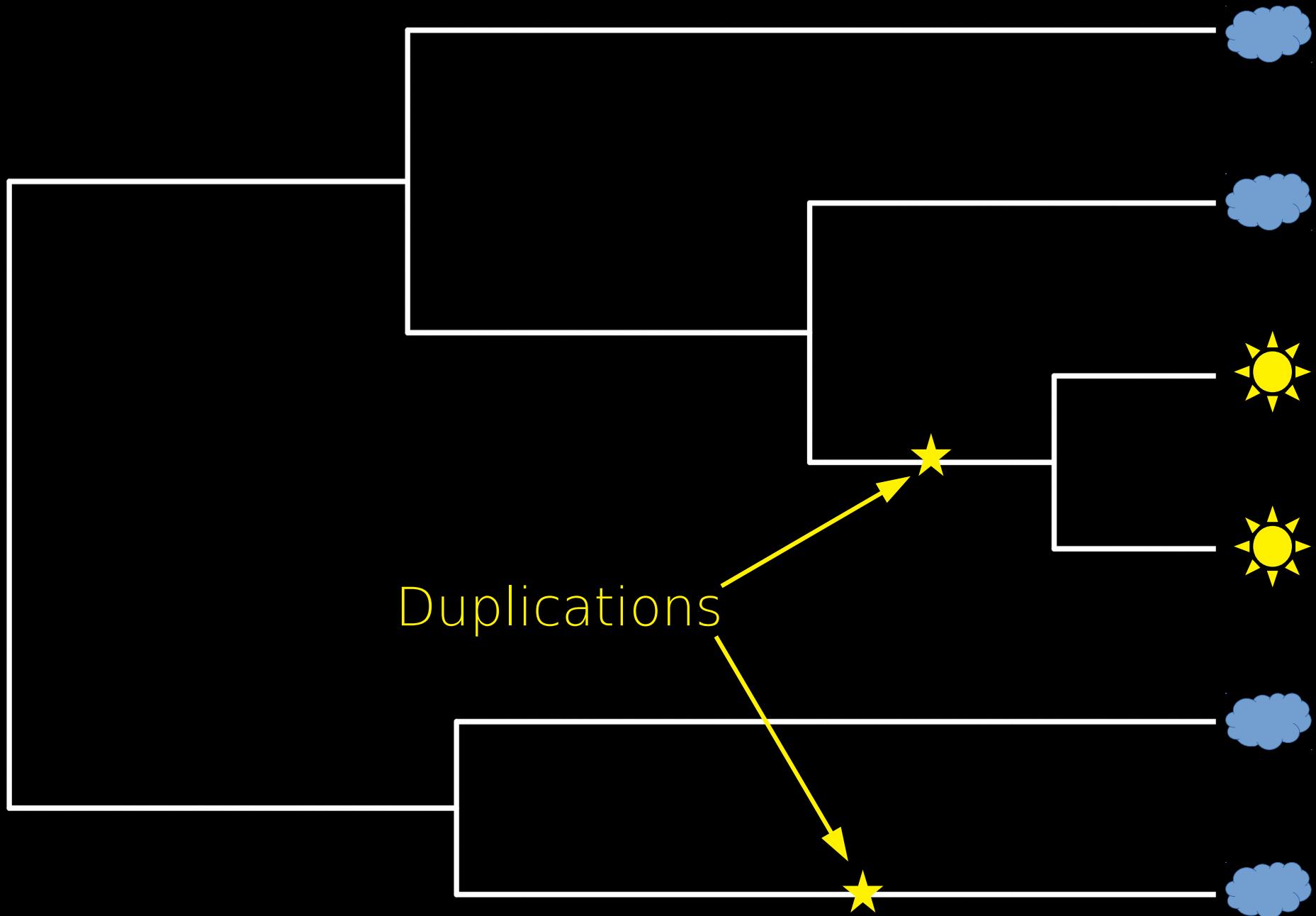
Date: Friday, July 23

Time: 10:45 am

Reconstruct chromosomal evolution



Reconstruct climate evolution



Climate variable reconstructions

Generate niche model with variables of interest

Extract predicted niche occupancies (PNOs) for each variable

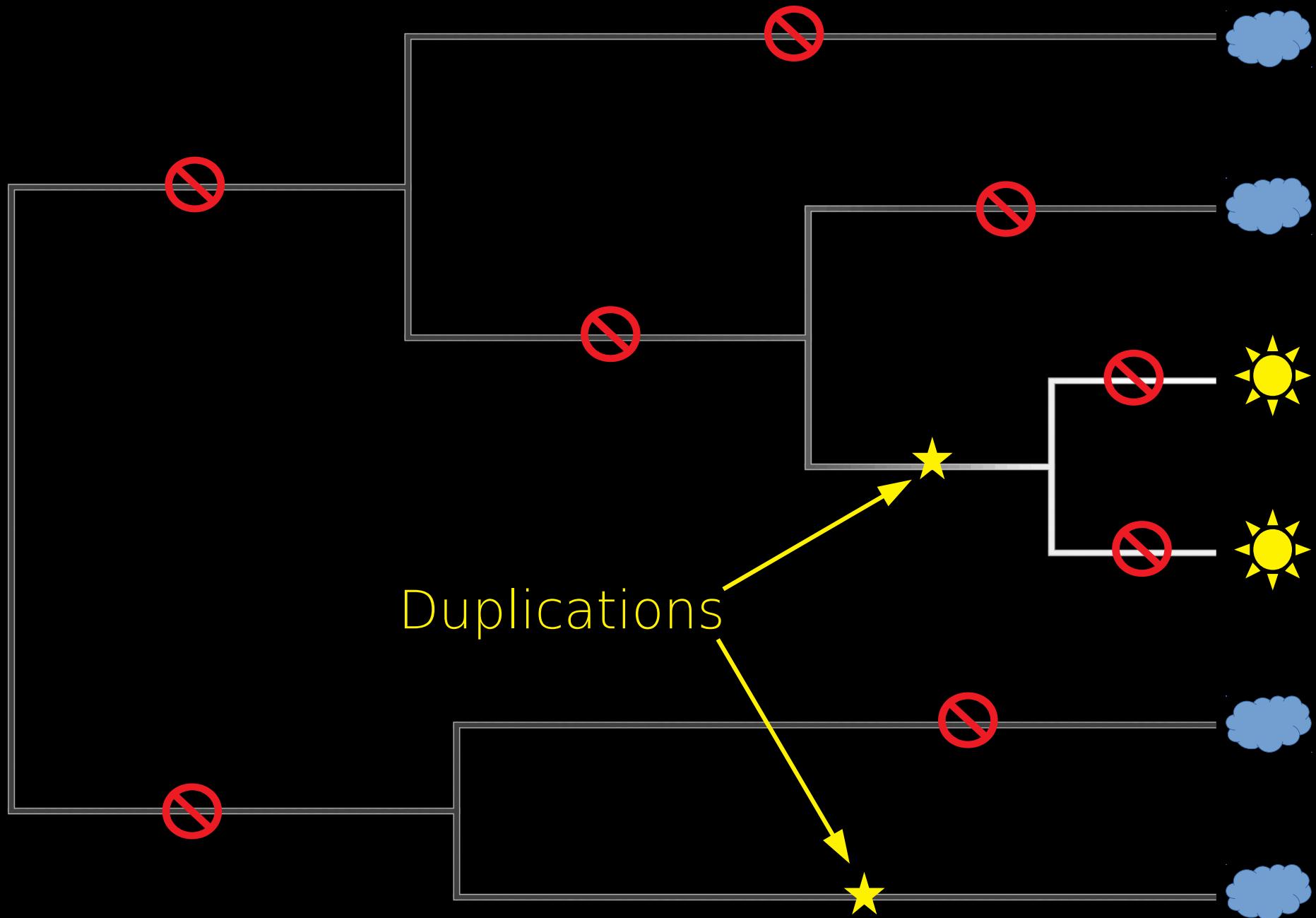
Reconstruct evolution for a single variable or multiple variables

Approach 1

Reconstruct climatic evolution
under a simple model

Compare climatic changes
along branches with or
without chromosomal
changes

Reconstruct climate evolution



Test Case: Gymnosperms

391 species with chromosome counts, occurrences

- Chromosome counts from Kew C-values database, Plant chromosome counts database

- specimen-based occurrences from GBIF, iDigBio

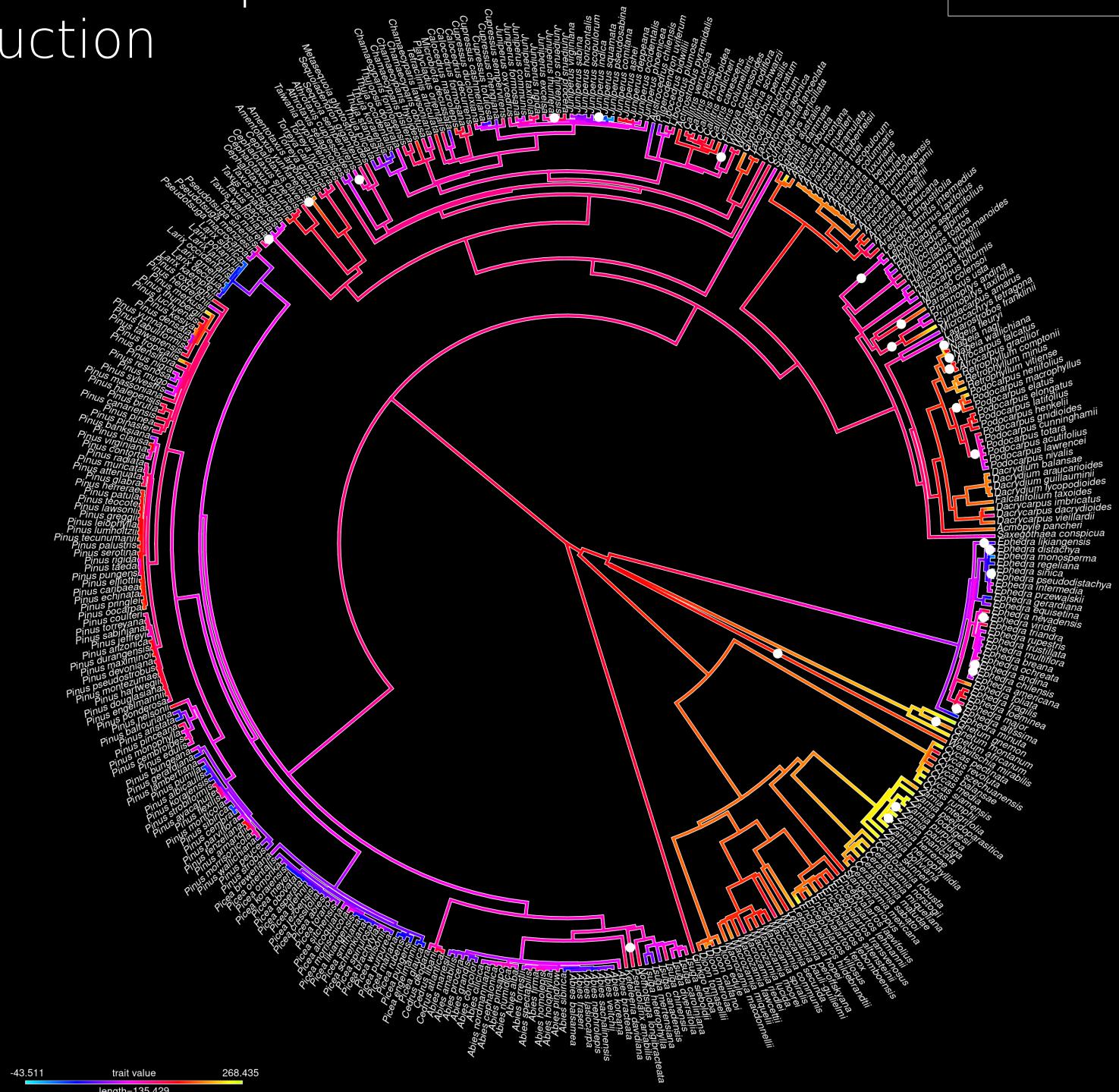
MaxEnt models based on Bioclim variables

Pruned seed plant phylogeny ('gbotb')
From Smith & Brown, 2018

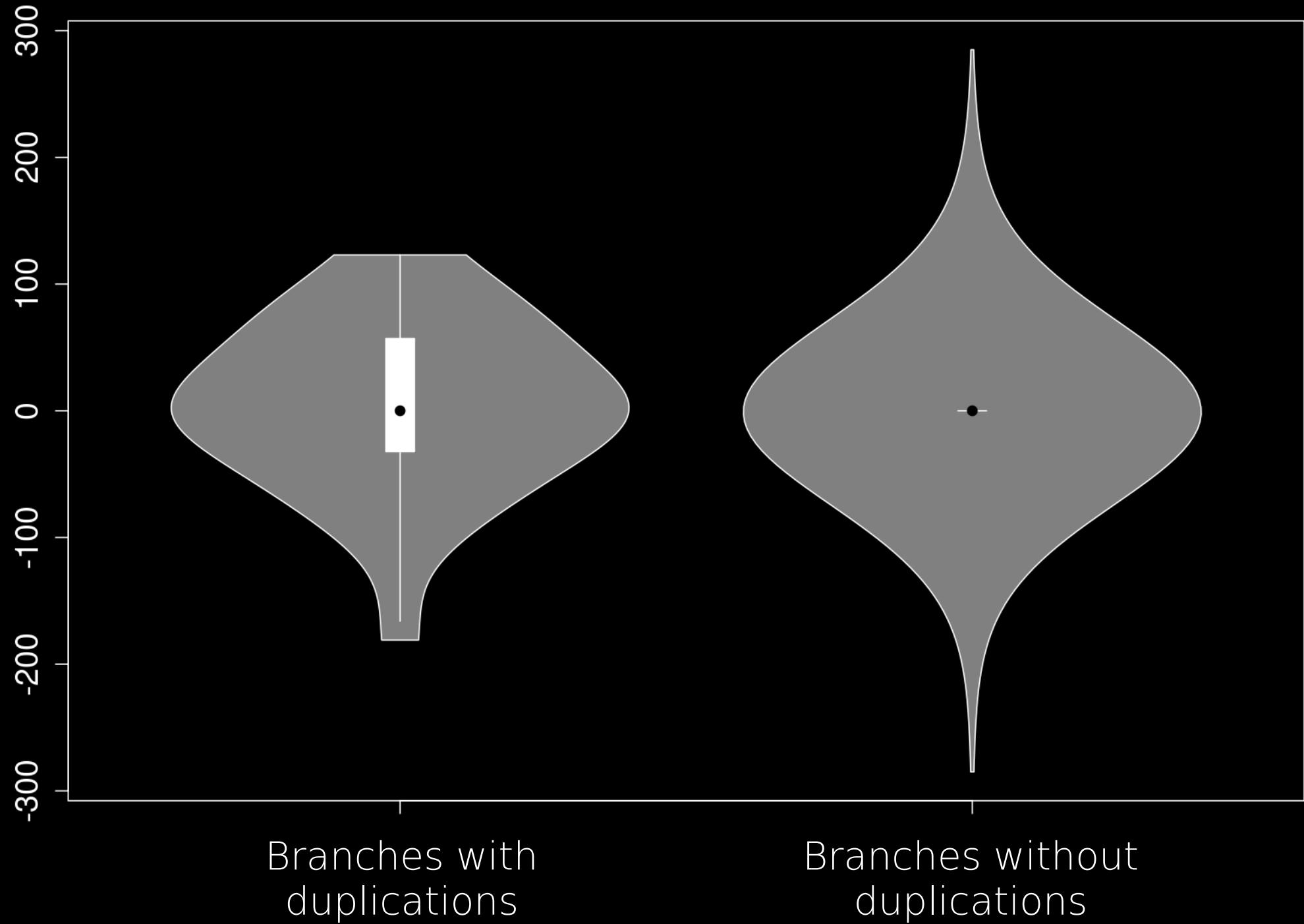
Niche reconstructions based on
PNOs from MaxEnt

Mean annual temperature reconstruction

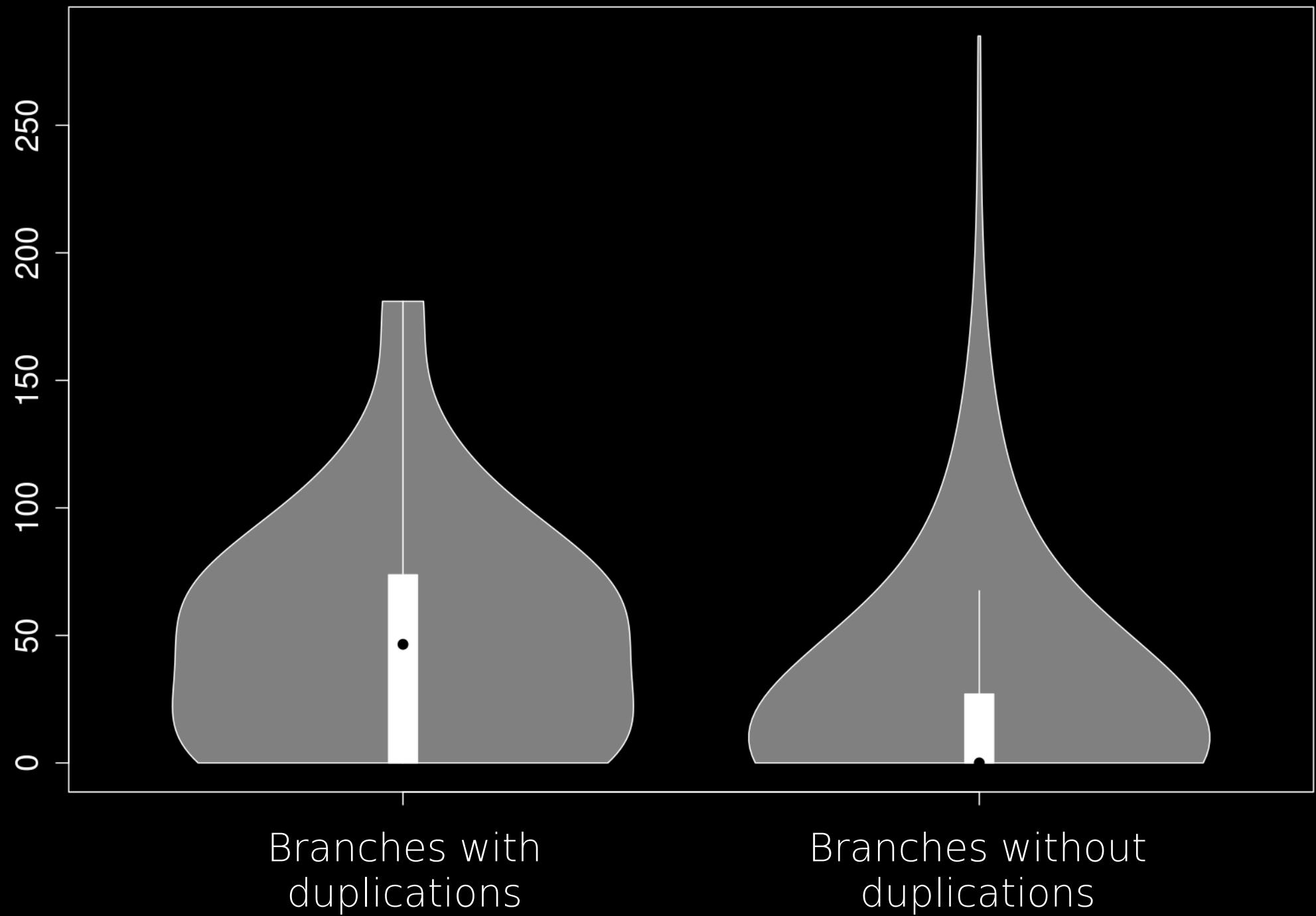
- Duplication



Variable change along each branch of the phylogeny



Absolute change along each branch of the phylogeny

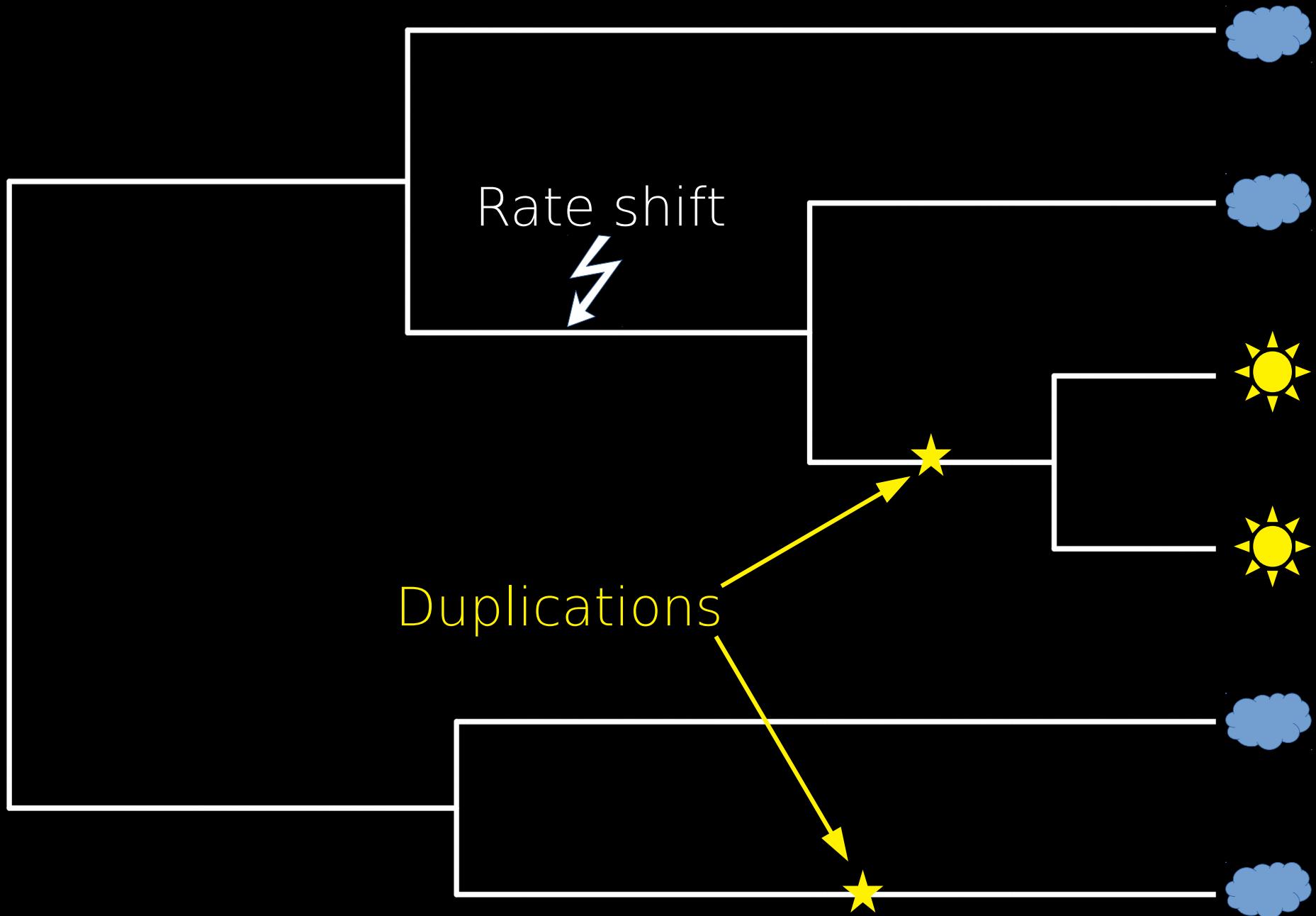


Approach 2

Reconstruct climatic evolution
using a complex model with
shifts in evolutionary
rates

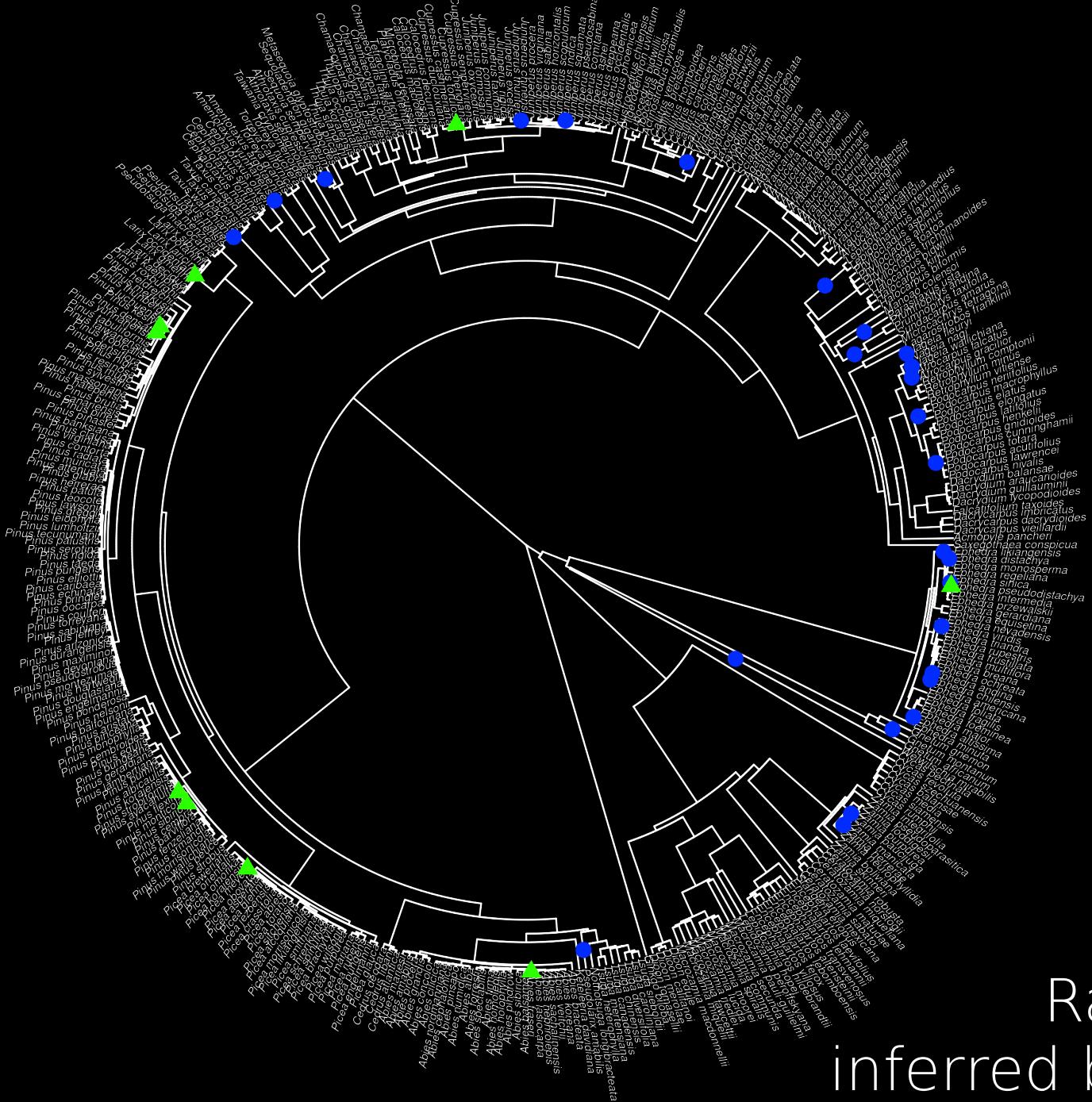
Compare the positions of
evolutionary rate shifts
and chromosomal
changes

Reconstruct climate evolution



univariate reconstruction -mean annual temp.

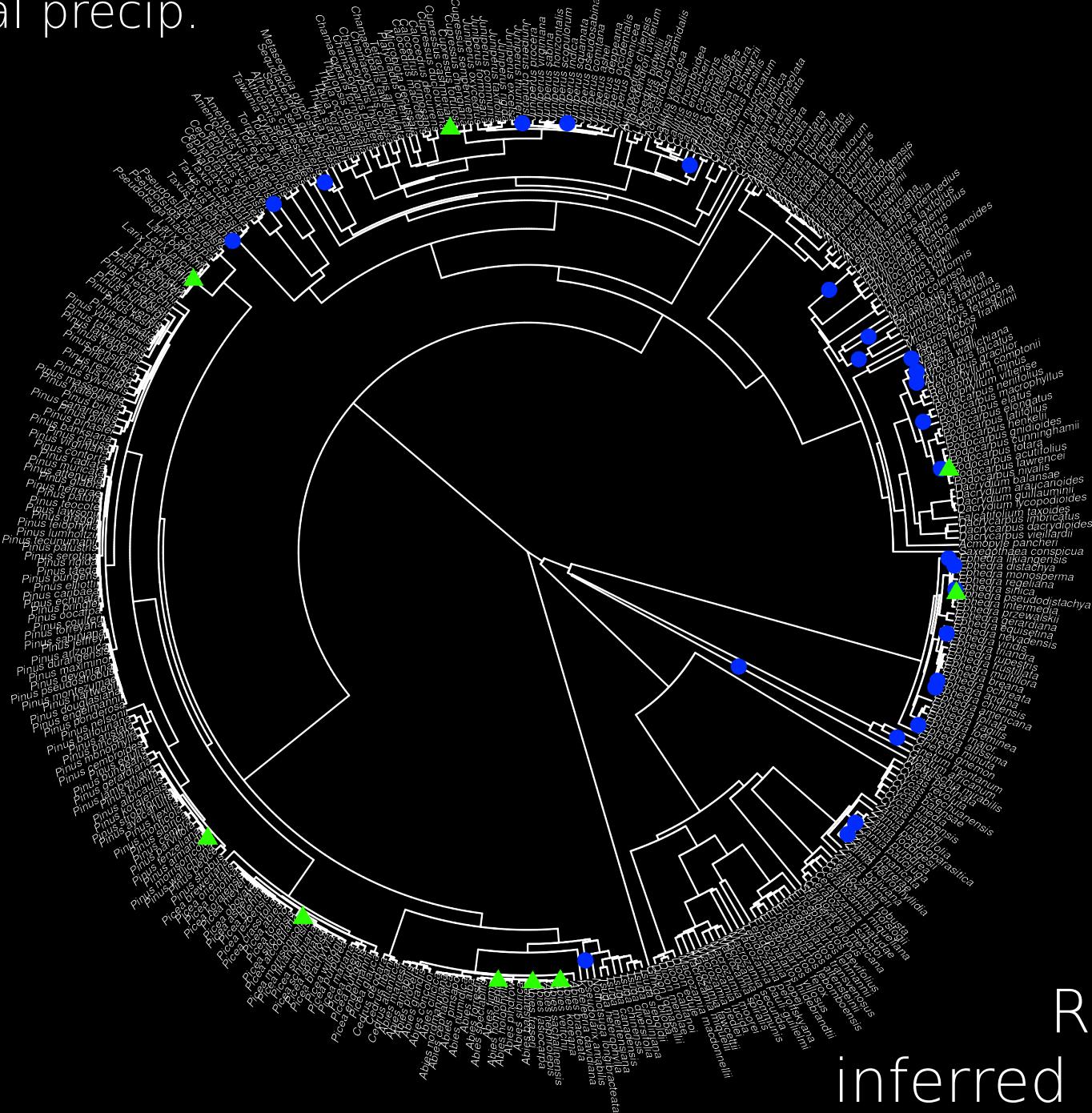
- Duplication
- ▲ Rate shift



Rate shifts inferred by model

Multivariate reconstruction

- mean annual temp.
- mean annual precip



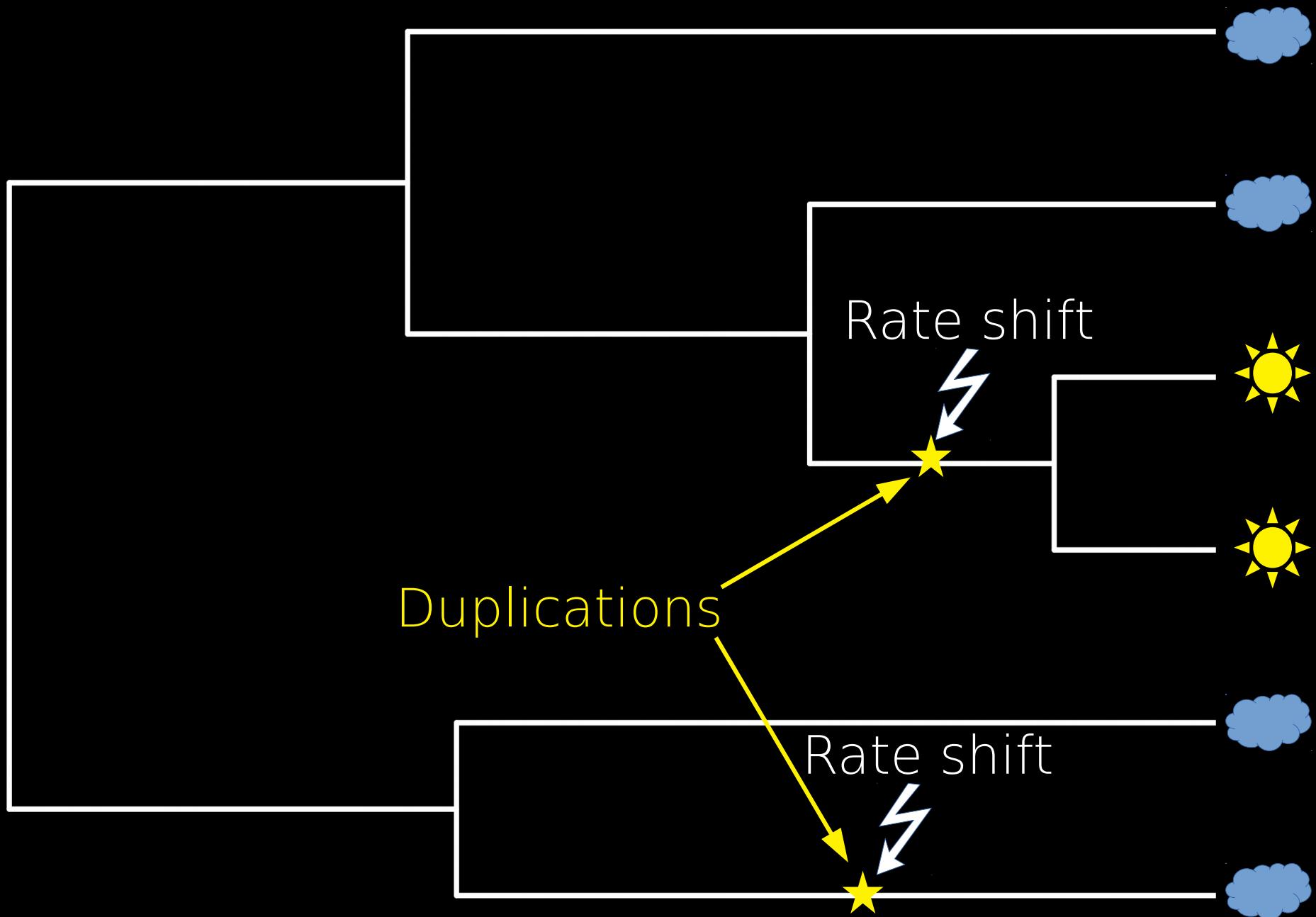
Rate shifts inferred by model

Approach 3

Reconstruct climatic evolution
under a complex model using
chromosomal states as
a priori assumptions
about evolutionary
rates

Compare model fit to a
null (simple) model

Reconstruct climate evolution



Acknowledgments



iDigBio
Integrated Digitized Biocollections



Resources

Chromevol software
<http://chromevol.tau.ac.il/>

R packages for discrete character evolution
and reconstruction

- 'phytools' (make.simmap) - incredibly flexible
- 'geiger' (fitDiscrete) - includes tree transformation options
- 'corHMM' (corHMM) - fit multiple evolutionary rates

R packages for working with niche models

- 'maxnet' (maxnet) - R-based version of maxent software
- 'phyloclim' (pno) - generates PNOs from maxent outputs
- 'phyloclim' (anc.clim) - simple univariate reconstruction

Resources, cont.

R packages for discrete character evolution and reconstruction (incl. climate variables)

- 'ape' (ace) - Simple, univariate reconstructions
- 'phytools' (fastAnc) - Simple, univariate reconstructions
- 'Rphylopars' (phylopars) - simple, uni- or multivariate reconstructions, allows multiple observations, missing data
- 'PhylogeneticEM' (phyloEM) - complex, uni- or multivariate reconstructions, rate shift detection
- 'motmot' (transformPhylo.ML) - complex, uni- or multivariate reconstructions, rate shift detection and *a priori* specification