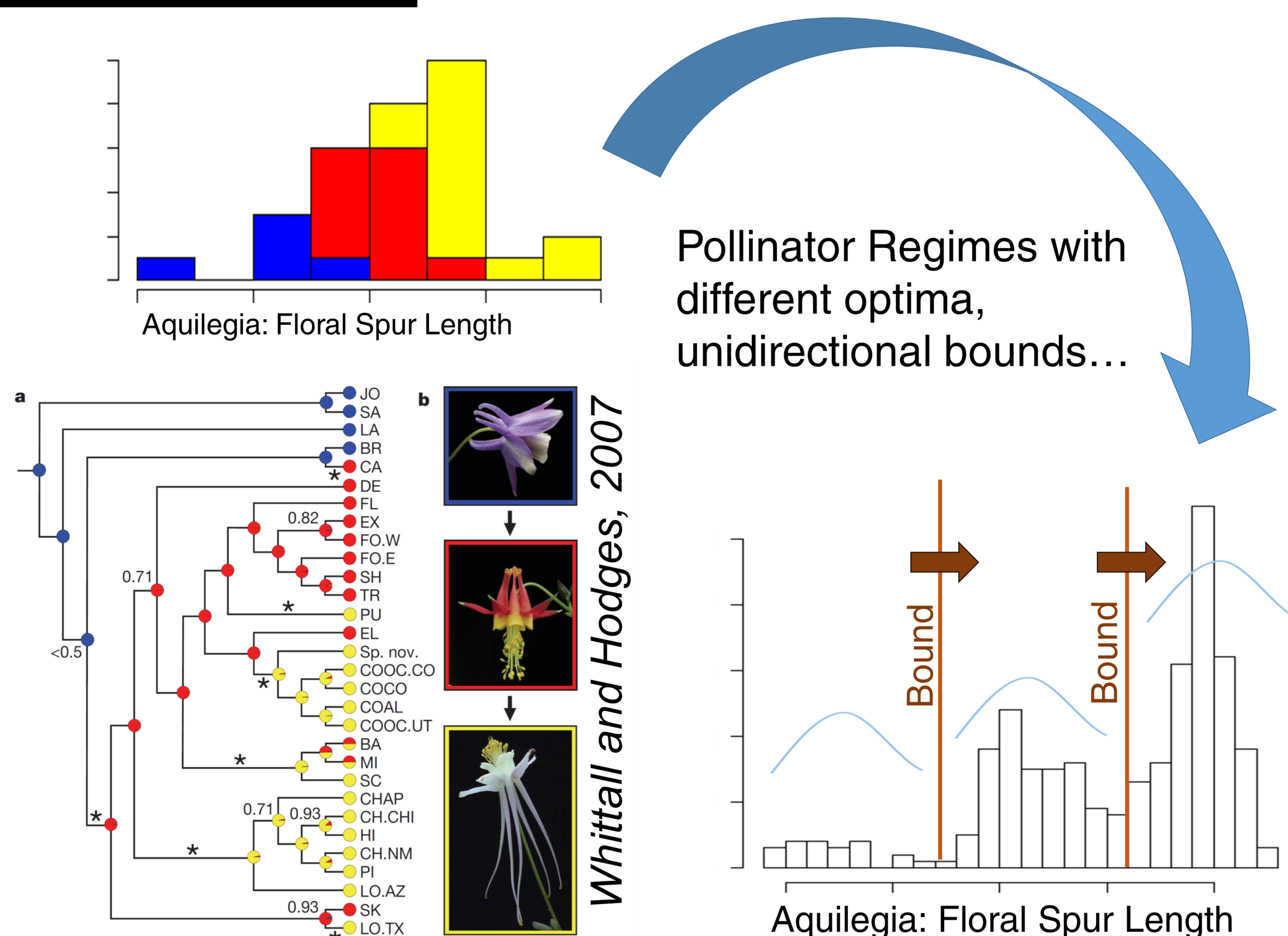


If You Can Simulate It, You Can Fit It

Do-It-Yourself Phylogenetic Models of Trait Evolution for the Fossil Record with the R Package **TreEvo**

*David Bapst, Brian O'Meara
& Barb Banbury*

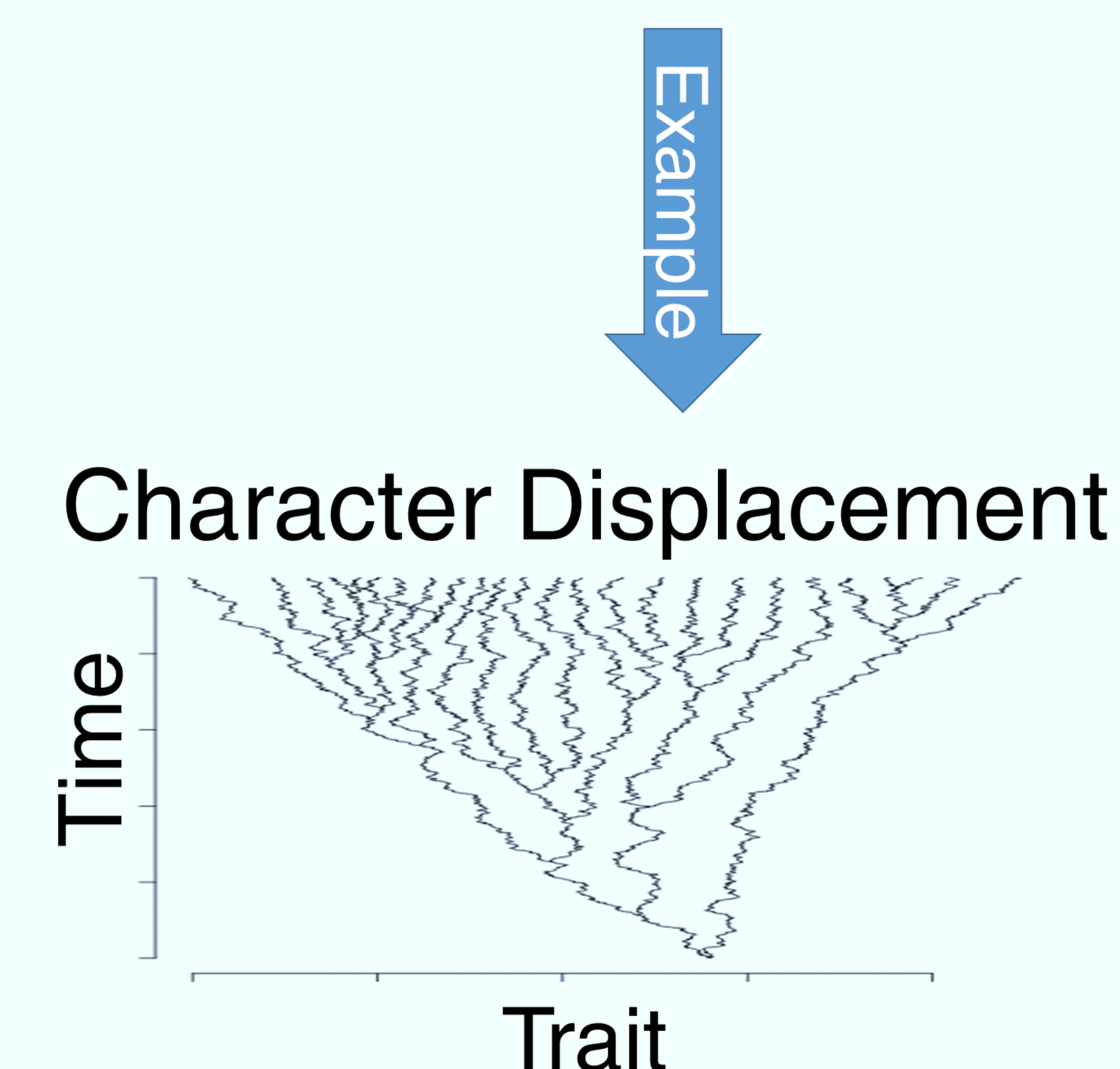
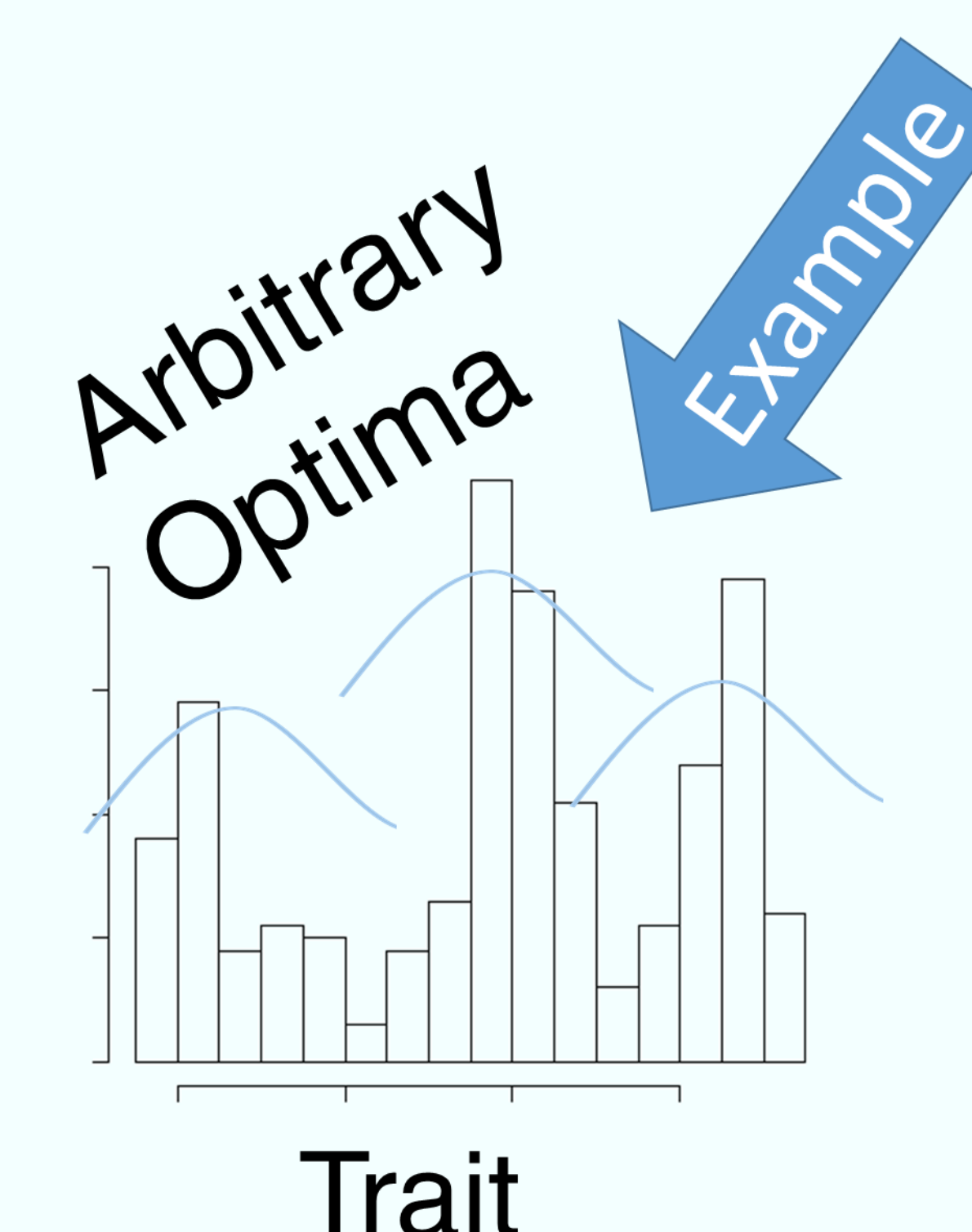
The Problem



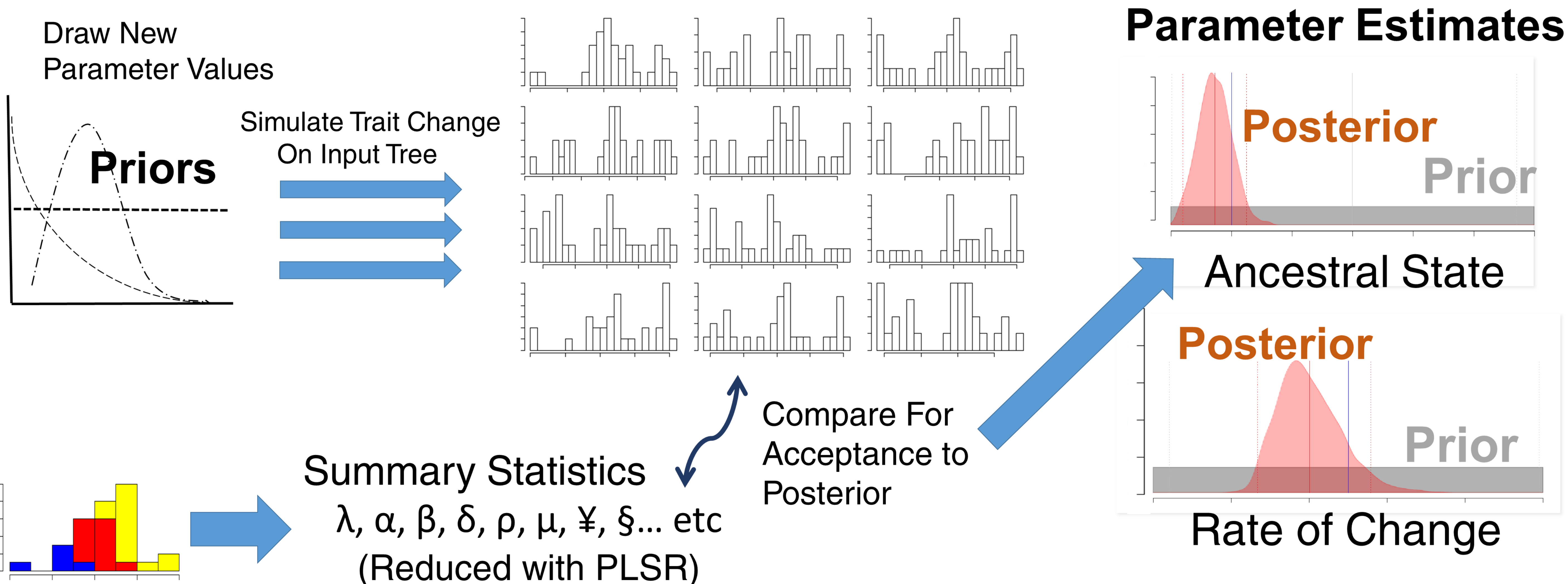
Parameter Estimates?
Model Likelihood = ???

Modeling Trait Evolution with **TreEvo**

$$X_t \sim X_{t-1} + \text{function}() \text{ Intrinsic } \Delta + \text{function}() \text{ Extrinsic } \Delta$$



The Solution: Approximate Bayesian Computation (ABC)



Limits of ABC

- Slow
- Identifiability

Trait evolution models should be match our biological understanding, not methodological limits. What new models can you imagine?



For the package, see:
<https://github.com/bomeara/treevo>