

BCB 503: RevBayes Intro



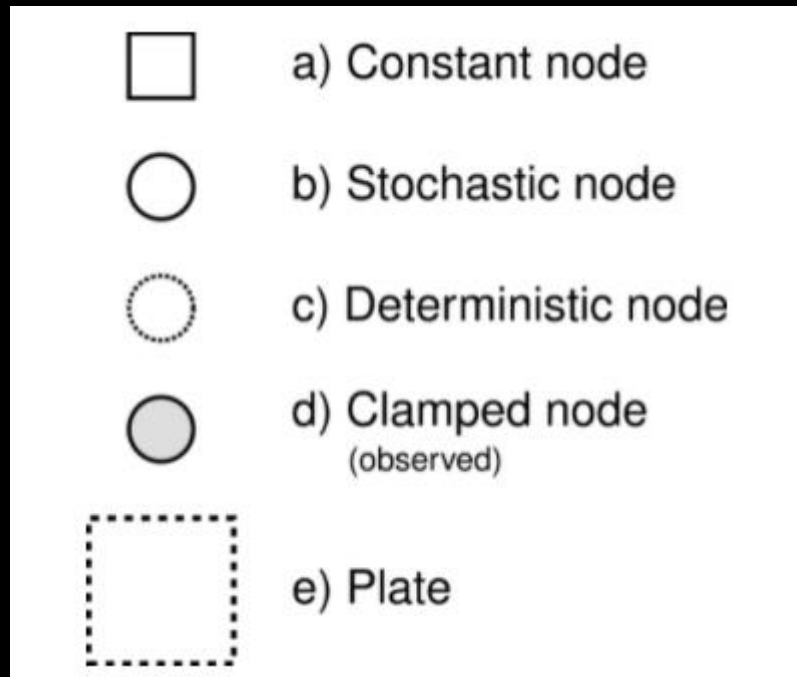
Last session: Joint Analysis

Orlando Schwery, 26. Oct. 2021, University of Idaho

A quick recap...

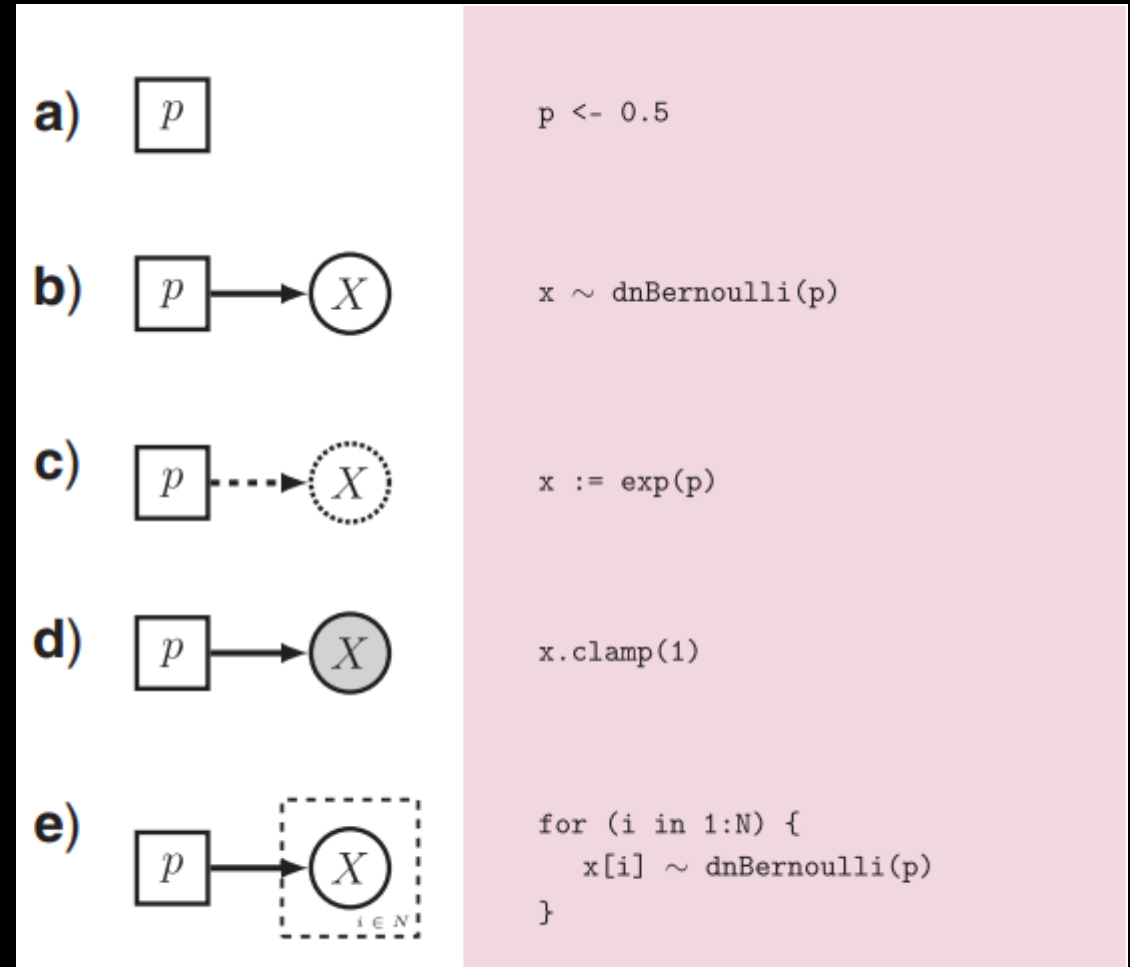
- Let's see what we've done so far
- **24. Aug.:** Intro [Graphical Models & Rev Lang.]
- **31. Aug.:** Trait Evolution [Simple Brownian Motion & OU]
- **07. Sep.:** Biogeography [Simple DEC]
- **14. Sep.:** Diversification [BD, BiSSE, MuSSE]
- **12. Oct.:** Div. Add-On [CID-2, HiSSE]
- **19. Oct.:** Tree-Building & -Dating [Substitution- & Clock-Models]
- **26. Oct.:** Joint Analyses [Mix & Match]

Graphical Models

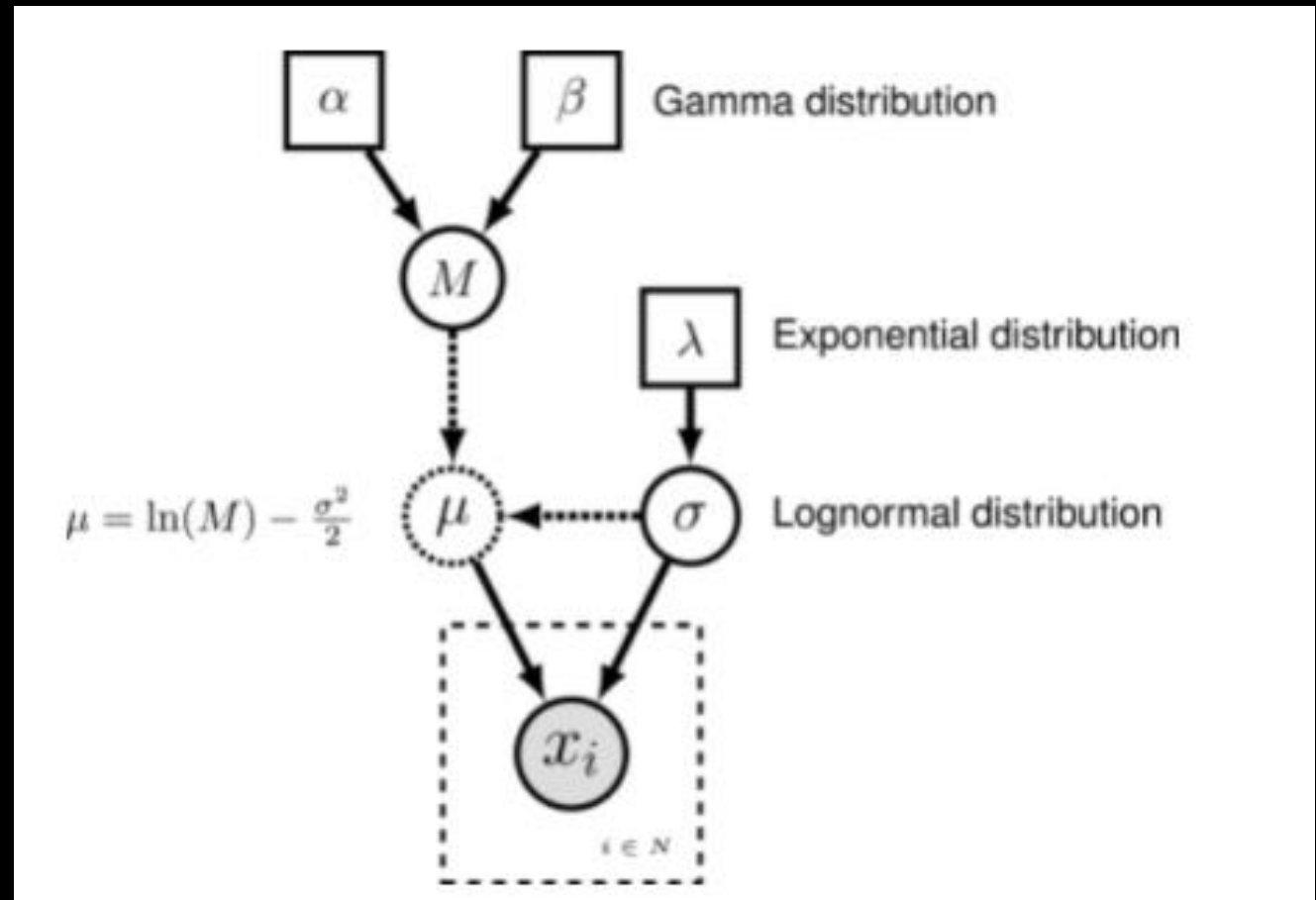
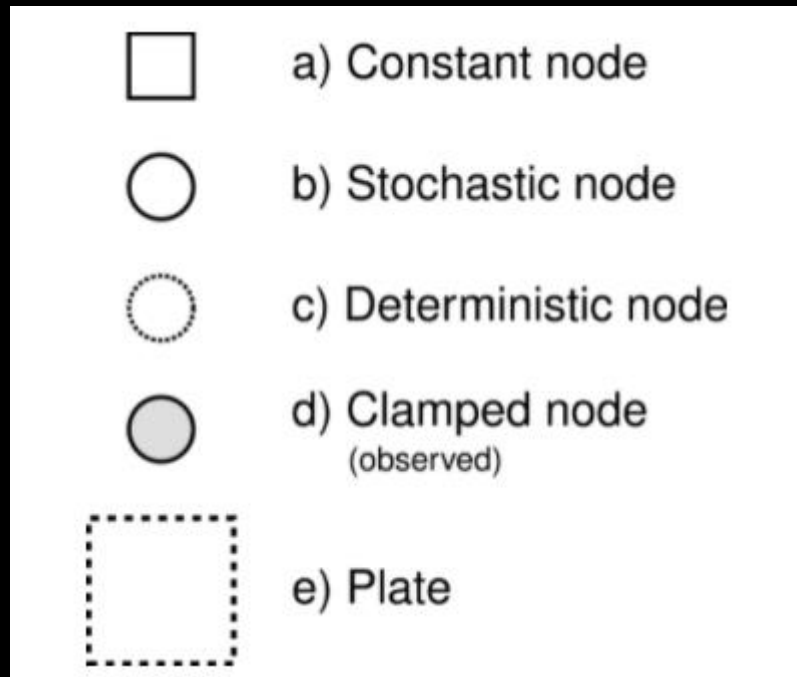


Directed Acyclic Graph (DAG)

→ Nodes (vertices) and Edges (circles/squares and arrows)



Graphical Models

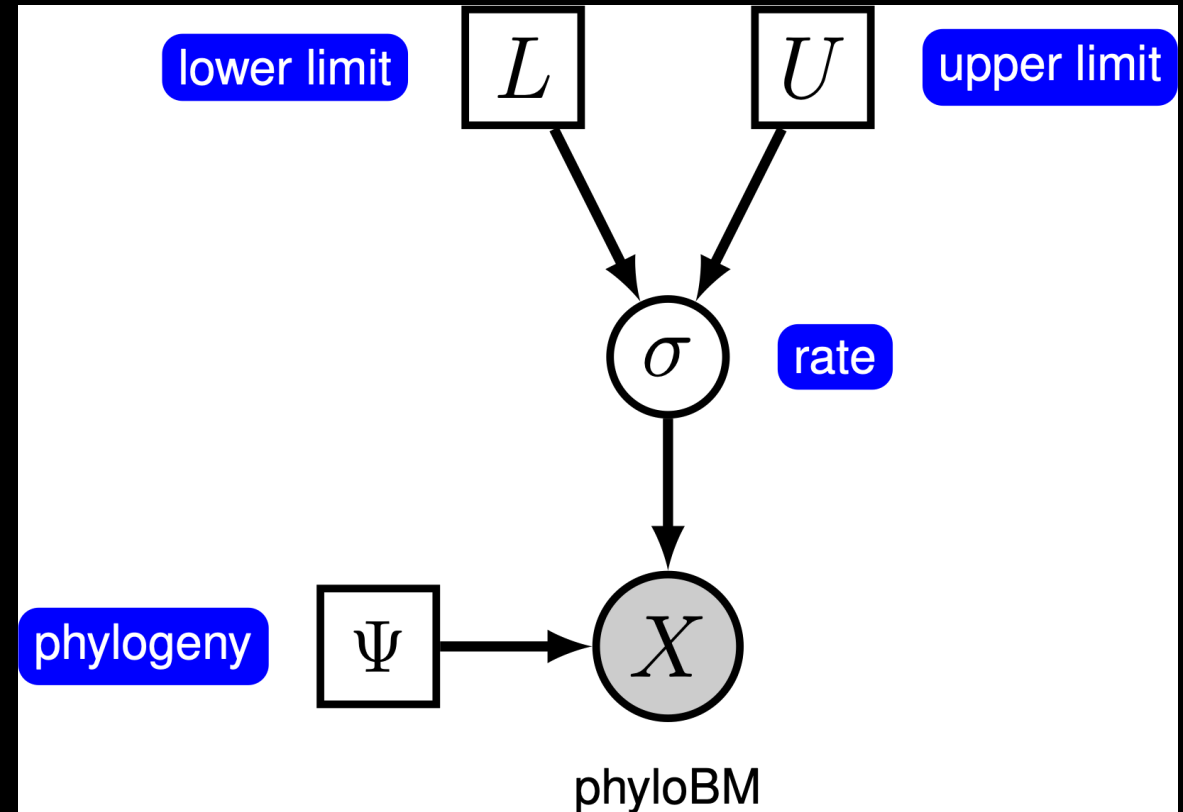


Lognormal Model/Distribution:

$$X = e^{\mu + \sigma z} \quad [\mu: \text{location parameter (log mean)}; \sigma: \text{standard deviation}]$$

Trait Evolution: Simple Brownian-Motion

- Single rate parameter σ^2
 - Drawn from loguniform distribution
 - Lower bound L
 - Upper bound U
- The phylogeny is assumed to be fixed, thus added as a constant node
- The node X contains the BM model for trait data based on tree and rate, with observed data clamped to it

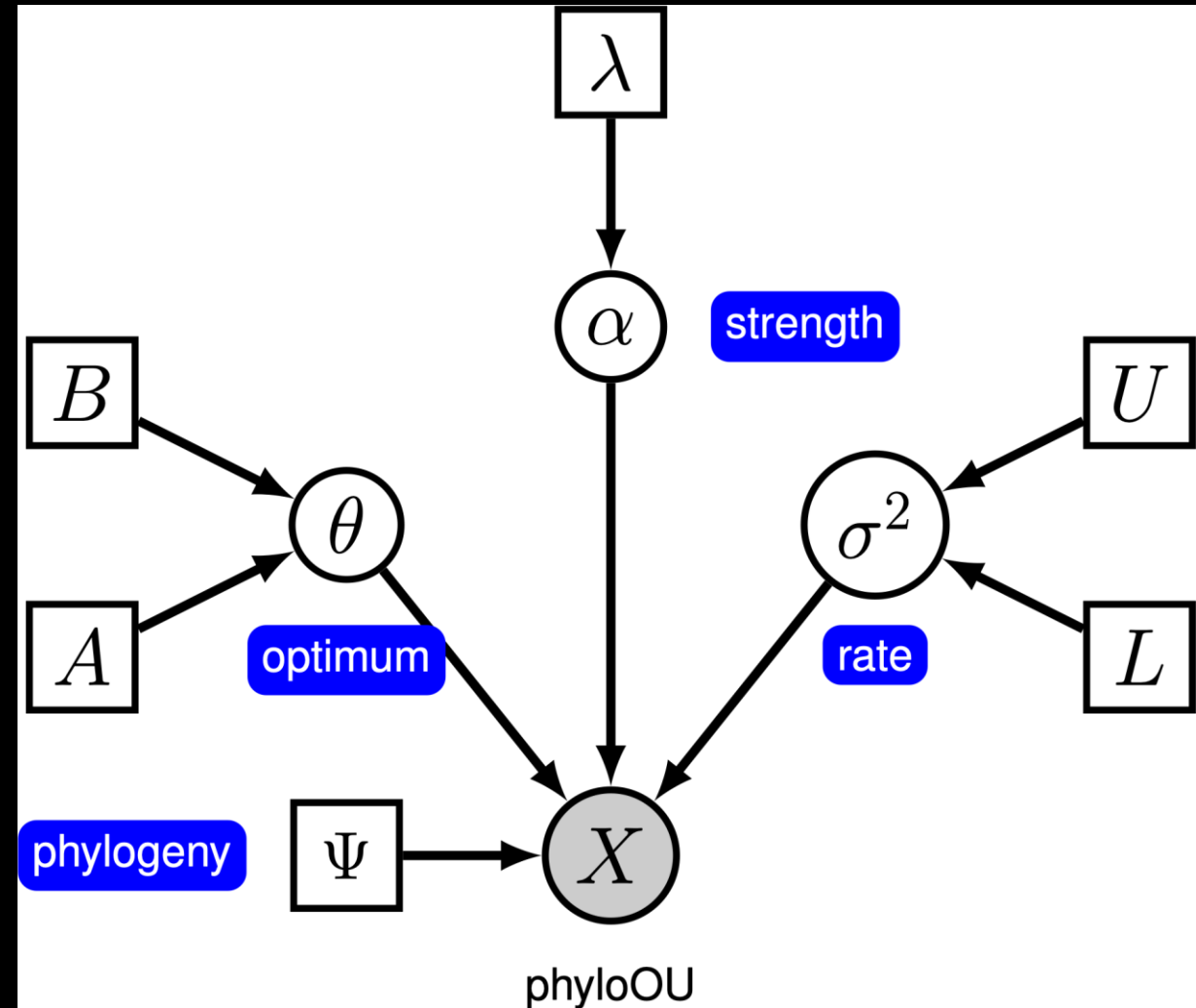


Trait Evolution: Ornstein-Uhlenbeck Model

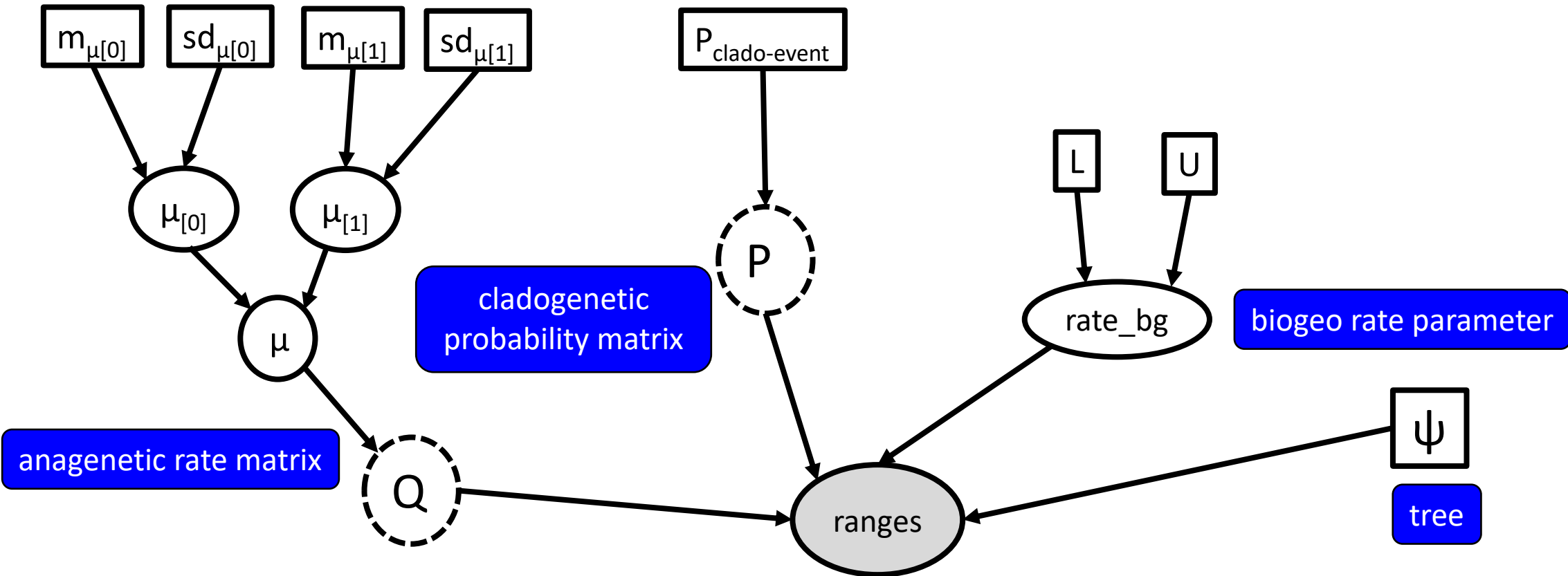
Trait Strength Optimum Rate

$$dX_{(t)} = \alpha (\theta - X_{(t)}) dt + \sigma dB_{(t)}$$

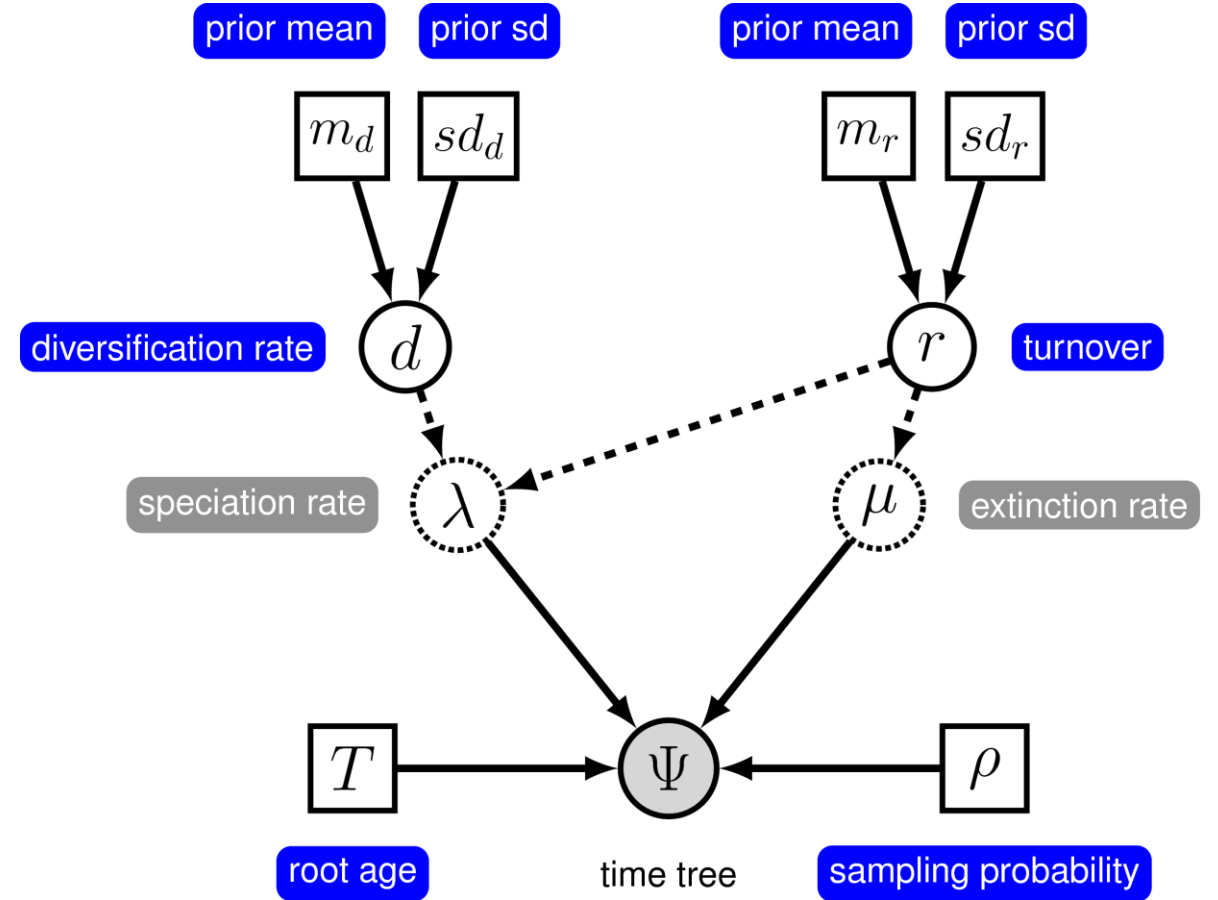
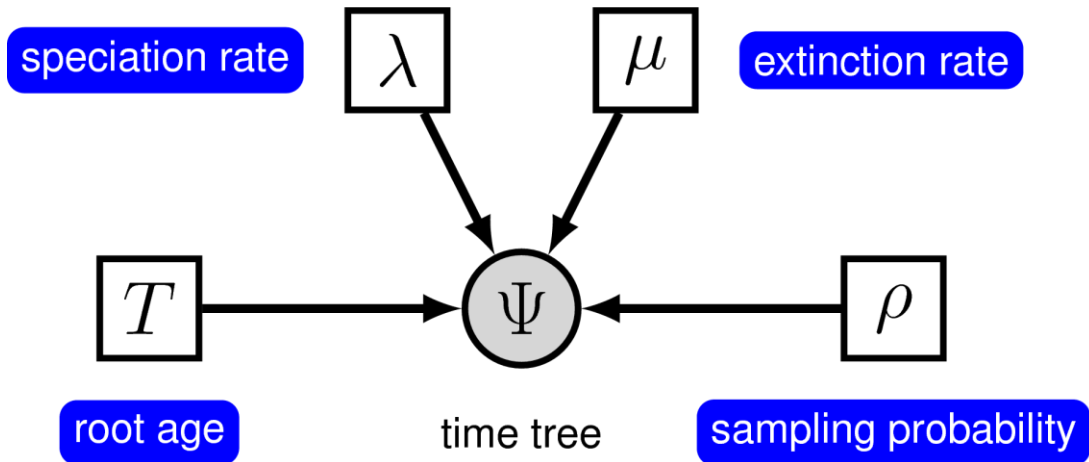
Change in Trait Change towards Optimum Brownian Motion



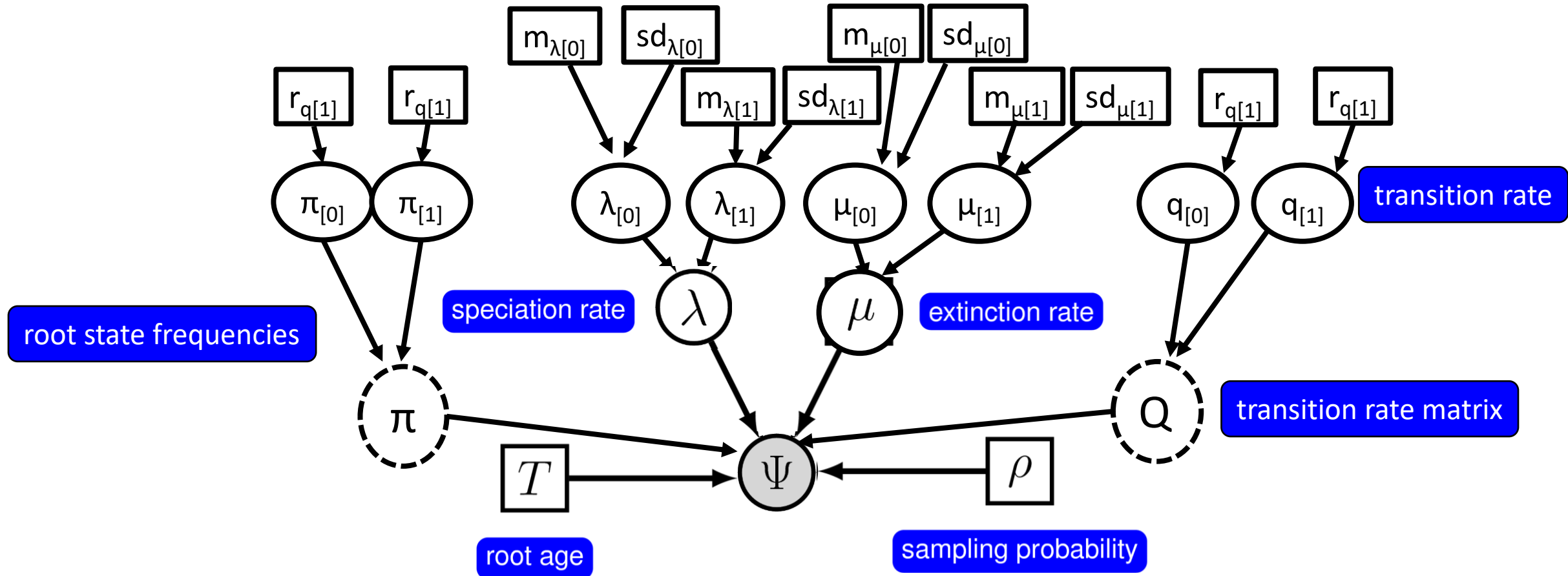
Biogeography: DEC



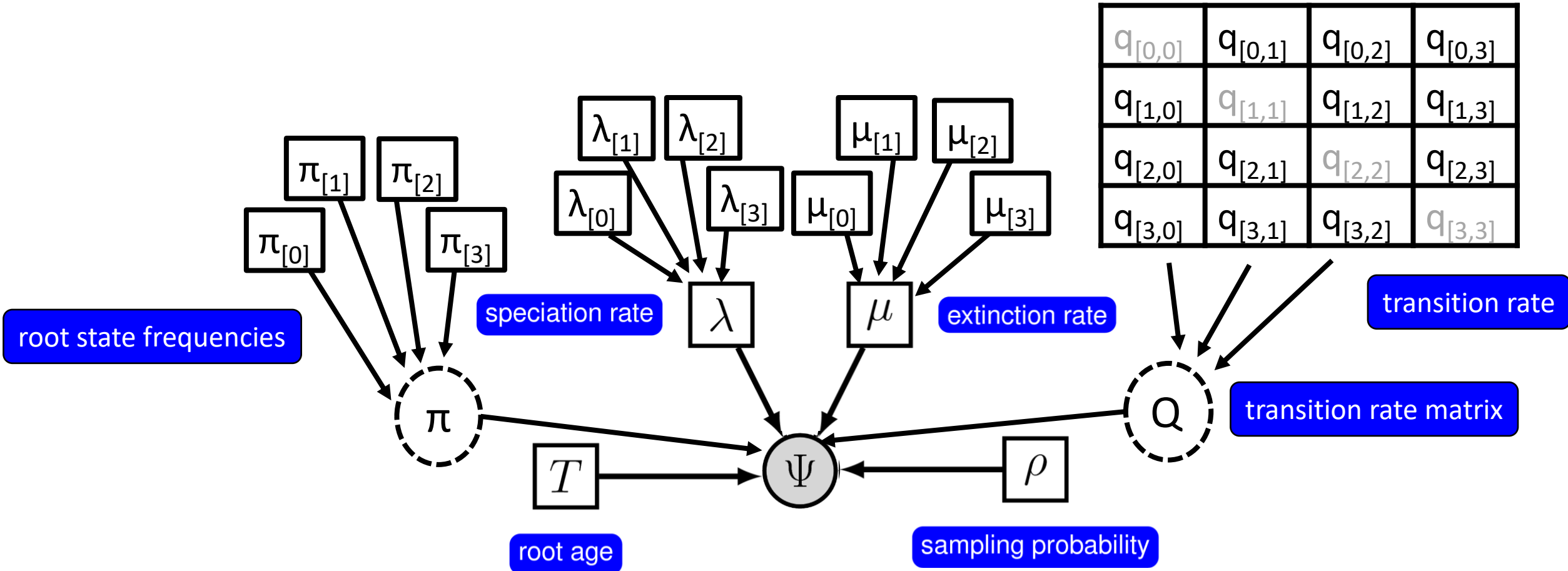
Diversification: Birth Death



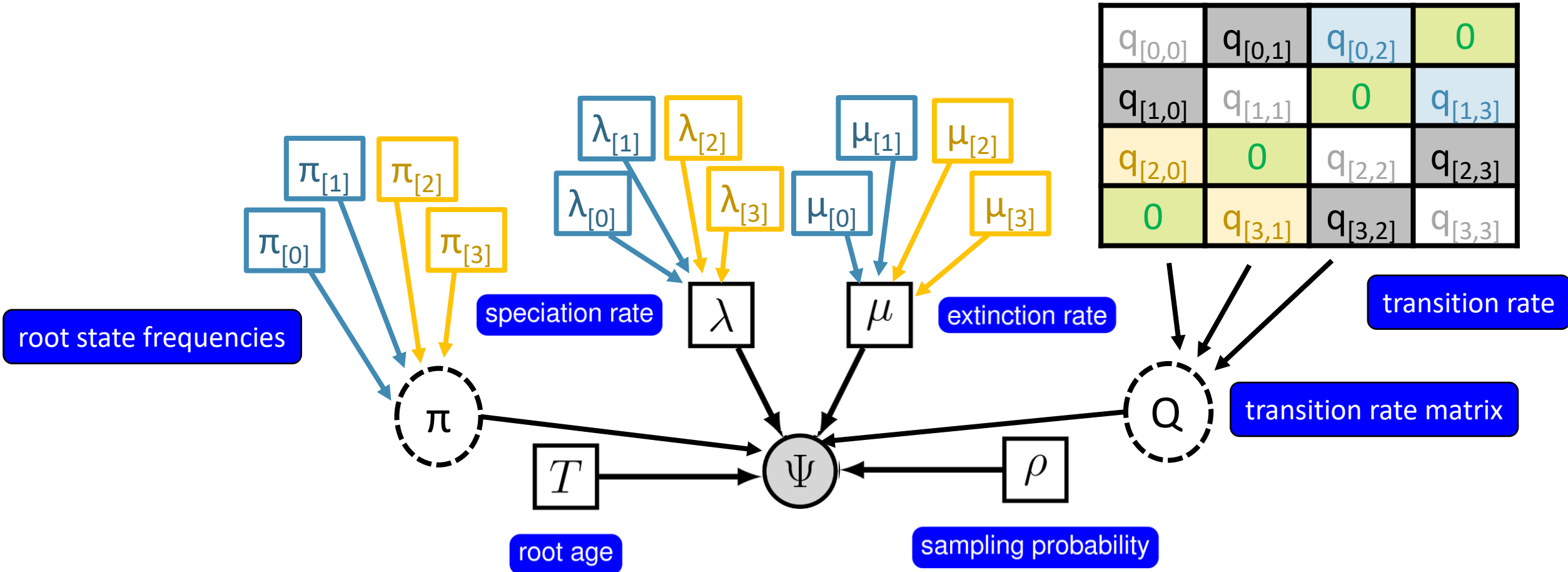
Diversification: BiSSE



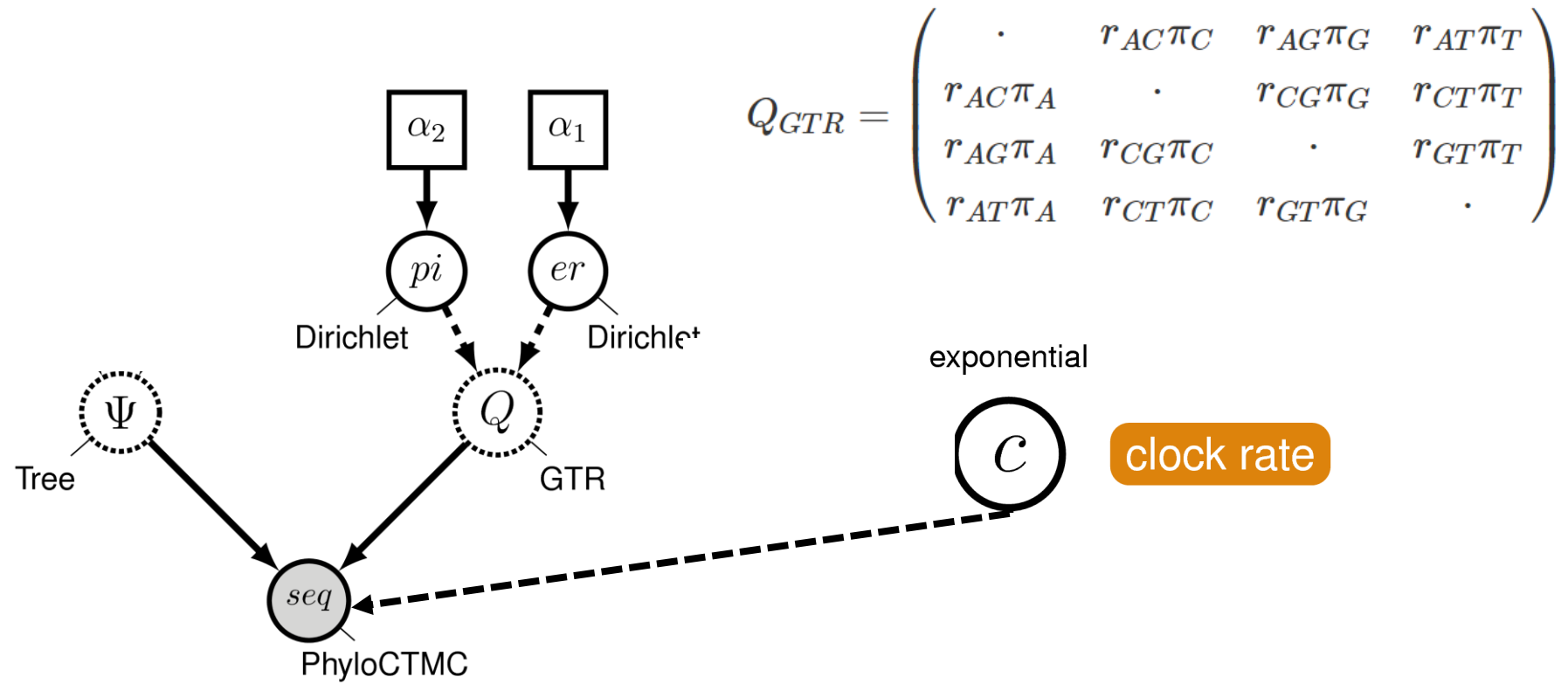
Diversification: MuSSE



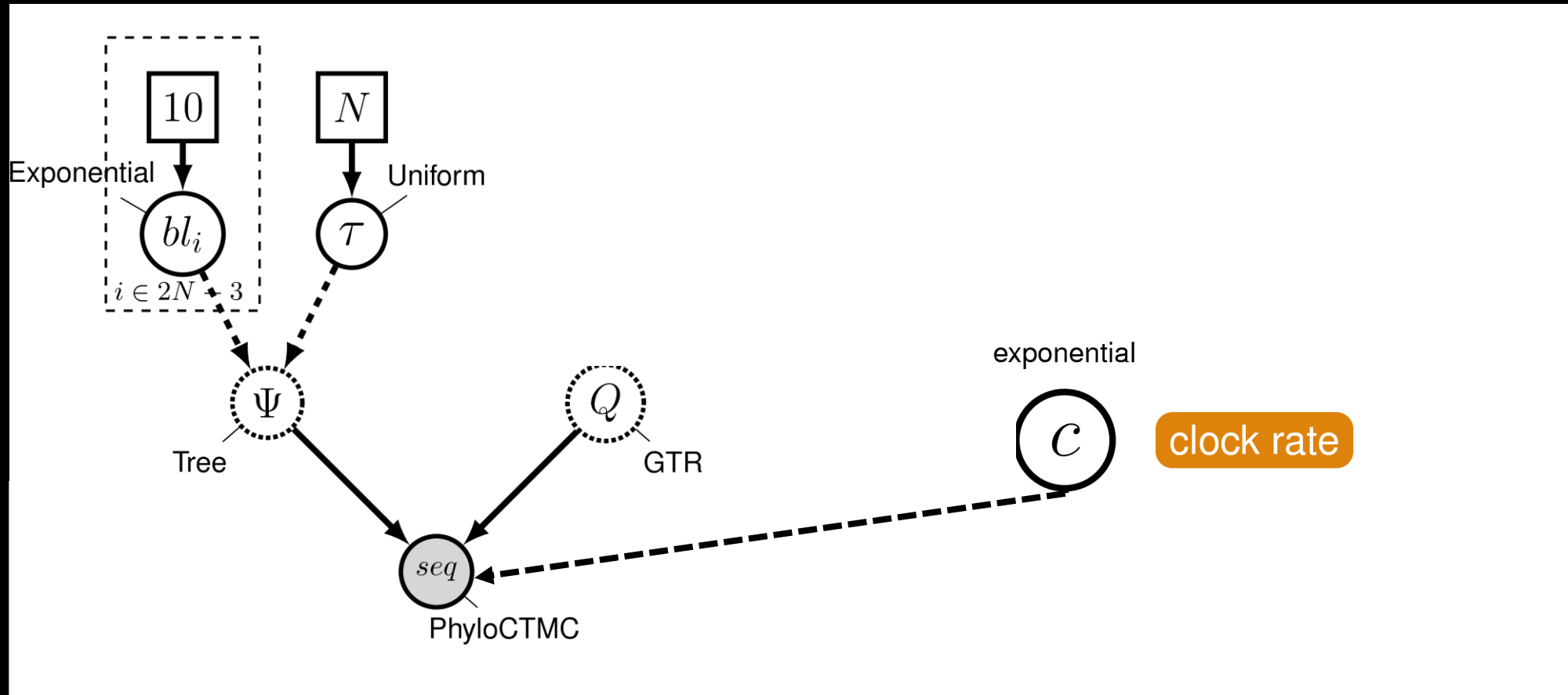
Diversification: CID-2



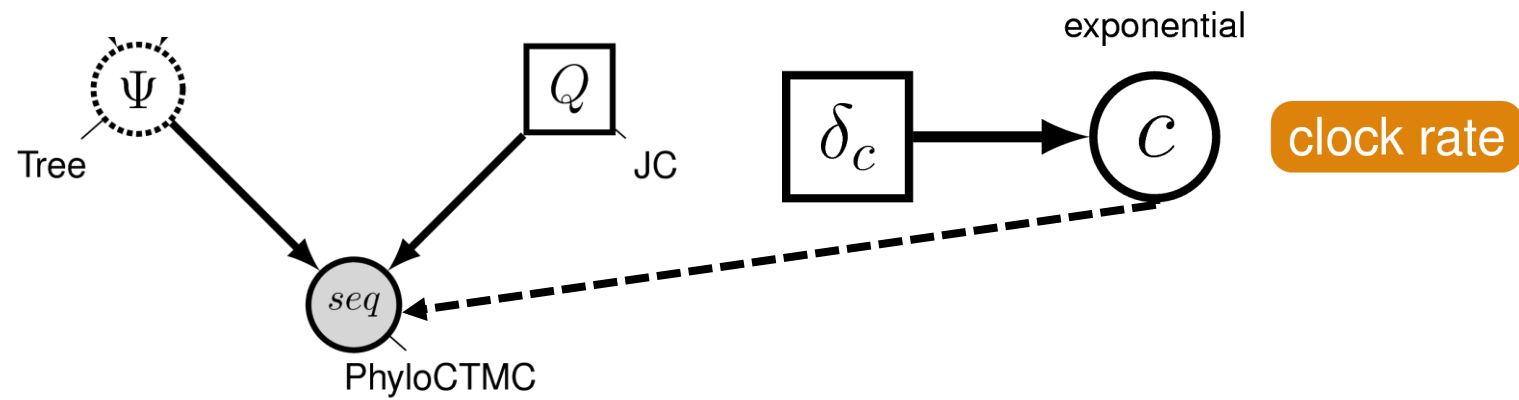
Tree Building & Dating: GTR Nucleotide Substitution Model



Tree Building & Dating: Tree Model

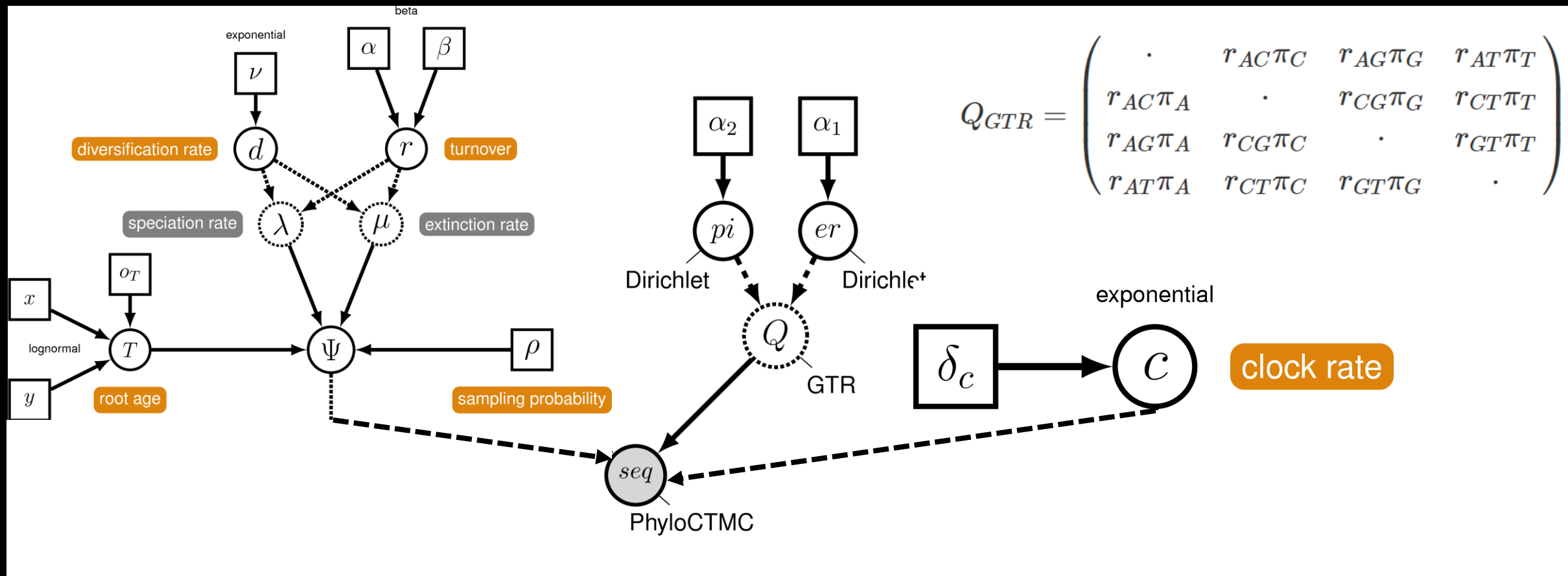


Tree Building & Dating: Global Molecular Clock



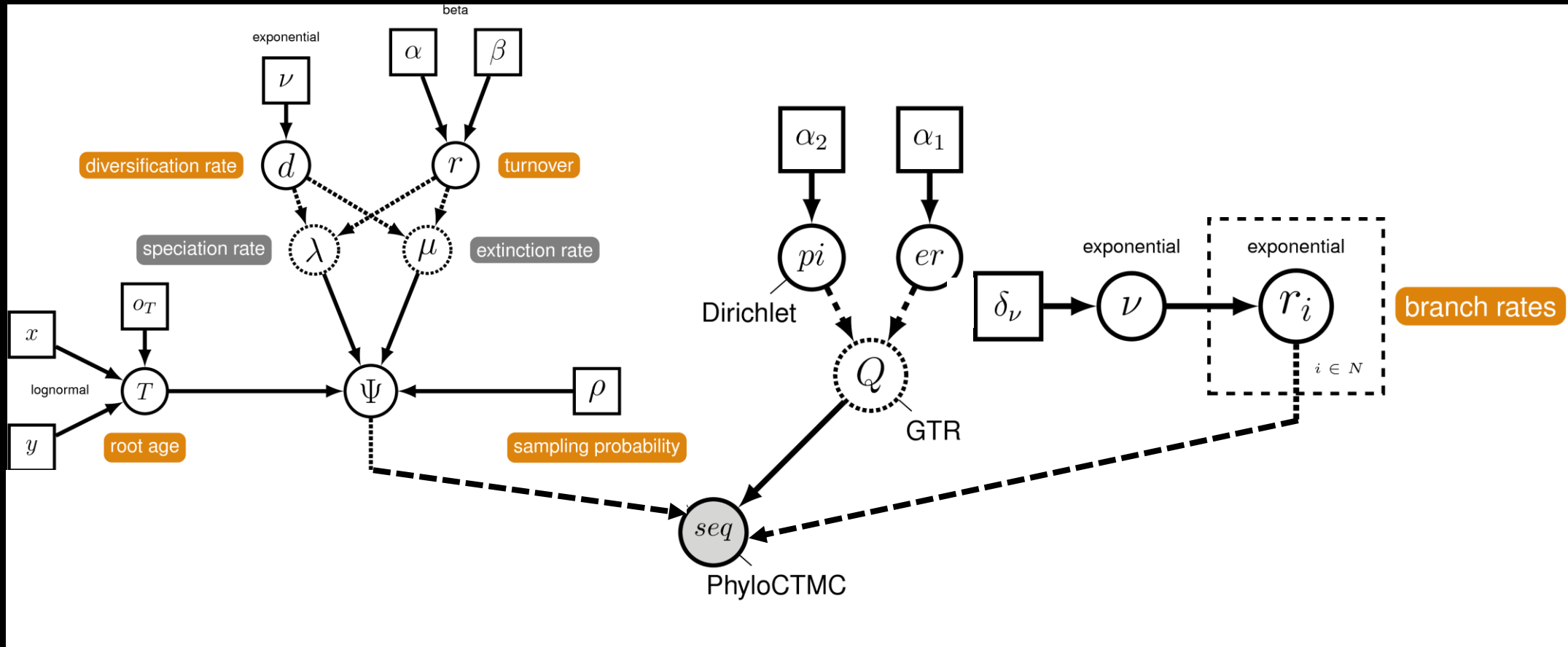
Tree Building & Dating:

BD – GTR – Global Molecular Clock

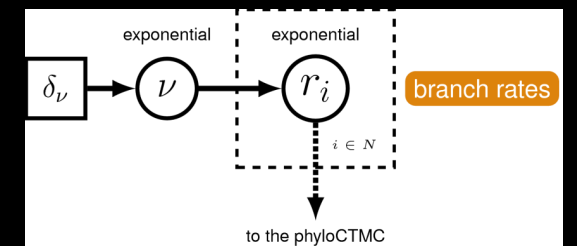
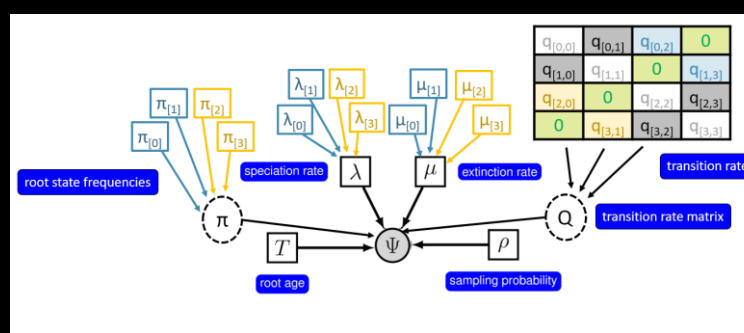
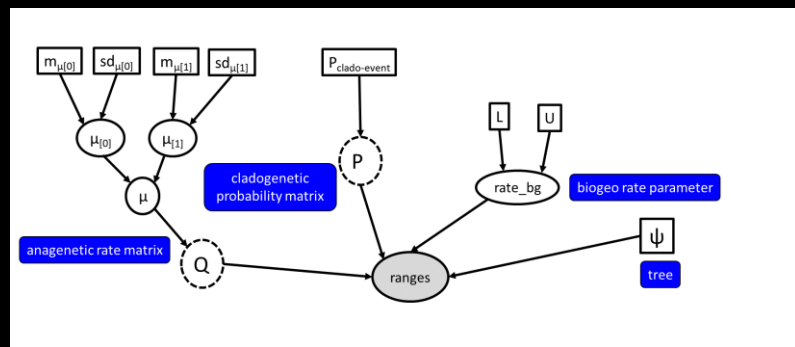
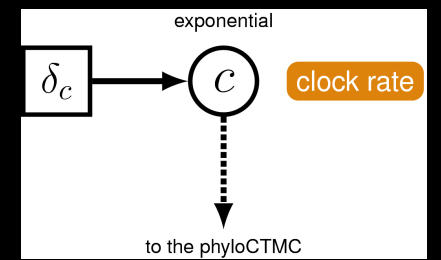
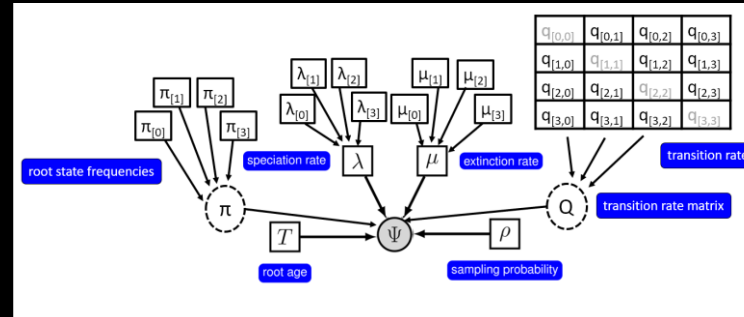
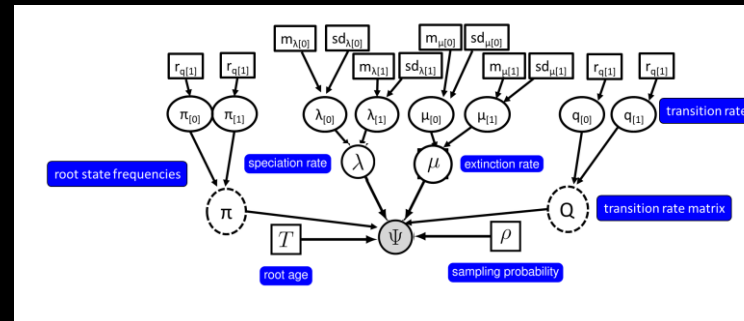
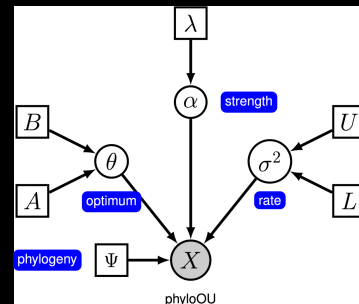
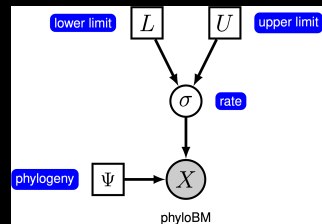
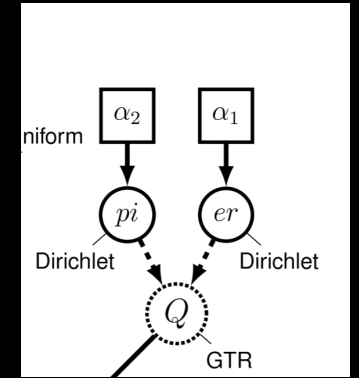
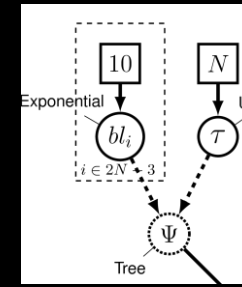
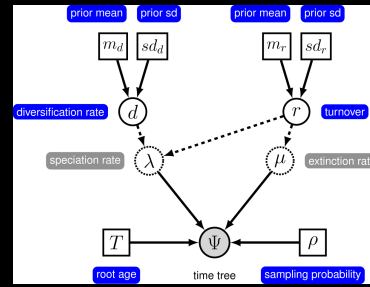


Tree Building & Dating:

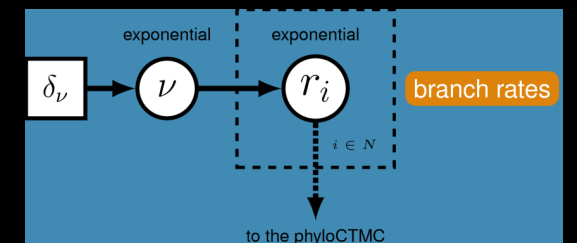
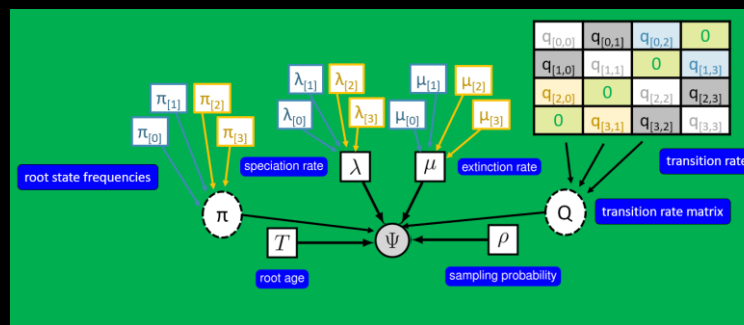
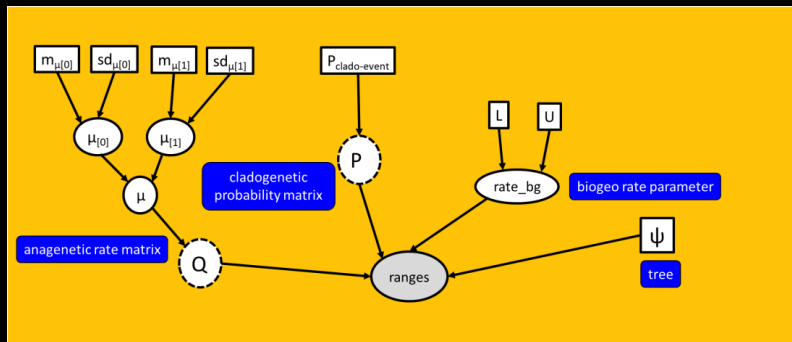
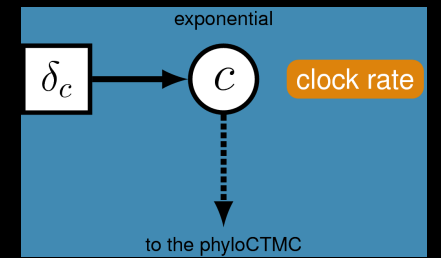
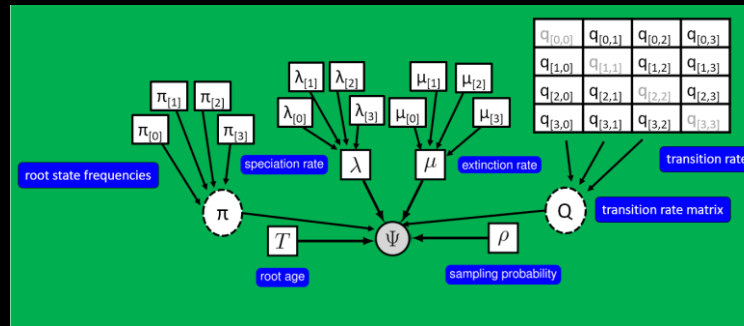
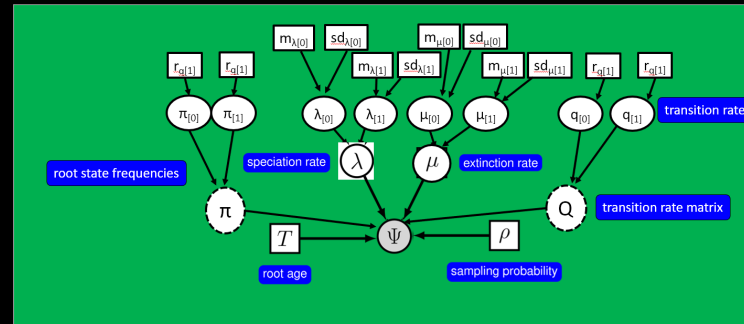
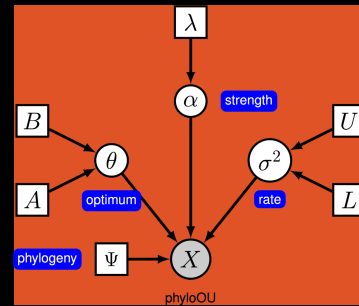
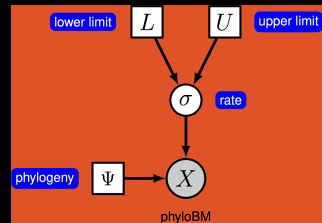
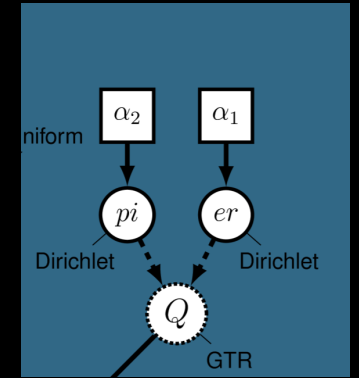
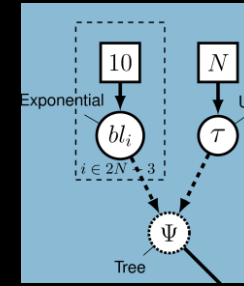
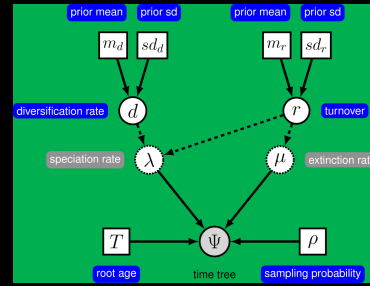
BD – GTR – Relaxed Molecular Clock



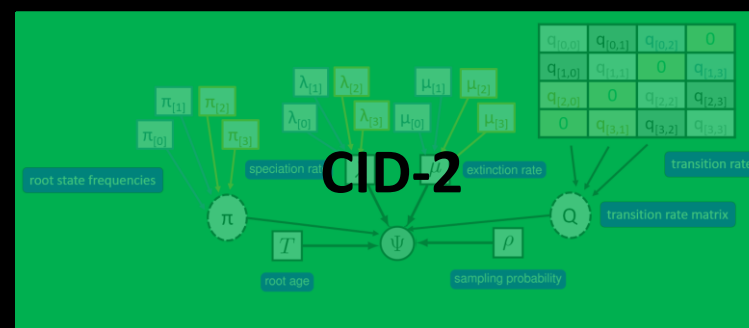
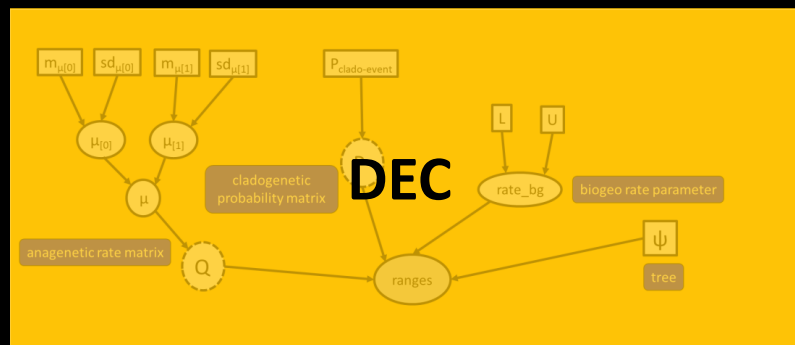
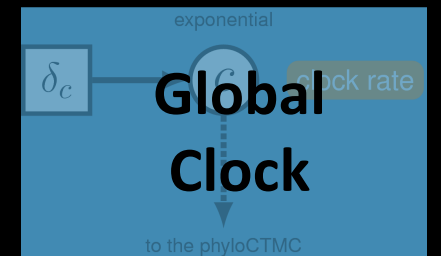
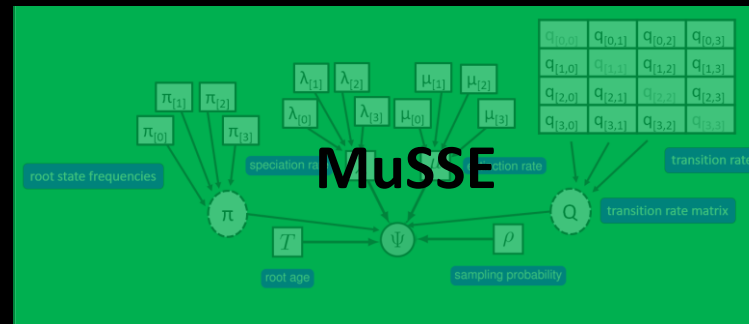
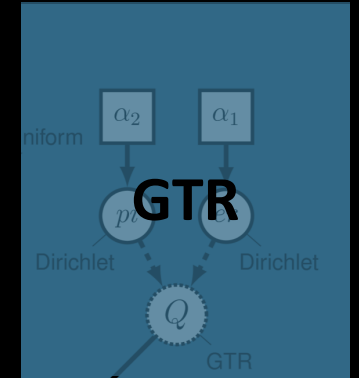
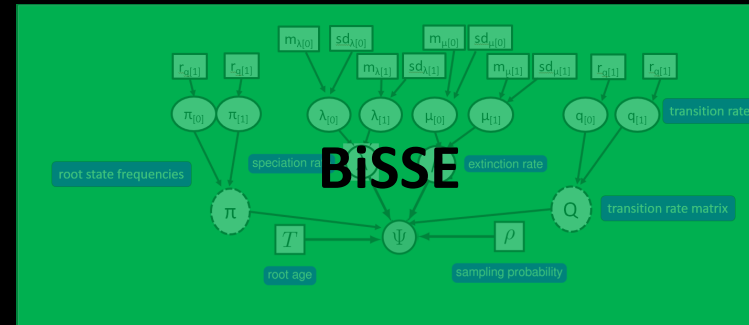
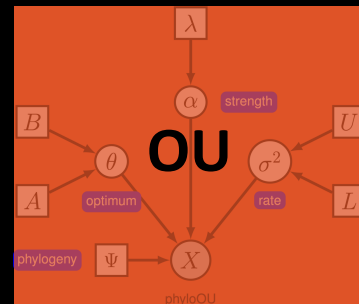
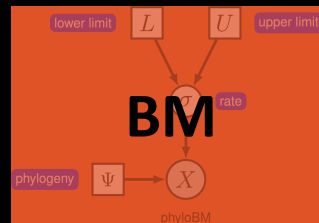
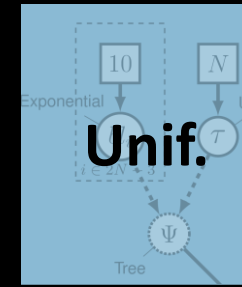
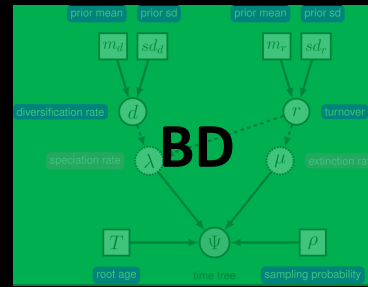
Our Models



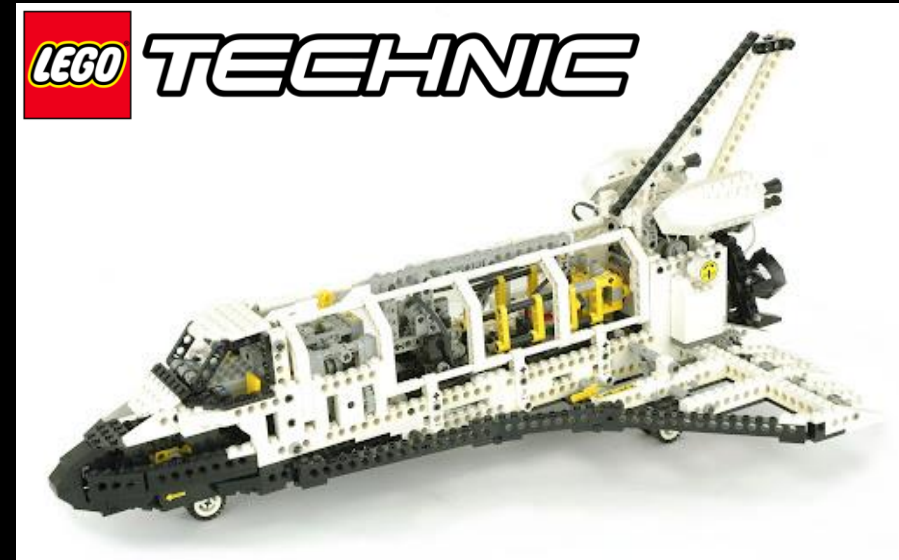
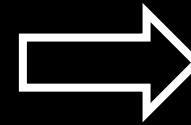
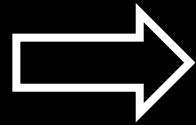
Our Models



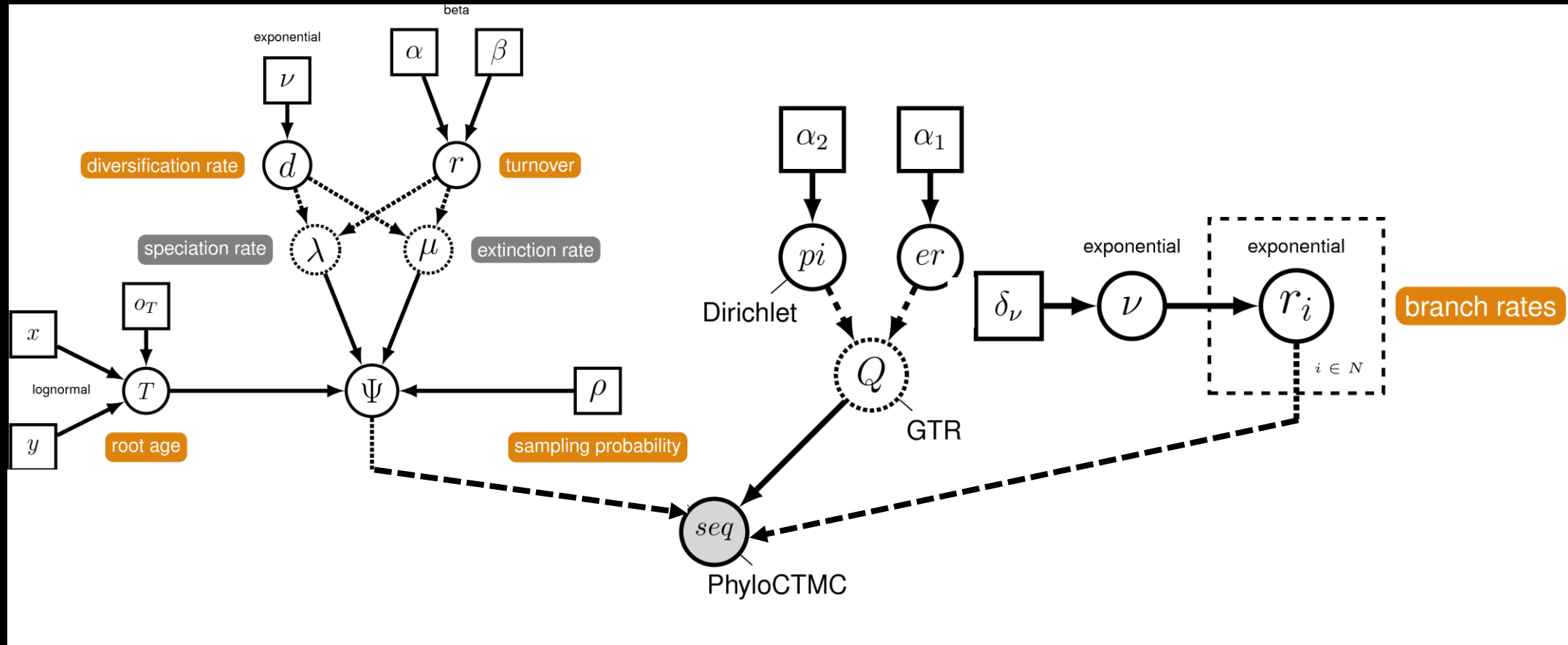
Our Models



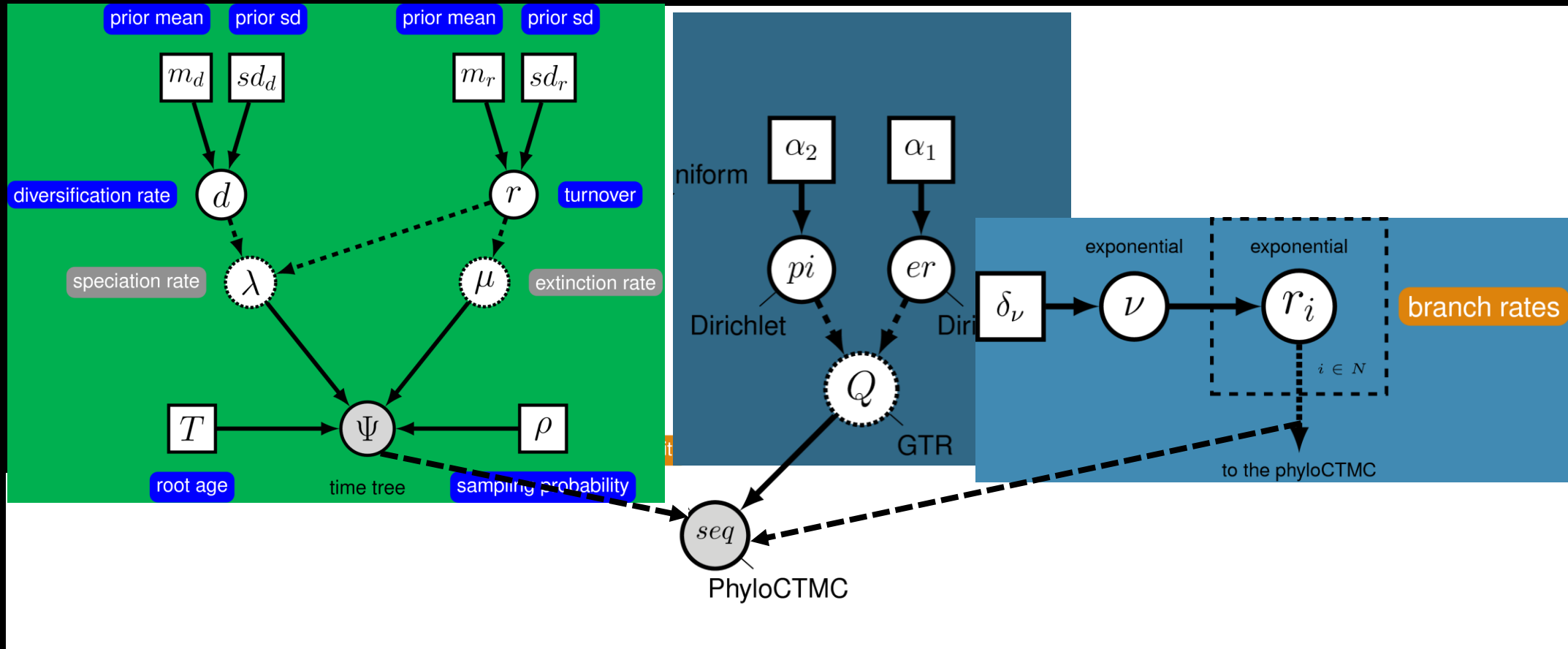
Syntax and more...



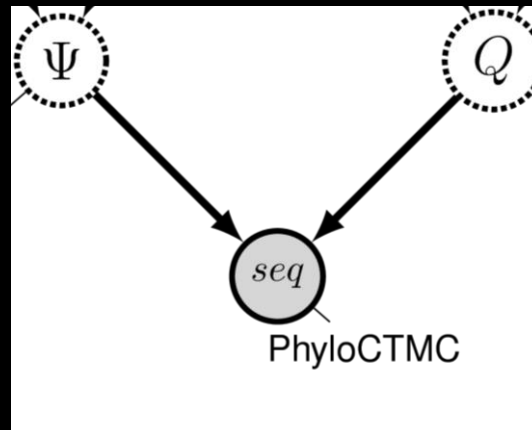
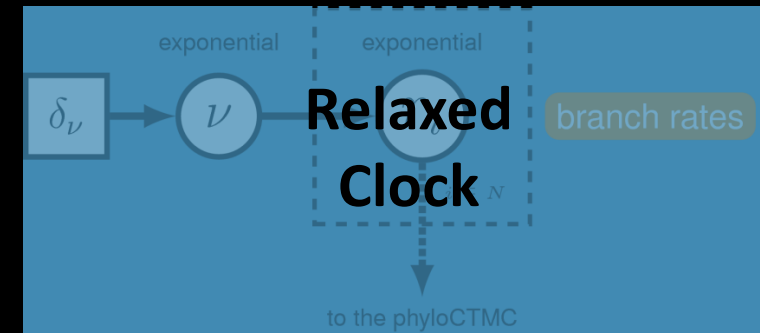
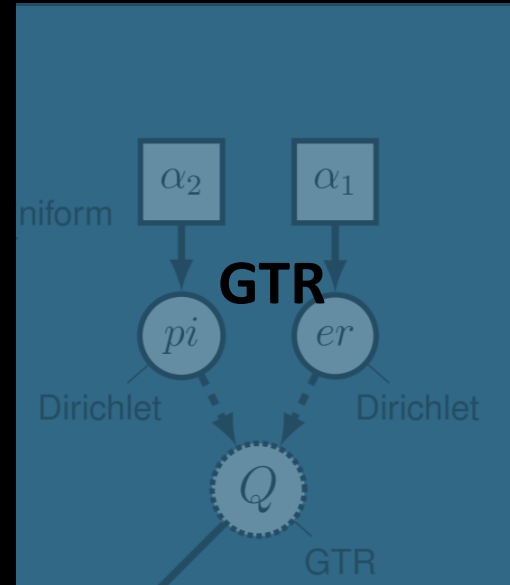
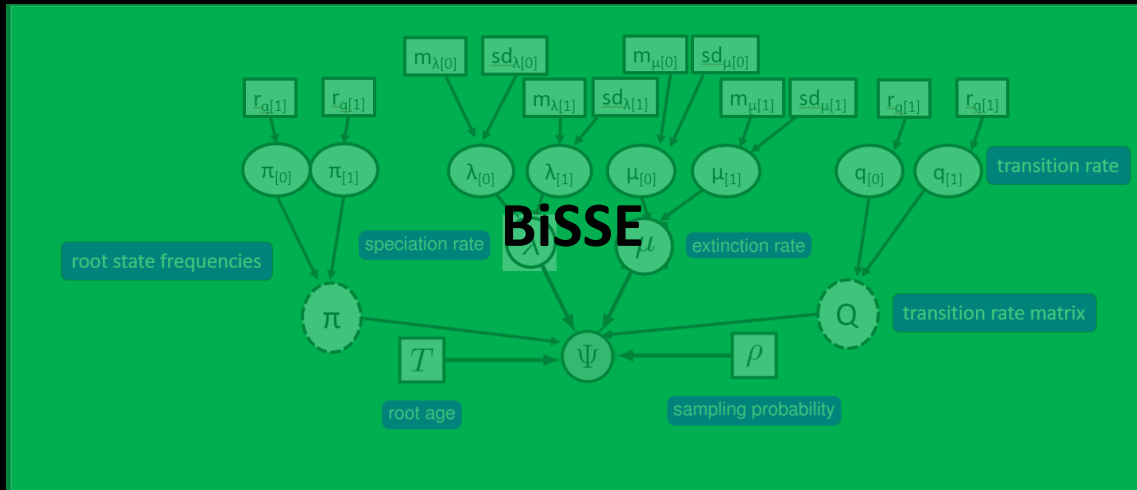
BD – GTR – Relaxed Molecular Clock



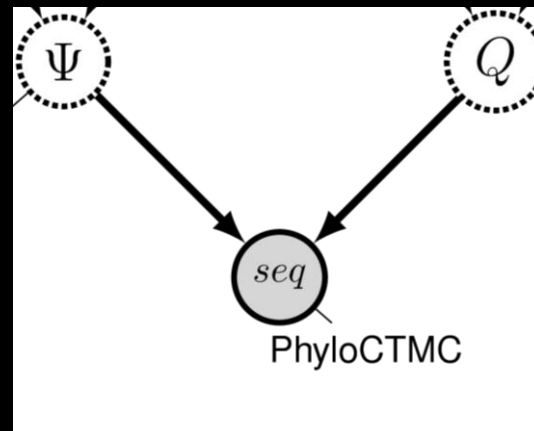
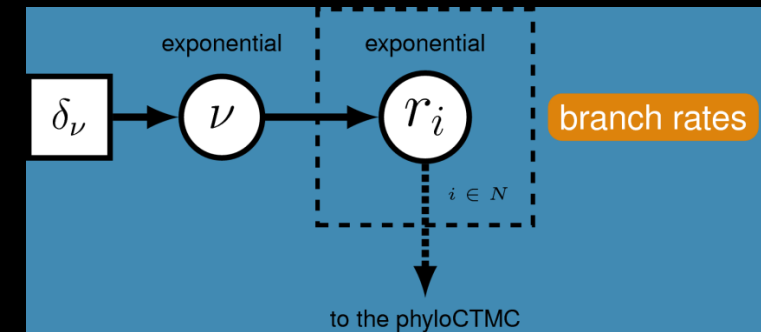
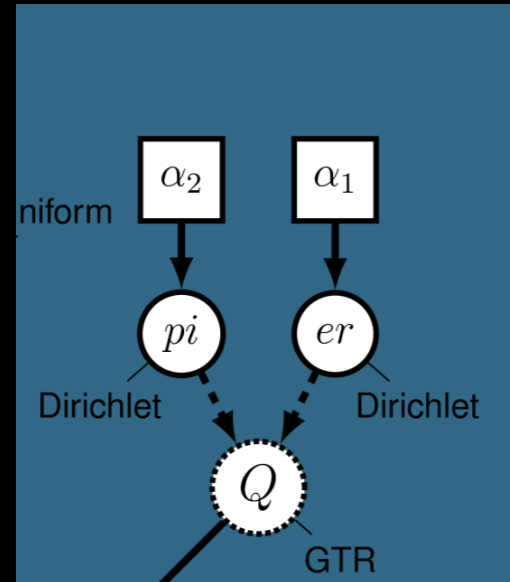
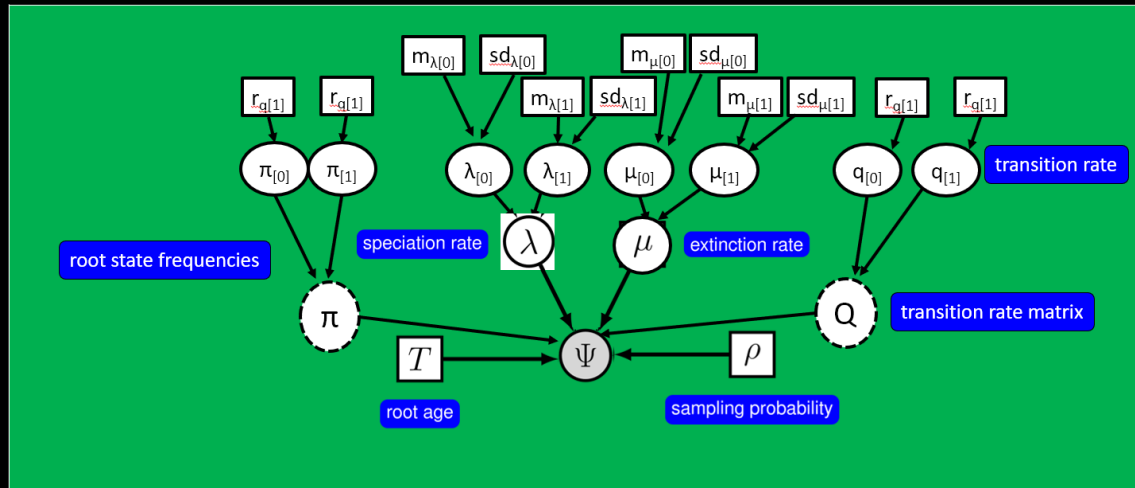
BD – GTR – Relaxed Molecular Clock



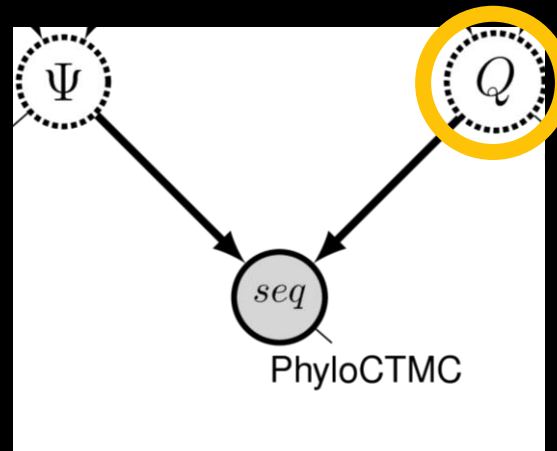
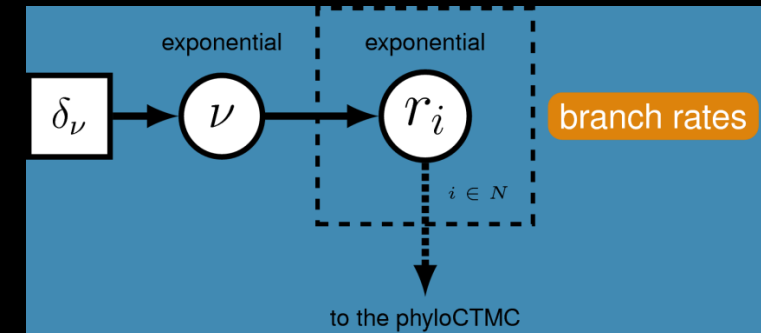
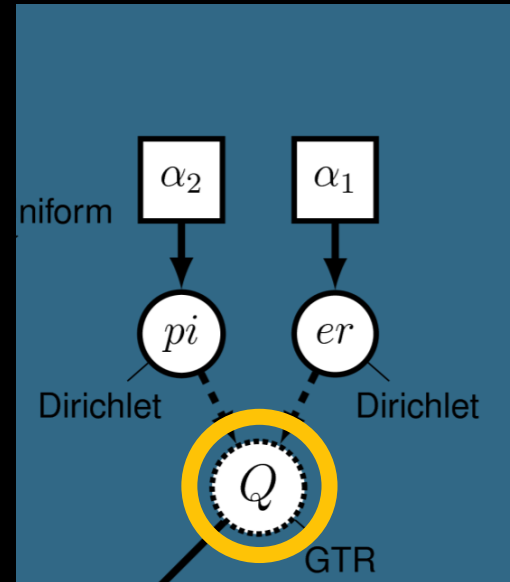
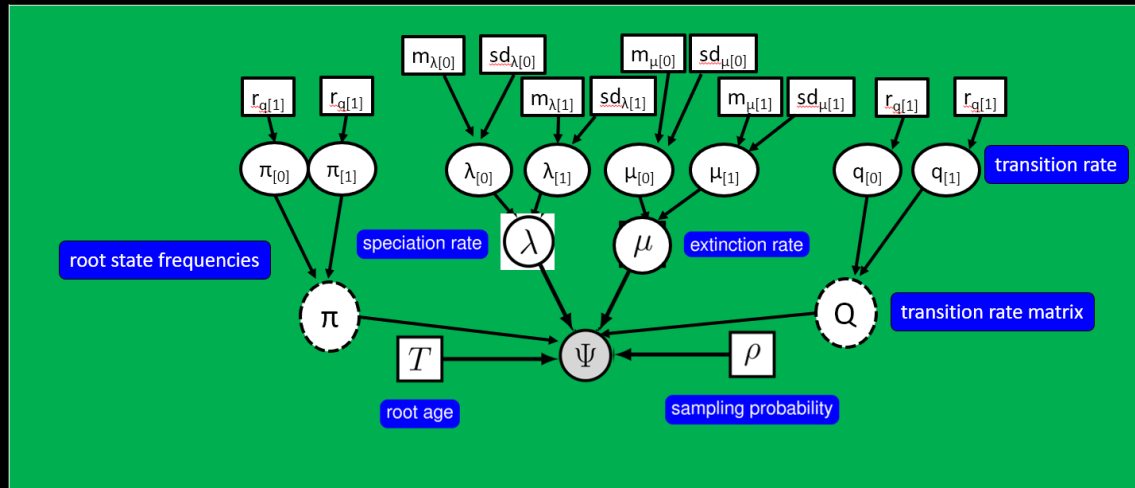
Build & Date Tree with BiSSE



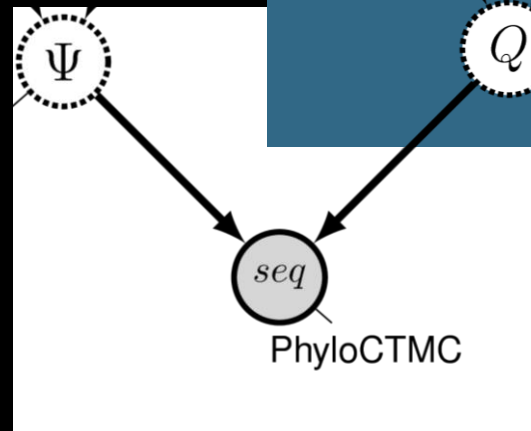
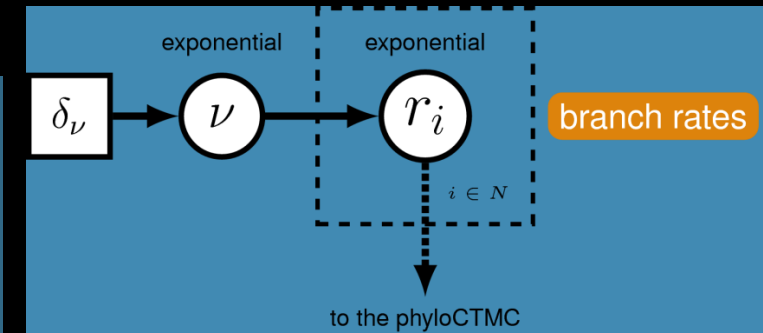
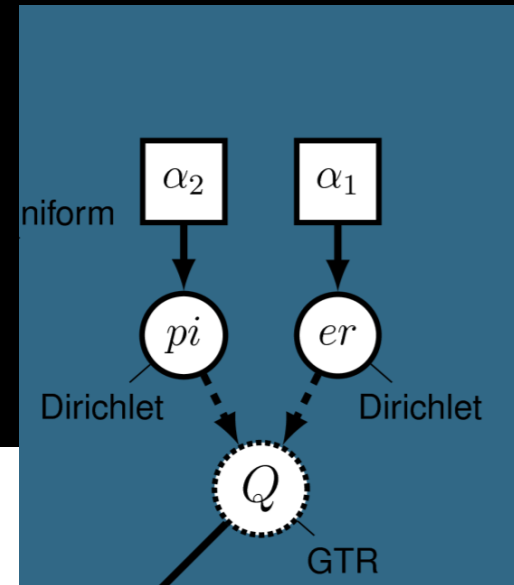
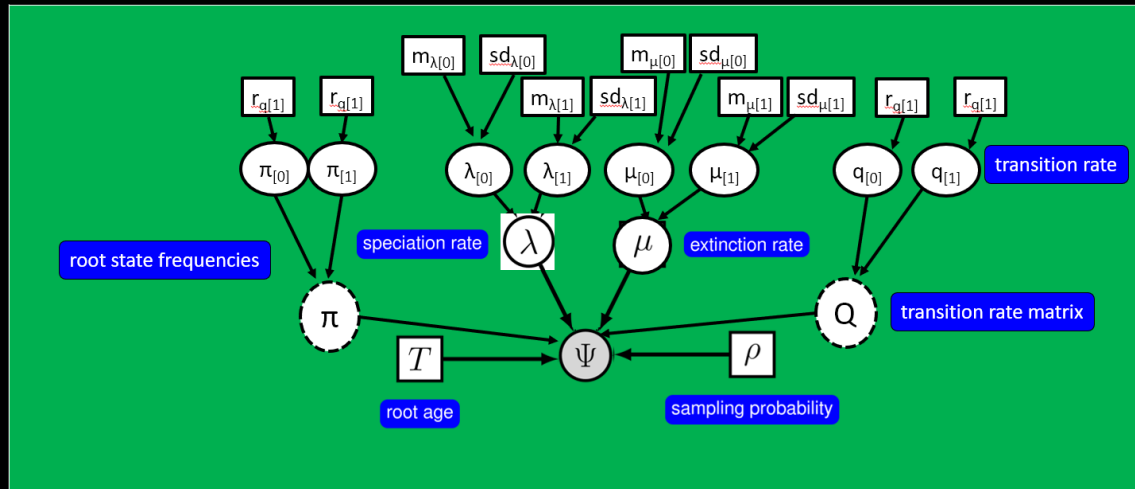
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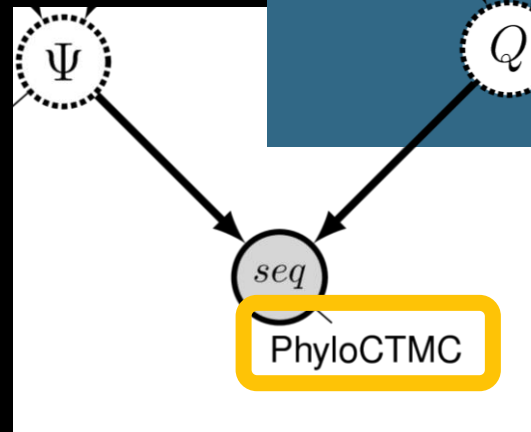
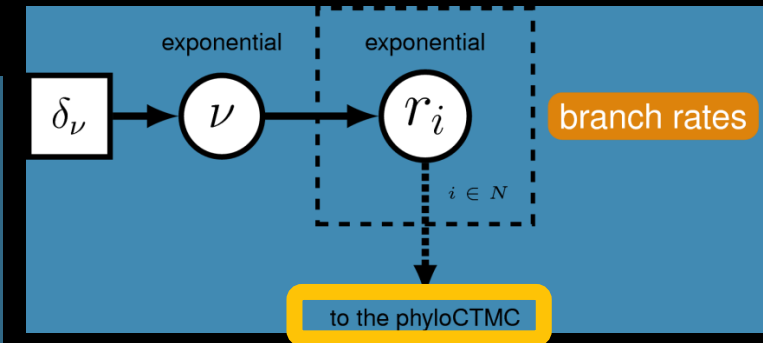
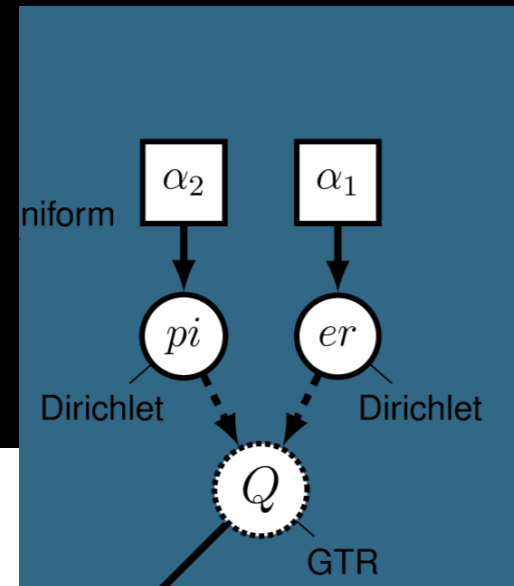
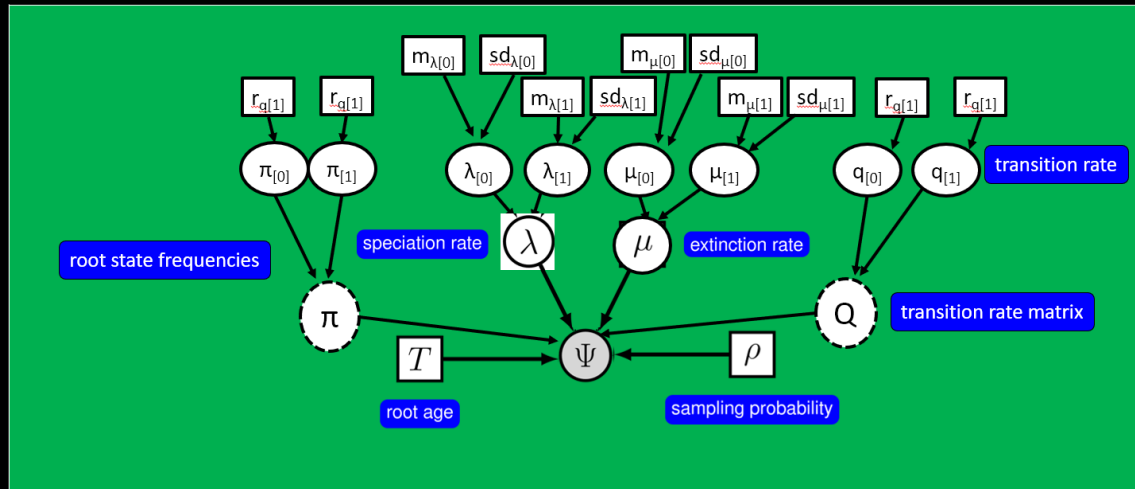
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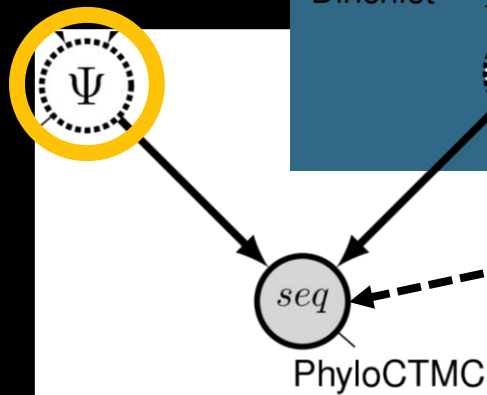
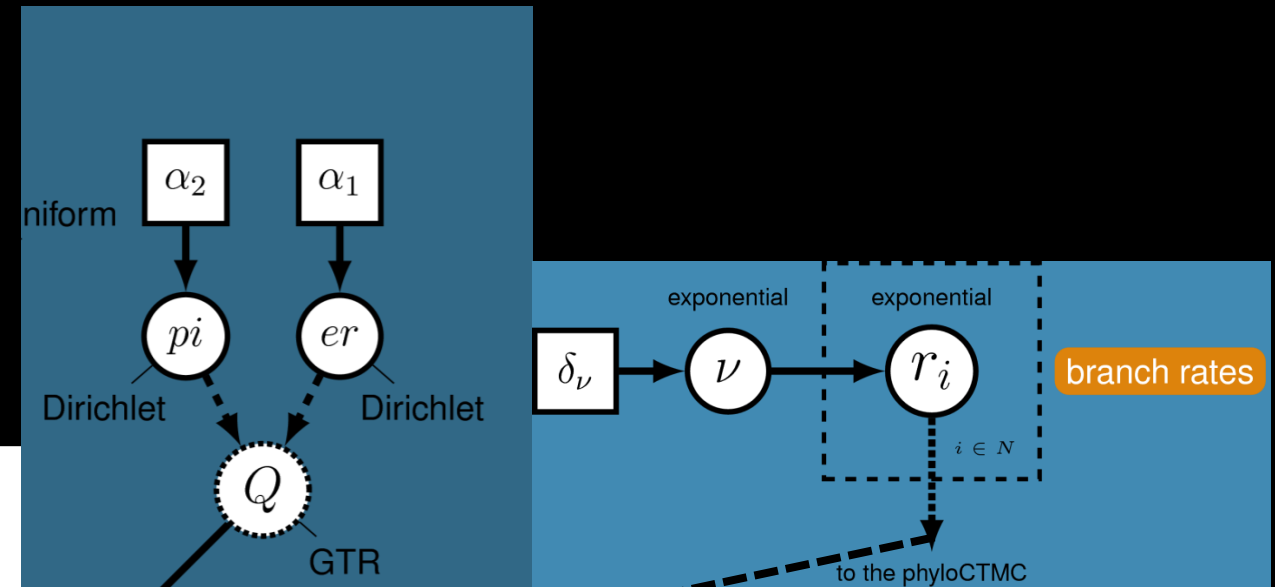
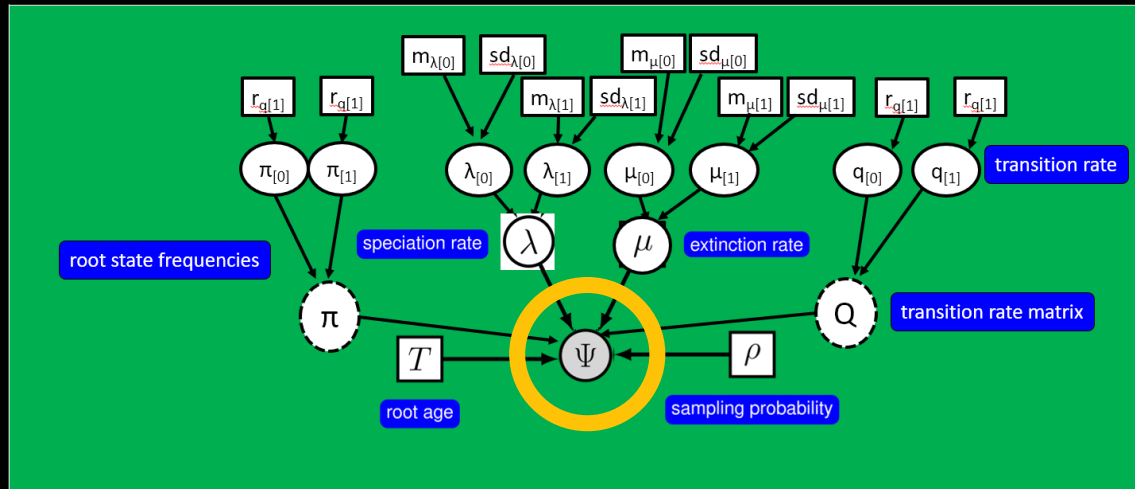
Build & Date Tree with BiSSE



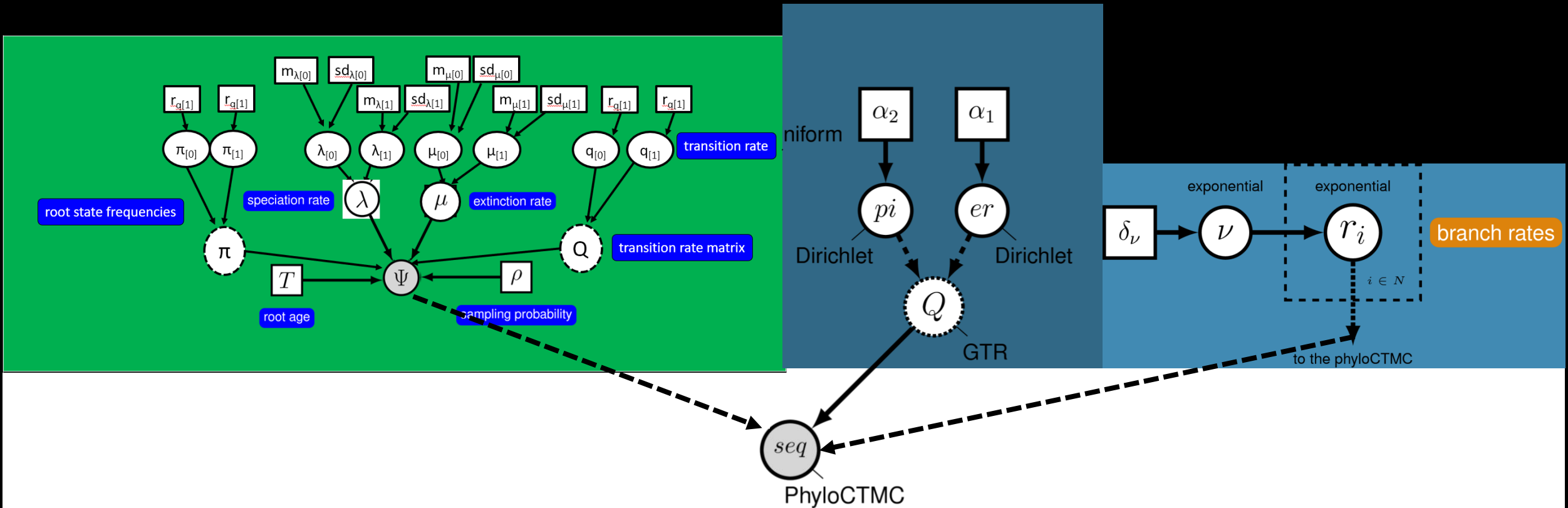
Build & Date Tree with BiSSE



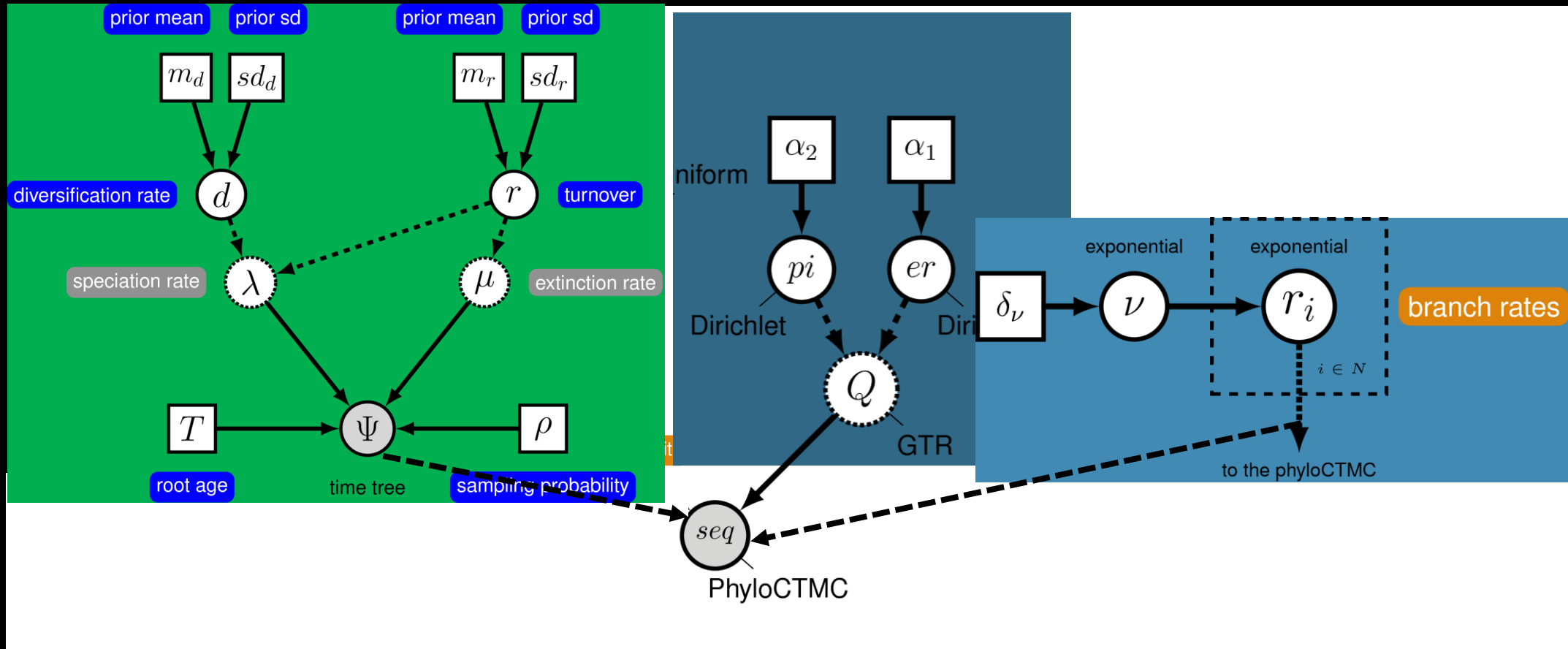
Build & Date Tree with BiSSE



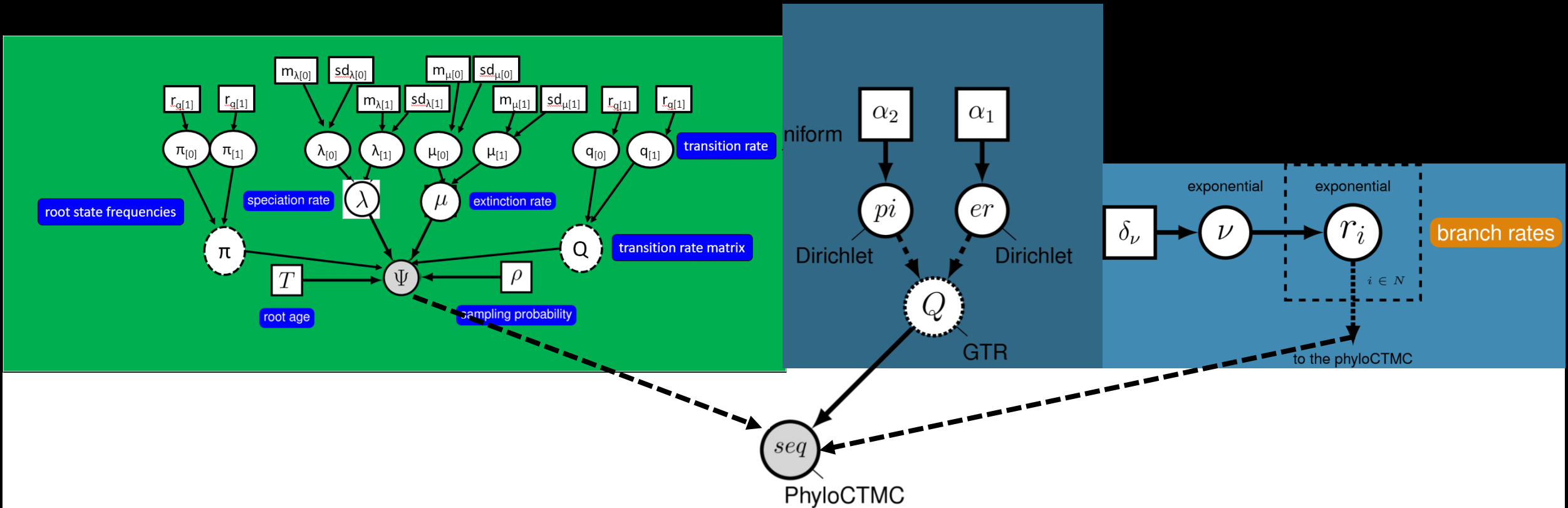
Build & Date Tree with BiSSE



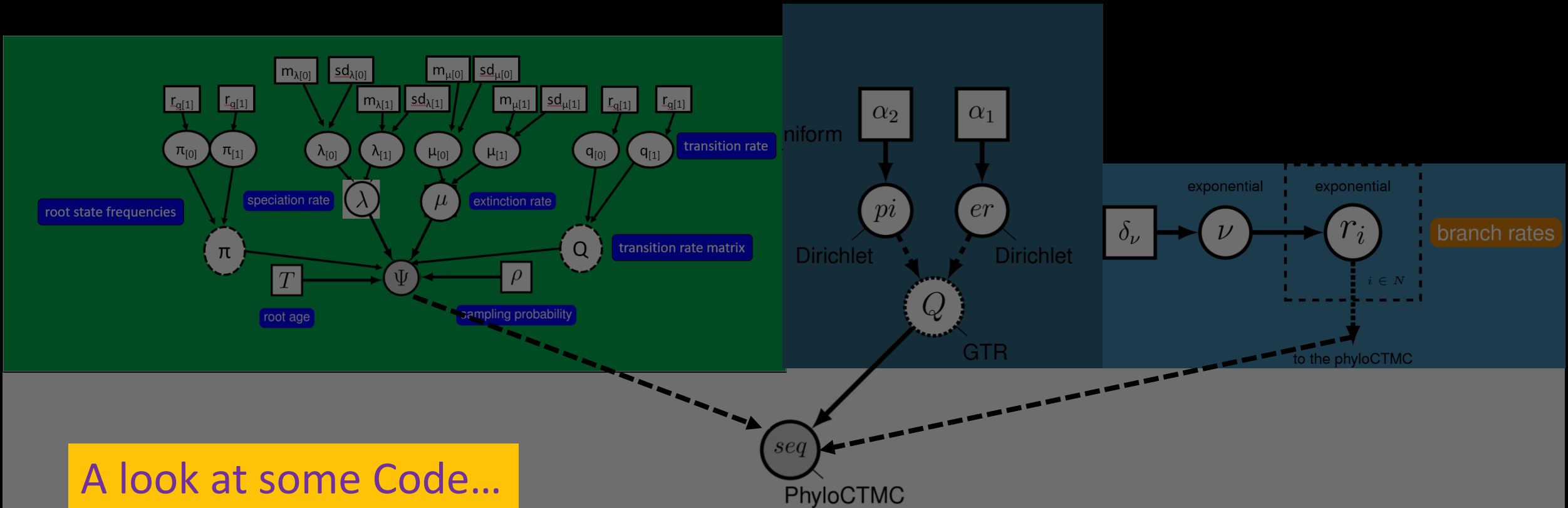
BD – GTR – Relaxed Molecular Clock



Build & Date Tree with BiSSE

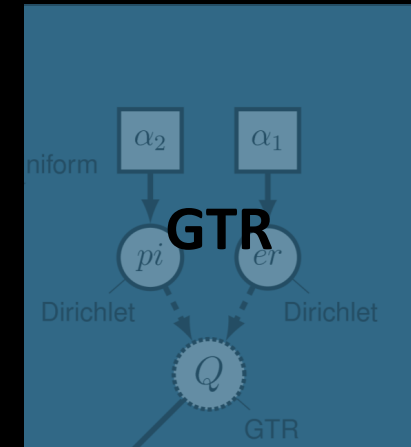
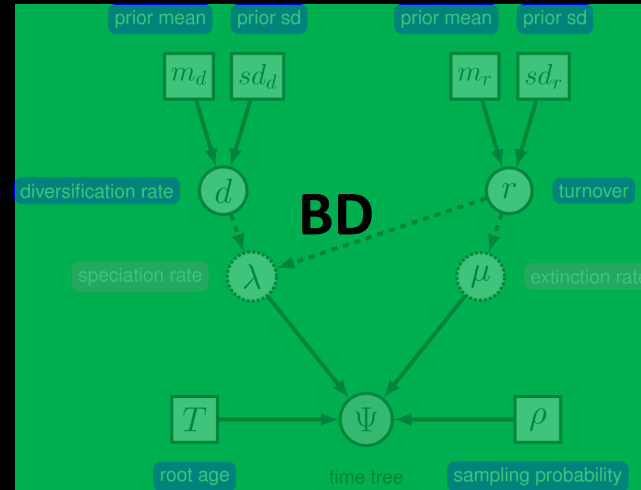
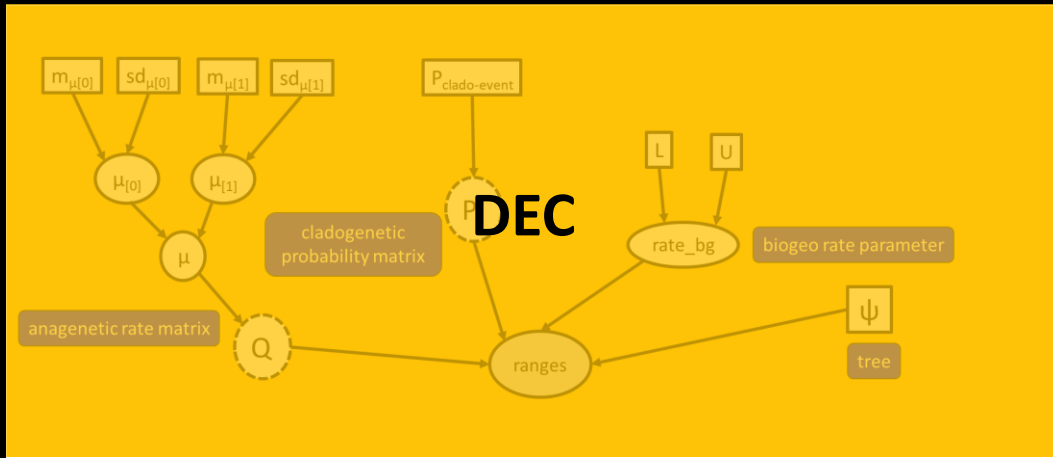


Build & Date Tree with BiSSE

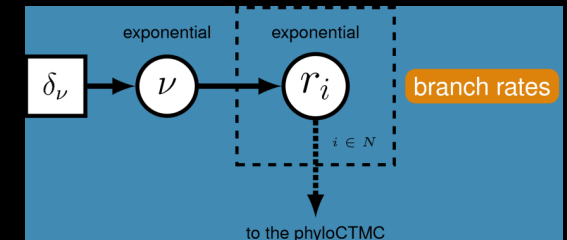
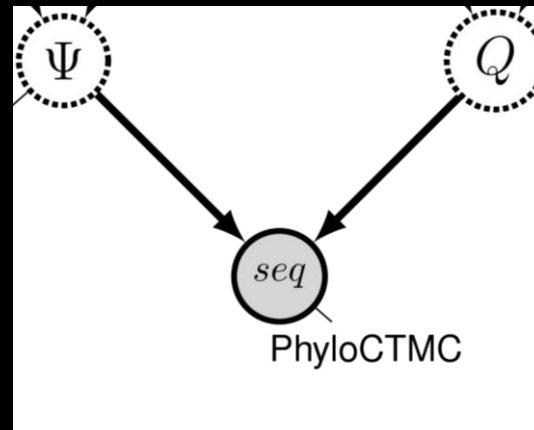
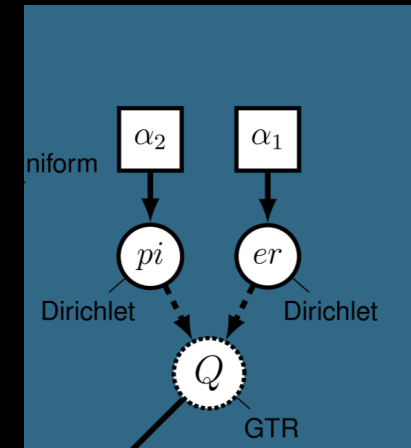
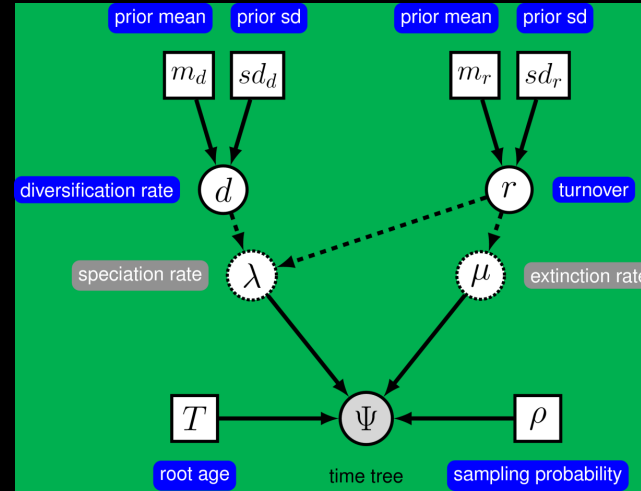
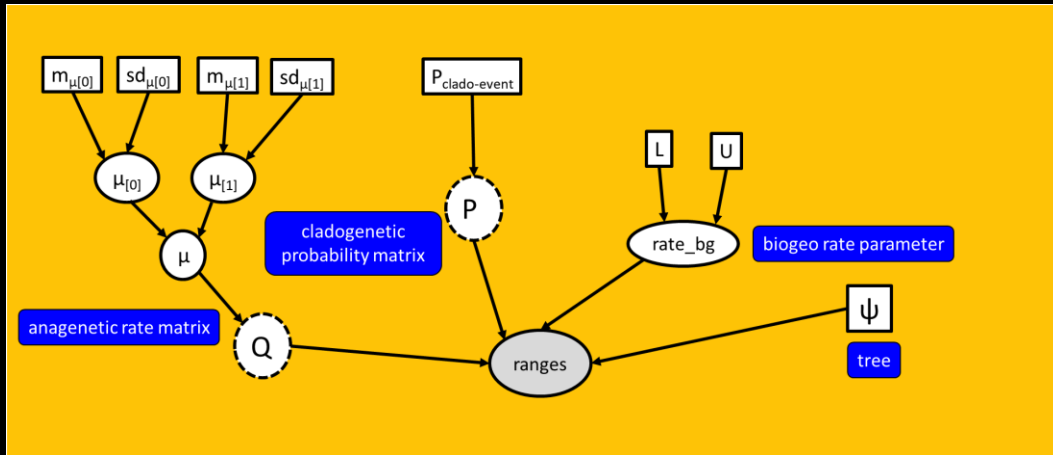


A look at some Code...

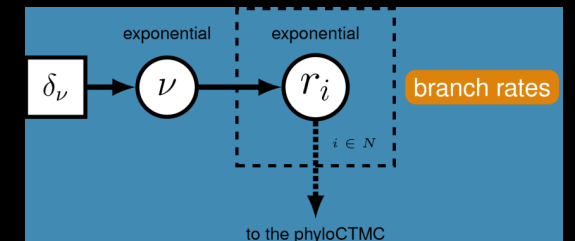
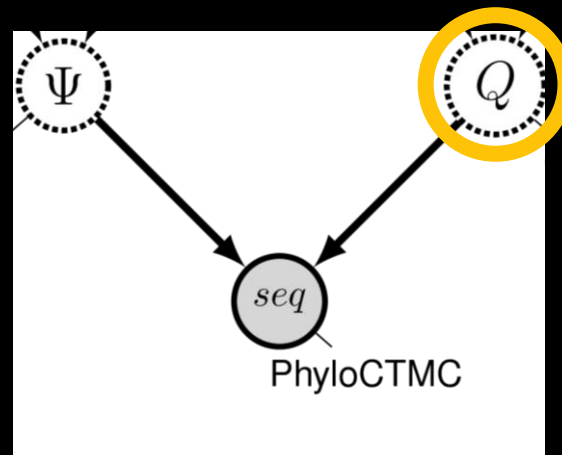
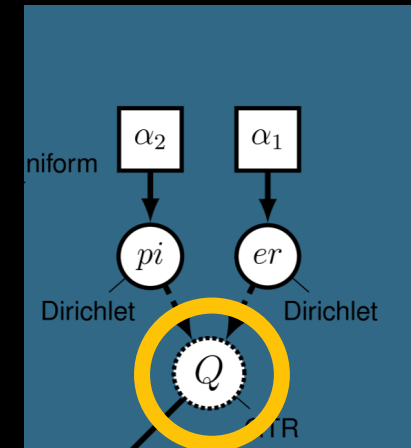
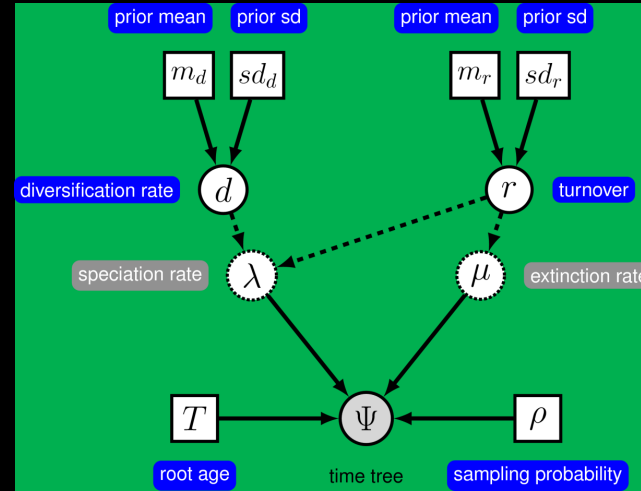
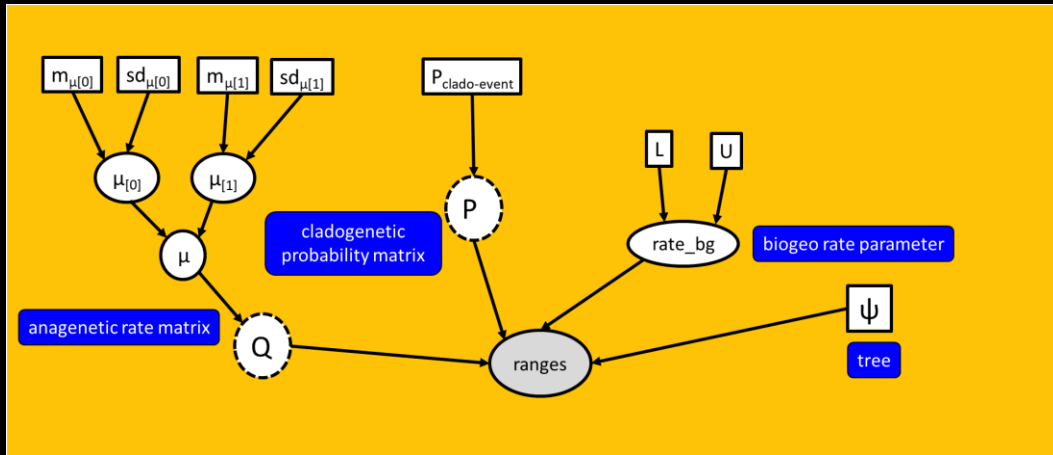
Stratigraphic Dating



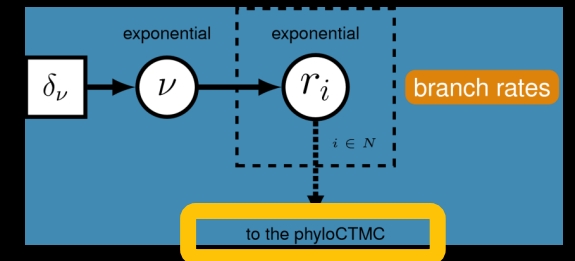
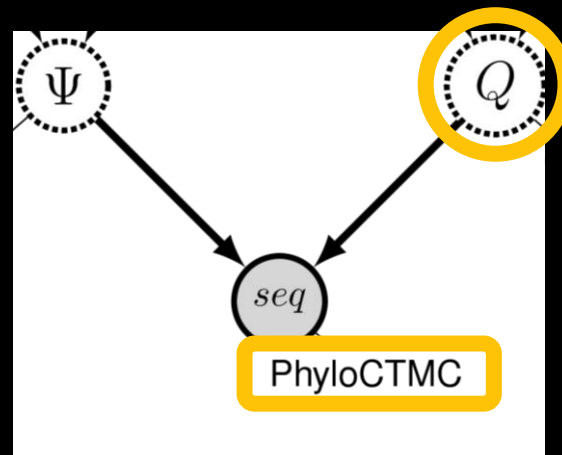
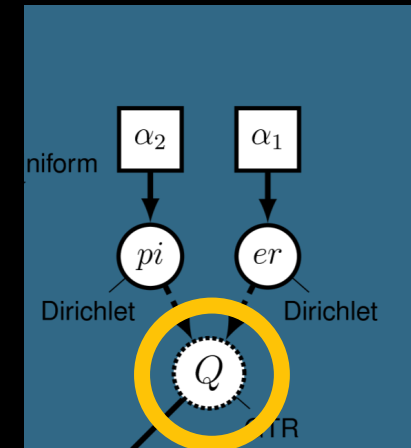
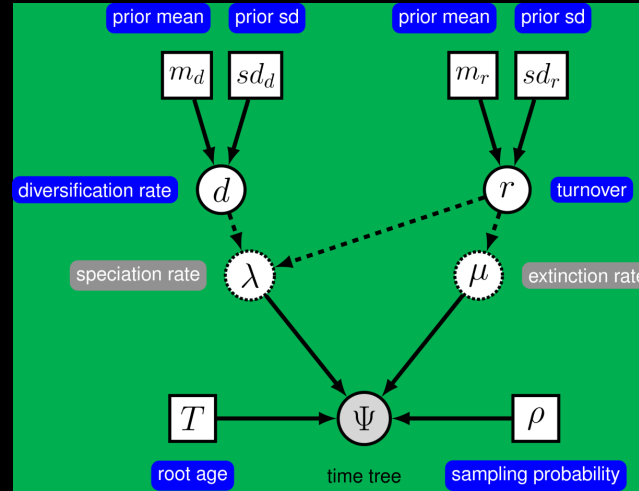
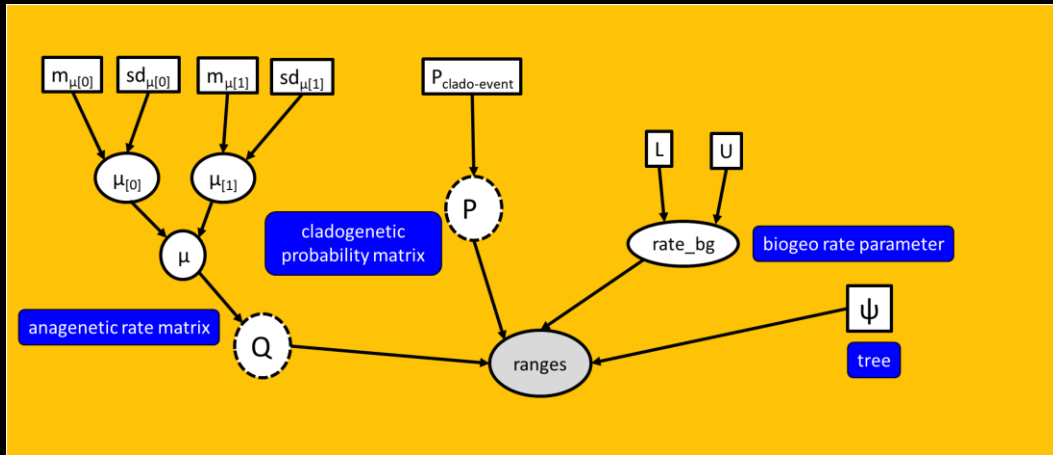
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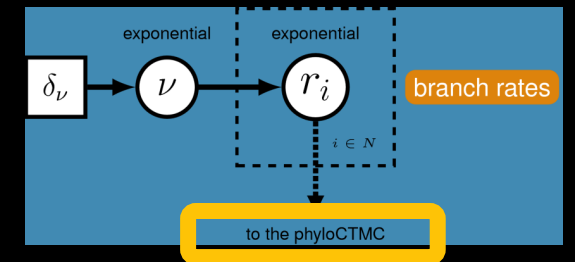
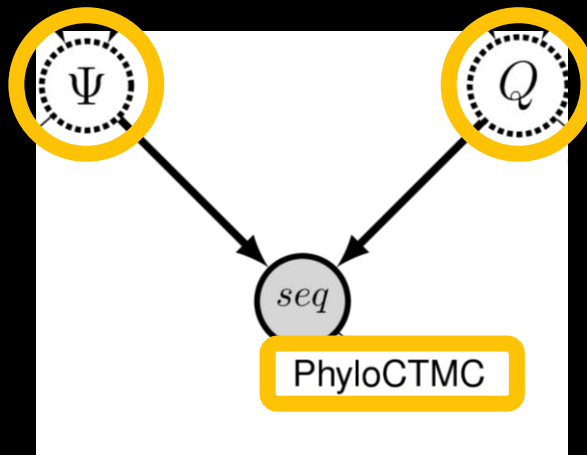
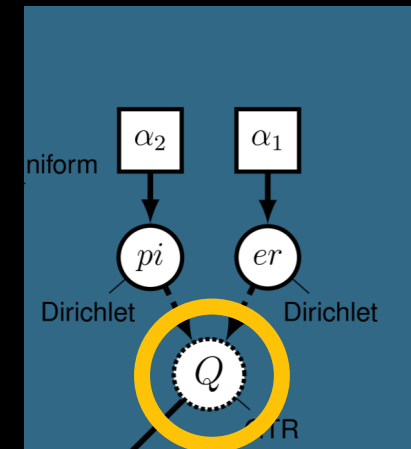
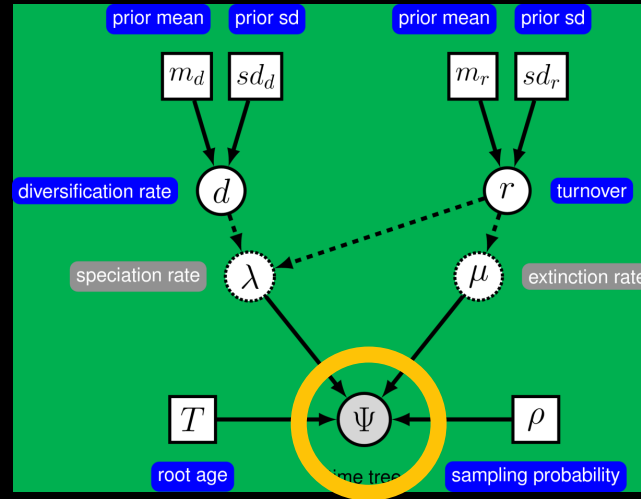
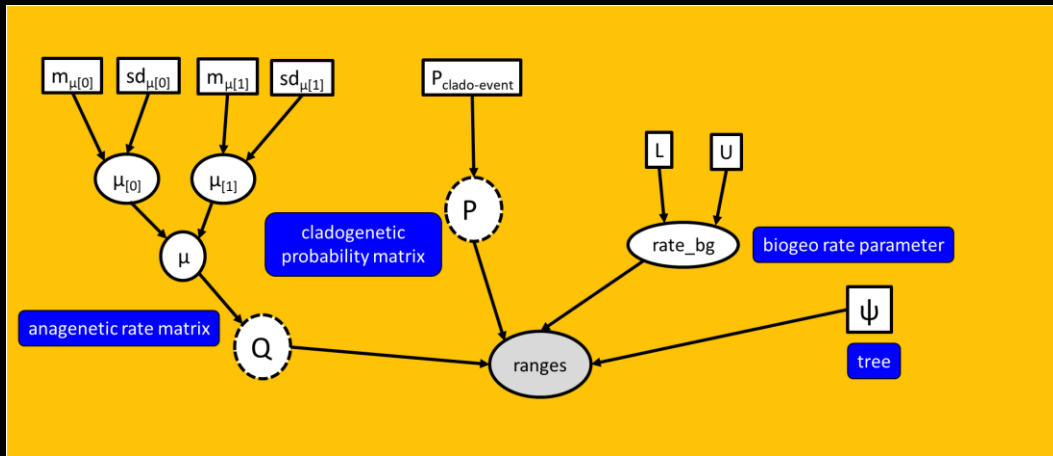
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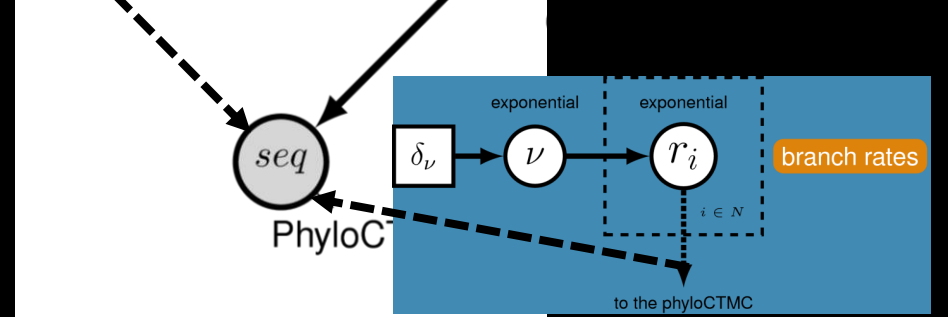
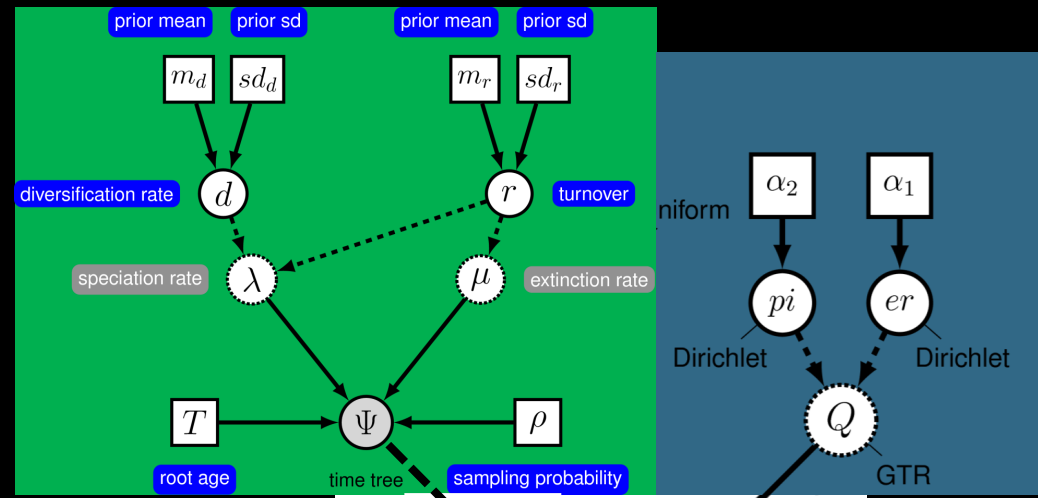
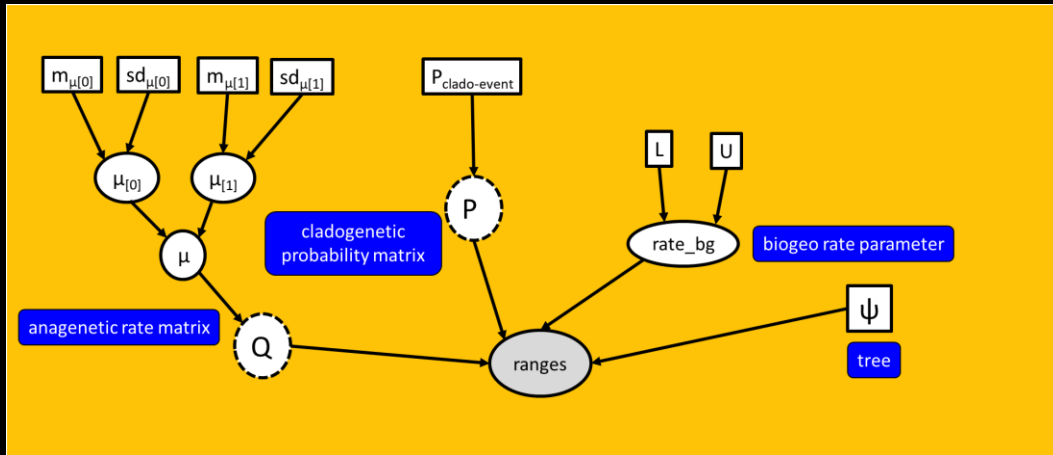
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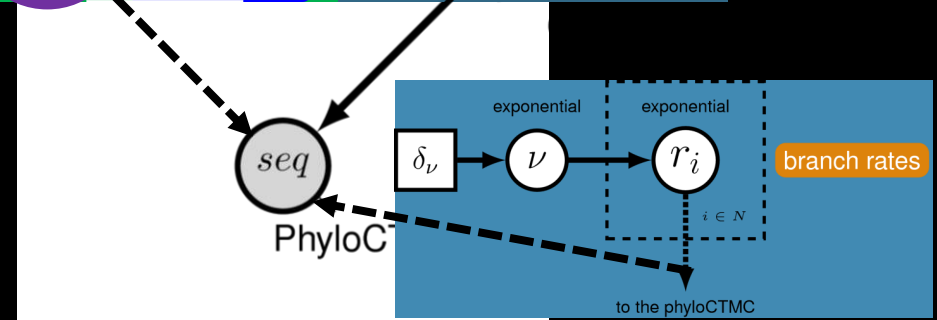
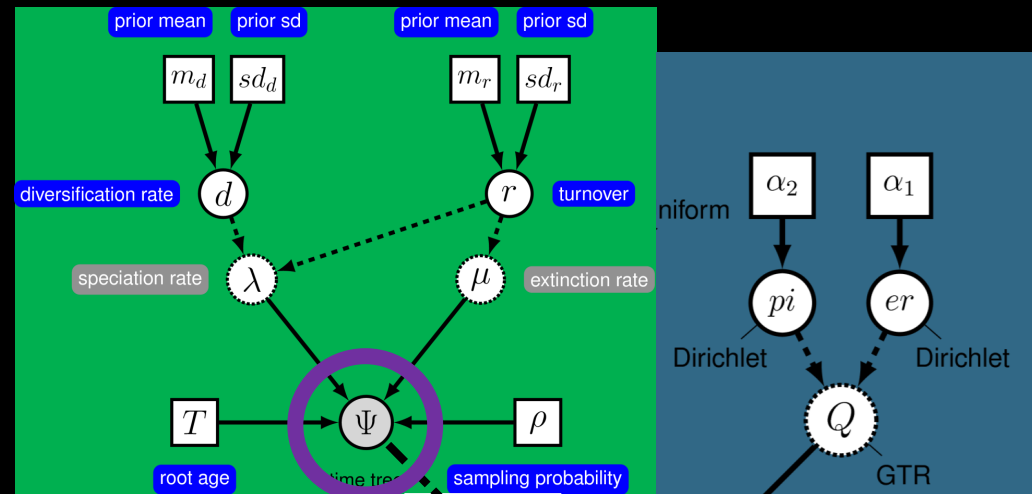
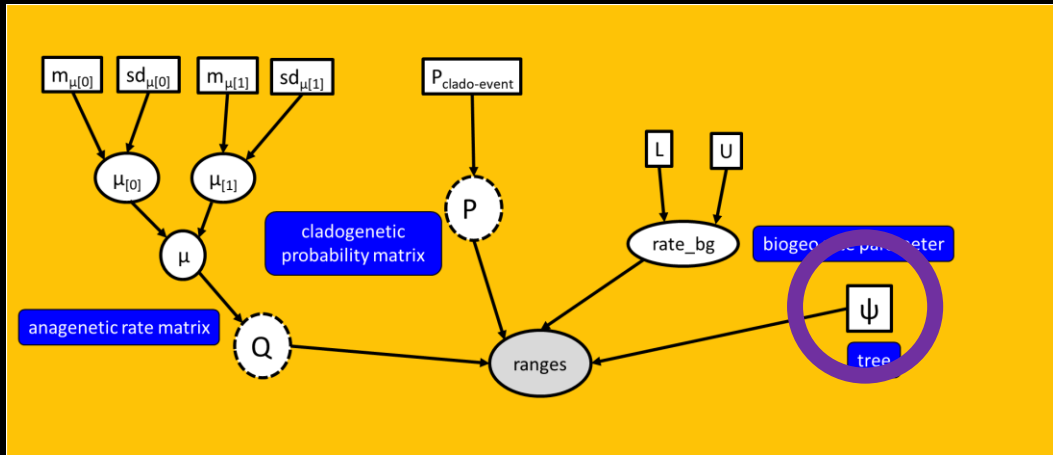
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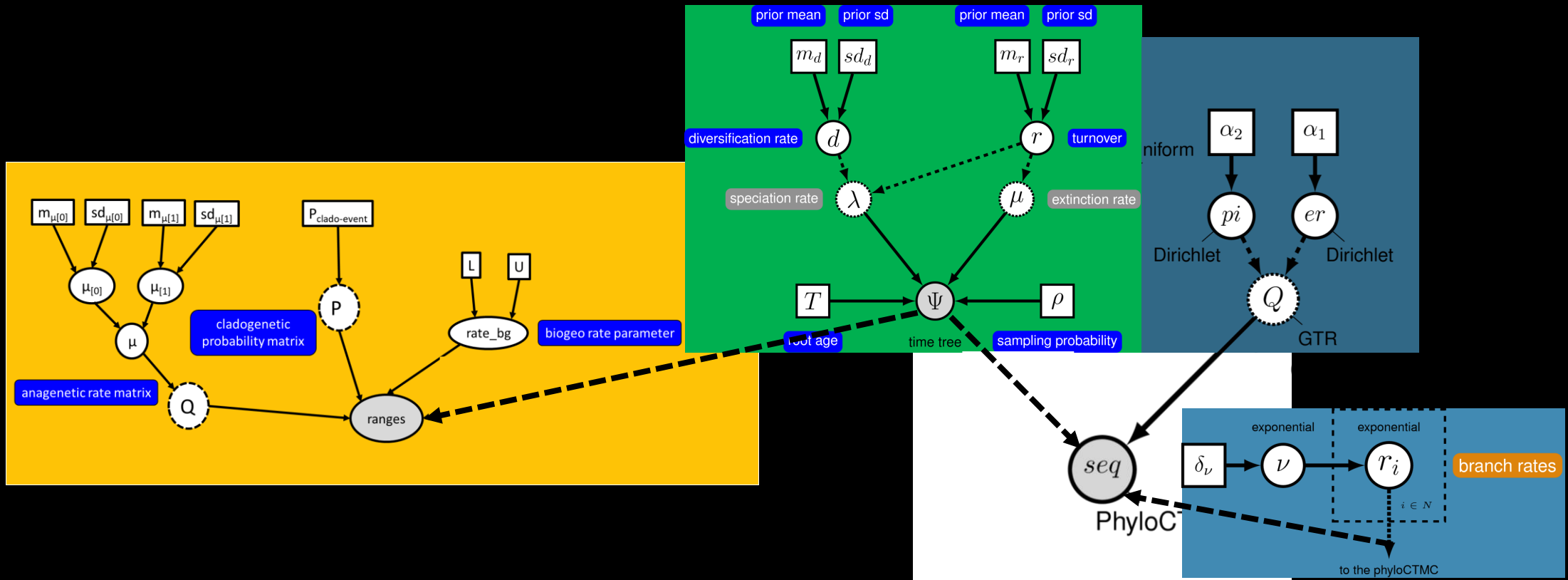
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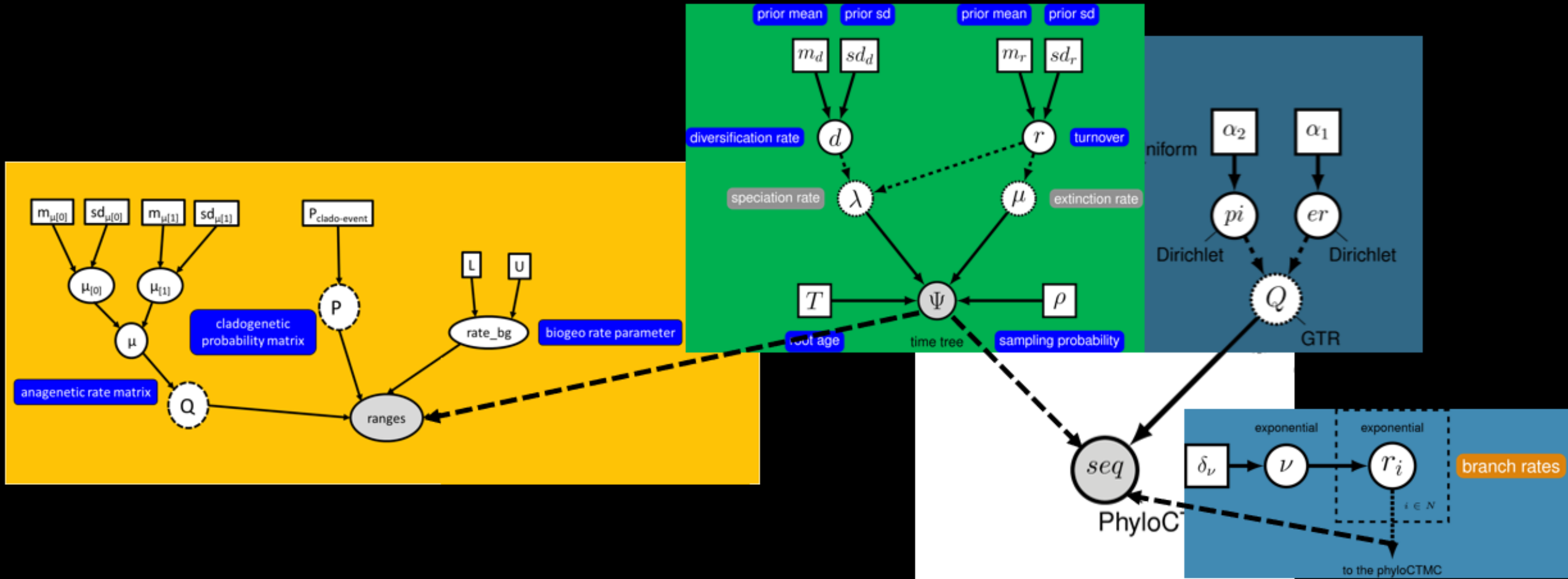
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Disclaimer & the Actual People Behind This

Höhna, Landis, Heath, Boussau, Lartillot, Moore, Huelsenbeck, Ronquist. **2016**. RevBayes: Bayesian phylogenetic inference using graphical models and an interactive model-specification language. *Systematic Biology*, 65:726-736.

Höhna, Heath, Boussau, Landis, Ronquist, Huelsenbeck. **2014**. Probabilistic graphical model representation in phylogenetics. *Systematic Biology* 63:753–771.



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