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1 Simulation of Summary Statistics

1. Generate target host tree \bar{H} .

Inputs

- Sequence data.
- Divergence time calibration priors.

Outputs

- Time-calibrated phylogeny, \bar{H} .

Procedure

- Use **BEAST** to generate sample from the posterior distribution of trees given the data, \mathcal{H} .
- Summarize \mathcal{H} using MCCT or other criteria to produce \bar{H} .

2. Generate samples of augmented host trees, \mathbf{h}^* , conditioned on target host tree, \bar{H} .

Inputs

- Time-calibrated phylogeny, \bar{H} .
- Labeling of tips on \bar{H} by geography (distributional range, specified as presence/absence over set of areas, for each tip).

Outputs

- Samples of host tree augmented with biogeographical history \mathbf{h}^* .

Procedure

- Use **BayArea** or **RevBayes** to generate stochastic mapped samples.

3. Generate samples of schedule of host events, \mathbb{E} .

Inputs

- Samples of host tree augmented with biogeographical history \mathbf{h}^* .

Outputs

- Samples of a schedule of host events, \mathbb{E} , where each distinct element $\mathcal{E}_i, \mathcal{E}_i \in \mathbb{E}$ bijectively corresponds to a distinct tree from \mathbf{h}^* , and consists of a vector of ordered pairs of (τ, η) , where τ is the simulation time of an event and η is the event (host speciation, host extinction, host dispersal, etc.) that occurs at that time on the particular tree to which it corresponds.

4. For *each* simulation replicate:

- (a) Sample a schedule of host tree events, \mathcal{E}_i , from \mathbb{E} .
- (b) Simulate symbiont tree, ψ , conditioned on \mathcal{E} and other parameters.
- (c) Calculate summary statistics on the symbiont tree, ψ .