Distinguishing Causal Scenarios Using SSE Models

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Photo: L. Alencar

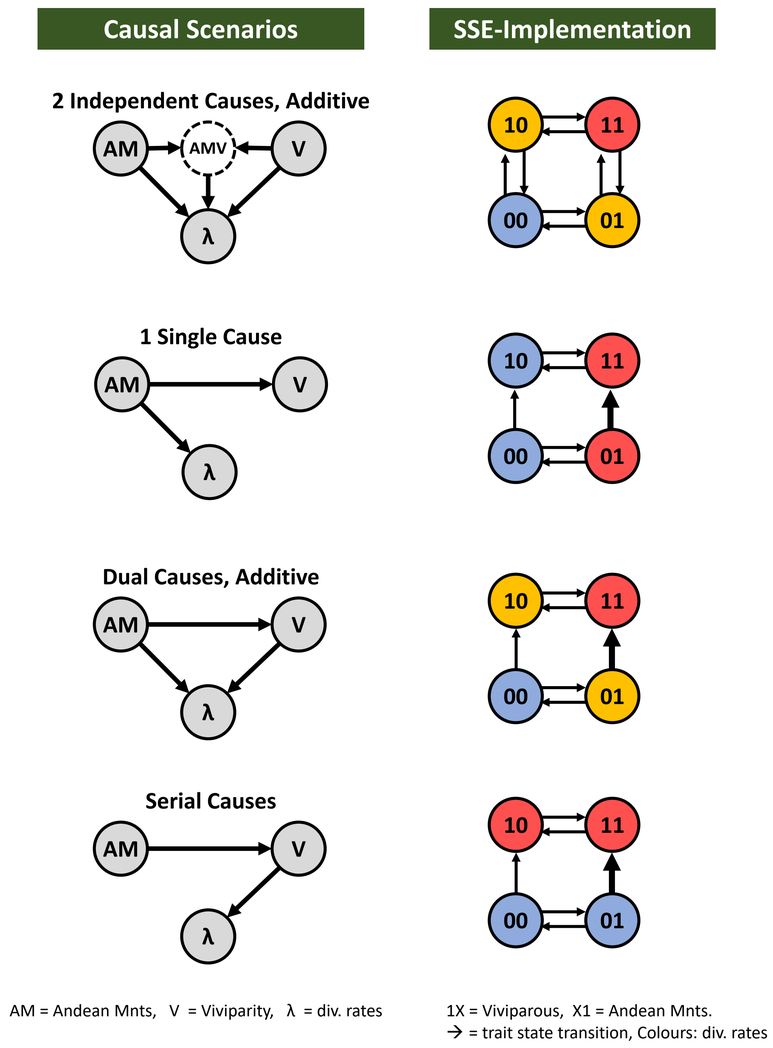
Background

- SSE models are popular tools to study adaptive radiations but can be misled (Rabosky & Goldberg 2015).
- Hidden states (HiSSE; Beaulieu & O'Meara, 2016) detect confounding factors to rate heterogeneity.
- Adequacy tests (adequaSSE; Schwery, Freyman & Goldberg, *in prep*.) can detect mismatches between data and model due to other processes.
- Correlative nature of models and confounding factors limit possible conclusions to be drawn from results.

Questions/Goals

- Pleurodonta radiation due to ecological opportunity.
- Previously inferred to be linked to viviparity, but here we consider occurrence in Andean mountains as possible confounding (real) cause.
- Formulate alternative causal scenarios where Andean mountains, viviparity, or both are the ecological opportunities causing increased diversification rates – or also causing the evolution of the respective other trait.

Can the combination of **causal models** and **adequacy tests** help rule out competing causal scenarios?



Methods

Dated phylogeny:
- 733 out of 1111 species of Pleurodonta
- Based on trees by Tonini *et al.* (2016)

Data:
- Reproductive mode (oviparous/viviparous)
- Occurrence in Andean mountains.

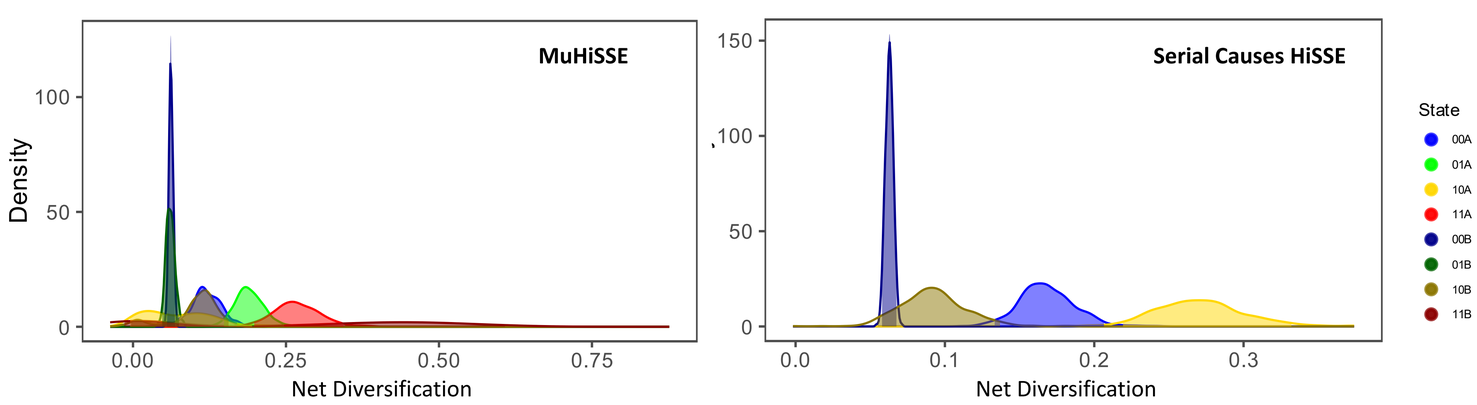
Diversification Models:
- 4 causal scenarios implemented in SSE models
- MuSSE or MuHiSSE (2 hidden states) in RevBayes.

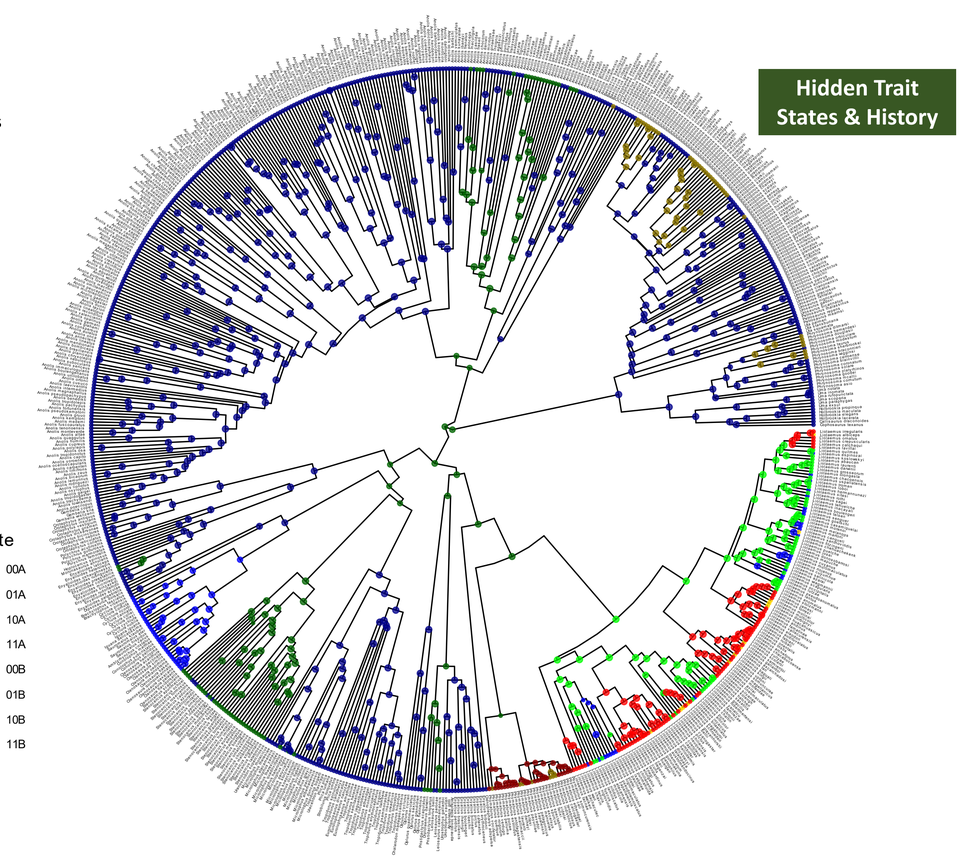
Model Fit:
- Bayes Factors using stepping stone sampling

Model Adequacy:
- Simulated posterior predictive data sets for each model
- 4 different conditionings
- Calculated a large number of summary statistics on empirical and simulated data

Main Findings

- Best fitting: MuHiSSE, (followed by Serial Causes HiSSE & MuSSE)
- Different hidden states for Liolaemidae (or Liolaemus) and large bodied iguanids
- Clear inadequacy of models without hidden states





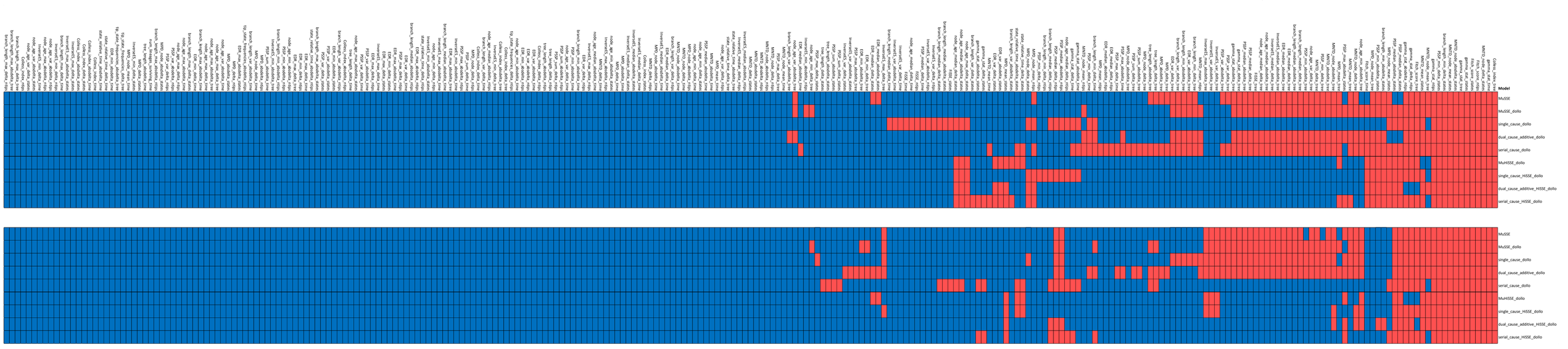


Photo: Marcio Borges-Martins

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References

- Rabosky, D. L., & Goldberg, E. E. (2015). Model inadequacy and mistaken inferences of trait-dependent speciation. *Systematic biology*, *64*(2), 340-355.
- Beaulieu, J. M., & O'Meara, B. C. (2016). Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Systematic biology*, *65*(4), 583-601
- Schwery, O., Freyman, W., & Goldberg, E. E. (*in prep*) adequaSSE: model adequacy testing for trait-dependent diversification models
- Tonini, J. F. R., Beard, K. H., Ferreira, R. B., Jetz, W., & Pyron, R. A. (2016). Fully-sampled phylogenies of squamates reveal evolutionary patterns in threat status. *Biological Conservation*, *204*, 23-31.