Tracking the formation of a species assemblage over time: phylogenetic reconstruction of patterns of colonisation and speciation

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Division of Evolution, Ecology and Genetics
Australian National University

Presented by Xia Hua, 11-08-13

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Colonisation **In-situ speciation**

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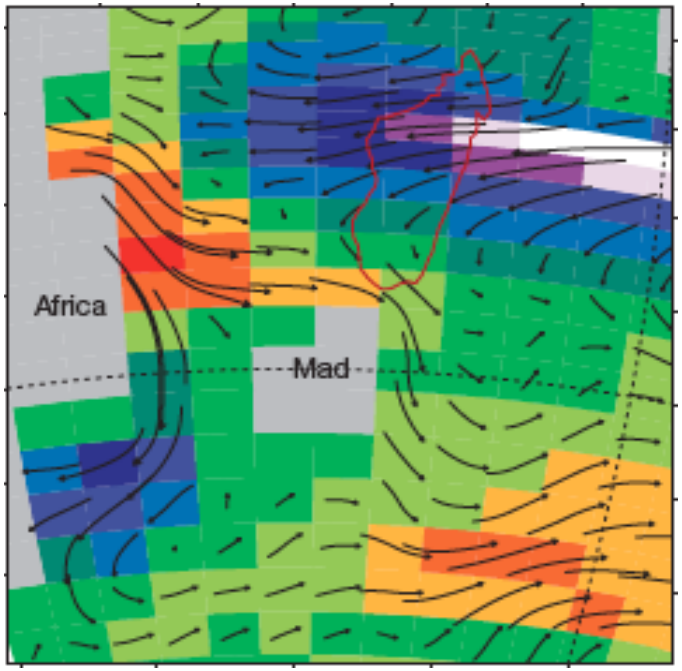
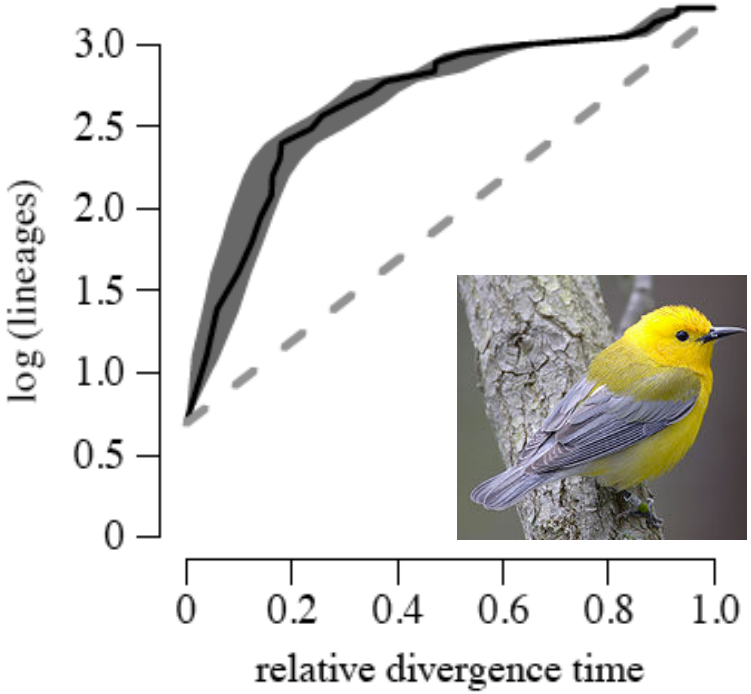


Uneven colonization rate due to geographical events

Ali & Huber 2010 Nature



Slow-down in speciation rate due to saturation

Rabosky & Lovette 2008 Proc.R.Soc.B

Approaches to reconstruct patterns of speciation and colonisation

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Use paleontological data

Need continuous fossil record and adequate taxonomic and temporal resolution

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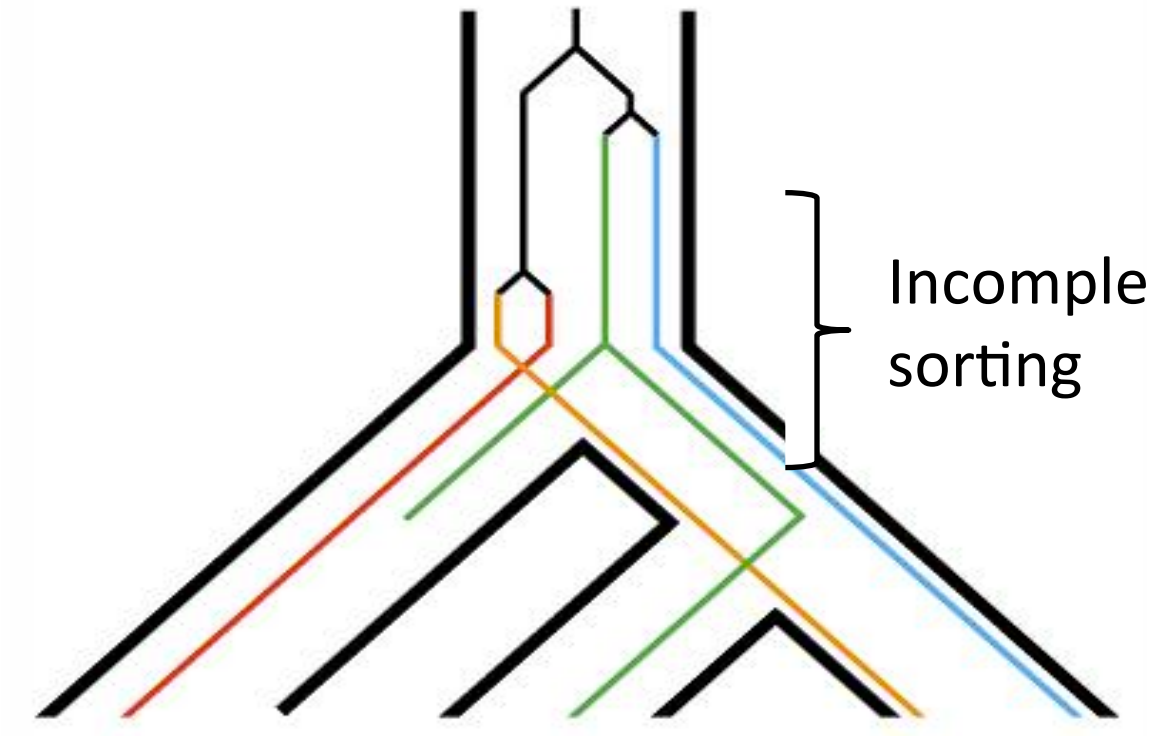

Uncertainty in localize speciation and colonization events on a node

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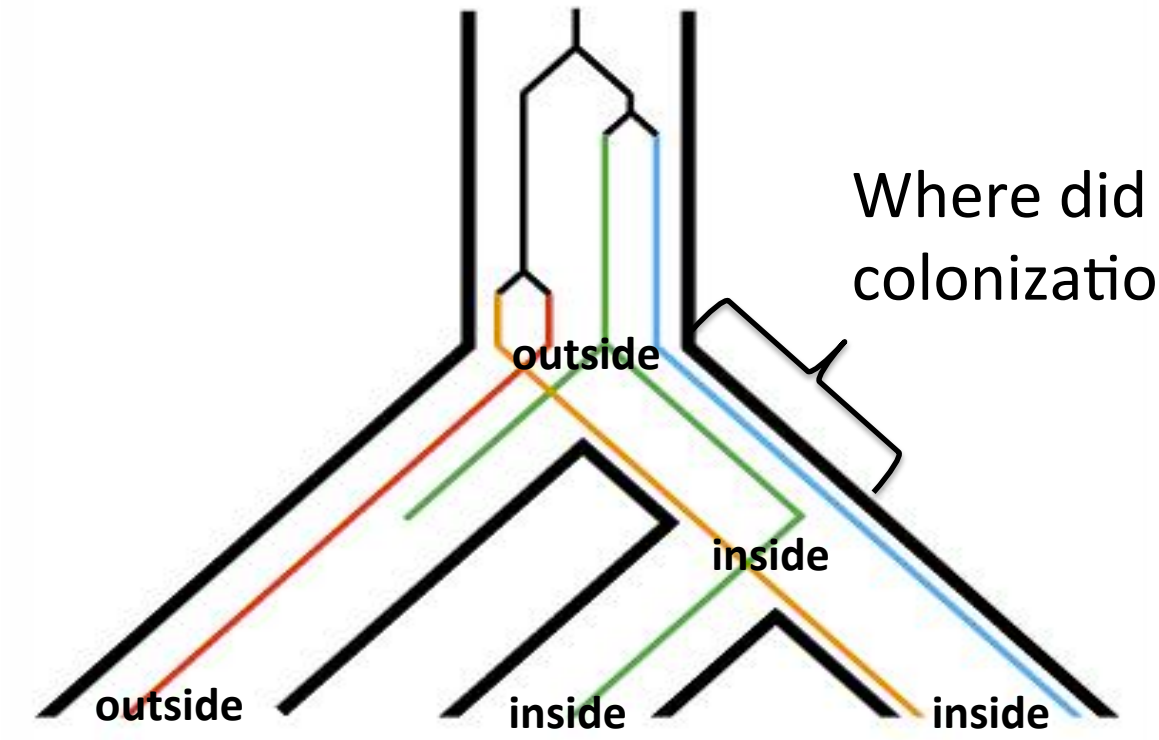

Uncertainty in localize speciation and colonization events on a node

Framework of testing assemblage formation using phylogenies

How likely it is to observe the extant species assemblage if it was formed in the way as the null hypothesis predicts ?

$$L(\text{assemblage} \mid \mathrm{H}_0) =$$

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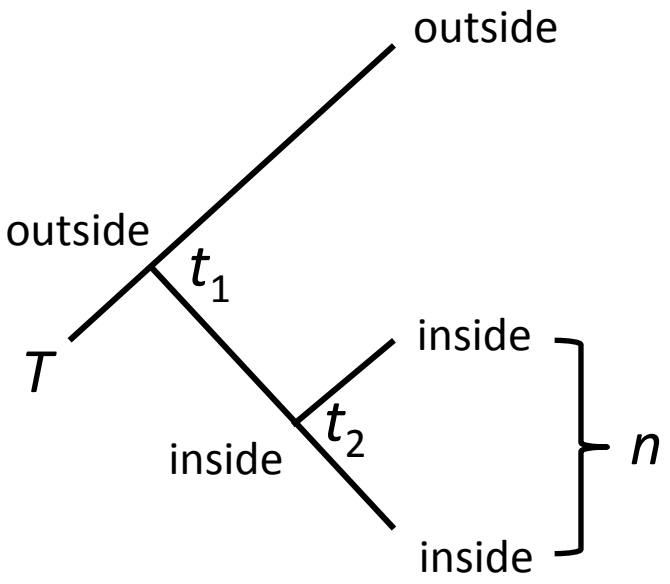

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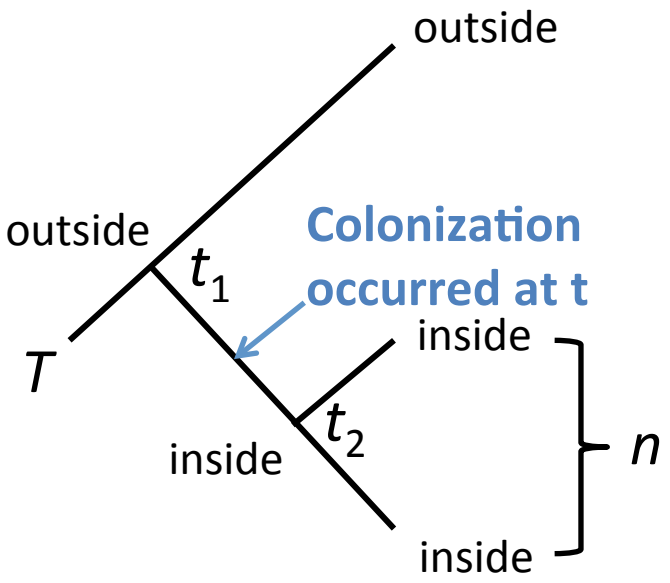

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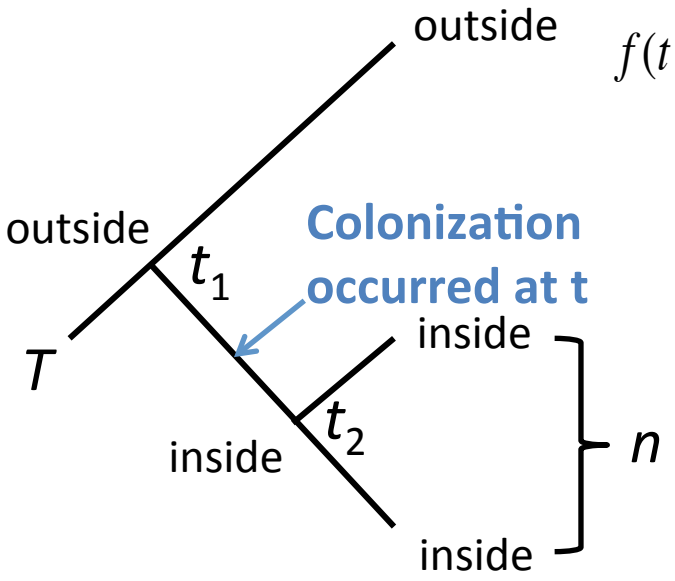

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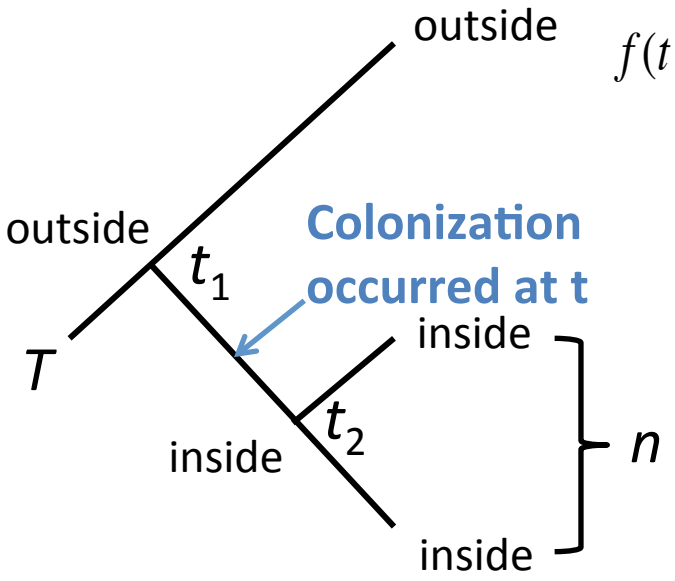

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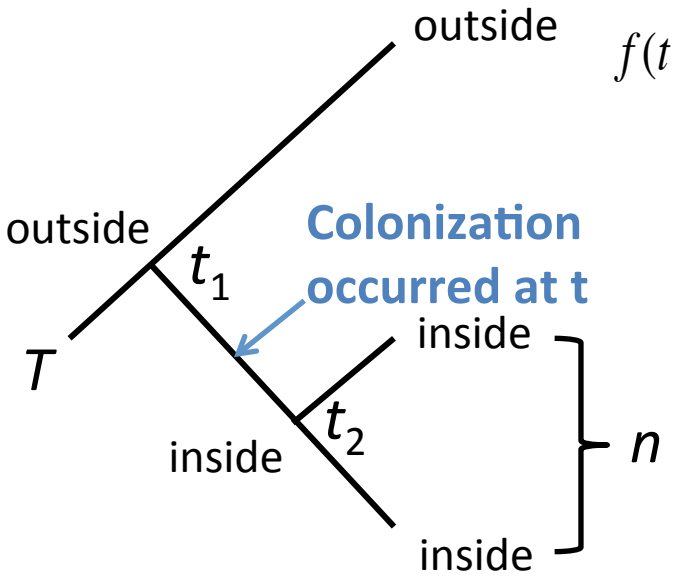

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$N_0(t)$ follows deterministic two state birth-death model in macroevolution study

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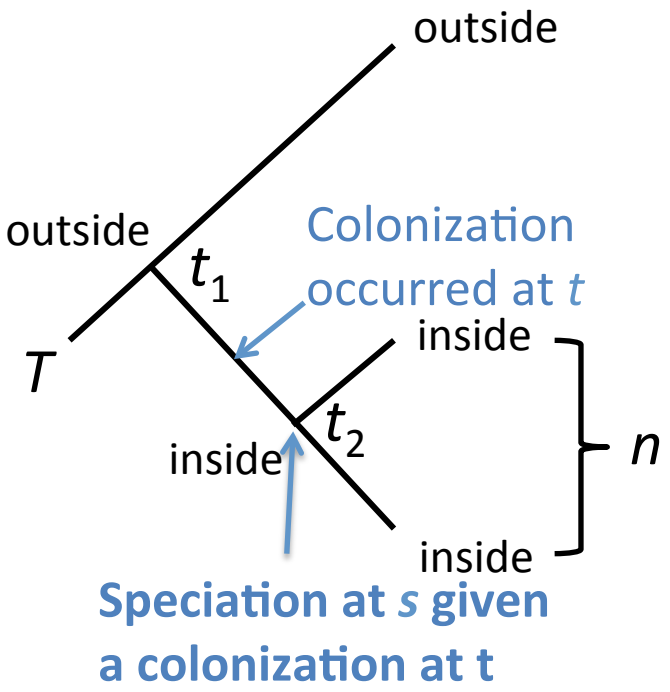

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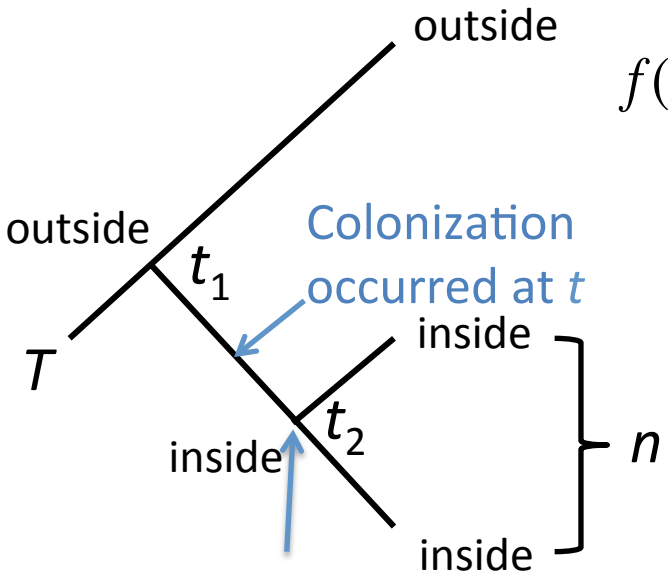

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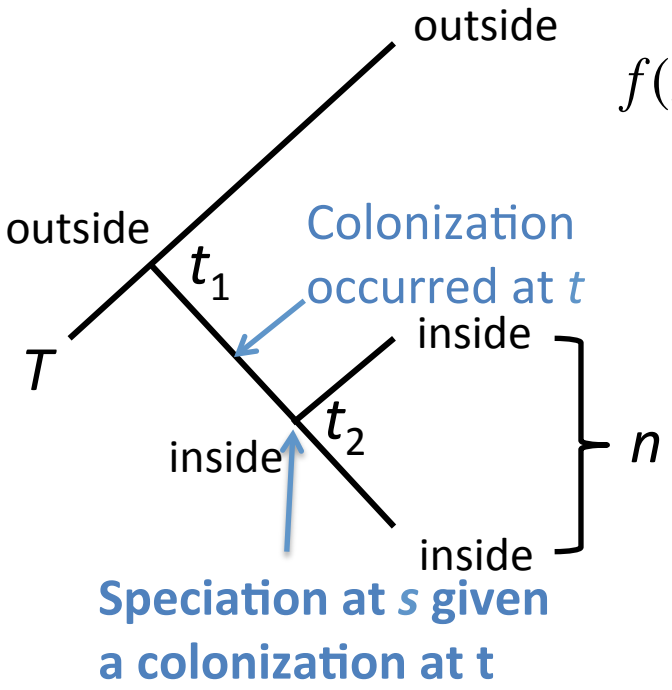

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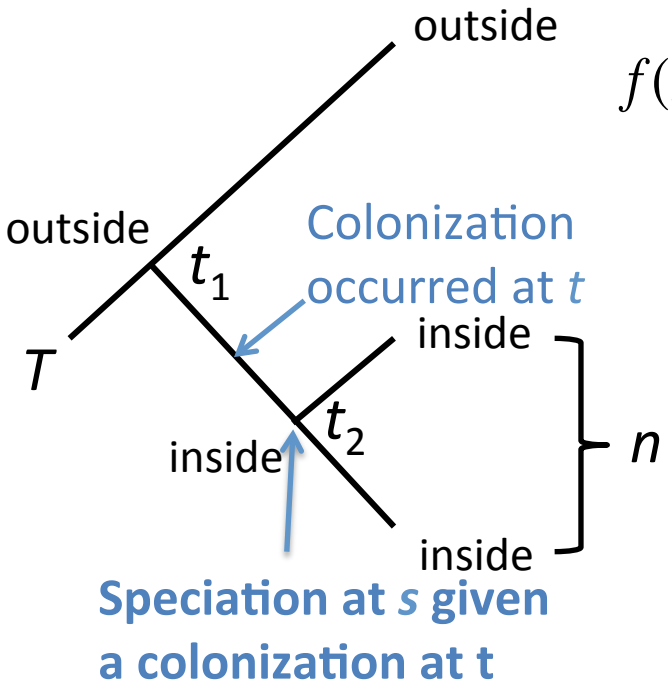

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Prior $f(s)$ follows coalescent theory if using species tree approach

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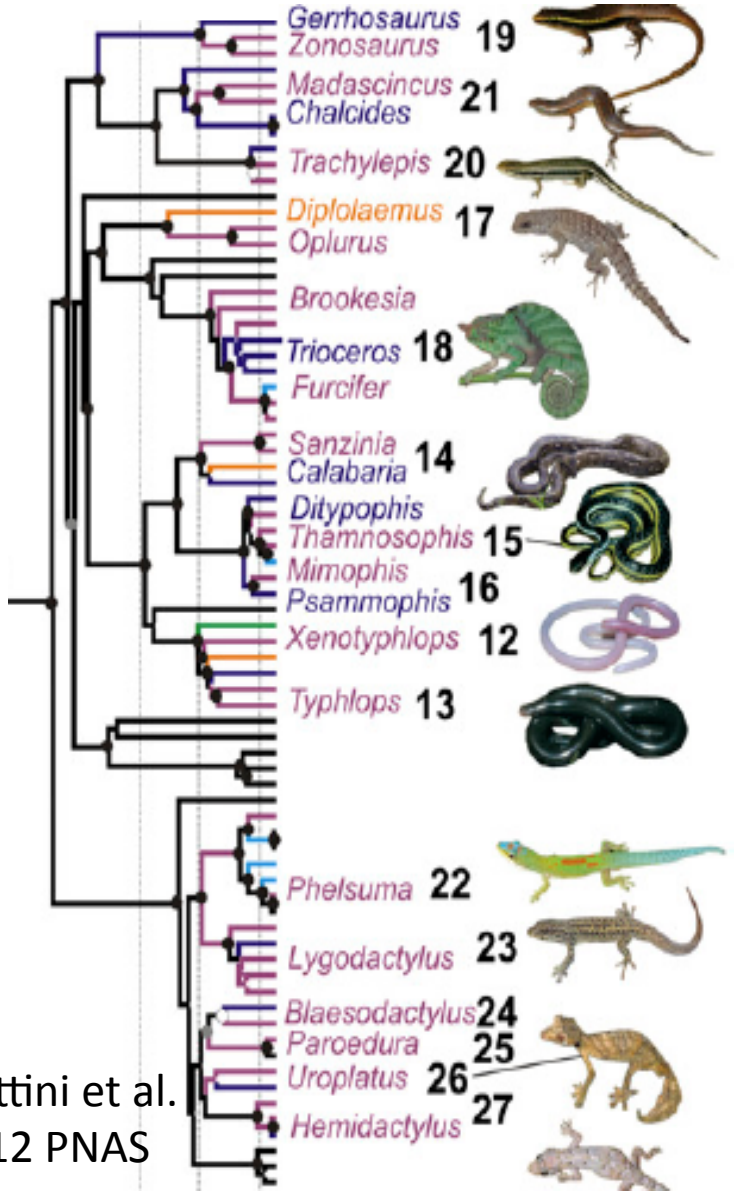
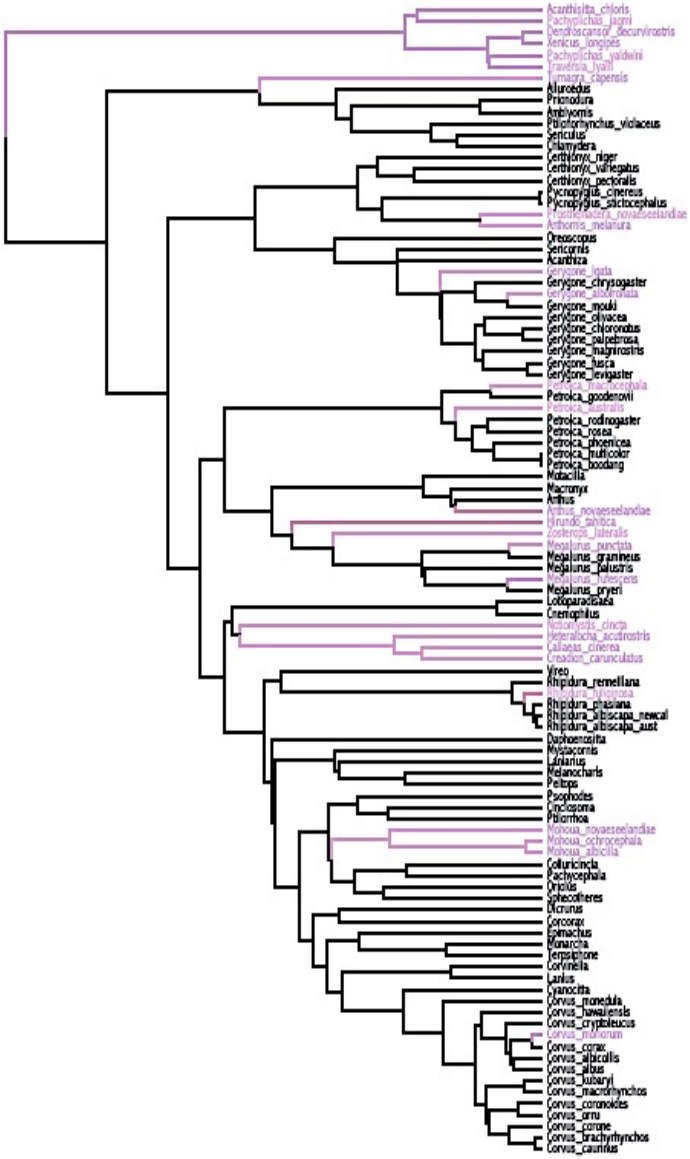
Step 4: Construct CI of simulated and observed histories:
Colonization frequency over time
Number of extant lineages per colonization

Madagascar squamates



Crottini et al.
2012 PNAS

New Zealand passerines



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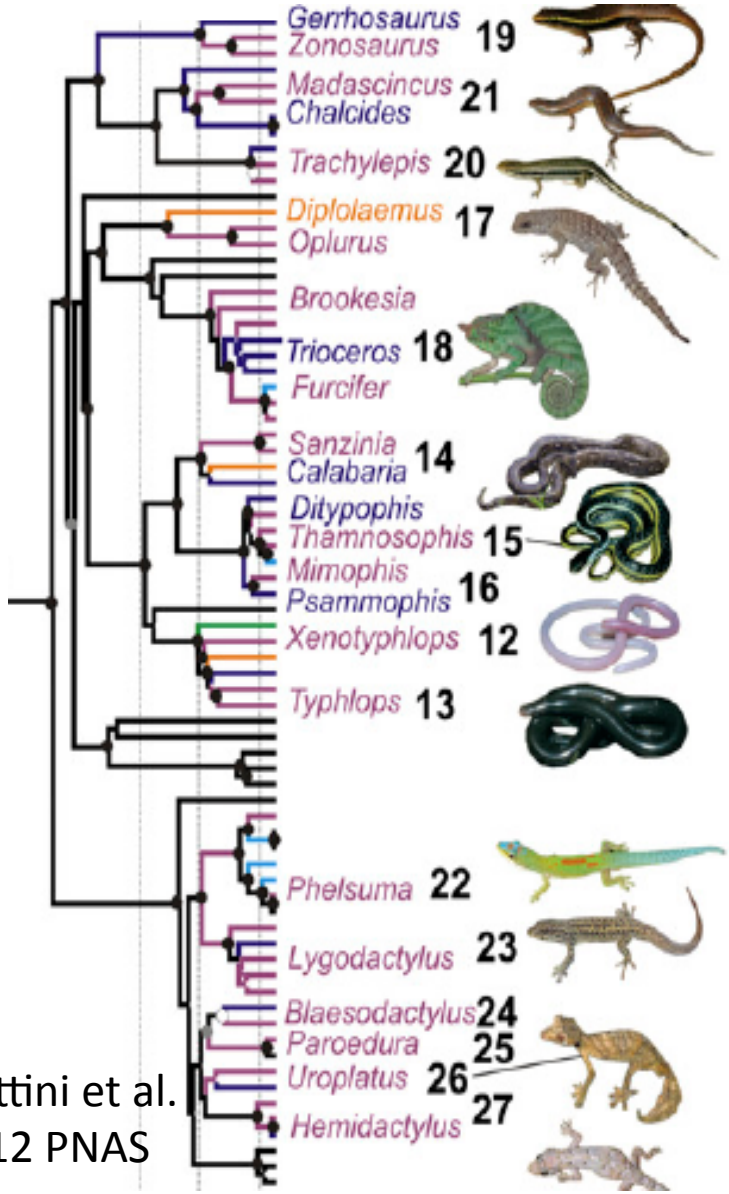

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Include all the taxa in the assemblage

← Genus-level

Species-level →

Include the closest relatives of each taxon outside the assemblage

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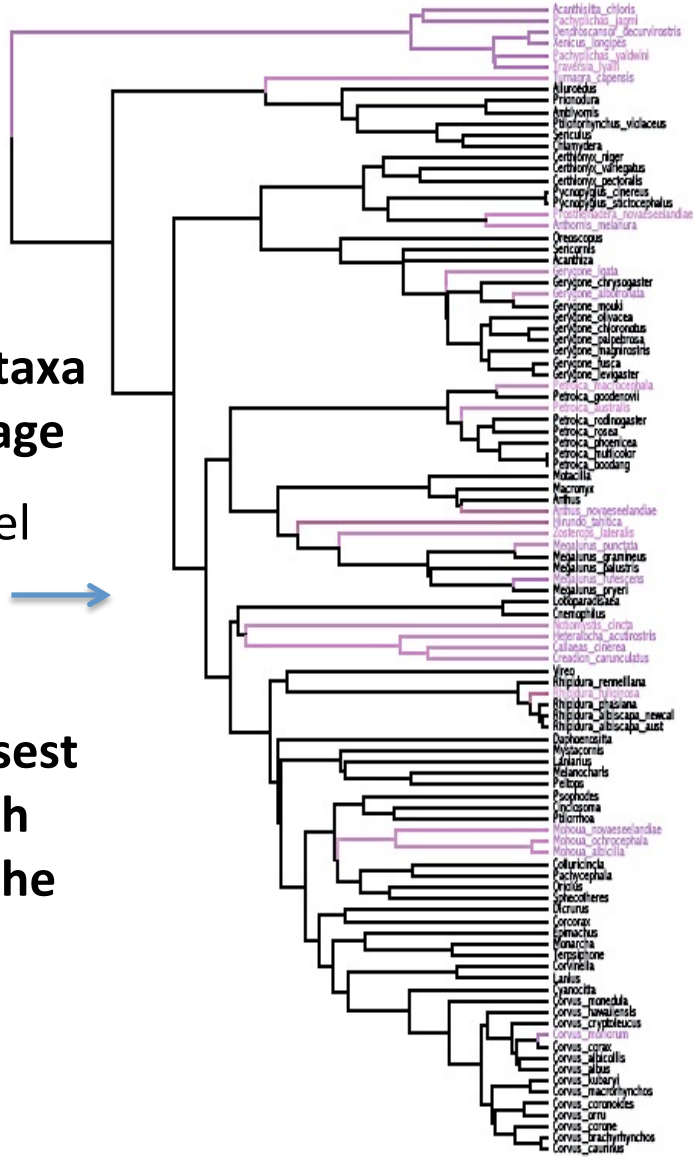
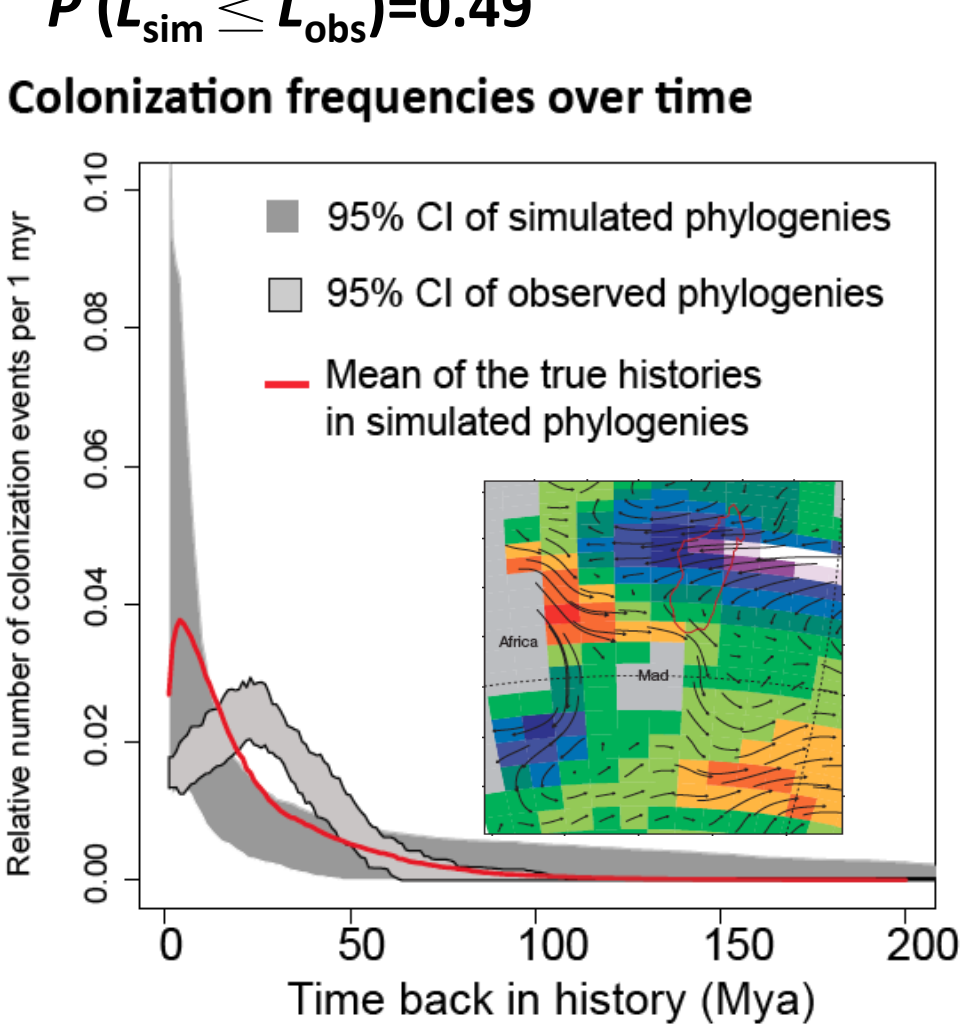
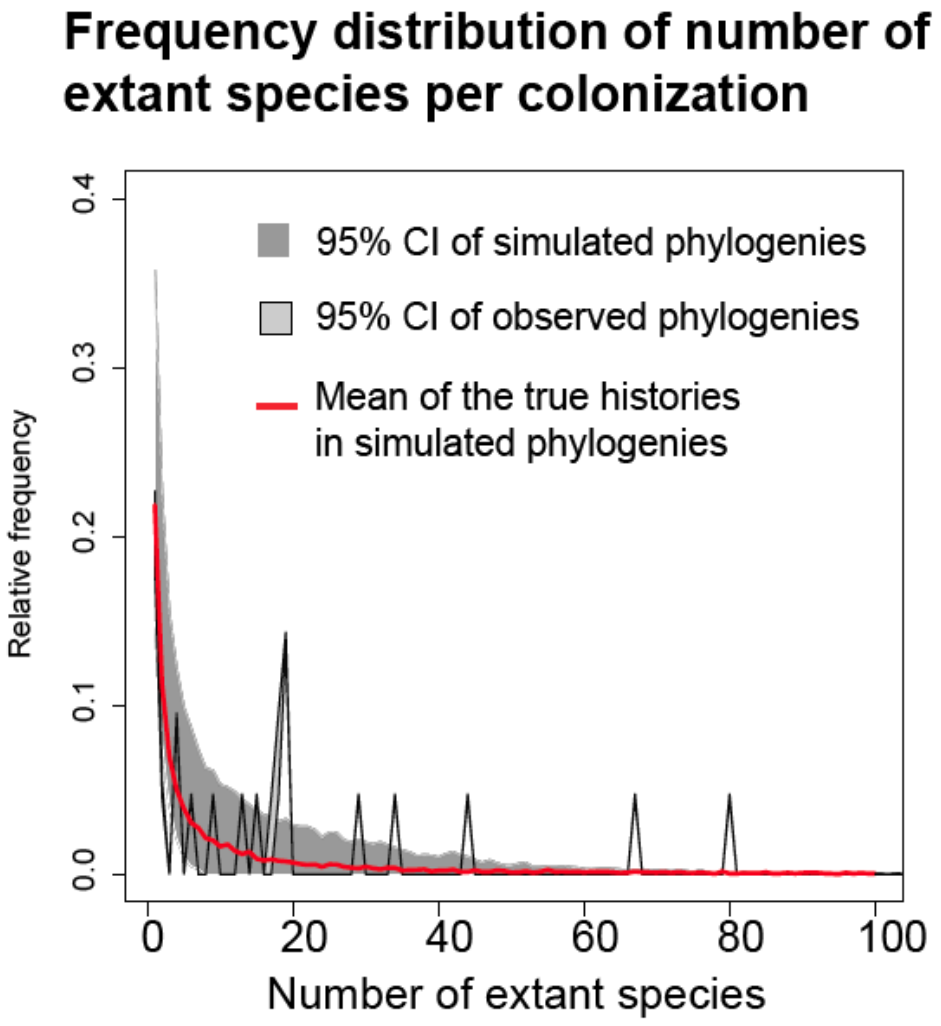


More colorizations during Cenozoic Era in Madagascar squamates

$P\ (L_{sim} \leq L_{obs})$=0.49

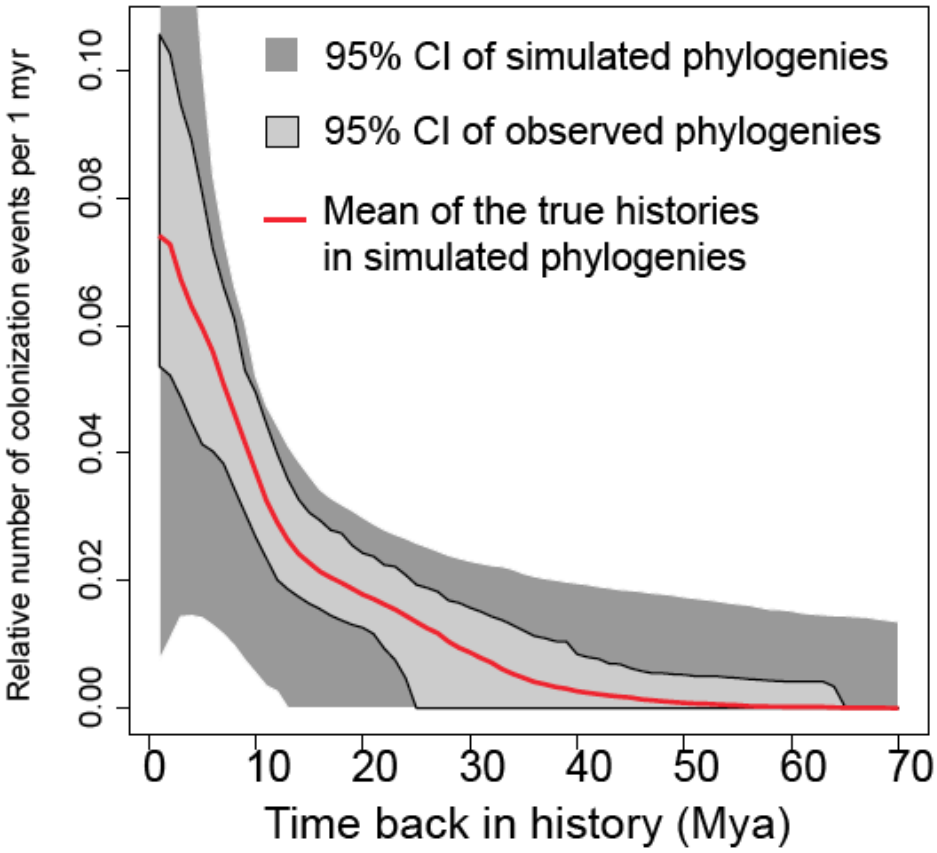




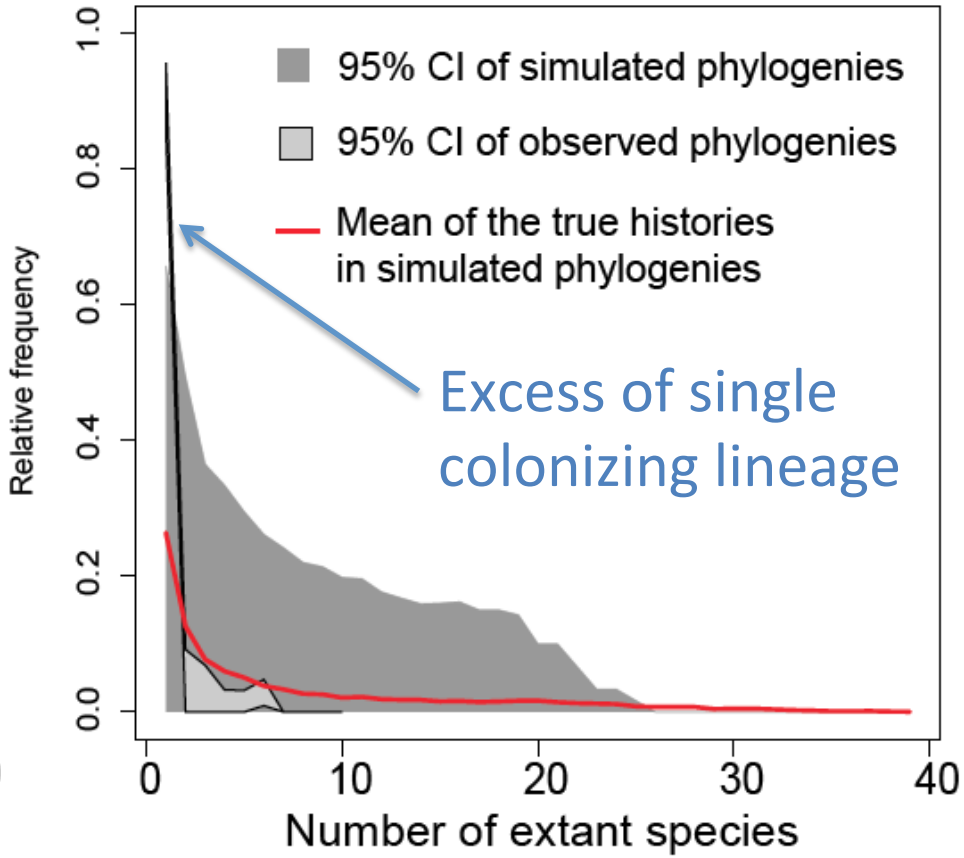
Constant colonization but inconstant speciation in New Zealand passerines

$P(L_{sim} \leq L_{obs})=0.04$

Colonization frequencies over time



Frequency distribution of number of extant species per colonization



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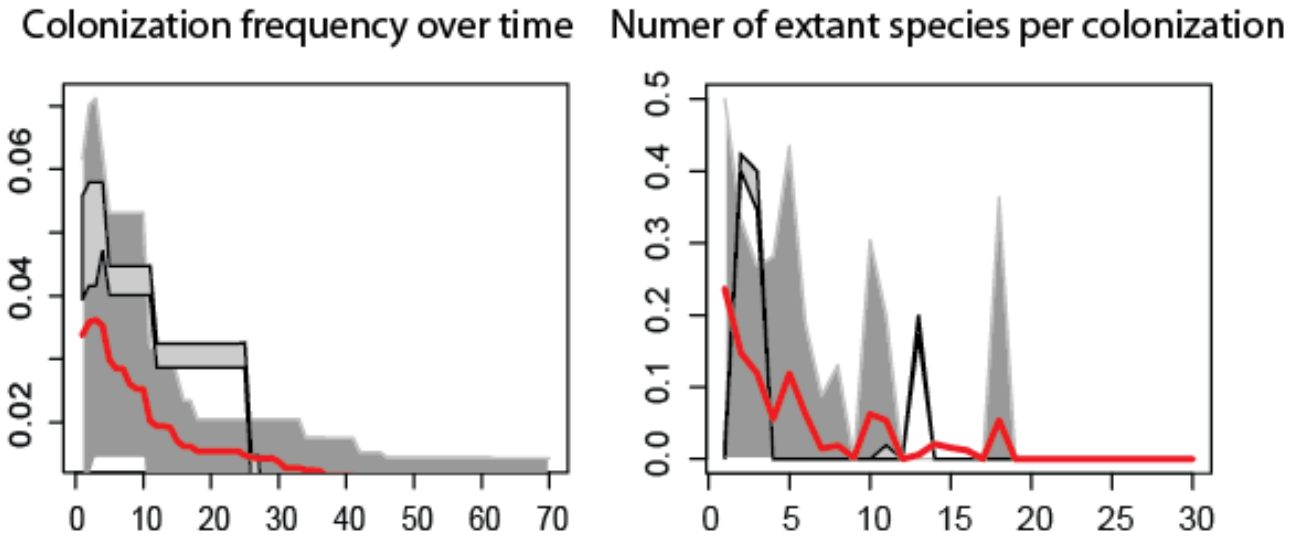

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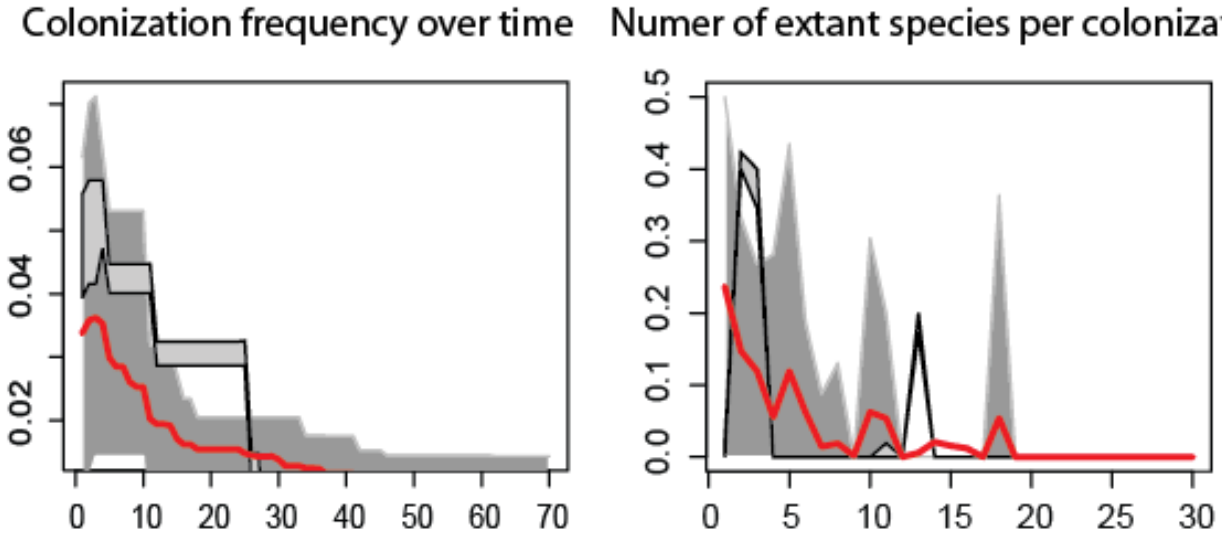

Sample size?

MCMC sampling ?

Type II error?

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Compare performance between hidden Markov methods and our analytical approach in reconstructing assemblage histories

Acknowledgements

To Celine Poux, Miguel Vences, and Ted Townsend for providing their data and analysis files

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Thanks!