Diversification in Space and Time:
Using phylogenies to understand the formation of species assemblages

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Why Care?

1. How do species assemblages form?
2. What are the properties of colonising lineages?
3. Do colonisation rates decline over time?
4. Are colonisation and speciation rates independent?
Species Assemblages

‘species assemblage’ is a neutral term for the species found in a defined location

Species are added by:
1. colonization
2. speciation

Species are subtracted by:
3. extinction
Species Assemblages

What can phylogenies do for us?
Species Assemblages

What can phylogenies do for us?

1. Tell us when in-situ diversification events and colonisation events happened

✓

2. Allow us to compare different models of colonisation and diversification

Work in progress*
Null Models

Expected arrival rate of extant species, with diversification, but no colonisation or extinction

(count)

(mid)

0.004

0.003

0.002

0.001
Null Models

Expected arrival rate of extant species, with constant diversification rate, variable extinction rates, and no colonisation

diversification = 0.004
Species Assemblages

What can phylogenies tell us about these processes?
Species Arrival

What can molecular phylogenies tell us about these processes?

Colonisation
Diversification
Sources of Uncertainty

1. Topology

- Colonisation
- Diversification
Sources of Uncertainty

2. Colonisation times

- Colonisation
- Diversification
Sources of Uncertainty

3. Node heights

- Colonisation
- Diversification
Sources of Uncertainty

4. Ancestral states

- Colonisation
- Diversification
Sources of Uncertainty

1. Topology ✔
2. Node Heights ✔
3. Ancestral States
4. Colonisation Times
Sources of Uncertainty

1. Topology ✔
2. Node Heights ✔
3. Ancestral States ✔
4. Colonisation Times
Sources of Uncertainty

1. Topology ✓
2. Node Heights ✓
3. Ancestral States ✓
4. Colonisation Times ✓
The Method

1. Collect dataset of all members of an assemblage
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2. Add in phylogenetic nearest neighbours
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1. Collect dataset of all members of an assemblage
2. Add in phylogenetic nearest neighbours
3. Estimate the posterior distribution of the dated phylogeny
4. For each tree, probabilistically reconstruct ancestral states
5. Reconstruct colonisation and diversification events
Arrival Rate

NZ passerine
Colonisation
Diversification
A single estimate of in-situ diversification rate
401 estimates of in-situ diversification rate
401 estimates of
in-situ diversification rate
Colonisation and diversification
In all nine models, the speciation rate is assumed greater than or equal to the extinction rate at all times. To our knowledge, all models in the cladogenesis literature for which likelihood expressions are available also make this assumption. In nature, however, there is evidence that some clades have lost diversity towards the present, suggesting that extinction events are sometimes more frequent than speciation events [32]. Our coalescent likelihood expression can be used to investigate a scenario with decreasing diversity by assuming an instantaneous mass extinction event in the history of a clade. However, further work remains before the coalescent approach can accommodate general patterns of decreasing diversity (see Materials and Methods).

**Results**

**Likelihood of Internode Distances**

Consider a clade with $N_0$ species at the present time, which has evolved according to one of the nine diversification scenarios illustrated in Figure 1. We denote by $N(t)$ the expected number of species at time $t$ in the past, given the model of diversification and its corresponding parameters (e.g., $N(t)$: $N_0$ under Models 1 and 2, and $N(t)$ ~ $N_0 e^{l(t)}$ under Model 5). We denote by $l(t)$ the speciation rate at time $t$ in the past (under Model 1 and 2, $l(t)$ ~ $t(t)$, where $t(t)$ is the turnover rate at time $t$ in the past). We consider a phylogeny of $k$ species randomly sampled in the clade at the present time. This phylogeny has $k$ internal nodes, and...
When they vary, rates either decay or grow exponentially. The parameters of each model are shown in Table 1.
Comparing models of assemblage formation