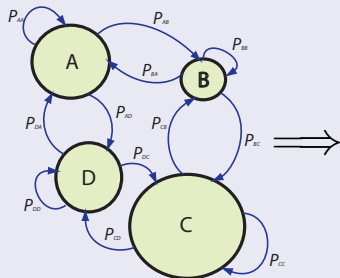


The Simulation Model

The Birth-Death Process

- Probability of speciation, birth rate = λ
- Probability of extinction, death rate = μ

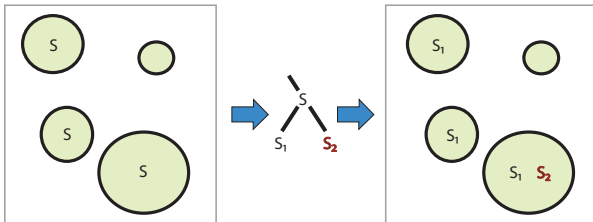
The Geographical Template



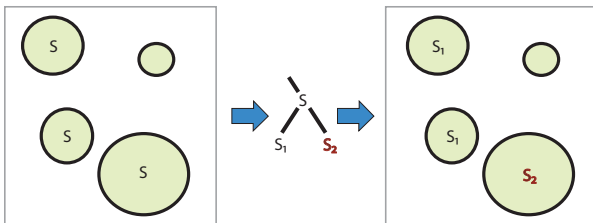
	A	B	C	D
A	P_{AA}	P_{AB}	P_{AC}	P_{AD}
B	P_{BA}	P_{BB}	P_{BC}	P_{BD}
C	P_{CA}	P_{CB}	P_{CC}	P_{CD}
D	P_{DA}	P_{DB}	P_{DC}	P_{DD}

Speciation Modes

- Sympatric



- Allopatric



Simulation Set Up

- Set model parameters:
 - Birth (speciation) rate, λ .
 - Death (extinction) rate, μ .
 - Geographic template.
 - Speciation mode.
- Set termination condition:
 - Target diversity: run until total number of species = T .
 - Number of generations: run until number of generations = G .
- Specify random number seed.

Simulation Procedure

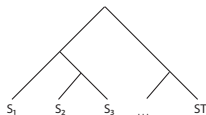
- ① Initialize: introduce single lineage into a region.
- ② Repeat until T species or G generations, or all species extinct:
 - Migration:
 - For each species in each region, select a destination region for dispersal (including current region, i.e., no dispersal) according to dispersal probability.
 - Add species to destination region if not already present.
 - Diversification:
 - For each species in the system, draw a uniform random number, $u \sim U(0, 1)$.
 - If $u < \lambda$: split lineage.
 - If $u > \lambda$ and $u < (\lambda + \mu)$: remove lineage.
- ③ Report results.

Simulation Output

- Incidence (presence/absence) matrix:

	A	B	C	D
S_1	0	0	1	1
S_2	1	0	0	1
S_3	0	1	1	0
\vdots	\vdots	\vdots	\vdots	\vdots
\vdots	\vdots	\vdots	\vdots	\vdots
\vdots	\vdots	\vdots	\vdots	\vdots
S_T	1	0	1	1

- Phylogeny:



- Summary of total number of lineages and total number of endemic lineages in each region.
- Classification tree of areas based on shared species.

Is This Model Biologically Realistic?

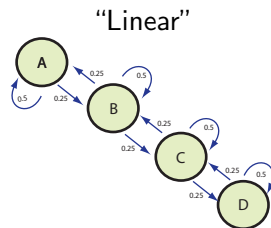
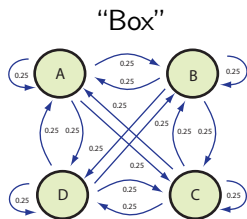
NO!

YES!

- As a null model, to assess various beta diversity and community diversity studies and statistics that do **not** take into account evolutionary history.
- As a null model, to assess various macro-evolutionary diversification studies and statistics that do **not** take into account spatial relationships.
- To determine whether observed patterns of distributions of island diversity are random with respect to ecological relationships, competition, etc.: if the observed patterns can be replicated under this model, which does not take into account these factors, then we can conclude that simple (random) speciation and (random) dispersal are sufficient explanations for the generation of the observed biotic patterns.

Application: Geography and the Mid-Domain Effect

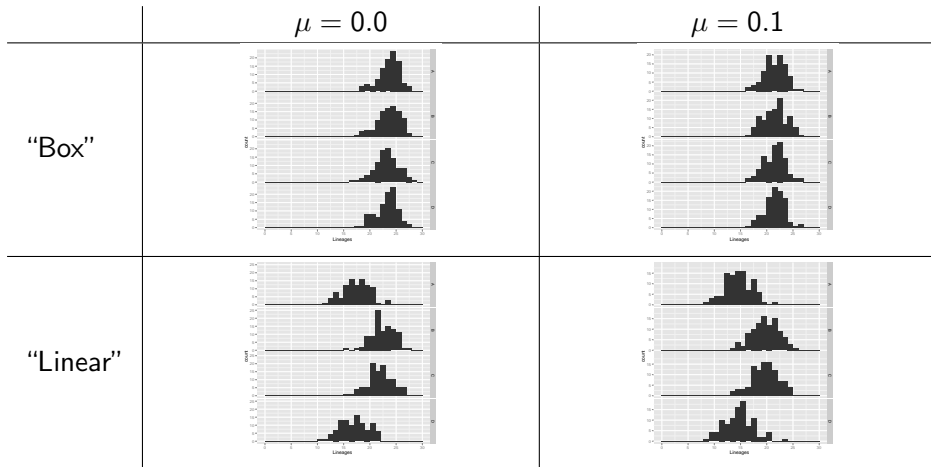
- The Mid-Domain Effect as an explanation for the latitudinal gradient in species diversity has been analyzed in terms of "packing" overlapping species ranges into a finite bounded space.
- Here, I analyze it as a random effect of cycles of dispersal and diversification under different geographical configurations:



- Each geographical configuration was run under two birth-death processes: (a) $\lambda = 0.1$, $\mu = 0.0$ and (b) $\lambda = \mu = 0.1$.

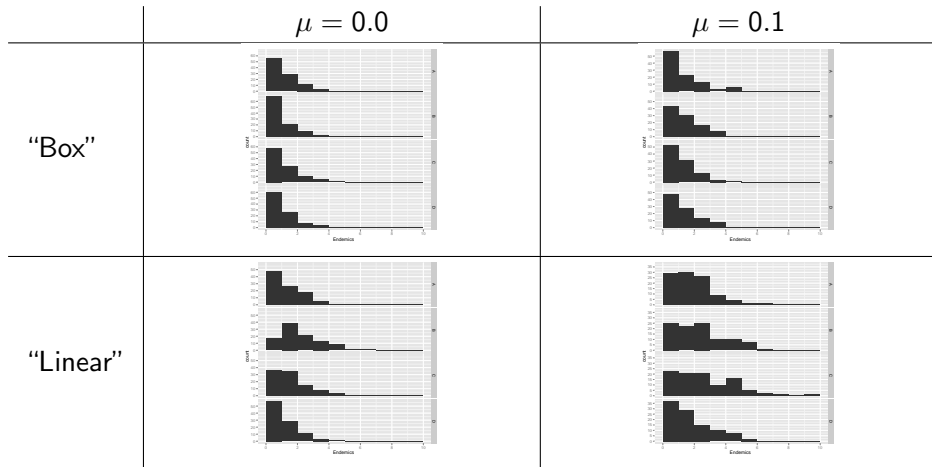
Geography and the Mid-Domain Effect: Results

Number of Lineages by Region



Geography and the Mid-Domain Effect: Results

Number of Endemic Lineages by Region



Future Applications

- Comparative Island Biogeographical Analysis of Diversity
 - The distribution of diversity in the Philippine Islands is uneven: different islands have different numbers of species.
 - Not related to island size: islands of similar sizes have different diversity.
 - Different groups have different distributions of diversity.
 - No satisfactory explanation for the differences within groups, though many suggestions: ecology, history, random, etc.
 - No comparison of difference between groups.
- Assessment of Beta and Community Diversity Statistics and Studies in a Phylogenetic Context
 - Most studies, and statistics underlying those studies, of beta and community diversity ignore analysis of evolutionary and phylogenetic history.
 - And yet:
 - Evolutionary history plays a role in the generation of **beta** diversity.
 - These same studies usually invoke evolutionary history as the ultimate explanation (e.g. competitive exclusion in evolutionary time).
 - Classic debates, e.g. the “checkerboard score” and species distribution, need to be re-assessed in a phylogenetic context.