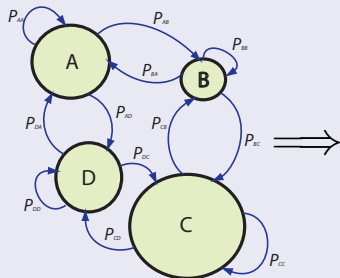


The Simulation Model

The Birth-Death Process

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

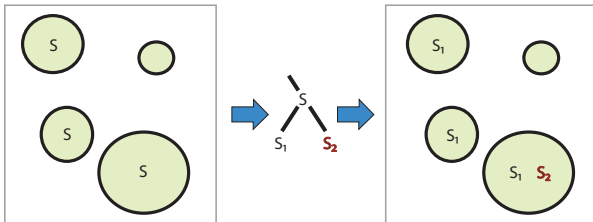
The Geographical Template



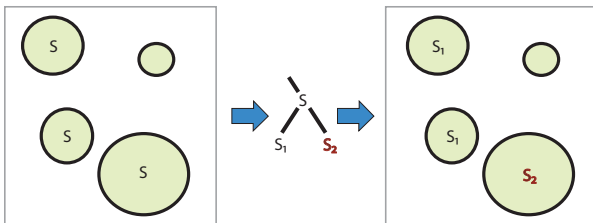
	A	B	C	D
A	P_{AA}	P_{AB}	P_{AC}	P_{AD}
B	P_{BA}	P_{BB}	P_{BC}	P_{BD}
C	P_{CA}	P_{CB}	P_{CC}	P_{CD}
D	P_{DA}	P_{DB}	P_{DC}	P_{DD}

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
\cdot	\cdot	\cdot	\cdot	\cdot
\cdot	\cdot	\cdot	\cdot	\cdot
\cdot	\cdot	\cdot	\cdot	\cdot
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.