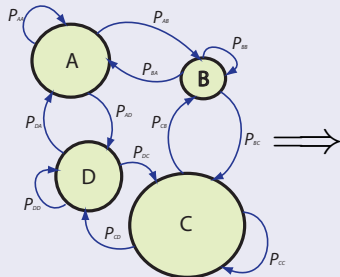


# The Simulation Model

## The Birth-Death Process

- Probability of speciation, birth rate =  $\lambda$
- Probability of extinction, death rate =  $\mu$

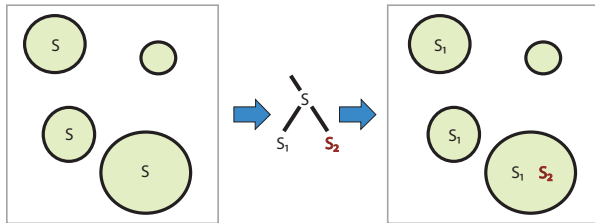
## The Geographical Template



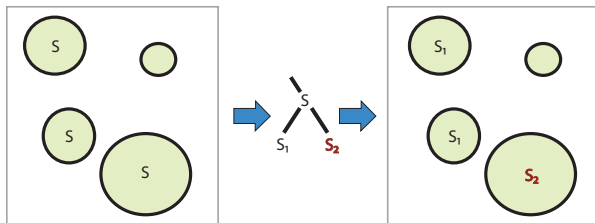
	A	B	C	D
A	$P_{AA}$	$P_{AB}$	$P_{AC}$	$P_{AD}$
B	$P_{BA}$	$P_{BB}$	$P_{BC}$	$P_{BD}$
C	$P_{CA}$	$P_{CB}$	$P_{CC}$	$P_{CD}$
D	$P_{DA}$	$P_{DB}$	$P_{DC}$	$P_{DD}$

# Speciation Modes

- Sympatric



- Allopatric



# Simulation Set Up

- Set model parameters:
  - Birth (speciation) rate,  $\lambda$ .
  - Death (extinction) rate,  $\mu$ .
  - 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

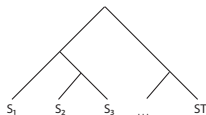
- ① Initialize: introduce single lineage into a region.
- ② Repeat until  $T$  species or  $G$  generations, or all species extinct:
  - Migration:
    - For each species in each region, select a destination region for dispersal (including current region, i.e., no dispersal) according to dispersal probability.
    - 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:

