

Biogeography

April 20, 2009

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- Goals of biogeographic studies
- Classic approaches
- Newer model-fitting methods for biogeography

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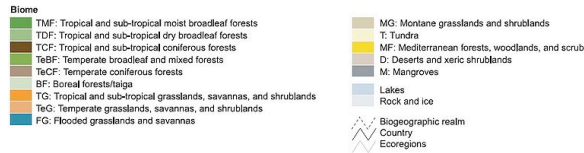
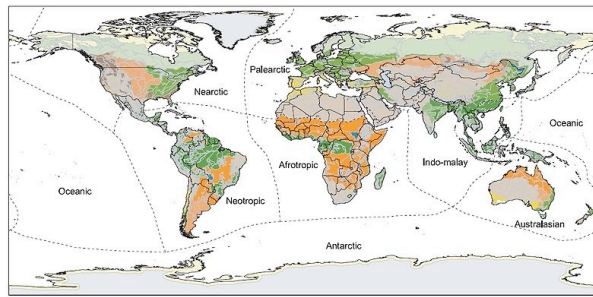
Goals of Biogeographic Studies

- The study of the distribution of biodiversity over space and time
- Use historical factors to explain species distributions
- Speciation, extinction, vicariance, dispersal, etc.

Father of Biogeography

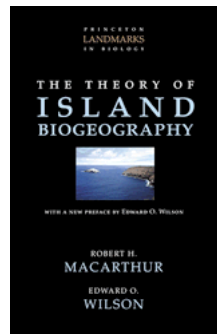
- Alfred Russel Wallace
- Extensive field work in the Malay Archipelago
- Identified Wallace's line, a major biogeographic break between Asiatic and Australian species





Radical Biogeography

- Theory explaining the distribution of species on islands
- Used immigration and extinction to explain species counts on isolated islands



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Classic Approaches

- Area cladograms
- Event-based parsimony
- Topological tests of trees

Area Cladograms

- Assume speciation events are caused by vicariance (separation by a geographic barrier)
- Use phylogeny of species to infer the history of areas
- Goal: reconstruct an area cladogram

Constructing Area Cladograms

- Use areas as taxonomic units, construct a set of “characters” representing clades
- Convert each tree into a set of 0-1 characters
- Reconstruct the area cladogram using parsimony

Event-based parsimony

- Model the events needed to make a particular tree match the known history of an area
- Possible events: vicariance, extinction, speciation within area, dispersal
- Find the area cladogram that minimizes the total number of events across a set of trees

DIVA (Ronquist)

- Dispersal-Vicariance Analysis
- method in which ancestral distributions are inferred based on a three-dimensional cost matrix derived from a simple biogeographic model
- Allows different events, weighted with cost matrix, to model geographic ranges in a phylogenetic context

DIVA (Ronquist)

1. Speciation is assumed to be by vicariance separating a wide distribution into two mutually exclusive sets of areas. This event costs nothing.
2. A species occurring in a single area may speciate within the area by allopatric (or possibly sympatric) speciation giving rise to two descendants occurring in the same area. The cost is zero.
3. Dispersal costs one per unit area added to a distribution.
4. Extinction costs one per unit area deleted from a distribution.

Topology-based tests

- Are all of the lineages within a region monophyletic?
- Can I statistically reject trees that are not compatible with a particular biogeographic story?
- KH test, SH test, etc.

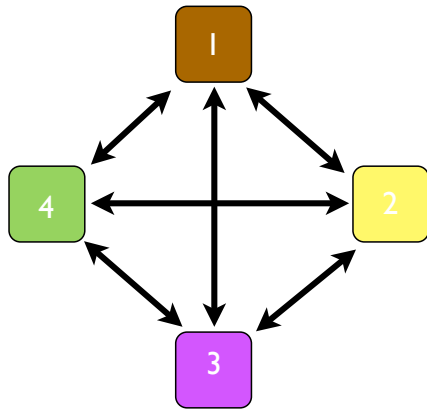
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Models and Biogeography

- Exciting recent developments: application of models (and model selection) to biogeography
- DEC model (Ree et al. 2005; Ree and Smith 2008)

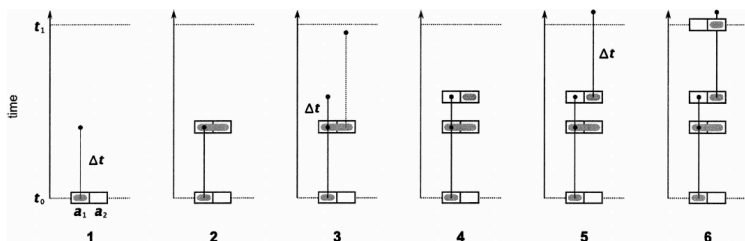
Why not just use standard character models?



Why not just use standard character models?

- Characters change along branches, not at speciation events
- Daughter species always inherit parental phenotype
- Species can only have one character state at a time

A Different Model



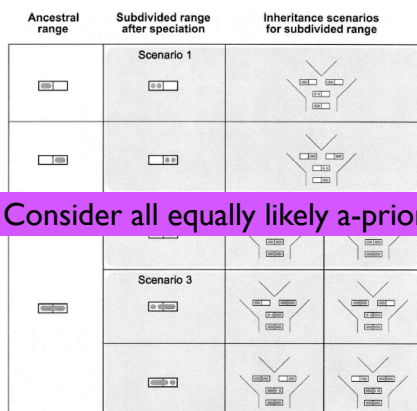
from Ree et al. 2005



Where could a species be?

0, 1, 2, 3, 12, 13, 23, 123

$$Q = \begin{bmatrix} & \emptyset & 1 & 2 & 3 & 12 & 13 & 23 & 123 \\ \emptyset & - & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & E_1 & - & 0 & 0 & D_{12} & D_{13} & 0 & 0 \\ 2 & E_2 & 0 & - & 0 & D_{21} & 0 & D_{23} & 0 \\ 3 & E_3 & 0 & 0 & - & 0 & D_{31} & D_{32} & 0 \\ 12 & 0 & E_2 & E_1 & 0 & - & 0 & 0 & D_{13} + D_{23} \\ 13 & 0 & E_3 & 0 & E_1 & 0 & - & 0 & D_{12} + D_{32} \\ 23 & 0 & 0 & E_3 & E_2 & 0 & 0 & - & D_{21} + D_{31} \\ 123 & 0 & 0 & 0 & 0 & E_3 & E_2 & E_1 & - \end{bmatrix}.$$



Consider all equally likely a-priori

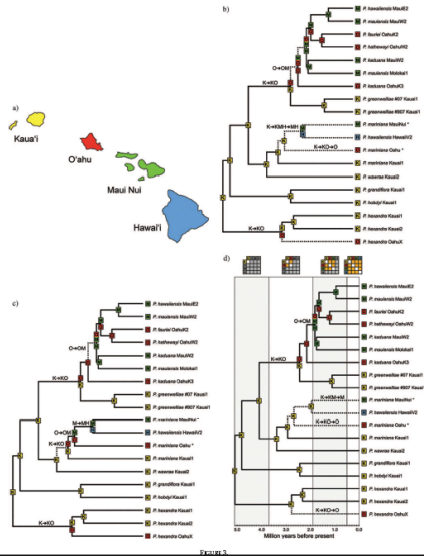
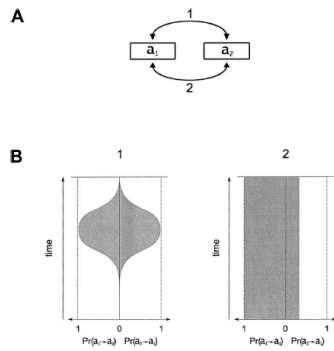
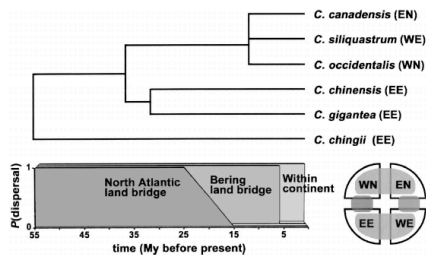


TABLE 1. Inferences about the ancestral area and range evolution parameters of Hawaiian *Pygostictus* under DEC models. The unconstrained model (M0) allows geographic ranges to include any combination of islands in the archipelago and permits direct dispersal between any pair of islands. M1 and M2 restrict ranges to include a maximum of two adjacent islands. M2 further limits dispersal to be eastward between adjacent islands. The stratified model permits dispersal to islands only after their time of geological origin, thus with a root age of 5.1 Ma, the only ancestral area possible is Kaua'i.

Model	Area	-ln(L)	Dispersal	Extinction
M0	Kaua'i	35.758	0.040	0.058
	O'ahu	40.700	0.041	0.024
	Maui Nui	44.378	0.054	0.076
	Hawai'i	45.323	0.058	0.085
M1	Kaua'i	34.636	0.093	0.017
	O'ahu	38.877	0.112	0.052
	Maui Nui	48.683	0.207	0.164
	Hawai'i	55.396	0.377	0.280
M2	Kaua'i	32.434	0.132	0.009
	O'ahu	106.018	0.174	0.103
	Maui Nui	107.701	0.216	0.101
	Hawai'i	118.930	0.173	0.066
Stratified	Kaua'i	40.777	0.075	0.082



DEC Model

- Promising, especially when areas can be broken into a few discrete units
- Parameter estimates can be pretty far off (see Ree and Smith 2008)

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