

Historical biogeography methods

1. Estimate a dated phylogeny
2. Put the geographic ranges at the tips
- 3. Assume some process(es)**
4. Conduct inference

Summary of previous lectures:

Different authorities have different assumptions about what processes matter!

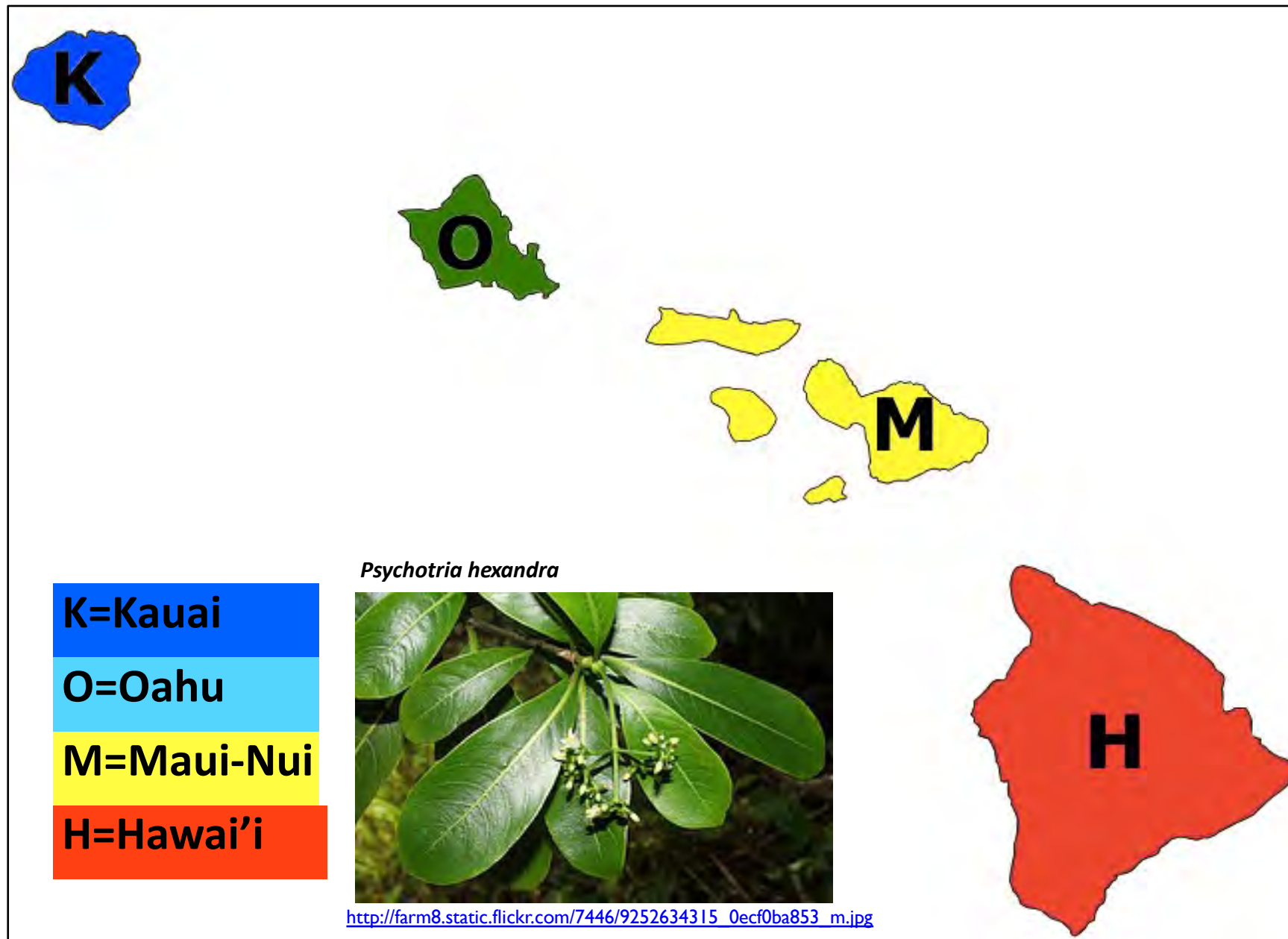
Your inferences will depend on your assumptions

Vicariance: deterministic vision where geology determines ranges

Dispersal: “unpredictable” “chance events”

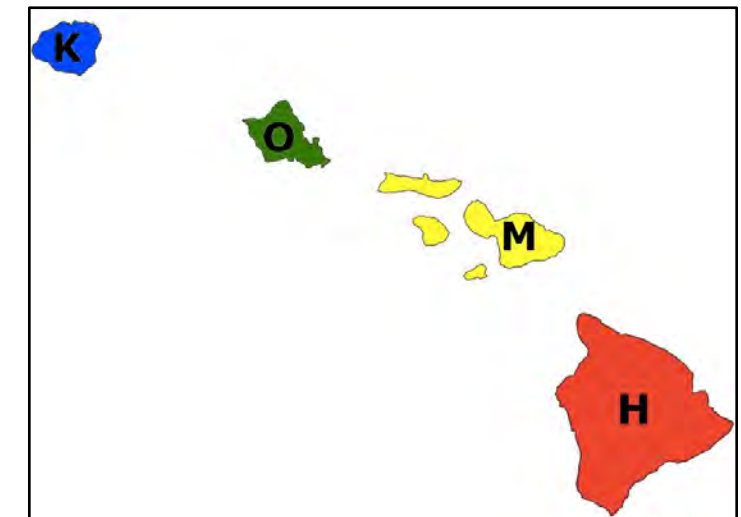
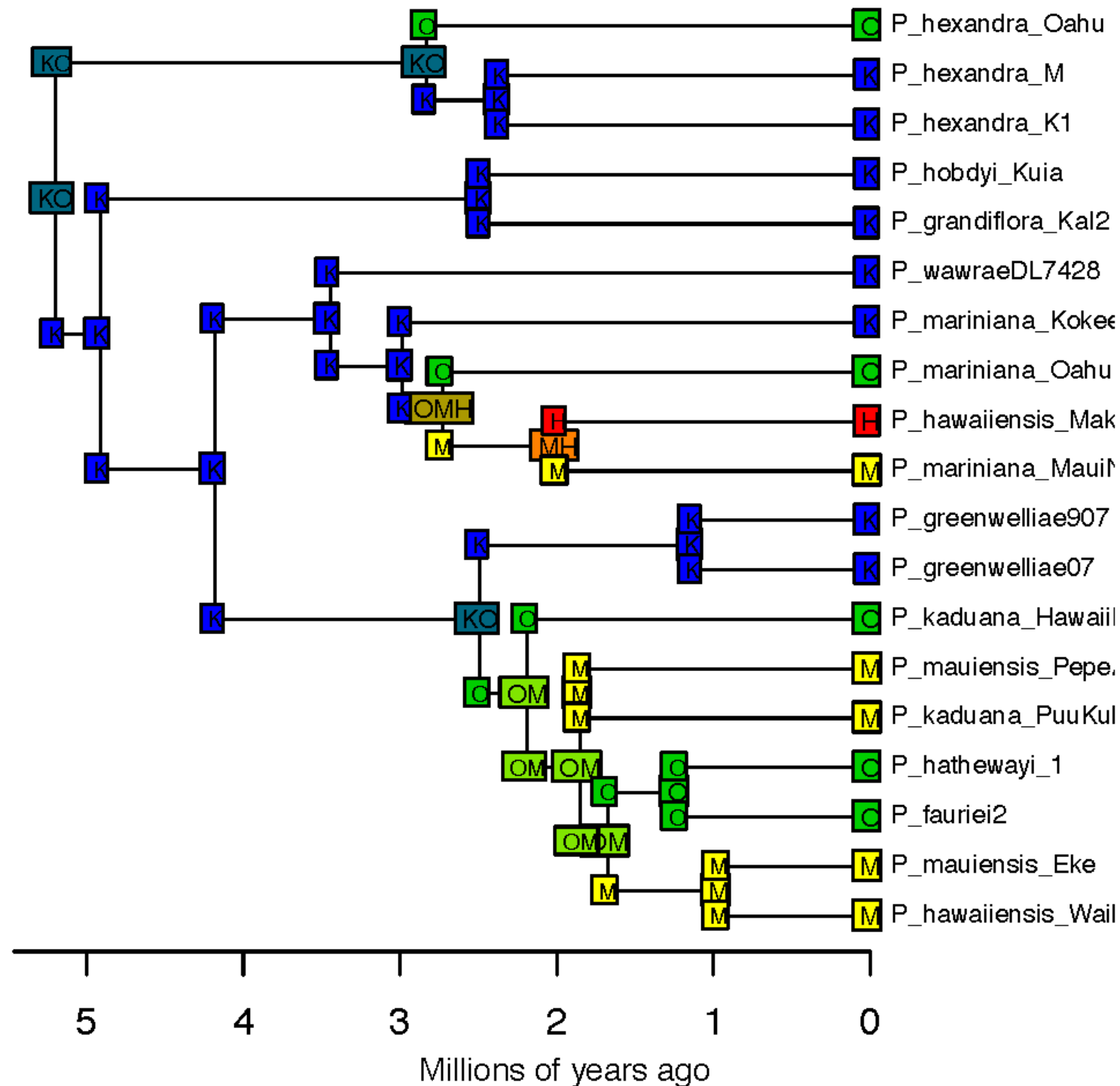
Me: “Unpredictable” doesn’t mean intractable – we can address using probabilistic models

Results of different biogeography models on same dataset:



Example of biogeographic history: *Psychotria*

Model: DEC



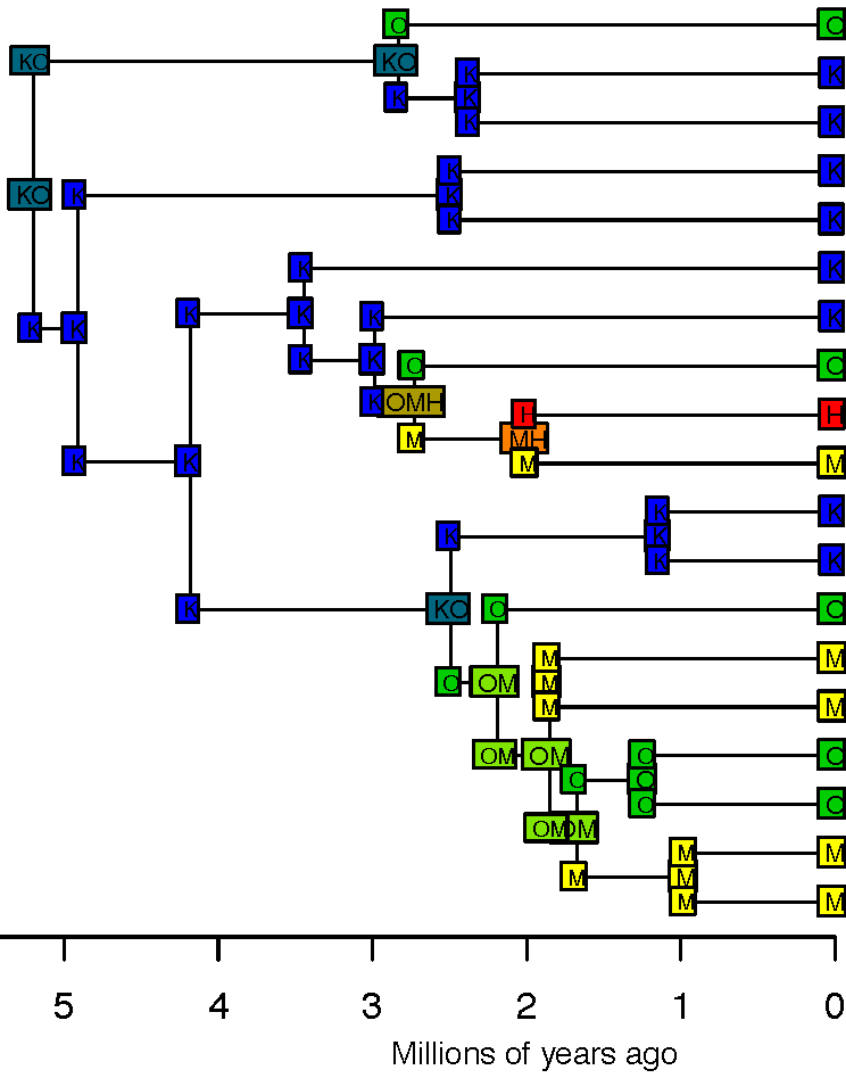
Psychotria hexandra



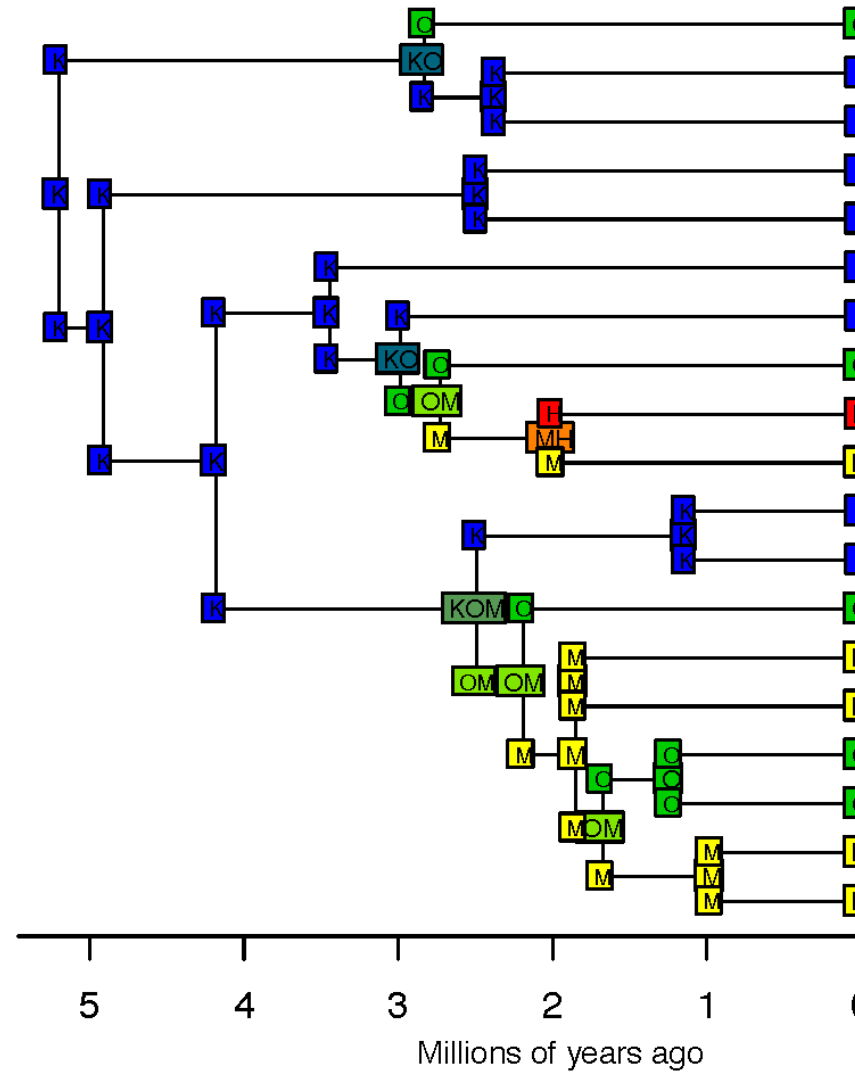
K=Kauai
O=Oahu
M=Maui-Nui
H=Hawai'i

Comparison: 3 models

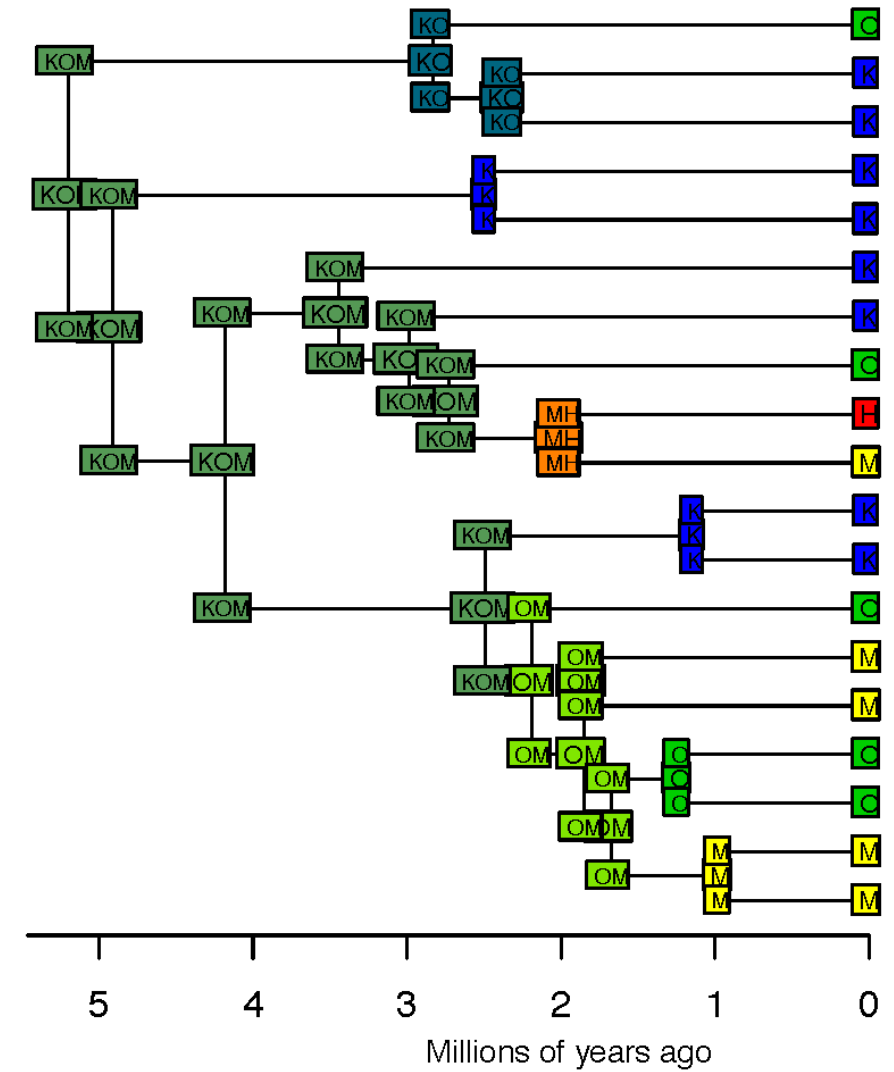
Model: DEC



Model: DIVA



Model: BayArea



K=Kauai
O=Oahu
M=Maui-Nui
H=Hawaii'i

Psychotria hexandra



http://farm8.static.flickr.com/7446/9252634315_0ecf0ba853_m.jpg

I think we should use statistical model choice in biogeography

Comparison of two models:

- 1. model without founder-event speciation**
- 2. model with founder-event speciation**

		Ranges		Character mapping	DIVA	DEC (LAGRANGE)	BayArea, BBM (RASP)
		Before	After				
Anagenetic	Dispersal				✓	✓	✓
	Extinction				✓	✓	✓
	Range-switching			✓			
Cladogenetic	Sympatry (narrow)			✓	✓	✓	✓
	Sympatry (widespread)						✓
	Sympatry (subset)					✓	
	Vicariance (narrow)				✓	✓	
	Vicariance (widespread)				✓		
	Founder						

Which model should we use?

What about founder-event speciation?

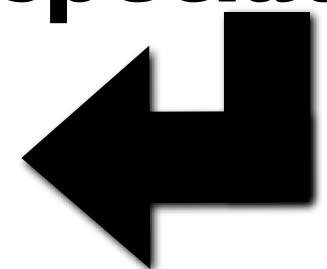
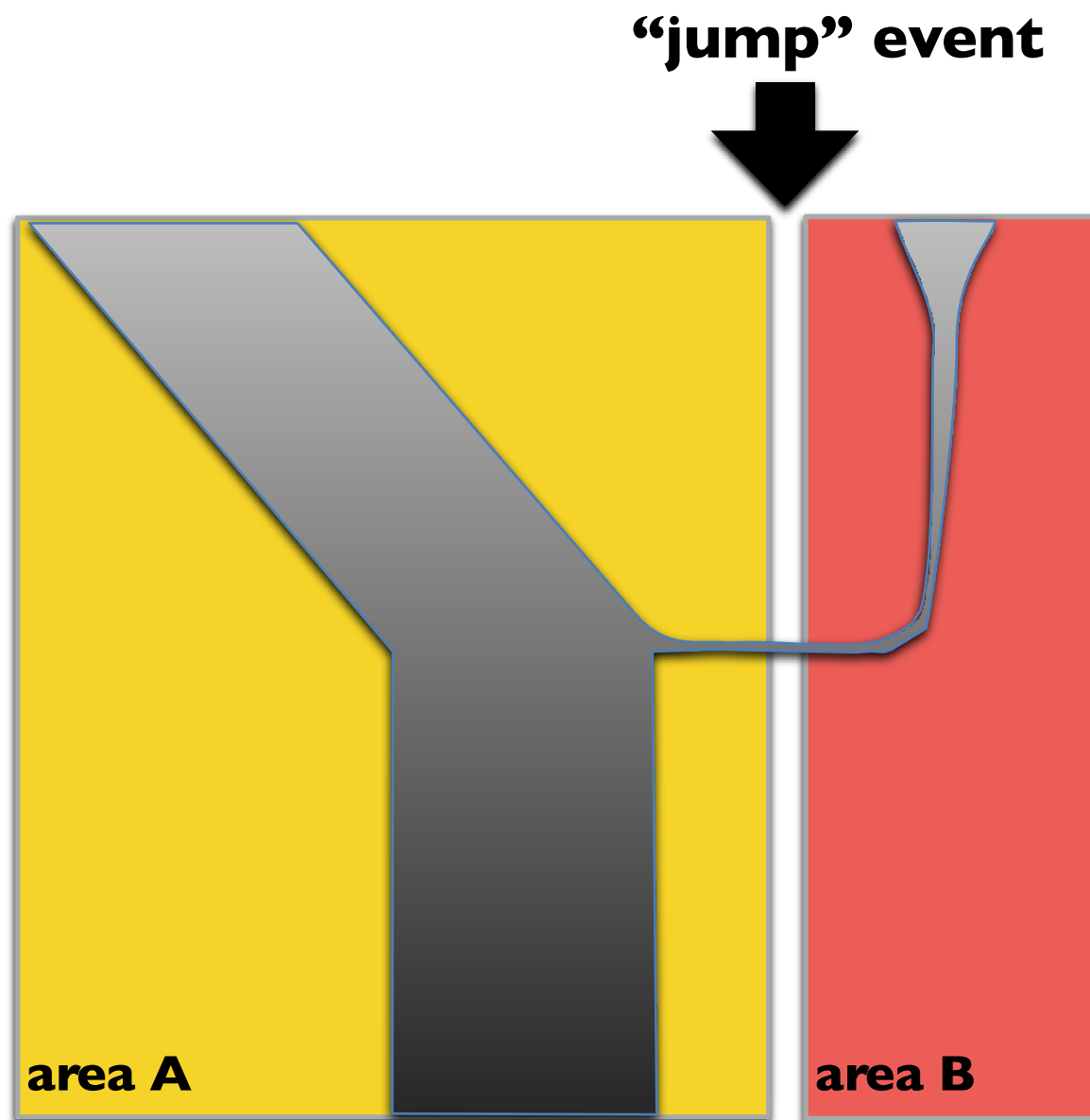


Figure 1, Matzke 2013, *Frontiers of Biogeography*

Founder-event speciation



- In founder-event speciation, a rare dispersal event “instantaneously” establishes a geographically isolated new lineage with one or a few individuals
- Widely discussed in population genetics, speciation literature, island biogeography
- However, ignored in traditional historical biogeography computer models

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