Organism traits must be important in historical biogeography. In particular, rates of dispersal (both range-expansion dispersal, and jump dispersal leading to founder-event speciation) must depend to some degree on traits such as flight and its loss, and seed dispersal mechanisms and the dispersal abilities of animals that transport seeds. However, to date no probabilistic historical biogeographical models have been available that allow geographic range and traits to co-evolve on the phylogeny, with traits influencing dispersal ability. In purely continuous-time Markov models, adding a trait is just a matter of doubling the size of the rate matrix; however, biogeographical models also include a much more complex discrete-time model describing how geographic range can change during cladogenesis. Traits might also influence this process.

I present an addition to the R package BioGeoBEARS that enables an evolving discrete trait to influence dispersal ability for both anagenetic and cladogenetic range change. This model can be freely combined with models adding jump dispersal (e.g., DEC+), distance as a predictor of dispersal (vs models, with dispersal rate multiplied by distance*s), and other variants. I test the model against simulations and datasets where large evolutionary changes in dispersal ability are highly likely (e.g., Pacific rails, which have repeatedly lost flight).

### Study system: “typical” rails of the Pacific

![Image of Rails](https://en.wikipedia.org/wiki/Snoring_rail)

**G. pacifica**, from Tahiti, “known only from a painting made by Georg Forster on James Cook’s second voyage.”

### Data from: Kirchman (2012)

Collaborators: Jeremy J. Kirchman, Curator of Birds, New York State Museum

### Results: Ancestral geography

![Ancestral Area Estimation](https://en.wikipedia.org/wiki/Snoring_rail)

- Ancestral area estimate: Philipines & nearby (the 2-area species are actually more widespread)
- Founder-events colonizing remote islands are new areas are associated with rapid (evolutionary) loss of flight

### Conclusions

Linked trait-dispersal model allows statistical inferences not possible with either individually. Although this case is “obvious,” in many datasets, the influence of traits on dispersal may be unknown.

- Flightlessness is more frequent at the tips, so models that allow reversal are favored. Regardless, the trait inference is improved (not perfect, see root).
- Inferred m2 is difficult, but tixing to 0 is feasible and nearly as good (~1 Lnl.).
- Founder-event speciation is a key process, as is founder-flight loss.
- The base model matters a lot. This must be part of the model choice!
- These models ignore lineage extinction, but CluSSE models feasible.
- Models with more areas will be slower, but BioGeoBEARS is parallelized.

Check out BioGeoBEARS, updated code at [PhyloWiki](http://phylo.wikidot.com), references & more info: Use QR code or go to: http://phylo.wikidot.com/nicholas-j-matzke