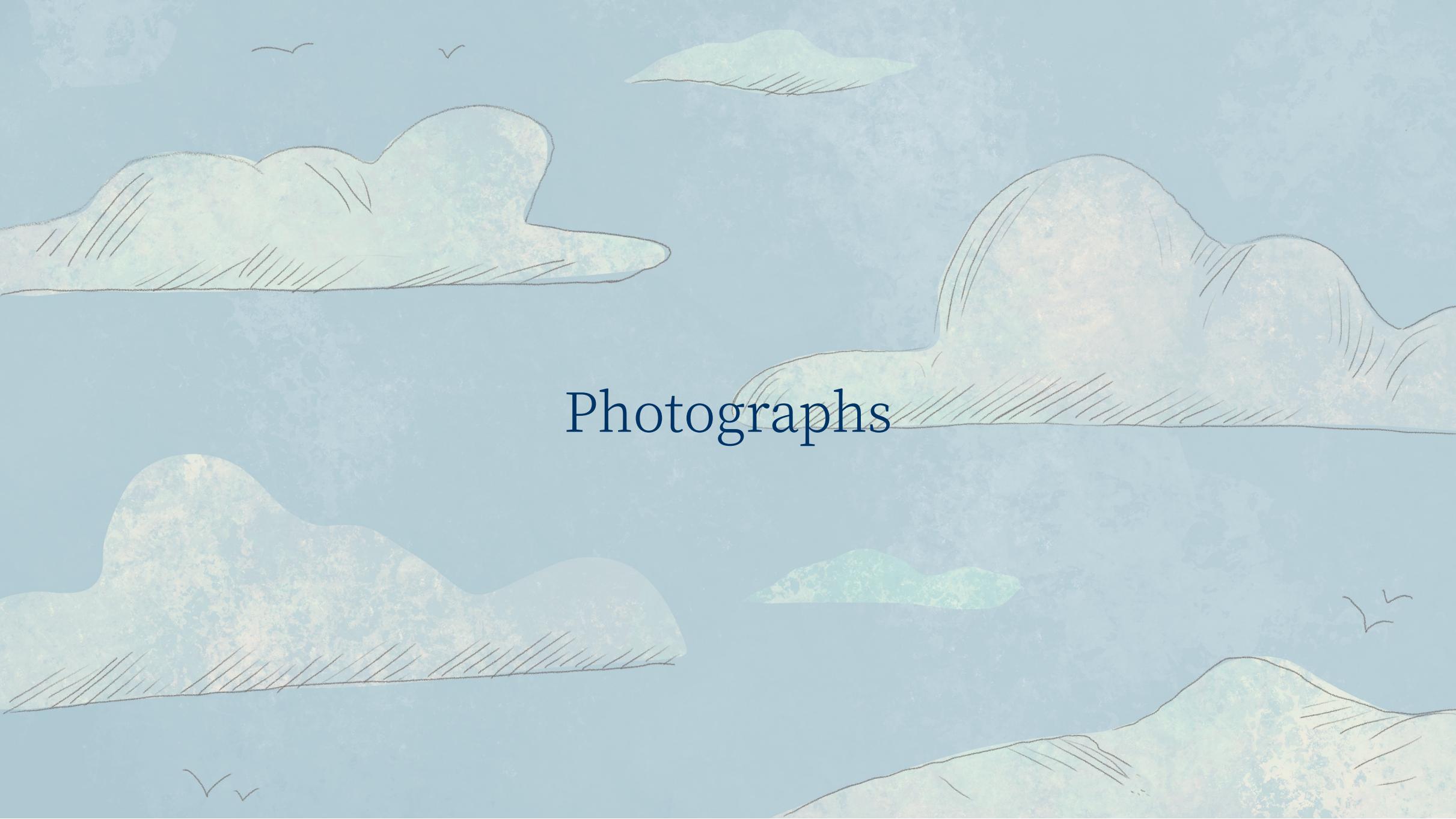


Bridging the gap among community phylogenetics, biogeography and macroevolution: moving from patterns to process

Gabriel Nakamura, Ph.D (Postdoctoral Research Associate - Daru Lab - Texas A&M University Corpus Christi)



The background of the image is a soft, blue-tinted collage of various cloud shapes. Some clouds are filled with a textured, mottled pattern in shades of grey, white, and light blue. Others are solid or have thin, dark outlines. Scattered throughout the sky are small, white bird silhouettes, some with simple V-shaped wings and others more detailed. The overall effect is dreamlike and atmospheric.

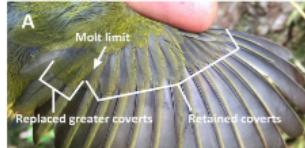
Photographs

For example..



✓ But... the interpretation it is not always
straighforward

Ecology - the challenge of working with limited information



Looking to the past to understand the present....





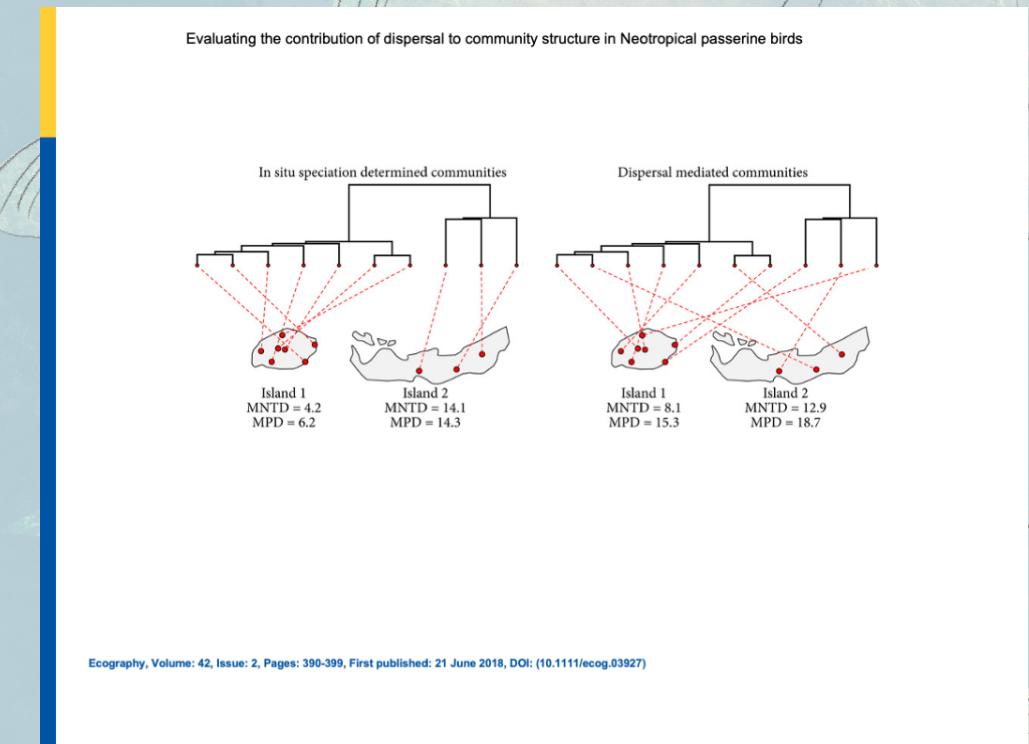
The nature's photograph album

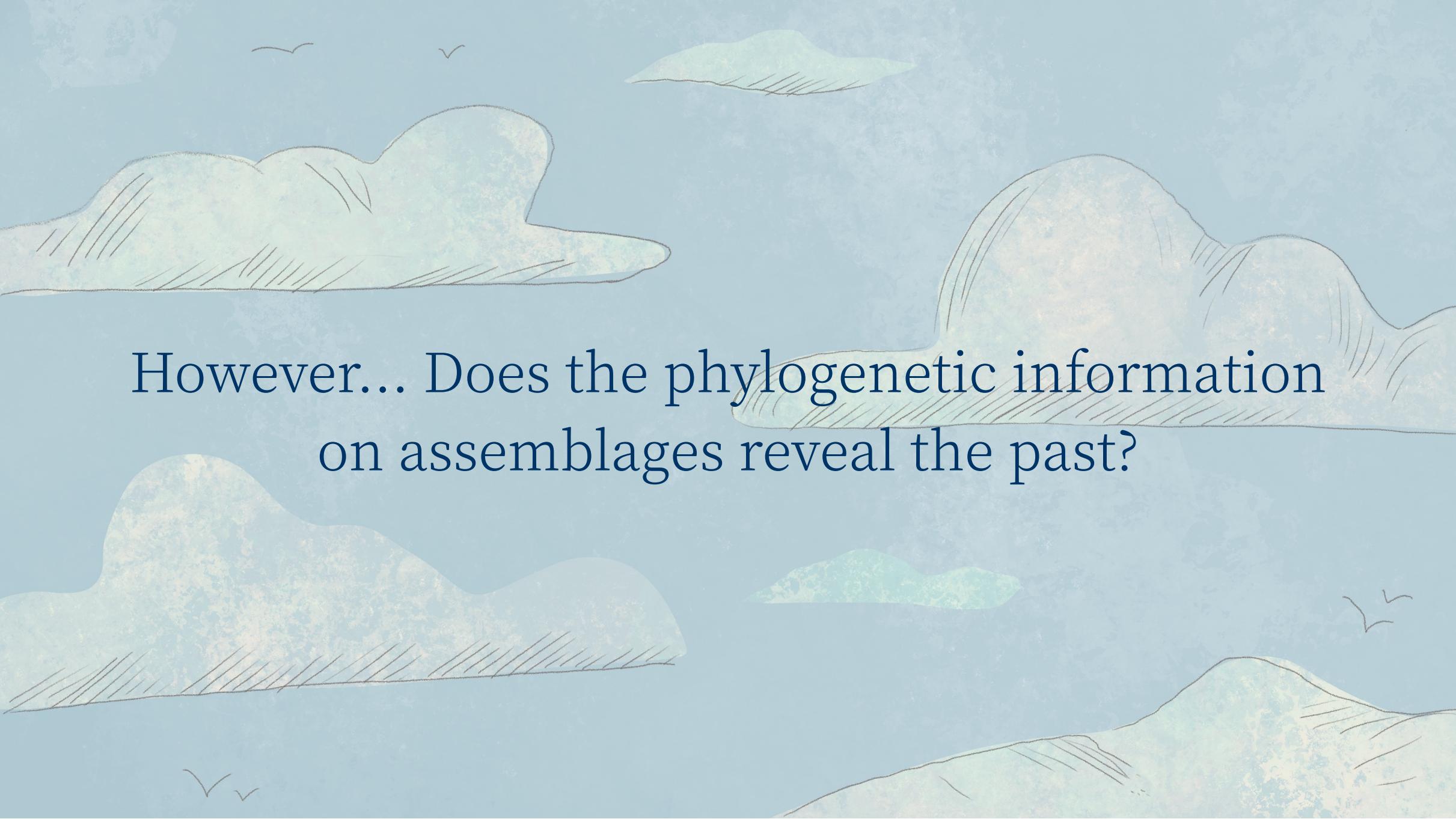


Phylogenetic history + Patterns of distribution of species = More comprehensive view of nature?

Phylogenies + Data in assemblage scale (local/regional)

- Assemblages with species with **similar evolutionary history** (clustered) -> effects of **diversification**
- Assemblages with species with **distinct evolutionary history** (overdispersed) -> effects of **dispersal**





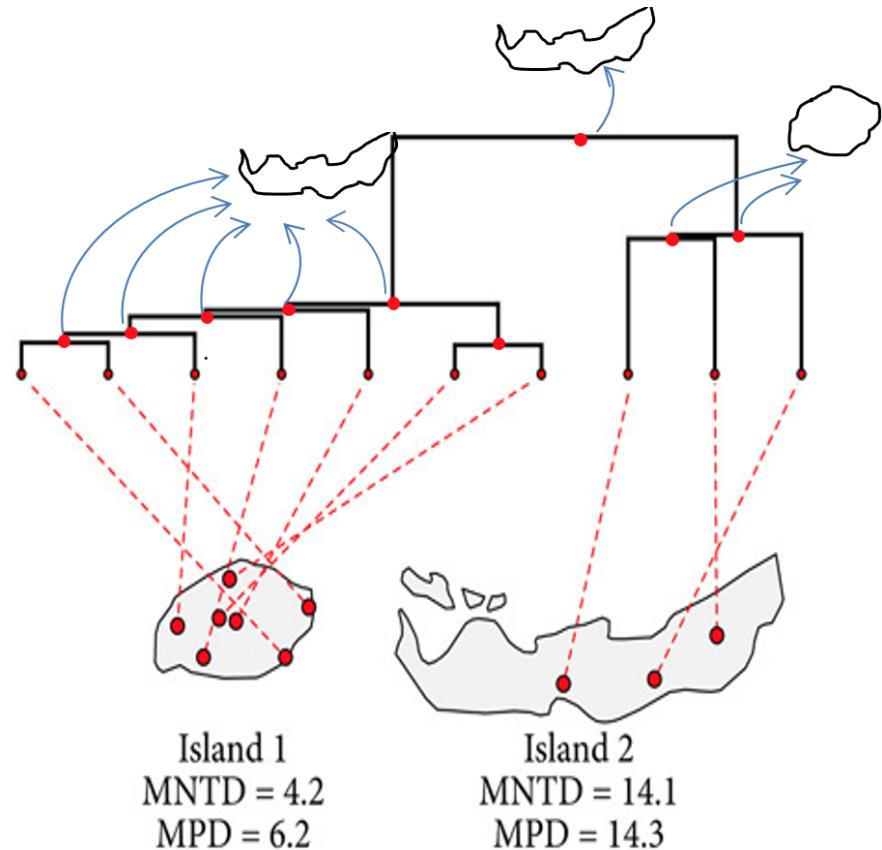
However... Does the phylogenetic information
on assemblages reveal the past?

Sometimes, under some assumptions

- All ancestors of present day species were always in the same place (or biome/region)
- The dispersal is a characteristic that is conserved along the phylogeny
- The potential of speciation is always conserved along the phylogeny

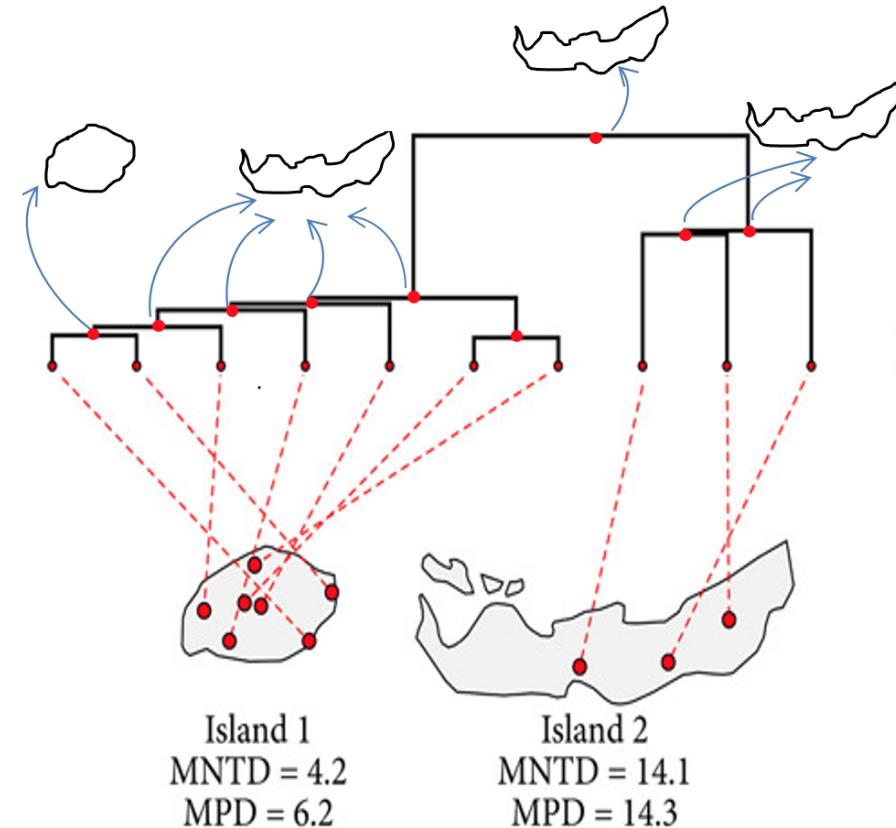
Different scenarios...

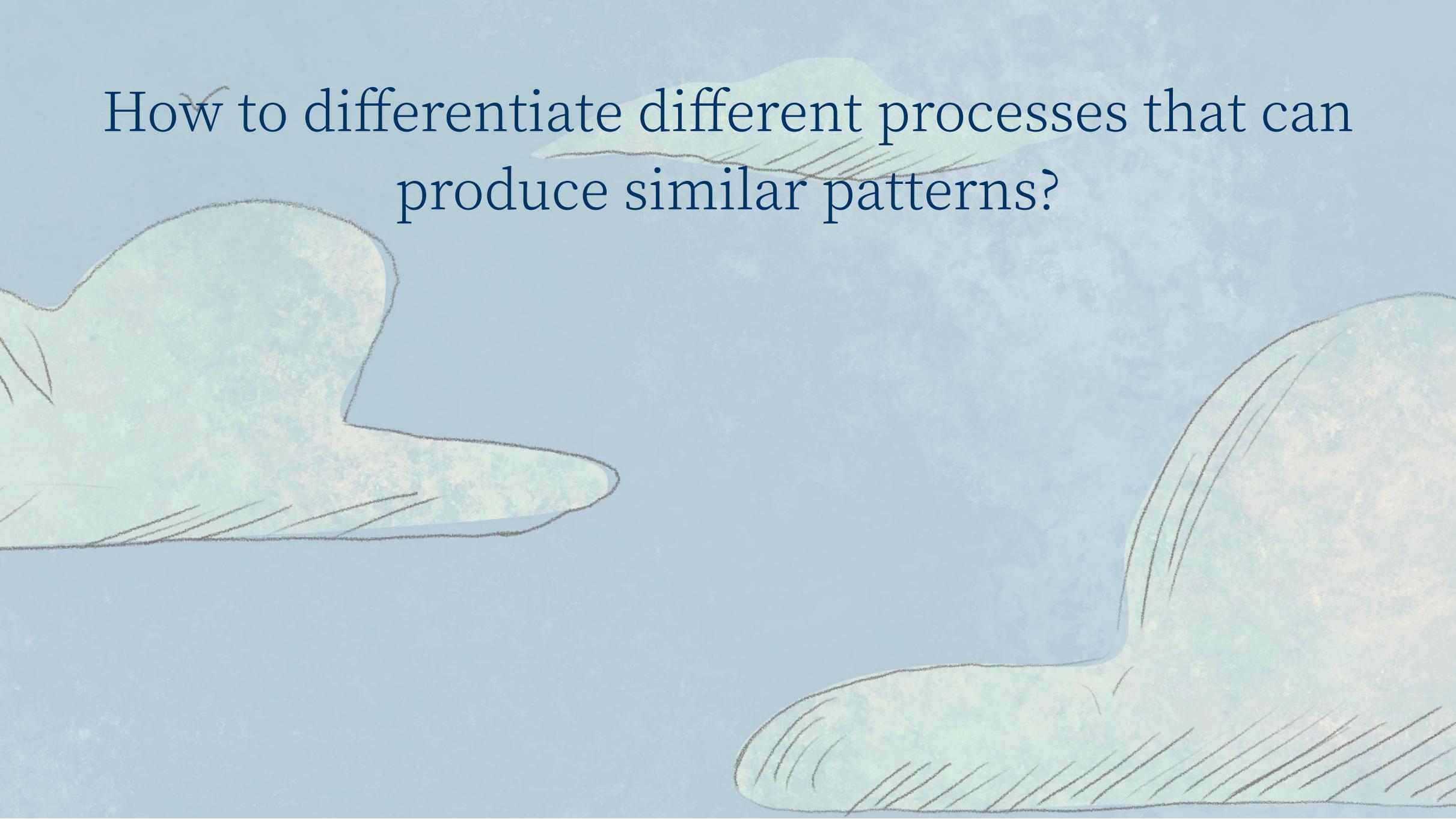
- Dispersion can play an important role
- As well as **in situ diversification**
- Specially if the traits associated with area occupation **are not conserved in phylogeny**



Different scenarios...

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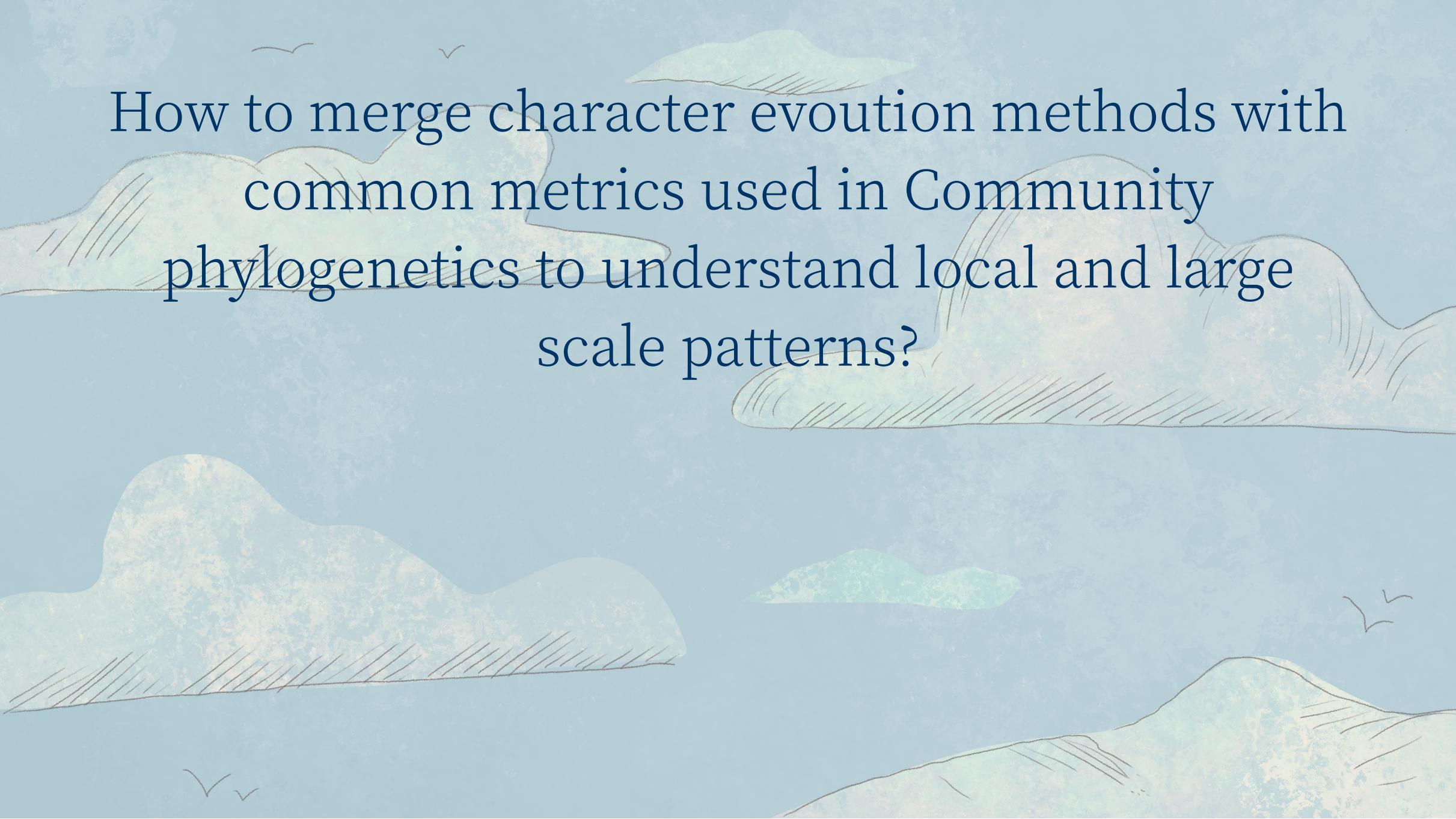


How to differentiate different processes that can produce similar patterns?

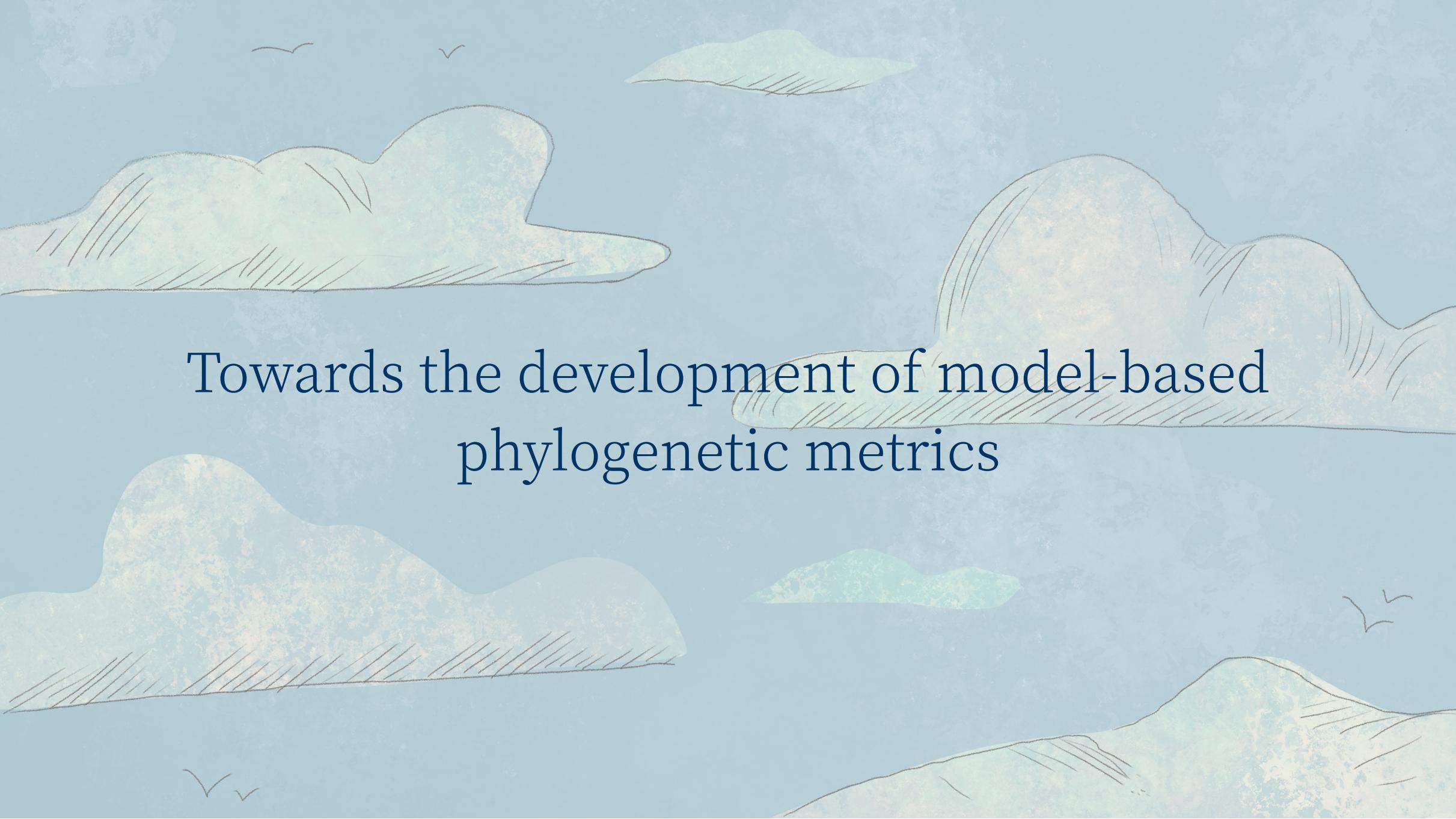
The importance to look at the deep past

- The deep past provides a **complementary vision history**
- For example, using **fossils**
- But... fossils are scarce, so we can use **character reconstruction models**





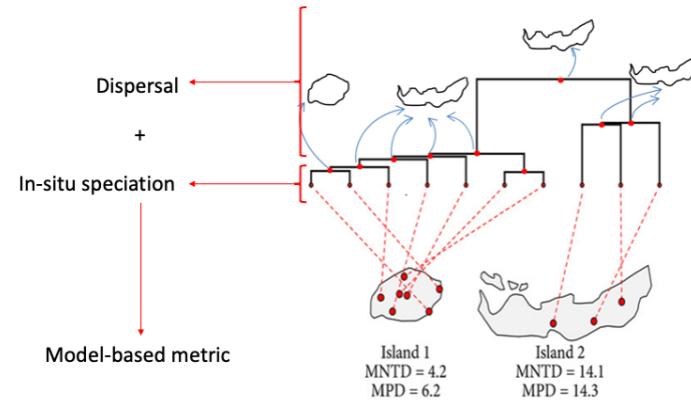
How to merge character evolution methods with
common metrics used in Community
phylogenetics to understand local and large
scale patterns?



Towards the development of model-based phylogenetic metrics

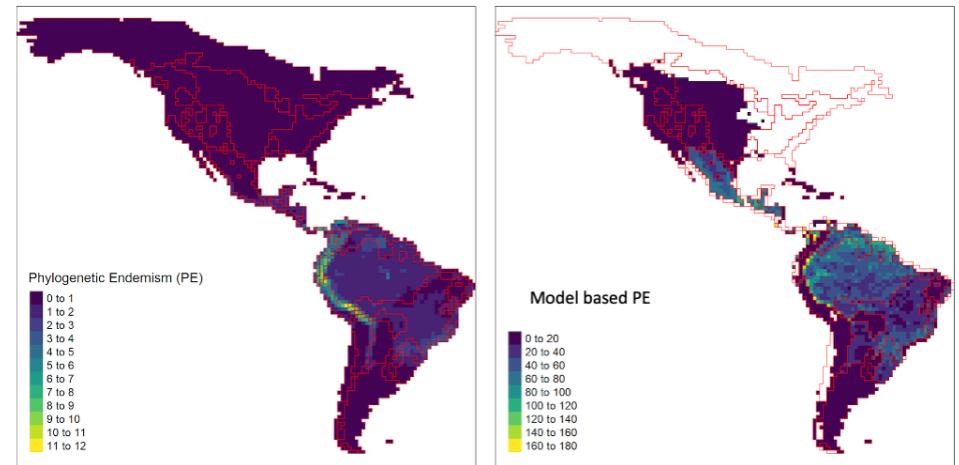
How can we differentiate between historical dispersal and diversification (speciation + extinction)

- estimating the range of species through **ancestral area reconstruction**
- **decomposing** the amount of evolutionary history that comes from **dispersal events** and from **diversification**



What does this approach brings as new information

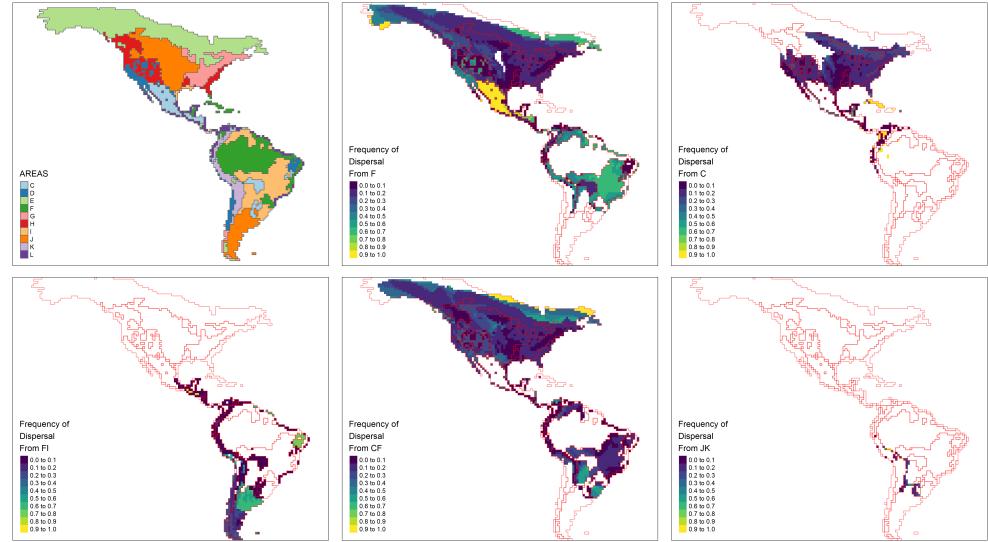
- More direct and **realistic estimate of evolutionary dynamics** in assemblages
- **Link between patterns and processes** generating biodiversity
- **Unambiguous interpretation** and better decisions regarding long term conservation actions



Differences between traditional approaches and
model-based metrics

Application in regionalization schemes

Understanding the role of historical dispersion and different regions in regionalization schemes



Main contributions

- Theoretical perspective: directly assessment of **deep time processes**
- Practical: conservation decision can be based on **both patterns and processes**

Thank you for your attention



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