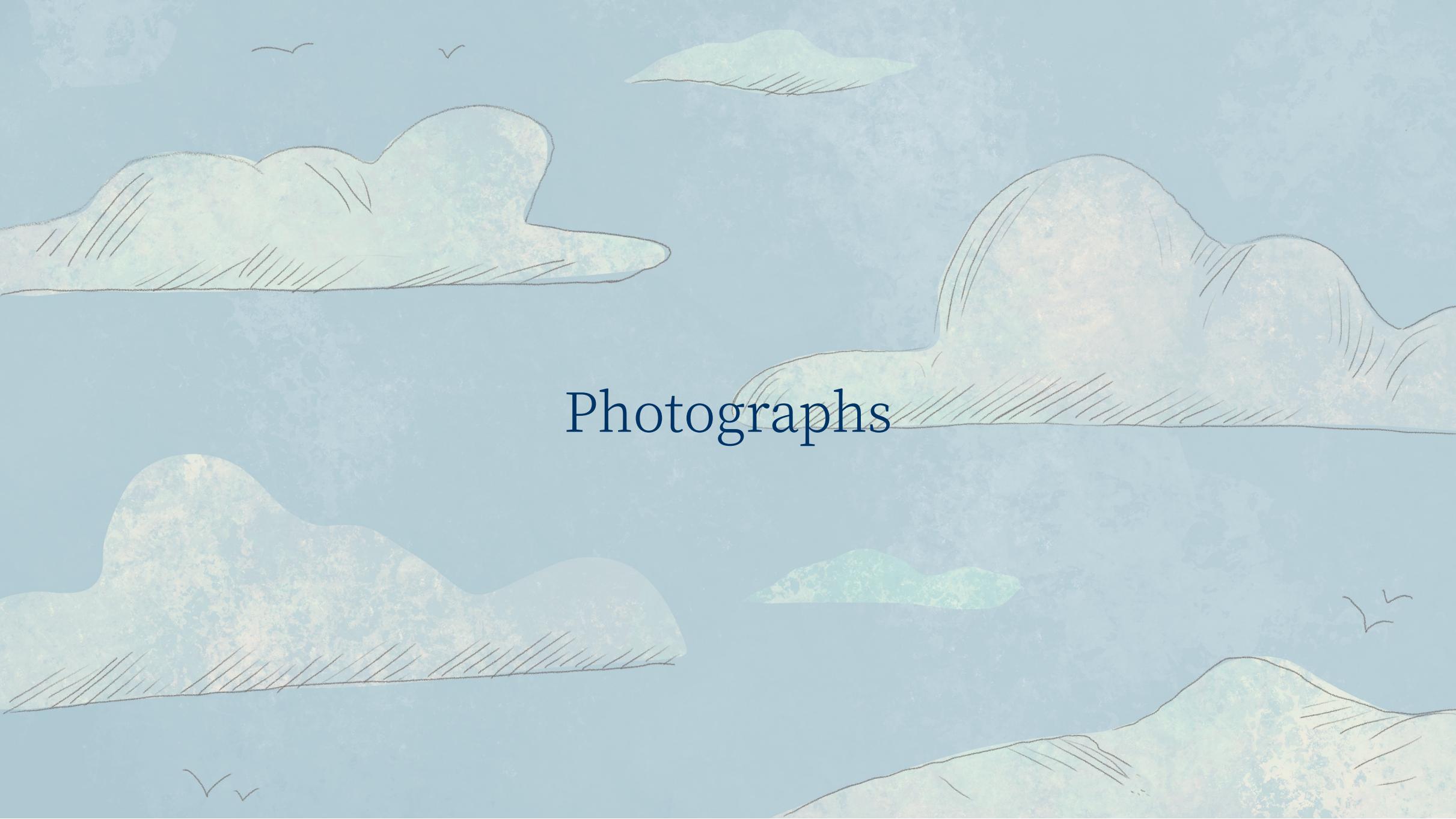


Bridging the gap among community phylogenetics, biogeography and macroevolution: moving from patterns to process

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. Small, dark bird silhouettes are scattered across the sky, particularly visible in the upper left and lower right corners.

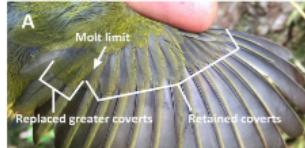
Photographs

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....





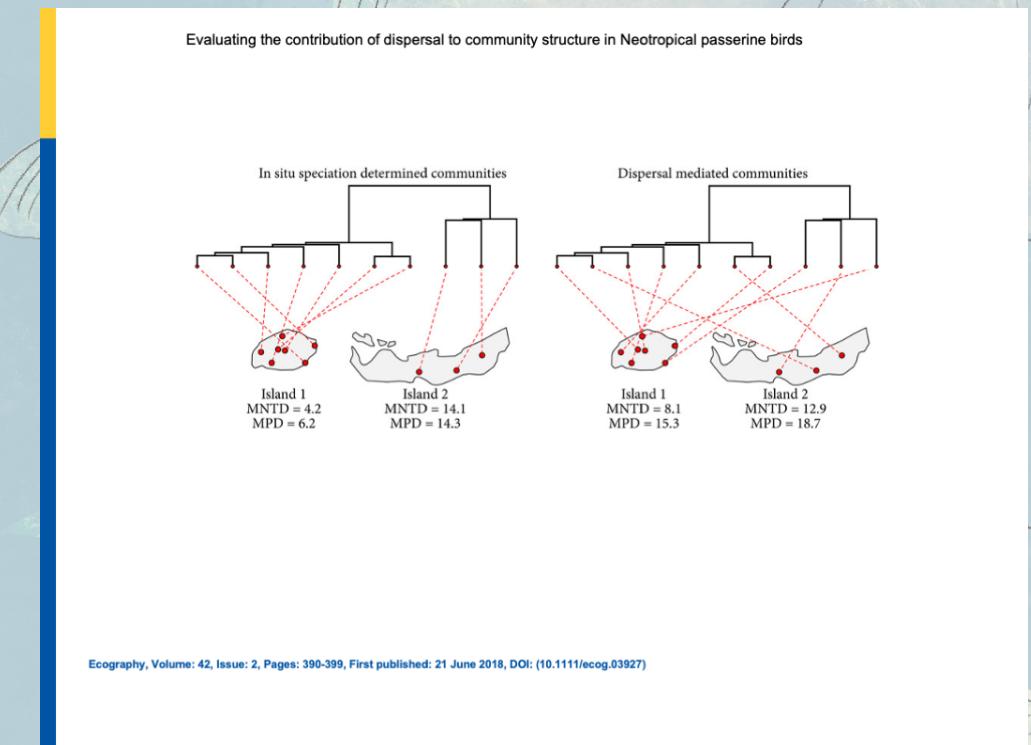
The nature's photograph album

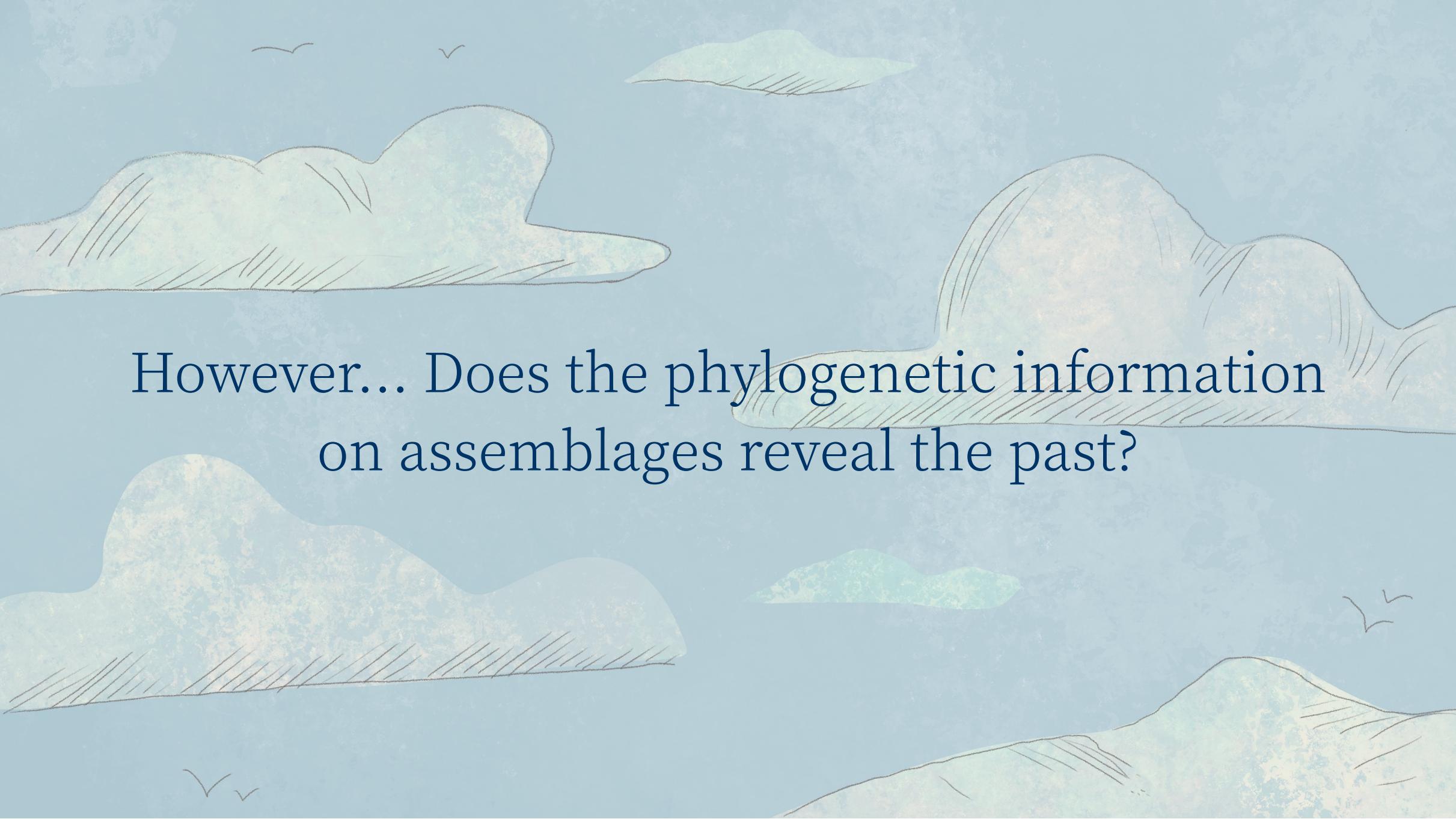


Phylogenetic history + Patterns of distribution of species = More comprehensive view of nature?

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**





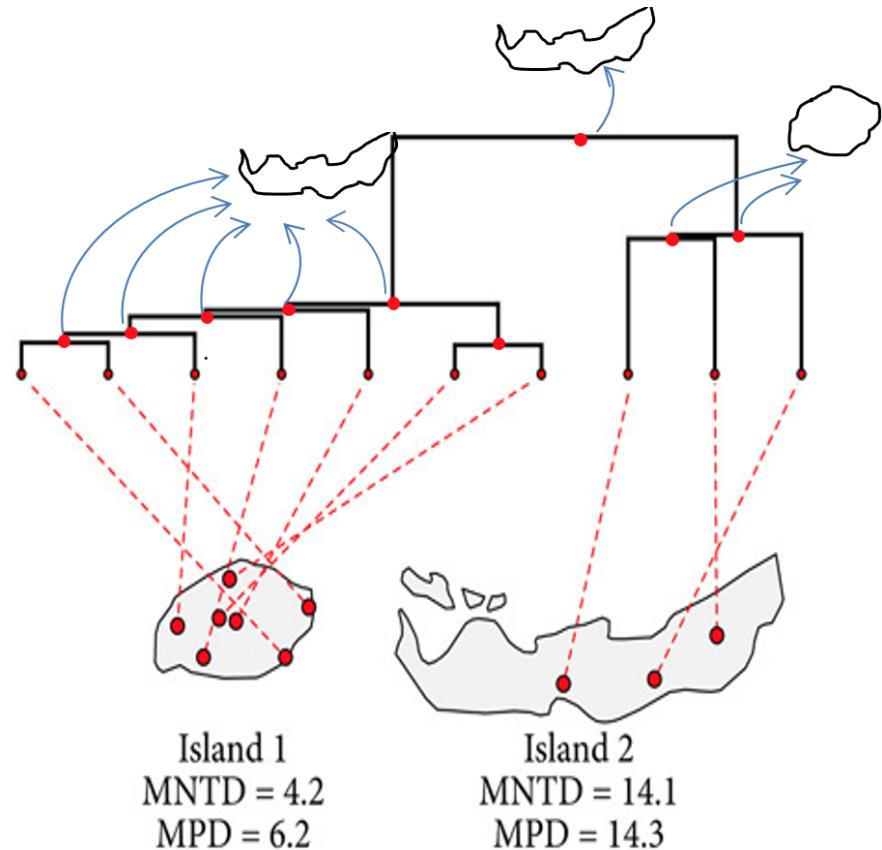
However... Does the phylogenetic information
on assemblages reveal the past?

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

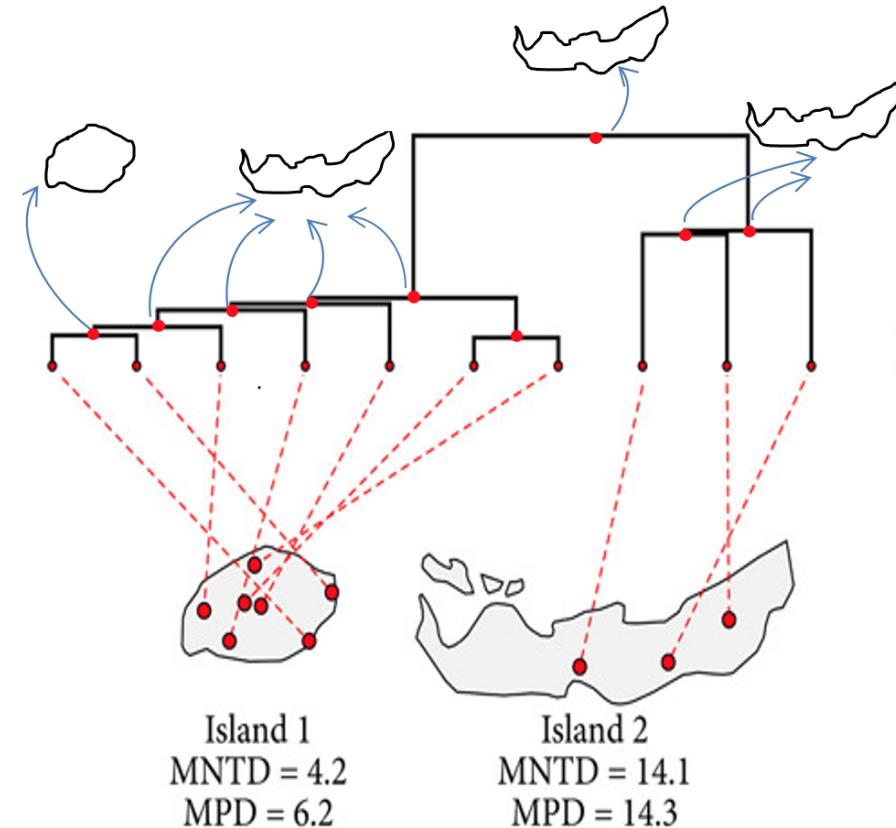
Different scenarios...

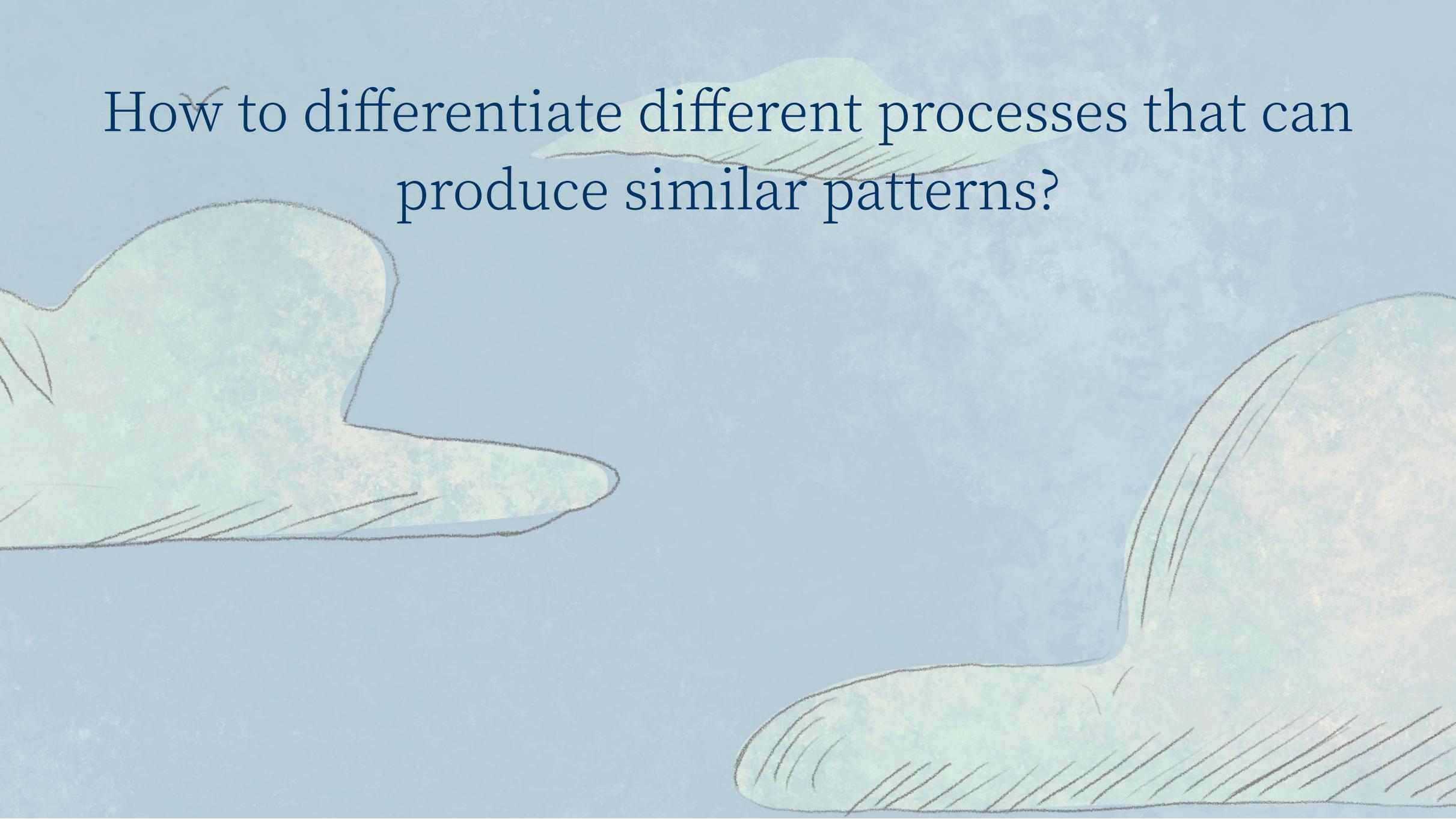
- Dispersion can play an important role
- As well as **in situ diversification**
- Specially if the traits associated with area occupation **are not conserved in phylogeny**



Different scenarios...

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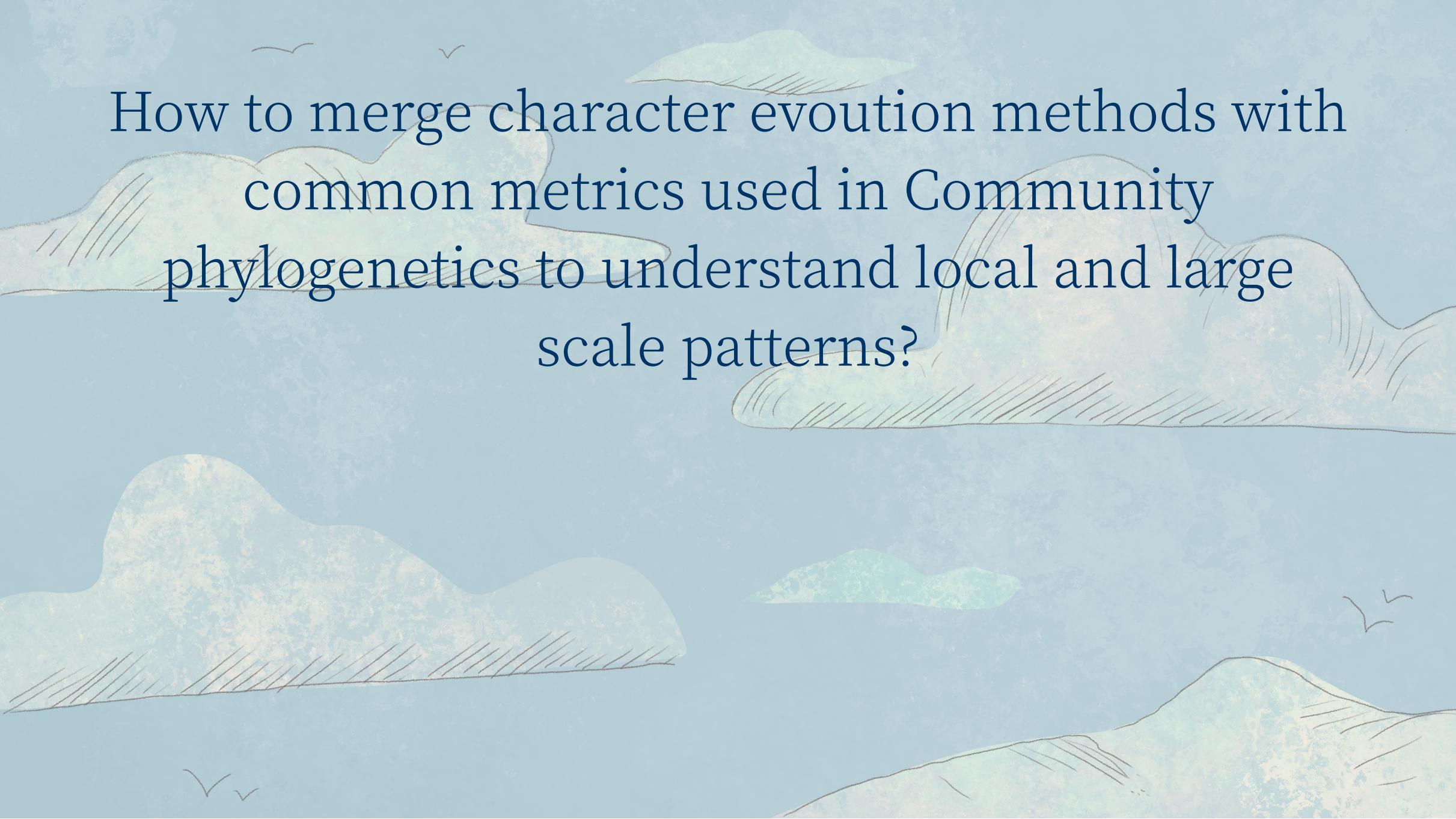


How to differentiate different processes that can produce similar patterns?

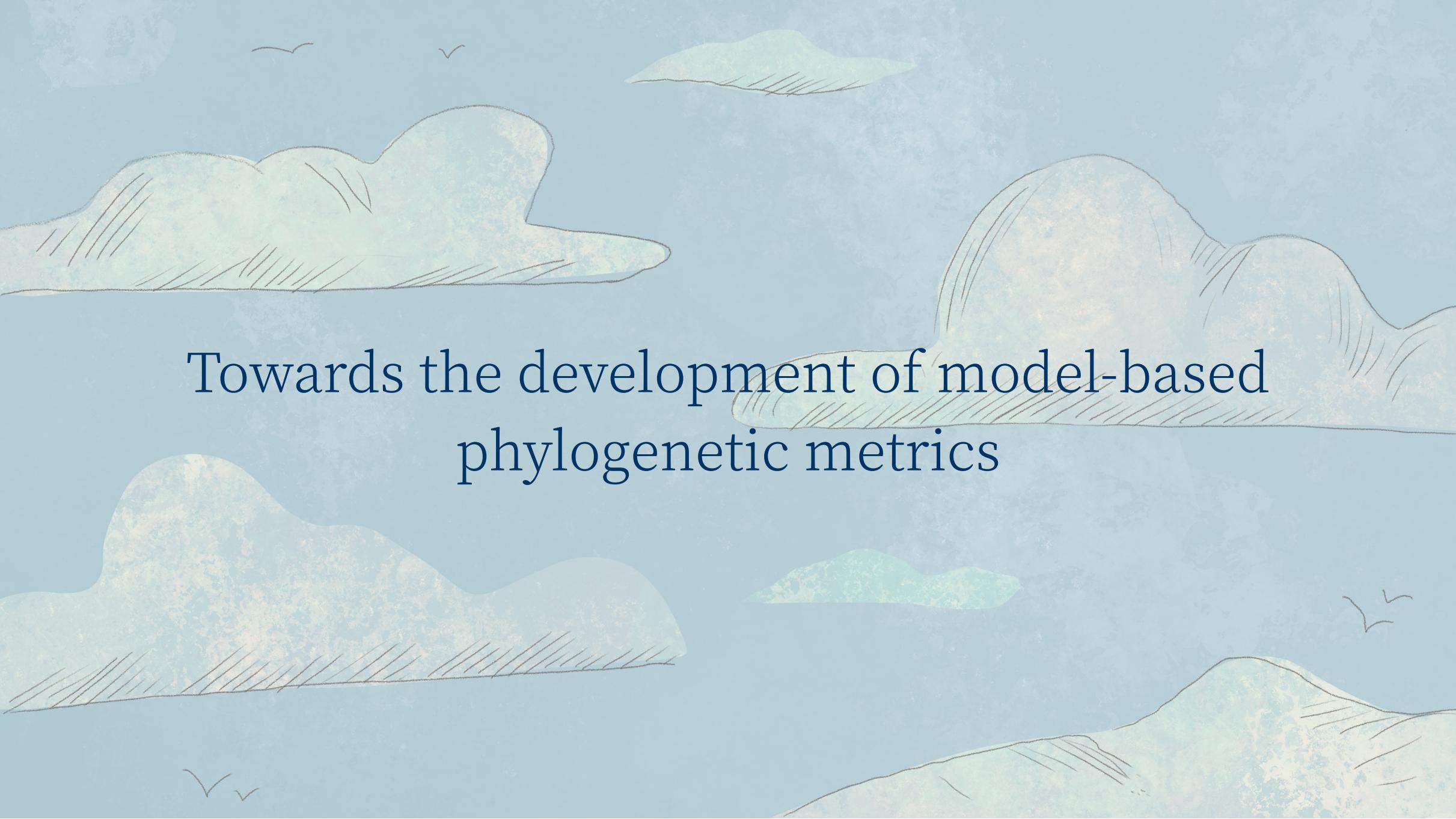
The importance to look at the deep past

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





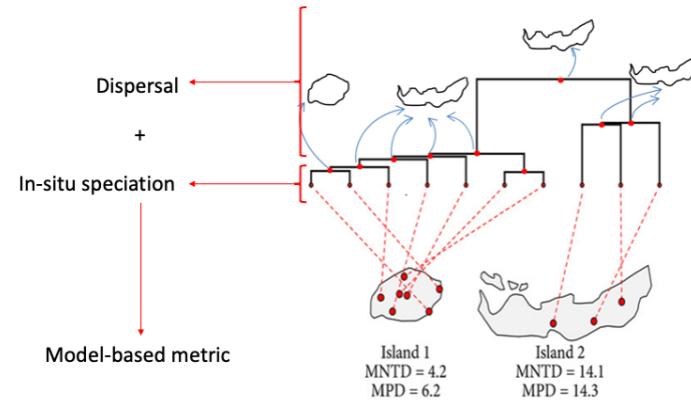
How to merge character evolution methods with
common metrics used in Community
phylogenetics to understand local and large
scale patterns?



Towards the development of model-based phylogenetic metrics

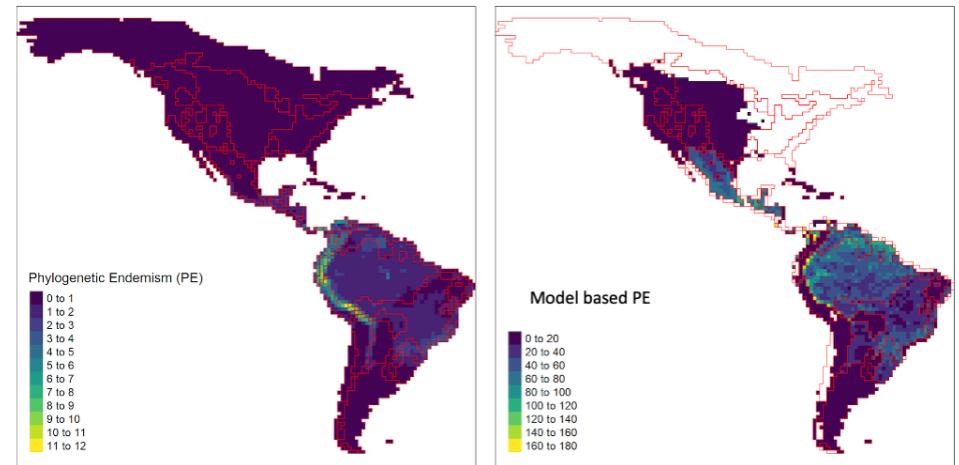
How can we differentiate between historical dispersal and diversification (speciation + extinction)

- 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

Further possibilities: 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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