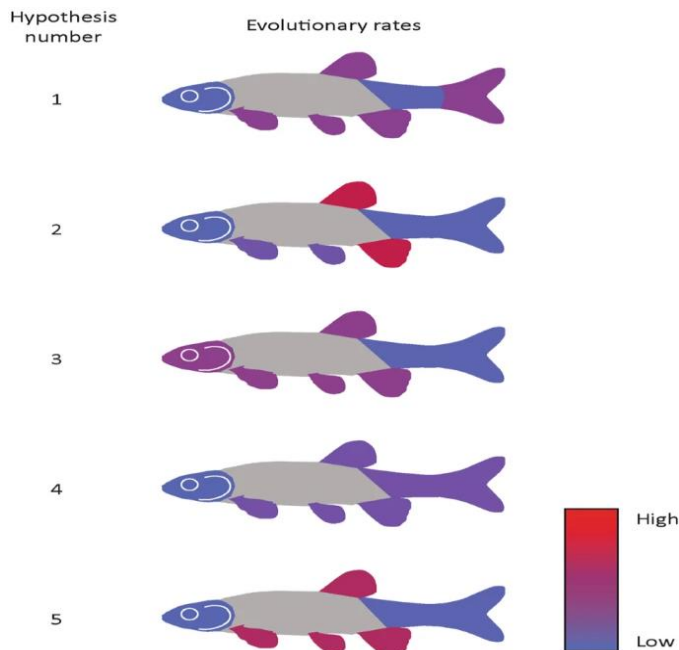


Can we make multivariate methods of how biological anatomy evolve more flexible?
What can this reveal about how biological diversity has evolved?

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Recent proposals about how different parts of living fishes (where each colour represents anatomy that is more correlated / integrated with objects of the same colour than to anatomy within alternative colours), and how these different correlated units / modules evolve at different rates (high vs. low), which may explain the diversity and success of different groups of fishes.



Generally, biologists have lacked explicit mathematical models that describe how the many features of organisms evolved, and how they interact during evolution. In the last decade, methods have become available to allow biologists to better fit such models to their data, as best exemplified by R packages such as mvSLOUCH and mvMORPH. However, even these models have been somewhat limited in scope due to computational demands. In the last 2 years, this situation has changed, spurring innovation in the mvSLOUCH R package in particular, whose latest version allows users to specify many ways in which the traits of organisms interact (e.g. how the length of an organism can drive the evolution of its head shape and crushing ability of its jaws). These vast improvements are only starting to be explored by biologists, but they nevertheless enforce the interactions between traits (e.g. length, head shape, jaw crushing ability) to be the same throughout the group under study. This may clearly present a problem, as we may expect these relationships to differ according to the ecology of species (e.g. herbivore jaws may respond differently to head shape and body length than carnivores). **Thus, the goal of this project is to make these methods more realistic for biological applications, using a large dataset of fish traits as an empirical test case.**

Teleost fishes, with 34,000+ extant species, represent half of vertebrate species today. While scientists have sought to explain the success of teleost fishes by heavily testing environmental drivers (e.g. salinity, mass extinction, water depth, coral reef living, latitude), comparatively little attention has been paid to intrinsic drivers of teleost fish success, such as how different parts of their anatomy co-evolve. Under certain combinations of trait co-evolution, fishes may flourish into many weird and wonderful forms, while under others, they may be highly constrained, and unable to diversify into numerous forms. **Without a method of trait co-evolution that is flexible, it is not possible to test such theories. Therefore, the goals are to:**

- Use R package PCMfit in a manner comparable to mvSLOUCH, so the user can specify how different traits interact.
- Use the additional functionality of PCMfit that allow it to fit different models of trait co-evolution in different groups of fishes, when these instructions are set by the biologist user.
- Use the additional functionality of PCMfit so that it tells the user, when given a dataset, which parts of the tree have traits co-evolving in different patterns and combinations.
- Apply this new method to a large dataset of living fishes (over 6000 species), to learn which trait co-evolution patterns exist in the dataset.

Supervision comes from Krzysztof Bartoszek, who developed R package mvSLOUCH (Bartoszek et al. 2012) and contributed to R package PCMfit, and John Clarke, an empirical biologist studying how traits evolve in fishes with interests and experience implementing a variety of phylogenetic evolutionary methods.

Relevant references:

Bartoszek K. et al. (2012). A phylogenetic comparative method for studying multivariate adaptation. *Journal of Theoretical Biology*

Mitov, Venelin, Krzysztof Bartoszek, and Tanja Stadler. (2019). Automatic Generation of Evolutionary Hypotheses Using Mixed Gaussian Phylogenetic Models. *Proceedings of the National Academy of Sciences of the United States of America*.