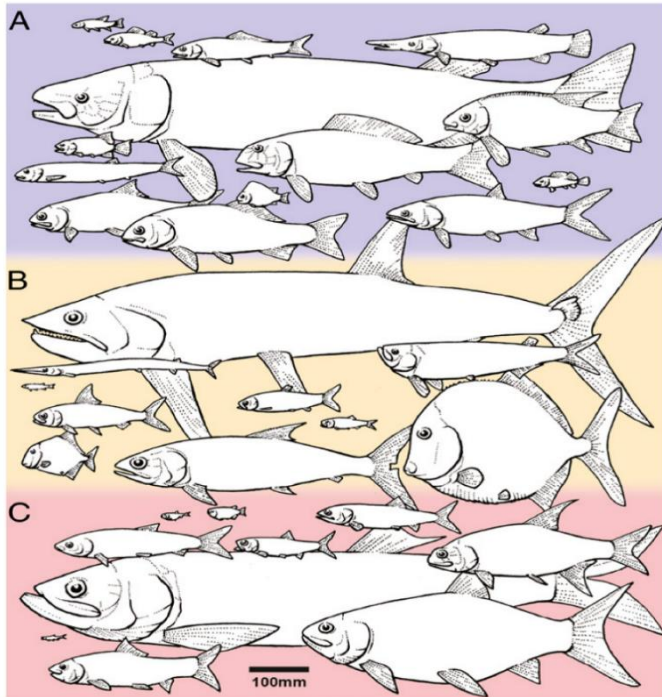


Testing how salinity habitat influences shape evolution in deep-time

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The vast, but poorly studied diversity of Mesozoic fishes will be your dataset for this work. These include **A**: the holostean fishes, highly diverse in the past, but known from only bowfin and gars today. **B**: fossil stem teleost fishes; and **C**: fossil crown teleost fishes.



Teleost fishes, with 32000+ extant species, represent half of vertebrate diversity. An important part of their evolutionary success is their ability to successfully explore both marine and freshwater environments, a divide many other groups of organisms struggle to cross. Distinct evolutionary pressures in these settings provide expectations for how size and shape might vary across this divide. For example, marine settings have fewer barriers to species movement, and the dominance of phytoplankton at the marine food-web base (relative to freshwater) is associated with longer trophic chains (Potapov et al., 2019) that are expected to sustain larger taxa in marine settings. Conversely, freshwater environments are more fragmented, and may act as refugia that encourage the evolution of functionally extreme geologically old taxa termed ‘living fossils’ (Darwin, 1859). Fortunately, fishes have repeatedly crossed this salinity divide, providing natural replicates in which evidence for repeated evolutionary pressures and outcomes can be tested.

Study of living fishes has revealed a pattern whereby the body shapes (represented by PC1) occupied by marine and freshwater fishes are remarkably similar between marine and freshwater environments (Friedman et al. 2021), but that these

similar shapes were attained via very different evolutionary patterns. Specifically, marine clades fill the PC1 axis by spreading out efficiently across the space, with different subclades occupying different shapes (results more consistent with a Brownian null model, where closely related taxa are likely to be similar, but more distantly related clades likely to be dissimilar in shape; shape variance is therefore mainly partitioned between clades, rather than between them). In contrast, freshwater clades relatedly explore very similar shapes to other freshwater clades, with shape variance within clades greater than would be expected under a null model. Despite these similarities in shape evolution, freshwater fishes are consistently smaller than marine fishes (Clarke 2021). With a dataset of fossil fishes assembled by John Clarke, the student could therefore seek to:

- replicate the analyses of Friedman et al. 2021 with landmark based fossil fish dataset. Do the same patterns emerge, or is there something fundamentally different about the biology, or evolutionary pressures of a geological old group of fishes that brings about a different evolutionary outcome?
- fit a variety of alternative evolutionary models to characterise differences in phenotypic evolution to learn if, and how, shape evolution differs between marine and freshwater environments. This can be achieved within mvSLOUCH, an R package developed in-house by Krzysztof Bartoszek (Bartoszek et al. 2012).
- given the expected size differences between marine and freshwater habitats, one could explore if the relationship between size and body shape varies substantially between these two environments (e.g. using OUOU and OUBM models) and consider how this might influence evolutionary outcomes in the two settings.
- provide some recommendations to the broader community about how best to utilise landmarks in analyses, versus use of PCA axes.

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

Clarke J.T (2021). Evidence for general size-by-habitat rules in actinopterygian fishes across nine scales of observation. *Ecology Letters*.

Friedman S.T. et al. (2021). Divergent processes drive parallel evolution in marine and freshwater fishes. *Systematic Biology*.