



## **Journeys through discrete character morphospace**

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The fossil record represents a rich morphological data set that can be captured as discrete categorical data. This typically results in the generation of discrete character-taxon matrices that are themselves the starting point for analyses of evolutionary tempo, relationships, and measuring morphological diversity (often termed disparity). However, these three endeavours have historically been treated separately despite having a common starting point and similar overall goal: understanding morphological evolution. Here I argue that it may be more fruitful to consider these three research strands simultaneously, and further that the way to do this is the deployment of "phylo-morphospaces". In an ideal scenario such spaces capture how morphospace has been explored by phylogeny over geologic time and hence can be used to test hypotheses relating to evolutionary rates, constraints, convergence, and directional trends. However, there are many challenges to generating such spaces, including ordinating non-Euclidean distances into Euclidean spaces, an inability to convert points in such spaces back into tangible morphologies (sets of discrete character states), and an unexamined variation in approaches to generating such spaces, particularly whether or not the reconstructed ancestors are generated prior to, or after, ordination. Here I focus on this last issue and use a large (152 taxa, 853 characters) data set for coelurosaurian theropod dinosaurs to compare these two approaches. It is not yet clear what might be considered optimal, but I was particularly interested in how much of the resulting spaces reflected phylogenetic signal. This is important as phylogenetic distances will constantly diverge, making it less likely that patterns of convergent or constrained evolution will be recognised. Across five different approaches (I applied four subversions of the pre-ordination approach) the percentage of phylogenetic signal in the resulting phylomorphospace varied from 22.4% to 77.6%, minimally exhibiting just how different a phylomorphospace methodological approach choice can generate. Here I favour a pre-ordination ancestral state reconstruction approach, but one that minimises the amount of phylogenetic signal added to the data by reconstructing ancestors or estimating missing values. Finally I consider how stochastic character maps may represent the future in generating such spaces. In particular, how they may allow us to properly reconstruct the transistional morphologies passed through along the branches of a phylogenetic tree.