BALL STATE
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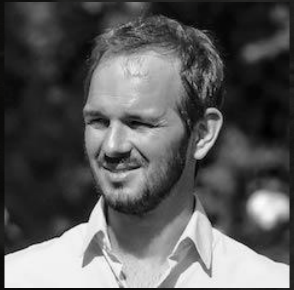
The Mathematical Laws of Morphology and Biomechanics

PURDUE
FORT WAYNE

Tuesday 7th February 2023 @ noon EST

Virtual Presentation: https://purdue.webex.com/meet/aselvite



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Modelling phenotypic traits evolution in deep times: a phylogenetic approach

The use of statistical approaches for modeling the evolution of species traits on phylogenetic trees, also known as phylogenetic comparative methods, have exploded since Felsenstein's seminal paper in 1985. Developed first as a statistical fix for comparative analyses, these approaches are now routinely used to address fundamental questions in macroevolution and macroecology from extant and fossil data. However, their use has been often limited to simplistic models assuming that traits or species are evolving independently of each other's and from their environment. Here, I present a suite of models that we developed in the past years to infer the effect of inter-specific interactions and past environmental changes on the evolution of phenotypic traits as well as for understanding the evolution of multidimensional traits – high dimensional multivariate datasets such as 3D geometric morphometrics. These methods show that phylogenies of extant taxa provide valuable information about past and present biodiversity and offer a unified analytical framework for the study of extant and fossil taxa. Future developments of these models and statistical tools will further allow a better integration of data types and research fields for a better understanding of the processes driving the evolution of taxonomic and phenotypic diversity.

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