

Functional Data Analysis in Continuous Reaction Norms: Identifying Nonlinear Variations

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A continuous reaction norm in evolutionary biology is a trait or characteristic of an individual or genotype that varies as a continuous function of some aspect of the environment. The trait value as a function of the environment for an individual could be represented by a curve, and the set of curves for distinct clones, families or genotypes in the population shows the genetic variations in that population. Directions of variations of the curves are of importance to evolutionary biologists because they provide information on the genetic constraints to evolution. In this talk, I will first define three directions of variations of biological interest for continuous reaction norms: Faster-Slower direction or vertical shift, Hotter-Colder direction or horizontal shift, and Generalist-Specialist direction or change in width. Then, I will propose a method to identify and quantify those directions. The Faster-Slower direction allows for standard linear analysis (e.g. by PCA), but effective analysis of the other directions has motivated the development of a new non-linear methodology. Results of this methodology will be illustrated on curves of growth rate of caterpillars as a function of temperature.