

STANFORD UNIVERSITY  
DEPARTMENT OF STATISTICS  
JOINT STATISTICS/BIOSTATISTICS SEMINAR

4:15 p.m., Thursday, March 11, 2004  
Sequoia Hall Room 200  
(Cookies at 3:45 in 1st Floor Lounge)

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**Analysis of Nonlinear Variation in Curves, New Look at Genetic Tradeoffs**

Abstract:

I present a new Functional Data Analysis method for analyzing variations in curves of common shape. The motivation of this methodology and its results will be illustrated on examples of reaction norms from Evolutionary Biology including curves of growth rate of caterpillars as a function of temperature. The new method achieves two important goals. First, it allows for the decomposition of variation in a set of curves of common shape into predetermined linear and nonlinear modes of interest. Second, it quantifies each mode leading to meaningful comparisons. Such comparison in the biological data gives an insight into the evolutionary responses of a population under selection and shows that non-linear components can be dominant. Variation along a linear mode is quantified, in methods such as Principal Component Analysis, by a ratio of sums of squares. As this ratio is not accurate for the quantification of nonlinear modes, a new ratio is proposed which takes into account the geometry of the manifold of variation.