Statistics Seminar

Department of Mathematical Sciences

DATE:	Thursday, November 5, 2020
TIME:	1:15pm – 2:15pm
LOCATION:	ZOOM meeting
SPEAKER:	Yifei Zhang, Binghamton University
TITLE:	Comparison of shape quantification methods for genomic study

Abstract

Among geometric morphometrics methods, elliptic Fourier analysis and semi-landmark analysis are often used for the quantification of biological shape variations. Elliptic Fourier analysis is an approximation process of a shape contour while semi-landmark is a method of superimposed points in which the difference of multiple contour positions are minimized. These two methods will give us two different responses. Moreover, different direction standardization and different scaling procedures can also lead to different responses. This paper showed how different combinations of geometric morphometrics methods and standardization & scaling procedures affect principal component scores, average shape, prediction accuracy and association study by analyzing the association between Sorghum seed's shape variations and genome-wide single-nucleotide polymorphisms (SNP).

From:
http://www2.math.binghamton.edu/ - **Department of Mathematics and Statistics, Binghamton University**

Permanent link:
http://www2.math.binghamton.edu/p/seminars/stat/201105

Last update: **2020/10/29 00:39**