The Southwest Michigan chapter of the American Statistical Association presents:

Computationally efficient genome-scale evolutionary inference: creating a sustainable future for African smallholder farmers

Laura Kubatko, Professor of Statistics and Professor of Evolution, Ecology, and Organismal Biology at The Ohio State University

Abstract: The era of rapid and inexpensive genome sequencing has ushered in a range of computational and modeling challenges in the effective analysis of such data. A problem of fundamental importance in evolutionary biology is the inference of a phylogenetic tree — a directed, bifurcating graph that represents the ancestry-descent relationships among a collection of distinct species. Given DNA sequence data from many species and from many genes within each of the species, the goal is to infer a robust estimate of the phylogenetic tree, along with a quantification of the uncertainty in this estimate. In this talk, I will discuss a computationally efficient method for inferring the phylogeny arising from the application of methods from algebraic statistics. I will demonstrate the success of the method by application to the problem of estimating evolutionary relationships among viruses that infect cassava plants in East Africa, for which computationally efficient methods for inference are imperative for real-time crop protection strategies.

Brief Biography: Dr. Laura Kubatko is Professor of Statistics and Professor of Evolution, Ecology, and Organismal Biology at the The Ohio State University in Columbus, Ohio. Dr. Kubatko holds BA degrees in Mathematics and Biology from Hiram College (Ohio, USA), and an MS in Statistics and PhD in Biostatistics (both from The Ohio State University). From 1999-2006, Dr. Kubatko was Assistant Professor of Mathematics and Statistics at the University of New Mexico (USA) before moving to her present position. Her research interests are broadly in statistical genetics, with a focus on the development of statistical and computational methods for inferring phylogenies from molecular data. Her recent work is focused on bridging the gap between traditional phylogenetic techniques and methodology used in population genetics analyses, primarily through the application of coalescent theory to species-level phylogenetic inference.

Where: On the **downtown Grand Rapids** campus of Grand Valley State University, **DEV 136 E**

When: 5:00 PM Friday November 10, 2017

Agenda:

- Chapter business meeting at 5pm (this will be short!), Dr. Kubatko's talk
- Afterward, we will eat dinner at **Slows Bar BQ** (435 Ionia Ave. SW), one mile from DEV. Chapter members will dine free (does not include parking).