

American Statistical Association Mid-Michigan Chapter

The Chapter is pleased to announce its 2015 fall meeting. Our guest speaker is Dr. Gustavo de los Campos, Departments of Epidemiology & Biostatistics and Probability & Statistics, Michigan State University, East Lansing, MI.

Gustavo de los Campos is Associate Professor at the Epidemiology & Biostatistics and at the Probability & Statistics departments of Michigan State University. His academic background and research interests center on Statistical and Quantitative Genetics methods with emphasis on the use of high-dimensional inputs (e.g., SNPs, environmental covariates other omics) for analysis and prediction of complex traits and diseases in humans, plant and animal breeding.



Thursday, November 12, 2015, 7:00 – 8:30 pm

Chapter business meeting and presentation Social hour & meeting: 7:00 – 7:30 pm Presentation: **7:30 – 8:30 pm** Location: **Michigan State University, C405 Wells Hall** Title of presentation: **Integrating Multi-Layer High-Dimensional Inputs for Analyses and Prediction of Complex Traits**

Abstract: The availability of data sets comprising multiple layers of genetic and environmental information has grown recently, and the growth is expected to continue. Integrating these high-dimensional inputs into models poses important statistical and computational challenges. In this presentation I will show how Bayesian Generalized Additive Models (BGAM), with layer-specific priors and data-estimated hyper-parameters, can be used to integrate multi-layer high-dimensional inputs for analysis and prediction of complex traits and diseases. Two applications will be introduced. The first one, based on Jarquín et al. (2014, PMC3931944), uses a BGAM for integrating high-dimensional molecular markers (SNPs) and high-dimensional environmental covariates for prediction of wheat yield in multi-environment trials. The second one (Vazquez et al., submitted) uses a BGAM for integration of multi-layer omic data (SNPs, methylation, gene expression) for prediction of survival of breast cancer. Both applications used the BGLR R-package (https://github.com/gdlc/bglr-r) which implements a wide array of BGAM.