



A Knight's Welcome To: Michael DeGiorgio



DATE: Tuesday November 20, 2018

TIME: 11:00AM-12:00PM

LOCATION: HEC-101A

(Harris Engineering Corporation Building)

HOSTED BY: Wei Zhang and Shibu Yooseph

Genomics and Bioinformatics Cluster

Bio: Michael received his B.S. in mathematics and in computer science from the University of Central Florida in 2006, and his Ph.D. in bioinformatics from the University of Michigan in 2011. He was subsequently a postdoctoral fellow at the University of California, Berkeley and joined the faculty of the Departments of Biology and Statistics and the Institute for CyberScience at Pennsylvania State University in January 2014. He was named an Alfred P. Sloan fellow in 2017.

“Uncovering footprints of adaption from ancient and modern genomes”

The study of genomic variation is fundamental to population and evolutionary genetics, as it provides a basis for understanding differences among individuals, populations, and species. Because a number of adaptive and non-adaptive processes work in concert to shape genomic variation, strategic study designs and powerful statistical approaches are often needed to tease apart these forces. In this talk, I will focus on the development and application of statistical approaches for identifying adaptive processes that shaped the current distribution of genomic variation within and across populations. During the first half of my talk, I will discuss a set of collaborative studies in which we analyzed genomic data from ancient and living Native Americans from the Pacific Northwest to examine temporal effects of European colonization on genomic diversity. In particular, we discovered evidence of a population collapse and genomic mixture between Europeans and Native Americans, as well as shifts in selection pressures correlating to regional European-borne epidemics of the 1800s. During the second half of my talk, I will introduce several new powerful and robust statistical methods for detecting and classifying genomic targets of natural selection. These approaches contribute to the current state-of-the-art in evolutionary genomics, and have been applied by our group and others to address evolutionary problems that were previously difficult or inaccessible with previous methods

