



The Math/Stats Colloquium
Department of Mathematics and Statistics
San José State University



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*Machine Learning Methods
in Genomic Variation*

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Abstract: Genomic anomalies, or variations, are often shared between members of the same species. Although rare, these changes may result in disease or an increase in host fitness. Most approaches for detecting structural variation rely on high quality data and are typically limited to one type of structural variant such as deletions or inversions. Standard approaches for identifying such variation involves comparing fragments of DNA from the genome of interest to a reference genome. In this work, we describe gradient boosting, neural network, and recommendation systems approaches in the context of genomic variants.

Background: Calculus II and a first course in linear algebra.

About the speaker: Mario Banuelos is a first generation college student from Delano, California. He attended Fresno State for his B.A. in Mathematics, CSU Bakersfield for his preliminary teaching credential, and UC Merced for his Ph.D. in Applied Mathematics.

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