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**Erica L Sawyer\***, ericasawyer@mail.fresnostate.edu, and **Mario Banuelos**. *Deep Learning Methods for Detecting Structural Variants in Related Individuals*. Preliminary report.

Structural variants (SVs) are observed differences between the sequenced genome of an individual as compared to a reference genome for that species. These differences include deletions, inversions, insertions, and duplications. Since some genomic variations are associated with certain diseases, our work focuses on developing methods to detect such changes. Current methods to detect structural variation still suffer from high false positive rates, and we seek to develop machine learning and deep learning methods for identifying probable deletions in DNA based on genomic information of related individuals.

In this talk, we explain the implementation of neural networks, gradient descent, and logistic regression to predict SVs. We then introduce our preliminary model, which uses the observed genomic information of two parents and an offspring to predict locations of SVs in the genome of the child. Furthermore, we discuss the expansion of our model to simultaneously predict SVs for both the parents and the child and investigate the performance of this model under different neural network architectures using various performance metrics. (Received March 03, 2020)