

1135-VL-2919      **Tanner J Rosenberg\*** (tjr268@nau.edu). *Computing maximal genetic distance in terms of signed permutations*. Preliminary report.

One can model a configuration of genes as a permutation of the numbers 1 through  $n$ , where each number can be right-side-up or upside-down. In this model, one type of mutation corresponds to performing  $180^\circ$  reversals of consecutive subsequences of the permutation. The genetic distance between two configurations of genes is the minimum number of reversals needed to convert one permutation to the other. While there exist algorithms for computing genetic distance between two given permutations, our goal is to determine the maximum genetic distance between any permutation of 1 through  $n$  and the identity permutation. This maximum determines an upper bound for the evolutionary distance between any two gene sequences of the same length. In this presentation, we will discuss our current progress on the gene sorting problem. (Received September 26, 2017)