Nataša Jonoska* (jonoska@mail.usf.edu) and Masahico Saito (saito@usf.edu). Detecting complexities in a scrambled genome through spacial graphs.

DNA rearrangement is a process found on both developmental and evolutionary scale. The process itself and the molecular shape at the time of the rearrangement can be modeled through 4-regular spacial graphs. These graph models are used to illustrate the rearrangement processes in a well studied ciliate species *Oxytricha trifallax* where DNA recombination is observed on a massive scale. Our studies show that there are two general patterns, reoccurring genome-wide, that describe over 90% of the *Oxytricha*’s scrambled genes. Further, gene segments that recombine during DNA rearrangement processes may be organized on the chromosome in a variety of ways. They can overlap, interleave or one may be a subsegment of another. We use colored directed graphs to represent contigs containing rearranged segments where edges represent recombining segment organization. Using graph properties we associate a point in a higher dimensional Euclidean space to each graph such that cluster formations and analysis can be performed with various methods. The analysis shows some emerging graph structures indicating that segments of a single gene can interleave, or even contain, all of the segments from several other genes in between its segments. (Received January 29, 2019)