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*Detecting complexity and patterns in a scrambled genome.*

DNA recombination occurs at both evolutionary and developmental levels, and is often studied through model organisms such as ciliate species *Oxytricha* and *Stylonychia*. These species undergo massive genome rearrangements during their development of a somatic macronucleus from a zygotic micronucleus. 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 recombined 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 methods from topological data analysis. We find that there are specific star-like graph structures that describe most complex interleaving gene patterns. We also use word patterns to investigate genome-wide scrambled gene architectures that describe the precursor-product relationships. Our studies show that there are two general patterns, reoccurring genome wide, that describe over 90% of the *Oxytricha*'s scrambled genes. (Received September 26, 2017)