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Nataša Jonoska* (jonoska@mail.usf.edu), Department of Mathematics and Statistics, USF, 4202 E. Fowler Av. CMC 342, Tampa, FL 33620, and **Masahico Saito** (saito@usf.edu), Tampa, FL 33620. *DNA Recombination Through Spatial Graphs*.

Certain species of ciliates undergo massive DNA rearrangements during their development. taking these species as model organisms, we study DNA recombination, in particular, rearrangements guided by RNA templates. We use spacial rigid vertex graphs, possibly with end points. Single gene rearrangements can be described by double occurrence words (unsigned Gauss codes), also used in knot theory. Assembled DNA segments are modeled by certain types of paths in graphs called Hamiltonian polygonal paths, while the homologous recombination is modeled by vertex smoothings. We discuss properties of such graphs motivated by DNA assembly, such as the minimum number of polygonal paths, genus ranges, and rearrangement pathways. In particular we analyze these properties for recently sequenced thousands of scrambled genes in ciliate *Oxytricha*. (Received August 27, 2014)