

DEPARTMENT OF MATHEMATICS AND STATISTICS
MISSISSIPPI STATE UNIVERSITY

COLLOQUIUM

Gene Rearrangements through Assembly Graphs

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Thursday, February 12 at 3:30 pm

Allen 14

Abstract. The genome rearrangements, which have been observed in broad range of cells, play an important role in the heredity, the genetic diversity and with it, in the evolution in general. We propose molecular and combinatorial models that explain and formalize these biomolecular processes. Motivated by DNA rearrangements in certain species of ciliates, we investigate spatial graphs that consist of 4-valent rigid vertices, called assembly graphs. We introduce a notion of polygonal path in an assembly graph to model a single gene. The smoothing of the vertices in an assembly graph can be seen as a DNA homologous recombination. We study the simultaneous recombination events through subsets of vertices, called successful sets, whose simultaneous smoothing keep all of the gene segments on a single DNA molecule. Recent experimental results suggest that there are rearrangements that are likely to happen before others and furthermore there might be different pathways for unscrambling a gene. These results lead to a development of a mathematical model for recombination that uses formal words and circular strings.

Ms Angeleska is a candidate for a position in our department. There will be a reception for her in Allen 467 at 4:30 pm following her talk.