1145-VP-478   **Hays W. Whitlatch*** (`hww@math.sc.edu`) and **Joshua N. Cooper**. *Pressing Sequences in Genome Graphs.*

In the 1930's, two biologists, Dobzhansky and Sturtevant, introduced the idea that the degree of disorder between the genes in two genomes is an indicator of the evolutionary distance between two organisms. This has inspired extensive work in the fields of computational biology, bio-informatics and phylogenetics. In particular, researchers have pursued the question of how a common ancestral genome may have been transformed by evolutionary events into distinct, yet homologous, genomes. In mathematics, we often represent genomes as signed permutations, and evolutionary events are encoded as operations on signed permutations. Hannenhalli and Pevzner famously showed that sorting such sequences can be done in polynomial time and that they are essentially equivalent to a certain sequences of operations - "vertex pressing" - on bicolored graphs. In this talk we examine the combinatorial matrix algebra over GF(2) that arises from the theory of such sequences, providing a collection of equivalent conditions for their existence and showing how linear algebra, poset theory, and group theory can be used to study them. We also discuss enumeration, characterization, and recognition of uniquely pressable graphs (those with exactly one pressing sequence). (Received September 07, 2018)