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**Jennifer F. Vasquez\*** ([jennifer.vasquez@scranton.edu](mailto:jennifer.vasquez@scranton.edu)) and **Michael Allocca** ([mallocca@muhlenberg.edu](mailto:mallocca@muhlenberg.edu)). *Combinatorial Rearrangements of Bacterial Genomes via Circular Permutations*. Preliminary report.

In this talk, we will discuss how circular permutations can be used to help understand and model the evolution process of genomes. Specifically, we will discuss an analogue of the classical bubble sort algorithm that can be used to sort circular permutations and thus model rearrangement sequences between similar genomes. (Received September 16, 2014)