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Heather C Smith* (heather.smith@math.gatech.edu), 686 Cherry Street, Atlanta, GA 30332,
and **István Miklós**. *The Single Cut-or-Join Model for Genome Rearrangement*.

Represent a genome with an edge-labelled, directed graph having maximum total degree two. We explore a number of questions regarding genome rearrangement, a common mode of molecular evolution. In the single cut-or-join model, a genome can mutate in one of two ways at any given time: a cut divides a degree two vertex into two degree one vertices while a join merges two degree one vertices into one degree two vertex.

Fix a set of genomes, each having the same set of edge labels. The number of ways for one genome to mutate into another can be computed in polynomial time. The number of medians can also be computed in polynomial time. While single cut-or-join is, computationally, the simplest mathematical model for genome rearrangement, determining the number of most parsimonious median scenarios is #P-complete. We will discuss these and other complexity results that arose from an abstraction of this problem. (Received January 12, 2016)