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Heather Smith* (smithhc5@email.sc.edu) and **István Miklós**. *Sampling Single Cut-or-Join Scenario*.

Gene rearrangement is a common mode of molecular evolution. One basic mathematical model which prescribes a set of allowable moves for gene rearrangement is single cut-or-join. It is reasonable then to ask how the genes of one genome can be “rearranged” so that it evolves into another quickly.

To take this one step farther, fix a collection of genomes $\mathcal{G} = \{\mathcal{G}_1, \mathcal{G}_2, \dots, \mathcal{G}_n\}$. Label the leaves of a star with the genomes in \mathcal{G} . The middle of the star will be labelled with a genome \mathcal{G}_M which is “close” to \mathcal{G} . The number of rearrangements admitted by \mathcal{G}_M is the product of the number of ways one can evolve \mathcal{G}_M into each \mathcal{G}_i . Over all possible \mathcal{G}_M , we would like to uniformly sample from the admitted rearrangements.

Miklós, Kiss, and Tannier (2014) examined this same question, but for binary trees rather than stars. They found that no polynomial-time algorithm exists which will sample the rearrangements almost uniformly unless $\text{RP}=\text{NP}$. In this talk, I will present a complexity result for the analogous problem on the star. (Received September 13, 2014)