Abstract

The focus of this talk lies in gene rearrangement, a common mode of molecular evolution. A given collection of genes can be combined in a number of different ways, each of which is a genome. Comparing two genomes with the same gene content, it is reasonable to ask how to transform one into the other.

We explore the basic mathematical model, Double Cut-and-Join, which provides a set of rules for gene rearrangement. In particular, we are interested in the shortest sequences of transformations to move between two genomes. These shortest sequences are called scenarios. From a single scenario, certain biological hypotheses can be tested. While conclusions from a single scenario may be biased, the difficulty lies in the fact that there are too many to construct and test each one or even to list them all and choose one at random.

In "Approximating the number of Double Cut-and-Join scenarios," (2012) István Miklós constructs a rapidly mixing Markov chain to sample, with near uniformity, the scenarios between two fixed genomes. Following this work, I joined Miklós on a similar project involving the Single Cut-or-Join model and median genomes. This work is on-going.

In the talk, I will walk through the major ideas of the Double Cut-and-Join paper and then give a flavor of the work I am doing on the Single Cut-or-Join problem. I will not assume any prior knowledge of Markov chains or genome rearrangement.