



Colloquium

December 7, 4:05 p.m. (9th Period)
(in the Atrium)

Speaker: Dr. Miklos Bona

Title: Permutations and Genome Sorting

Abstract

Genomes can be modeled by permutations, the entries playing the role of the genes. We may be interested in knowing the evolutionary distance between two genomes. Translated into the language of permutations, this means to find the number of steps it takes to turn a permutation into another one.

For instance, given a permutation written in the one-line notation, such as 3147526, we can ask how many block transpositions (interchanges of two adjacent substrings) are needed to turn this permutation into the increasing one. This has turned out to be a surprisingly difficult problem, and a long-standing conjecture has recently been disproved in this area.

If, on the other hand, we are allowed to interchange any two blocks, then the best sorting algorithm is known. The average number of necessary block interchanges has recently been computed, using some very unexpected tools from remote-looking areas of mathematics.

In this talk, we will review the results and open problems of these two families of questions, and suggest another interesting open problem connected to them.

No previous knowledge of sorting algorithms is necessary.