

Time: Wednesday May 4th, 2011 9:00am
Location: Buchanan A203

**Tractability results for the Double-Cut-and-Join multichromosomal
median problem**

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Genomes can be modeled by sets of adjacencies between genomic markers. There are different ways of measuring the dissimilarity between pairs of genomes, in terms of genome rearrangements. The most widely used are distances and define a metric space. In the present work, we consider the Double-Cut-and-Join (DCJ) distance model. In a given dissimilarity model D , the median of three genomes G_1 , G_2 , and G_3 is a genome M which minimizes the sum $D(M, G_1) + D(M, G_2) + D(M, G_3)$. The problem of computing a DCJ median has been shown to be NP-hard.

For studying the genomes we consider a graph, called breakpoint graph, and we show that for breakpoint graphs of maximum degree 2, the optimal median for this dissimilarity can be computed in polynomial time (In general the breakpoint graph maximum degree is at most 3).