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*Topological analysis of chromosome conformation capture data.*

Chromosome conformation capture (CCC) data provides an unprecedented opportunity to analyze the three dimensional organization of genomes. The richness of the data, the apparently endless 3D trajectories that explain the data and their accuracy call for new mathematical methods. In this talk I will present new topological tools for analyzing three dimensional reconstructions of the genome and show that knotted trajectories are consistent with the CCC experimental data available. Since multiple 3D models of the genome fit the CCC data we suggest that CCC data are inconclusive about the topology of the genome.