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Lila Kari* (lila@uwaterloo.ca), School of Computer Science, University of Waterloo, Waterloo, ON N2L 3G1, Canada. *Was the Chimaera a reptile or mammal? Measuring (real or synthetic) species' relatedness using genome syntactic information.*

Phylogenetic trees have been the traditional means to represent evolutionary history and species classification, but there is a growing realization that some type of graphs or networks rather than trees are often needed, to take into account phenomena such as recombination, hybridization, horizontal gene transfer, and convergent evolution. We propose Molecular Distance Maps (MoDMaps), a novel alignment-free method for computing and displaying sequence and species' relatedness.

MoDMaps compute pairwise distances between Chaos Game Representations (CGR) of all input DNA sequences, and visualize the interrelationships thus obtained as an interactive map in three-dimensional Euclidean space: Each point on a map represents a DNA sequence, and the spatial proximity between any two points reflects the degree of structural similarity between the corresponding sequences.

MoDMaps is a general-purpose method that can compute and display the interrelationships within any set of sequences, biological, simulated, synthetic or computer-generated, sequences that closely related or completely unrelated, of the same length or of different lengths, several kilo-basepair-long or complete genomes. (Received July 08, 2017)