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Towards generating random mammalian genomes

Genome arrangements, a major mechanism of evolution, shuffle genetic material along chromosomes. Thus, a now standard approach models groups of close genomes as signed permutations. The correct data structure to study permutations in this context is the common interval tree. In this talk we will describe the process of considering tree parameters to refine the class of common interval trees (hence permutations) to those that represent mammalian genomes well. These refinements are particularly amenable to Boltzmann random generation and analytic enumerative techniques. Work in collaboration with Mathilde Bouvel, Cedric Chauve, Rosemary McCloskey, Cyril Nicaud and Carine Pivoteau.