

celebrating the end of the project Konstanz Women in Mathematics



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**Abstract.** The 3D organization of the genome plays an important role for gene regulation. Chromosome conformation capture techniques allow one to measure the number of contacts between genomic loci that are nearby in the 3D space. In this talk, we study the problem of reconstructing the 3D organization of the genome from whole genome contact frequencies in diploid organisms, i.e. organisms that contain two indistinguishable copies of each genomic locus. In particular, we study the identifiability of the 3D organization of the genome and optimization methods for reconstructing it. Since every possible 3D organization is a solution to a system of polynomial equations, the identifiability question reduces to a question in algebraic geometry. For reconstruction, we use semidefinite programming methods. This talk is based on joint work with Anastasiya Belyaeva, Lawrence Sun and Caroline Uhler.