

## **Chromosome communities in the human pangenome**

Experimental evidence indicates the presence of a common subfamily of alpha satellite DNA on the five acrocentric human chromosomes, compatible with an evolutionary process consistent with the recombination exchange of sequences between the nonhomologous. The latest T2T-CHM13 assembly confirms a high degree of similarity between the acrocentric chromosomes, nevertheless, no strong direct evidence of recombination has yet been found. Thanks to advances in sequencing technologies, new genome assemblies are produced at a high rate, enabling the discovery of unknown genomic variation. Pangenome models encode the mutual relationship between all the genomes represented. This allows us to avoid the reference-bias problem which affects genome-based approaches that relate sequences to a single reference model of the genome. Reference-free pangenomic methods and high-quality T2T assemblies open the door to the study of the most difficult regions of the human genome, finally allowing us to decrypt possible traces of recombination between non-homologous chromosomes.