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Haplotype resolved genomes

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STELLINGEN

behorende bij het proefschrift

Haplotype resolved genomes: Computational challenges and applications

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1. In order to extract biological insight from sequencing data the tools, specifically designed to process such data, are as important as the data itself (This thesis).

2. The directionality of single stranded DNA tracked using Strand-seq can be used to directly phase genomic regions where the directionality of inherited parental homologues differs (This thesis).

3. Genome-wide haplotype scaffolds provided by Strand-seq can serve to anchor various structural variants distributed around the genome into separate haplotypes (This thesis).

4. The concept of having a single reference genome for any given organism does not reflect the true architecture of individual genomes and will soon become obsolete (This thesis).

5. The future genomic studies will benefit from approaches that integrate the power of multiple sequencing techniques or protocols to gain more confidence in mapping of complex structural variants in haplotype resolved fashion (This thesis).

6. Long repetitive regions of the genome still represent the biggest hurdle that prevents routine *de novo* assembly of haplotype resolved genomes (This thesis).