

Seminar CMM-Bio

Title: New algorithmic ideas for the "de novo" assembly of human populations

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Abstract:

Decoding the genome of the entire human population is currently regarded as a feasible task due to the accelerated development of sequencing technologies. Two major approaches have been proposed to decode the genomic sequence of human individuals namely resequencing and de novo assembly. Currently, resequencing is the dominant approach and consists in sequencing genomic fragments (reads) and compares them to the human reference sequence. Contrary to the resequencing idea, the de novo assembly approach compute overlaps among the sequenced reads and build the genome sequence without previous information. The de novo assembly of human genomes, as opposed to comparing to a reference, promises a more accurate and comprehensive understanding of the human genetic variation. In this talk I will present de novo genome assembly using current sequencing technologies as well as WENGAN a new hybrid genome assembler that is able to produce accurate and contiguous genome assemblies using modest computational resources. WENGAN is an important step toward the democratization of the de novo assembly of human genomes.

Room: BP401; Beauchef 851, East Tower, 4th floor.