

Presentation title: Short read mapping

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Abstract

Sequence alignment is a well-studied problem with the Smith-Waterman algorithm being published in the mid 1980's and the BLAST and FASTA alignment programs both being published and released in 1990. Although newer and faster algorithms appeared periodically (such as BLAT in 2002) the field seemed largely settled until the advent of next-generation sequencing in 2007. The automated capillary sequencers in use prior to 2007 produced thousands of reads of average lengths approaching 1000 bases but the next-generation sequencing platforms were massively parallel short-read sequencers producing tens of millions of reads of approximately 25 bases. Effectively overnight, read lengths dropped by 1.5 logs and the number of reads increased by 4 logs and taken together, these changes rendered the majority of existing sequence aligners obsolete and triggered a renaissance of research into new sequence alignment methods. This session will detail some of the newer approaches to short-read sequence alignment with reference to a number of the new aligners including MAQ, BMA, Bowtie, mapreads and BFAST.