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Fast combinatorial computation of good seeds for genome alignment

Aligning entire genomes requires high sensitivity and speed. Whereas other methods trade one for the other, multiple spaced seeds increase both. They have many applications to homology search, alignment of next generation sequencing reads, oligonucleotide design, etc. Finding optimal seeds is a hard problem and even heuristic algorithms are exponential. We present the only polynomial-time algorithm, whose ideas stemmed from stringology. It is much faster and computes better seeds than all the other programs.