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場所: 臨海副都心センター別館8階コラボレーションコーナー

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タイトル

Next-generation genome alignment with LAST

概要

We present LAST, an open-source software package to replace BLAST.

BLAST and related sequence similarity tools are arguably the most successful of all bioinformatics applications. However they are not fully adequate for important tasks such as mammalian genome-genome alignment and tera-scale mapping of sequence reads.

While BLAST searchers are based on fixed length exact match "seeds", LAST employs the concept of adaptive length seeds. We show that adaptive seeds are robust to highly repetitive (e.g. mammalian) and biased composition (e.g. malaria) genomes. LAST also introduces improved methods for xeno-mapping, e.g. of mammoth reads to an elephant genome.

For the task of genome vs genome alignment, LAST is often 10-100 times faster than BLAST for similar levels of sensitivity. In fact, LAST is the first method that can sensitively compare giga-scale, repeat-rich sequences -- all previous methods either have low sensitivity e.g. DNA read mappers, or must heavily suppress repeats e.g. BLASTZ.