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Reference free, ultra fast valid statistical inference for sequencing data and biological sequences

Stanford scientists have created a statistical framework for interpreting next generation sequencing data which obviates the need for sequence alignment references in the most common and fundamental problems in genomics. The technology includes a unifying statistical formulation and proposes a solution to problems like finding genetic DNA nomads within and across species and identifying differential RNA expression or splicing that is near optimal in its computational efficiency with model-free valid statistical inference. The invention includes a reproducible computational workflow and the inventors have demonstrated the algorithm's ability to make biological discoveries missed by reference-based approaches.

Applications

- Diagnostic or research computational platform for identifying the following from next generation sequencing data without the need for reference sequences:
    - Genetic DNA nomads within and across species
    - Mobile DNA elements
    - Differential RNA expression or splicing

Advantages

- 100+ times faster than current methods
- More unbiased than current methods
- Reference-free

Patents

- Published Application: WO2023245068
- Published Application: 20260269008

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