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Dual phenotype and target discovery from statistical and machine learning

Stanford researchers have developed a novel technology called FLASH (Functional Assigning Sequence Homing) that predicts phenotypes directly from raw sequencing data, bypassing assembly and alignment, while revealing the biological features driving those predictions.

Genome-to-phenotype prediction is currently slow, complex, and incomplete. Existing methods depend on genome assembly, alignment, and highly customized statistical approaches. These workflows miss features absent from reference genomes, require organism-specific tailoring, and involve time-consuming computational and experimental steps. As a result, discovery is limited and translation to diagnostics or therapeutics is delayed.

Stanford researchers have developed a novel approach called FLASH (Functional Assigning Sequence Homing), which predicts phenotypes directly from raw sequencing data, completely bypassing assembly and alignment. Using the proprietary sequence feature extraction method (SPLASH), FLASH simultaneously provides accurate phenotype predictions and interpretable sequence features driving those predictions. It is fast, simple to run, and generalizable across the tree of life, achieving accuracy equal to or better than bespoke, resource-intensive studies.

Stage of Development
Prototype

Applications

- Diagnostics
- Drug discovery
- Clinical trials

Advantages

- Speed
- Discovery power
- Generality
- Interpretability

Innovators

- Julia Salzman
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