SnakeSplice: A seamless workflow for splice variant discovery and visualization in RNA-Seq data

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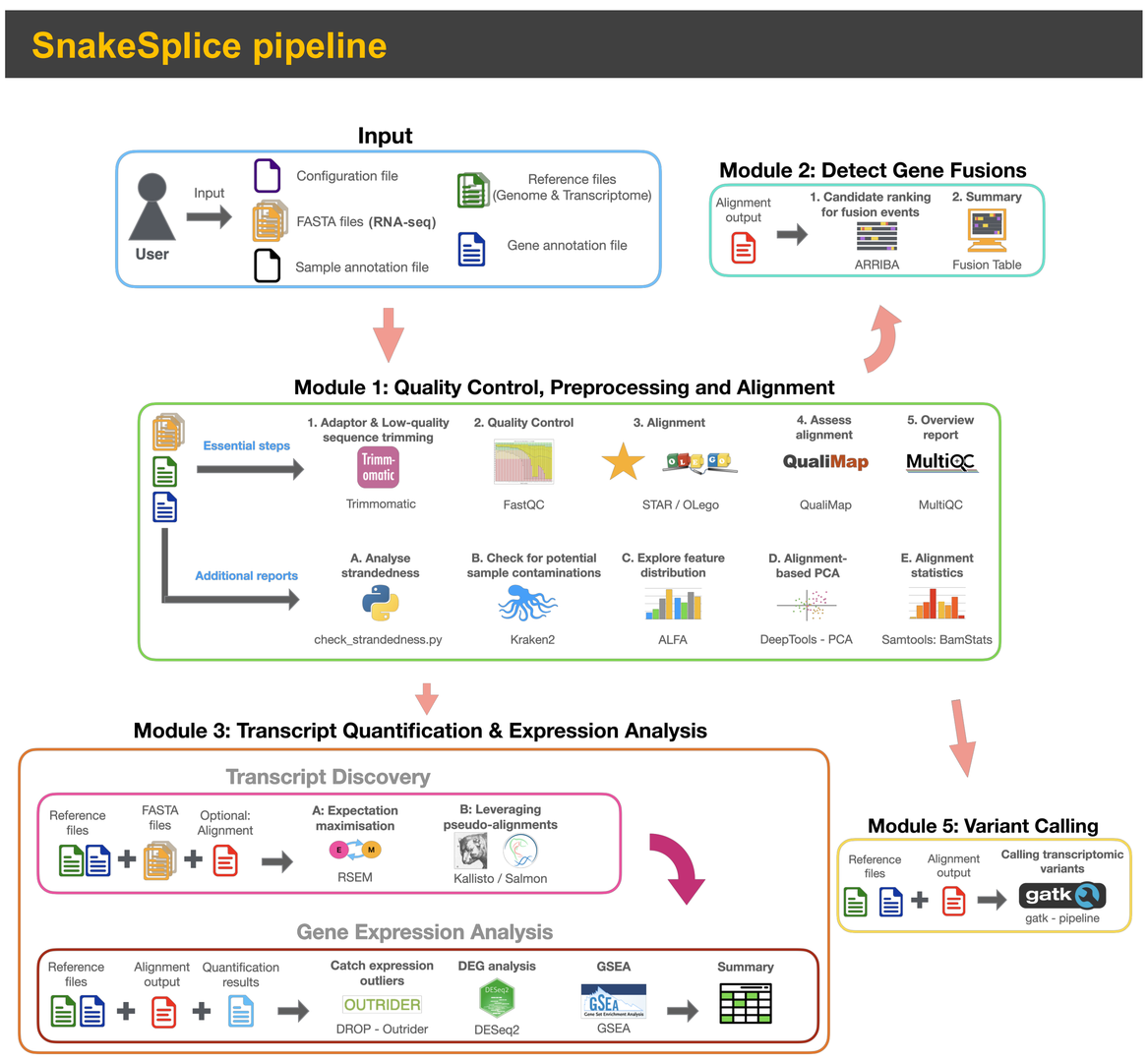
Abstract

Splicing defects are a major cause of human genetic disease, yet detecting them from RNA-Seq data remains a complex and fragmented process. SnakeSplice is a scalable, ***Snakemake***-based workflow that streamlines RNA-Seq analysis from quality control to splice variant detection. It combines robust preprocessing, diverse splicing analysis tools, and novel junction discovery in a single, scalable workflow optimized for high-performance computing. It enables efficient analysis of large RNA-Seq datasets and generates dynamic, interactive HTML reports that make results easy to interpret across research and clinical settings. By bridging deep analysis with intuitive visualization, SnakeSplice empowers transcriptome-driven disease gene discovery and variant prioritization.

SnakeSplice pipeline

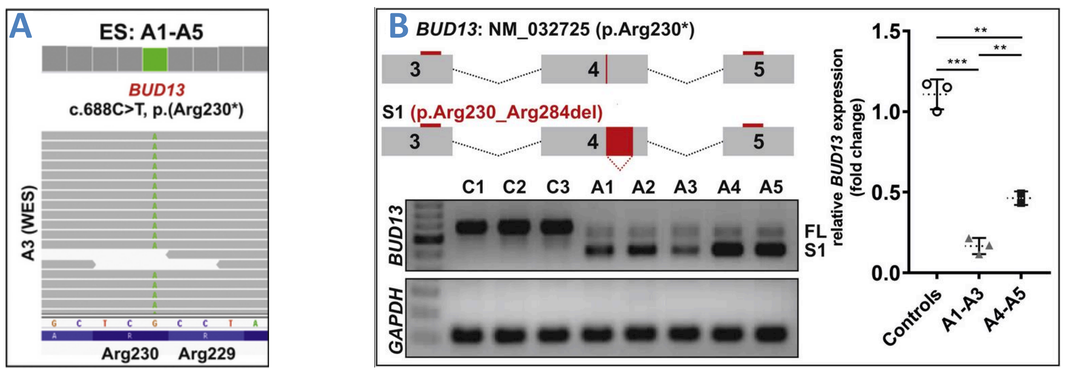


Final step: Generation of an interactive, shareable HTML report

HTML

Uncovering both known and novel splicing events with confidence

Application case: Alternative splicing of *BUD13*



A: A homozygous nonsense variant in *BUD13* (c.688C>T; p.Arg230*) was identified in five individuals presenting with syndromic lipodystrophy and variable disease severity*. **B:** The variant leads to aberrant splicing and production of a truncated transcript (S1), whose abundance correlates with patient survival.

C: HTML report displaying SnakeSplice's analysis of RNA-Seq data from individual A1-A5 highlights this splicing defect and its molecular signature.

* KORNAK, Uwe, et al. Alternative splicing of BUD13 determines the severity of a developmental disorder with lipodystrophy and progeroid features. Genetics in Medicine, 2022, 24. Jg., Nr. 9, S. 1927-1940.

SnakeSplice report: Alternative splicing of *BUD13*

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