DNASTAR’s Lasergene Genomics Suite for RNA-Seq Alignment and Analysis of Three Bos taurus Breeds

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Abstract

DNASTAR offers an integrated suite of software for assembling and analyzing sequence data from all major next-generation sequencing platforms supporting key workflows on both a desktop computer as well as the DNASTAR Cloud. Our RNA-Seq alignment and analysis workflow employs the DNASTAR SeqMan NGen, SeqMan Pro, and ArrayStar applications, all components of the Lasergene Genomics Suite. Here, next-gen RNA reads from Jersey, Holstein, and Cholistani cattle are aligned against the Bos taurus reference sequence in SeqMan NGen. Next, visualize the three samples and perform SNP analysis in SeqMan Pro. SeqMan Pro additionally offers the ability to look at the alignment of the reads to the reference and analyze what reads map to different isoforms or exons to explore differences in splice patterns. Finally, we can import the three experiments into ArrayStar for multi-sample analysis where advanced filtering options can be utilized for large-scale gene expression analysis. Innovative algorithms and highly interactive views within these three software applications offer a powerful, integrated, and user-friendly alignment and analysis workflow for RNA-Seq data.

Workflow

Align RNA-Seq data with reference genome → Visualize alignment and analyze SNPs → Multi-sample gene expression analysis

RNA-Seq Alignment

Align RNA-seq reads from Jersey, Holstein, and Cholistani cattle breeds against Bos taurus reference genome in SeqMan NGen.

Analyze

Utilize advanced filtering options for multi-sample gene expression analysis. Compare gene expression levels between breeds using the scatter plot, and compare sets of genes using Venn diagrams.

Visualize

Visualize the alignment of reads to the reference sequence for each strain, examine coverage, and explore differences in splice site patterns.

Discover SNPs using the interactive SNP report. Filter, sort, and evaluate variants.