Strand

Analyze Visualize Annotate Discover

strand NGS

About Strand NGS

Strand NGS-formerly known as Avadis NGS, is an integrated platform that provides analysis, management and visualization tools for next-generation sequencing data. It supports extensive workflows for alignment, RNA-Seq, DNA-Seq, ChIP-Seq, Methyl-Seq and small RNA-Seq data.

Strand NGS comes pre-packaged with comprehensive annotations for several standard organisms from various sources and enables you to create annotations for other organisms.

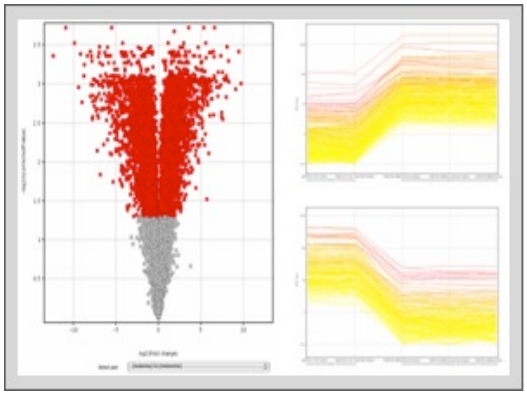
Various quality control plots and filtering steps ensure that any poor quality data is kept out of downstream analysis. Biological interpretation and discovery tools such as Gene Ontology enrichment, GSEA, NLP derived interaction network analysis, and significant pathways analysis enable taking the analysis all the way from reads to the end goal of the experiment.

Strand NGS is also available in an enterprise version for large-scale analysis with ability to share data in a controlled way. The enterprise version meets the needs of multi-member teams working on NGS data analysis and facilitates collaborative analysis through group and individual level permissions. It enables central storage of data and analysis results with support for scheduled and incremental backups. The Extensive API allows the use of third party applications and it is optimized for scalable and efficient NGS data analysis.

Alignment

Strand NGS provides support for aligning reads to a genome for small RNA reads, DNA reads (for ChIP-Seq and DNA-Seq applications), and RNA reads (spliced and unspliced reads) from sequencing platforms like Illumina, Ion Torrent, ABI, 454 (Roche), and Pac Bio. The tool is equipped with the Strand NGS aligner, a proprietary algorithm based on the Burrows Wheeler Transform. The significance of the Strand NGS alignment algorithm compared to other alignment algorithms is to handle both short reads and long reads, allows an arbitrary number of gaps and mismatches, and handles both single and paired end reads. Wherein, the other algorithms are often limited to either a specific class of reads or alignment characteristics.

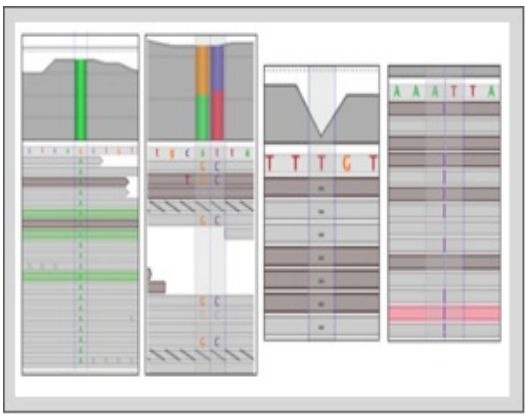
RNA-Seq



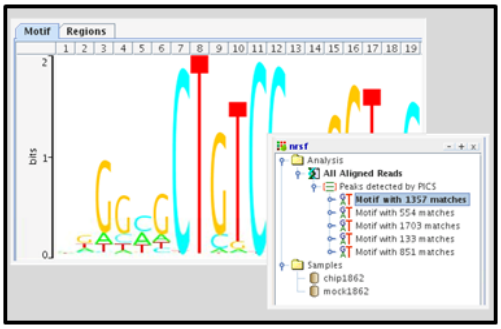
Strand NGS supports an extensive workflow for the analysis and visualization of RNA-Seq data, which includes standard differential expression analysis for different experimental conditions, as well as differential splicing analysis. It supports novel discovery including identifying novel genes and exons and novel splice junctions. It includes the ability to detect variants in the transcriptome, and the ability to detect gene fusion events.

DNA-Seq

In the DNA-Seq workflow, Strand NGS has analysis and visualization options for whole genome, whole exome or targeted resequencing experiments. The workflow includes the ability to detect variants (SNPs, MNPs and short InDels), annotate them with dbSNP, and identify the effect on transcripts of non-synonymous coding SNPs. Large structural variations, including large insertions, deletions, inversions, and translocations, can also be detected with paired-end or mate-paired data. In addition, copy number variations can be detected using tumor-normal pairs.



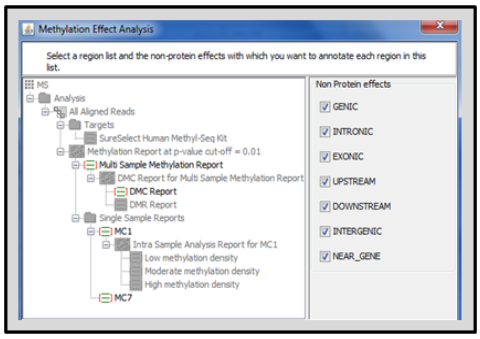
ChIP-Seq



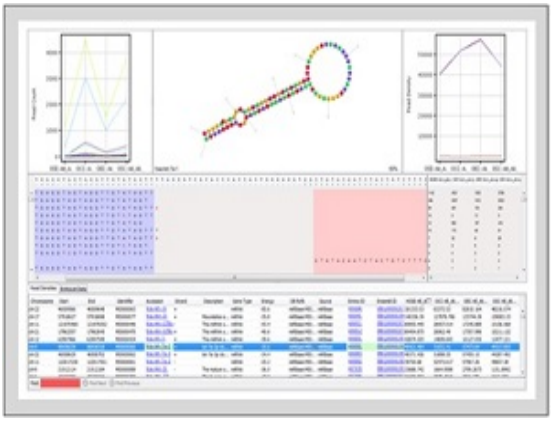
The ChIP Seq workflow provides the ability to identify transcription factor binding sites and histone modification sites using the PICS and MACS peak detection algorithms. It supports the ability to detect motifs in the peak regions using GADEM, and scan for known motifs in the genome or region of interest.

Methyl-Seq

Strand NGS supports analysis and visualization of bisulfite treated methyl-seq data – from whole genome or targeted enrichment experiments. The workflow provides steps to detect differentially methylated cytosines across samples/target regions and also study methylation effects at the genic level. Further downstream analysis such as GO, and pathway analysis can be performed on the set of affected genes



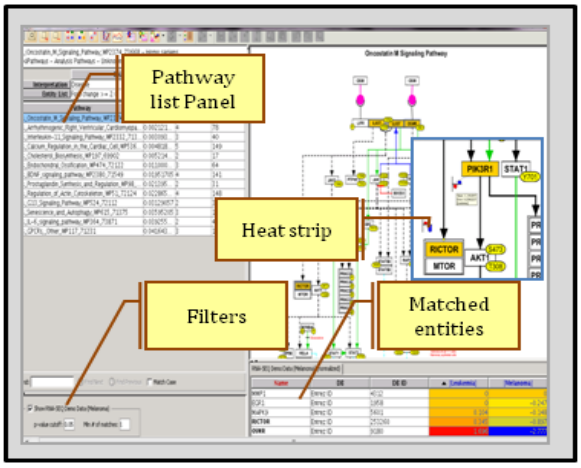
Small RNA-Seq



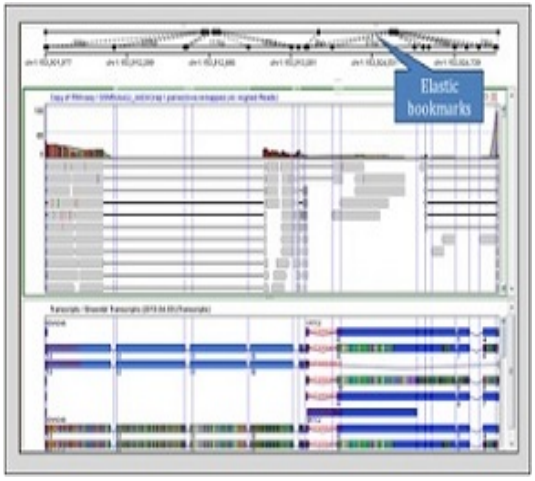
In case of small RNA Data, Strand NGS provides the ability to determine the expression levels of various small RNA species, supports detection of novel small RNA genes, and prediction of their type. It provides the ability to identify differentially expressed small RNA genes, and visualize the results in a small RNA-specific gene view. The mRNA targets of interesting small RNA genes can be identified from multiple target prediction databases.

Pathway Analysis

Strand NGS provides the capability to learn how genes interact with each other using information extracted from the literature as well as from canonical pathways. Strand NGS allows the user to ask and answer questions like: Which small molecules or other genes might interact with my list of genes? Interactions between genes and small molecules may provide insight into the functionality of the genes. The Pathway module supports pathway rendering from WikiPathways, BioCyc and BioPAX.

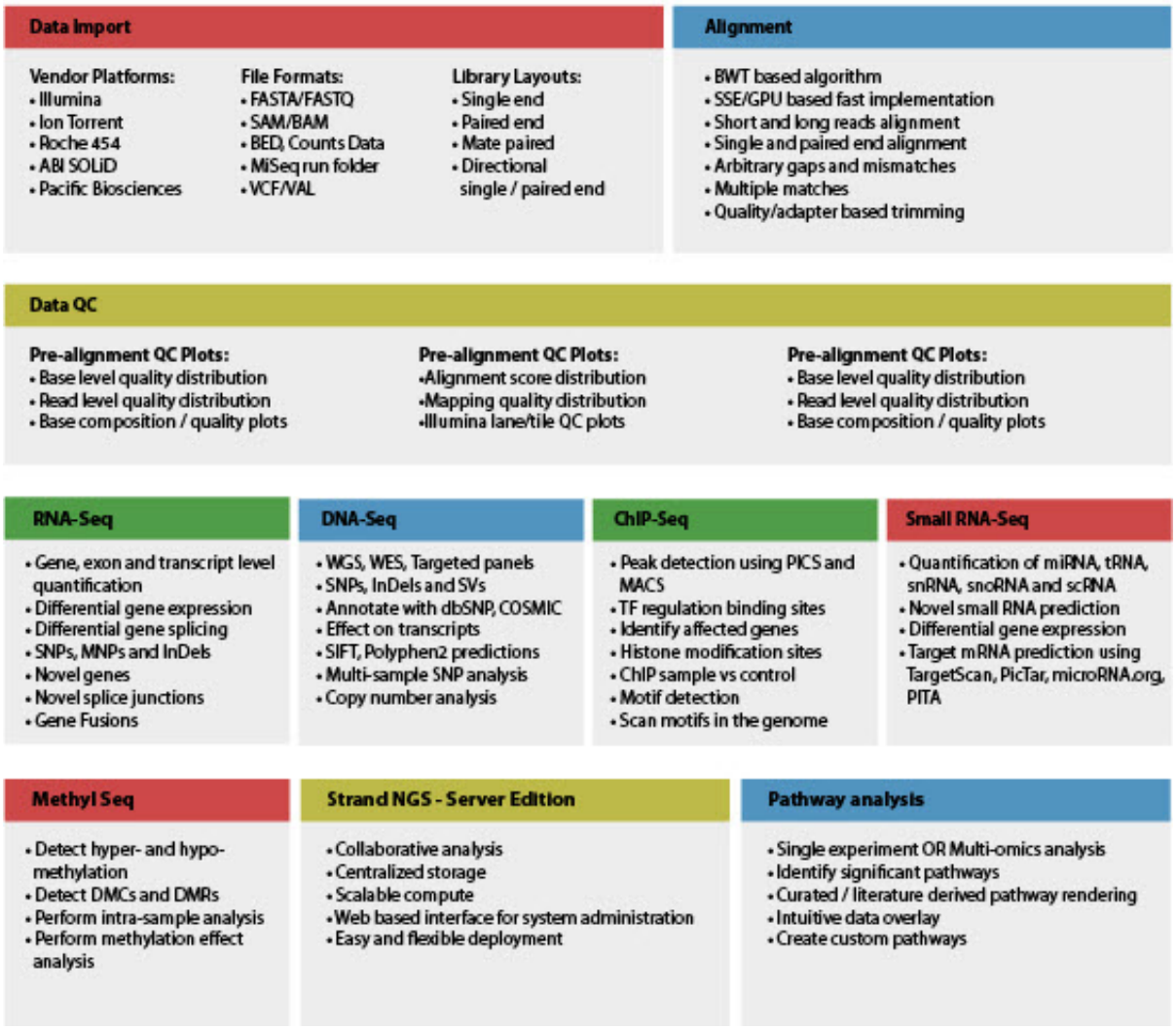


Genome Browser



Feature rich Genome Browser provides custom visualizations to provide an intuitive feel for analysis results. Annotation data, such as cytobands, genes, and transcripts, can be superimposed, as well as results from various analyses, such as peak regions, SNPs, and gene fusions. The elastic genome browser can display multiple genomic regions simultaneously. Each genomic region can be viewed at a different zoom level allowing for uninteresting regions to be collapsed and interesting regions to be expanded.

Product Overview



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