BIOVIA PIPELINE PILOT
NEXT GENERATION SEQUENCING COLLECTION

Datasheet

The BIOVIA Pipeline Pilot Next Generation Sequencing (NGS) Collection offers a comprehensive set of NGS data analysis pipelines for easy analysis and interpretation of the massive datasets generated by DNA sequencing platforms. The unparalleled power and flexibility of the NGS Collection allows you to accommodate current analysis needs, as well as adapt to novel applications and computational methods that are rapidly emerging in the NGS landscape.

BENEFITS OF BIOVIA PIPELINE PILOT NGS COLLECTION

- Accelerate creation, modification, and distribution of new analysis methods to suit your specific research needs

- Create new data processing pipelines using simple drag-and-drop construction and automate the execution of protocols
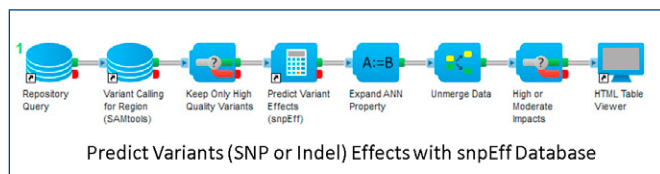

Predict Variants (SNP or Indel) Effects with snpEff Database

Figure 1: A typical NGS protocol that identifies SNPs using SAMtools, determines which ones are in coding regions and are non-synonymous, then displays the results in a web page.

- Gain valuable research insight from your NGS data by using widely applied and validated analysis methods for major types of NGS experiments

- Ensure quality of results based on NGS data by creating and using standard protocols throughout your research organization, avoiding duplication of effort and costly analysis mistakes

- Augment your NGS analysis with BIOVIA Pipeline Pilot's full breadth of advanced capabilities, including sequence analysis, gene expression, mass spec and proteomics, statistics, data modeling, reporting, cheminformatics, and text analytics

KEY CAPABILITIES

- Perform comprehensive NGS analyses with a wide selection of algorithms, including methods for de novo assembly, mapping to reference sequences, identifying polymorphisms and structural variants (SNPs, insertions and deletions, and copy number variations), measuring RNA expression levels (RNA-Seq), and identifying transcription factor binding sites (ChIP-Seq)
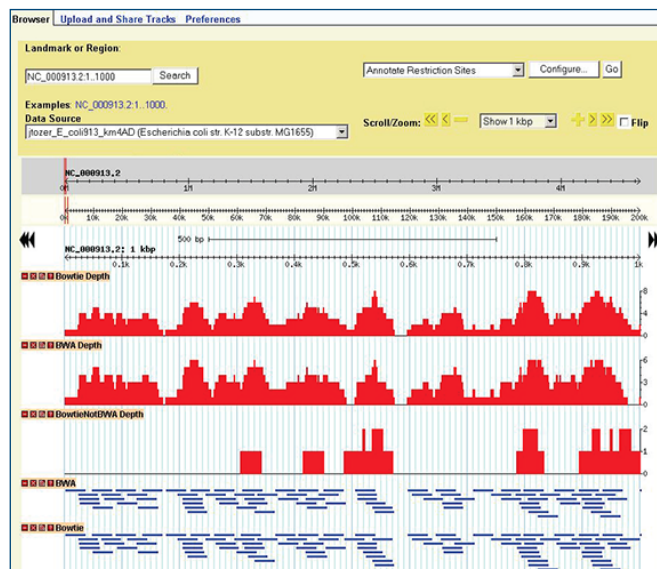

Figure 2: Use popular tools like GBrowse2 to visualize your NGS data.

- Integrate other command-line algorithms into your NGS pipelines using our industry-leading integration framework

- Efficiently manage data using powerful repository components that enable combining data across experiments, adding annotations, and performing region-based queries

- Visualize results with popular genomic browsers and visualization tools, and augment these with BIOVIA Pipeline Pilot's interactive tables and graphs

- Maximize compute performance by deploying on grids or clusters using BIOVIA Pipeline Pilot's own parallel processing management capabilities or those in popular grid management systems

WHO BENEFITS FROM THE NGS COLLECTION?

Genomics and Translational Research Scientists

- Create and duplicate standard processing pipelines for major types of NGS experiments with unmatched processing flexibility and ease of use

- Visualize results using popular visualization tools

- Save and share pipelines to be applied to new datasets and for easy collaboration across the organization
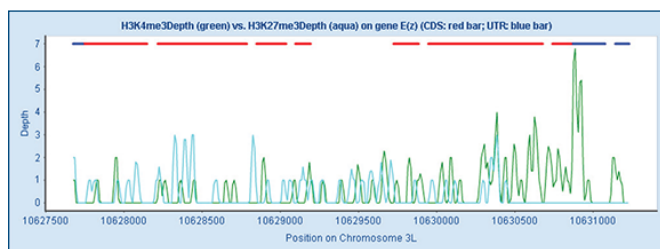

Figure 3: Comparison of transcription-factor binding patterns for 2 samples of ChIP data.

Bioinformatics and Research IT Experts

- Develop "best practice" processing pipelines to be applied to new datasets by other users

- Evaluate computational approach by comparing results from different algorithms

- Incorporate new algorithms and accommodate dynamic user requirements

- Integrate advanced computational methods for NGS into existing in-house applications via web services

Research Managers

- Consolidate and simplify complex and redundant applications into a single platform, making it far simpler to deploy new applications and less expensive to support existing needs

- With hundreds of public domain algorithms and dozens of commercial software applications, stay abreast of the NGS innovation curve with BIOVIA Pipeline Pilot platform, without sacrificing capability

LEARN MORE

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