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FlowJo is a wholly owned subsidiary of BD.

Unique Specifications of FlowJo™ November 2024

FlowJo™ is the leading analysis platform for flow cytometry data analysis.

Patent Information

- Reg. No. 4,731,268
- Registered May 5th, 2015
- Int. Cl.:9 For: Computer Software For Data Analysis, In Class 9 (U.S. CLS. 21,23,26,36 and 38).

Benefits

- Single solution for flow analysis. Compatible with all data files from all acquisition software packages and cytometers (including FCS2.0, FCS3.0, FCS3.1, LMD, MQD, and CSV).
- Models for advanced data analysis:
 - » Proliferation
 - » Cell Cycle
 - » Kinetics
 - » Population Comparison
- Novel combinatorial feature-sets available in one platform:
 - » Plugin architecture has fast updates with novel algorithms
 - » Plate Editor
 - » Compensation Calculation Wizard
 - » Derived Parameter tool
- Visualize and share with ease:
 - » Publication-quality customizable figures from the Layout Editor
 - » Intuitive drag-and-drop analysis in Workspace
 - » Add statistics and export using the Table Editor
 - » Color Mapping
 - » Customizable parameter scaling and transforms with the T button in the Graph Window



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Unique Specifications of SeqGeq™ November 2024

SeqGeq™ provides powerful tools for exploring next-generation sequencing (NGS) data with an intuitive drag-and-drop interface that makes it easy to get up to speed.

Patent Information

- Reg. No. 5,318,597
- Registered Oct. 24, 2017
- Int. Cl.: 9,41,42 Class 9: Computer software for analyzing single cell gene sequencing and gene expression data.

Benefits

- SeqGeq™ v1.4.0+ analyzes data from bulk RNA-sequencing (RNA-seq) and single-cell RNA-sequencing (scRNA-seq) data matrices.
- Intuitive drag-and-drop analysis in Workspace
- Add statistics to subpopulations for any features of interest
- Single solution for all NGS data import and analysis. Compatible with data files from most sequencing pipelines (including CSV, TSV, TXT, TAB, MTX, H5, and HDF5)
- A host of platforms are available within the FlowJo-like workspace (graphic user interface) for:
 - » Quality Control
 - » Dimensionality Reduction
 - » Differential Expression Analysis
 - » Geneset Enrichment Analysis
- Advanced analysis functionality:
 - » Multi-omics support built right into the intuitive user interface
 - » Geneset export and import functionality
 - » Add statistics to subpopulations for any features of interest
 - » Plugin architecture allows for fast updates of bleeding edge machine learning and other computational biology techniques
- Visualize and share with ease:
 - » Publication-quality customizable figures exportable directly from the Layout Editor
 - » Intuitive drag-and-drop analysis in Workspace
 - » Share your entire analysis with one easy to create archived Workspace file
 - » Heatmap gene expression profiles for features and cells of interest
 - » Color Map features within dot plots
 - » Create powerful overlays to illustrate clustering relationships