Flexible Enterprise Solutions for Genomic Data Analysis

Partek® Flow® Enterprise Edition provides organizations with diverse needs and geographic locations the tools needed to store, manage, and collaboratively analyze large genomic data sets. Whether a cloud, cluster, or server deployment, it provides the elastic computing resources and flexibility to scale with ever-changing needs.

Partek® Flow®

Partek Flow Enterprise Edition Overview

Collaboration
Analysis tools and data accessible on a central server makes data management and collaboration easy and efficient. Simply grant users and groups the necessary permissions and enable your scientific team to work together from virtually anywhere.

Security
Security is a top priority at Partek. We have strong data access controls, authentication, data transit, auditing, application, infrastructure, and data integrity security protocols in place to protect your data.

Infrastructure
Partek Flow Enterprise Edition can be deployed on a desktop, cluster or private/public cloud and accessed by any connected device via a web browser. All major operating systems are supported (Linux and Macintosh).

Scalability
To support many users and compute-intensive work Partek Flow can automatically allocate and deallocate computing resources as needed. This elastic scaling makes processing more efficient, thereby reducing the time to complete analyses and your computing costs.

Pipelines and Toolkits
Partek Flow provides single cell, RNA-Seq, DNA-Seq, ChIP-Seq, metegenomics, and microarray toolkits. Install them all or just what you need to support the needs of your research teams. You can download prebuilt pipelines or easily build and share your own custom analysis pipelines.

Visualization
Partek Flow delivers many rich and interactive visualizations including chromosome views, dot plots, heat maps, scatterplots, principal component analysis, sample-to-sample correlation plots, volcano plots, Venn diagrams, Sankey plots, and more.

Reproducibility
All analysis performed in Partek Flow produces an audit trail that can be reviewed, downloaded, and shared at any point. This allows for transparency, verification, and replication of results by anyone.

User Added Tasks
Administrators can add their own executables and scripts to Partek Flow Enterprise Edition. Users can then run them using the graphical user interface and include them as part of analysis pipelines.

Partek Flow Enterprise Edition Tools

User, Data, and Process Management
- Sample metadata, data management, and import
- Controlled vocabulary
- Import/Export projects
- Computing resource and user utilization reports
- Flexible sample and feature filtering
- Job scheduling and prioritization
- Per-user and per-group disk quotas
- Share projects with selected individuals or groups
- Live system usage dashboard

Statistics
- Wide variety of normalization and scaling options (RPKM, TMM, Quantile Normalization)
- Multi-factor and mixed model Analysis of Variance (ANOVA, GLM)
- Multi-factor Poisson test
- Multi-factor Negative Binomial test
- Normal or Lognormal test with shrinkage (Limma)
- Linear contrasts
- Akaike information criterion (AIC)
- Bayesian information criterion (BIC)
- FDR Stepup
- Storey q-value
- F and Wald p-values
- Hierarchical Clustering
- Dimensional reduction (PCA, t-SNE)
- Non-parametric tests (Kruskal-Wallis/Dunn's tests)
- DESeq2
- Batch effect removal

Input File Types Supported
- NGS (SAM, BAM, FASTA, FASTQ, BCL, UBAM, SRA, VCF)
- Microarray (Affymetrix CEL, Illumina IDAT)
- Count matrix (TXT)

Visualizations
- Chromosome viewer
- Dot plot
- Principal Components Analysis (PCA)
- t-SNE plots
- Hierarchical clustering, heat maps
- Volcano plot
- Sample-to-sample correlation scatterplots
- Venn diagram
- Sankey plot
- Bar chart
- Pie chart
- Histogram
- Violin plots

RNA-Seq
- RNA-Specific aligners (e.g. STAR, Bowtie/Tophat)
- Quantify aligned reads to gene and transcript annotations of your choice
- Fusion detection
- Detect differential expression
- Find enriched gene sets, biological themes, GO terms, pathways

Noncoding RNA
- Flexible aligner options (e.g. Bowtie, STAR)
- Quantify to any noncoding RNA annotation of your choice
- Detect differential expression

Whole Genome / Whole Exome Sequencing (WGS/WES)
- Variant callers (e.g. LoFreq, FreeBayes, SAMtools, Strelka, GATK4 HaplotypeCaller)
- Copy number variation caller (CNVKit)
- Variant annotation (dbSNP, 1000 genomes)
- Functional annotation (SnpEff, VEP)
- Variant validation, recalibration, and filtering
- Cohort summarization

ChIP-Seq
- MACS2 peak caller
- Visualize reads and peaks in chromosome view
- Annotate with genes/transcripts
- Transcription start site (TSS) plot
- Detect known motifs
- Discover novel motifs
- Filter peaks

Metagenomics
- Classify whole genome shotgun data (Kraken)
- Hierarchical Pie Chart of species
- Alpha & Beta diversity reports

Single Cell
- Parse multiplexed data with unique molecular identifiers (UMIs) and barcodes
- Cell quality QA/QC
- Cluster cells (K-means, graph-based clustering, t-SNE, PCA)
- Identify biomarkers
- Flexible filtering

Scalability
- Elastic computing allocates more workers when needed and frees them up when not needed

Customization
- Users can add 3rd party or own custom scripts and programs
- Embed Partek Flow into existing pipelines via API
- Define user roles/privileges

Auditing
- Audit trail tracks exactly what was done to data at each step
- Including who made the change and when
- Exact parameters of each step
- Computing time used at each step
- Disk usage at each step

Security
- Access logs
- Data access controls
- Isolated data per user/group
- Authentication
- HTTPS
- Configurable login and password controls
- LDAP integration

Miscellaneous NGS Tools
- QA/QC reports (both pre and post alignment)
- Trim reads based on quality score
- Demultiplex reads
- Trim adapters
- Deduplicate UMIs
- Wide range of aligners (BWA, STAR, Bowtie/2, TopHat/2, GSNAP, Isaac2, TMAP)

Partek®
turning data into discovery®

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