Release Notes Archive - Partek Flow 10

Includes performance optimizations and fixes for improved speed and usability of Partek Flow software. To upgrade to this version, please follow the steps outlined in our Installation Guide.

10.0.23.0720

- Added option to report down regulated genes (negative biomarkers) for each cluster in compute biomarkers
- Added option to specify input data is linear or log scale
- Added split sample option in single cell QA/QC task
- Improvement on memory usage for variant validation task
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0720.334

10.0.23.0531

- Improved 2D scatterplot labeling up to 2000 selected points
- Added option for deselected point color to be the same as selected point color
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0531.320

10.0.23.0519

- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0519.317

10.0.23.0425

- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0425.313

10.0.23.0414

- Added FDR adjusted p-value in the enrichment report
- Added a function to remove empty folders on the settings menu
- Improved the bar chart to display text attributes
- Improved single cell count matrix import to allow user to filter cells with low umi counts
- Simplified the wording on the settings menu
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0414.312

10.0.23.0326

- Improved gene set enrichment analysis by adding feature identifier selector
- Improved data import to set the most recently opened directory as the default directory
- Upgraded Cutadapt to version 4.2
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0326.310

10.0.23.0312

- Added links to the number of genes to download gene list in biological interpretation report
- Added a filter task on differential analysis report data node to extend the flexibility
- Improved GSEA task to perform on attributes with more than 2 groups
- Upgraded Space Ranger to 2.0.1
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0312.310

10.0.23.0214

- Added rich factor in enrichment analysis report

- Added function to download gene lists in biological interpretation reports
- Improved Violin plot to have different Max on Y-axis in different groups
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0214.305

10.0.23.0131

- Added an optional t-statistic value output to the ANOVA report
- Added support for the Parse Bio SPLiT-Seq count matrix data format
- Allowed the Annotate feature task to be performed on count matrix data nodes
- Added Survival analysis task options
- Added function allowing the selection of cells based on a score from a list of genes
- Added motif detection function to the gene list report in the RNA-Seq assay
- Added primary ID option to allow selection when there are two IDs in the file to import
- Added support for single sign-on
- Improved the transfer file function to not observe the time out setting
- Refined the import for single cell sparse matrix files (3 files per sample) to support multiple samples at one time
- Improved the Correlation analysis task to allow the user to search for specific features to perform correlation with all the features
- Optimized the default Volcano plot display
- Changed the default settings on a 2D scatterplot to fill the view
- Upgraded SCTransform v2
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0131.304

10.0.23.0124

- Improved the I/O performance on the coverage report task
- Minor bug fixes

Latest docker image: registry.partek.com/rtw:23.0124.298

10.0.22.1204

- Added an importer for Parse Biosciences single cell count sparse matrix file format
- Allowed the use of a feature list summary score to select cells, the score can be published to project level from the data viewer
- Switched the default feature scaling setting to standardize for a bubble map
- Changed the default settings to compute biomarkers for both graph-based clustering and K-means clustering dialogs
- Allowed the export of data as matrix from the heatmap viewer
- Minor bug fixes

Latest Docker image: registry.partek.com/rtw:22.1204.290

10.0.22.1111

- Bug fixes

10.0.22.1107

- Upgraded peak detection method to MACS 3.0
- Added leading edge genes generation in GSEA report details
- Improved speed and performance on UI
- Minor bug fixes

10.0.22.1023

- Improved the KEGG pathway image update with version number
- Added a function to allow any project level attributes as sample ID when creating project from a data node
- Added stretch to view point option on axes configuration for more efficient space in 2D plots
- Minor bug fixes

10.0.22.1003

- Added annotate features task on single cell count data node
- Added round normalization method
- Added filter task on gene set enrichment report data node

- Added LIMMA-trend and LIMMA VOOM method options in differential analysis
- Minor bug fixes

10.0.22.0828

- Improved the Data viewer interface to make it more user friendly and more flexible, added how-to video link in each dialog
- Improved the speed and memory efficiency for the Seurat3 integration task
- Improved TF-IDF normalization memory usage
- Improved import of scATAC count matrix to be more memory efficient
- Changed the classify tool by removing the data node selection step when using apply classifications
- Changed the computation of median, Q1, Q3 on the Box & Whisker plot using a different method to match the descriptive statistics method
- Changed the default promoter regions to be up/down 1000bp from TSS for annotate regions
- Added function to save video for 3D scatterplot rotation
- Added import for VDJ annotation combined with gene expression data generated from the Cell Ranger pipeline
- Added support for Space Ranger 2.0 outputs
- Added a function to compute descriptive statistics on observations to use a list of features
- Added Spot clean task on Space ranger output data node
- Combined differential analysis methods into one task on the menu
- Minor bug fixes

10.0.22.0727

- Added a task to merge adjacent regions
- Added a function to remove data published in data repository
- Improved scATAC data import to be more efficient on RAM usage
- Allow user to select whether to display shrinkage plot on GSA nd hurdle model report in advanced option
- Changed the default graph-based clustering resolution to 0.5
- Reorganized the task menu, added Statistics section
- Minor bug fixes

10.0.22.0703

- Upgrade MACS to version 3.0.0a7
- Added a function to allow user to perform motif detection on quantify region report
- Added flexibility to allow user to define TSS, TTS regions when perform peak annotation
- Renamed the default quantify region task report data node as region counts
- Added compare region tasks to allow user to compare regions among samples
- Added promoter sum task for scATAC data analysis
- Added down scale alignment tasks on aligned data node
- Allow user to run gene set enrichment task on filtered gene count matrix data node
- Merged Gene set enrichment and pathway enrichment tasks into one to reduce confusion
- Changed the graph-based clustering default resolution setting from 1 to 0.5
- Minor bug fixes

10.0.22.0524

- Added a function to allow user to create annotation model from the reference
- Added a function to allow user to create new annotation model by merging to existing annotation models
- Improved the user interface on differential analysis tasks
- Minor bug fixes

10.0.22.0428

- Fixed the refresh delay issue on library file management dialog

10.0.22.0424

- Added sorting observations based numeric attribute function on heatmap
- Added a function to allow user to create a new assembly reference by providing sequence
- Added a function to allow user to create a new assembly reference by merging two existing assembly
- Added case insensitive option when filter features based on a list
- Improved the interface of generating heatmap and bubble map
- Improved list creating to handle leading and trailing white space in the list
- Added function to allow user access read only directory
- Minor bug fixes

10.0.22.0410

- Improved feature on generating filtered node operation on differential analysis report page, the page will not redirect automatically after clicking the button
- Changed some import task labels

- Minor bug fixes

10.0.22.0330

- Changed the order of Annotation models section in library file management page, Genomics library files tab
- Removed selecting files from local computer option, instead files need to be transferred to server to be used in tasks
- Improved the speed of UI
- Minor bug fixes

10.0.22.0321

- Bug fix on enrichment report visualization
- Bug fix on Seurat3 integration task excluding feature IDs with hyphen

10.0.22.0313

- Added option to allow features to be sorted based on a feature list in heatmap
- Allow to invoke WNN on SVD data node
- Minor bug fixes

10.0.22.0228

- Improved on handling big genome alignment like wheat
- Added classification summary report on Garnett classify cell type task
- Allow to sort heatmap samples/cells using numeric attributes
- Improved the speed on sctransform task
- Minor bug fixes

10.0.22.0213

- Added TF_IDF normalization task
- Added singular value decomposition task
- Improved the Seurat3 integration computation on normalized with SCTransformed data by adding PrepSCTIntegration function
- Changed the Seurat object importer, added convert Seurat to matrix task
- Removed Shrimp aligner support
- Minor bug fixes

10.0.22.0130

- Improved Flow homepage layout
- Improved the pipeline management page
- Minor bug fixes

10.0.22.0121

- Added sorting observations based numeric attribute function on heatmap
- Added gene labeling option in heatmap when use Ensembl annotation
- Added CellRanger ATAC wrapper
- Improved filter observation tasks to easily choose multiple subgroups from the same attribute
- Improved feature list creation after features selected on data viewer
- Minor bug fixes

10.0.22.0102

- Added GSEA task for biological interpretation
- Extend Cell ranger task to support custom assemblies
- Improved Space ranger interface to be more intuitive
- Upgraded GATK to version 4.2
- Removed standardization option in t-SNE dialog
- Added learning rate parameter in t-SNE advanced dialog
- Added function to allow to specify multiple levels in each comparison panel in non-parametric ANOVA and Welch's ANOVA task
- Minor bug fixes

10.0.21.1116

- Sped up h5 file import
- Sped up transfer file process
- Added a new peak filter task

- Added log transformation on Scran deconvolution output data
- Added option to use gene name or gene ID to filter features based on gene list task
- Added region length information on differential analysis report on regions
- Improved creating factorial comparisons on differential analysis dialog
- Added feature list creation function in data viewer on selected features
- Minor bug fixes

10.0.21.1026

- Sped up sparse matrix import
- Added poscounts normalization method for DESeq2
- Added support on .gaf file as gene set library file format
- Minor bug fixes

10.0.21.1014

- Added feature to allow search a list of gene names in volcano plot
- Added S1 and SUM_MS values to INFO column in Pindel vcf files
- Added Space ranger task in Flow for hg38, mm10 and hg38-mm10 assembly
- Improved UMAP speed
- Improved task graph drawing speed
- Improved sra file importer
- Improved h5 importer to handle both 32bit and 64bit values
- Minor bug fixes

10.0.21.0929

- Added Salmon algorithm to compute gene count from fastq files
- Added Garnett cell type classification function
- Added support on import and export of h5ad file format on scRNA-seq project
- Added weighted nearest neighbor algorithm for multimodal single cell datasets analysis
- Improved speed on user interface interaction
- Minor bug fixes

10.0.21.0912

- Improved PCA dialog when there is only one sample in the project, no need to select split sample option
- Improved cell number and cell percentage descriptive statistics computation to give more options
- Improved cell ranger functions to handle CITE-seq data
- Improved post-alignment QA/QC speed
- Improved heatmap export to allow entire data after zoom in
- Changed TPM normalization method, remove scaling across sample step
- Added 10X CellRager HDF5 file format option when download single cell data matrix data node
- Added visualization on enrichment report
- Minor bug fixes

10.0.21.0816

- Added a function to allow manually drag&drop to change the order of features/observations on heatmap
- Minor bug fixes

10.0.21.0801

- Improvement Kraken on handling samples with multiple files
- Added report transcript assemblers option in HISAT2
- Added download option on multiple fastq/bam files associated with one sample to allow download one merged file fastq/bam per sample
- Minor bug fixes

10.0.21.0723

- Updated bioproject download link based on the changes on ENA website
- Minor bug fixes

10.0.21.0718

- Added function to display both Ensembl gene ID and gene name in differential analysis report
- Improvement on interface response
- Minor bug fixes

10.0.21.0707

- Added Flow version in each task details
- Allow to change group order by drag and drop directly on the axis on scatter plot
- Added re-order mode in heatmap to allow to drag and drop observation/feature labels to swap
- Added function to display both Ensembl gene ID and gene name in data viewer table
- Added support on .tsv file format as cell annotation file
- Added more descriptive statistics to filter cell task report
- Output STAR fusion in vcf format
- Improved speed on interface and visualization
- Minor bug fixes

10.0.21.0621

- Improve 10X Genomics Visium image annotation to handle multiple samples
- Added 10X Genomics Cellranger to handle scRNA-seq data from 10X Genomics on human, mouse and human-mouse assemblies
- Improve PCA computation on memory usage on large datasets
- Added more functions on metagenomics data analysis
- Added STAR fusion function
- Minor bug fixes

10.0.21.0602

- Added a sample level box plot on the sctransform task report
- Added Cell Ranger to process 10X Genomics fastq files and generate count matrix data on hg38, mm10 and hg38-mm10 references
- Improved library file deletion function – list all projects that using the file
- Improved hierarchical clustering visualization – allow user to manually adjust dendrogram size
- Removed log transformation section in PCA and hierarchical clustering dialogs
- Added more options in the STAR configuration dialog
- STAR aligner is upgraded to 2.7.8a
- Added support on Seurat4 objects import (requires R version 4 and above)
- Minor bug fixes

10.0.21.0509

- Added a feature of allowing manually type in a list of features to color in scatterplot
- Added annotate Visium task to add tissue position and image information on 10X Genomics Visium data
- Added compute biomarker as an independent task in addition to the subtask in any classification task
- Improved the Seurat3 integration task
- Enable both Monocle 2 and Monocle 3 in trajectory analysis
- Added download options for mm39 assembly library files
- Minor bug fixes

10.0.21.0411

- Added number of genes for up and down regulation separately in volcano plot
- Annotate Visium task to add tissue position and image information on 10X Genomics Visium data
- Minor bug fixes

10.0.21.0328

- Added HTSeq quantification method to Microarray data analysis
- Added BWA method on ERCC in pre-alignment QA/QC
- Added project statistics information on homepage
- Improvement Monocle 3 (trajectory analysis) to automatically detect the input data is in log scale or not
- Minor bug fixes

10.0.21.0302

- Upgrade trajectory analysis using monocle 3 algorithm
- Added bubble map shortcut in data viewer
- Added function to specify gene list in filter feature dialog without creating a list beforehand
- Added more options in usage report
- Changed the graph-based clustering nearest neighbor type default from KNN to NN-Descent
- Improvement on interface
- Minor bug fixes

10.0.21.0201

- Added publish cell attributes to project task

- Scatterplot selection labeling is turned off by default
- Minor bug fixes

10.0.21.0117

- Added more options to generate usage report
- Added more configuration options in BWA-MEM
- Added download to the user management table
- Minor bug fixes

10.0.20.1231

- Added heatmap plot type in data viewer, hierarchical cluster report is in data viewer
- Added pie chart on visualizing categorical sample/cell annotation
- Added Harmony algorithm for data transformation
- Added Scran normalization method
- Added Seurat 3 integration task
- Added more options on descriptive statistics task
- Added filtering capability on task management page
- Added ability to perform biological interpretation on miRNA data
- Added similarity matrix task on bulk RNA count matrix data node
- Added correlation section on task menu and move sample correction, correlation analysis under this menu
- Added function to import count matrix to allow import multiple files
- Added function to use sample name to split attribute on single cell data node
- Improved text importer to handle text file generated from R which has the first column shifted
- Improved speed on data viewer
- Improved volcano plot display
- Improved filter feature task dialog speed and added filter based on feature meta data
- Changed the default calculation on features in descriptive statistics dialog
- Changed single cell QA/QC plot to display 4 plots by default
- Changed DESeq2 only normalization report not using per million scale
- Changed the per million normalization using the sum of input count instead of aligned read counts
- Removed the log transformation in tSNE, UMAP and graph-base clustering dialog to reduce confusion
- Minor bug fixes