Release Notes

To install or upgrade to the latest version of Partek Genomics Suite software, follow the directions outlined in the Installation Guide.

PGS7.21.1119

Bug fixes:

- Support MacOS 12
- Minor bug fixes

PGS7.20.0831

Bug fixes:

- Minor bug fixes

PGS7.19.1125

Bug fixes:

- Improved memory efficiency
- Minor bug fixes

PGS7.18.0723

General Improvement:

- Microarray methylation workflow to make it more intuitive

Bug fixes:

- Minor bug fixes

PGS7.18.0518

General Improvement:

- Implemented DMRCate algorithm for differential methylated regions detection
- Added false discovery rate report in html format
- Add options to delete rows contains missing value only during text import

Bug fixes:

- Minor bug fixes

PGS7.18.0402

General Improvement:

- Sped up multidimensional scaling function
- Added chi-square analysis for categorical data
- Improved Fisher exact test on integer columns with two distinct values
- Improved handling beta value as 0 or 1 during M value transformation, instead of output "?", we set the value as 1e-6 or 9e-6 by default

Bug fixes:

- Fixed GEO downloader issue
- Fixed scatterplot set cutoff line and regression line button issue
- Fixed a dot plot close issue
- Bug fixes on OSX

PGS7.18.0130

General Improvement:

- Improved the methylation workflow – add region methylation analysis workflow
- Added correlation analysis across two spreadsheets when they have the same set of samples

Bug fixes:

- Bug fixes on OSX

PGS7.17.1222

General Improvement:

- Improved the ANOVA contrast dialog; added the option to output difference between the two groups instead of fold change
- Added new options on the Illumina methylation array importer to allow filtering of probes based on detection p-value and XY chromosomes
- Improved Illumina methylation array analysis workflow to compute differential methylation sites based on M value and report the difference of M and beta values

Bug fixes:

- Fix Tk event crashes on OSX
- Other minor bug fixes

PGS7.17.1103

General Improvement:

- Sped up genome view with large annotation files
- Added option to specify output file name on task dialogs
- Added option to save merged spreadsheet to a new spreadsheet

Bug fixes:

- Fixed a hierarchical clustering viewer bug on Mac version
- Other minor bug fixes

PGS7.17.1018

General Improvement:

- Partek spreadsheet can only be saved as binary format
- Partek spreadsheet can be exported as text format. The name of the exported spreadsheet will not be changed
- "Import Text File" will not change the input text file, the imported file will be saved as user-defined name in binary format
- When there are unsaved spreadsheets, "Save Project..." and "Export Zipped Project..." will give a warning message to save each unsaved spreadsheet
- When cloning a spreadsheet, the newly generated spreadsheet name is unique by default
- Re-ordered the File menu to improve usability
- Added a function to impute missing values with random numbers from a defined distribution
- Improved the "Save Image As..." dialog on Mac and Linux
- Added support for save image as JPEG on Mac and Linux
- Added file type selector for open and save file dialogs on Mac
- Violin Plot displays the properties tab by default
- Gene Expression workflow "Import from Affymetrix CEL Files" and File menu "Import Affymetrix .CEL Files" produce the same output spreadsheet for gene expression arrays
- Improved graphics for visualizations on Mac

Bug fixes:

- Fixed a bug on "Split Column" dialog on Mac
- Fixed a bug in "Import Affymetrix .ARR File..."
- Other minor bug fixes

PGS7.17.0918

General Improvement:

- Most of the computations are multi-threaded, which drastically increases the speed
- Viewers generated from spreadsheets are new tabs within the same window frame by default; viewer windows can be docked back to the main window frame
- Workflow panel is visible in any invoked viewers, order of the workflow steps is more intuitive
- Updated with modern icons and graphics color palette
- Mixed model ANOVA uses REML by default
- Sample ID factor is not included in the model of Alt-splicing ANOVA, GO ANOVA, pathway ANOVA
- Apply button are removed from most of the dialogs
- Improved interface is cleaner and more user friendly
- New functional normalization method in the Illumina methylation array importer (450K and 850K)
- Improved SWAN normalization in the Illumina methylation array importer
- Allows import of different versions of the Illumina methylation arrays when using the same set of library files
- Improved text file importer by adding wizard for specifying the properties of the spreadsheet
- Removed repeated measures menu option, it is recommended to use ANOVA doing repeated measures analysis
- Simplified menus and dialogs, removed obsolete functions, improved wording

- Automatically downloads annotation files, even from sites with HTTPS or redirects (e.g. Affymetrix and GEO)
- Logged data is detected and appropriate defaults are automatically set

Older release notes are available on our website at Partek® Genomics Suite™ Software Update Archive.