

Singular Analysis Toolset 3.6.2

This version of the Singular™ Analysis Toolset is an update from version 3.6.1 (limited release) to 3.6.2. To download the latest version of the software for Singular Analysis Toolset, go to fluidigm.com/software.

For more information, see the Singular Analysis Toolset User Guide (PN 100-5066) or the Singular Analysis Toolset Practice Sets Instructions (PN 100-6270).

v3.6.2 Bug Fixes

- The analyzeGeneDetection function:
 - Counts failed data correctly for qPCR data.
 - Applies the default threshold for qPCR data.
 - Uses the custom color assignment set by the setSampleGroupColorAndSymbols function.
- The violinPlotBySamples function uses the color assignment set by the setSampleGroupAndSymbols function.
- The readCtExp function imports NoCall as missing data.

v3.6.1 Enhancements

The main features of this release include:

- t-Distributed Stochastic Neighbor Embedding (tSNE) analysis of gene expression data
- Addition of the k-mean clustering function to cluster PCA and tSNE results
- Ability to display the tSNE and PCA score plots using a different sample list
- Addition of an interactive method to change the outlier threshold for outlier identification function when there are too many data points for individual sample selection
- Ability to select greater than 400 top genes with the autoAnalysis function, and the top genes are unchanged as the selected number increases (up to 1000)
- Addition of gene names to the gene list function for ease of use
- Addition of a display range in the foldChangeAnalysis function
- A range of 0 to max instead of max to max for the displayHC function where display = "expression"

- A method to filter unwanted columns and rows when importing data with the functions `autoAnalysis`, `identifyOutliers`, and `readLinearExp`

v3.6.1 Bug Fixes

- The `autoAnalysis` and hierarchical clustering function works for R version 3.3.
- The HC plot is properly displayed for all computer display resolutions (equal to or greater than 1024x768) and all system font size.
- All pairwised combinations are calculated when the number of sample groups is greater than 3 in ANOVA analysis.
- The genes are correctly labelled in the `foldChangeAnalysis` when `Locate = TRUE`.
- The samples are correctly labelled in the `analyzeGeneDetection` function.
- The `autoAnalysis` function displays the correct message for the PCA analysis step, which finds high variance genes instead of differentially expressed genes.
- The `foldChangeAnalysis` function returns proper value when no gene or only one gene meets the criteria.
- The `foldChangeAnalysis` calculates fold change using the criterion $(A-B)/B$ instead of A/B .
- The `displayHC` function displays the proper heatmap when `display = "gene_z_score"`.

v3.5.2 Enhancements

Process Whole exome scale DNA Seq data for identification of somatic mutations and variants at single-cell resolution.

v3.5.2 Bug Fixes

- The `readCtExp` function reads custom Ct data with non-equal sample and assay numbers.
- The `vcEvalSampleVariants()` and `vcEvalSampleGroupVariants()` functions can calculate nonreference discrepancies correctly.
- The `vcUpdateVariantListFromVariantAnnotation(vc, by_annotation = " ")` function can update annotation in a Variant List of a VCF.

v3.0.3 Enhancements

None

v3.0.3 Bug Fixes

- The readCtExp function does not invalidate the failed Ct values.

v3.0.2 Enhancements

- Gene Group ID. Annotate and update genes in a gene list using the column GroupID.
- Outlier Analysis. Identify outliers by sample group directly from an existing EXP object, EXP object file, or gene expression file.
- Apply HC. Apply a new HC dendrogram to an existing dendrogram for visual, side-by-side comparison of two EXP data sets.
- Volcano Plots. Identify significant changes in gene expression during ANOVA analysis between two sample groups in terms of fold-change and p-value.
- 3D PCA Analysis. Generate a rotatable 3D PCA Score plot for sample data.
- Find Genes Co-Expressed with Target Genes. For gene targets of interest, find co-expressed genes and display them for a set of samples using the Pearson method of calculating the Correlation Coefficient.
- Custom Colors and Symbols for Sample and Gene Groups. Display your choice of colors and symbols for sample and gene groups in HC and PCA plots.

v3.0.2 Bug Fixes

None

v3.0.1 Enhancements

Differential Expression Gene Analysis Enhancements

- Gene Group ID. Annotate and update genes in a gene list using the column GroupID.
- Outlier Analysis. Identify outliers by sample group directly from an existing EXP object, EXP object file, or gene expression file.
- Apply HC. Apply a new HC dendrogram to an existing dendrogram for visual, side-by-side comparison of two EXP data sets.
- Volcano Plots. Identify significant changes in gene expression during ANOVA analysis between two sample groups in terms of fold-change and p-value.
- 3D PCA Analysis. Generate a rotatable 3D PCA Score plot for sample data.

- Find Genes Co-Expressed with Target Genes. For gene targets of interest, find co-expressed genes and display them for a set of samples using the Pearson method of calculating the Correlation Coefficient.
- Custom Colors and Symbols for Sample and Gene Groups. Display your choice of colors and symbols for sample and gene groups in HC and PCA plots.

Variant Analysis for DNA Seq Data

- Read single or multiple VCF files and return the created VC object. You can also restrict the import of specific target chromosome coordinates and genes.
- Update samples and genes with group information.
- Choose either a control sample or a control sample group for variant calling.
- Define outlier samples by user-defined threshold values for coverage of variant calls (DP), conditional genotype quality (GQ), allele frequency (AF), and minimum variant number in samples (VNS); and display all as histograms.
- Filter variant calls in any of the following ways:
 - All Variants. Considers all variant calls in the analysis and filters any calls having low-quality in all samples.
 - Significant Variants. Performs Fisher's Exact Test for variant calls between sample group pairs, and then filters variants having a p-value greater than the defined threshold (default 0.05) in all sample pairs.
 - Control Variants. Filters out all non-variant calls in the control sample or control sample group.
 - Control Calls. Gets a common call list in the control sample group with call concordance greater than the defined threshold in control samples (default is 0.51), and then filters out any variant calls that are not on the common call list.
- Filter samples in any of the following ways:
 - All Samples. Uses all samples in variant analysis.
 - High Quality Samples. Filters out all low-quality samples, which are defined as all variants having a percentage of No-Call or Missing data greater than the defined threshold; the default is 0.5. © Fluidigm Corporation. All rights reserved.
- Perform HC analysis to display variant calls in samples. Do HC Analysis on the filtered variant calls and identify sample and variant clusters via GUI.
- Write out VC object data back to VCF format.
- You can also:
 - Perform a Fisher's Exact Test to get the p-value for each pairwise sample group and display a Manhattan plot.
 - Do evaluation performance of variant calls: Compare genotyping from control sample and control sample groups (common GT calls in control group), evaluate performance of variant calls in individual samples and sample groups, and return

performance table including Allele Dropout (ADO), Locus Dropout (LDO), Genotyping overall concordance, non-reference sensitivity, and non-reference discrepancy

v3.0.1 Bug Fixes

None

For technical support visit fluidigm.com/support

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