Package ‘CONSTANd’

February 19, 2024

Type Package
Title Data normalization by matrix raking
Version 1.10.0
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Description Normalizes a data matrix `data` by raking (using the RAS method by Bacharach, see references) the Nrows by Ncols matrix such that the row means and column means equal 1. The result is a normalized data matrix `K=RAS`, a product of row multipliers `R` and column multipliers `S` with the original matrix `A`. Missing information needs to be presented as `NA` values and not as zero values, because CONSTANd is able to ignore missing values when calculating the mean. Using CONSTANd normalization allows for the direct comparison of values between samples within the same and even across different CONSTANd-normalized data matrices.

License file LICENSE
Encoding UTF-8
LazyData true

biocViews MassSpectrometry, Cheminformatics, Normalization, Preprocessing, DifferentialExpression, Genetics, Transcriptomics, Proteomics

NeedsCompilation no
Depends R (>= 4.1)
Suggests BiocStyle, knitr, rmarkdown, tidyr, ggplot2, gridExtra, magick, Cairo, limma

SystemRequirements

BugReports https://github.com/PDiracDelta/CONSTANd/issues
URL qcquan.net/constand
VignetteBuilder knitr

Related

git_url https://git.bioconductor.org/packages/CONSTANd

git_branch RELEASE_3_18

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Description

Normalizes the data matrix by raking the Nrows by Ncols matrix such that the row means and column means equal Ncols and Nrows, respectively.

Usage

`CONSTANd(data, precision=1e-5, maxIterations=50, target=1)`

Arguments

data: Nrows by Ncols matrix.

precision: Combined allowed deviation (residual error) of col and row means from target value.

maxIterations: Maximum amount of iterations (1x row and 1x col per iteration).

target: The mean value of quantifications in each row and column after normalization.

Details

Normalizes the data matrix <data> by raking (using the RAS method by Bacharach, see references) the Nrows by Ncols matrix such that the row means and column means equal 1. The result is a normalized data matrix K=RAS, a product of row multipliers R and column multipliers S with the original matrix A. Missing information needs to be presented as nan values and not as zero values, because CONSTANd is able to ignore nan-values when calculating the mean. The variable <maxIterations> is an integer value that denotes the number of raking cycles. The variable <precision> defines the stopping criteria based on the L1-norm as defined by Friedrich Pukelsheim, Bruno Simeone in "On the Iterative Proportional Fitting Procedure: Structure of Accumulation Points and L1-Error Analysis".
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Value:
- normalized_data: Normalized data matrix ‘K=RAS’ in the RAS-formulation of the problem.
- convergence_trail: Precision acquired after each raking iteration (last value is the final precision).
- R: Row multipliers in the ‘K=RAS’ formulation of the problem.
- S: Column multipliers in the ‘K=RAS’ formulation of the problem.

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References:

Examples:
# generic use (mock data)
data_matrix <- matrix(runif(20), c(5,4))normalized_matrix <- CONSTANd(data_matrix)$normalized_data

# customize parametersresult <- CONSTANd(data_matrix, precision=1e-3, maxIterations=30)

# explore parts of the result objectnormalized_matrix <- result$normalized_datanum_iterations_performed <- length(result$convergence_trail)attained_precision <- result$convergence_trail[num_iterations_performed]
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