

Package ‘proteomicsCV’

February 17, 2024

Type Package

Title Calculates the Percentage CV for Mass Spectrometry-Based Proteomics Data

Version 0.1.0

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Description Calculates the percentage coefficient of variation (CV) for mass spectrometry-based proteomic data. Intensity based quantification is log normal, there the CV is calculated with the log-normal function. This package currently does not reference any academic publication.

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Encoding UTF-8

Imports stats

RoxygenNote 7.2.3

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-02-17 21:00:02 UTC

R topics documented:

proteomicsCV	1
------------------------	---

Index	3
--------------	---

proteomicsCV	<i>logCV</i>
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Description

Calculates the percentage CV for intensity based proteomic data.

Usage

```
logCV(data, log_transformed)
```

Arguments

data input dataframe of the intensity values. These should be normalised already for optimal results.

log_transformed 'no' for data that has not been log transformed. 'yes' for natural log transformed data. (`log()` function in R)

Value

returns a list of percentage CVs

Author(s)

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Examples

```
library(proteomicsCV)
intensity_df<-data.frame(intensity1=c(23.88,23.55,23.41,23.15),
                           intensity2=c(23.98,23.56,23.43,23.29),
                           intensity3=c(23.94,23.635,23.37,23.21),
                           intensity4=c(23.81,23.57,23.54,23.08))
cvs<-logCV(intensity_df, "yes")

not_log_intensity_df<-exp(1)^intensity_df
cvs<-logCV(not_log_intensity_df,"no")
```

Index

```
* ~CV
  proteomicsCV, 1
* ~proteomics
  proteomicsCV, 1
logCV (proteomicsCV), 1
proteomicsCV, 1
```