Package 'GeneScoreR'

January 20, 2025

Title Gene Scoring from Count Tables

Version 0.1.1

Description

Provides two methods for automatic calculation of gene scores from gene count tables: the z-score method, which requires a table of samples being scored and a count table with control samples, and the geometric mean method, which does not rely on control samples. The mathematical methods implemented are described by Kim et al. (2018) <doi:10.1089/jir.2017.0127>.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

Author Aris Syntakas [aut, cre]

Maintainer Aris Syntakas <sejjsyn@ucl.ac.uk>

Repository CRAN

Date/Publication 2024-10-25 09:10:10 UTC

Contents

---

geomean	*Calculate Geometric Means from Count Tables*

Description

This function computes the geometric mean for each sample in the given count table.

Usage

```
geomean(count_table)
```

Arguments

count_table   A data frame of gene count data (genes as rows, samples as columns). All columns must be numeric.

Value

A data frame with the geometric means per sample and the sample IDs.

Examples

```
# Example data to be scored
count_table <- data.frame(
  sample1 = c(1, 10, 100),
  sample2 = c(2, 20, 200),
  sample3 = c(3, 30, 300)
)
rownames(count_table) <- c("gene1", "gene2", "gene3")

# Calculate Geometric Mean per sample in the count_table
geomean(count_table)
```

---

   zscore   *Calculate Z-Scores from Count Tables*

Description

This function computes a Z-score sum for each sample in the given "scored" count table, based on the means and SDs of the genes in the control table.

Usage

```
zscore(scored_table, control_table)
```

Arguments

scored_table   Data frame of samples to be scored (genes as rows, samples as columns). All columns must be numeric.

control_table   Data frame of control samples (genes as rows, samples as columns). All columns must be numeric.

Value

A data frame with the sum of Z-scores per sample and the sample IDs.

Examples

```
# Example data to be scored
scored_table <- data.frame(
  sample1 = c(1, 2, 3),
  sample2 = c(4, 5, 6),
  sample3 = c(7, 8, 9)
)
rownames(scored_table) <- c("gene1", "gene2", "gene3")

# Example control data
control_table <- data.frame(
  control1 = c(1, 1, 1),
  control2 = c(2, 2, 2),
  control3 = c(3, 3, 3)
)
rownames(control_table) <- c("gene1", "gene2", "gene3")

# Calculate Z-score for each sample of the scored_table
zscore(scored_table, control_table)
```

Index