Package ‘ProliferativeIndex’

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Title Calculates and Analyzes the Proliferative Index
Version 1.0.1
Description Provides functions for calculating and analyzing the proliferative index (PI) from an RNA-seq dataset. As described in Ramaker & Lasseigne, et al. bioRxiv, 2016 <doi:10.1101/063057>.
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Author Brittany Lasseigne [aut, cre], Ryne Ramaker [aut]
Maintainer Brittany Lasseigne &lt;brittany.lasseigne@gmail.com&gt;
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R topics documented:

  calculatePI .......................................................... 2
  compareModelToPI .................................................. 2
  comparePI ............................................................. 3
  exReadDataObj ....................................................... 3
  exVSTPI ............................................................... 4
  readDataForPI ......................................................... 4
  vstTCGA_ACCData_sub ................................................. 5

Index 6
**calculatePI**

A function for calculating proliferative index from variance stabilized RNA-seq data in the ProliferativeIndex package

**Description**

This function allows the user to read in data for subsequent proliferative index calculation and analysis

**Usage**

`calculatePI(userObject)`

**Arguments**

- `userObject` Output from ProliferativeIndex readDataForPI function

**Examples**

`calculatePI(exReadDataObj)`

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**compareModeltoPI**

A function for comparing proliferative indices from variance stabilized RNA-seq data to model principal components in the ProliferativeIndex package

**Description**

This function allows the user to calculate a correlation between their model and PI

**Usage**

`compareModeltoPI(userObject, vstPI)`

**Arguments**

- `userObject` Output from ProliferativeIndex readDataForPI function (user data)
- `vstPI` Output from ProliferativeIndex calculatePI function

**Examples**

`compareModeltoPI(exReadDataObj, exVSTPI)`
**comparePI**

A function for comparing proliferative indices from variance stabilized RNA-seq data in the ProliferativeIndex package

**Description**

This function allows the user to examine a summary and plot of their PIs

**Usage**

```
comparePI(vstPIinput)
```

**Arguments**

- `vstPIinput` Output from ProliferativeIndex calculatePI function (PI of user vst data)

**Examples**

```
comparePI(exVSTPI)
```

---

**exReadDataObj**

TCGA ACC data set output from readDataForPI function

**Description**

This object is the output from readDataForPI taking vstTCGA_ACCData_sub and this model:

```
c("AIFM3", "ATP9B", "CTRC", "MCL1", "MGAT4B", "ODF2L", "SNORA65", "TPPP2")
```

as inputs.

**Usage**

```
data(exReadDataObj)
```

**Format**

A list of the vstData (vstTCGA_ACCData_sub data frame with 20501 rows and 10 columns) and the modelIDs (character vector of "AIFM3", "ATP9B", "CTRC", "MCL1", "MGAT4B", "ODF2L", "SNORA65", "TPPP2")
**exVSTPI**

*TCGA ACC data set output from calculatePI function*

**Description**

This object is the output from calculatePI from the exReadDataObj as input.

**Usage**

```r
data(exVSTPI)
```

**Format**

A numeric vector of the calculated Proliferation Indices for the vstTCGA_ACCData_sub data

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**readDataForPI**

*A function for reading data in for use with the ProliferativeIndex package*

**Description**

This function allows the user to read in variance stabalized RNA-seq data and gene model names for subsequent proliferative index calculation and analysis.

**Usage**

```r
readDataForPI(vstData, modelIDs)
```

**Arguments**

- `vstData` : Dataframe of user variance stabalized count data (from DESeq2) with samples in columns and genes in rows. Rownames must be genes.
- `modelIDs` : Genes in user identified model for comparison to proliferative index

**Examples**

```r
readDataForPI(vstTCGA_ACCData_sub, c("AIFM3", "ATP9B", "CTRC", "MCL1", "MGAT4B", "ODF2L", "SNORA65", "TPPP2"))
```
Description

A dataset containing data from the The Cancer Genome Atlas (TCGA) Adrenocortical Carcinoma (ACC) dataset. This data was obtained from the TCGA data portal (tcga-data.nci.nih.gov) in June 2015. Level 3 RNASeqV2 raw count data was variance stabalized with the DESeq2 v1.8.2 varianceStabilizingTransformation:

Usage

data(vstTCGA_ACCData_sub)

Format

A data frame with 20501 rows and 10 variables
Index

* datasets
  - exReadDataObj, 3
  - exVSTPI, 4
  - vstTCGA_ACCData_sub, 5

  calculatePI, 2
  compareModeltoPI, 2
  comparePI, 3

  exReadDataObj, 3
  exVSTPI, 4

  readDataForPI, 4
  vstTCGA_ACCData_sub, 5