

# 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](https://doi.org/10.1101/063057)>.

**Depends** R (>= 3.0.0)

**Imports** graphics, stats

**License** MIT + file LICENSE

**LazyData** true

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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calculatePI	<i>A function for calculating proliferative index from variance stabilized RNA-seq data in the ProliferativeIndex package</i>
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**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	<i>A function for comparing proliferative indices from variance stabilized RNA-seq data to model principal componenets in the ProliferativeIndex package</i>
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**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)
```



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exVSTPI	<i>TCGA ACC data set output from calculatePI function</i>
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### Description

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

### Usage

```
data(exVSTPI)
```

### Format

A numeric vector of the calculated Proliferation Indices for the vstTCGA\_ACCData\_sub data

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readDataForPI	<i>A function for reading data in for use with the ProliferativeIndex package</i>
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### Description

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

### Usage

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

### Arguments

vstData	Dataframe of user variance stabilized 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

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

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vstTCGA\_ACCData\_sub    *TCGA ACC data set*

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**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](http://tcga-data.nci.nih.gov)) in June 2015. Level 3 RNASeqV2 raw count data was variance stabilized with the DESeq2 v1.8.2 varianceStabilizingTransformation:

**Usage**

```
data(vstTCGA_ACCData_sub)
```

**Format**

A data frame with 20501 rows and 10 variables

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