Package 'Group5Project'

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Type Package

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Description Implements various methods for pooling statistical evidence from multiple datasets.

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RoxygenNote 6.1.1

R topics documented:

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getFramePvals	*Helper method which populates a vector with p-values for group dif-ference in each biomarker from a single frame.*

Description

This function tests for normality within groups, then applies the appropriate test for group difference.

Usage

```
getFramePvals(dataFrame)
```

Arguments

dataFrame   The data frame to generate p-values from.

Value

A vector containing the p-values for group difference for each biomarker in the specified data frame. Note that if there are p biomarkers, this vector will be of length p.

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isInputValid   *Helper method for the main method.*

Description

Tests to see if the input to the main function is valid. Valid input is defined as 2-5 data frames, each with:

- The same number of columns.
- At least 2 unique values in the first column.

Usage

```
isInputValid(input)
```

Arguments

input   A list() of the data frames passed as input to the main function.

Value

True if the input is valid, as defined above; false otherwise.

---

isNormByGroup   *Helper method which determines if a biomarker is normally distributed by group at alpha level 0.05.*

Description

This function will be called by the implementations of bullet 1 and 2 on page 7 of the project slides. Note that the shapiro.test() function limits sample size to 5000.

Usage

```
isNormByGroup(dataFrame, marker)
```

Arguments

`dataFrame`	The data frame to test for normality by group.
`marker`	The biomarker number to be tested; e.g., for the nth biomarker, input integer n. Note that marker n corresponds to column n+1 in the data frame.

Value

True if normality cannot be rejected for all groups; false otherwise.

---

pooledPValues	*Pools the p-values between data frames using the specified method.*

Description

Pools the p-values between data frames using the specified method.

Usage

```
pooledPValues(method = "Fisher", ...)
```

Arguments

`method`	The desired pooling method: "Fisher" for Fisher, "Stouffer" for Stouffer, "minP" for minimum p-value, or "maxP" for maximum p-value.
`...`	The data frames to pool the p-values from. Must be between 2 and 5 data frames, all with the same number of columns, and at least 2 groups per data frame.

Value

A vector containing pooled p-values for each biomarker. For p biomarkers, the vector will be of length p.

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poolFisher	*Pools the p-values using the Fisher method.*

Description

Pools the p-values using the Fisher method.

Usage

```
poolFisher(unpooledPvalsList, frameList)
```

Arguments

`unpooledPvalsList`	
	A list (by data frame) of vectors (by biomarker in data frame) of p-values for group difference in each biomarker. E.g., p-value for group difference in biomarker j from data frame i is given by `unpooledPvalsList[[i]][j]`.
`frameList`	A list of the original 2-5 data frames. Note that data frame i is given by `frameList[[i]]`.

Value

A vector containing pooled p-values for each biomarker. For p biomarkers, the vector will be of length p.

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poolMaxP	*Pools the p-values using the Maximum p-value method.*

Description

Pools the p-values using the Maximum p-value method.

Usage

```
poolMaxP(unpooledPvalsList, frameList)
```

Arguments

unpooledPvalsList

A list (by data frame) of vectors (by biomarker in data frame) of p-values for group difference in each biomarker. E.g., p-value for group difference in biomarker j from data frame i is given by `unpooledPvalsList[[i]][j]`.

frameList   A list of the original 2-5 data frames. Note that data frame i is given by `frameList[[i]]`.

Value

A vector containing pooled p-values for each biomarker. For p biomarkers, the vector will be of length p.

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poolMinP	*Pools the p-values using the Minimum p-value method.*

Description

Pools the p-values using the Minimum p-value method.

Usage

```
poolMinP(unpooledPvalsList, frameList)
```

Arguments

unpooledPvalsList

A list (by data frame) of vectors (by biomarker in data frame) of p-values for group difference in each biomarker. E.g., p-value for group difference in biomarker j from data frame i is given by `unpooledPvalsList[[i]][j]`.

frameList   A list of the original 2-5 data frames. Note that data frame i is given by `frameList[[i]]`.

Value

A vector containing pooled p-values for each biomarker. For p biomarkers, the vector will be of length p.

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poolStouffer	*Pools the p-values using the Stouffer method.*

Description

Pools the p-values using the Stouffer method.

Usage

```
poolStouffer(unpooledPvalsList, frameList)
```

Arguments

unpooledPvalsList

A list (by data frame) of vectors (by biomarker in data frame) of p-values for group difference in each biomarker. E.g., p-value for group difference in biomarker j from data frame i is given by unpooledPvalsList[[i]][j].

frameList A list of the original 2-5 data frames. Note that data frame i is given by frameList[[i]].

Value

A vector containing pooled p-values for each biomarker. For p biomarkers, the vector will be of length p.

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