

# Package ‘pathVar’

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**Type** Package

**Title** Methods to Find Pathways with Significantly Different Variability

**Version** 1.17.0

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**Description** This package contains the functions to find the pathways that have significantly different variability than a reference gene set. It also finds the categories from this pathway that are significant where each category is a cluster of genes. The genes are separated into clusters by their level of variability.

**License** LGPL (>= 2.0)

**Collate** classdef.R pipeline.final.R

**LazyData** true

**Depends** R (>= 3.3.0), methods, ggplot2, gridExtra

**Imports** EMT, mclust, Matching, data.table, stats, grDevices, graphics, utils

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| pathVar-package | <i>Detects pathways with different levels of variance than reference gene set variability.</i> |
|-----------------|--|

---

## Description

This package contains functions used to determine pathways with significant differences in variability.

## Details

```

Package: pathVar
Type: Package
Version: 1.11.2
Date: 2018-06-29
License: LGPL
Depends: R (>= 3.2.2), methods, ggplot2, gridExtra
Imports: EMT, mclust, Matching, reshape, data.table

```

1. Compute the standard deviation for each gene.
2. Classify the genes with respect to sd in at most 4 clusters.
3. For each pathway, we extract the gene in our dataset and in which cluster they belong.
4. For each pathway, we look how its genes are distributed in each category and compare it to the expected number with all the gene from the dataset with the chisq.
5. Same as 4. but with the exact test.
6. find significant pathway(s), which category(ies) from this pathway are significant and which gene(s) belongs to this(ese) category(ies)

## Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
results_kegg=pathVarOneSample(bock,pways.kegg,test="chisq",varStat="sd")
sig_kegg=sigPway(results_kegg,0.05)
```

---

**bock***Gene Expression Matrix of Published Data*

---

**Description**

This is a matrix object containing genes as rows and the samples as columns, where each element in the matrix is an expression value. The dataset contains 12900 genes and 32 samples.

**Usage**

```
data(bock)
```

**Value**

A matrix with expression values for 12900 genes probes on 32 samples.

**See Also**

[pways.kegg](#), [pways.reactome](#)

**Examples**

```
data(bock)
```

---

**diagnosticsVarPlots***Plots the average expression against variability using different summary statistics.*

---

**Description**

Plots the average expression against variability using different summary statistics to help decide which statistic would be the best with your dataset.

**Usage**

```
diagnosticsVarPlots(dat.mat)
```

**Arguments**

`dat.mat` a matrix with rows as genes and columns as samples.

**Details**

This function gives you 3 plots one for SD, one for MAD and one for CV against the mean to help you decide which one would be the best with your dataset. It also returns the correlation between each variability statistics and the mean.

**Value**

3 scatter plots where average expression is on the X-axis and SD, MAD, and CV are on the Y-axis.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
diagnosticsVarPlots(bock)
```

---

```
diagnosticsVarPlotsTwoSample
```

*Plots the average expression against variability using different summary statistics when comparing 2 groups of samples to each other.*

---

**Description**

Plots the average expression against variability using different summary statistics to help decide which statistic would be the best with your dataset when comparing 2 groups of samples to each other.

**Usage**

```
diagnosticsVarPlotsTwoSample(dat.mat, groups)
```

**Arguments**

|                      |  |
|----------------------|--|
| <code>dat.mat</code> | a matrix with rows as genes and columns as samples.                    |
| <code>groups</code>  | vector indicating the amount of samples and replicates of each sample. |

**Details**

This function gives you 3 plots one for SD, one for MAD and one for CV against the mean to help you decide which one would be the best with your dataset. It also returns the correlation between each variability statistics and the mean.

**Value**

3 scatter plots where average expression is on the X-axis and SD, MAD, and CV are on the Y-axis.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
diagnosticsVarPlotsTwoSample(bock[1:5000,], groups=as.factor(c(rep(1,10),rep(2,10))))
```

---

```
geneDistributionSet-class  
  Class "geneDistributionSet"
```

---

### Description

This is a class representation for storing the output of the `pathVarOneSample` function.

### Objects from the Class

Objects are output by the function `pathVarOneSample`. Objects can also be created by calls of the form `new("geneDistributionSet", ...)`.

### Slots

**tablePway:** A "data.table" of pathway name, pathway IDs, adjusted p-value from the chisq test or exact test, the number of genes from our dataset inside the pathway and the total number of genes inside the pathway.

**NAPways:** A character object that contains the pathway names of the pathway having less than 10 genes for the Chi-Squared or also more than 500 genes for the exact test.

**genesInPway:** A list object that contains each pathway with the genes from the datasets belonging to it and in which cluster they were classified.

**refProb:** A table object that contains the probability of the reference in each cluster.

**refCounts:** A table object that contains the genes counts of the reference in each cluster.

**pwayCounts:** A list object that contains the genes counts of the each pathway in each cluster.

**numOfClus:** A numeric object that contains the number of clusters.

**varStat:** A character object that contains the statistics sd, mad, cv or mean chosen for the analysis.

**genesInClus:** A numeric object that contains all the genes from the dataset and in which cluster they belong.

**var:** A numeric object that contains the statistics value (sd, mad, cv or mean) for each gene.

### Methods

No methods defined with class "geneDistributionSet" in the signature.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
out <- new("geneDistributionSet", tablePway=data.table::data.table(), NAPways=character(), genesInPway=list(),  
showClass("geneDistributionSet"))
```

---

```
geneDistributionSet2-class  
  Class "pathVarTwoSamplesCont"
```

---

## Description

This is a class representation for storing the output of the `pathVarTwoSamplesCont` function.

## Objects from the Class

Objects are output by the function `pathVarTwoSamplesCont`. Objects can also be created by calls of the form `new("geneDistributionSet2", ...)`.

## Slots

**tablePway:** A "data.table" of pathway name, pathway IDs, adjusted p-value from the boot KS test, the number of genes from our dataset inside the pathway and the total number of genes inside the pathway.

**NAPways:** A character object that contains the pathway names of the pathway having no genes inside the dataset.

**genesInPway:** A list object that contains the genes from the dataset belonging to each pathway.

**groups:** A factor object that contains the groups in which group each sample belongs to.

**groupNames:** A character object that contains the names of the two groups.

**var1:** A numeric object that contains the statistics (sd, mad, cv or mean) for each gene for group 1.

**var2:** A numeric object that contains the statistics (sd, mad, cv or mean) for each gene for group 2.

**varStat:** A character object that contains the statistics sd, mad, cv or mean chosen for the analysis.

## Methods

No methods defined with class "geneDistributionSet2" in the signature.

## Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

## Examples

```
out <- new("geneDistributionSet2", tablePway=data.table::data.table(), NAPways=character(), genesInPway=list())  
showClass("geneDistributionSet2")
```

---

```
geneDistributionSet3-class  
  Class "pathVarTwoSamplesDisc"
```

---

### Description

This is a class representation for storing the output of the `pathVarTwoSamplesDisc` function.

### Objects from the Class

Objects are output by the function `pathVarTwoSamplesDisc`. Objects can also be created by calls of the form `new("geneDistributionSet3", ...)`.

### Slots

**tablePway:** A "data.table" of pathway name, pathway IDs, adjusted p-value from the boot KS test, the number of genes from our dataset inside the pathway and the total number of genes inside the pathway.

**NAPways:** A character object that contains the pathway names of the pathway having no genes inside the dataset.

**genesInPway1:** A list object that contains the genes from the dataset belonging to each pathway in the first group.

**genesInPway2:** A list object that contains the genes from the dataset belonging to each pathway in the second group.

**pwayCounts1:** A list object that contains tables of the number of genes in each cluster per pathway for the first group

**pwayCounts2:** A list object that contains tables of the number of genes in each cluster per pathway for the second group

**groups:** A factor object that contains the groups in which group each sample belongs to.

**groupNames:** A character object that contains the names of the two groups.

**var1:** A numeric object that contains the statistics (sd, mad, cv or mean) for each gene for group 1.

**var2:** A numeric object that contains the statistics (sd, mad, cv or mean) for each gene for group 2.

**varStat:** A character object that contains the statistics sd, mad, cv or mean chosen for the analysis.

### Methods

No methods defined with class "geneDistributionSet3" in the signature.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
out <- new("geneDistributionSet3", tablePway=data.table::data.table(), NAPways=character(), genesInPway1=list(),  
showClass("geneDistributionSet3"))
```

---

|               |                        |
|---------------|------------------------|
| geneSet-class | <i>Class "geneSet"</i> |
|---------------|------------------------|

---

### Description

This is a class representation for storing the output of the getGenes function.

### Objects from the Class

Objects are output by the function `getGenes`. Objects can also be created by calls of the form `new("geneSet", ...)`.

### Slots

`genes1`: A character object that contains the genes belonging to the pathway in the given window for group 1.

`genes2`: A character object that contains the genes belonging to the pathway in the given window for group 2.

`genesAll`: A character object that contains the genes from the dataset belonging to the pathway.

### Methods

No methods defined with class "geneSet" in the signature.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
out <- new("geneSet", genes1=character(), genes2=character(), genesAll=character())
showClass("geneSet")
```

---

|          |   |
|----------|---|
| getGenes | <i>Gets significant genes within a certain window of variability.</i> |
|----------|---|

---

### Description

Gets significant genes within a certain window of variability.

### Usage

```
getGenes(pvalue_results, pathway, window)
```

### Arguments

`pvalue_results` output of `pathVarTwoSamplesCont` step.

`pathway` A pathway name.

`window` A vector with a min and max range to specify the window of genes to grab with a certain level of variance.



**Details**

It takes the result of `pathVarTwoSamplesCont`, a given pathway and "window". It will give you the genes having their variability value in the window for group 1 and another set of genes for group 2 corresponding to the given pathway. It also returns the set of all the genes from your dataset that belong to this pathway.

**Value**

An object of class `geneSet` with 3 properties. The first 2 are the genes in the window from each group. The third are all the genes.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
# we run the 2 samples analysis on the first 10 pathways from kegg
pways.kegg.10pways <- lapply(pways.kegg, function(x) x[1:10])
results_2samples=pathVarTwoSamplesCont(bock,pways.kegg.10pways,groups=as.factor(c(rep(1,10),rep(2,10))))
genes_window=getGenes(results_2samples,pways.kegg$PATHNAME[10],c(0.25,0.75))
```

---

makeDBList

*Puts your own list of pathways and genes related to them into a list.*

---

**Description**

Puts your own list of pathways and genes related to them into a list.

**Usage**

```
makeDBList(file,pID=TRUE)
```

**Arguments**

|      |  |
|------|--|
| file | a tab delimited text file where the first and second columns are pathwayID and pathway name. The third, or last column, is the genes associated with each pathway, seperated by commas. If no pathwayIDs are available, the first column should be the pathway name. |
| pID  | boolean expression specifying where the pathways have an ID or not.  |

**Details**

This function is given a tab delimited text file with the pathwayID (if available), the pathway name, and the genes associated with each pathway. It outputs a list where the first element is the pathway names, the second is the Pathway IDs and the third is a list of genes for each pathway. The first row should be the column names.

**Value**

A list of pathway names, IDs, and genes in each pathway is returned.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
## Not run:
pways.ipa <- makeDBList("fileName",pID=FALSE)

## End(Not run)
```

---

|                  |   |
|------------------|---|
| pathVarOneSample | <i>Compares the distribution of genes in each cluster to the distribution of genes in each cluster for every pathway.</i> |
|------------------|---|

---

**Description**

Compares the distribution of genes in each cluster to the distribution of genes in each cluster for every pathway.

**Usage**

```
pathVarOneSample(dat.mat, pways, test=c("chisq", "exact"), varStat=c("sd", "mean", "mad", "cv"))
```

**Arguments**

|         |   |
|---------|---|
| dat.mat | matrix with the genes on the rows and the samples on the columns.   |
| pways   | list which contains a vector of pathway IDs, a vector of pathway names, and a list of genes in each pathway.            |
| test    | a string specifying the type of significance test to perform. The options are "exact" or "chisq".                       |
| varStat | a string specifying the type of variability summary statistic to perform. The options are "sd", "mean", "mad", or "cv". |

**Details**

This function classifies your genes into one to four clusters with respect to the standard deviation (SD), median absolute deviation (MAD), coefficient of variation (CV) or mean. Then, it compares the counts of genes in each class from your dataset in one pathway with the counts of the genes in each class from the whole dataset. For that, it uses a Chi-square or an exact test. You can give your own list of pathways (using the output of `makeDBList`) or use Reactome and KEGG pathways that are already included.

**Value**

A `geneDistributionSet` object is returned.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
results_kegg=pathVarOneSample(bock,pways.kegg, test="chisq", varStat="sd")
```

---

pathVarTwoSamplesCont *Compares the distribution of genes in each pathway for two groups of samples that you define.*

---

### Description

Compares the distribution of genes in each pathway for two groups of samples that you define.

### Usage

```
pathVarTwoSamplesCont(dat.mat, pways, groups, boot=1000, varStat=c("sd", "mean", "mad", "cv"))
```

### Arguments

|         |   |
|---------|---|
| dat.mat | matrix with the genes on the rows and the samples on the columns.   |
| pways   | list which contains a vector of pathway IDs, a vector of pathway names, and a list of genes in each pathway.            |
| groups  | vector indicating the amount of samples and replicates of each sample.  |
| boot    | number of bootstraps to be performed.   |
| varStat | a string specifying the type of variability summary statistic to perform. The options are "sd", "mean", "mad", or "cv". |

### Details

This function splits the samples into two groups that you define. It compares the density of the variability (SD, MAD, CV) or of the mean of the genes in a pathway from group 1 with the density from group 2. For that, it uses the bootstrap Kolmogorov-smirnov test. You can give your own list of pathways (using the output of makeDBList) or use Reactome and KEGG pathways that are already included.

### Value

A geneDistributionSet2 object is returned.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
# we run the 2 samples analysis on the first 10 pathways from kegg
pways.kegg.10pways <- lapply(pways.kegg, function(x) x[1:10])
results_2samples=pathVarTwoSamplesCont(bock,pways.kegg.10pways,groups=as.factor(c(rep(1,10),rep(2,10))),bo
```

---

pathVarTwoSamplesDisc *Compares the number of genes in clusters in each pathway for two groups of samples that you define.*

---

### Description

Compares the distribution of genes in each pathway for two groups of samples that you define.

### Usage

```
pathVarTwoSamplesDisc(dat.mat, pways, groups, perc=c(1/3, 2/3), test=c("chisq", "exact"), varStat=c("s
```

### Arguments

|         |  |
|---------|--|
| dat.mat | matrix with the genes on the rows and the samples on the columns.  |
| pways   | list which contains a vector of pathway IDs, a vector of pathway names, and a list of genes in each pathway.               |
| groups  | vector indicating the amount of samples and replicates of each sample.   |
| perc    | numeric vector of probabilities with values between 0 and 1. Used to put genes into clusters                               |
| test    | a string, either "exact" or "chisq" which are tests to see if clusters in the 2 samples are sig. different from each other |
| varStat | a string specifying the type of variability summary statistic to perform. The options are "sd", "mean", "mad", or "cv".    |

### Details

This function splits the samples into two groups that you define. It computes the variability (sd, mad, cv, or mean) for each gene in each group. Then it classifies the genes with respect to the variability in at most 4 clusters. For each pathway, we extract the gene in our dataset and in which cluster they belong. Then for each pathway we look at the gene counts in each category and compare the 2 samples to each other with all the genes from the data set with the Chi-Squared or exact test.

### Value

A geneDistributionSet3 object is returned.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
# we run the 2 samples analysis on the first 10 pathways from kegg
pways.kegg.10pways <- lapply(pways.kegg, function(x) x[1:10])
results_2samples=pathVarTwoSamplesDisc(bock, pways.kegg.10pways, groups=as.factor(c(rep(1, 10), rep(2, 10))), per
```

---

plotAllTwoSampleDistributionCounts

*Compares the distribution of genes in clusters for every gene in your data set for two groups of samples that you define and plot the counts.*

---

### Description

Compares the distribution of genes for every gene in your data set for two groups of samples that you define and plot the counts of each gene.

### Usage

```
plotAllTwoSampleDistributionCounts(dat,pvalue_results,perc=c(1/3,2/3),pvalue,plotName)
```

### Arguments

**dat** matrix with the genes on the rows and the samples on the columns.

**pvalue\_results** output of pathVarTwoSamples step.

**perc** numeric vector of probabilities with values between 0 and 1. Used to put genes into clusters

**pvalue** the significance level to test.

**plotName** a string specifying the file name of the output plot. Default value is NULL which prints, but does not save the graph in a pdf.

### Details

This function looks at the gene counts in each category of 2 groups previously defined in the pathVarTwoSamples step and compare the 2 samples to each other with all the genes from the data set. Then it plots the counts for each group.

### Value

A plot of results returned.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
# we run the 2 samples analysis on the first 10 pathways from kegg
pways.kegg.10pways <- lapply(pways.kegg, function(x) x[1:10])
results_2samples=pathVarTwoSamplesDisc(bock,pways.kegg.10pways,groups=as.factor(c(rep(1,10),rep(2,10))),perc=c(1/3,2/3))
plotAllTwoSampleDistributionCounts(bock, results_2samples, perc=c(1/3,2/3), pvalue=0.05, "bock.group1.group2")
```

---

|          |  |
|----------|--|
| plotPway | <i>Checks if an object is from the one sample or two samples cases and then plots reference distribution and the chosen pathway.</i> |
|----------|--|

---

**Description**

Checks if an object is from the one sample or two samples cases and then plots reference distribution and the chosen pathway.

**Usage**

```
plotPway(pvalue_results, pathway, sig)
```

**Arguments**

`pvalue_results` output of `pathVarTwoSamples` or `pathVarOneSample` step.  
`pathway` the chosen pathway you want to plot.  
`sig` output of `sigPway` or `NULL`.

**Details**

Plots the results of the one or two samples case for a chosen pathway.

**Value**

A plot of the results from `sigPway`.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
# we run the 2 samples analysis on the first 10 pathways from kegg
pways.kegg.10pways <- lapply(pways.kegg, function(x) x[1:10])
results_2samples=pathVarTwoSamplesCont(bock,pways.kegg.10pways,groups=as.factor(c(rep(1,10),rep(2,10))))
sigPways <- sigPway(results_2samples,0.05)
plotPway(results_2samples,"Glycolysis / Gluconeogenesis",sigPways)
```

---

|            |  |
|------------|--|
| pways.kegg | <i>List containing pathway IDs, names, and genes in each pathway</i> |
|------------|--|

---

**Description**

This is a list containing a vector of pathway IDs, a vector of pathway names, and a list of the genes in each pathway. There are a total of 272 KEGG pathways.

**Usage**

```
data(pways.kegg)
```

**Value**

A list containing a vector of pathway IDs, a vector of pathway names, and a list of the genes in each pathway for 272 pathways.

**See Also**

[bock](#), [pways.reactome](#)

**Examples**

```
data(pways.kegg)
```

---

|                |  |
|----------------|--|
| pways.reactome | <i>List containing pathway IDs, names, and genes in each pathway</i> |
|----------------|--|

---

**Description**

This is a list containing a vector of pathway IDs, a vector of pathway names, and a list of the genes in each pathway. There are a total of 946 reactome pathways.

**Usage**

```
data(pways.reactome)
```

**Value**

A list containing a vector of pathway IDs, a vector of pathway names, and a list of the genes in each pathway for 946 pathways.

**See Also**

[bock](#), [pways.kegg](#)

**Examples**

```
data(pways.reactome)
```

---

|           |   |
|-----------|---|
| saveAsPDF | <i>Save the plots of the significant pathway or a chosen list of pathways as a pdf.</i> |
|-----------|---|

---

**Description**

Save the plots of the significant pathway or a chosen list of pathways as a pdf.

**Usage**

```
saveAsPDF(pvalue_results,sig,listPath="significant")
```

**Arguments**

`pvalue_results` output of `pathVarTwoSamples` or `pathVarOneSample` step.  
`sig` output of `sigPway` or `NULL`.  
`listPath` the string "significant" if you want to save the plots of the significant pathways or a list of names of pathways of interest.

**Details**

Save the plots of the significant pathway or a chosen list of pathways as a pdf.

**Value**

A pdf of the results from `sigPway`.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
# we run the 2 samples analysis on the first 10 pathways from kegg
pways.kegg.10pways <- lapply(pways.kegg, function(x) x[1:10])
results_2samples=pathVarTwoSamplesCont(bock, pways.kegg.10pways, groups=as.factor(c(rep(1,10), rep(2,10))))
sigPways <- sigPway(results_2samples, 0.05)
saveAsPDF(results_2samples, sigPways, listPath="significant")
```

---

```
significantPathway-class
      Class "significantPathway"
```

---

**Description**

This is a class representation for storing the output of the `sigPway` function in the one sample case.

**Objects from the Class**

Objects are output by the function `sigPway` in the one sample case. Objects can be created by calls of the form `new("significantPathway", ...)`.

**Slots**

`genesInSigPways1`: A "list" object that contains the genes per significant pathway belonging to the significant category.

`sigCatPerPway`: A "list" object that contains the category(ies) per pathway that are significant.

`thresPValue`: A "numeric" object that contains the chosen p-value for the significance.

**Methods**

No methods defined with class "significantPathway" in the signature.



**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
sig <- new("significantPathway", genesInSigPways1=list(), sigCatPerPway=list(), thresPValue=numeric())
showClass("significantPathway")
```

---

```
significantPathway2-class
      Class "significantPathway2"
```

---

**Description**

This is a class representation for storing the output of the sigPway function in the two sample case.

**Objects from the Class**

Objects are output by the function [sigPway](#) in the two sample case. Objects can be created by calls of the form `new("significantPathway2", ...)`.

**Slots**

**genesInSigPways1:** A "list" object that contains the genes belonging to each significant pathway.

**thresPValue:** A "numeric" object that contains the chosen p-value for the significance.

**Methods**

No methods defined with class "significantPathway2" in the signature.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
sig <- new("significantPathway2", genesInSigPways1=list(), thresPValue=numeric())
showClass("significantPathway2")
```

---

```
significantPathway3-class
      Class "significantPathway3"
```

---

### Description

This is a class representation for storing the output of the sigPway function in the two sample case.

### Objects from the Class

Objects are output by the function `sigPway` in the two sample case. Objects can be created by calls of the form `new("significantPathway3", ...)`.

### Slots

`genesInSigPways1`: A "list" object that contains the genes belonging to each significant pathway in group 1.

`genesInSigPways2`: A "list" object that contains the genes belonging to each significant pathway in group 2.

`sigCatPerPway`: A "list" object that contains the significant categories in each pathway.

`thresPValue`: A "numeric" object that contains the chosen p-value for the significance.

### Methods

No methods defined with class "significantPathway3" in the signature.

### Author(s)

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

### Examples

```
sig <- new("significantPathway3", genesInSigPways1=list(), genesInSigPways2=list(), sigCatPerPway=list(), thresPValue=0.05)
showClass("significantPathway3")
```

---

```
sigPway
```

*A function checks if an object is from the one sample or two samples cases and then finds the significant pathways.*

---

### Description

A function checks if an object is from the one sample or two samples cases and then finds the significant pathways.

### Usage

```
sigPway(pvalue_results, pvalue)
```

**Arguments**

`pvalue_results` geneDistributionSet2 object and the output of the pathVarTwoSamples function or geneDistributionSet object and the output of the pathVarOneSample.  
`pvalue` the significance level to test.

**Details**

This function takes the output pathVarTwoSamples or pathVarOneSample and returns a significantPathway2 or significantPathway object specifying the significant pathway(s) and which gene(s) belongs to the significant pathway(s).

**Value**

A significantPathway2 object or significantPathway object is returned.

**Author(s)**

Laurence de Torrente, Samuel Zimmerman, Jessica Mar

**Examples**

```
results_2samples=pathVarTwoSamplesCont(bock,pways.kegg,groups=as.factor(c(rep(1,10),rep(2,10))),boot=1000,  
sig_kegg=sigPway(results_2samples,0.05)
```

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