

# Package ‘GISPA’

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**Type** Package

**Title** GISPA: Method for Gene Integrated Set Profile Analysis

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**Description** GISPA is a method intended for the researchers who are interested in defining gene sets with similar, a priori specified molecular profile. GISPA method has been previously published in Nucleic Acid Research (Kowalski et al., 2016; PMID: 26826710).

**Depends** R (>= 3.3.2)

**Imports** Biobase, changepoint, data.table, genefilter, graphics, GSEABase, HH, lattice, latticeExtra, plyr, scatterplot3d, stats

**License** GPL-2

**LazyData** true

**Collate** 'cptPlot.R' 'cptModel.R' 'computePS.R' 'GISPA.R'  
'cptSlopeplot.R' 'data.R' 'propBarplot.R' 'stackedBarplot.R'

**biocViews** StatisticalMethod, GeneSetEnrichment, GenomeWideAssociation

**Suggests** knitr

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/GISPA>

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cnvset	<i>Copy Number Variation (CNV) data</i>
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### Description

A dataset containing the genome-wide gene copy change identified in the 3 multiple myeloma cell line samples. The variables are as follows

### Usage

```
cnvset
```

### Format

A data matrix with 534 genes copy change and 3 samples

### Details

- gene
- copy number variation segment ID
- sample 1 copy change segment mean value
- sample 2 copy change segment mean value
- sample 3 copy change segment mean value

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computePS	<i>Computes the profile statistics</i>
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### Description

Computes the increased or decreased profile statistics for each row (or gene) across the three samples within a feature or data type (expression, methylation, or copy-number variation)

### Usage

```
computePS(rd1, cd1, cd2, profile)
```

### Arguments

rd1	: A numeric value of the reference sample (R) on which to estimate the profile statistics for a given gene, gene probe or gene copy segment
cd1	: A numeric value of the comparison sample 1 (S1) for a given gene, gene probe or gene copy segment
cd2	: A numeric value of the comparison sample 2 (S2) for a given gene, gene probe or gene copy segment
profile	: The desired direction of genomic change. The values are "up" (default) or "down" to select for increased or decreased gene set profile, respectively

### Details

This function requires three data values corresponding to three samples for a given gene (or row), respectively

### Value

The returned value is profile statistics computed considering the specified change in the reference sample when compared to the remaining two relative samples.

### Author(s)

Bhakti Dwivedi & Jeanne Kowalski

### Examples

```
rd1 = 40  
cd1 = 20  
cd2 = 20  
computePS(rd1, cd1, cd2, profile="up")
```

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cptModel	<i>Computes within and between gene feature profile statistics by feature and amongst features</i>
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### Description

Computes the percentiles on the estimated profile statistics within a gene and across genes for one or more combination of feature or data types (expression, methylation, copy-number variation, or variant change)

### Usage

```
cptModel(psm, genelist, cpt.data, cpt.method, cpt.max)
```

### Arguments

psm	: A data matrix of estimated gene profile statistics for each feature
genelist	: A vector of gene names or gene symbols corresponding to the profile statistics
cpt.data	: Identify changepoints in the data using variance (cpt.var), mean (cpt.mean) or both (meanvar). Default is cpt.var.
cpt.method	: Choice of single or multiple changepoint model. Default is "BinSeg".
cpt.max	: The maximum number of changepoints to search for using "BinSeg" method. Default is 60. This number is dependent on the number of input data points

### Details

This function estimates within and between feature profile statistics by gens in addition to the summed percentiles and successive differences

### Value

Estimated change points in the input data set

### Author(s)

Bhakti Dwivedi & Jeanne Kowalski

### Examples

```
id <- 1000 ## number of probes
s <- 3 ## number of sample groups
dm <- matrix(runif(id*s,0,200), nrow=id, ncol=s, dimnames=list(paste("gene", 1:id, sep=""), paste("fs", 1:s, sep="")))
genelist <- rownames(dm)
cptModel(dm, genelist, cpt.data="var", cpt.method="BinSeg", cpt.max=60)
```

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`cptPlot`*Scatterplot representation of gene sets by change points*

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**Description**

Scatterplot representation of identified change points on the estimated profile statistics within the data

**Usage**

```
cptPlot(psv, cut.pts)
```

**Arguments**

`psv` : A data vector of estimated profile statistics on which changepoints are identified  
`cut.pts` : The estimated profile statistics cutoffs corresponding to the locations in `psv`

**Details**

This function expects 'gispa.output' profile statistics output from GISPA.R main function

**Value**

Plot representing all the identified gene sets by change points in the data

**Author(s)**

Bhakti Dwivedi & Jeanne Kowalski

**Examples**

```
x <- runif(100, 0.0, 1.0)
y <- c(0.2, 0.6, 0.8)
cpt.plot <- cptPlot(psv=x, cut.pts=y)
```

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`cptSlopeplot`*Scatterplot representation of identified change points gene set slopes*

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**Description**

This function will plot the average slopes estimated over all gene sets within each change point by data types

**Usage**

```
cptSlopeplot(gispa.output, feature, type)
```

**Arguments**

- `gispa.output` : A data matrix of between gene feature profile statistics for each feature with corresponding identified changepoints. The row names should correspond to genes or names to be displayed on y-axis
- `feature` : Analysis type i.e., one ('1'), two ('2') or three ('3') dimensional feature analysis.
- `type` : Type of data, e.g., EXP (default) for expression, VAR of variants, CNV for copy number change.

**Details**

This function expects the output from GISPA function of GISPA package, and highlights the gene set slope profile in the selected changepoints

**Value**

Scatterplot illustrating the average slopes by change point to access the best gene set profile

**Author(s)**

Bhakti Dwivedi & Jeanne Kowalski

**Examples**

```
id <- 200 ## number of rows
s <- 3 ## number of columns
dm <- matrix(runif(id*s,0,10), nrow=id, ncol=s,
             dimnames=list(paste("gene", 1:id, sep=""),
                           paste("sample", 1:s, sep="")))
changepoints <- sort(sample(1:2, id, replace=TRUE))
dm <- cbind(dm,changepoints)
cptSlopeplot(gispa.output=dm,feature=1,type="EXP")
```

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exprset

*Gene Variant (EXP) data*

---

**Description**

A dataset containing the genome-wide gene expression values from 3 multiple myeloma cell line samples. The variables are as follows

**Usage**

exprset

**Format**

A data matrix with 1500 genes and 3 samples

**Details**

- gene
- gene names
- sample 1 log2 transformed normalized expression count values
- sample 2 log2 transformed normalized expression count values
- sample 3 log2 transformed normalized expression count values

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GISPA

*Gene Integrates Set Profile Analysis*


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**Description**

Identifies gene sets with a similar a prior defined profile using any combination of three feature or data types

**Usage**

```
GISPA(feature, f.sets, g.set, ref.samp.idx, comp.samp.idx, f.profiles, cpt.data, cpt.method, cpt.max)
```

**Arguments**

feature	: Analysis type i.e., one ('1'), two ('2') or three ('3') dimensional feature analysis.
f.sets	: A list of ExpressionSet data objects corresponding to a data type
g.set	: A GeneSet from an ExpressionSet to subset the f.sets for analysis purposes. 'geneIds' should correspond to the gene names. Default is null, i.e., genome-wide analysis
ref.samp.idx	: Reference sample column index on which to determine the gene set profile. The default is 3
comp.samp.idx	: The other two relative sample column index against which the profile is being determined. The default is 4 and 5
f.profiles	: A vector of the desired direction of genomic change (or profile) corresponding to each data type. The values are "up" or "down" for increased and decreased gene set profile, respectively
cpt.data	: Identify changepoints for data using variance (cpt.var), mean (cpt.mean) or both (meanvar). Default is cpt.var.
cpt.method	: Choice of single or multiple changepoint model. Default is "BinSeg".
cpt.max	: The maximum number of changepoints to search for using "BinSeg" method. Default is 60. This number is dependent on the number of input data points

**Value**

The returned value is a data matrix including the original data along with between gene profile statistics and identified changepoints.

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propBarplot                      *A plotting function for proportion by sample*

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### Description

Given a gene, this function will plot the proportion of each sample over the three samples within each data type

### Usage

```
propBarplot(gispa.output, feature, cpt, input.cex, input.cex.lab, ft.col, strip.col)
```

### Arguments

gispa.output    : A data matrix of between gene feature profile statistics for each feature with corresponding identified changepoints. The row names should correspond to genes or names to be displayed on y-axis

feature         : Analysis type i.e., one ('1'), two ('2') or three ('3') dimensional feature analysis.

cpt             : Changepoints to be plotted.

input.cex       : character (or symbol expansion) for the x- and y-axis labels

input.cex.lab   : character (or symbol expansion) for the horizontal and vertical strip labels

ft.col          : a vector of colors of the bar for the features or data types

strip.col       : color to be used for the vertical strip

### Details

This function expects the output from the main function of GISPA package, and highlights the gene set in the selected changepoints and their proportion in each of the three sample groups by data type.

### Value

Barplot illustrating each sample proportion for each gene in the selected change point

### Author(s)

Bhakti Dwivedi & Jeanne Kowalski

### Examples

```
id <- 20 ## number of rows
s <- 3 ## number of columns
dm <- matrix(runif(id*s,0,10), nrow=id, ncol=s,
             dimnames=list(paste("gene", 1:id, sep=""),
                           paste("fs", 1:s, sep="")))
changepoints <- sort(sample(1:2, id, replace=TRUE))
dm <- cbind(dm, changepoints)
propBarplot(gispa.output=dm, feature=2, cpt=1,
            input.cex=0.5, input.cex.lab=0.5,
            ft.col=c("grey0", "grey60"), strip.col="yellow")
```



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stackedBarplot                      *A plotting function for each sample proportion*

---

### Description

Given a gene, this function will plot the proportion of each sample over all the samples for each gene or row within each data type

### Usage

```
stackedBarplot(gispa.output, feature, cpt, type, input.cex, input.cex.lab, input.gap, samp.col, strip.col)
```

### Arguments

`gispa.output` : A data frame containing genes as rows followed by between gene feature profile statistics for each sample.

`feature` : Analysis type i.e., one ('1d'), two ('2d') or three ('3d') dimensional feature analysis.

`cpt` : Change point gene set to be plotted.

`type` : Type of data, e.g., EXP (default) for expression, VAR of variants, CNV for copy number change.

`input.cex` : character (or symbol expansion): x- and y-axis labels

`input.cex.lab` : character (or symbol expansion) for the horizontal and vertical strip labels

`input.gap` : gap or distance between each data type plot

`samp.col` : a vector of colors of the bar for the three sample groups, reference followed by other two samples

`strip.col` : color to be used for the vertical strip

### Details

This function expects the output from GISPA function of GISPA package, and highlights the gene set in the selected change points and their proportion in each of the three sample groups.

### Value

Barplot illustrating each sample proportion for each gene in the selected change point

### Author(s)

Bhakti Dwivedi & Jeanne Kowalski

### Examples

```
id <- 20 ## number of rows
s <- 4 ## number of columns
dm <- matrix(runif(id*s,min=0,max=100), nrow=id, ncol=s,
             dimnames=list(paste("gene", 1:id, sep=""),
                           paste("sample", 1:s, sep="")))
changepoints <- sort(sample(1:2, id, replace=TRUE))
dm <- cbind(dm, changepoints)
```

```
stackedBarplot(gispa.output=dm, feature=1, cpt=1, type="EXP",
               input.cex=1.5, input.cex.lab=1.5, input.gap=0.5,
               samp.col=c("red", "green", "blue"), strip.col="yellow")
```

---

varset	<i>Variant (VAR) data</i>
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### **Description**

A dataset containing the genome-wide gene variant proportion from 3 multiple myeloma cell line samples. The variables are as follows

### **Usage**

```
varset
```

### **Format**

A data matrix with 1101 genes variants and 3 samples

### **Details**

- gene
- gene names
- sample 1 transformed variant proportion data
- sample 2 transformed variant proportion data
- sample 3 transformed variant proportion data

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