

# Package ‘SMITE’

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**Type** Package

**Title** Significance-based Modules Integrating the Transcriptome and Epigenome

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**Description** This package builds on the Epimods framework which facilitates finding weighted subnetworks (“modules”) on Illumina Infinium 27k arrays using the SpinGlass algorithm, as implemented in the iGraph package. We have created a class of gene centric annotations associated with p-values and effect sizes and scores from any researchers prior statistical results to find functional modules.

**License** GPL (>=2)

**Depends** R (>= 3.5), GenomicRanges

**Imports** scales, plyr, Hmisc, AnnotationDbi, org.Hs.eg.db, ggplot2, reactome.db, KEGGREST, BioNet, goseq, methods, IRanges, igraph, Biobase,tools, S4Vectors, geneLenDataBase, grDevices, graphics, stats, utils

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**VignetteBuilder** knitr

**biocViews** ImmunoOncology, DifferentialMethylation, DifferentialExpression, SystemsBiology, NetworkEnrichment,GenomeAnnotation,Network, Sequencing, RNASeq, Coverage

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SMITE-package	<i>Significance-based Modules Integrating the Transcriptome and Epigenome</i>
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## Description

SMITE provides a method of scoring and visualizing multi-level epigenomic data in order to prioritize genes within a genome-wide experiment. These scores can then be used to identify subnetworks within an interaction network called modules. Each module represents a collection of highly interacting genes that are implicated by the experiment.

## Details

Package: SMITE  
Type: Package  
Version: 1.0.0  
Date: 2015-07-06  
License: GPL (>=2)

## Author(s)

Neil Ari Wijetunga, Andrew Damon Johnston

Maintainer: Neil.Wijetunga@med.einstein.yu.edu, Andrew.Johnston@med.einstein.yu.edu

## See Also

FEM BioNet

## Examples

```
## NOTE: commented out for example. See vignette for better explanation ##  
  
options(stringsAsFactors=FALSE)  
  
data(methylationdata)  
methylation <- methylation[-which(is.na(methylation[, 5])), ]  
methylation[,5] <- replace(methylation[,5],methylation[,5] == 0,  
  min(subset(methylation[,5], methylation[,5]!=0), na.rm=TRUE))  
  
data(curated_expressiondata)  
  
data(hg19_genes_bed)  
data(histone_h3k4me1)
```

```
#test_annotation<-makePvalueAnnotation( data=hg19_genes,
#other_data=list(h3k4me1=h3k4me1), gene_name_col=5, other_tss_distance=5000)

##fill in expression data
#test_annotation<-annotateExpression(test_annotation, expression_curated)

##fill in methylation data

#test_annotation<-annotateModification(test_annotation, methylation,
#weight_by=c(promoter="distance", body="distance", h3k4me1="distance"),
#verbose=TRUE, mod_corr=TRUE)

##create a pvalue object that will count the effect of the h3k4me1 as
##bidirectional

#test_annotation<-makePvalueObject(test_annotation,
#effect_directions=c(methylation_promoter="decrease",
#methylation_body="decrease",
#methylation_h3k4me1="bidirectional"))

##normalize the pvalues compared to colExp

#test_annotation<-normalizePval(test_annotation,ref="expression_pvalue",
#method="rescale")

##score with all four features contributing

#test_annotation<-SMITEScorePval(test_annotation,
#weights=c(methylation_promoter=.3,methylation_body=.1,expression=.3,
#methylation_h3k4me1=.3))

##load REACTOME
#load(system.file("data","Reactome.Symbol.Igraph.rda", package="SMITE"))

##run Spinglass using REACTOME network

#test_annotation<-runSpinglass(test_annotation, REACTOME, maxsize=50,
#num_iterations=10)

##run goseq on individual modules to determine bias
#test_annotation <- runGOseq(test_annotation,
#coverage=read.table(system.file("extdata",
#"hg19_symbol_hpaii_sites_inbodyand2kbupstream.bed.gz", package="SMITE")),
#type="kegg")

##search go seq output for keywords
#searchGOseq(test_annotation, "Cell")

##Draw a network
#plotModule(test_annotation, which_network=6, layout="fr")

##sample final file ##
```

```
data(test_annotation_score_data)
```

---

addShadowText	<i>Add shadow text (a second color bordering the text) to a plot</i>
---------------	--

---

### Description

This is a usefule function to help text stand out on busy backgrounds like gene networks

### Usage

```
addShadowText(x, y = NULL, labels, col = "white", bg = "black",  
theta = seq(pi/4, 2 * pi, length.out = 8), r = 0.1, ...)
```

### Arguments

x	A numeric vector of x coordinates
y	A numeric vector of y coordinates
labels	A character vector to be plotted at the specified coordinates
col	The text color
bg	The color of the outline
theta	The number of shadows to plot
r	The radius for the shadows
...	Additional plotting arguments

### Details

The function creates its effect by plotting theta shadows at r radius around the text to create the illusion of a text shadow

### Value

Adds shadow text to plot

### Note

This function was adapted by N. Ari Wijetunga for SMITE.

### Author(s)

Greg.Snow <at> imail.org

### References

<http://article.gmane.org/gmane.comp.lang.r.general/147787>

**See Also**

text, mtext

**Examples**

```
plot.new()

addShadowText(x = .5,y = .5,"TEST",col="white",bg="gray")
```

---

annotateExpression      *Adding expression data to a PvalueAnnotation*

---

**Description**

This function is used to create and load an ExpressionSet into a PvalueAnnotation. Using specified effect and p-value column or named columns that the function will use to determine the effect and p-value columns, it loads the data it into the PvalueAnnotation.

**Usage**

```
annotateExpression(pvalue_annotation, expr_data, effect_col = NULL, pval_col = NULL)
```

**Arguments**

pvalue_annotation	An S4 object of class PvalueAnnotation
expr_data	An object of class data.frame or matrix with row names corresponding to genes and atleast two columns with an effect and p-value for expression.
effect_col	A numeric specifying the column with an effect direction. If not specified the function will grep for a single named column from: "effect", "odds", "coeff" or "B"
pval_col	A numeric specifying the column with p-values. If not specified the function will grep for a single named column from: "pval", "p.val", "p_val" or "sig"

**Details**

The function will load the entire given expression dataset as an ExpressionSet in the expression slot, while the effect and p-value data will also be stored as an "AnnotatedDataFrame" in the phenodata slot of the ExpressionSet.

**Value**

A PvalueAnnotation, an S4 object with the slot "expression" filled in.

**Author(s)**

N. Ari Wijetunga

**See Also**

annotateModification makePvalueAnnotation createPvalueObject

**Examples**

```
data(curated_expressiondata)
data(test_annotation_score_data)
## Load Expression data into PvalueAnnotation ##
test_annotation <- annotateExpression(pvalue_annotation=test_annotation,
expression_curated)

## Extract entire ExpressionSet with expression data ##
#slot(test_annotation,"expression")

## Extract expression data summary ##
#head(extractExpression(pvalue_annotation=test_annotation))
```

annotateModification *Adding modification data to a PvalueAnnotation*

**Description**

This function is the main "workhorse" function for SMITE because given a specific epigenetic modification (e.g. DNA methylation) it will 1) assess an internal correlation structure and 2) aggregate the modification over all intervals associated with a gene in the "makePvalueAnnotation" function.

**Usage**

```
annotateModification(pvalue_annotation, mod_data, weight_by = NULL,
weight_by_method = "Stouffer", mod_included = NULL, mod_corr = TRUE,
mod_type = "methylation", verbose = FALSE)
```

**Arguments**

- pvalue\_annotation      An S4 object of class PvalueAnnotation.
- mod\_data                A dataframe or matrix derived from a bed file with thhe the first three columns as (chromosome, start, end), column 4 is the effect, and column 5 is the p-value.
- weight\_by               A vector with named elements specifying how modifications should be weighted within an interval. Must be one of:  
"distance" Use the distance from the gene TSS to weight the p-values and the combined effect such that events closer to the TSS are weighted more. Log distances are used.

	"pval" "p.value" "pvalue" "p_val" (DEFAULT) Do not weight p-values but weight the combined effect such by the significance of that effect. ELSE Do not weight p-values or the combined effect.
weight_by_method	A character specifying which method should be used to combine p-values. Must be one of: "Stouffer" (DEFAULT) Stouffer's method for combing pvalues involves first taking the inverse standard normal CDF transformation of a vector of p-values followed by a weighted sum creating a new Z score with a standard normal distribution "Fisher" "fisher" "chisq" "chi" Fisher's method involves summing the $-2\ln(p)$ for each of k p's which follows an approximate chi square distribution with 2k degrees of freedom "Sidak" "sidak" "minimum" Sidak's adjustment is essentially the minimum p-value, with an added transformation to account for multiple comparisons. "binomial" The binomial probability assesses the probability of observing the observed number of p-value below a threshold ( $\alpha=0.05$ ) given the total number of p values and the probability of a false positive.
mod_included	A vector of named elements specifying for which intervals in the annotation the function should find combined scores (e.g. promoters). If not specified the assumption is that all type of intervals associated with a gene should be included.
mod_corr	A logical (TRUE/FALSE) specifying whether a correlation matrix should be estimated. The DEFAULT is TRUE.
mod_type	A character naming the modification that is being loaded. The DEFAULT is "methylation" and any modType string can be used, but will be referred to in downstream analysis. A unique name must be used for each modification that is loaded. When picking a variable modType should also avoid using "_" as it is used to split column names containing modType.
verbose	A logical specifying if the user wants updates about the progress of the function.

## Details

This function is the main "workhorse" function for SMITE because given a specific epigenetic modification (e.g. DNA methylation) it will 1) assess an internal correlation structure and 2) aggregate the modification over all intervals associated with a gene in the "makePvalueAnnotation" function.

## Value

A an S4 object of class PvalueAnnotation with the slot modification (a GrangesList) filled in for each additional modification.

## Author(s)

N. Ari Wijetunga

## References

Fisher R. Statistical methods for research workers. Oliver and Boyd; Edinburgh: 1932.

Stouffer S, DeVinney L, Suchmen E. The American soldier: Adjustment during army life. Vol. 1. Princeton University Press; Princeton, US: 1949.

Sidak, Z. (1967). Rectangular confidence regions for the means of multivariate normal distributions, Journal of the American Statistical Association 62, 626-633.

### See Also

removeModification annotateExpression makePvalueAnnotation createPvalueObject

### Examples

```
options(stringsAsFactors=FALSE)

## Commented out below See vignette for more detailed usage information ##
## Load genome bed file ##
#data(hg19_genes_bed)

## Create a PvalueAnnotation with defaults for promoter size##
#test_annotation<-makePvalueAnnotation(data=hg19_genes, gene_name_col=5)

## Load DNA methylation bed file ##
#data(methylationdata)
#methylation<-methylation[-which(is.na(methylation[,5])),]
#methylation[,5]<-replace(methylation[,5],methylation[, 5] == 0,
#min(subset(methylation[,5], methylation[,5]!=0), na.rm=TRUE))

## Load DNA methylation into PvalueAnnotation modCorr=F for example##
## NOTE: Commented out below. See vignette for better example ##
#test_annotation <- annotateModification(pvalue_annotation=test_annotation,
#mod_data=methylation, weight_by=c(promoter="distance", body="distance"),
#verbose=FALSE, mod_corr=FALSE, mod_type="methylation")
```

---

convertGeneIds

*Convert between gene ids*

---

### Description

A convenient function used to convert between gene ids from different gene annotations.

### Usage

```
convertGeneIds(gene_IDs, ID_type, ID_convert_to, delim = NULL, verbose = FALSE)
```

### Arguments

gene\_IDs            A vector of gene names.

ID_type	A character specifying the type of given annotation. Currently one of "refseq", "ensembleprot", "uniprot" or "ensemble". In the case of ID_convert_to="entrez", "symbol"
ID_convert_to	A character specifying the type of desired annotation. Currently one of "symbol" or in they case of ID_type="symbol", "entrez"
delim	An optional character that will be removed from the beginning of each gene name. It can be a long string.
verbose	TRUE/FALSE Should the function be verbose? DEFAULTS to FALSE.

### Details

This is a very usefule function to efficently convert between gene ids. It currently relies on enumeration of each possible conversion, which has limited it's use to mainly converting to gene symbol.

### Value

A character vector formatted to ID\_convert\_to

### Note

The function has enumerated combinations using AnnotationDBI. We can provide additional functionality if needed.

### Author(s)

N. Ari Wijetunga <Neil.Wijetunga@med.einstein.yu.edu >

### See Also

AnnotationDBI, Biomart

### Examples

```
data(genes_for_conversiontest)

genes[,1] <- convertGeneIds(gene_IDs=genes[,1], ID_type="refseq",
                           ID_convert_to="symbol")
```

---

curated\_expressiondata

*A toy dataset of curated RNA-seq to test within SMITE*

---

### Description

A toy dataset of pre-cleaned gene expression data from RNA-seq. The file is effect and p-value with gene names as rownames.

**Usage**

```
data("curated_expressiondata")
```

**Format**

A data frame with 20819 observations on the following 2 variables.

**rownames** a character vector specifying gene

**column1** an numeric vector specifying effect (log fold change)

**column2** a numeric vector with a two sided p-value from DESeq analysis

**Details**

This gene expression dataset is a randomized version of the Toxoplasma dataset used to benchmark SMITE. It no longer has NAs or p-values=0. Gene names were converted to gene symbols.

**Value**

A dataframe with rownames as genes in Refseq format and columns for effects and pvalues derived from negative binomial testing of DESeq normalized values from RNA-seq.

**Source**

Manuscript in preparation. Please see <https://github.com/GreallyLab> for more details.

**Examples**

```
data(curated_expressiondata)
```

---

extractExpression	<i>View the expression data stored in a PvalueAnnotation</i>
-------------------	--

---

**Description**

This function allows the user to see the effect and p-value data that was loaded into a PvalueAnnotation before performing downstream analysis.

**Usage**

```
extractExpression(pvalue_annotation)
```

**Arguments**

pvalue\_annotation

An S4 object of class PvalueAnnotation for which expression data has already been loaded via annotateExpression

**Value**

A data.frame pulled from the phenoData of the expression slot within a load PvalueAnnotation. The phenoData specifically hold the effect and p-value information.

**Author(s)**

N. Ari Wijetunga

**See Also**

annotateExpression

**Examples**

```
data(test_annotation_score_data)
data(curated_expressiondata)
## Load Expression data into PvalueAnnotation ##
test_annotation<-annotateExpression(test_annotation, expression_curated)

## Extract entire ExpressionSet with expression data ##
#slot(test_annotation,"expression")

## Extract expression data summary ##
head(extractExpression(pvalue_annotation=test_annotation))
```

---

extractGOseq	<i>View the GOseq pathway analysis after having run Goseq, or search for a term.</i>
--------------	--

---

**Description**

Having defined at least one genomic module using runSpinglass or runBioNet, this function allows you to interrogate the enriched terms for a specific module or combination of modules.

**Usage**

```
extractGOseq(pvalue_annotation, which_network = NULL)
searchGOseq(pvalue_annotation, search_string, wholeword = FALSE)
```

**Arguments**

**pvalue\_annotation** An S4 object of class PvalueAnnotation, for which module-finding and GOseq analysis have already been performed

**which\_network** A numeric vector of a length of at least one, corresponding to a particular functional module specifically for the extract function.

`search_string` A character specifying a search string specifically for the search function.

`wholeword` A logical (TRUE/FALSE) determining whether the search string must be matched for whole word specifically for the search function.

### Details

Goseq analysis is useful since it allows you to assess term/pathway enrichment in a collection of genes, while adjusting for bias data. Potential bias can be from aspects like gene length or probe density that influence the likelihood of finding a particular gene. For more information please see the goseq reference.

### Value

`##Extract##` A list with each element matching the specified module. Has columns identifying the term id, the over represented p-value, underrepresented p-value the total number in the category found in the module, the total number in the category and a more descriptive pathway name.

`##Search##` A matrix with columns identifying the module name, module position/significance, the specific enriched term, the rank of that term within all enriched terms and the total number of enriched terms.

### Author(s)

N. Ari Wijetunga

### References

Young MD, Wakefield MJ, Smyth GK and Oshlack A (2010). Gene ontology analysis for RNA-seq: accounting for selection bias. *Genome Biology*, 11, pp. R14.

### See Also

`runGOseq` `runSpinglass` `runBioNet` `extractModules` `plotModule`

### Examples

```
## Commented out below. See vignette for more details ##

##load sample data with only PvalueObject filled in##
data(test_annotation_score_data)

## show goseq analysis for module 1 ##
extractGOseq(test_annotation, 1)

## show goseq analysis for module 1 and 2 ##
#extractGOseq(test_annotation, 1:2)

## search for term ##

#searchGOseq(test_annotation, "Cell cycle")
```

---

extractModification    *Extract some or all loaded modifications or a the summary of combined effects*

---

### Description

After having loaded modifications into a PvalueAnnotation, these functions can be used to display the GRanges with the modification of interest, or the data frame containing a summary of the combined effects.

### Usage

```
extractModification(pvalue_annotation, mod_type = "methylation")
extractModSummary(pvalue_annotation)
```

### Arguments

pvalue\_annotation    An s4 object of class PvalueAnnotation

mod\_type    A string or character vector that must match one or more of the loaded modifications. If NULL (DEFAULT) then it will show all modifications.

### Value

A GRanges object containing the modification(s) of interest or a data frame with a summary of the combined p-values and effects

### Author(s)

N. Ari Wijetunga

### See Also

extractExpression    annotateModification    removeModification

### Examples

```
##NOTE: Comment out in example see vignette for more detailed usage ##

## Load genome bed file ##
data(hg19_genes_bed)

## Load curated DNA methylation bed file ##
#data(methylationdata)
#methylation <- methylation[-which(is.na(methylation[,5])),]
#methylation[, 5] <- replace(methylation[,5],methylation[,5] == 0,
#min(subset(methylation[, 5], methylation[, 5] !=0 ), na.rm=TRUE))

## Create a PvalueAnnotation with defaults for promoter size##
```

```
test_annotation<-makePvalueAnnotation(data=hg19_genes, gene_name_col=5)

## Load DNA methylation into PvalueAnnotation ##
#test_annotation <- annotateModification(pvalue_annotation=test_annotation,
#methylation, weight_by=c(promoter="distance", body="distance"), verbose=TRUE,
#mod_corr=FALSE, mod_type="methylation")

## Extract GRanges with modification data ##
#extractModification(pvalue_annotation=test_annotation)
```

---

extractModules	<i>View specific modules within a PvalueAnnotation</i>
----------------	--

---

### Description

Having identified modules within a Pvalue annotation, this function allows the user to display 1 or more of the module genes.

### Usage

```
extractModules(pvalue_annotation, which_module = NULL)
```

### Arguments

`pvalue_annotation` An S4 object of class PvalueAnnotation for which Spinglass or BioNet has already been run.

`which_module` A numeric vector specifying one or more module to display

### Value

A list with each element containing the requested modules

### Author(s)

N. Ari Wijetunga

### See Also

plotModule runGOseq extractGOseq runSpinglass runBioNet

### Examples

```
data(test_annotation_score_data)

extractModules(pvalue_annotation=test_annotation, which_module=1)
```

---

extractScores	<i>Extract scores for all genes</i>
---------------	-------------------------------------

---

**Description**

A function to obtain all gene scores

**Usage**

```
extractScores(pvalue_annotation)
```

**Arguments**

`pvalue_annotation`  
An S4 object of class `PvalueAnnotation` for which scores have already been calculated

**Value**

A named vector containing all gene scores

**Author(s)**

N. Ari Wijetunga

**See Also**

`scorePval` `extractModules` `highScores`

**Examples**

```
data(test_annotation_score_data)
out <- extractScores(pvalue_annotation=test_annotation)
head(out)
```

---

genes\_for\_conversiontest

*A small set of RefSeq genes for converting*

---

**Description**

This toy dataset has 100 randomly selected RefSeq genes and can be used to test conversion functionality in SMITE

**Usage**

```
data("genes_for_conversiontest")
```

**Format**

A data frame with 100 observations on the following 1 variables.

**column1** a character vector of RefSeqGene IDs

**Value**

A dataframe with genes in Refseq format for conversion testing.

**Examples**

```
data("genes_for_conversiontest")  
genes[,1]<-convertGeneIds(gene_IDs=genes[,1], ID_type="refseq",  
                          ID_convert_to="symbol")
```

---

hg19\_genes\_bed

*A bed file annotating Refseq genes for the hg19 genome build*

---

**Description**

A gene annotation BED file containing columns for RefSeq name and Gene Symbol

**Usage**

```
data("hg19_genes_bed")
```

**Format**

A data frame with 41633 observations on the following 6 variables.

- column 1** a character vector for chromosome
- column 2** an integer vector for start position
- column 3** an integer vector for end position
- column 4** an character vector for RefSeq gene names
- column 5** an character vector for Gene Symbol names
- column 6** an character vector for strand

**Details**

A BED files taken from the table browser.

**Value**

A dataframe in BED format (chromosome, start, end) with additional columns for gene name as Refseq and gene symbol and strand.

**Source**

Karolchik D, Hinrichs AS, Furey TS, Roskin KM, Sugnet CW, Haussler D, Kent WJ. The UCSC Table Browser data retrieval tool. Nucleic Acids Res. 2004 Jan 1;32 (Database issue):D493-6.

**References**

<http://genome.ucsc.edu/>

**Examples**

```
data(hg19_genes_bed)
```

---

highScores

*Generate a vector of the highest scoring genes*

---

**Description**

This function can be used to extract a subset of the highest scoring genes for other downstream analysis.

**Usage**

```
highScores(pvalue_annotation, alpha = 0.05)
```

**Arguments**

pvalue_annotation	An S4 object of class PvalueAnnotation for which scoring has already been performed
alpha	A numeric specifying a threshold at significant genes can be determined. DEFAULT is alpha=0.05.

**Details**

This function randomly samples the scores with replacement 100 times and for within each random sample for each score it determines the proportion of scores at or greater than the score. The average of these proportions over the 100 samples will be the new p-value/scores. All scores falling below the threshold will be returned.

**Value**

A named vector of scores.

**Author(s)**

N. Ari Wijetunga

**See Also**

scorePval plotCompareScores runSpinglass runBioNet

**Examples**

```
data(test_annotation_score_data)

## Note: commented out for example. See vignette for better example ##

#out <- highScores(pvalue_annotation=test_annotation, alpha=0.01)
```

---

histone\_h3k4me1      *A toy dataset of H3k4me1 peaks to test within SMITE*

---

**Description**

A toy dataset of H3k4me1 peaks from liver ChIP-seq through the encode project. The file is a BED file.

**Usage**

```
data(histone_h3k4me1)
```

**Format**

A data frame with 75448 observations on the following 3 variables.

**column1** a character vector specifying chromosome

**column2** an integer vector specifying start

**column3** an integer vector specifying end

**Details**

This is a BED file that specifies the consensus locations of three H3K4me1 ChIP-seq experiments performed on normal adult liver.

**Value**

A dataframe in BED format (chromosome, start, end).

**Source**

GSM669972, GSM621654, GSM537706

Roadmap Epigenomics Lister R, et al. Nature. 2009 Nov 19;462(7271):315-22 ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. Nature. 2012 Sep 6;489(7414):57-74.

**Examples**

```
data(histone_h3k4me1)
head(h3k4me1)
```

---

makePvalueAnnotation *Initialize a PvalueAnnotation*

---

**Description**

This function initializes a PvalueAnnotation using a gene BED file and optional BED files corresponding to interval datasets. This is a necessary first step in order to establish for each gene the gene promoter, body and associated intervals.

**Usage**

```
makePvalueAnnotation(data, other_data = NULL, other_tss_distance = 10000,
  promoter_upstream_distance = 1000, promoter_downstream_distance = 1000,
  strand_col = NULL, gene_name_col = NULL)
```

**Arguments**

<code>data</code>	A required gene annotation BED file like that obtained from the UCSC Table Browser. At a minimum BED files must have the first three columns as (chromosome, start, end). Additional required columns should correspond to the strand and gene name. The gene name needs to match the gene format desired for the interaction network. Duplicated gene names and associated gene annotations are removed.
<code>other_data</code>	A list of BED files corresponding to each additional interval file to be associated with genes. The function will use the <code>other_tss_distance</code> variable and the gene transcription start site (TSS) to find for each gene all intervals within <code>[tss-other_tss_distance, tss+other_tss_distance]</code> .
<code>other_tss_distance</code>	A vector specifying for each element of <code>otherdata</code> a distance from the gene TSS to consider that interval as related to a gene. If the length of <code>other_tss_distance</code> does not match the length of the <code>otherdata</code> list, then the first value is used for all datasets in the <code>otherdata</code> list. DEFAULTS to 10,000 base pairs.
<code>promoter_upstream_distance</code>	A numeric specifying how far upstream from the gene TSS is considered part of the gene promoter. DEFAULTS to 1,000 base pairs.
<code>promoter_downstream_distance</code>	A numeric specifying how far downstream from the gene TSS is considered part of the gene promoter. Gene bodies subtract the <code>promoter_downstream</code> region. DEFAULTS to 1,000 base pairs.
<code>strand_col</code>	A numeric specifying the column of the gene BED file ( <code>data</code> ) corresponding to the gene strand. If this is not provided, the function will attempt to determine the strand.
<code>gene_name_col</code>	A numeric specifying the column of the gene BED file ( <code>data</code> ) corresponding to the gene name.

**Details**

The required only input file is the gene annotation BED file that should have (as all BED files) the chromosome, start and end in columns 1,2 and 3, respectively. Also, there should be a column for gene name and gene strand. The user needs to determine distance from the gene transcription start site that will define the gene promoter. The gene body will then be calculated as the non-promoter overlapping sequence. If optional BED files are given as `otherdata` (e.g. transcription factor binding sites, histone modification peaks), then the user will also decide a distance from the gene TSS to associate each BED interval with a gene. For a particular BED file, each genes may have more than one interval that falls within the desired range around a TSS. Unique gene names are required and the function will automatically remove duplicated genes. We recommend deciding on an interaction network first and then loading a gene annotation BED file with the same names. This will likely necessitate allowing the function to pick one annotation of a gene, or pre- processing using some criteria (e.g. longest transcript).

**Value**

An S4 object of class `PvalueAnnotation` containing slots for an annotation (`GRangesList`), an expression set, modifications (`GRangesList`), and a `PvalueObject`.

**Author(s)**

N. Ari Wijetunga

**See Also**

SMITE vignette

**Examples**

```
## Note: Commented out below. See vignette for more detailed usage information##  
  
## Load genome bed file ##  
data(hg19_genes_bed)  
  
## Create a PvalueAnnotation with defaults for promoter size##  
test_annotation <- makePvalueAnnotation(data=hg19_genes, gene_name_col=5)
```

---

makePvalueObject	<i>Function to make a PvalueObject within a PvalueAnnotation</i>
------------------	--

---

**Description**

Having annotated modifications and expression data this function will assemble a PvalueObject within the slot "score\_data" of a PvalueAnnotation. This is a necessary step before being able to run downstream functions.

**Usage**

```
makePvalueObject(pvalue_annotation, effect_directions = NULL)
```

**Arguments**

`pvalue_annotation`  
An S4 object of class PvalueAnnotation

`effect_directions`  
A character vector with optional names specifying "increase" Modification is expected to increase as expression increase "decrease" Modification is expected to decrease as expression decreases "bidirectional" No direction is assumed between modification and direction

**Details**

The specified relationship between the modification and expression will be stored and then used when scoring.

**Value**

An S4 object of class PvalueAnnotation with a slot for score\_data filled it

**Author(s)**

N.Ari Wijetunga

**See Also**

makePvalueAnnotation

**Examples**

```

#NOTE: Commented out in example, please see vignette for more details##
options(stringsAsFactors=FALSE)

data(methylationdata)
methylation <- methylation[~which(is.na(methylation[, 5])), ]
#methylation[, 5] <- replace(methylation[, 5],methylation[, 5] == 0,
#min(subset(methylation[, 5], methylation[, 5] != 0), na.rm=TRUE))

#data(curated_expressiondata)
#data(hg19_genes_bed)
#data(histone_h3k4me1)

#test_annotation<-makePvalueAnnotation(data=hg19_genes,
#other_data=list(h3k4me1=h3k4me1), gene_name_col=5,other_tss_distance=5000)

#fill in expression data
#test_annotation<-annotateExpression(test_annotation, expression_curated)

#fill in methylation data
#this step takes ~10 minutes
#test_annotation<-annotateModification(test_annotation, methylation,
#weight_by=c(promoter="distance",body="distance",h3k4me1="distance"),
#verbose=TRUE, mod_corr=FALSE)

#create a pvalue object that will count the effect of the h3k4me1 as
#bidirectional
#test_annotation<-makePvalueObject(pvalue_annotation=test_annotation,
#effect_directions=c(methylation_promoter="decrease",
#methylation_body="decrease", methylation_h3k4me1="bidirectional"))

```

---

methylationdata

*A toy dataset of DNA methylation to test within SMITE*


---

**Description**

A toy dataset of raw DNA methylation from HELP-tagging. The file is a BED file with columns added for effect and p-value.

**Usage**

```
data(methylationdata)
```

**Format**

A data frame with 40000 observations on the following 5 variables.

**column1** a character vector specifying chromosome

**column2** an integer vector specifying start

**column3** an integer vector specifying end

**column4** a numeric vector with an effect direction (here it is average difference between two groups)

**column5** a numeric vector with a two sided t-test p-value

**Details**

This is a small subset of a DNA methylation dataset is a randomized version of the Toxoplasma dataset used to benchmark. We could not include the larger version do to package size requirements but larger versions are available. See Github source below. It still has NAs and p-values=0.

**Value**

A dataframe in BED format (chromosome, start, end) with additional columns for and effect direction and p-value derived from T-tests of HELP-tagging DNA methylation data.

**Source**

Manuscript in preparation. Please see <https://github.com/GreallyLab/SMITE> for more details.

**Examples**

```
data(methylationdata)
```

```
any(is.na(methylation[, 4]))
```

```
any(methylation[, 4] == 0)
```

---

normalizePval

*This function normalizes p-values (Scores) that are otherwise on different scales.*

---

**Description**

This function is a used to rescale component scores when distributions have been altered. There are two methods available.

**Usage**

```
normalizePval(pvalue_annotation, trans, ref = "expression_pvalue", method = "rescale")
```

**Arguments**

pvalue_annotation	An S4 object of class p-value annotation
trans	A vector specifying a specific Box-cox power transformation to use. If not specified, the optimal transformation powers will be estimated.
ref	A string that will be grepped from the names of the loaded expression data or modification/context pairing. All scores will be rescaled to match this reference's range. The DEFAULT is expression.
method	A string of either "Rescale" DEFAULT "rescale" Performs a logit transform and rescales all probabilities to the reference's logit transformed scale, then back-transforms "Box-Cox" "box-cox" "boxcox" "Boxcox" For each probability vector does a logit transform and then iterates between 0.5 and 0.95 by 0.05 to determine the most similar transformation to the logit transformed reference by a Wilcoxon- test

**Details**

Normalization may not be necessary but should improve some p-values from driving the majority of downstream scores and modules solely because of the scale of their p-values. All transformations are monotonic and are controlled for by use of randomization procedure downstream. procedures downstream should

**Value**

An S4 object of class PvalueAnnotation with normalized p-values within the pval\_data slot of the PvalueObject "score\_data" slot

Plots densities of p-values before and after transform

**Author(s)**

N. Ari Wijetunga

**See Also**

makePvalueObject scorePval plotDensityPval

**Examples**

```
data(test_annotation_score_data)

#test_annotation<-normalizePval(pvalue_annotation=test_annotation)
```

---

plotCompareScores	<i>Compare two genomic features by score and display them in a hexbin plot</i>
-------------------	--

---

### Description

This function creates a hexbin of the log transformed p-value/score for any two expression or modification-context pairing within a PvalueObject inside of a PvalueAnnotation

### Usage

```
plotCompareScores(pvalue_annotation, x_name, y_name, ...)
```

### Arguments

pvalue_annotation	An S4 object of class PvalueAnnotation for which a PvalueObject has already been created
x_name	A string to be grepped from the columns within the slot "pval_data" that is within the PvalueAnnotation slot "score_data." This column will be plotted on the x-axis with a direction specified from the corresponding effect column.
y_name	A string to be grepped from the columns within the slot "pval_data" that is within the PvalueAnnotation slot "score_data." This column will be plotted on the y-axis with a direction specified from the corresponding effect column.
...	Other plotting parameters

### Details

This plotting function creates a hexbin plot of any two p-value vectors stored within a p-value object. It can be used to define relationships between direction and significance in different genomic contexts after having combined p-values.

### Value

A hexbin plot

### Author(s)

N. Ari Wijetunga

### See Also

makePvalueObject plotDensityPval

**Examples**

```
data(test_annotation_score_data)

plotCompareScores(pvalue_annotation=test_annotation, x_name="expression",
y_name="methylation_promoter")
```

---

plotDensityPval            *Plot the density of the combined scores stored in a PvalueObject*

---

**Description**

This function is called by the normalizePval function, but can also be called by the user to visualize the relative densities of combined p-values (scores).

**Usage**

```
plotDensityPval(pvalue_annotation, ref = "expression_pvalue", ...)
```

**Arguments**

pvalue_annotation	An S4 object of class PvalueAnnotation.
ref	A character specifying the name of the reference category. DEFAULT is "expression_pvalue"
...	Additional plotting arguments

**Value**

Plots a multidensity plot.

**Author(s)**

N. Ari Wijetunga

**Examples**

```
## Load test annotation with only score data ##
data(test_annotation_score_data)

plotDensityPval(pvalue_annotation=test_annotation)
```

---

plotModule

*Plot a specific module after running Spinglass algorithm*


---

## Description

This function is an adapted version of renderModule available through Epimods. We have added optional functionality including plotting the actual raw data onto the node edges, adding goseq annotation to the plot, legends and plotting modes.

## Usage

```
plotModule(pvalue_annotation, p_thresh = 0.05, which_network = 1, goseq = FALSE,
  layout = "fr", legend = TRUE, namestyle = "symbol", suppress_details = FALSE,
  meth_hi_col = "blue", meth_low_col = "yellow1",
  meth_mid_col = "gray90", exp_hi_col = "red1", exp_low_col = "chartreuse1",
  exp_mid_col = "gray90", label_scale = TRUE, label_shadow = FALSE, compare_plot=FALSE,
  pdf_out=NULL)
```

## Arguments

pvalue_annotation	An S4 object of class PvalueAnnotation
p_thresh	A numeric specifying a threshold for plotting raw data on edges of nodes. DEFAULT is alpha=0.05. Items above this threshold will be classified as "mid" instead of "high" or "low" "
which_network	A numeric specifying which network to plot. DEFAULTS to 1, and will not plot another network until specified explicitly.
goseq	A logical indicating whether to plot goseq results for the module on the right hand side of the plot.
layout	A character string as either "fr" (DEFAULT) for fruchterman.reingold or "circle" for a circular plot.
legend	A logical (TRUE(DEFAULT)/FALSE) specifying whether a legend should be drawn.
namestyle	A character string as either "symbol" (DEFAULT) for gene symbols or "refseq" for RefSeq genes. If modules were performed on RefSeq genes, then the function will plot with gene symbols so that it is more useful.
suppress_details	A logical (TRUE(DEFAULT)/FALSE) indicating whether border raw data information should be plotted.
meth_hi_col	A color to be associated with significant modification data with positive effects
meth_low_col	A color to be associated with significant modification data with negative effects
meth_mid_col	A color to be associated with non-significant modification data
exp_hi_col	A color to be associated with significant expression data with positive effects

exp_low_col	A color to be associated with significant expression data with negative effects
exp_mid_col	A color to be associated with non-significant expression data
compare_plot	A logical (TRUE/FALSE(DEFAULT)) indicating whether two plots should be drawn side by side, one with raw data and one without
label_scale	A logical (TRUE(DEFAULT)/FALSE) indicating whether whether the node label should be scaled with the node score
label_shadow	A logical (TRUE/FALSE(DEFAULT)) indicating whether whether the node label should have a white text shadow for easier label reading
pdf_out	A string indicating a location to which the function should output a pdf. If NULL (DEFAULT) then no pdf is made.

**Value**

A plot of the module

**Author(s)**

N. Ari Wijetunga

**See Also**

extractModules

**Examples**

```
data(test_annotation_score_data)

#plotModule(pvalue_annotation=test_annotation, which_network=2)

#plotModule(pvalue_annotation=test_annotation, which_network=2,
#suppressDetails=TRUE)
```

---

Reactome.Symbol.Igraph

*An Igraph network for REACTOME with nodes as gene symbols*

---

**Description**

This is an Igraph network that was created using the REACTOME protein-protein interaction database.

**Usage**

```
data("Reactome.Symbol.Igraph")
```

**Format**

An igraph object with 5770 nodes and 114288 edges

**nodes** gene names as gene symbols

**edges** paired genes that interact

**Details**

The provided igraph file was created using the igraph package and the interaction file provided from the reference.

**Value**

An Igraph network based off of REACTOME interactions

**Source**

REACTOME

**References**

<http://www.reactome.org/pages/download-data/>

**Examples**

```
data(Reactome.Symbol.Igraph)
head(igraph::V(REACTOME))
```

---

removeModification      *A function to "unload" a modification that has already been added.*

---

**Description**

After using the annotateModification function to load a modification into a PValue annotation, you may wish to remove a modification or reannotate one, which requires removing it first.

**Usage**

```
removeModification(pvalue_annotation, mod_type = "methylation")
```

**Arguments**

pvalue\_annotation      An S4 object of class PvalueAnnotation

mod\_type                A character string that identifies a type of modification within a PvalueAnnotation.

**Value**

An S4 object of class PvalueAnnotation

**Author(s)**

N. Ari Wijetunga

**See Also**

annotateModification extractModification extractModSummary

**Examples**

```
##NOTE: Commented out in example. ##
## Please see vignette for more detailed usage information ##

## Load genome bed file ##

#data(hg19_genes_bed)

## Load curated DNA methylation bed file ##

data(methylationdata)
methylation <- methylation[-which(is.na(methylation[, 5])), ]
methylation[, 5] <- replace(methylation[, 5], methylation[, 5] == 0,
  min(subset(methylation[, 5], methylation[, 5] != 0), na.rm=TRUE))

#meth1<-methylation

## make second curated test methylation bed file ##

#meth2<-methylation

## Create a PvalueAnnotation with defaults for promoter size##
#test_annotation<-makePvalueAnnotation(data=hg19_genes, gene_name_col=5)

## Load DNA methylation into PvalueAnnotation ##
#test_annotation<-annotateModification(annotation=test_annotation,
#mod_data=meth1, weight_by=c(promoter="distance",body="distance"),verbose=TRUE,
#mod_corr=TRUE,mod_type="methylation")

## Extract GRanges with modification data ##
#extractModification(test_annotation)

## Load second dataset bed file ##
#test_annotation<-annotateModification(pvalue_annotation=test_annotation,
#mod_data=meth2, weight_by=c(promoter="distance",body="distance"),
#verbose=TRUE, mod_corr=TRUE,mod_type="hydroxy")

## Extract GRanges with both modification dataset loaded ##
#head(extractModification(test_annotation,"hydroxy"))
```

```
## Unload DNA hydroxymethylation form PvalueAnnotation ##  
  
#test_annotation<-removeModification(pvalue_annotation=test_annotation,  
                                     #mod_type="hydroxy")  
  
## Extract GRanges to see only one modification dataset loaded ##  
#head(extractModification(pvalue_annotation=test_annotation))
```

---

runBioNet

*Perform BioNet Analysis on a PvalueAnnotation*

---

## Description

With BioNet, a researcher can find a single interconnected gene module using the highest scoring genes generated in a PvalueAnnotation. This function will load the module into the PvalueAnnotation for visualization and downstream analysis.

## Usage

```
runBioNet(pvalue_annotation, network, alpha = 0.05)
```

## Arguments

pvalue_annotation	An S4 object of class PvalueAnnotation that has already had scores generated.
network	An interaction network of class graphNEL or igraph.
alpha	A numeric specifying a cutoff for high scoring genes to be return with the high-Scores function.

## Details

The input of p-values to BioNet discussed in the BioNet vignette involves first modeling p-values as a Beta-uniform mixture model to obtain the actual corresponding probability function values. Since our scoring method produces p-values/scores that are uniform in distribution, we input them directly into the BioNet algorithm. For more details on BioNet see the reference or runFastHeinz in the BioNet package.

## Value

A PvalueAnnotation with a loaded module.

## Note

This is a wrapper function to run BioNet. The actual BioNet code was created by Beisser et al.

## Author(s)

N. Ari Wijetunga

## References

Beisser et al. BioNet: an R-Package for the functional analysis of biological networks. *Bioinformatics*. 2010 Apr 15;26(8):1129-30. doi: 10.1093/bioinformatics/btq089. Epub 2010 Feb 25.

## See Also

plotModule extractModule runGOseq

## Examples

```
## load test data ##
data(test_annotation_score_data)

## NOTE: commented out for example. See vignette for better explanation ##

#load reactome network with gene symbols ##
#load(system.file("data", "Reactome.Symbol.Igraph.rda", package="SMITE"))

## run BioNet ##
#test_annotation<-runBioNet(pvalue_annotation=test_annotation,
#network = REACTOME)

## view module ##
#extractModules(pvalue_annotation=test_annotation, 1)

## plot module ##
#plotModule(pvalue_annotation=test_annotation, which.network=1)
```

---

runGOseq

*Run a GoSeq pathway analysis*

---

## Description

This function allows pathway annotation of identified modules.

## Usage

```
runGOseq(pvalue_annotation, p_thresh = 0.05, supply_cov=TRUE, coverage=NULL, type = "reactome")
```

## Arguments

pvalue_annotation	An S4 object of class PvalueAnnotation, for which module-finding has already been performed
p_thresh	A numeric specifying a threshold for significance of FDR (q-values). DEFAULT is alpha=0.05

supply_cov	A logical specifying whether or not the user wants to supply their own coverage (TRUE), or would like SMITE to calculate the coverage based on methylation data already inputted. DEFAULT is TRUE.
coverage	A data.frame that is a bed file (chr start stop) folowed by a gene name and a numeric specifying the bias data (e.g. gene length or number of probes related to gene). DEFAULT is null
type	Either "kegg" to run KEGG analysis or "reactome" to run a REACTOME analysis

### Details

Goseq analysis is useful since it allows you to assess term/pathway enrichment in a collection of genes, while adjusting for bias data. Potential bias can be from aspects like gene length or probe density that influence the likelihood of finding a particular gene. For more information please see the goseq reference.

The function will compare all of the genes within a module to known pathways and terms to find the terms that are most enriched within a module. In this way, this tool allows a reasearch to find a functional importance of a module.

We currently offer KEGG and REACTOME analysis, although additional pathway tools may be added in the near future.

### Value

A PvalueAnnotation with goseq annotated modules.

### Note

This is a wrapper function written by N. Ari Wijetunga for the package SMITE.

### Author(s)

Matthew D. Young myoung at wehi.edu.au

### References

Young MD, Wakefield MJ, Smyth GK and Oshlack A (2010). Gene ontology analysis for RNA-seq: accounting for selection bias. *Genome Biology*, 11, pp. R14.

### See Also

searchGOseq extractGOseq runSpinglass runBioNet extractModules plotModule

### Examples

```
##load sample data with only PvalueObject filled in##
data(test_annotation_score_data)

## NOTE commented out in example. Please see Vignette for better example ##
#test_annotation<-runGOseq(pvalue_annotation=test_annotation,
```

```
#coverage=read.table(
#system.file("extdata", "hg19_symbol_hpaii_sites_inbodyand2kbupstream.bed.gz",
#package="SMITE"),stringsAsFactors=FALSE),type="kegg")

## search for a term ##
searchGOseq(test_annotation,"Cell cycle")

## show goseq analysis for module 1 ##
#extractGOseq(test_annotation,1)
```

---

runSpinglass

*Run Spinglass algorithm on a Scored PvalueAnnotation*


---

## Description

This function is a function to prepare the data for calling the Spinglass network algorithm.

## Usage

```
runSpinglass(pvalue_annotation, network, random_alpha = 0.05, gam = 0.5,
node_alpha = 0.05, maxsize = 500, minsize = 8, num_iterations = 1000, simplify = TRUE)
```

## Arguments

pvalue_annotation	An S4 object of class PvalueAnnotation
network	An graph object of class graphNEL or igraph
random_alpha	A numeric specifying a threshold with which to determine module significance after randomization
gam	A parameter used by the Spinglass algorithm
node_alpha	The proportion of nodes to be used as seeds for the community detection
maxsize	The maximum module size
minsize	The minimum module size
num_iterations	The number of randomizations that will be computed to determine whether the module is significant by chance
simplify	A logical (TRUE(DEFAULT)/FALSE) that specifies whether network should be simplified by removing self loops and repeated edges

## Details

In the provided Epimods reference, West et al outlined the advantages of using the spin-glass algorithm in the detection of modules. Please consult the reference for more detailed information on the spin-glass algorithm implemented in the package igraph.

Like Epimods, this function employs the spin-glass algorithm implemented in igraph and uses random permutations to assess the "modularity," the number and strength of connected nodes, of a module. However, SMITE scores are interpreted as Chi-square distributed statistics whenever possible, rather than the weighted-T-statistic in Epimods.

## Value

An S4 object of class PvalueAnnotation with modules loaded

## Note

This function was adapted from a function in the Epimods package that employs the spin-glass algorithm and uses random permutations to assess the "modularity" of a module . The original function was created by West et al.

## Author(s)

N. Ari Wijetunga

## References

James West, Stephan Beck, Xiangdong Wang & Andrew E. Teschendorff An integrative network algorithm identifies age-associated differential methylation interactome hotspots targeting stem-cell differentiation pathway. Scientific Reports 3, Article number: 1630 (2013)

<https://code.google.com/p/epimods/>

## See Also

FEM runBioNet extractModules plotModule

## Examples

```
data(test_annotation_score_data)

#load(system.file("data", "Reactome.Symbol.Igraph.rda", package="SMITE"))

## NOTE: commented out for example. See vignette for better explanation ##
#test_annotation <- runSpinglass(pvalue_annotation=test_annotation,
#network=REACTOME, maxsize=50, num_iterations=10)

plotModule(test_annotation, which_network=6, layout="fr")
```

---

`scorePval`*Making a single combined score for each gene*

---

**Description**

This function uses an a priori weighting scheme to combine scores for a given gene.

**Usage**

```
scorePval(pvalue_annotation, weights)
```

**Arguments**

`pvalue_annotation`

An S4 object of class `PvalueAnnotation`, for which `makePvalueObject` has already been run.

`weights`

A numeric vector of the relative importance of expression, modifications, and genomic contexts toward the final score. Names should be provided that match the "modification\_genomicfeature" format, except for expression. While the scores do not have to add up to 1, it is good practice to impose this restriction in order to track the relative importance.

**Details**

Because each weighting scheme generates scores from a distribution that will change depending on the analysis inputs, the function will randomly sample the final scores and compare each derived score to this simulated distribution.

If no names are given, then the function will assume the weights are in the order that it finds a particular "modification\_genomicfeature" and it will print the weighting scheme so that you can verify it is correct. The total number of weights must match the total number of modifications\*genomicfeatures+1 for expression.

After calculating a combined score (using a Stouffer's weighted statistic), a new p-value is derived using a non-parametric sampling approach.

**Value**

An S4 object of class `PvalueAnnotation`.

**Author(s)**

N. Ari Wijetunga

**Examples**

```
options(stringsAsFactors=FALSE)

data(test_annotation_score_data)

## NOTE: commented out for example. See vignette for better explanation ##
#test_annotation<-scorePval(pvalue_annotation=test_annotation,
#weights=c(methylation_promoter=.3,methylation_body=.1,expression=.3,
#methylation_h3k4me1=.3))
```

---

 stoufferTest

*Stouffer's Test*


---

**Description**

This function performs a weighted Stouffer's method of combining p-values.

**Usage**

```
stoufferTest(pvalues, weights)
```

**Arguments**

pvalues	A vector of p-values.
weights	Optional weights used when combining probabilities. If no weights are given then the p-values are equally weighted.

**Details**

For each p-value the inverse standard normal CDF is applied and Z scores are derived. Z-scores are then summed and a new Z score is transformed back to a p-value.

**Value**

A numeric p-value that represents the standard normal CDF of the combined Z statistic.

**Note**

This function was adapted from the function written on the Fisher's Method wikipedia page.

**References**

[https://en.wikipedia.org/wiki/Fisher's\\_method](https://en.wikipedia.org/wiki/Fisher's_method)  
 Stouffer S, DeVinney L, Suchman E. The American soldier: Adjustment during army life. Vol. 1. Princeton University Press; Princeton, US: 1949.

### Examples

```
## Generate test weights ##
weights<-runif(10, 1,100)
weights<-sort(weights)

## Generate test p-values##
pvals<-runif(10,0,1)

## run stoufferTest ##
stoufferTest(pvalues = pvals, weights=1/weights)
```

---

```
test_annotation_score_data
      A toy PvalueAnnotation
```

---

### Description

This Pvalue annotation has only scoring data filled in to use in late pipeline "SMITE" functions. It can be used to skip the loading data phase of analysis and test latter functionality.

### Usage

```
data("test_annotation_score_data")
```

### Format

A PvalueAnnotation with the following slots

**score\_data** a PvalueObject with slots corresponding to pval\_data, effect\_data, genes, signs\_index, scores, trans, scoring\_vector, and module\_otuput

### Details

This is a PvalueAnnotation which has had all of the pre-scoring data removed so that it is only usefull for using functions beginning with SMITE and SMITE plotting functions.

### Value

A PvalueAnnotation with the score\_data slot containing toy scores

### Examples

```
data(test_annotation_score_data)
plotDensityPval(test_annotation)
head(extractScores(test_annotation))
```

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