Package 'regionalpcs'

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Title Summarizing Regional Methylation with Regional Principal Components Analysis

Version 1.10.0

Description Functions to summarize DNA methylation data using regional principal components. Regional principal components are computed using principal components analysis within genomic regions to summarize the variability in methylation levels across CpGs. The number of principal components is chosen using either the Marcenko-Pasteur or Gavish-Donoho method to identify relevant signal in the data.

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Encoding UTF-8

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URL https://github.com/tyeulalio/regionalpcs

BugReports https://github.com/tyeulalio/regionalpcs/issues

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Imports dplyr, PCAtools, tibble, GenomicRanges

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`combine_results` *Combine results dataframes across regions*

Description

Combine results dataframes across regions

Usage

```
combine_results(res, df_name)
```

Arguments

`res`	List of lists; contains summarized region results
`df_name`	String; name of result being combined (sig_pcs or percent_var)

Value

Data Frame containing results

Examples

```
# Create example data for 'sig_pcs' and 'percent_var'
    sig_pcs_example <- data.frame(pcs = c("PC1", "PC2"),
value = c(0.2, 0.4))
percent_var_example <- data.frame(pcs = c("PC1", "PC2"),
value = c(0.7, 0.3))

# Create 'res' list containing both 'sig_pcs' and 'percent_var'
res <- list(region = "Region1", sig_pcs = sig_pcs_example,
percent_var = percent_var_example)
```

```
# Example function use: Combine 'sig_pcs' across regions
combined_sig_pcs <- combine_results(res, df_name = "sig_pcs")
print(combined_sig_pcs)
```

`compute_dimension` *Compute significant dimensions of a matrix using the Marchenko-Pastur or Gavish-Donoho methods*

Description

Compute significant dimensions of a matrix using the Marchenko-Pastur or Gavish-Donoho methods

Usage

```
compute_dimension(
  x,
  var_explained,
  noise_select,
  pc_method = c("gd", "mp"),
  verbose = FALSE
)
```

Arguments

`x`	A data frame or matrix of methylation values; rows = features, columns = samples
`var_explained`	A numeric vector containing the variance explained by successive PCs, sorted in decreasing order. (Used for PCAtools)
`noise_select`	Numeric scalar specifying the variance of the random noise (Used for PCAtools)
`pc_method`	String indicating the method for estimating dimension; "gd" = Gavish-Donoho, "mp" = Marchenko-Pastur
`verbose`	Boolean indicating whether to print statements while running, default = FALSE

Value

Numeric scalar representing the optimal number of PCs to retain using the specified method

Examples

```
x <- diag(4)
pca_res <- PCAtools::pca(x) # Run PCA
eig_sq <- pca_res$sdev^2 # Compute variance explained
compute_dimension(x, eig_sq, 1, "gd")
```

compute_regional_pcs *Compute regional principal components for methylation data*

Description

Compute regional principal components for methylation data

Usage

```
compute_regional_pcs(
  meth,
  region_map,
  pc_method = c("gd", "mp"),
  verbose = FALSE
)
```

Arguments

meth	Data frame of methylation beta values, with CpGs in rows and samples in columns
region_map	Data frame mapping CpGs to gene regions
pc_method	Method to use for PC computation, either 'gd' (Gavish-Donoho) or 'mp' (Marchenko-Pastur)
verbose	Logical, should progress messages be displayed?

Value

A list containing several elements, including the regional PCs, percent variance, and other information

Examples

```
# Create synthetic methylation data
meth_data <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(meth_data) <- paste0("CpG", 1:100)
colnames(meth_data) <- paste0("Sample", 1:10)

# Create a synthetic region map
region_map_data <- data.frame(
    region_id = rep(c("Gene1", "Gene2"), each = 50),
    cpg_id = rownames(meth_data)
)

# Run the function
compute_regional_pcs(meth_data, region_map_data, pc_method = 'gd')
```

create_region_map *Create a Region Map Between CpGs and Gene Regions*

Description

This function generates a map that assigns CpG sites to gene regions, establishing a linkage based on their genomic coordinates and providing a foundation for subsequent region-specific analyses.

Usage

```
create_region_map(cpg_gr, genes_gr, verbose = FALSE)
```

Arguments

cpg_gr	A GRanges object containing the genomic positions of CpG sites.
genes_gr	A GRanges object containing the genomic positions of gene regions (e.g., promoters) of interest.
verbose	Boolean; print output statements

Value

A data.frame with mappings between gene IDs and CpG IDs, facilitating associating CpG sites with their corresponding gene regions for downstream analyses.

Examples

```
library(GenomicRanges)

# Creating dummy GRanges objects for CpG sites and gene regions
cpg_gr <- GRanges(seqnames=c("chr1", "chr1", "chr2"),
                  ranges=IRanges(start=c(100, 200, 150),
                  end=c(100, 200, 150)))
genes_gr <- GRanges(seqnames=c("chr1", "chr2", "chr2"),
                  ranges=IRanges(start=c(50, 100, 130),
                  end=c(150, 180, 160)))
# Creating a region map using the function
region_map <- create_region_map(cpg_gr, genes_gr)
```

get_sig_pcs *Get significant principal components*

Description

Get significant principal components

Usage

```
get_sig_pcs(x, pc_method = c("mp", "gd"), verbose = FALSE)
```

Arguments

x	A data frame or matrix of methylation values; rows = features, columns = samples
pc_method	String indicating the method for estimating dimension; "gd" = Gavish-Donoho (default), "mp" = Marchenko-Pastur
verbose	Boolean; print output statements

Value

List containing four elements; sig_pcs = significant PCs, percent_var = percent variance explained, loadings = PC loadings, est_dim = estimated dimension

Examples

```
x <- diag(4)
get_sig_pcs(x, "gd")
```

summarize_region *Summarize a region using regional principal components*

Description

Summarize a region using regional principal components

Usage

```
summarize_region(region, region_map, meth, pc_method, verbose = FALSE)
```

Arguments

region	String; name of region being processed
region_map	Data frame; Mapping of CpGs to regions, column 1 should be regions, column 2 should be CpGs with the same names as the rows of meth
meth	Data frame or matrix; Methylation values to summarize; rows=CpGs, columns=samples
pc_method	String; indicating the method for estimating dimension; "gd"=Gavish-Donoho (default), "mp"=Marchenko-Pastur
verbose	Boolean; print output statements

Value

list containing PC results

Examples

```
# Create the region map with just one region containing 10 CpGs
region_map <- data.frame(region_id = rep(1, 10), cpg_id = seq(1, 10))

# Create methylation data frame
set.seed(123)
meth <- as.data.frame(matrix(runif(10 * 20, min = 0, max = 1), nrow = 10))
rownames(meth) <- seq(1, 10)

# Call the function
summarize_region(1, region_map, meth, 'gd')
```

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