Package ‘regionalpcs’

February 2, 2024

Title  Summarizing Regional Methylation with Regional Principal Components Analysis

Version  1.0.0

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

Roxygen  list(markdown = TRUE)

RoxygenNote  7.2.3

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

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

biocViews  DNAMethylation, DifferentialMethylation, StatisticalMethod, Software, MethylationArray

Imports  dplyr, PCAtools, tibble, GenomicRanges

Suggests  knitr, rmarkdown, RMTstat, testthat (>= 3.0.0), BiocStyle, tidyr, miniData, TxDb.Hsapiens.UCSC.hg19.knownGene, IRanges

Config/testthat/edition  3

VignetteBuilder  knitr

Depends  R (>= 4.3.0)

LazyData  false

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git_last_commit_date  2023-10-24

Repository  Bioconductor 3.18
combine_results

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
```r
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**

```r
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**

```r
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

**Usage**

```r
compute_regional_pcs(
  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 = c("gd", "mp"),  # Method to use for PC computation, either 'gd' (Gavish-Donoho) or 'mp' (Marchenko-Pastur)
  verbose = FALSE  # Logical, should progress messages be displayed?
)
```

**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**

```r
# 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**

```r
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**

```r
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)))
genesis_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)
summarize_region

Arguments

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<td>region</td>
<td>String; name of region being processed</td>
</tr>
<tr>
<td>region_map</td>
<td>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</td>
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<tr>
<td>meth</td>
<td>Data frame or matrix; Methylation values to summarize; rows=CpGs, columns=samples</td>
</tr>
<tr>
<td>pc_method</td>
<td>String; indicating the method for estimating dimension; &quot;gd&quot;=Gavish-Donoho (default), &quot;mp&quot;=Marchenko-Pastur</td>
</tr>
<tr>
<td>verbose</td>
<td>Boolean; print output statements</td>
</tr>
</tbody>
</table>

Value

list containing PC results

Examples

```r
# 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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