

# Package ‘regionalpcs’

December 16, 2025

**Title** Summarizing Regional Methylation with Regional Principal Components Analysis

**Version** 1.8.0

**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>

**biocViews** DNAMethylation, DifferentialMethylation, StatisticalMethod, Software, MethylationArray

**Imports** dplyr, PCAtools, tibble, GenomicRanges

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|                 |                                                  |
|-----------------|--------------------------------------------------|
| combine_results | <i>Combine results dataframes across regions</i> |
|-----------------|--------------------------------------------------|

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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)
```

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|                   |                                                                                                       |
|-------------------|-------------------------------------------------------------------------------------------------------|
| compute_dimension | <i>Compute significant dimensions of a matrix using the Marchenko-Pastur or Gavish-Donoho methods</i> |
|-------------------|-------------------------------------------------------------------------------------------------------|

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## 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")
```

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compute\_regional\_pcs    *Compute regional principal components for methylation data*

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## 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 | <i>Create a Region Map Between CpGs and Gene Regions</i> |
|-------------------|----------------------------------------------------------|

---

### 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)
```

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|             |                                             |
|-------------|---------------------------------------------|
| get_sig_pcs | <i>Get significant principal components</i> |
|-------------|---------------------------------------------|

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### 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")
```

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summarize\_region

*Summarize a region using regional principal components*


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**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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