

# Package ‘fCCAC’

October 10, 2021

**Version** 1.18.0

**Date** 2020-07-02

**Type** Package

**Title** functional Canonical Correlation Analysis to evaluate Covariance  
between nucleic acid sequencing datasets

**Author** Pedro Madrigal <bioinformatics.engineer@gmail.com>

**Description** An application of functional canonical correlation  
analysis to assess covariance of nucleic acid sequencing  
datasets such as chromatin immunoprecipitation followed by deep  
sequencing (ChIP-seq). The package can be used as well with other types  
of sequencing data such as neMeRIP-seq (see PMID: 29489750).

**Depends** R (>= 3.3.0), S4Vectors, IRanges, GenomicRanges, grid

**Maintainer** Pedro Madrigal <bioinformatics.engineer@gmail.com>

**Imports** fda, RColorBrewer, genomation, ggplot2, ComplexHeatmap,  
grDevices, stats, utils

**Suggests** RUnit, BiocGenerics, BiocStyle

**License** Artistic-2.0

**LazyLoad** yes

**LazyData** yes

**biocViews** Transcription, Genetics, Sequencing, Coverage

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

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** 9de3dbd

**git\_last\_commit\_date** 2021-05-19

**Date/Publication** 2021-10-10

## R topics documented:

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**Description**

An application of functional canonical correlation analysis to assess covariance of nucleic acid sequencing datasets such as chromatin immunoprecipitation followed by deep sequencing (ChIP-seq).

**Details**

|           |              |
|-----------|--------------|
| Package:  | fCCAC        |
| Type:     | Package      |
| Version:  | 0.99.0       |
| Date:     | 2016-09-09   |
| License:  | Artistic-2.0 |
| LazyLoad: | yes          |

**Author(s)**

Pedro Madrigal,  
 Maintainer: Pedro Madrigal <dnaseiseq@gmail.com>

**References**

Madrigal P (2016) fCCAC: functional canonical correlation analysis to evaluate covariance between nucleic acid sequencing datasets. Bioinformatics: <http://doi.org/10.1093/bioinformatics/btw724>.

**Examples**

```
## hg19. chr21:40000000-48129895 H3K4me3 data from Bertero et al. (2015)
if (.Platform$OS.type == "unix") {

  owd <- setwd(tempdir())

  bigwig1 <- "chr21_H3K4me3_1.bw"
  bigwig2 <- "chr21_H3K4me3_2.bw"
  bigwig3 <- "chr21_H3K4me3_3.bw"
  peakFile <- "chr21_merged_ACT_K4.bed"
  labels <- c( "H3K4me3", "H3K4me3", "H3K4me3" )
  ti <- "H3K4me3 peaks"
```

```

r1 <- system.file("extdata", bigwig1, package="fCCAC", mustWork = TRUE)
r2 <- system.file("extdata", bigwig2, package="fCCAC", mustWork = TRUE)
r3 <- system.file("extdata", bigwig3, package="fCCAC", mustWork = TRUE)
r4 <- system.file("extdata", peakFile, package="fCCAC", mustWork = TRUE)

fc <- fccac(bar=NULL, main=ti, peaks=r4, bigwigs=c(r1,r2,r3), labels=labels, splines=15, nbins=100, ncan=15)

head(fc)

setwd(owd)
}

```

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|       |                                                                                                                  |
|-------|------------------------------------------------------------------------------------------------------------------|
| fccac | <i>functional Canonical Correlation Analysis to evaluate Covariance between nucleic acid sequencing datasets</i> |
|-------|------------------------------------------------------------------------------------------------------------------|

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## Description

functional Canonical Correlation Analysis to evaluate Covariance between nucleic acid sequencing datasets.

## Usage

```
fccac(peaks, bigwigs, labels, splines=10, nbins=100, ncan=5 , tf=c(), main="",
bar=NULL, outFiles=FALSE )
```

## Arguments

|          |                                                                                                                                                   |
|----------|---------------------------------------------------------------------------------------------------------------------------------------------------|
| peaks    | BED file. Column 1: chr, Column 2: start, Column 3: end (REQUIRED).                                                                               |
| bigwigs  | A vector of characters containing the path to bigwigs files. Replicates of the same samples should be entered consecutive one another (REQUIRED). |
| labels   | IDs for each sample. Replicates should have the same label and be ordered (vector of characters, REQUIRED)                                        |
| splines  | Number of cubic B-splines used to smooth the data and to estimate the canonical variate weight functions (default: 15)                            |
| nbins    | Integer value representing the number of bins that should be used for each window (default: 100)                                                  |
| ncan     | Number of canonical components to report in the results. It cannot be higher than number of splines or the number of peaks (default: 15)          |
| tf       | Plot results involving only this TF or TF-replicate (character). Eg., "SOX2" or "SOX2\_Rep1" (default: empty vector. plot all)                    |
| main     | Title of the plot generated (default: no title)                                                                                                   |
| bar      | In the barplot, plot only first bar[1] and last bar[2] interactions after ranking by F-value (default: NULL, plots all the combinations).         |
| outFiles | If TRUE, the function writes two files in the working directory, fCCAC.pdf and fCCAC.txt (tabulated text-file with results). (default: FALSE)     |

## Details

Detailed information about the methodology can be found in Madrigal (2016).

## Value

The function reports a dataframe with the following columns: pairwise samples, F value, k (order of the first canonical correlation), and value of the first canonical correlation.

## Author(s)

Pedro Madrigal, <dnaseiseq@gmail.com>

## References

Madrigal P (2016) fCCAC: functional canonical correlation analysis to evaluate covariance between nucleic acid sequencing datasets. Bioinformatics: <http://doi.org/10.1093/bioinformatics/btw724>.

## See Also

[fCCAC-package](#)

## Examples

```
## hg19. chr21:40000000-48129895 H3K4me3 data from Bertero et al. (2015)
if (.Platform$OS.type == "unix") {

  owd <- setwd(tempdir())

  bigwig1 <- "chr21_H3K4me3_1.bw"
  bigwig2 <- "chr21_H3K4me3_2.bw"
  bigwig3 <- "chr21_H3K4me3_3.bw"
  peakFile <- "chr21_merged_ACT_K4.bed"
  labels <- c( "H3K4me3", "H3K4me3", "H3K4me3" )

  r1 <- system.file("extdata", bigwig1, package="fCCAC", mustWork = TRUE)
  r2 <- system.file("extdata", bigwig2, package="fCCAC", mustWork = TRUE)
  r3 <- system.file("extdata", bigwig3, package="fCCAC", mustWork = TRUE)
  r4 <- system.file("extdata", peakFile, package="fCCAC", mustWork = TRUE)
  ti <- "H3K4me3 peaks"

  fc <- fccac(bar=NULL, main=ti, peaks=r4, bigwigs=c(r1,r2,r3), labels=labels, splines=15, nbins=100, ncan=15)

  head(fc)

  setwd(owd)
}
```

heatmapfCCAC

*Heatmap of F values obtained by Canonical Correlation Analysis***Description**

Heatmap of F values obtained by Canonical Correlation Analysis. This function can only be used if all pairwise comparisons were computed previously with the function 'fccac', i.e., using "tf=c()".

**Usage**

```
heatmapfCCAC(fc)
```

**Arguments**

fc                      Output of the function 'fccac'.

**Value**

Plots a Heatmap of F values using the package 'ComplexHeatmap'.

**Author(s)**

Pedro Madrigal, <dnaseiseq@gmail.com>

**References**

Madrigal P (2016) fCCAC: functional canonical correlation analysis to evaluate covariance between nucleic acid sequencing datasets. Bioinformatics: <http://doi.org/10.1093/bioinformatics/btw724>.

**See Also**

[fccac](#)

**Examples**

```
## hg19. chr21:40000000-48129895 H3K4me3 data from Bertero et al. (2015)
if (.Platform$OS.type == "unix") {

  owd <- setwd(tempdir())

  bigwig1 <- "chr21_H3K4me3_1.bw"
  bigwig2 <- "chr21_H3K4me3_2.bw"
  bigwig3 <- "chr21_H3K4me3_3.bw"
  peakFile <- "chr21_merged_ACT_K4.bed"
  labels <- c( "H3K4me3", "H3K4me3", "H3K4me3" )

  r1 <- system.file("extdata", bigwig1, package="fCCAC",mustWork = TRUE)
  r2 <- system.file("extdata", bigwig2, package="fCCAC",mustWork = TRUE)
  r3 <- system.file("extdata", bigwig3, package="fCCAC",mustWork = TRUE)
```

```
r4 <- system.file("extdata", peakFile, package="fCCAC", mustWork = TRUE)
ti <- "H3K4me3 peaks"

fc <- fccac(bar=NULL, main=ti, peaks=r4, bigwigs=c(r1,r2,r3), labels=labels, splines=15, nbins=100, ncan=15)

head(fc)

heatmapfCCAC(fc)

setwd(owd)

}
```

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