

Package: fCCAC (via r-universe)

June 9, 2026

Version 1.38.0

Date 2025-04-07

Type Package

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

Description Computational evaluation of variability across DNA or RNA sequencing datasets is a crucial step in genomics, as it allows both to evaluate reproducibility of replicates, and to compare different datasets to identify potential correlations. fCCAC applies functional Canonical Correlation Analysis to allow the assessment of: (i) reproducibility of biological or technical replicates, analyzing their shared covariance in higher order components; and (ii) the associations between different datasets. fCCAC represents a more sophisticated approach that complements Pearson correlation of genomic coverage.

Depends R (>= 4.2.0), S4Vectors, IRanges, GenomicRanges, grid

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

Suggests RUnit, BiocGenerics, BiocStyle, knitr, rmarkdown

License Artistic-2.0

LazyLoad yes

LazyData yes

biocViews Epigenetics, Transcription, Sequencing, Coverage, ChIPSeq, FunctionalGenomics, RNASeq, ATACSeq, MNaseSeq

URL <https://github.com/pmb59/fccac>

BugReports <https://github.com/pmb59/fccac/issues>

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev perl libx11-dev xz-utils zlib1g-dev

Repository <https://bioc-release.r-universe.dev>

Date/Publication 2026-04-28 12:44:39 UTC

RemoteUrl <https://github.com/bioc/fCCAC>

RemoteRef RELEASE_3_23

RemoteSha 5e50dd8a5d97fe41bbe0d4082091c1614ecdf703

Contents

fCCAC-package	2
fccac	3
heatmapfCCAC	5

Index	7
--------------	----------

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

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:	1.23.1
Date:	2022-05-28
License:	Artistic-2.0
LazyLoad:	yes

Author(s)

Pedro Madrigal,
 Maintainer: Pedro Madrigal <pmadrigal@ebi.ac.uk>

References

Madrigal P (2017) 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)
}
```

fccac

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

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)

<code>nbins</code>	Integer value representing the number of bins that should be used for each window (default: 100)
<code>ncan</code>	Number of canonical components to report in the results. It cannot be higher than number of splines or the number of peaks (default: 15)
<code>tf</code>	Plot results involving only this TF or TF-replicate (character). Eg., "SOX2" or "SOX2_Rep1" (default: empty vector. plot all)
<code>main</code>	Title of the plot generated (default: no title)
<code>bar</code>	In the barplot, plot only first <code>bar[1]</code> and last <code>bar[2]</code> interactions after ranking by F-value (default: NULL, plots all the combinations).
<code>outFiles</code>	If TRUE, the function writes two files in the working directory, <code>fCCAC.pdf</code> and <code>fCCAC.txt</code> (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, <pmadrigal@ebi.ac.uk>

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, <pmadrigal@ebi.ac.uk>

References

Madrigal P (2017) 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)
}
```

Index

fCCAC (fCCAC-package), [2](#)

fccac, [3](#), [5](#)

fCCAC-package, [2](#)

heatmapfCCAC, [5](#)