

Package ‘hicream’

January 30, 2026

Title HIC diffeREntial Analysis Method

Version 0.0.4

Date 2026-01-30

Maintainer Elise Jorge <elise.jorge@inrae.fr>

Description Perform Hi-C data differential analysis based on pixel-level differential analysis and a post hoc inference strategy to quantify signal in clusters of pixels. Clusters of pixels are obtained through a connectivity-constrained two-dimensional hierarchical clustering.

License GPL (>= 3)

URL <https://scales.pages-forge.inrae.fr/hicream/>,
<https://forge.inrae.fr/scales/hicream>

BugReports <https://forge.inrae.fr/scales/hicream/-/issues>

Depends R (>= 4.0.0), reticulate

SystemRequirements Python (>= 3.9)

Imports adjclust, auk, BiocGenerics, csaw, diffHic, dplyr, edgeR, GenomeInfoDb, GenomicRanges, InteractionSet, limma, Matrix, methods, reshape2, rlang, S4Vectors, stats, SummarizedExperiment, utils, viridis

Suggests knitr, rmarkdown

Encoding UTF-8

RoxygenNote 7.3.3

VignetteBuilder knitr

NeedsCompilation no

Author Elise Jorge [aut, cre],
Sylvain Foissac [aut] (ORCID: <<https://orcid.org/0000-0002-2631-5356>>),
Toby Hocking [aut] (ORCID: <<https://orcid.org/0000-0002-3146-0865>>),
Pierre Neuvial [aut] (ORCID: <<https://orcid.org/0000-0003-3584-9998>>),
Nathalie Vialaneix [aut] (ORCID:
<<https://orcid.org/0000-0003-1156-0639>>),
Gilles Blanchard [ctb],

Guillermo Durand [ctb] (ORCID: <<https://orcid.org/0000-0003-4056-5631>>),
Nicolas Enjalbert-Courrech [ctb],
Etienne Roquain [ctb]

Repository CRAN
Date/Publication 2026-01-30 15:50:02 UTC

Contents

AggloClust2D	2
loadData	3
performTest	4
pighic	6
postHoc	7
Index	9

AggloClust2D	<i>Perform Constrained 2D Agglomerative Clustering</i>
--------------	--

Description

This function performs a connectivity constrained 2D agglomerative clustering using scikit-learn function AgglomerativeClustering and outputs an object of class hclust that stores the hierarchy of merges and value of criterion at each merge. It also outputs the optimal level of the hierarchy with respect to the elbow heuristic.

Usage

```
AggloClust2D(counts, nbClust = NULL)

## S3 method for class 'res2D'
print(x, ...)

## S3 method for class 'res2D'
summary(object, ...)

## S3 method for class 'res2D'
plot(x, ...)
```

Arguments

- | | |
|---------|--|
| counts | an object of class InteractionSet obtained from the function loadData or an object of class resdiff obtained from function performTest . |
| nbClust | integer. Number of clusters to obtain. Set to NULL by default. |
| x | a res2D object to plot |
| ... | not used |
| object | a res2D object to summarize |

Value

An object of class res2D containing:

tree	an object of class hclust
nbClust	the number of clusters corresponding either to the value passed by the user or to the optimal level of clusters as provided by the elbow heuristic
clustering	obtained clustering

Author(s)

Élise Jorge <elise.jorge@inrae.fr>
 Sylvain Foissac <sylvain.foissac@inrae.fr>
 Toby Dylan Hocking <toby.hocking@r-project.org>
 Pierre Neuvial <pierre.neuvial@math.univ-toulouse.fr>
 Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

Examples

```
data("pighic")

res2D <- AggloClust2D(pighic$data)
if (!is.null(res2D)) { # in case Python or modules are not available
  clusters <- res2D$clustering
  print(res2D)
  summary(res2D)
  plot(res2D)
}
```

loadData

Load and Normalize Hi-C Data

Description

This function loads data necessary for the analysis and outputs them in a suitable format for performTest and 2Dclust.

Usage

```
loadData(files, index, chromosome, normalize = TRUE)
```

Arguments

files	character vector. Paths to Hi-C matrices in bed format.
index	character. A path to an index file in bed format.
chromosome	character or integer. Chromosome to select.
normalize	logical. Whether or not to normalize the output (with MA method). Set to TRUE by default.

Value

An [InteractionSet](#) corresponding to all interactions present in at least one of the input matrices and corresponding counts across all matrices.

Author(s)

Élise Jorge <elise.jorge@inrae.fr>
 Sylvain Foissac <sylvain.foissac@inrae.fr>
 Toby Dylan Hocking <toby.hocking@r-project.org>
 Pierre Neuvial <pierre.neuvial@math.univ-toulouse.fr>
 Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

Examples

```
replicates <- 1:2
cond <- "90"
allBegins <- interaction(expand.grid(replicates, cond), sep = "-")
allBegins <- as.character(allBegins)
chromosome <- 1
nbChr <- 1
allMat <- sapply(allBegins, function(ab) {
  matFile <- paste0("Rep", ab, "-chr", chromosome, "_200000.bed")
})
index <- system.file("extdata", "index.200000.longest18chr.abs.bed",
  package = "hicream")
format <- rep("HiC-Pro", length(replicates) * length(cond) * nbChr)
binsize <- 200000
files <- system.file("extdata", unlist(allMat), package = "hicream")
exData <- loadData(files, index, chromosome, normalize = TRUE)
```

performTest

Perform diffHic Test

Description

This function performs diffHic differential analysis for every pixel of the matrix.

Usage

```
performTest(
  matrices,
  cond,
  outFile = NULL,
  filterLc = FALSE,
  filterFlank = FALSE,
  flank = NULL
)
```

```
## S3 method for class 'resdiff'
print(x, ...)

## S3 method for class 'resdiff'
summary(object, ...)

## S3 method for class 'resdiff'
plot(x, whichPlot = c("p.value", "p.adj", "logFC"), ...)
```

Arguments

matrices	an object of class InteractionSet obtained from the function loadData . Conditions correspond to the columns (one column per replicate).
cond	a vector indicating the condition of each column of matrices.
outFile	path to export outputs of the function, set to NULL by default, in which case results are not exported.
filterLc	logical. Whether to filter out low counts or not. Set to FALSE by default, in which case no filtering is performed. See filterTrended for more details.
filterFlank	logical. Whether to filter out on enriched pairs. Set to FALSE by default, in which case no filtering is performed. See enrichedPairs and filterPeaks for more details.
flank	flank parameter used only if filterFlank = TRUE. Set to NULL by default. See enrichedPairs for more details.
x	a resdiff object to plot
...	not used
object	a resdiff object to print
whichPlot	a character string indicating which plot to display. Possible values are "p.value", "p.adj" and "logFC". Set to "p.value" by default.

Value

An object of class `resdiff` with the following entries:

region1	the first bin of the interaction
region2	the second bin of the interaction
p.value	the p-value of the diffHic test
p.adj	the adjusted p-value of the diffHic test
logFC	the log2-fold-change of the interaction

Author(s)

Élise Jorge <elise.jorge@inrae.fr>
 Sylvain Foissac <sylvain.foissac@inrae.fr>
 Toby Dylan Hocking <toby.hocking@r-project.org>
 Pierre Neuvial <pierre.neuvial@math.univ-toulouse.fr>
 Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

Examples

```
data("pighic")
resdiff <- performTest(pighic$data, pighic$conditions)
resdiff
summary(resdiff)
plot(resdiff)
plot(resdiff, whichPlot = "p.adj")
plot(resdiff, whichPlot = "logFC")
```

pighic

Dataset "pighic"

Description

6 Hi-C matrices (3 in each condition) obtained from two different developmental stages of pig embryos (90 and 110 days of gestation) corresponding to chromosome 1.

Format

An object with two entries:

data an object of class `InteractionSet` containing 6 Hi-C matrices from 2 conditions (3 each) for 21 interactions.

conditions a two-level factor indicating the condition of each matrix in data.

Details

The data are identical to the dataset present in the package `treediff`.

References

Nathalie Vialaneix, Gwendaelle Cardenas, Marie Chavent, Sylvain Foissac, Pierre Neuvial, and Nathanael Randriamihamison (2023). `treediff`: Testing Differences Between Families of Trees. <https://cran.r-project.org/package=treediff>

Examples

```
data(pighic)
```

postHoc	<i>Perform Post Hoc Inference</i>
---------	-----------------------------------

Description

This function performs post-hoc inference on all provided clusters using [performTest](#) results.

Usage

```
postHoc(resdiff, clusters, alpha, fill = FALSE, stepDown = TRUE)
```

```
## S3 method for class 'resposthoc'
print(x, ...)
```

```
## S3 method for class 'resposthoc'
summary(object, ...)
```

```
## S3 method for class 'resposthoc'
plot(x, ...)
```

Arguments

resdiff	An object of class resdiff obtained from the function performTest .
clusters	A vector corresponding to a clustering of resdiff rows.
alpha	A number between 0 and 1 at which the computed post hoc bounds will be valid.
fill	A boolean value. If TRUE (the default), enforce the total number of tests to be $p*(p+1)/2$ by adding ones to the p-value vector for non tested entries.
stepDown	A boolean value. If FALSE, the single step Simes method is used. If TRUE (the default), the step-down Simes method is used. The latter is more powerful when the signal is strong.
x	a resposthoc object to plot
...	not used
object	a resposthoc object to summarize

Value

An object of class resposthoc containing a matrix with true positive proportions for each interaction and a dataframe with the following entries:

region1	The first bin of the interaction.
region2	The second bin of the interaction.
clust	The cluster the interaction belongs to.
TDP	The minimal post hoc true discovery (positive) proportion of the cluster the interaction belongs to.

p.value	The p-value of the diffHic test.
p.adj	The adjusted p-value of the diffHic test.
logFC	The log2-fold-change of the interaction.
meanlogFC	The mean of the log2-fold-change for the cluster the interaction belongs to.
varlogFC	The variance of the log2-fold-change for the cluster the interaction belongs to.
propPoslogFC	The proportion of interactions with positive log2-fold-change in the cluster the interaction belongs to.

Author(s)

Élise Jorge <elise.jorge@inrae.fr>
Sylvain Foissac <sylvain.foissac@inrae.fr>
Toby Dylan Hocking <toby.hocking@r-project.org>
Pierre Neuvial <pierre.neuvial@math.univ-toulouse.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

Examples

```
data("pighic")
resdiff <- performTest(pighic$data, pighic$conditions)
res2D <- AggloClust2D(pighic$data)
if (!is.null(res2D)) { # in case Python or modules are not available
  clusters <- res2D$clustering
  alpha <- 0.05
  resposthoc <- postHoc(resdiff, clusters, alpha)
  resposthoc
  summary(resposthoc)
  plot(resposthoc)
}
```

Index

AggloClust2D, [2](#)

diffHic, [5](#)

enrichedPairs, [5](#)

filterPeaks, [5](#)

filterTrended, [5](#)

InteractionSet, [2](#), [4–6](#)

loadData, [2](#), [3](#), [5](#)

performTest, [2](#), [4](#), [7](#)

pighic, [6](#)

plot.res2D (AggloClust2D), [2](#)

plot.resdiff (performTest), [4](#)

plot.resposthoc (postHoc), [7](#)

postHoc, [7](#)

print.res2D (AggloClust2D), [2](#)

print.resdiff (performTest), [4](#)

print.resposthoc (postHoc), [7](#)

summary.res2D (AggloClust2D), [2](#)

summary.resdiff (performTest), [4](#)

summary.resposthoc (postHoc), [7](#)