

# Package ‘HiTC’

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**Type** Package

**Title** High Throughput Chromosome Conformation Capture analysis

**Description** The HiTC package was developed to explore high-throughput 'C' data such as 5C or Hi-C.

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**Collate** AllGenerics.R HTCexp-class.R HTClst-class.R qualityControl.R  
normalize\_5C.R normalize\_hiC.R mapC.R mapC\_tracks.R binningC.R  
import.R export.R pca.R deprecated.R

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binningC	<i>Windowing of high-throughput 'C' contact matrix</i>
----------	--

---

## Description

Windowing of 'C' contact map

## Usage

```
binningC(x, binsize=100000, bin.adjust=TRUE, upa=TRUE,
method=c("median", "mean", "sum"), use.zero=TRUE, step=1, optimize.by = c("speed", "memory"))
```

## Arguments

x	object that inherits from class HTCexp
binsize	size of the bin to consider for windowing
bin.adjust	logical; adjust the size of the bin to the size of the genomic region
upa	logical; unique primer assignment. Allow one primer to belong to one or several bins
method	the method used to combine the counts. Must be 'mean', 'median' or 'sum'
use.zero	logical; use the zero values in the method calculation
step	numeric; binning step size in n coverage <i>i.e.</i> window step
optimize.by	"speed" will use faster methods but more RAM, and "memory" will be slower, but require less RAM

**Details**

`bin.adjust` allows to work with bin of the same size. Otherwise, the last bin will has a size different from `binsize`. A primer is assigned to a bin, if there is at least one base overlap between the bin and the primer region.

The method is used to combine the counts in a bin, must be 'mea', 'median' or 'sum'. The step parameter allows to choose the overlap between the bins. A step of 2 means a 50% overlap between two bins, a step of 3 means a 60% overlap between two bins, *etc.*

**Value**

An `HTCexp`-class object with binned intraction data. In this case, the genomic intervals are converted into bins of fixed size. The contact matrix is symmetric.

**Author(s)**

N. Servant, B. Lajoie

**See Also**

[HTCexp-class](#)

**Examples**

```
data(Nora_5C)

## Data binning 100kb, with a 1/3 overlap
E14.bin <- binningC(E14$chrXchrX, binsize=100000, step=3)
show(E14.bin)
```

---

CQC

*Quality Control for high-throughput 'C' experiment*

---

**Description**

Quality Control for high-throughput 'C' experiment

**Usage**

```
CQC(x, cis.trans.ratio = TRUE, hist.interac=TRUE, scat.interac.dist=TRUE,
hist.dist=TRUE, trim.range=0.98, winsize=NA, dev.new=TRUE)
```

**Arguments**

<code>x</code>	object that inherits from class <code>HTCexp</code> or <code>HTClist</code>
<code>cis.trans.ratio</code>	logical; barplot of percentage of inter-intrachromosomal interactions
<code>hist.interac</code>	logical; histogram of the interaction frequency

<code>scat.interac.dist</code>	logical; scatter plot of interaction count versus the genomic distance between two elements
<code>hist.dist</code>	logical; histogram of the distance between the 'x' and 'y' intervals
<code>trim.range</code>	remove the extreme values by trimming the counts. Only use for plotting functions. [0,1]
<code>winsize</code>	used for the <code>scat.interac.dist</code> . If specify, the data are windowed before plotting
<code>dev.new</code>	if true, each graphs is plotted in a new device

### Details

If `x` is a `HTClist` object, all `HTCexp` objects are merged. The zero values are not used to compute the descriptive statistics and to display the data. If `trim.range` are lower than 1. The highest values (quantile probability is equal to `trim.range`) are discarded.

### Value

Create quality plots and return a `matrix` with some simple statistics on all, cis and trans data.

### Author(s)

N. Servant, B. Lajoie

### See Also

[HTCexp-class](#)

### Examples

```
data(Nora_5C)

## Quality Control
CQC(E14)
```

---

discretize

*Transform matrix of counts data into discrete matrix*

---

### Description

Transform matrix of counts data into discrete matrix

### Usage

```
discretize(x, nb.lev=4, quant=TRUE)
```

**Arguments**

x                    data matrix  
nb.lev              number of discretization level  
quant                logical; use quantile distribution or split data into equals 'nb.lev' levels

**Value**

A discrete matrix

**Author(s)**

N. Servant

**See Also**

quantile

**Examples**

```
## Not run:  
data(Nora_5C)  
  
## Data binning  
E14bin<-binningC(E14$chrXchrX)  
  
## Discretize matrix  
dismat<-discretize(intdata(E14bin))  
mapC(dismat)  
  
## End(Not run)
```

---

export.my5C

*Export HTCexp object to my5C website format*

---

**Description**

Export HTCexp object to my5C website format

**Usage**

```
export.my5C(x, file, format=c("mat","list"), genome="mm9", header=TRUE)
```

**Arguments**

x	object that inherits from class HTCexp
file	character; the name of the output file
format	Either 'list' or 'mat'. See details
genome	The genome version. This information is only used for the 'mat' export format. See details
header	if true; a header is added in the output file with the package version and the date

**Details**

If 'format=list', a my5C tabbed delimited file is created, with :  
 Y\_INTERVAL\_NAME/X\_INTERVAL\_NAME/INTERACTION\_COUNT  
 Otherwise, a tab-delimited matrix file is generated with the row and colnames defined as follow as in the my5C web tool :  
 REV\_2lmm9lchrX:98831149-98834145

**Author(s)**

N. Servant

**See Also**

[exportC](#)

**Examples**

```
## Not run:
data(Nora_5C)

## Data binning
E14.bin<-binningC(E14$chrXchrX)

## Export the new intervals definition
export.my5C(E14.bin, file="E14my5C.csv")

## End(Not run)
```

---

exportC

*Export HTCexp object*

---

**Description**

Export HTCexp object to csv format

**Usage**

```
exportC(x, file)
```

**Arguments**

x                    object that inherits from class HTCexp  
 file                character; the basename of the output file

**Value**

Three output files will be created ; 2 BED files for each genomic intervals, and one matrix file

**Author(s)**

N. Servant

**See Also**

[export.my5C](#), [importC](#)

**Examples**

```
## Not run:
data(Nora_5C)

## Data binning
E14.bin<-binningC(E14$chrXchrX)

## Export the new intervals definition
exportC(E14.bin, file="E14")

## End(Not run)
```

---

extractRegion	<i>Extract a subset of the HTCexp object</i>
---------------	--

---

**Description**

Extract a subset of the HTCexp object based on genomic ranges

**Usage**

```
extractRegion(x, MARGIN, chr, from, to, exact=FALSE)
```

**Arguments**

x                    object that inherits from class HTCexp  
 MARGIN            a vector giving the subscripts which the function will be applied over as in 'apply' function. E.g., '1' for the 'x' intervals, and '2' for the 'y' intervals, 'c(1, 2)' indicates 'x' and 'y' intervals.  
 chr                character; the chromosome of the genomic region

from	numeric; start of the genomic region
to	numeric; end of the genomic region
exact	logical; exact genomic region

### Details

By default, only the intervals fully included in the genomic ranges are returned. If `exact` is true, the overlapping intervals are also used, and forced to start/end at the specified position. If no intervals are overlapping, an interval with NA values is added.

### Value

A `HTCexp` object

### Author(s)

N. Servant

### See Also

[GRanges-class](#)

### Examples

```
data(Nora_5C)

## Focus on the genomic region chrX:98000000-100000000
E14sub<-extractRegion(E14$chrXchrX, c(1,2), chr="chrX", from=98000000, to=100000000)
show(E14sub)
```

---

`getAnnotatedRestrictionSites`  
*Annotation of restriction sites*

---

### Description

Performs the annotation of all restriction sites of a given genome (i.e. GC content, mappability, effective fragment length)

### Usage

```
getAnnotatedRestrictionSites(resSite="AAGCTT", overhangs5=1,
chromosomes=NA, genomePack="BSgenome.Mmusculus.UCSC.mm9", mappability=NULL, wingc=200, winmap=500)
```



**Arguments**

resSite	the sequence of the restriction site to look for. Default is HindIII restriction site
overhangs5	5' overhangs on the DNA resulted from the cutting
chromosomes	vector of chromosome number to focus on. Default all the chromosomes for the specified genome.
genomePack	name of the genome package to access the DNA sequence
wingc	size of the window upstream and downstream the restriction site used to calculate the GC content
mappability	a GRanges with a 'score' describing the mappability of the genome
winmap	size of the window upstream and downstream the restriction site used to calculate the mappability

**Details**

This function automatically annotate all the restriction sites of a given chromosome. The mappability is optional but strongly advice for Hi-C contact map normalization. This information can be easily download from public ressources like <ftp://hgdownload.cse.ucsc.edu/gbdb/mm9/bbi/>.

**Value**

Returns a GRanges object annotation data upstream (U) and downstream (D) the restriction sites.

**Author(s)**

N. Servant

**See Also**

[normLGF](#), [setGenomicFeatures](#)

**Examples**

```
## Not run:
## Mappability data From http://hgdownload.cse.ucsc.edu/goldenPath/hg18/encodeDCC/wgEncodeMapability/
map_hg18<- import("wgEncodeCrgMapabilityAlign100mer.bw",format="BigWig", asRangedData=FALSE)

## 1- Example of restriction sites annotation
cutSites <- getAnnotatedRestrictionSites(resSite="AAGCTT", overhangs5=1, chromosomes="chr1", genomePack="BSgenome")

## End(Not run)
```

---

getExpectedCounts	<i>Estimate expected interaction counts of a High-Throughput C intra-chromosomal map based on the genomic distance between two loci</i>
-------------------	---

---

### Description

The expected interaction is defined as the linear relationship between the interaction counts and the distance between two loci. See details for additional informations.

### Usage

```
getExpectedCounts(x, span=0.01, bin=0.005, stdev=FALSE, plot=FALSE)
```

### Arguments

x	object that inherits from class HTCexp
span	fraction of the data used for smoothing at each x point.
bin	interpolation parameter
stdev	logical, calculate the variance
plot	logical, display lowess smoothing and variance estimation points

### Details

The expected value is the interaction frequency between two loci that one would expect based on a sole dependency on the genomic proximity of these fragments in the linear genome. This can be estimated using a Lowess regression model. The lowess smoothing has two parameters : span and bin. The span corresponds to the fraction of the data used for smoothing. Instead of computing the local polynomial fitting at each data point, a window of size delta (bin parameter) is applied on the data and a linear interpolation is used to fill in the fitted values within the window. The default is 1% of the range of x. If delta=0 all but identical x values are estimated independently. The variance is then estimated using the same span and bin parameter, at each interpolation points. The points inside a window are weighted so that nearby points get the most weight (tricube weight function).

### Value

A list with the expected interaction map and the estimated variance

### Author(s)

N. Servant, B. Lajoie

### See Also

[HTCexp-class](#), [normPerExpected](#), [normPerExpected](#), [lowess](#)

**Examples**

```
data(Nora_5C)

## Estimate expected interaction from distance between intervals
E14.exp<-getExpectedCounts(E14$chrXchrX, stdev=TRUE, plot=FALSE)
mapC(HTCexp(E14.exp$exp.interaction, xgi=x_intervals(E14$chrXchrX), ygi=y_intervals(E14$chrXchrX)))
```

---

HTCexp-class

*Class 'HTCexp'*


---

**Description**

A class for representing high throughput Chromosome Conformation Capture data from next-generation sequencing experiments.

**Details**

The `normPerExpected` method estimates the expected interactions based on a the dependency on the genomic proximity between two loci. If `stdev` is false, the ratio observed/expected is returned, otherwise, the `zscore` ((observed-expected)/stdev) is returned Look at the [getExpectedCounts](#) function for details.

The `normPerTrans` method is based on the assumption that all trans contacts should be the same. Thus, the cis contacts can be normalized by the interaction level of trans data. The `xtrans` trans map has to share its 'xgi' ranges with the cis map, and the `ytrans` has to share its 'ygi' ranges with the cismap. The method is used to combine the normalization factor from x and y ranges. Must be 'sum', 'mult' or 'mean'.

**Objects from the Class**

Objects can be created either by:

1. calls of the form `new("HTCexp", intdata, GRanges, GRanges)`.
2. using the auxiliary function `HTCexp` and supplying contact Matrix with x and y intervals definition.

**Slots**

**intdata:** Dense or Sparse Matrix, holding the interaction level between each pairs of 'x-y' intervals. The 'y' intervals must be in rows, and the 'x' in columns.

**ygi:** Genomic ranges of y intervals; see class `granges` for details

**xgi:** Genomic ranges of x intervals; see class `granges` for details

**Methods**

- c(x, ...)** Combines 'x' and the signature("HTCexp") objects in '...' together. The results is an object of class signature("HTCList")
- detail(x)** signature("HTCexp"): a more detailed output of the experiment than provided by show.
- divide(x)** comparison of two signature("HTCexp") objects. Perform the division of the two contact matrices on the common 'x' and 'y' intervals. The operation is done only on the common intervals of both objects. If one of the two objects has a count to zero, the divided value will be NA
- intdata(x)** return the intdata Matrix counts
- export(x)** Defunct. See exportC method
- isBinned** return TRUE if the data are binned. The method tests if the 'x' and 'y' genome intervals are the same, if 90% of the bins have the same size and if the full genomic range is covered
- isIntraChrom(x)** return TRUE if the current signature("HTCexp") object contains intrachromosomal contact data
- isSymmetric(x)** return TRUE if the contact map is symmetrical, i.e inherits the symmetricMatrix class
- normPerReads(x)** normalize the contact matrix by the total number of reads of the matrix.
- normPerExpected(x, stdev=TRUE)** normalize the contact matrix by the expected number of reads based on the distance between two loci. See details.
- normPerZscore(x)** Defunct. See normPerExpected method
- normPerTrans(x, xtrans, ytrans, method="sum")** Normalize cis contact map based on the trans interactions. See details
- plot(x)** visualization method; Display an heatmap of the contact data. Refer to the documentation of [mapC](#) for more details of the plotting function
- range(x)** return the genomic range of the signature("HTCexp") object
- seq\_name(x)** Defunct. See seqlevels method
- seqlevels(x)** return the sequence levels of the signature("HTCexp") object
- show(x)** summarized output of the experiment, with informations about the data dimension and the genomic region studied
- subtract(x)** comparison of two signature("HTCexp") objects. Perform the subtraction of the two contact matrices on the common 'x' and 'y' intervals. The operation is done only on the common intervals of both objects. If one of the two objects has a count to zero, the divided value will be NA
- summary(x)** return descriptive summary statistics about the contact map
- x\_intervals(x)** return the xgi GRanges object defining the x intervals
- y\_intervals(x)** return the ygi GRanges object defining the y intervals
- xy\_intervals(x)** return both xgi and ygi objects as a GRangesList object

**Author(s)**

Nicolas Servant

**See Also**

[GRanges-class](#), [GRangesList-class](#), [Matrix-class](#)

**Examples**

```

data(Nora_5C)

## HTCexp descriptio
show(E14)
detail(E14)

## Is binned data ?
isBinned(E14$chrXchrX)

## Is a inter or intrachromosomal experiment ?
isIntraChrom(E14$chrXchrX)

## Divide by expected interaction counts
E14norm<-normPerExpected(E14$chrXchrX)

## Operation on HTCexp object
E14_d_MEF<-divide(normPerReads(E14$chrXchrX), normPerReads(MEF$chrXchrX))
E14_s_MEF<-subtract(normPerReads(E14$chrXchrX), normPerReads(MEF$chrXchrX))

## Overlap with genomic annotation
require(rtracklayer)
gene <- import(file.path(system.file("extdata", package="HiTC"), "refseq_mm9_chrX_98831149_103425150.bed"), format="bed")
plot(E14$chrXchrX, tracks=list(RefSeqGene=gene))

## Not run:
## normPerTrans data normalization applied on http://genome.ucsc.edu/cgi-bin/hgFileUi?db=hg19&g=wgEncodeUm
ENCODE=import.my5C("./ENM-GM12878-R1.matrix")

## Look at raw contact map
mapC(ENCODE$chr7chr7)

## look at normalize by trans contact map
mapC(normPerTrans(ENCODE$chr7chr7, xtrans=ENCODE$chr7chr5, ytrans=ENCODE$chr5chr7))

## End(Not run)

## Not run:
## Export
exportC(E14$chrXchrX, con="E14.csv")

## End(Not run)

```

**Description**

A class for representing a list of high throughput Chromosome Conformation Capture data from next-generation sequencing experiments.

**Constructor**

The HTClist represents a list of HTCexp objects and can be created as follow :

HTClist(...): Creates a HTClist object using HTCexp objects supplied in '...'

**Methods**

**c(x, ...)** Combines a signature("HTClist") object 'x' with signature("HTClist") or signature("HTCexp") objects in '...'. The results is an object of class signature("HTClist")

**detail(x)** signature("HTClist"): a more detailed output of the experiment than provided by show.

**isBinned(x)** applies 'isBinned' to each element in 'x'

**isIntraChrom(x)** applies 'isIntraChrom' to each element in 'x'

**ranges(x)** applies 'range' to each element in 'x'

**range(x)** return the reduce range of all elements in 'x'

**seqlevels(x)** return the sequence levels of all elements in 'x'

**as.list(x)** coercion to simple list object

**names(x)** get the names of the elements

**show(x)** summarized output of the experiment, with informations about the data dimension

**summary(x)** return descriptive summary statistics for each interaction map

**x[i ]** Get elements i from x. Can be the positional index or its name.

**Author(s)**

Nicolas Servant

**See Also**

[GRangesList-class](#), [HTCexp-class](#)

**Examples**

```
exDir <- system.file("extdata", package="HiTC")
l <- sapply(list.files(exDir, pattern=paste("HIC_gm06690_"), full.names=TRUE),
            import.my5C)
hiC <- HTClist(l)
names(hiC)

## Methods
ranges(hiC)
range(hiC)
isBinned(hiC)
isIntraChrom(hiC)
seqlevels(hiC)
```

---

import.my5C	<i>Import data from my5C webtool</i>
-------------	--------------------------------------

---

**Description**

Import data from my5C webtool

**Usage**

```
import.my5C(my5C.datafile, xgi.bed=NULL, ygi.bed=NULL, all.pairwise=TRUE, forceSymmetric=FALSE)
```

**Arguments**

my5C.datafile	input file from the my5C webtool
xgi.bed	BED file describing the 'x' Intervals (i.e. column names) of the contact map. Required for the my5C list format
ygi.bed	BED file describing the 'y' intervals (i.e. row names) of the contact map. Required for the my5C list format
all.pairwise	logical; generate all pairwise chromosomal contact maps, i.e chr1-chr2, chr2-chr1
forceSymmetric	Force the Matrix to be symmetrical

**Details**

This function allows data import from the [the my5C webtool](#).

Two input formats can be used :

- The list format is composed of three files; two BED files describing the genomic intervals (i.e. primers); and a tabbed delimited format to specify the interaction between each genomic regions, with :  
FORWARD\_PRIMER\_NAME/REVERSE\_PRIMER\_NAME/INTERACTION\_COUNT. In this case, **BED files** describing the genomic coordinates are required.

- The matrix format is a tab-delimited format, corresponding to the contact map. The rownames and columnnames are splitted to created the genome intervals (example : REV\_2lmm9|chrX:98831149-98834145).

The all.pairwise option is not necessary in case of symmetric design. Otherwise, it will return all the pairwise contact maps.

The matrix will be stored as a matrix inheriting from Matrix class. If forcesymmetrical=TRUE, the matrix as forced to symmetricMatrix class allowing a much more efficient memory usage.

**Value**

A HTCList object(s)

**Author(s)**

N. Servant

**See Also**

[import](#), [codeHTClist-class](#), [codeMatrix-class](#), [symmetricMatrix-class](#)

**Examples**

```
exDir <- system.file("extdata", package="HiTC")
## Load my5C matrix format
hiC<-import.my5C(file.path(exDir, "HIC_gm06690_chr14_chr14_1000000_obs.txt"))
detail(hiC)
```

---

importC

---

*Import high-throughput 'C' data*


---

**Description**

Import 5C or Hi-C data from csv file

**Usage**

```
importC(con, xgi.bed, ygi.bed = NULL, all.pairwise=TRUE)
```

**Arguments**

con	input csv file. See details
xgi.bed	BED file describing the 'x' Intervals (i.e. column names) of the contact map. Required for the my5C list format
ygi.bed	BED file describing the 'y' intervals (i.e. row names) of the contact map. Required for the my5C list format
all.pairwise	logical; generate all pairwise chromosomal contact maps, i.e chr1-chr2, chr2-chr1

**Details**

This function import high-throughput data from a matrix file.

**Value**

A list of HTCexp object(s)

**Author(s)**

N. Servant

**See Also**

[exportC](#), [import.my5C](#), [HTCexp-class](#)



**Examples**

```
## Not run:
data(Nora_5C)

## Data binning
E14.bin<-binningC(E14$chrXchrX)

## Export the new intervals definition
exportC(E14.bin, file="E14")

##Import
importC("E14.csv")

## End(Not run)
```

---

intervalsDist	<i>intervalsDist</i>
---------------	----------------------

---

**Description**

Compute the distance of intrachromosomal contacts of a 'C' experiment

**Usage**

```
intervalsDist(x, use.zero=TRUE)
```

**Arguments**

`x` object that inherits from class HTCexp  
`use.zero` if FALSE, the distance for non interacting regions (zero counts) are not reported

**Details**

If  $A$  and  $B$  are the two sets of intervals and  $s$  and  $e$ , the start and end of an interval, the distance is calculated as :

$$\min(|A_e - B_s|, |A_s - B_e|)$$

Only intrachromosomal contact maps can be use for this operation.

**Value**

A matrix of distances between genomic intervals

**Author(s)**

N. Servant

**See Also**[HTCexp-class](#)**Examples**

```
data(Nora_5C)

## Calculate distances between primers/intervals
d<-intervalsDist(E14$chrXchrX)
```

mapC

*Visualize 'C' ontact map***Description**

Visualize 'C' contact map

**Details**

This function implements the `plot` method for objects of class `HTCexp` and `HTClist`.

By default, the `maxrange` and `minrange` values are fixed as the 98th percentile (resp. 2th percentile) of the interaction matrix. These values are useful to play with the contrast and remove the extreme values from the matrix.

The `HTCexp` and `HTClist` are not represented in the same way. The heatmap view is used to display the `HTClist` objects in two dimension. This view is mainly useful to have an overview of the data, as Hi-C data. The triangle view is used for `HTCexp` only and represent the top-right part the interaction matrix. If two `HTCexp` objects are specified, they will be displayed in order to compare both contact maps. The two maps have to be binned to ensure comparison between genomic ranges.

Annotation tracks can be added to both views. In case of binned data, the exact genomic positions of each features are taken into account. Otherwise, the 'C' intervals which overlap with the annotation features are colored.

**Value**

Returns NULL; this function is called for the side-effect of creating the plot.

**For `HTCexp` and `HTClist` objects**

**x** object that inherits from class `HTCexp` or `HTClist`

**tracks** List of `GRanges` objects of data to display as annotation track(s)

**minrange** the minimum range of values used to define the color palette

**maxrange** the maximum range of values used to define the color palette

**trim.range** define the `maxrange` and `minrange` values using the percentile of the interaction matrix

**show.zero** logical; plot the zero values

**show.na** logical; show the NA values in gray

**log.data** logical; do you want to log the data before plotting the heatmap

**col.pos** color for (low,mid,high) positive contact counts. Must be a vectore of size 3. mid can be NA

**col.neg** color for (low,mid,high) negative contact counts. Must be a vectore of size 3. mid can be NA

**col.na** color for NA values

**grid** logical; add a grid on the heatmap

**title** character; add a title to the HTCexp plot(s)

**value** logical; display the contact values on the matrix. Useful for small matrices

#### For HTCexp objects only

**y** optional. object that inherits from class HTCexp.

#### For HTClisT objects only

**names** logical; display the names of the intervals. Useful for small matrices

#### Author(s)

N. Servant, B. Lajoie

#### See Also

[HTCexp-class](#), [HTClisT-class](#)

#### Examples

```
data(Nora_5C)

## Contact map
## HTClisT view
mapC(E14)

## HTCexp view
mapC(E14$chrXchrX)

## Play with contrast and color
mapC(E14$chrXchrX, maxrange=100, col.pos=c("black","red","yellow"))

## Add annotation and change view
require(rtracklayer)
exDir <- system.file("extdata", package="HiTC")
gene <- import(file.path(exDir,"refseq_mm9_chrX_98831149_103425150.bed"), format="bed", asRangedData=FALSE)
mapC(E14$chrXchrX, tracks=list(Refseq=gene))

## Compare two samples
mapC(binC(E14$chrXchrX), binC(MEF$chrXchrX), tracks=list(Refseq=gene))
```

---

Nora\_5C

*HiTC - 5C data*

---

### **Description**

5C data described by Nora et al. (2012)

### **Usage**

```
data(Nora_5C)
```

### **Format**

Contains two `HTClist` objects (E14 and MEF). Each of them containing the ChrX intrachromosomal maps as a `HTCexp` object.

### **Details**

This 5C dataset published by Nora et al ([GSE35721](#)), contains two different samples, a male undifferentiated ES cells (E14, GSM873935) and a mouse embryonic fibroblasts (MEF, GSM873924). This dataset is mainly used to describe the available functionalities of the HiTC package. The data provided with the package are count data.

### **Source**

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35721>

### **References**

Nora EP, Lajoie BR, Schulz EG, Giorgetti L et al. Spatial partitioning of the regulatory landscape of the X-inactivation centre. *Nature* 2012 Apr 11;485(7398):381-5. PMID: 22495304

### **Examples**

```
data(Nora_5C)
show(E14)
show(MEF)
```

---

normICE	<i>Iterative Correction of Hi-C data (ICE)</i>
---------	--

---

## Description

Iterative correction leverages the unique pairwise genome-wide structure of Hi-C data to decompose the data into a set of biases and a map of relative contact probabilities between any two genomic loci, achieving equal visibility across all genomic regions.

## Usage

```
normICE(x,max_iter=200, eps=1e-4, sparse.filter=0.02)
```

## Arguments

x	object that inherits from class HTCexp
max_iter	maximum number of iteration
eps	the relative increment in the results before declaring convergence
sparse.filter	Define which pourcentage of bins with high sparsity should be force to zero

## Details

The imakaev normalization of Hi-C data consists of iteratively estimating the bias using the l1 norm. Note that the original method is applied on the genome-wide Hi-C map. For computation reason, we will applied the normalization to each chromosome separatly.

## Value

Returns a HTCexp object with a corrected contact map.

## Author(s)

N. Servant, N. Varoqaux

## References

Imakaev M, Fudenberg G, McCord RP, Naumova N, Goloborodko A, Lajoie BR, Dekker J, Mirny LA. Iterative correction of Hi-C data reveals hallmarks of chromosome organization. Nat Methods. 2012 Oct;9(10):999-1003.

## See Also

[normLGF](#)

**Examples**

```
## Not run:
##Lieberman data
exDir <- system.file("extdata", package="HiTC")
l <- sapply(list.files(exDir, pattern=paste("HIC_gm06690_"), full.names=TRUE),
            import.my5C)
hiC <- HTcList(l)
hiC <- hiC[isIntraChrom(hiC)]

## Run ICE
hiC_iced <- HTcList(lapply(hiC, normICE))

## End(Not run)
```

normLGF

*Local Genomic Feature (LGF) normalization***Description**

Parametric model to remove systematic biases in the raw contact maps

**Usage**

```
normLGF(x, family=c("poisson", "nb"))
```

**Arguments**

x	object that inherits from class HTCexp
family	parametric model to fit (poisson or nb)

**Details**

This function implements the HiCNorm method proposed by Hu et al. Briefly, the method uses a generalized linear model to correct the systematic biases (effective fragment length, GC content, mappability) in a Hi-C contact map.

Note : v1.7.3. works only for intrachromosome data

**Value**

Returns a HTCexp object with a normalized contact map.

**Author(s)**

N. Servant, M. Hu, S. Selvaraj

**References**

Hu M, Deng K, Selvaraj S, Qin Z, Ren B, Liu JS. HiCNorm: removing biases in Hi-C data via Poisson regression. *Bioinformatics*. 2012;28(23):3131-3.

**See Also**

[getAnnotatedRestrictionSites](#), [setGenomicFeatures](#)

**Examples**

```
## Not run:
require(HiTC)
require(BSgenome.Hsapiens.UCSC.hg18)

##Lieberman data
exDir <- system.file("extdata", package="HiTC")
l <- sapply(list.files(exDir, pattern=paste("HIC_gm06690_"), full.names=TRUE),
            import.my5C)
hiC <- HTCList(l)
hiC <- hiC[isIntraChrom(hiC)]
names(hiC)

## Mappability data From http://hgdownload.cse.ucsc.edu/goldenPath/hg18/encodeDCC/wgEncodeMapability/
map_hg18<- import("wgEncodeCrgMapabilityAlign100mer.bw", format="BigWig", asRangedData=FALSE)

## Get the genomic feature of the chromosome 12
hiC_annot <- HTCList(lapply(hiC, setGenomicFeatures, resSite="AAGCTT", overhangs5=1, genomePack="BSgenome.Hsapiens.UCSC.hg18"))
hiC_annot$chr12chr12

## Normalize the data
hiCnorm <- HTCList(lapply(hiC_annot, normLGF))

## End(Not run)
```

---

pca.hic

*Perform Principle Component Analysis on Hi-C contact map*

---

**Description**

Perform Principle Component Analysis on Hi-C contact map

**Usage**

```
pca.hic(x, normPerExpected=TRUE, npc=2, asGRangesList=TRUE)
```

**Arguments**

x	object that inherits from class HTCexp
normPerExpected	normalized by expected interaction using the loess calculation of distance dependency. see normPerExpected
npc	numeric; number of first principal component to return
asGRangesList	if TRUE a GRangesList object is returned where the scores represent the eigenvector

**Details**

This method was apply by Lieberman-Aiden et al. 2009 to correlate the annotation profiles (genes, ChIP-seq, etc.) with the topological domains observed in Hi-C (see Fig3G of Lieberman-Aiden et al. 2009)

**Value**

A list with the eigen vector(s) of the npc first principal component(s), and their importance

**Author(s)**

N. Servant, B. Lajoie, R. McCord

**See Also**

[normPerExpected](#)

**Examples**

```
## Get Lieberman-Aiden Hi-C data
exDir <- system.file("extdata", package="HiTC")
l <- sapply(list.files(exDir, pattern=paste("HIC_gm06690_"), full.names=TRUE),
import.my5C)
hiC <- HTClist(l)

## Performed PCA
pr<-pca.hic(hiC$chr14chr14, npc=1, asGRangesList=TRUE)
```

---

removeIntervals

*Remove intervals from HTCexp object*

---

**Description**

Remove primers intervals from HTCexp object

**Usage**

```
removeIntervals(x, ids)
```

**Arguments**

x                    object that inherits from class HTCexp  
ids                   character; vector of primers Ids to remove from the object

**Value**

A HTCexp object without the discarded intervals



**Author(s)**

N. Servant

**See Also**[GRanges-class](#)**Examples**

```
data(Nora_5C)

## Remove intervals from a HTCexp object
removeIntervals(E14$chrXchrX, ids=c("5C_938_XIC-3_REV_2", "5C_938_XIC-3_REV_4"))
```

---

setGenomicFeatures      *Annotation of Hi-C contact map*

---

**Description**

Annotate a Hi-C contact map with the genomic local features (i.e. GC content, mappability, effective fragment length)

**Usage**

```
setGenomicFeatures(x, cutSites, minFragMap=.5, effFragLen=1000)
```

**Arguments**

x	HTCexp object to annotate
cutSites	GRangesList or GRanges object with restriction sites annotation obtained using the getAnnotatedRestrictionSites function
minFragMap	Minimum Fragment Mappability. All fragments with a lower mappability are not used for the annotation.
effFragLen	Effective Fragment Length. Size of specific fragment ligation

**Details**

The function require the restriction sites annotation as provided by the getAnnotatedRestrictionSites function. The restriction sites are first filtered according to their mappability. This threshold has to be defined according to the data pre-processing. All remaining restriction sites are then intersected with the genomic bins of the contact map. All restriction sites included within a bin are averaged. The effective fragment length is defined as the size of specific ligation product. (See Yaffe and Tanay, 2011). In this paper, the authors define specific ligation as sum of distance to cutter sites  $(d1+d2) \leq 500$  bp. Such criterion implies that  $d1 \leq 500$  bp and  $d2 \leq 500$  bp. So for each fragment end, only reads mapped within 500 bp to cutter sites are used for downstream analysis. All defaults paramters correspond to the ones used in the HiCNorm method.

**Value**

Returns a HTCexp object with local genomic features annotations.

**Author(s)**

N. Servant

**See Also**

[normLGF](#), [setGenomicFeatures](#)

**Examples**

```
## Not run:
require(BSgenome.Hsapiens.UCSC.hg18)
require(rtracklayer)

##Lieberman data
exDir <- system.file("extdata", package="HiTC")
l <- sapply(list.files(exDir, pattern=paste("HIC_gm06690_"), full.names=TRUE),
            import.my5C)
hiC <- HTClust(l)
hiC <- hiC[isIntraChrom(hiC)]
names(hiC)

## Mappability data From http://hgdownload.cse.ucsc.edu/goldenPath/hg18/encodeDCC/wgEncodeMapability/
map_hg18<- import("wgEncodeCrgMapabilityAlign100mer.bw", format="BigWig", asRangedData=FALSE)

## Get the genomic feature of the HiC chr12 data
cutSites <- getAnnotatedRestrictionSites(resSite="AAGCTT", overhangs5=1, chromosome=seqlevels(hiC), genomePack="")

chr12_annot <- setGenomicFeatures(hiC$chr12chr12, cutSites)

## End(Not run)
```

---

setIntervalScale      *Set x and y interval of the HTCexp object*

---

**Description**

Set x and y interval of the HTCexp object and update the contact map accordingly

**Usage**

```
setIntervalScale(x, xgi, ygi, upa=TRUE, method=c("median", "mean", "sum"),
use.zero=TRUE, optimize.by = c("speed", "memory"))
```

**Arguments**

x	object that inherits from class HTCexp
ygi	y intervals; see class GRanges for details
xgi	x intervals; see class GRanges for details
upa	logical; unique primer assignment. Allow one primer to belong to one or several bins
method	the method used to combine the counts. Must be 'mean', 'median' or 'sum'
use.zero	logical; use the zero values in the method calculation
optimize.by	"speed" will use faster methods but more RAM, and "memory" will be slower, but require less RAM

**Details**

Define new contact map based on the specified xgi and ygi intervals.

This function has to be used carefully and can has important impact on the contact map. It is important to note that the `setIntervalScale` function is different from the `binningC` function in the way that the output is not symmetrical.

**Value**

A HTCexp object

**Author(s)**

N. Servant

**See Also**

[HTCexp-class](#)

**Examples**

```
data(Nora_5C)

E14.bin<-binningC(E14$chrXchrX)

## I have two HTCexp samples defined with different intervals.
show(E14.bin)
show(MEF$chrXchrX)

## How to compare them ?
## One idea is to force the intervals definition of one object using the
## intervals of the other.

setIntervalScale(MEF$chrXchrX, xgi=x_intervals(E14.bin), ygi=y_intervals(E14.bin))
```

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