

# Package ‘bnbc’

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**Title** Bandwise normalization and batch correction of Hi-C data

**Description** Tools to normalize (several) Hi-C data from replicates.

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GenomicRanges

**Suggests** BiocStyle, knitr, rmarkdown, RUnit

**Imports** Rcpp (>= 0.12.12), IRanges, rhdf5, data.table, GenomeInfoDb,  
S4Vectors, matrixStats, preprocessCore, sva, parallel, EBImage,  
utils

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**VignetteBuilder** knitr

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**BugReports** <https://github.com/hansenlab/bnbc/issues>

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bnc-package	<i>Bandwise normalization and batch correction of Hi-C data</i>
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## Description

Tools to normalize (several) Hi-C data from replicates.

## Details

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The package implements the bnc method for normalizing Hi-C data across samples. The name is short for band-wise normalization and batch correction. The main workhorse is the bnc function. We recommend using smoothing and library size normalization first.

The package implements the ContactGroup class for storing multiple Hi-C contact matrices. This is most naturally done with one object per chromosome, which is ugly.

We also have functions for applying over a ContactGroup (cgApply) and working with matrix bands band, getBandIdx.

## Author(s)

NA

Maintainer: NA

## References

Fletez-Brant et al. *Distance-dependent between-sample normalization for Hi-C experiments*. In preparation.

## See Also

[bnc](#), [ContactGroup](#), [band](#), [cgApply](#).

## Examples

```
data(cgEx)
batches <- colData(cgEx)$Batch
cgEx.cpm <- logCPM(cgEx)
cgEx.smooth <- boxSmoother(cgEx, 5, mc.cores=1)
cgEx.bnbc <- bnbc(cgEx.smooth, batches, 1e7, 4e4, bstart=2, nbands=4)
```

---

band	<i>Get Band</i>
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---

## Description

Get or set band from matrix.

## Usage

```
band(mat, band.no)
band(mat, band.no) <- value
```

## Arguments

mat	A matrix.
band.no	Integer specifying which matrix band. band.no = 1 retrieves the main diagonal.
value	A scalar or vector equal in length to the matrix band.

## Details

A matrix band is the set of elements in a matrix from a specific off-diagonal.

## Value

A matrix band in the form of a vector.

## See Also

[getBandIdx](#)

## Examples

```
mat <- matrix(1:9, 3, 3)
band(mat, band.no = 2)
mat
band(mat, band.no = 2) <- c(9,10)
mat

data(cgEx)
tact.1 <- contacts(cgEx)[[1]]
b2 <- band(tact.1, 2)
band(tact.1, 2) <- b2
```

bnc

*Normalize Contact Matrices with BNBC***Description**

Applies BNBC method to normalize contact matrices.

**Usage**

```
bnc(cg, batch, threshold = NULL, step = NULL, qn = TRUE, nbands
    = NULL, mod = NULL, mean.only = FALSE, tol = 5, bstart = 2, verbose = TRUE)
```

**Arguments**

<code>cg</code>	A ContactGroup object.
<code>batch</code>	A single batch indicator variable.
<code>threshold</code>	The maximum distance interacting loci are allowed to be separated by.
<code>step</code>	The step size, or the number of bases a contact matrix cell represents.
<code>qn</code>	Whether to apply quantile normalization on each band matrix. Defaults to TRUE.
<code>bstart</code>	The first band to normalize. Defaults to 2.
<code>nbands</code>	The last band to normalize. Defaults to <code>nrow(cg) - 1</code> .
<code>mod</code>	A model matrix specifying which sample information is to be preserved by ComBat. Optional.
<code>mean.only</code>	Whether ComBat should not correct for batch effect in the variances of band matrix rows. Defaults to FALSE, which means variances are corrected. Set to TRUE if there is only one observation per batch.
<code>tol</code>	The number of significant digits for which the mean value of a band matrix must be greater than 0 to be processed by ComBat.
<code>verbose</code>	Should the function print progress?

**Details**

Normalization and batch correction is performed in a band-wise manner, correcting all samples' observations of one matrix off-diagonal (which we refer to as a matrix "band") at a time. For each matrix band, we collect all samples' observations into a single matrix. We then apply quantile normalization to ensure distributional similarity across samples. Finally, we perform batch effect correction using ComBat on this matrix. Each samples' matrix band is then replaced with its corrected version. We refer to this process of Band-Wise Normalization and Batch Correction as BNBC.

This function applies BNBC to the set of contact matrices and returns a ContactGroup object with matrix bands `bstart:nbands` corrected. For those rows in the matrix bands which cannot be corrected we set all elements to 0.

Very high bands contain little data in Hi-C experiments, and we don't recommend to analyze those or apply this function to high bands, see the `nbands` argument to the function.

We recommend performing bnbc on contact matrices which have been converted to log-CPM and smoothed, see the example.

### Value

A ContactGroup object for which matrix bands bstart:nbands have had BNBC applied.

### References

Johnson, W.E., Li, C. and Rabinovic, A. *Adjusting batch effects in microarray expression data using empirical Bayes methods*. Biostatistics 2007, 8:118-127. doi:10.1093/biostatistics/kxj037

Fletez-Brant et al. *Distance-dependent between-sample normalization for Hi-C experiments*. In preparation.

### See Also

[ContactGroup](#), [logCPM](#), [boxSmoother](#), [band](#)

### Examples

```
data(cgEx)
batches <- colData(cgEx)$Batch
cgEx.cpm <- logCPM(cgEx)
cgEx.smooth <- boxSmoother(cgEx, 5, mc.cores=1)
cgEx.bnbc <- bnbc(cgEx.smooth, batches, 1e7, 4e4, bstart=2, nbands=4)
```

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cgApply

*Apply-type methods*

---

### Description

These functions are apply-type functions for ContactGroup objects.

### Usage

```
cgApply(cg, FUN, mc.cores=1, ...)
cgBandApply(cg, FUN, nbands=NULL, mc.cores=1, bstart=2, ...)
```

### Arguments

cg	A ContactGroup object.
FUN	A function to be applied. For cgApply this function should operate on a square matrix. For cgBandApply this function should operate on a band, ie. a vector (see <a href="#">band</a> ).
mc.cores	The number of cores to be used. Defaults to 1
bstart	The first band to apply a function to. Defaults to 2. Only applicable to cgBandApply.
nbands	The last band to apply a function to. Default is nrow(cg) - 1. Only applicable to cgBandApply.
...	Passed to mclapply.

## Details

These methods make it easy to apply functions to either all contact matrices or a set of bands in all contact matrices. Both methods accept a function FUN. For `cgApply`, the first argument should be `cg`, the contact group itself. For `cgBandApply`, the first argument should also be `cg`, and the second argument should be a specific band number. Additionally, the bands to be iterated are specified through `bstart:nbands`: `bstart` indicates the starting band, and `nbands` indicates the last band.

## Value

For `cgApply`, a `ContactGroup` object. For `cgBandApply`, a list whose elements are the returned value of FUN.

## See Also

[ContactGroup](#), [getBandMatrix](#), [band](#)

## Examples

```
data(cgEx)
cgEx.1 <- cgApply(cgEx, FUN=function(xx){ xx + 1 })
band.matrix.list <- cgBandApply(cgEx, FUN=getBandMatrix, bstart=2, nbands=5)
```

---

cgEx

*Sample chr22 Data*

---

## Description

This is a sample `ContactGroup` object representing observations on chr22 from 3 1k Genomes trios' lymphoblastoid cell lines (LCL). `colData(cgEx)` gives the cell line name (`CellLine`), the ethnicity of the individual (`Population`), the family (`Family`), the gender (`Gender`), the relationship of the individuals within a trio (`Role`), the replicate number (`Tech`) and each sample's batch (`Batch`).

These data were generated by the dilution Hi-C method using HindIII (Lieberman-Aiden et al.). Hi-C contact matrices were generated by tiling the genome into 40kb bins and counting the number of interactions between bins.

These data have undergone no preprocessing.

## Format

The data is an object of class `ContactGroup`.

## Source

Raw data are available from the 4D nucleome data portal (<https://data.4dnucleome.org>) under accessions 4DNESYUYFD6H, 4DNESVKLYDOH, 4DNESHGL976U, 4DNESJ1VX52C, 4DNESI2UKI7P, 4DNESTAPSPUC, 4DNES4GSP9S4, 4DNESJIYRA44, 4DNESE3ICNE1.

## References

Lieberman-Aiden, E, et al. *Comprehensive mapping of long-range interactions reveals folding principles of the human genome*. Science 2009, 326:289-293. doi:10.1126/science.1181369

## See Also

[ContactGroup](#)

---

ContactGroup-class	Class "ContactGroup"
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---

## Description

The ContactGroup class represents a collection of contact matrices which are observations from different samples on the same set of genomic loci.

## Usage

```
ContactGroup(rowData, contacts, colData)
```

## Arguments

rowData	Object of class GenomicRanges equal in length to the number of rows/columns in contact matrices.
contacts	Object of class list that contains all contact matrices.
colData	Object of class DataFrame containing sample-level information.

## Details

The ContactGroup class contains a set of contact matrices in the slot 'contacts'. All matrices are required to be of the same dimensionality. 'ContactGroup()' expects a list of symmetric matrices to be passed to the constructor. Data about these contact matrices is held in two other slots. Data about the genomic loci represented in the ContactGroup is found in the 'rowData' slot as a GenomicRanges objects, and sample-level information is located in the 'colData' slot as a DataFrame.

## Value

A ContactGroup object.

## Methods

In the code snippets below, x is a ContactGroup object.

[ signature(x = "ContactGroup", i = "ANY", j = "ANY", drop = "ANY")]: Allows for subsetting the contact matrices through use of i or of samples through j.

**colData** signature(x = "ContactGroup"): Get sample-level information about samples in x

- colData<-** signature(x = "ContactGroup", value = "DataFrame"): Set sample-level information about samples in x. value is expected to be a DataFrame object.
- dim** signature(x = "ContactGroup"): Obtain the dimensions of a ContactGroup. Returns 2 values: one representing the number of bins in the contact matrices and another representing the number of samples.
- rowData** signature(x = "ContactGroup"): Get the GenomicRanges object describing the loci in the ContactGroup. value is expected to be a GenomicRanges object.
- rowData<-** signature(x = "ContactGroup"): Set the GenomicRanges object describing the bins in the ContactGroup. value is expected to be a GenomicRanges object.
- show** signature(object = "ContactGroup"): Method to display summary information about a ContactGroup: the number of bins, the width of the bins and the number of samples.
- librarySize** signature(x = "ContactGroup"): Method to compute the library size of each contact matrix in x. Library size is defined to be the sum of the upper triangle of a contact matrix.
- logCPM** signature(x = "ContactGroup"): Method to transform each contact matrix to logCPM scale.

### Utilities

- contacts(x), contacts(x) <- value**: Method to extract the list of contact matrices from a ContactGroup. value is expected to be a list object.
- distanceIdx** signature(cg = "ContactGroup", threshold="ANY", step="ANY"): Method to identify which matrix bands are no more than threshold bins apart, where each bin represents step base pairs.

### References

Law, C.W., Chen, Y., Shi, W. and Smyth G.K. *voom: Precision weights unlock linear model analysis tools for RNA-seq read counts*. Genome Biology 2014, 15:R29. doi:10.1186/gb2014152r29.

### Examples

```
data(cgEx)

cgEx[1,]
cgEx[,1]

cd <- colData(cgEx)
colData(cgEx) <- cd

gr <- rowData(cgEx)
rowData(cgEx) <- gr

cgEx

cl <- contacts(cgEx)
contacts(cgEx) <- cl

d.idx <- distanceIdx(cgEx, 1e7, 4e4)
```



```

libs <- librarySize(cgEx)

cgEx.cpm <- logCPM(cgEx)

## below, upper.mats.list is a list of upper triangular matrices
## SampleData is a DataFrame of sample data and LociData is a GenomicRanges objec
## Not run:
MatsList <- lapply(upper.mats.list, function(M) M[lower.tri(M)] = M[upper.tri(M)])
cg <- ContactGroup(LociData, MatsList, SampleData)

## End(Not run)

```

---

cooler\_methods

*Methods for manipulating cooler files*


---

## Description

These are a set of methods for working with data in cooler file format. At present this assumes there is one sample's data at one resolution per cooler file, for all observations from one sample.

## Usage

```

getGenomeIdx(file, step)
getChrCGFromCools(bin.ixns, files, chr, colData)
cg2bedgraph2(cg, out.dir)

```

## Arguments

file	The name of a cooler file.
step	The resolution of the data inside the cooler file.
bin.ixns	A list that contains a list of interactions and the bins involved; output of getGenomeIdx.
files	A vector of cooler file names.
chr	The target chromosome to be read.
colData	A data.frame or DataFrame of metadata for the ContactGroup object.
cg	A ContactGroup object.
out.dir	A directory in which individual bedgraph2 (BG2) files are to be written.

## Details

These methods allow for the normalization of cooler files. Users must first generate an index of the genome represented in all cooler files (it is assumed the same loci pair's interactions are observed in all samples), which allows for subsequent efficient I/O operations. `getGenomeIdx` generates this index. The index can then be used to pull data for one chromosome for all cooler files using `getChrCGFromCools`. Users can then follow the standard pipeline, and save their data in bedgraph2 (BG2) format using `cg2bedgraph2`. cooler provides a tool to convert this format to cooler and users are encouraged to make use of this tool.

**Value**

For `getGenomeIdx`, a list that contains a set of all interactions, as well as a listing of all bins present in the cooler file `cool.fh`. For `getChrCGFromCools`, a `ContactGroup` object. There is nothing returned by `cg2bedgraph2`.

**See Also**

[ContactGroup](#)

**Examples**

```
coolerDir <- system.file("cooler", package = "bnbc")
cools <- list.files(coolerDir, pattern="cool$", full.names=TRUE)

step <- 4e4

bin.ixns.list <- bnbc::getGenomeIdx(cools[1], step)
bin.ixns <- bin.ixns.list$bin.ixns

data(cgEx)
cool.cg <- bnbc::getChrCGFromCools(bin.ixns,
                                   files = cools,
                                   chr = "chr22",
                                   colData = colData(cgEx)[1:2,])
all.equal(contacts(cgEx)[[1]], contacts(cool.cg)[[1]])
```

---

getBandIdx

*Get Band Indices*

---

**Description**

Get the indices corresponding to a matrix band.

**Usage**

```
getBandIdx(n, band.no)
```

**Arguments**

<code>n</code>	The number of rows/columns of a contact matrix
<code>band.no</code>	Integer specifying which matrix band. <code>band.no = 1</code> retrieves the main diagonal.

**Details**

This function is used in subsetting contact matrices, primarily in [getBandMatrix](#). However, users wishing to extract band matrices directly may find this useful

**Value**

A matrix with 2 columns and as many rows as entries in the matrix band.

**See Also**

[ContactGroup](#), [getBandMatrix](#), [band](#)

**Examples**

```
data(cgEx)
b2.idx <- getBandIdx(nrow(cgEx), 2)
```

---

getBandMatrix	<i>Get Band Matrix</i>
---------------	------------------------

---

**Description**

Get band matrix from ContactGroup.

**Usage**

```
getBandMatrix(cg, band.no=1)
```

**Arguments**

cg	A ContactGroup object.
band.no	Integer specifying which matrix band. band.no = 1 retrieves the main diagonal.

**Details**

A band matrix is a matrix whose columns are the band.no-th off-diagonal of each sample's contact matrix. If there are k samples and matrix band band.no has r entries, then the returned band matrix is of dimension r x k.

**Value**

A matrix with one column per sample in the ContactGroup and number of rows equal to the length of the matrix band.

**See Also**

[ContactGroup](#), [getBandIdx](#), [band](#)

**Examples**

```
data(cgEx)
b2 <- getBandMatrix(cgEx, 2)
```

---

`groupZeros`*Group Zero Operations*

---

## Description

These functions find and remove rows in the set of contact matrices for which all elements in the row are 0 in all samples.

## Usage

```
getGroupZeros(cg)
dropGroupZeros(cg, g0s)
```

## Arguments

<code>cg</code>	A <code>ContactGroup</code> object.
<code>g0s</code>	A list of elements identified as group zeros.

## Details

Group zeros are those rows for which all elements of the row in all samples are 0. These can impact estimation of features such as A/B compartment status and so should be removed for many analyses.

## Value

A `ContactGroup` object with the group zeros removed from all rows in all contact matrices.

## See Also

[ContactGroup](#)

## Examples

```
data(cgEx)
g0s <- getGroupZeros(cgEx)
cgEx <- dropGroupZeros(cgEx, g0s)
```

---

`smoothing`*Smoothing Operations*

---

**Description**

These functions apply a smoothing kernel to all contact matrices in a ContactGroup object.

**Usage**

```
boxSmoother(cg, h, mc.cores)
gaussSmoother(cg, radius, sigma, mc.cores)
```

**Arguments**

<code>cg</code>	A ContactGroup object.
<code>h</code>	The desired smoother radius. Only applies to box smoother. This is an integer.
<code>radius</code>	The desired smoother width. Only applies to Gaussian smoother. This is an integer.
<code>sigma</code>	The desired smoother standard deviation. Only applies to Gaussian smoother. This is a positive number.
<code>mc.cores</code>	The number of cores to be used.

**Details**

`boxSmoother` applies a square smoothing kernel of radius  $h$  to all contact matrices in a ContactGroup object. Specifying radius  $h$  implies that the width of the kernel is  $2 * h + 1$  matrix cells.

`gaussSmoother` applies a square Gaussain smoothing kernel of width `radius` with standard deviation `sigma` to all contact matrices in a ContactGroup object.

**Value**

A ContactGroup object is returned that contains the smoothed matrices.

**See Also**

[ContactGroup](#)

**Examples**

```
data(cgEx)
cgEx.smooth <- boxSmoother(cgEx, h=5, mc.cores=1)
cgEx.smooth <- gaussSmoother(cgEx, radius=3, sigma=0.5, mc.cores=1)
```

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