

# Package ‘genomicInstability’

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**Title** Genomic Instability estimation for scRNA-Seq

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**Imports** mixtools, SummarizedExperiment

**Description** This package contain functions to run genomic instability analysis (GIA) from scRNA-Seq data.

GIA estimates the association between gene expression and genomic location of the coding genes.

It uses the aREA algorithm to quantify the enrichment of sets of contiguous genes (loci-blocks) on the gene expression profiles and estimates the Genomic Instability Score (GIS) for each analyzed cell.

**License** file LICENSE

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## Contents

genomicInstability-package . . . . .	2
geneLength . . . . .	3
genePosition . . . . .	3
generateChromosomeGeneSet . . . . .	4
genomicInstabilityScore . . . . .	4
giDensityPlot . . . . .	5
giLikelihood . . . . .	6
inferCNV . . . . .	7
plot.inferCNV . . . . .	8
<b>Index</b>	<b>10</b>

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genomicInstability-package

*genomicInstability: Genomic Instability estimation for scRNA-Seq*

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## Description

This package contain functions to run genomic instability analysis (GIA) from scRNA-Seq data. GIA estimates the association between gene expression and genomic location of the coding genes. It uses the aREA algorithm to quantify the enrichment of sets of contiguous genes (loci-blocks) on the gene expression profiles and estimates the Genomic Instability Score (GIS) for each analyzed cell.

## Details

The basic functionality of this package can be performed by `inferCNV()`, to infer the enrichment of loci-blocks on gene expression; `genomicInstabilityScore()`, to estimate the genomic instability for each of the cells in the scRNASeq dataset; `giLikelihood()`, to estimate the relative likelihood for each cell to be normal (low genomic instability) or tumor (high genomic instability); `plot()` and `giDensityPlot()` to plot the scores per loci-block and the distribution of the genomic instability score, respectively.

## Author(s)

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- DarwinHealth [copyright holder]

**See Also**

[inferCNV()] for estimating loci-block enrichment, [genomicInstabilityScore()] for estimating the genomic instability of each cell in the dataset, [giLikelihood()] for estimating the relative likelihood for the cells to be normal or neoplastic, [plot.inferCNV()] and [giDensityPlot()] to plot the results.

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geneLength	<i>Average length of human and mouse known genes</i>
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**Description**

A dataset containing the average length for known mouse and human genes

**Usage**

```
geneLength
```

**Format**

Vector of integers indicating the average length in bp for each gene, indicated with EntrezIDs as name argument. To access this data use:

**data(hg38)** Human

**data(mm10)** Mouse

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genePosition	<i>Chromosomal coordinate of human and mouse known genes</i>
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**Description**

A dataset containing the chromosomal coordinate for known human and mouse genes

**Usage**

```
genePosition
```

**Format**

data.frame with 2 columns: Chromosome and Coordinate. To access this data use:

**data(hg38)** Human

**data(mm10)** Mouse

generateChromosomeGeneSet  
*Topological gene sets*

---

**Description**

This function generates a list of sets of k genes encoded by neighbor loci

**Usage**

```
generateChromosomeGeneSet(species = c("human", "mouse"), k = 100, skip = 25)
```

**Arguments**

species	Character string indicating the species, either human or mouse
k	Integer indicating the number of genes per set
skip	Integer indicating the displacement of the window for selecting the k genes

**Value**

List of topologically-close gene sets

**Examples**

```
chrom_set <- generateChromosomeGeneSet('human')
length(chrom_set)
chrom_set[seq_len(2)]
```

---

genomicInstabilityScore  
*Genomic Instability Analysis*

---

**Description**

This function computes the genomic instability for an object of class inferCNV

**Usage**

```
genomicInstabilityScore(cnv, likelihood = FALSE)
```

**Arguments**

cnv	Object of class inferCNV generated by inferCNV() function
likelihood	Logical, whether the genomic instability likelihood should be estimated

**Value**

Object of class inferCNV with updated slots for gis and gisnull

**See Also**

[inferCNV()] to infer the enrichment of loci-blocks in the gene expression data.

**Examples**

```
eh <- ExperimentHub::ExperimentHub()
dset <- eh[["EH5419"]]
tpm_matrix <- SummarizedExperiment::assays(dset)$TPM
set.seed(1)
tpm_matrix <- tpm_matrix[, sample(ncol(tpm_matrix), 500)]
cnv <- inferCNV(tpm_matrix)
cnv <- genomicInstabilityScore(cnv)
plot(density(cnv$gis))
```

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giDensityPlot

*Genomic instability plot*

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**Description**

This function plot the genomic instability distribution, gaussian fits and null distribution if available

**Usage**

```
giDensityPlot(inferCNV, legend = c("topleft", "top", "topright", "none"), ...)
```

**Arguments**

inferCNV	Object of class inferCNV
legend	Character string indicating the location of the legend. none to not include it
...	Additional parameters for plot()

**Value**

None, a figure is created in the default output device

**See Also**

[giLikelihood()] to estimate the relative likelihood, [genomicInstabilityScore()] to estimate the genomic instability score for each cell in the dataset, and [inferCNV()] to infer the enrichment of loci-blocks in the gene expression data.

**Examples**

```

eh <- ExperimentHub::ExperimentHub()
dset <- eh[["EH5419"]]
tpm_matrix <- SummarizedExperiment::assays(dset)$TPM
set.seed(1)
tpm_matrix <- tpm_matrix[, sample(ncol(tpm_matrix), 500)]
cnv <- inferCNV(tpm_matrix)
cnv <- genomicInstabilityScore(cnv)
cnv <- giLikelihood(cnv, distros=c(3, 3), tumor=2:3)
giDensityPlot(cnv)

```

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giLikelihood

*Genomic instability likelihood*


---

**Description**

This function computes the genomic instability likelihood

**Usage**

```

giLikelihood(
  inferCNV,
  recompute = TRUE,
  distros = c(1, 3),
  tumor = NULL,
  normal = NULL
)

```

**Arguments**

inferCNV	InferCNV-class object
recompute	Logical, whether the model fits should be re-computed
distros	Vector of 2 integers indicating the minimum and maximum number of Gaussian models to fit
tumor	Optional vector of integers indicating the Gaussians considered as tumors
normal	Optional vector of integers indicating the Gaussians considered as normal. This is only useful when no null model has been provided for the analysis

**Value**

Updated inferCNV-class object with `gi_likelihoood` slot

**See Also**

[`genomicInstabilityScore()`] to estimate the genomic instability score for each cell in the dataset, and [`inferCNV()`] to infer the enrichment of loci-blocks in the gene expression data.

**Examples**

```

eh <- ExperimentHub::ExperimentHub()
dset <- eh[["EH5419"]]
tpm_matrix <- SummarizedExperiment::assays(dset)$TPM
set.seed(1)
tpm_matrix <- tpm_matrix[, sample(ncol(tpm_matrix), 500)]
cnv <- inferCNV(tpm_matrix)
cnv <- genomicInstabilityScore(cnv)
cnv <- giLikelihood(cnv, distros=c(3, 3), tumor=2:3)
print(cnv$gi_fit)
plot(density(cnv$gi_likelihoood, from=0, to=1))

```

inferCNV

*Inference of CNV from expression data***Description**

This function estimates the CNV score based on expression data

**Usage**

```

inferCNV(
  expmat,
  nullmat = NULL,
  species = c("human", "mouse"),
  k = 100,
  skip = 25,
  min_geneset = 10,
  verbose = TRUE
)

```

**Arguments**

expmat	Matrix of gene expression profiles or signatures with genes '(entrezID) in rows and samples in columns
nullmat	Optional matrix with same number of rows as expmat to be used as null model
species	Character string indicating the species, either human or mouse
k	Integer indicating the number of genes per set
skip	Integer indicating the displacement of the window for selecting the k genes
min_geneset	Integer indicating the minimum size for the genesets
verbose	Logical, whether progress should be reported

**Value**

Object of class inferCNV, which is a list containing matrix of nes, and parameters (param), including species, window (k) and skip

**Examples**

```
eh <- ExperimentHub::ExperimentHub()
dset <- eh[["EH5419"]]
tpm_matrix <- SummarizedExperiment::assays(dset)$TPM
set.seed(1)
tpm_matrix <- tpm_matrix[, sample(ncol(tpm_matrix), 500)]
cnv <- inferCNV(tpm_matrix)
class(cnv)
names(cnv)
cnv$nes[1:5, 1:3]
```

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plot.inferCNV	<i>Plot chromosome map</i>
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**Description**

This function generates a chromosomes map plot for the inferred CNVs

**Usage**

```
## S3 method for class 'inferCNV'
plot(x, output = NULL, threshold = 0.2, gamma = 1.5, resolution = 150, ...)
```

**Arguments**

x	Object of class inferCNV
output	Optional output PDF file name (with extension)
threshold	Likelihood threshold for identifying genomically instable cells/samples, 0 disables this filter
gamma	Number indicating the gamma transformation for the colors
resolution	Integer indicating the ppi for the png and jpg output files
...	Additional parameters for plot

**Value**

Nothing, a plot is generated in the default output devise

**See Also**

[giLikelihood()] to estimate the relative likelihood, [genomicInstabilityScore()] to estimate the genomic instability score for each cell in the dataset, and [inferCNV()] to infer the enrichment of loci-blocks in the gene expression data.



### **Examples**

```
eh <- ExperimentHub::ExperimentHub()
dset <- eh[["EH5419"]]
tpm_matrix <- SummarizedExperiment::assays(dset)$TPM
set.seed(1)
tpm_matrix <- tpm_matrix[, sample(ncol(tpm_matrix), 500)]
cnv <- inferCNV(tpm_matrix)
cnv <- genomicInstabilityScore(cnv)
cnv <- giLikelihood(cnv, distros=c(3, 3), tumor=2:3)
plot(cnv, output='test.png')
```

# Index

- \* **datasets**

- geneLength, 3
  - genePosition, 3

- \* **internal**

- genomicInstability-package, 2

- geneLength, 3

- genePosition, 3

- generateChromosomeGeneSet, 4

- genomicInstability

- (genomicInstability-package), 2

- genomicInstability-package, 2

- genomicInstabilityScore, 4

- giDensityPlot, 5

- giLikelihood, 6

- inferCNV, 7

- plot.inferCNV, 8