Package 'TranScan'

July 12, 2022

Type Package

Title Translocation Detection from Hi-C data via Scan Statistics

Version 1.0

Date 2020-09-19

Author Anthony Cheng, Disheng Mao, Yuping Zhang, Joseph Glaz, Zhengqing Ouyang

Maintainer
Yuping Zhang <yuping.zhang@uconn.edu> and Zhengqing Ouyang <ouyang@schoolph.umass.edu>

Description
R-package for the paper entitled ``Translocation Detection from Hi-C data via Scan Statistics" by Anthony Cheng, Disheng Mao, Yuping Zhang, Joseph Glaz, Zhengqing Ouyang

Imports Matrix, dplyr, ggplot2, ggpubr, MASS, reshape2

Depends R (>= 3.2.3)

License GPL (>= 3)

RoxygenNote 7.1.1

NeedsCompilation no

R topics documented:

`chr10` *Chromosome 10 of T47D*

Description

Intra region of chromosome 10 in cell line T47D (500kb resolution)

Usage

```
data(chr10)
```

Format

The third column refers to rounded log count

`chr10_20` *Chromosome 10_20 of T47D*

Description

Inter region between chromosome 10 and 20 in cell line T47D (500kb resolution)

Usage

```
data(chr10)
```

Format

The third column refers to rounded log count

`chr20` *Chromosome 20 of T47D*

Description

Intra region of chromosome 20 in cell line T47D (500kb resolution)

Usage

```
data(chr20)
```

Format

The third column refers to rounded log count

TranScan *Hi-C inter-chromosomal translocation detection via Scan clustering*

Description

This function allows you to detect the inter-chromosomal translocation from Hi-C data. It requires two intra-regions and the corresponding inter-region as inputs. We suggest rounded log counts as inputs.

Usage

```
TranScan(
  chr1,
  chr2,
  chr1_2,
  outputpath,
  sizes,
  resolution = 5e+05,
  quantitest = 256,
  alpha = 0.05,
  gammath = 0.1,
  number_of_bandwidth = 20,
  diag_remove = 2e+06,
  add_gap = 2500000
)
```

Arguments

chr1	First chromosome
chr2	Second chromosome
chr1_2	Inter-chromosomal region of chr1 and chr2
outputpath	The path to store all results
sizes	Chrom sizes of chr1_2; vector of length 2
resolution	Resolution of Hi-C data
quantitest	Grid of testing, must be 2^k, default 256, meaning 256 * 256
alpha	FDX, default 0.05
gammath	Gamma threshold, default 0.1
number_of_bandwidth	Number of bandwidths used, default 20
diag_remove	Removed short-range interactions, must be k * resolution, default 2e+06
add_gap	Added gap between two chromosomes, must be k * resolution, defult 2500000

Value

A heatmap and a rejected region plot will be generated under the output folder. The matrix form of rejected region is saved as RR.txt. All intermediate objects will also be saved.

Examples

```
data(chr10)
data(chr20)
data(chr10_20)
p_sizes = "../hg38.sizes"
p_outdir = "output"
sizes = read.table(p_sizes, col.name=c("chrom", "size"))
chr10_l = subset(sizes, chrom=="chr10")$size
chr20_l = subset(sizes, chrom=="chr20")$size
size_dim = c(chr10_l, chr20_l)
TranScan(chr10, chr20, chr10_20, p_outdir, size_dim)
```

Index