

rGMAP

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Type Package

Title Call hierarchical chromatin domains from HiC matrix by GMAP

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Description Call hierarchical chromatin domains from HiC contact matrix by Gaussian Mixture model And Proportion test

BugReports <https://github.com/wbaopaul/rGMAP/issues>

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LazyData TRUE

Imports data.table,
ggplot2,
mclust,
EMD,
caTools,
Matrix,
Rcpp (>= 0.12.5)

LinkingTo Rcpp

RoxygenNote 6.0.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

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data_simu	<i>generate simulated hic_mat and true tads</i>
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Description

generate simulated hic_mat and true tads

Usage

```
data_simu(stype = "poisson-dist", nratio = 2.5, mu0 = 200, resl = 1)
```

Arguments

stype	One of four types of simulated data in the manuscript: poisson-dist, poisson-dist-hier, nb-dist, nb-dist-hier; poisson- or nb- indicates poisson distribution or negative binomial distribution -hier indicated subtads are generated nestly
nratio	The effect size between intra- and inter domain, larger means higher intra-tad contacts
mu0	The mean parameter, default 200
resl	Resolution, default set to 1

Value

A list includes following elements:

hic_mat	n by n contact matrix
hierTads	True heirarchical domains
tads_true	True TADs

hic_rao_IMR90_chr15	<i>Normalized Hi-C data for IMR90, chr15 with resolution 10kb.</i>
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Description

Normalized Hi-C data for IMR90, chr15 with resolution 10kb.

Usage

```
hic_rao_IMR90_chr15
```

Format

A data table with 3 variables:

n1 bin 1

n2 bin 2

count normalized counts

Source

Rao et al., Cell 2014, A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping

plotdom	<i>visualize hierarchical domains</i>
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Description

visualize hierarchical domains

Usage

```
plotdom(hic_dat, hiertads_gmap, start_bin, end_bin, cthr = 20, resl = 10000)
```

Arguments

hic_dat	hic contact matrix for a given chromosome, either a n by n matrix, or a 3 columns data.frame <bin1> <bin2> <counts>
hiertads_gmap	the hierarchical domains called by GMAP
start_bin	the start bin of the genome
end_bin	the end bin of the genome
cth	the upper bound count threshold for color, default 20
resl	reslution of Hi-C data, default 10000

rGMAP	<i>Detect hierarchical choromotin domains by GMAP</i>
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Description

Detect hierarchical choromotin domains by GMAP

Usage

```
rGMAP(hic_mat, resl = 10 * 10^3, logt = T, dom_order = 2,
      maxDistInBin = min(200, 2 * 10^6/resl), min_d = 25, max_d = 100,
      min_dp = 5, max_dp = 10, hthr = 0.95, t1thr = 0.5)
```

Arguments

<code>hic_mat</code>	Either a 3 columns Hi-C contact matrix for a given chromosome, with each row corresponding to the start bin, end bin and the contact number; or a n by n matrix, n is the number of bins for a given chromosom
<code>resl</code>	The resolution (bin size), default 10kb
<code>logt</code>	Do log-transformation or not, default TRUE
<code>dom_order</code>	Maximum level of hierarchical structures, default 2 (call TADs and subTADs)
<code>maxDistInBin</code>	Only consider contact whose distance is not greater than maxDistInBin bins, default 200 bins (or 2Mb)
<code>min_d</code>	The minimum d (d: window size), default 25
<code>max_d</code>	The maximum d (d: window size), default 100
<code>min_dp</code>	The minmum dp (dp: lower bound of tad size), default 5
<code>max_dp</code>	The maximum dp (dp: lower bound of tad size), default 10. <code>min_d</code> , <code>max_d</code> , <code>min_dp</code> and <code>max_dp</code> should be specified in number of bins
<code>hthr</code>	The lower bound cutoff for posterior probability, default 0.95
<code>t1thr</code>	Lower bound for t1 for calling TAD, default 0.5 quantile of test statistics of TADs, 0.9 of subTADs

Value

A list includes following elements:

<code>tads</code>	A data frame with columns start, end indicates the start and end coordinates of each domain, respectively
<code>hierTads</code>	A data frame with columns start, end, dom_order, where dom_order indicates the hierarchical status of a domain, 1 indicates tads, 2 indicates subtads, and so on
<code>params</code>	A data frame gives the final parameters for calling TADs

Examples

```
## On simulated data:
library(rGMAP)
simu_res = data_simu('poisson-dist-hier')
true_domains = simu_res$hierTads
simu_mat = simu_res$hic_mat
predicted_domains = rGMAP(simu_mat, resl = 1)$hierTads
true_domains
predicted_domains

## On an real data example
hic_rao_IMR90_chr15 # normalized Hi-C data for IMR90, chr15 with resolution 10kb
res = rGMAP(hic_rao_IMR90_chr15, resl = 10 * 1000, dom_order = 2)
names(res)
#quickly visualize some hierarchical domains
pp = plotdom(hic_rao_IMR90_chr15, res$hierTads, 6000, 7000, 30, 10)
pp$p2
```

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