Package ‘geneRxCluster’

March 27, 2024

Date 2013-02-13
Version 1.38.0
License GPL (>= 2)

Description Detect Differential Clustering of Genomic Sites such as
gene therapy integrations. The package provides some functions
for exploring genomic insertion sites originating from two
different sources. Possibly, the two sources are two different
gene therapy vectors. Vectors are preferred that target
sensitive regions less frequently, motivating the search for
localized clusters of insertions and comparison of the clusters
formed by integration of different vectors. Scan statistics
allow the discovery of spatial differences in clustering and
calculation of False Discovery Rates (FDRs) providing
statistical methods for comparing retroviral vectors. A scan
statistic for comparing two vectors using multiple window
widths to detect clustering differentials and compute FDRs is
implemented here.

Title gRx Differential Clustering
Author Charles Berry
Maintainer Charles Berry <ccberry@ucsd.edu>
Depends GenomicRanges,IRanges
Suggests RUnit, BiocGenerics
biocViews Sequencing, Clustering, Genetics

git_url https://git.bioconductor.org/packages/geneRxCluster
git_branch RELEASE_3_18
git_last_commit aad4ae6
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-27
**R topics documented:**

- `critVal.alpha` .......................... 2
- `critVal.power` .......................... 3
- `critVal.target` .......................... 4
- `geneRxCluster` .......................... 5
- `gRxCluster` .............................. 6
- `gRxCluster-object` ........................ 7
- `gRxPlot` ................................. 8
- `gRxPlotClumps` ........................... 9
- `gRxSummary` .............................. 10
- `noprune` ................................. 11
- `plot.cutpoints` ........................... 12
- `prune.loglik` ............................. 12

**Index**

14

---

### `critVal.alpha`

**description**

Critical region cutpoints

**usage**

```r
critVal.alpha(k, p0, alpha, posdiff)
```

**arguments**

- `k` - window width(s)
- `p0` - length 2 probabilities
- `alpha` - two tailed
- `posdiff` - position difference matrix

**details**

This version uses alpha and will find TFD

**value**

List of cutoffs and attributes

**author(s)**

Charles Berry
critVal.power

See Also

gRxCluster for how and why this function is used

Examples

# symmetric odds:
crit <- critVal.alpha(5:25, c(1,1)/2, alpha=0.05,
                       matrix(1,nr=50,nc=21))
crit[[1]]
sapply(crit,c)
# 5:1 odds
asymmetric.crit <- critVal.alpha(5:25, c(1,5)/6, alpha=0.05,
                                  matrix(1,nr=50,nc=21))
# show the critical regions
par(mfrow=c(1,2))
gRxPlot(crit,method="critical")
gRxPlot(asymmetric.crit,method="critical")
rm(crit, asymmetric.crit)

Description

critical region cutpoints

Usage

critVal.power(k, p0, target, pwr = 0.8, odds = 7)

Arguments

k - window width(s)
p0 - length 2 probabilities
target - false discoveries wanted
pwr - desired power
odds - alternative odds ratio

Details

This version uses power and TFD and will limit windows screened

Value

list of cutoffs and attributes
critVal.target

Author(s)
Charles Berry

See Also
gRxCluster for how and why this function is used

Examples

# symmetric odds:
crit <-
critVal.power(5:25,c(1,1),5,pwr=0.8,odds=7)
crit[[1]]
sapply(crit,c)
# 5:1 odds
asymmetric.crit <-
critVal.power(5:25,c(1,5),5,pwr=0.8,odds=7)
# show the critical regions
par(mfrow=c(1,2))
gRxPlot(crit,method="critical")
gRxPlot(asymmetric.crit,method="critical")
rm(crit,asymmetric.crit)

critVal.target  critical regions

description

critical region cutpoints

Usage

critVal.target(k, p0, target, posdiff = NULL, ns)

Arguments

- k window width(s)
- p0 length 2 probabilities
- target - two tailed
- posdiff - position difference matrix
- ns the number of windows passing filter at each k

details

This version uses TFD and will find alpha implicitly
**geneRxCluster**

**Value**

list of cutoffs and attributes

**Author(s)**

Charles Berry

**See Also**

`gRxCluster` for how and why this function is used

**Examples**

```r
# symmetric odds:
crit <- critVal.target(5:25,c(1,1),1,ns=rep(10,21))
crit[[1]]
sapply(crit,c)
# 5:1 odds
asymmetric.crit <- critVal.target(5:25,c(1,5),1,ns=rep(10,21))
# show the critical regions
par(mfrow=c(1,2))
gRxPlot(crit,method="critical")
gRxPlot(asymmetric.crit,method="critical")
rm(crit,asymmetric.crit)
```

---

geneRxCluster  

**Differential Clustering of Integration Sites**

**Description**

geneRxCluster provides the function `gRxCluster` and friends.

**Details**

Windows defined by \( k \) consecutive integration sites are scanned. A two class indicator is tallied to determine whether one class dominates. If one does, a flag is set and the window is retained. Various values of \( k \) are used. Conflicts between overlapping windows with the same value of \( k \) can occur — two windows are dominated by the two different classes. In that case, the sites of overlap are marked and neither window is retained. Conflicts can also arise between windows differing in their values of \( k \). In that case, the window having the smaller value of \( k \) is retained and the other is discarded.

Permutation tests and permutation based false discovery rates are available.
Filtering of windows is allowed so that regions which are sparsely populated need not be studied.
gRxCluster

Description

Cluster integration sites - optionally perform the permutations needed to estimate the discoveries expected under a null hypothesis

Usage

gRxCluster(object, starts, group, kvals, nperm = 0L,
pruneFun = prune.loglik, ..., cutpt.filter.expr, cutpt.tail.expr, tmp.env,
sample.id, sample.tab)

Arguments

object chromosome names or other grouping of starts
starts ordered chromosome position or ordered integer vector
group logical vector separating two groups
kvals integer vector of window widths
nperm number of permutations for FDR calculation
pruneFun a function like prune.loglik.
... other args
cutpt.filter.expr (optional) R object or call (or variable naming a call) with (optional) var x (window widths in base pairs) to filter windows. It must evaluate to mode "double". If not specified, as.double(apply(x,2,median,na.rm=TRUE)) is used. If an atomic vector of length one is supplied it is expanded to the proper length and coerced to double. If this arg is the name of a variable provided in tmp.env, it must be protected with quote(...).
cutpt.tail.expr R object or call (or variable naming a call) with (optional) vars: k,n, and x (as above). Returns list like critVal.target. k is a vector of the number of sites in a collection of windows, and n is a vector of counts or proportions for the two classes of insertion. If not supplied, critVal.target(k,n,target=5,posdiff=x) is used. If this arg is the name of a variable provided in tmp.env, it must be protected with quote(...).
tmp.env (optional) environment to use in evaluation of cutpt.* expressions. This is usually needed for critVal.power, which is first calculated and placed in the environment, and the supplied object is used in the expression for cutpt.filter.expr.
sample.id (optional) integer vector indexing cells in sample.tab to be looked up to determine group under permutation. A factor can be used, too, but will be coerced to integer.
sample.tab (optional) integer vector containing 0 or 1 in each cell. Its length is the same as max(sample.id). Both or neither sample.id and sample.tab should be supplied. When supplied sample.tab[sample.id] must equal group. If the arguments are supplied, permutations are of the form sample(sample.tab)[sample.id]. Otherwise they are of the form sample(group).

Value

da GRanges object with a special metadata slot, see gRxCluster-object

Author(s)

Charles Berry example inst/ex-gRxCluster.R

gRxCluster-object  gRxCluster object

Description

Overview of the result of gRxCluster(...) 

Details

The object returned is a GRanges object.
If the object is x, seqnames(x) and ranges(x) slots demarcate the clusters discovered. There will be one element for each cluster (aka 'clump') discovered.
Using the default argument pruneFun=prune.loglik or pruneFun=noprune, mcols(x) will have these columns:

value1 and value2 are the counts of the two classes of insertion sites for the clusters of object x
clump.id numbers each cluster.

If the user supplies a custom pruneFun, it should return a GRanges with those columns and one element for each unique clump.id. The column target.min has the smallest nominal False Discoveries Expected for each cluster and is added to (or replaces) the mcols(x) produced by the argument supplied as pruneFun.
metadata(x) will include these components:

criticalValues A list object such as supplied by critVal.target whose elements each give the cutpoints to be used for a window with k sites. attributes(metadata(object)$criticalValues[[i]]) will contain elements

  fdr with dimension c(k+1,4) of target false discovery expectations and and the one-sided p-values
  target the target for false discovery which sometimes is specified a priori and sometimes results from calculation
  n an upper bound on the number of windows to screen, if this number is needed.
In some cases, an attribute is attached to `metadata(object)$criticalValues`, see `critVal.power` for an example.

- **kvals** the number of sites, k, to include in a window
- **perm_cluster_best** a list whose canonical element is a vector of values like `x$target.min` obtained from a permutation of the class indicators
- **summary_matrix** a matrix giving the start, end, depth, and counts in each class for every cluster and depth in sequential order
- **call** the call invoking `gRxCluster` which may include some arguments added by default.

**Author(s)**

Charles Berry <ccberry@ucsd.edu>

---

**gRxPlot**

**Description**

Plot Clumps and/or Critical Regions

**Usage**

```r
gRxPlot(object, pi.0 = NULL, method = c("odds", "criticalRegions"),
        xlim = NULL, main = NULL, xlab = "log odds ratio", breaks = "Sturges",
        kvals = NULL, ...)
```

**Arguments**

- **object** either the results of `gRxCluster` or a list containing cutpoints for critical regions.
- **pi.0** the background proportion for vector 2
- **method** character vector of “odds” and/or “criticalRegions”
- **xlim** limits of the log odds histogram
- **main** a title for the panel(s)
- **xlab** label for the x-axis of the log odds plot
- **breaks** see `hist`
- **kvals** values to use in selecting a subset of the critical regions to display
- **...** other args to pass to the plotting routine(s)

**Details**

The results of a call to `gRxCluster` are plotted. Optionally, with `method="criticalRegions"` only the critical regions are plotted or with `method="odds"` the log odds only are plotted.
**gRxPlotClumps**

**Value**

see hist

**Author(s)**

Charles Berry

**See Also**

gRxPlotClumps for a more fine grained display

**Examples**

```r
x.seqnames <- rep(letters[1:3], each=500)
x.starts <- c(seq(1, length=500), seq(1, by=2, length=500), seq(1, by=3, length=500))
x.lens <- rep(c(5, 10, 15, 20, 25), each=20)
x.group <- rep(rep(c(TRUE, FALSE), length=length(x.lens)), x.lens)
## add a bit of fuzz:
x.group <- 1==rbinom(length(x.group), 1, pr=ifelse(x.group,.8,.2))
x.kvals <- as.integer(sort(unique(x.lens)))
x.res <- gRxCluster(x.seqnames, x.starts, x.group, x.kvals)
gRxPlot(x.res)
```

---

**Description**

Plot gRxCluster object clumps

**Usage**

```r
gRxPlotClumps(object, data, seqlens, panelExpr = quote(grid()))
```

**Arguments**

- **object**: result of gRxCluster
- **data**: (optional) GRanges like that from which args to gRxCluster were derived
- **seqlens**: (optional) seqlens(data) or similar. Can be given if data is missing
- **panelExpr**: - an expression to evaluate after drawing each panel

**Details**

Plot Relative Frequencies of the two classes according to region. Regions typically alternate between clusters and non-clusters on each chromosome.
Author(s)

Charles Berry

Examples

```r
x.seqnames <- rep(letters[1:3], each=50)
x.starts <- c(seq(1, length=50), seq(1, by=2, length=50), seq(1, by=3, length=50))
x.lens <- rep(c(5, 10, 15, 20, 25), each=2)
x.group <- rep(rep(c(TRUE, FALSE), length=length(x.lens)), x.lens)
## add a bit of fuzz:
x.group <- 1==rbinom(length(x.group), 1, pr=ifelse(x.group,.8,.2))
x.kvals <- as.integer(sort(unique(x.lens)))
x.res <- gRxCluster(x.seqnames, x.starts, x.group, x.kvals)
gxPlotClumps(x.res)
rm(x.seqnames, x.starts, x.lens, x.group, x.kvals, x.res)
```

Description

Summarize gRxCluster Results

Usage

```r
gRxSummary(object, targetFD = NULL)
```

Arguments

- **object**: the result of gRxCluster
- **targetFD**: the critical value target in each tail

Details

Get the FDR and related data for a run of gRxCluster. By selecting a value for targetFD that is smaller than what was used in constructing the object, fewer clumps will be included in the computation for the False Discovery Rate - akin to what would have been obtained from the object if it had been constructed using that value.

Value

- a list containing the summarized results

Author(s)

Charles Berry
Examples

```r
x.seqnames <- rep(letters[1:3], each=50)
x.starts <- c(seq(1, length=50), seq(1, by=2, length=50), seq(1, by=3, length=50))
x.lens <- rep(c(5, 10, 15, 20, 25), each=2)
x.group <- rep(rep(c(TRUE, FALSE), length=length(x.lens)), x.lens)
x.kvals <- as.integer(sort(unique(x.lens)))
x.res <- gRxCluster(x.seqnames, x.starts, x.group, x.kvals, nperm=100L)
gRxSummary(x.res)
rm(x.seqnames, x.starts, x.lens, x.group, x.kvals, x.res)
```

Description

join contiguous windows

Usage

```r
noprune(x, ...)
```

Arguments

- `x`: a GRanges object
- `...`: currently unused

Details

return all the candidate sites in a clump without pruning
this is to be used as the pruneFun argument of `gRxCluster`

Value

same as `gRxCluster` less the metadata

Author(s)

Charles Berry

See Also

`gRxCluster-object` for more details on what this function returns.
plot.cutpoints - Utility

Description
Plot a set of cutpoints - Utility

Usage
## S3 method for class 'cutpoints'
plot(crit, pi.0 = NULL, kvals = NULL, ...)

Arguments
- crit - a cutpoint object see gRxCluster
- pi.0 - optional null value to plot
- kvals - which cutpoints to include in the plot
- ... passed to barplot

Details
NOT FOR USERS. Not exported.

Value
list with components of “bar.x” (the value of hist()), “kvals” (window widths plotted), and “pi.0” (the input value of pi.0)

Author(s)
Charles Berry

prune.loglik - prune.loglik

Description
best contiguous region

Usage
prune.loglik(x, p.null = 0.5)
prune.loglik

Arguments

  x          a GRanges object
  p.null     the probability of category 1 (FALSE)

Details

  prune each end of the region using loglik criterion
  this is to be used as the pruneFun are of gRxCluster

Author(s)

  Charles Berry

See Also

  gRxCluster-object for details on what this function returns.
Index

* cluster
  gRxCluster-object, 7

critVal.alpha, 2
critVal.power, 3, 6, 8
critVal.target, 4, 7
geneRxCluster, 5
geneRxCluster-package (geneRxCluster), 5
GRanges, 7
gRxCluster, 3–5, 6, 8, 11, 12
gRxCluster-object, 7
gRxPlot, 8
gRxPlotClumps, 9, 9
gRxSummary, 10

hist, 8, 9

noprun, 11

plot.cutpoints, 12
prune.loglik, 12