

Package ‘BubbleTree’

October 27, 2015

Type Package

Title BubbleTree: an intuitive visualization to elucidate tumoral aneuploidy and clonality in somatic mosaicism using next generation sequencing data.

Version 2.0.0

Date 2015-08-27

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Description CNV analysis in groups of tumor samples (Publication Pending).

License LGPL (>= 3)

Imports BiocGenerics (>= 0.7.5), BiocStyle, Biobase, ggplot2, WriteXLS, gtools, RColorBrewer, limma, scales, rgl, grid, gtable, gridExtra, biovizBase, rainbow

Depends R (>= 3.2.1), IRanges, GenomicRanges, plyr, dplyr, magrittr

Suggests methods, knitr, rmarkdown

biocViews CopyNumberVariation, Software, Sequencing, Coverage

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

all.somatic.lst	2
allCall.lst	2
allCNV.lst	3
allHetero.lst	3
allRBD.lst	3
annoByGenesAndCyto	4
Annotate	5
bafTrack	5
btcompare	6
btpredict	7
BTreePlotter	8

BTreePredictor	8
cancer.genes.minus2	8
centromere.dat	8
cyto.gr	9
drawBTree	9
drawBubbles	10
drawFeatures	11
gene.uni.clean.gr	12
getTracks	12
heteroLociTrack	13
hg19.seqinfo	14
info	14
loadRBD	15
RscoreTrack	16
saveXLS	17
trackBTree	18
TrackPlotter	19
vol.genes	19
xyTrack	19

Index **21**

all.somatic.lst	<i>all.somatic.lst</i>
-----------------	------------------------

Description

A dataset containing pre-calculated BAF scores for annotated SNVs.

Format

S4 object with seqnames, genomic ranges, strand, BAF score

Source

internal

allCall.lst	<i>allCall.lst</i>
-------------	--------------------

Description

A dataset containing precalculated data from CNV segment analysis.

Format

S4 object with rbd, rbd.adj, results

Source

internal

`allCNV.lst`*allCNV.lst*

Description

A dataset containing pre-calculated segment calls.

Format

S4 object with seqnames, genomic ranges, num.mark, score

Source

internal

`allHetero.lst`*allHetero.lst*

Description

S4 GRanges dataset containing pre-calculated heterozygosity data.

Format

S4

Source

internal

`allRBD.lst`*allRBD.lst*

Description

A dataset containing precalculated data from CNV segment analysis.

Format

S4 object with rbd, rbd.adj

Source

internal

annoByGenesAndCyto *annoByGenesAndCyto*

Description

annoByGenesAndCyto

Usage

```
annoByGenesAndCyto(.Object, chr, beg, end, critical.genes, gene.uni.clean.gr,
  cyto.gr)
```

```
## S4 method for signature 'Annotate'
annoByGenesAndCyto(.Object, chr, beg, end, critical.genes,
  gene.uni.clean.gr, cyto.gr)
```

Arguments

.Object	the objet
chr	the chromosome
beg	genomic start coord
end	genomic end coord
critical.genes	set of critical genes
gene.uni.clean.gr	gr object of genes
cyto.gr	gr object of cyto positions

Value

list of annotation for genes and cytobands

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "cancer.genes.minus2.rda", package="BubbleTree"))
load(system.file("data", "vol.genes.rda", package="BubbleTree"))
load(system.file("data", "gene.uni.clean.gr.rda", package="BubbleTree"))
load(system.file("data", "cyto.gr.rda", package="BubbleTree"))

comm <- btcompare(vol.genes, cancer.genes.minus2)
btreeplotter <- new("BTreePlotter", branch.col="gray50")
annotator <-new("Annotate")
nn <- "sam2"
cc <- allCall.lst[[nn]]
z <- drawBTree(btreeplotter, cc@rbd.adj) + ggplot2::labs(title=sprintf("%s (%s)", nn, info(cc)))
out <- cc@result$dist %>%
  filter(seg.size >= 0.1 ) %>%
  arrange(gtools::mixedorder(as.character(seqnames)), start) # needs to be relevel

ann <- annoByGenesAndCyto(annotator,
```

```

as.character(out$seqnames),
as.numeric(out$start),
as.numeric(out$end),
comm$comm,
gene.uni.clean.gr=gene.uni.clean.gr,
cyto.gr=cyto.gr)

```

Annotate

*Annotate***Description**

Annotate

Examples

```
annotate <- new("Annotate")
```

bafTrack

*bafTrack***Description**

bafTrack

Usage

```
bafTrack(.Object, result.dat, gr2, somatic.gr = NULL, min.prev = 0.15,
cex = 1.2)
```

```
## S4 method for signature 'TrackPlotter'
bafTrack(.Object, result.dat, gr2, somatic.gr = NULL,
min.prev = 0.15, cex = 1.2)
```

Arguments

.Object	the object
result.dat	the result dataframe
gr2	the gr2 object
somatic.gr	somatic gr object annotation
min.prev	previous min
cex	the cex

Value

the highlighted BAF track

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "centromere.dat.rda", package="BubbleTree"))
load(system.file("data", "all.somatic.lst.RData", package="BubbleTree"))
load(system.file("data", "hg19.seqinfo.rda", package="BubbleTree"))

trackplotter <- new("TrackPlotter")
gr2 = centromere.dat
nn <- "sam2"
p2 <- bafTrack(trackplotter,
               result.dat=allCall.lst[[nn]]@result,
               gr2=gr2,
               somatic.gr=all.somatic.lst[[nn]])
```

btcompare

btcompare

Description

btcompare

Usage

```
btcompare(set1, set2)
```

Arguments

set1	first set
set2	second set to compare

Value

combined, unique list of genes

Examples

```
load(system.file("data", "cancer.genes.minus2.rda", package="BubbleTree"))
load(system.file("data", "vol.genes.rda", package="BubbleTree"))

# 77 common cancer genes
comm <- btcompare(vol.genes, cancer.genes.minus2)
```

btpredict	<i>btpredict</i>
-----------	------------------

Description

btpredict

Usage

```
btpredict(.Object)

## S4 method for signature 'BTreePredictor'
btpredict(.Object)
```

Arguments

.Object the object

Value

.Object populated with the predictions

Examples

```
load(system.file("data", "allRBD.lst.RData", package="BubbleTree"))

btrepredictor <- new("BTreePredictor")
btrepredictor@config$cutree.h <- 0.15
high.ploidy <- rep(TRUE, length(allRBD.lst))
high.purity <- rep(TRUE, length(allRBD.lst))

high.ploidy[c("sam6",
              "ovary.wgs",
              "ovary.wes",
              "TCGA-06-0145-01A-01W-0224-08",
              "TCGA-13-1500-01A-01D-0472-01",
              "TCGA-AO-A0JJ-01A-11W-A071-09")] <- FALSE

high.purity[c("sam6", "ovary.wgs", "ovary.wes")] <- FALSE

rbd <- allRBD.lst[["sam6"]]
btrepredictor@config$high.ploidy <- high.ploidy["sam6"]
btrepredictor@config$high.purity <- high.purity["sam6"]
btrepredictor <- loadRBD(btrepredictor, rbd)
btrepredictor@config$min.segSize <- ifelse(max(btrepredictor@rbd$seg.size, na.rm=TRUE) < 0.4, 0.1, 0.4)
btrepredictor <- btpredict(btrepredictor)
cat(info(btrepredictor), "\n")
```

BTreePlotter *BTreePlotter*

Description

BTreePlotter

Examples

```
btreeplotter <- new("BTreePlotter")
```

BTreePredictor *BTreePredictor*

Description

BTreePredictor

Examples

```
btreepredictor <- new("BTreePredictor")
```

cancer.genes.minus2 *cancer.genes.minus2.rda*

Description

A dataset containing a list of known cancer genes.

Format

list

Source

internal

centromere.dat *centromere.dat*

Description

A dataset containing an annotated list of centromere locations.

Format

list

Source

internal

 cyto.gr

cyto.gr

Description

S4 GRanges object containing data on chromosomal locations with seqnames, genomic range, strand, name, gieStain.

Format

S4

Source

internal

 drawBTree

drawBTree

Description

drawBTree

Usage

```
drawBTree(.Object, rbd, size = 1)
```

```
## S4 method for signature 'BTreePlotter'
drawBTree(.Object, rbd, size = 1)
```

Arguments

.Object	the object
rbd	the rbd object
size	the size

Value

draw the BTree track

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "cancer.genes.minus2.rda", package="BubbleTree"))
load(system.file("data", "vol.genes.rda", package="BubbleTree"))
load(system.file("data", "gene.uni.clean.gr.rda", package="BubbleTree"))
load(system.file("data", "cyto.gr.rda", package="BubbleTree"))
```

```
# 77 common cancer genes
```

```

comm <- btcompare(vol.genes, cancer.genes.minus2)

btreeplotter <- new("BTreePlotter", branch.col="gray50")
annotator <-new("Annotate")
cc <- allCall.lst[["sam2"]]
z <- drawBTree(btreeplotter, cc@rbd.adj) + ggplot2::labs(title=sprintf("%s (%s)", "sam2", info(cc)))

```

drawBubbles

drawBubbles

Description

drawBubbles

Usage

```

drawBubbles(.Object, rbd, col = NULL)

## S4 method for signature 'BTreePlotter'
drawBubbles(.Object, rbd, col = "gray80")

```

Arguments

.Object	the object
rbd	the rbd object
col	the col value

Value

draw the bubbles on the track

Examples

```

load(system.file("data", "allCall.lst.RData", package="BubbleTree"))

btreeplotter <- new("BTreePlotter", max.ploidy=5, max.size=10)
nn <- "sam2"
rbd1 <- allCall.lst[[nn]]@rbd
rbd2 <- allCall.lst[[nn]]@rbd.adj
arrows <- trackBTree(btreeplotter, rbd1, rbd2, min.srcSize=0.01, min.trtSize=0.01)
btree <- drawBTree(btreeplotter, rbd1) + drawBubbles(btreeplotter, rbd2, "gray80") + arrows

```

drawFeatures	<i>drawFeatures</i>
--------------	---------------------

Description

drawFeatures

Usage

```
drawFeatures(.Object, rbd, col = NULL)

## S4 method for signature 'BTreePlotter'
drawFeatures(.Object, rbd, col = "black")
```

Arguments

.Object	the object
rbd	the rbd object
col	the col value

Value

draw the annotation on the track

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "cancer.genes.minus2.rda", package="BubbleTree"))
load(system.file("data", "vol.genes.rda", package="BubbleTree"))
load(system.file("data", "gene.uni.clean.gr.rda", package="BubbleTree"))
load(system.file("data", "cyto.gr.rda", package="BubbleTree"))

# 77 common cancer genes merged from 2 sets
comm <- btcompare(vol.genes, cancer.genes.minus2)

btreeplotter <- new("BTreePlotter", branch.col="gray50")
annotator <- new("Annotate")

nn <- "sam12"
cc <- allCall.lst[[nn]]
z <- drawBTree(btreeplotter, cc@rbd.adj) + ggplot2::labs(title=sprintf("%s (%s)", nn, info(cc)))
out <- cc@result$dist %>% filter(seg.size >= 0.1) %>% arrange(gtools::mixedorder(as.character(seqnames)), s

ann <- with(out, {
  annoByGenesAndCyto(annotator,
    as.character(out$seqnames),
    as.numeric(out$start),
    as.numeric(out$end),
    comm$comm,
    gene.uni.clean.gr=gene.uni.clean.gr,
    cyto.gr=cyto.gr)
})
```

```
out$cyto <- ann$cyto
out$genes <- ann$ann
v <- z + drawFeatures(btreeplotter, out)
print(v)
```

gene.uni.clean.gr *gene.uni.clean.gr*

Description

S4 GRanges object containing human gene annotation with seqnames, genomic coordinates, stand, gene.symbol.

Format

S4

Source

internal

getTracks *getTracks*

Description

getTracks

Usage

```
getTracks(p1, p2, title = "")
```

Arguments

p1	set 1
p2	set 2
title	the title

Value

all of the requested tracks

Examples

```

load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "centromere.dat.rda", package="BubbleTree"))
load(system.file("data", "all.somatic.lst.RData", package="BubbleTree"))
load(system.file("data", "hg19.seqinfo.rda", package="BubbleTree"))

trackplotter <- new("TrackPlotter")
gr2 = centromere.dat
nn <- "sam2"
ymax <- ifelse(nn %in% c("lung.wgs", "lung.wes"), 9, 4.3)
p1 <- xyTrack(trackplotter,
              result.dat=allCall.lst[[nn]]@result,
              gr2=gr2,
              ymax=ymax) + ggplot2::labs(title=nn)

p2 <- bafTrack(trackplotter,
              result.dat=allCall.lst[[nn]]@result,
              gr2=gr2,
              somatic.gr=all.somatic.lst[[nn]])

t1 <- getTracks(p1, p2)

```

heteroLociTrack

heteroLociTrack

Description

heteroLociTrack

Usage

```
heteroLociTrack(.Object, result.dat, gr2, hetero.gr = NULL, min.prev = 0.15,
               ymax = 4.3, cex = 0.5)
```

```
## S4 method for signature 'TrackPlotter'
heteroLociTrack(.Object, result.dat, gr2,
               hetero.gr = NULL, min.prev = 0.15, ymax = 4.3, cex = 0.5)
```

Arguments

.Object	the object
result.dat	the results
gr2	the gr2 object
hetero.gr	hetero annotation
min.prev	previous min
ymax	max y
cex	the cex

Value

the highlightted heterozygosity track

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "centromere.dat.rda", package="BubbleTree"))
load(system.file("data", "allHetero.lst.RData", package="BubbleTree"))
load(system.file("data", "hg19.seqinfo.rda", package="BubbleTree"))

trackplotter <- new("TrackPlotter")
gr2 = centromere.dat
nn <- "sam2"
z1 <- heteroLociTrack(trackplotter, allCall.lst[[nn]]@result, gr2, allHetero.lst[[nn]])
```

hg19.seqinfo	<i>hg19.seqinfo.Rd</i>
--------------	------------------------

Description

Seqinfo object containing names and lengths of each chromosome of the human genome.

Format

Seqinfo

Source

internal

info	<i>info</i>
------	-------------

Description

info

Usage

```
info(.Object)

## S4 method for signature 'BTreePredictor'
info(.Object)
```

Arguments

.Object the object

Value

print out info of prediction data

Examples

```

load(system.file("data", "allRBD.lst.RData", package="BubbleTree"))

btrepredictor <- new("BTreePredictor")
btrepredictor@config$cutree.h <- 0.15

high.ploidy <- rep(TRUE, length(allRBD.lst))
high.purity <- rep(TRUE, length(allRBD.lst))

high.ploidy[c("sam6",
              "ovary.wgs",
              "ovary.wes",
              "TCGA-06-0145-01A-01W-0224-08",
              "TCGA-13-1500-01A-01D-0472-01",
              "TCGA-AO-A0JJ-01A-11W-A071-09")] <- FALSE

high.purity[c("sam6", "ovary.wgs", "ovary.wes")] <- FALSE

nn <- "sam6"

rbd <- allRBD.lst[[nn]]
btrepredictor@config$high.ploidy <- high.ploidy[nn]
btrepredictor@config$high.purity <- high.purity[nn]
btrepredictor <- loadRBD(btrepredictor, rbd)
btrepredictor@config$min.segSize <- ifelse(max(btrepredictor@rbd$seg.size, na.rm=TRUE) < 0.4, 0.1, 0.4)
btrepredictor <- btpredict(btrepredictor)
cat(info(btrepredictor), "\n")

```

loadRBD

*loadRBD***Description**

loadRBD

Usage

loadRBD(.Object, rbd, total.mark = NA)

S4 method for signature 'BTreePredictor'

loadRBD(.Object, rbd, total.mark = NA)

Arguments

.Object	the object
rbd	rbd object
total.mark	total mark

Value

.Object populated with the RBD list with updated segment size

Examples

```

load(system.file("data", "allRBD.lst.RData", package="BubbleTree"))

btrepredictor <- new("BTreePredictor")
btrepredictor@config$cutree.h <- 0.15

high.ploidy <- rep(TRUE, length(allRBD.lst))
high.purity <- rep(TRUE, length(allRBD.lst))

high.ploidy[c("sam6",
              "ovary.wgs",
              "ovary.wes",
              "TCGA-06-0145-01A-01W-0224-08",
              "TCGA-13-1500-01A-01D-0472-01",
              "TCGA-AO-A0JJ-01A-11W-A071-09")] <- FALSE

high.purity[c("sam6", "ovary.wgs", "ovary.wes")] <- FALSE

nn <- "sam6"

rbd <- allRBD.lst[[nn]]
btrepredictor@config$high.ploidy <- high.ploidy[nn]
btrepredictor@config$high.purity <- high.purity[nn]
btrepredictor <- loadRBD(btrepredictor, rbd)

```

RscoreTrack

RscoreTrack

Description

RscoreTrack

Usage

```

RscoreTrack(.Object, result.dat, gr2, cnv.gr = NULL, min.prev = 0.15,
            ymax = 3, cex = 1.5)

```

```

## S4 method for signature 'TrackPlotter'
RscoreTrack(.Object, result.dat, gr2, cnv.gr = NULL,
            min.prev = 0.15, ymax = 3, cex = 1.5)

```

Arguments

.Object	the object
result.dat	the results
gr2	the gr2 object
cnv.gr	cnv annotation
min.prev	previous min
ymax	max y
cex	the cex

Value

the highlighted RScore track

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "centromere.dat.rda", package="BubbleTree"))
load(system.file("data", "allCNV.lst.RData", package="BubbleTree"))
load(system.file("data", "hg19.seqinfo.rda", package="BubbleTree"))

gr2 = centromere.dat
trackplotter <- new("TrackPlotter")
nn <- "sam2"
z <- RScoreTrack(trackplotter, allCall.lst[[nn]]@result, gr2, allCNV.lst[[nn]])
```

 saveXLS

saveXLS

Description

saveXLS

Usage

```
saveXLS(dat.lst, xls.fn, row.names = FALSE, ...)
```

Arguments

dat.lst	dataframe
xls.fn	filename
row.names	row names
...	misc

Value

new Excel file

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))

all.summary <- plyr::ldply(allCall.lst, function(.Object) {
  purity <- .Object@result$prev[1]
  adj <- .Object@result$ploidy.adj["adj"]
  ploidy <- (2*adj - 2)/purity + 2 # when purity is low the calculation result is not reliable

  with(.Object@result,
    return(c(Purity=round(purity,3),
             Prevalences=paste(round(prev,3), collapse=", "),
```

```

        "Tumor ploidy"=round(ploidy,1)))
  }) %>% plyr::rename(c(".id"="Sample"))

xls.filename <- paste("all_summary", "xlsx", sep=".")
saveXLS(list(Summary=all.summary), xls.filename)

```

 trackBTree

trackBTree

Description

trackBTree

Usage

```

trackBTree(.Object, rbd1, rbd2, is.matched = FALSE, min.srcSize = 0.5,
  min.trtSize = 0.1, min.overlap = 1e+05)

```

```

## S4 method for signature 'BTreePlotter'
trackBTree(.Object, rbd1, rbd2, is.matched = FALSE,
  min.srcSize = 0.5, min.trtSize = 0.1, min.overlap = 1e+05)

```

Arguments

.Object	the object
rbd1	rbd one
rbd2	rbd two
is.matched	is it matched
min.srcSize	min src size
min.trtSize	min trt size
min.overlap	min overlap

Value

geom_segment location of BTree track

Examples

```

load(system.file("data", "allCall.lst.RData", package="BubbleTree"))

btreeplotter <- new("BTreePlotter", max.ploidy=5, max.size=10)
nn <- "sam2"
rbd1 <- allCall.lst[[nn]]@rbd
rbd2 <- allCall.lst[[nn]]@rbd.adj
arrows <- trackBTree(btreeplotter, rbd1, rbd2, min.srcSize=0.01, min.trtSize=0.01)
btree <- drawBTree(btreeplotter, rbd1) + drawBubbles(btreeplotter, rbd2, "gray80") + arrows

```

TrackPlotter	<i>TrackPlotter</i>
--------------	---------------------

Description

TrackPlotter

Examples

```
trackplotter <- new("TrackPlotter")
```

vol.genes	<i>vol.genes</i>
-----------	------------------

Description

A dataset containing a list of known cancer genes.

Format

list

Source

internal

xyTrack	<i>xyTrack</i>
---------	----------------

Description

xyTrack

Usage

```
xyTrack(.Object, result.dat, gr2, min.prev = 0.15, ymax = 4.3)
```

```
## S4 method for signature 'TrackPlotter'
xyTrack(.Object, result.dat, gr2, min.prev = 0.15,
        ymax = 4.3)
```

Arguments

.Object	the object
result.dat	result dataframe
gr2	gr2 object
min.prev	previous min
ymax	the max y

Value

the highlighted xy track

Examples

```
load(system.file("data", "allCall.lst.RData", package="BubbleTree"))
load(system.file("data", "centromere.dat.rda", package="BubbleTree"))
load(system.file("data", "hg19.seqinfo.rda", package="BubbleTree"))

trackplotter <- new("TrackPlotter")
gr2 = centromere.dat
nn <- "sam2"
ymax <- ifelse(nn %in% c("lung.wgs", "lung.wes"), 9, 4.3)
p1 <- xyTrack(trackplotter,
              result.dat=allCall.lst[[nn]]@result,
              gr2=gr2,
              ymax=ymax) + ggplot2::labs(title=nn)
```

Index

*Topic **datasets**

- all.somatic.lst, 2
 - allCall.lst, 2
 - allCNV.lst, 3
 - allHetero.lst, 3
 - allRBD.lst, 3
 - cancer.genes.minus2, 8
 - centromere.dat, 8
 - cyto.gr, 9
 - gene.uni.clean.gr, 12
 - hg19.seqinfo, 14
 - vol.genes, 19
-
- all.somatic.lst, 2
 - allCall.lst, 2
 - allCNV.lst, 3
 - allHetero.lst, 3
 - allRBD.lst, 3
 - annoByGenesAndCyto, 4
 - annoByGenesAndCyto, Annotate-method (annoByGenesAndCyto), 4
 - Annotate, 5
 - Annotate-package (Annotate), 5
-
- bafTrack, 5
 - bafTrack, TrackPlotter-method (bafTrack), 5
 - btcompare, 6
 - btpredict, 7
 - btpredict, BTreePredictor-method (btpredict), 7
 - BTreePlotter, 8
 - BTreePlotter-package (BTreePlotter), 8
 - BTreePredictor, 8
 - BTreePredictor-package (BTreePredictor), 8
-
- cancer.genes.minus2, 8
 - centromere.dat, 8
 - cyto.gr, 9
-
- drawBTree, 9
 - drawBTree, BTreePlotter-method (drawBTree), 9
-
- drawBubbles, 10
 - drawBubbles, BTreePlotter-method (drawBubbles), 10
 - drawFeatures, 11
 - drawFeatures, BTreePlotter-method (drawFeatures), 11
-
- gene.uni.clean.gr, 12
 - getTracks, 12
-
- heteroLociTrack, 13
 - heteroLociTrack, TrackPlotter-method (heteroLociTrack), 13
 - hg19.seqinfo, 14
-
- info, 14
 - info, BTreePredictor-method (info), 14
-
- loadRBD, 15
 - loadRBD, BTreePredictor-method (loadRBD), 15
-
- RscoreTrack, 16
 - RscoreTrack, TrackPlotter-method (RscoreTrack), 16
-
- saveXLS, 17
-
- trackBTree, 18
 - trackBTree, BTreePlotter-method (trackBTree), 18
 - TrackPlotter, 19
 - TrackPlotter-package (TrackPlotter), 19
-
- vol.genes, 19
-
- xyTrack, 19
 - xyTrack, TrackPlotter-method (xyTrack), 19