

# Package: BubbleTree (via r-universe)

June 2, 2026

**Type** Package

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

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**Description** CNV analysis in groups of tumor samples.

**License** LGPL (>= 3)

**Imports** BiocGenerics (>= 0.31.6), BiocStyle, Biobase, ggplot2, WriteXLS, gtools, RColorBrewer, limma, grid, gtable, gridExtra, biovizBase, e1071, methods, grDevices, stats, utils

**Depends** R (>= 3.5), IRanges, GenomicRanges, plyr, dplyr, magrittr

**Suggests** knitr, rmarkdown

**biocViews** CopyNumberVariation, Software, Sequencing, Coverage

**VignetteBuilder** knitr

**RoxygenNote** 5.0.1

**PackageStatus** Deprecated

**Config/pak/sysreqs** cmake make libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl xz-utils zlib1g-dev

**Repository** <https://bioc-release.r-universe.dev>

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

## 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*                      *allCall.lst*

---

**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	<i>allHetero.lst</i>
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---

**Description**

S4 GRanges dataset containing pre-calculated heterozygosity data.

**Format**

S4

**Source**

internal

---

allRBD.lst	<i>allRBD.lst</i>
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---

**Description**

A dataset containing precalculated data from CNV segment analysis.

**Format**

S4 object with rbd, rbd.adj

**Source**

internal

---

annoByGenesAndCyto	<i>annoByGenesAndCyto</i>
--------------------	---------------------------

---

**Description**

get annotation for genes and cytobands

**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)

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	<i>bafTrack</i>
----------	-----------------

---

**Description**

get the BAF track

**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	<i>btcompare</i>
-----------	------------------

---

**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-A0-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**

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

---

BTreePredictor	<i>BTreePredictor</i>
----------------	-----------------------

---

**Description**

BTreePredictor

**Examples**

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

---

cancer.genes.minus2	<i>cancer.genes.minus2.rda</i>
---------------------	--------------------------------

---

**Description**

A dataset containing a list of known cancer genes.

**Format**

list

**Source**

internal

---

centromere.dat	<i>centromere.dat</i>
----------------	-----------------------

---

**Description**

A dataset containing an annotated list of centromere locations.

**Format**

list

**Source**

internal

---

cnv.gr	<i>cnv.gr</i>
--------	---------------

---

**Description**

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

**Format**

S4

**Source**

internal

---

cyto.gr	<i>cyto.gr</i>
---------	----------------

---

**Description**

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

**Format**

S4

**Source**

internal

---

drawBTree	<i>drawBTree</i>
-----------	------------------

---

**Description**

draw the BTree track

**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**

draw the Bubbles

**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

*drawFeatures*

---

**Description**

draw the features

**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)), start)

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	<i>getTracks</i>
-----------	------------------

---

**Description**

get all tracks

**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	<i>heteroLociTrack</i>
-----------------	------------------------

---

## Description

get the heteroLoci track

## 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

*hg19.seqinfo.Rd*

---

**Description**

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

**Format**

Seqinfo

**Source**

internal

---

info

*info*

---

**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"))
```

```
btreepredictor <- new("BTreePredictor")  
btreepredictor@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-A0-A0JJ-01A-11W-A071-09")] <- FALSE

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

nn <- "sam6"

rbd <- allRBD.lst[[nn]]
btreepredictor@config$high.ploidy <- high.ploidy[nn]
btreepredictor@config$high.purity <- high.purity[nn]
btreepredictor <- loadRBD(btreepredictor, rbd)
btreepredictor@config$min.segSize <- ifelse(max(btreepredictor@rbd$seg.size,
                                              na.rm=TRUE) < 0.4, 0.1, 0.4)

btreepredictor <- btpredict(btreepredictor)
cat(info(btreepredictor), "\n")

```

---

loadRBD

*loadRBD*


---

## Description

load the RBD data

## 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"))

btreepredictor <- new("BTreePredictor")
btreepredictor@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-A0-A0JJ-01A-11W-A071-09")] <- FALSE

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

nn <- "sam6"

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

---

makeRBD

*makeRBD*


---

**Description**

make the RBD object

**Usage**

```
makeRBD(.Object, ...)
```

```
## S4 method for signature 'RBD'
```

```
makeRBD(.Object, snp.gr, cnv.gr, unimodal.kurtosis = -0.1)
```

**Arguments**

.Object	the object
...	other input (not needed)
snp.gr	SNP GenomicRanges object
cnv.gr	CNV GenomicRanges object
unimodal.kurtosis	kurtosis

**Value**

RBD object

**Examples**

```
# load sample files
load(system.file("data", "cnv.gr.rda", package="BubbleTree"))
load(system.file("data", "snp.gr.rda", package="BubbleTree"))

# load annotations
load(system.file("data", "centromere.dat.rda", package="BubbleTree"))
load(system.file("data", "cyto.gr.rda", 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"))

# initialize RBD object
r <- new("RBD", unimodal.kurtosis=-0.1)

# create new RBD object with GenomicRanges objects for SNPs and CNVs
rbd <- makeRBD(r, snp.gr, cnv.gr)
head(rbd)

# create a new prediction
btrepredictor <- new("BTreePredictor", rbd=rbd, max.ploidy=6, prev.grid=seq(0.2,1, by=0.01))
pred <- btpredict(btrepredictor)

# create rbd plot
btrepplotter <- new("BTreePlotter", max.ploidy=5, max.size=10)
btree <- drawBTree(btrepplotter, pred@rbd)
print(btree)

# create rbd.adj plot
btrepplotter <- new("BTreePlotter", branch.col="gray50")
btree <- drawBTree(btrepplotter, pred@rbd.adj)
print(btree)

# create a combined plot with rbd and rbd.adj that shows the arrows indicating change
# THIS IS VERY MESSY WITH CURRENT DATA from Dong
btrepplotter <- new("BTreePlotter", max.ploidy=5, max.size=10)
arrows <- trackBTree(btrepplotter,
                    pred@rbd,
                    pred@rbd.adj,
                    min.srcSize=0.01,
                    min.trtSize=0.01)

btree <- drawBTree(btrepplotter, pred@rbd) + arrows
print(btree)

# create a plot with overlays of significant genes
```

```

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

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

sample.name <- "22_cnv_snv"

btree <- drawBTree(btreeplotter, pred@rbd.adj) +
  ggplot2::labs(title=sprintf("%s (%s)", sample.name, info(pred)))

out <- pred@result$dist %>%
  filter(seg.size >= 0.1 ) %>%
  arrange(gtools::mixedorder(as.character(seqnames)), start)

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

btree <- btree + drawFeatures(btreeplotter, out)
print(btree)

# print out purity and ploidy values
info <- info(pred)
cat("\nPurity/Ploidy: ", info, "\n")

```

---

mergeSnpCnv

*mergeSnpCnv*


---

## Description

merge snp and cnv data

## Usage

```
mergeSnpCnv(.Object, snp.gr, cnv.gr)
```

```
## S4 method for signature 'RBD'
mergeSnpCnv(.Object, snp.gr, cnv.gr)
```

**Arguments**

.Object	the object
snp.gr	SNP GenomicRanges object
cnv.gr	CNV GenomicRanges object

**Value**

combined, unique list of genes

---

RBD	<i>RBD</i>
-----	------------

---

**Description**

RBD

**Examples**

```
rbd <- new("RBD")
```

---

RscoreTrack	<i>RscoreTrack</i>
-------------	--------------------

---

**Description**

get the RScore track

**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"]
  # when purity is low the calculation result is not reliable
  ploidy <- (2*adj - 2)/purity + 2
})
```

```

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)

```

---

snp.gr

*snp.gr*


---

### Description

S4 GRanges object containing data on chromosomal locations with seqnames, genomic position, strand, name

### Format

S4

### Source

internal

---

trackBTree

*trackBTree*


---

### Description

get the geom\_segment location of the BTree track

### 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

*TrackPlotter*

---

**Description**

TrackPlotter

**Examples**

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

---

`vol.genes`*vol.genes*

---

**Description**

A dataset containing a list of known cancer genes.

**Format**

list

**Source**

internal

---

`xyTrack`*xyTrack*

---

**Description**

get the xy track

**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**

<code>.Object</code>	the object
<code>result.dat</code>	result dataframe
<code>gr2</code>	gr2 object
<code>min.prev</code>	previous min
<code>ymax</code>	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)
```

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