Package ‘CNViz’

May 17, 2024

Type Package
Title Copy Number Visualization
Version 1.12.0
Description CNViz takes probe, gene, and segment-level log2 copy number ratios and launches a Shiny app to visualize your sample's copy number profile. You can also integrate loss of heterozygosity (LOH) and single nucleotide variant (SNV) data.
Depends R (>= 4.0), shiny (>= 1.5.0)
Imports dplyr, stats, utils, grDevices, plotly, karyoploteR, CopyNumberPlots, GenomicRanges, magrittr, DT, scales, graphics
License Artistic-2.0
Encoding UTF-8
biocViews Visualization, CopyNumberVariation, Sequencing, DNASeq
RoxygenNote 7.1.1
Suggests rmarkdown, knitr
VignetteBuilder knitr
git_url https://git.bioconductor.org/packages/CNViz
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Description

A dataset containing the study name and aggregated gene level copy number data

Usage

all_tcga2018_data

Format

A data frame with 14944 rows and 6 variables:

- hugoGeneSymbol: hugo gene symbol
- Gain: proportion of cohort with gain in this gene
- Amplification: proportion of cohort with amplification in this gene
- ShallowDeletion: proportion of cohort with shallow deletion in this gene
- DeepDeletion: proportion of cohort with deep deletion in this gene
- study_name: cancer type and sample size

Source

**cbio_studies**

*Names of 2018 TCGA studies from cBioPortal*

**Description**

A dataset containing the names and studyIds of the 2018 TCGA studies from cBioPortal.

**Usage**

```r
cbio_studies
```

**Format**

A data frame with 32 rows and 2 variables:

- **Cancer** Name of diagnosis and sample size
- **studyId** studyId that can be used in the cBioPortalData R package

**Source**


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**cytoband_data**

*Genomic locations of cytoband labels*

**Description**

A dataset containing the chr, start and end position for cytobands according to hg38.

**Usage**

```r
cytoband_data
```

**Format**

A data frame with 863 rows and 6 variables:

- **chrom** chromosome
- **chromStart** start position
- **chromEnd** end position
- **name** cytoband name
- **gieStain** color
- **color** HEX color

**Source**

[https://genome.ucsc.edu/cgi-bin/hgTables](https://genome.ucsc.edu/cgi-bin/hgTables)
gene_data  

**Gene data for vignette example**

**Description**

A dataset containing simulated gene data as sample input for launchCNViz

**Usage**

```r
data(gene_data)
```

**Format**

A dataframe with 112 rows and 6 variables

- **chr** chromosome
- **start** start location
- **end** end location
- **gene** gene name
- **log2** log2 copy number ratio
- **weight** weight given to log2 value
- **loh** loss of heterozygosity

**Source**

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launchCNViz

**Launches CNViz, a shiny app to visualize your sample’s copy number data.**

**Description**

CNViz launches a shiny application to visualize your sample’s copy number data. At least one of probe_data, gene_data, or segment_data must be supplied; sample_name, variant_data and meta_data are all optional. The more inputs supplied, the more informative the application will be. See the CNViz vignette for more information. Use the hg38 reference genome. CNViz only displays a single sample’s data.
launchCNViz

Usage

launchCNViz(
    sample_name = "sample",
    probe_data = data.frame(),
    gene_data = data.frame(),
    segment_data = data.frame(),
    variant_data = data.frame(),
    meta_data = data.frame()
)

Arguments

sample_name A string with the ID/name of your sample.

probe_data A dataframe or GRanges object containing probe-level data. If a dataframe, column names must include chr, gene, start, end, log2. chr/seqnames column should be formatted as ‘chr1’ through ‘chrX’, ‘chrY’. start, end and log2 should be numeric. If a GRanges object, gene and log2 are metadata columns. Optional column/metadata: weight, where weight is numeric.

gene_data A dataframe or GRanges object containing gene-level data - one row per gene. If a dataframe, column names must include chr, gene, start, end, log2. chr/seqnames column should be formatted as ‘chr1’ through ‘chrX’, ‘chrY’. start, end and log2 should be numeric. If a GRanges object, gene and log2 are metadata columns. Optional columns/metadata: weight, loh; where weight is numeric and loh values are TRUE or FALSE.

segment_data A dataframe or GRanges object containing segment-level data. If a dataframe, column names must include chr, start, end, log2. chr column should be formatted as ‘chr1’ through ‘chrX’, ‘chrY’. start, end and log2 should be numeric. If a GRanges object, log2 is a metadata column. Optional column/metadata: loh; where loh values are TRUE or FALSE.

variant_data A dataframe or VRanges object containing SNVs and short indels and columns of your choosing. If a dataframe, the only required columns are gene and mutation_id. Optional column: start; where start indicates the starting position of the mutation. If a VRanges object, make sure gene is one of the metadata columns, so it can be tied to the gene or probe data; a mutation_id column can also be included, otherwise it will be constructed. Additional columns might include depth, allelic_fraction, ref, alt.

meta_data A dataframe containing your sample’s metadata - columns of your choosing. Optional column: ploidy; ploidy will be rounded to the nearest whole number. Additional columns might include purity. This dataframe should only have one row.

Value

a Shiny application
Examples

```r
probes <- data.frame(chr = c("chr1", "chr1", "chr4", "chr4", "chrX"),
gene = c("NOTCH2", "NOTCH2", "KIT", "TET2", "BTK"),
start = c(119922221, 119967406, 54732072, 105243553, 101360541),
end = c(119922461, 119967646, 54732192, 105243793, 101360781),
log2 = c(-0.0832403, -0.0578757, 0.2131540, -0.3189430, -0.7876670),
weight = c(0.684114, 0.681546, 0.606129, 0.682368, 0.405772))
segments <- data.frame(chr = c("chr1", "chr1", "chr4", "chr4", "chrX"),
start = c(1050069, 124932724, 1942322, 51743951, 1198732),
end = c(122026459, 246947668, 49712061, 188110779, 37098762),
log2 = c(1, 1, 1, 1, 0.5849625), loh = c(FALSE, FALSE, FALSE, TRUE, TRUE))
meta <- data.frame(purity = c(.5),
ploidy = c(2), sex = c("Female"))

launchCNViz(sample_name = "sample123", probe_data = probes,
segment_data = segments, meta_data = meta)
```

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**meta_data**

**Metadata for vignette example**

**Description**

A dataset containing simulated metadata as sample input for launchCNViz

**Usage**

```r
data(meta_data)
```

**Format**

A dataframe with 1 rows and 2 variables

- **purity** sample purity
- **ploidy** tumor ploidy

**Source**

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probe_data

Probe data for vignette example

Description
A dataset containing simulated probe data as sample input for launchCNViz

Usage
data(probe_data)

Format
A data frame with 2006 rows and 6 variables:
- **chr** chromosome
- **start** start location
- **end** end location
- **gene** gene name
- **log2** log2 copy number ratio
- **weight** weight given to log2 value

Source
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segment_data
Segment data for vignette example

Description
A dataset containing simulated segment data as sample input for launchCNViz

Usage
data(segment_data)

Format
A dataframe with 101 rows and 5 variables
- **chr** chromosome
- **start** start location
- **end** end location
- **log2** log2 copy number ratio
- **loh** loss of heterozygosity
**Source**

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**variant_data**

**Variant data for vignette example**

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**Description**

A dataset containing simulated SNV and indel data as sample input for launchCNViz

**Usage**

data(variant_data)

**Format**

A dataframe with 119 rows and 4 variables

- gene: gene name
- mutation_id: string with information about snv
- depth: read depth
- start: starting location

**Source**

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