

# Package ‘CNViz’

March 6, 2025

**Type** Package

**Title** Copy Number Visualization

**Version** 1.14.0

**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>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 0870fb9

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-03-06

**Author** Rebecca Greenblatt [aut, cre]

**Maintainer** Rebecca Greenblatt <[rebecca.greenblatt@gmail.com](mailto:rebecca.greenblatt@gmail.com)>

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<code>all_tcga2018_data</code>	<i>Data from 2018 TCGA studies from cBioPortal</i>
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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**

<https://github.com/waldronlab/cBioPortalData> See data-raw folder.

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<code>cbio_studies</code>	<i>Names of 2018 TCGA studies from cBioPortal</i>
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**Description**

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

**Usage**

`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**

<https://github.com/waldronlab/cBioPortalData> See data-raw folder.

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cytoband_data	<i>Genomic locations of cytoband labels</i>
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**Description**

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

**Usage**

```
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>

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gene_data	<i>Gene data for vignette example</i>
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**Description**

A dataset containing simulated gene data as sample input for launchCNViz

**Usage**

```
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	<i>Launches CNViz, a shiny app to visualize your sample's copy number data.</i>
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**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.

**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

```
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*

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## Description

A dataset containing simulated metadata as sample input for launchCNViz

## Usage

```
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	<i>Probe data for vignette example</i>
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**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	<i>Segment data for vignette example</i>
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**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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