

# Package ‘BOBaFIT’

January 31, 2025

**Type** Package

**Title** Refitting diploid region profiles using a clustering procedure

**Version** 1.11.0

**Description** This package provides a method to refit and correct the diploid region in copy number profiles. It uses a clustering algorithm to identify pathology-specific normal (diploid) chromosomes and then use their copy number signal to refit the whole profile. The package is composed by three functions: DRrefit (the main function), ComputeNormalChromosome and PlotCluster.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

**URL** <https://github.com/andrea-poletti-unibo/BOBaFIT>

**BugReports** <https://github.com/andrea-poletti-unibo/BOBaFIT/issues>

**Imports** dplyr, NbClust, ggplot2, ggbio, grDevices, stats, tidyr, GenomicRanges, ggforce, stringr, plyranges, methods, utils, magrittr

**Suggests** rmarkdown, markdown, BiocStyle, knitr, testthat (>= 3.0.0), utils, testthat

**Config/testthat/edition** 3

**biocViews** CopyNumberVariation, Clustering, Visualization, Normalization, Software

**Depends** R (>= 2.10)

**VignetteBuilder** knitr

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computeNormalChromosomes  
*computeNormalChromosomes*

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## Description

This function compute the DRrefits' input "chromosome list". It is a vector that contains the chromosomal arms considered "normal" in the cohort of samples tested (BED file), under a specific tolerance value

## Usage

```
computeNormalChromosomes(  
  segments,  
  tolerance_val = 0.15,  
  maxCN = 6,  
  min_threshold = 1.6,  
  max_threshold = 2.4,  
  verbose = FALSE  
)
```

## Arguments

segments	data.frame formatted with correct column names
tolerance_val	decimal value of alteration frequency. By default is 0.15
maxCN	threshold of max copy number to consider. By default is 6
min_threshold	minimum threshold to define a normal CN. By default is 1.60
max_threshold	maximum threshold to define a normal CN. By default is 2.40
verbose	print information about the processes of the function. By default is FALSE

**Value**

vector with chromosome names and plot with the alteration rate of each chromosomal arms

**Examples**

```
data("TCGA_BRCA_CN_segments")
chr_list <- computeNormalChromosomes(segments = TCGA_BRCA_CN_segments)
```

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DRrefit

*DRrefit*


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**Description**

This function refits the diploid region of input copy number profiles (segments - BED file)

**Usage**

```
DRrefit(
  segments_chort,
  chrlist,
  maxCN = 6,
  clust_method = "ward.D2",
  verbose = FALSE
)
```

**Arguments**

<code>segments_chort</code>	data.frame formatted with correct column names
<code>chrlist</code>	list of normal chromosome arms (pathology-specific)
<code>maxCN</code>	threshold of max copy number to consider. By default is 6
<code>clust_method</code>	clustering method. By default is "ward.D2"
<code>verbose</code>	print information about the processes of the function. By default is FALSE

**Value**

Return two data frames, one is the DRrefit-corrected segments and the other is the samples report. See the vignette for data frame descriptions.

**Examples**

```
data("TCGA_BRCA_CN_segments")

chr_list <- c("10q", "11p", "12p", "19q", "1p", "21q", "2q", "3p", "4p", "4q", "6p", "6q", "7p" )

results <- DRrefit(segments_chort = TCGA_BRCA_CN_segments,
  chrlist = chr_list)
```

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DRrefit_plot	<i>DRrefit_plot</i>
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### Description

The function plot the copy number profile before and after DRrefit recalibration

### Usage

```
DRrefit_plot(
  corrected_segments,
  DRrefit_report,
  plot_viewer = F,
  plot_save = F,
  plot_format = "png",
  plot_path
)
```

### Arguments

<code>corrected_segments</code>	DRrefit output dataframe.
<code>DRrefit_report</code>	DRrefit output dataframe.
<code>plot_viewer</code>	Logical parameter. When it is TRUE, the function print the output plot in the R viewer. By default is FALSE.
<code>plot_save</code>	Logical parameter. When it is TRUE, the function save the plot in the chosen path and format. By default is FALSE.
<code>plot_format</code>	File format for the output plots (accepts "png", "jpg", "pdf", "tiff"). By default is "png"
<code>plot_path</code>	Path to save output plots.

### Value

Return the sample copy number profile before and after DRrefit recalibration. The function can output the figure in the R viewer on save it in a specific path.

### Examples

```
data("TCGA_BRCA_CN_segments")

chr_list <- c("10q", "11p", "12p", "19q", "1p", "21q", "2q", "3p", "4p", "4q", "6p", "6q", "7p" )

results <- DRrefit(segments_chort = TCGA_BRCA_CN_segments, chrlist = chr_list)

my_segments <- results$corrected_segments
my_report <- results$report
```

```
DRrefit_plot(corrected_segments = my_segments,
             DRrefit_report = my_report,
             plot_viewer= FALSE,
             plot_save = FALSE)
```

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PlotChrCluster	<i>PlotChrCluster</i>
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## Description

The function clusters chromosomes based on the copy number (CN) and returns a graph where it is possible to observe the different groups and two data frames (report and plot\_table). See the vignette for the data frame descriptions.

## Usage

```
PlotChrCluster(
  segs,
  clust_method = "ward.D2",
  plot_output = TRUE,
  plot_viewer = TRUE,
  plot_save = FALSE,
  plot_format = "png",
  plot_path,
  verbose = FALSE
)
```

## Arguments

segs	data.frame with segments of samples. It must be formatted with correct column names (start, end, ID)
clust_method	clustering method. Default is "ward.D2"
plot_output	Whether to plot refitted profiles (logical)
plot_viewer	Logical parameter. When it is TRUE, the function print the output plot in the R viewer. By default is TRUE.
plot_save	Logical parameter. When it is TRUE, the function save the plot in the chosen path and format. By default is TRUE.
plot_format	File format for the output plots (accepts "png", "jpg", "pdf", "tiff"). By default is "png"
plot_path	Path to save output plots.
verbose	print information about the processes of the function. By default is FALSE

## Value

Plot with chromosomes clustered

**Examples**

```
data(TCGA_BRCA_CN_segments)
Cluster <- PlotChrCluster(segs=TCGA_BRCA_CN_segments,
                          clust_method= "ward.D2",
                          plot_output=FALSE)
```

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Popeye	<i>Popeye</i>
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**Description**

The function assign the chromosomal arm to each segment.

**Usage**

```
Popeye(segments)
```

**Arguments**

segments      data.frame formatted with correct column names (see package vignette)

**Value**

Return a data frame containg segments with the arm annotation.

**Examples**

```
data("TCGA_BRCA_CN_segments")
data <- TCGA_BRCA_CN_segments[1:9] #as it already presents the arm column
data_annotated <- Popeye(segments = data)
```

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TCGA_BRCA_CN_segments	<i>Segments of 100 Breast Cancer samples, downloaded from TCGA-BRCA.</i>
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**Description**

Segments of 100 Breast Cancer samples, downloaded from TCGA-BRCA.

**Usage**

```
TCGA_BRCA_CN_segments
```

### Format

A data frame with 79,607 rows and 12 variables:

- chr** Chromosome which the segment belong
- start** Starting point of the segment, in Mb
- end** Ending point of the segment, in Mb
- width** Width of the segment, in Mb
- strand** Strand of the segment
- ID** Sample name
- Num\_Probes** Probes involved
- Segment\_Mean** LogR of the segments
- Sample** Barcode of tCGA-BRCA database
- arm** Arm information, p o q
- chrarm** Chromosomal arm which the segment belong
- CN** Segments Copy Number value obtained by the logR

### Source

<https://portal.gdc.cancer.gov/projects/TCGA-BRCA>

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%>%

*Pipe operator*

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### Description

See `magrittr::%>%` for details.

### Usage

`lhs %>% rhs`

### Arguments

- `lhs` A value or the `magrittr` placeholder.
- `rhs` A function call using the `magrittr` semantics.

### Value

The result of calling `'rhs(lhs)'`.

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