

# Package ‘BOBaFIT’

December 15, 2025

**Type** Package

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

**Version** 1.14.0

**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

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Normalization, Software

**Depends** R (>= 2.10)

**VignetteBuilder** knitr

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|                                 |
|---------------------------------|
| computeNormalChromosomes        |
| <i>computeNormalChromosomes</i> |

---

## 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)
```

---

DRrefit

*DRrefit*


---

## 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)
```

---

DRrefit\_plot

*DRrefit\_plot*


---

## 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)
```

---

PlotChrCluster

*PlotChrCluster*


---

## 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)
```

---

Popeye

*Popeye*


---

**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)
```

---

TCGA\_BRCA\_CN\_segments *Segments of 100 Breast Cancer samples, downloaded from TCGA-BRCA.*


---

**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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|     |                      |
|-----|----------------------|
| %>% | <i>Pipe operator</i> |
|-----|----------------------|

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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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