

# Package ‘oncoscanR’

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**Type** Package

**Title** Secondary analyses of CNV data (HRD and more)

**Version** 1.8.0

**Description** The software uses the copy number segments from a text file and identifies all chromosome arms that are globally altered and computes various genome-wide scores. The following HRD scores (characteristic of BRCA-mutated cancers) are included: LST, HR-LOH, nLST and gLOH. the package is tailored for the ThermoFisher Oncoscan assay analyzed with their Chromosome Alteration Suite (ChAS) but can be adapted to any input.

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**BugReports** <https://github.com/yannchristinat/oncoscanR/issues>

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oncoscanR-package	<i>oncoscanR: an R package to perform secondary analysis of Copy Number Variation data.</i>
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## Description

Allows computation of different homologous recombination deficiency (HRD) scores to identify PARP inhibitors responders. The package also allows for computation of the tandem duplication plus score (TDplus; hallmark of CDK12-mutated tumors) and the identification of arm-level alterations (e.g. gain of chromosome arm 1p).

## Details

The package is tailored for the ThermoFisher Oncoscan assay analyzed with their Chromosome Alteration Suite (ChAS) but can be adapted to any input.

To learn more about oncoscanR, see the vignette using `browseVignettes(package = "oncoscanR")`.

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**See Also**

Useful links:

- <https://github.com/yannchristinat/oncoscanR>
- Report bugs at <https://github.com/yannchristinat/oncoscanR/issues>

---

adjust\_loh

*Trim LOH segments with respect to loss segments.*

---

**Description**

Trim LOH segments with respect to loss segments.

**Usage**

```
adjust_loh(segments)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
----------	--

**Details**

LOH segments completely contained within (or equal to) a copy loss segment are deleted. LOH segments partially overlapping (on one end only) with a copy loss segment are trimmed to remove the overlap or split into several segments.

**Value**

A GRanges object containing the cleaned segments, their copy number and copy number types.

**Examples**

```
segs.adj <- adjust_loh(segs.chas_example)
```

---

armlevel\_alt                      *Get all globally-altered chromosome arms.*

---

### Description

Get all globally-altered chromosome arms.

### Usage

```
armlevel_alt(segments, kit.coverage, threshold = 0.9)
```

### Arguments

segments	A GRanges object containing the segments.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.
threshold	The minimum percentage of the arm to be considered as globally altered. Defaults to 80%.

### Details

By default uses the sum of all alterations and set the arm as globally altered if  $\geq 80\%$  of the arm is altered. Does not account for alteration type and copy number. Will run the function `trim_to_coverage` on the segments.

### Value

A list of globally-altered chromosome arms with the percentage of arm altered.

### Examples

```
arms <- armlevel_alt(segs.chas_example, oncoscan_na33.cov, 0.9)
```

---

cntypes	<i>Accepted types of CN for the segments - 'Gain': 1-2 extra copies - 'Weak amplification': 3-7 extra copies - 'Strong amplification': 8 or more extra copies - 'Heterozygote loss': Loss of one copy out of two - 'Homozygote loss': Loss of all copies - 'LOH': copy-neutral loss of one parental allele</i>
---------	--

---

### Description

Accepted types of CN for the segments - 'Gain': 1-2 extra copies - 'Weak amplification': 3-7 extra copies - 'Strong amplification': 8 or more extra copies - 'Heterozygote loss': Loss of one copy out of two - 'Homozygote loss': Loss of all copies - 'LOH': copy-neutral loss of one parental allele

### Usage

```
cntypes
```

**Format**

A list of strings containing all CN types

**Source**

```
cntypes <- list(LOH='LOH', Gain='Gain', Loss='Loss')
```

---

*get\_amp\_segments*      *Return all segments with an amplification (5 or more copies).*

---

**Description**

Return all segments with an amplification (5 or more copies).

**Usage**

```
get_amp_segments(segments)
```

**Arguments**

*segments*      A GRanges object containing the segments, their copy number and copy number types.

**Value**

A GRanges object containing the selected segments, their copy number and copy number types.

**Examples**

```
segs.amp <- get_amp_segments(segs.chas_example)
```

---

*get\_gain\_segments*      *Return all segments with gain of copies.*

---

**Description**

Return all segments with gain of copies.

**Usage**

```
get_gain_segments(segments)
```

**Arguments**

*segments*      A GRanges object containing the segments, their copy number and copy number types.

**Value**

A GRanges object containing the selected segments, their copy number and copy number types.

**Examples**

```
segs.gain <- get_gain_segments(segs.chas_example)
```

---

```
get_hetloss_segments
```

*Return all segments with heterozygous loss.*

---

**Description**

Return all segments with heterozygous loss.

**Usage**

```
get_hetloss_segments(segments)
```

**Arguments**

`segments` A GRanges object containing the segments, their copy number and copy number types.

**Value**

A GRanges object containing the selected segments, their copy number and copy number types.

**Examples**

```
segs.hetloss <- get_hetloss_segments(segs.chas_example)
```

---

```
get_homloss_segments
```

*Return all segments with homozygous loss.*

---

**Description**

Return all segments with homozygous loss.

**Usage**

```
get_homloss_segments(segments)
```

**Arguments**

`segments` A GRanges object containing the segments, their copy number and copy number types.

**Value**

A GRanges object containing the selected segments, their copy number and copy number types.

**Examples**

```
get_homloss_segments <- get_homloss_segments(segs.chas_example)
```

---

get_loh_segments	<i>Return all segments of type LOH, independently of the copy number.</i>
------------------	---

---

**Description**

Return all segments of type LOH, independently of the copy number.

**Usage**

```
get_loh_segments(segments)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
----------	--

**Value**

A GRanges object containing the selected segments, their copy number and copy number types.

**Examples**

```
segs.loh <- get_loh_segments(segs.chas_example)
```

---

get_loss_segments	<i>Return all segments with loss of 1 or 2 copies.</i>
-------------------	--

---

**Description**

Return all segments with loss of 1 or 2 copies.

**Usage**

```
get_loss_segments(segments)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
----------	--

**Value**

A GRanges object containing the selected segments, their copy number and copy number types.

**Examples**

```
segs.loh <- get_loh_segments(segs.chas_example)
```

---

```
get_oscscan_coverage_from_bed
```

*Load the oncoscan coverage BED file into a GenomicRanges object.*

---

### Description

Load the oncoscan coverage BED file into a GenomicRanges object.

### Usage

```
get_oscscan_coverage_from_bed(filename)
```

### Arguments

filename            Path to the coverage BED file.

### Details

Expects the following columns from the BED file (no header): 1. Name of the chromosomal arm (e.g. "1p") 2. Start position of the arm 3. End position of the arm

### Value

A GRanges object containing the regions covered on each chromosome arm.

### Examples

```
oscscan_na33.cov <- get_oscscan_coverage_from_bed(
  system.file('extdata', 'Oncoscan.na33.r2.cov.processed.bed',
  package = 'oscscanR'))
```

---

```
load_ascat
```

*Load an ASCAT text export file.*

---

### Description

Load an ASCAT text export file.

### Usage

```
load_ascat(filename, kit.coverage)
```

### Arguments

filename            Path to the ASCAT file.

kit.coverage        A GRanges object containing the regions covered on each chromosome arm by the kit.



**Details**

The ASCAT file is expected to have the following column names: 'chr' (chromosome number), 'startpos' (first position of CNV segment), 'endpos' (last position of CNV segment), 'nMajor' (Number of copies of the major allele) and 'nMinor' (Number of copies of the minor allele).

The segments are attributed to each chromosome arm and split if necessary.

**Value**

A GRanges object containing the segments, their copy number (field cn), their copy number types (field cntype). cntype contains either 'Gain', 'Loss' or 'LOH'. If the file contains twice the same segment or does not respect the format specifications, then an error is raised. NB. If the chromosome name is in the format '1' and not 'chr1' and will be transformed if needed.

**Examples**

```
segs.filename <- system.file('extdata', 'ascat_example.txt',
  package = 'oncscanR')
segs.ascat_example <- load_ascat(segs.filename, oncscan_na33.cov)
```

---

load_chas	<i>Load a ChAS text export file.</i>
-----------	--------------------------------------

---

**Description**

Load a ChAS text export file.

**Usage**

```
load_chas(filename, kit.coverage)
```

**Arguments**

filename	Path to the ChAS file.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm by the kit.

**Details**

The ChAS file is expected to have the following column names: 'CN State' (number or empty), 'Type' (expected value: 'Gain', 'Loss' or 'LOH') and 'Full Location' (in the format 'chr:start-end').

The segments are attributed to each chromosome arm and split if necessary.

**Value**

A GRanges object containing the segments, their copy number (field cn), their copy number types (field cntype). cntype contains either 'Gain', 'Loss' or 'LOH'. If the file contains twice the same segment or does not respect the format specifications, then an error is raised. NB. The chromosome name is in the format '1' and not 'chr1' and will be transformed if needed.

## Examples

```
segs.filename <- system.file('extdata', 'chas_example.txt',  
  package = 'oncscanR')  
segs.chas_example <- load_chas(segs.filename, oncscan_na33.cov)
```

---

merge_segments	<i>Merge segments with respect to the kit resolution and the copy number.</i>
----------------	---

---

## Description

Merge segments with respect to the kit resolution and the copy number.

## Usage

```
merge_segments(segments, kit.resolution = 300)
```

## Arguments

segments	A GRanges object containing the segments, their copy number and copy number types.
kit.resolution	Number >0 indicating the minimum segment size detectable by the technique (in kilobases). Defaults to the Oncoscan assay resolution outside of cancer genes: 300Kb.

## Details

If two segments are at a distance smaller than the resolution, then the segments are merged if they share the same cn value. Note that the function does not look at the copy number type or subtype but only at the actual copy number to decide whether segments can be merged.

## Value

A GRanges object containing the cleaned segments, their copy number and copy number types.

## Examples

```
segs.merged <- merge_segments(segs.chas_example)  
segs.merged_50k <- merge_segments(segs.chas_example, 50)
```

---

oncoscan_na33.cov	<i>GenomicRanges object of the chromosomal arms coverage for the oncoscan assay (based on file extdata/Oncoscan.na33.r2.cov.processed.bed).</i>
-------------------	---

---

**Description**

GenomicRanges object of the chromosomal arms coverage for the oncoscan assay (based on file extdata/Oncoscan.na33.r2.cov.processed.bed).

**Usage**

```
oncoscan_na33.cov
```

**Format**

A GRanges object containing the region covered on each chromosome arm.

**Source**

```
oncoscan_na33.cov <- get_oncoscan_coverage_from_bed( system.file('extdata', 'Oncoscan.na33.r2.cov',
package = 'oncoscanR'))
```

---

prune_by_size	<i>Remove segments smaller than the kit resolution.</i>
---------------	---

---

**Description**

Remove segments smaller than the kit resolution.

**Usage**

```
prune_by_size(segments, threshold = 300)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
threshold	Number indicating the minimum segment size to be kept (in kilobases). Defaults to the Oncoscan assay resolution outside of cancer genes: 300Kb.

**Value**

A GRanges object containing the cleaned segments, their copy number and copy number types.

**Examples**

```
segs.300k <- prune_by_size(segs.chas_example)
segs.50k <- prune_by_size(segs.chas_example, 50)
```

---

score_avgcn	<i>Compute the average copy number variation across the genome.</i>
-------------	---

---

**Description**

Compute the average copy number variation across the genome.

**Usage**

```
score_avgcn(segments, kit.coverage)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.

**Details**

Compute the weighted average (by segment length) of the copy number variation. LOH segments and sexual chromosomes are excluded. Copy number variation is rounded to the next level (1.67 -> 1 but 2.33 -> 3).

**Value**

A decimal value

**Examples**

```
score_avgcn(segs.chas_example, oncoscan_na33.cov)
```

---

score_estwgd	<i>Estimates the number of whole-genome doubling events (WGD).</i>
--------------	--

---

**Description**

Estimates the number of whole-genome doubling events (WGD).

**Usage**

```
score_estwgd(segments, kit.coverage)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.

**Details**

Based on the publication from Carter et al. (Nature Biotechnology 2012; PubMed ID: 22544022). On a pan-cancer cohort, they observed that tumors that underwent one whole-genome doubling event had a ploidy (average copy number) between 2.2 and 3.4. This function relies on the function `score_avgcn` to compute the ploidy.

**Value**

A named list with two values: `WGD` (whole-genome doubling events) and `avgCN` (the average copy number). `WGD` values are 0 for no WGD event, 1 for one WGD event, 2 for several WGD events.

**Examples**

```
score_estwgd(segs.chas_example, oncoscan_na33.cov)
```

---

score\_gloh

*Compute the genomic LOH score.*

---

**Description**

Compute the genomic LOH score.

**Usage**

```
score_gloh(segments, arms.loh, arms.hetloss, kit.coverage)
```

**Arguments**

<code>segments</code>	A <code>GRanges</code> object containing the segments, their copy number and copy number types.
<code>arms.loh</code>	A list of arms with global/arm-level LOH alteration.
<code>arms.hetloss</code>	A list of arms with global/arm-level heterozygous loss.
<code>kit.coverage</code>	A <code>GRanges</code> object containing the regions covered on each chromosome arm.

**Details**

The percentage genomic LOH score is computed as described in the FoundationFocus CDx BRCA LOH assay; i.e. the percentage of bases covered by the Oncoscan that display a loss of heterozygosity independently of the number of copies, excluding chromosomal arms that have a global LOH ( $\geq 90$  arm length). To compute with the `armlevel_alt` function on LOH segments only). This score was linked to BRCA1/2-deficient tumors.

**Value**

An integer representing the percentage of LOH bases.

**Examples**

```

armlevel.loh <- armlevel_alt(get_loh_segments(segs.chas_example),
                           kit.coverage = oncoscan_na33.cov)
armlevel.hetloss <- armlevel_alt(get_hetloss_segments(segs.chas_example),
                                kit.coverage = oncoscan_na33.cov)
score_gloh(segs.chas_example, names(armlevel.loh), names(armlevel.hetloss),
           oncoscan_na33.cov)

```

score\_loh

*Compute the number HR deficiency-associated LOH regions.***Description**

Compute the number HR deficiency-associated LOH regions.

**Usage**

```
score_loh(segments, arms.loh, arms.hetloss, kit.coverage)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
arms.loh	A list of arms with global/arm-level LOH alteration.
arms.hetloss	A list of arms with global/arm-level heterozygous losses.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.

**Details**

Procedure based on the paper from Abkevich et al., Br J Cancer 2012 (PMID: 23047548). All LOH segments larger than 15Mb but excluding chromosome with a global LOH alteration (to compute with the armlevel\_alt function on LOH segments only). This score was linked to BRCA1/2-deficient tumors. Note that the function will merge overlapping or neighbor LOH segments (at a distance of 1bp).

**Value**

An integer representing the number of HRD-LOH regions.

**Examples**

```

armlevel.loh <- armlevel_alt(get_loh_segments(segs.chas_example),
                           kit.coverage = oncoscan_na33.cov)
armlevel.hetloss <- armlevel_alt(get_hetloss_segments(segs.chas_example),
                                kit.coverage = oncoscan_na33.cov)
score_loh(segs.chas_example, names(armlevel.loh), names(armlevel.hetloss),
           oncoscan_na33.cov)

```

---

score_lst	<i>Compute the number of Large-scale State Transitions (LSTs).</i>
-----------	--

---

**Description**

Compute the number of Large-scale State Transitions (LSTs).

**Usage**

```
score_lst(segments, kit.coverage)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.

**Details**

Procedure based on the paper from Popova et al, Can. Res. 2012 (PMID: 22933060). First segments smaller than 3Mb are removed, then segments are smoothed with respect to copy number at a distance of 3Mb. The number of LSTs is the number of breakpoints (breakpoints closer than 3Mb are merged) that have a segment larger or equal to 10Mb on each side. This score was linked to BRCA1/2-deficient tumors.

**Value**

An integer representing the number of LSTs.

**Examples**

```
score_lst(segs.chas_example, oncoscan_na33.cov)
```

---

score_mbalt	<i>Computes the total number of Mbp altered.</i>
-------------	--

---

**Description**

Computes the total number of Mbp altered.

**Usage**

```
score_mbalt(segments, kit.coverage, loh.rm = TRUE)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.
loh.rm	A boolean (TRUE by default) to indicate whether LOH segments should be excluded.

**Value**

A named list representing the Mbp altered in the sample and the total Mbp of the kit.

**Examples**

```
score_mbalt(segs.chas_example, oncoscan_na33.cov)
score_mbalt(segs.chas_example, oncoscan_na33.cov, FALSE)
```

---

score_nlst	<i>Compute the number of LSTs, normalized by the number of WGD events.</i>
------------	--

---

**Description**

Compute the number of LSTs, normalized by the number of WGD events.

**Usage**

```
score_nlst(segments, n.wgd, kit.coverage, threshold = 15)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
n.wgd	Number of whole-genome doubling events (0 if diploid).
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.
threshold	A number above which the test is returned positive ( $\geq$ ).

**Details**

Compute the number of LSTs in non-LOH segments via the `score_lst` function and subtract the extra noise induced by WGD events:  $nLST = LST - 7*W/2$  where  $W$  is the number of WGD events. A sample is HRD positive (deficient in HR pathway) if  $nLST$  is greater or equal to the threshold (15 by default). This score was linked to BRCA1/2-deficient tumors.

**Value**

A named list with the number of  $nLSTs$  and the corresponding label ('Positive', 'Negative').

**Examples**

```
w <- score_estwgd(segs.chas_example, oncoscan_na33.cov)
score_nlst(segs.chas_example, w['WGD'], oncoscan_na33.cov)
```



---

score_td	<i>Compute the number of large tandem duplication (TDplus).</i>
----------	---

---

**Description**

Compute the number of large tandem duplication (TDplus).

**Usage**

```
score_td(segments)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
----------	--

**Details**

Procedure based on the paper from Popova et al., Cancer Res 2016 (PMID: 26787835). The TDplus score is defined as the number of regions larger than 1Mb but smaller or equal to 10Mb with a gain of one or two copies. This score was linked to CDK12-deficient tumors. They also identified as second category of tandem duplication whose size is smaller or equal than 1Mb and around 300Kb but could not link it to a phenotype. Note that due to its resolution the Oncoscan assay will most likely miss this second category. Nonetheless it is reported by the function.

**Value**

A list of integer containing the TDplus score ('TDplus') and the small TD score ('TD').

**Examples**

```
score_td(segs.chas_example)
```

---

segs.chas_example	<i>Expected segments from loading the ChAS file 'chas_example.txt'.</i>
-------------------	---

---

**Description**

Expected segments from loading the ChAS file 'chas\_example.txt'.

**Usage**

```
segs.chas_example
```

**Format**

A GRanges object containing the segments, their copy number (field cn) and their copy number types (field cn.type).

**Source**

```
segs.filename <- system.file('extdata', 'chas_example.txt', package = 'ancoscanR') mykit.cov <-
get_ancoscan_coverage_from_probes() segs.chas_example <- load_chas(segs.filename, kit.coverage
= mykit.cov)
```

---

trim_to_coverage	<i>Trim segments with respect to the kit's coverage.</i>
------------------	--

---

**Description**

Trim segments with respect to the kit's coverage.

**Usage**

```
trim_to_coverage(segments, kit.coverage)
```

**Arguments**

segments	A GRanges object containing the segments, their copy number and copy number types.
kit.coverage	A GRanges object containing the regions covered on each chromosome arm.

**Details**

All segments that are not entirely contained within the kit coverage will be trimmed to the coverage's limits.

**Value**

A GRanges object containing the cleaned segments, their copy number and copy number types.

**Examples**

```
segs.trimmed <- trim_to_coverage(segs.chas_example, ancocan_na33.cov)
```

---

workflow_ancoscan.ascat	<i>Run the standard workflow for ASCAT files (from ancocan data).</i>
-------------------------	---

---

**Description**

Run the standard workflow for ASCAT files (from ancocan data).

**Usage**

```
workflow_ancoscan.ascat(ascat.fn)
```

**Arguments**

ascat.fn	Path to the text-export ASCAT file
----------	------------------------------------

**Details**

Identifies the globally altered arms ( $\geq 90\%$  of arm altered), computes the HRD and TD+ scores. The amplification is defined as a CN  $\geq 5$ . An arm is gained if of CN type `cntype.gain` unless the arm is amplified.

**Value**

A list of lists with the following elements: `armlevel = list(AMP= list of arms, GAIN= list of arms, LOSS= list of arms, LOH= list of arms)`, `scores = list(LST= number, LOH= number, TDplus= number, TD= number)`, `file = path of the ChAS file as given by the parameter`

**Examples**

```
segs.filename <- system.file('extdata', 'ascat_example.txt',
package = 'oncscanR')
workflow_oncscan.ascat(segs.filename)
```

---

```
workflow_oncscan.chas
```

*Run the standard workflow for Oncoscan ChAS files.*

---

**Description**

Run the standard workflow for Oncoscan ChAS files.

**Usage**

```
workflow_oncscan.chas(chas.fn)
```

**Arguments**

`chas.fn` Path to the text-export ChAS file

**Details**

Identifies the globally altered arms ( $\geq 90\%$  of arm altered), computes the HRD and TD+ scores. The amplification is defined as a CN subtype `cntype.weakamp` or `cntype.strongamp`. An arm is gained if of CN type `cntype.gain` unless the arm is amplified.

**Value**

A list of lists with the following elements: `armlevel = list(AMP= list of arms, GAIN= list of arms, LOSS= list of arms, LOH= list of arms)`, `scores = list(LST= number, LOH= number, TDplus= number, TD= number)`, `file = path of the ChAS file as given by the parameter`

**Examples**

```
segs.filename <- system.file('extdata', 'chas_example.txt',
package = 'oncscanR')
workflow_oncscan.chas(segs.filename)
```

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