Package: CNVfilteR (via r-universe)

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Type Package

Title Identifies false positives of CNV calling tools by using SNV calls

Version 1.27.0

Description CNVfilteR identifies those CNVs that can be discarded by using the single nucleotide variant (SNV) calls that are usually obtained in common NGS pipelines.

License Artistic-2.0

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`auxAddCNcolumn` *auxAddCNcolumn*

Description

Adds a 'cn' column to the `cnvs.gr` data.frame or GRanges.

Usage

```
auxAddCNcolumn(cnvs.gr)
```

Arguments

`cnvs.gr`	`data.frame` or `GRanges` containing the column 'cnv' with "deletion" or "duplication" as values

Details

For each row, `cn` column is filled with 1 if `cnv` is "deletion", 3 if `cnv` is "duplication"

Value

input `cnvs.gr` with the new column 'cn'

`auxGetVcfSource` *auxGetVcfSource*

Description

Obtains VCF source from a given VCF file path. Auxiliar function used by `loadSNPsFromVCF`.

Usage

```
auxGetVcfSource(vcf.source = NULL, vcf.file)
```

Arguments

`vcf.source`	VCF source. Leave NULL to allow the function to recognize it. Otherwise, the function will not try to recognize the source. (Defaults to NULL)
`vcf.file`	VCF file path

Value

VCF source

`auxProcessVariants` *auxProcessVariants*

Description

Auxiliar function called by `loadVCFs` to process variants

Usage

```
auxProcessVariants(
  vars,
  cnvGR,
  heterozygous.range,
  homozygous.range,
  min.total.depth,
  exclude.indels,
  regions.to.exclude
)
```

Arguments

vars	GRanges object containing variants for a certain sample.
cnvGR	GRanges object containg CNV calls for a certain sample.
heterozygous.range	Heterozygous range. Variants not in the homozygous/heterozygous intervals will be excluded.
homozygous.range	Homozygous range. Variants not in the homozygous/heterozygous intervals will be excluded.
min.total.depth	Minimum total depth. Variants under this value will be excluded.
exclude.indels	Whether to exclude indels when loading the variants. TRUE is the recommended value given that indels frequency varies in a different way than SNVs.
regions.to.exclude	A GRanges object defining the regions for which the variants should be excluded.

Value

Processed vars

---

filterCNVs *filterCNVs*

Description

Identifies those copy number calls that can be filtered out

Usage

```
filterCNVs(
  cnvs.gr,
  vcfs,
  expected.ht.mean = 50,
  expected.dup.ht.mean1 = 33.3,
  expected.dup.ht.mean2 = 66.6,
  sigmoid.c1 = 2,
  sigmoid.c2.vector = c(28, 38.3, 44.7, 55.3, 61.3, 71.3),
  dup.threshold.score = 0.5,
  ht.deletions.threshold = 30,
  verbose = FALSE,
  margin.pct = 10
)
```

Arguments

cnvs.gr	GRanges containing CNVs to be filtered out. Use loadCNVcalls to load them.
vcfs	List of GRanges containing all variants (SNV/indel) obtaining with the loadVCFs function.
expected.ht.mean	Expected heterozygous SNV/indel allele frequency (defaults to 50)
expected.dup.ht.mean1	Expected heterozygous SNV/indel allele frequency when the variant IS NOT in the same allele than the CNV duplication call. (defaults to 33.3)
expected.dup.ht.mean2	Expected heterozygous SNV/indel allele frequency when the variant IS in the same allele than the CNV duplication call. (defaults to 66.6)
sigmoid.c1	Sigmoid c1 parameter. (defaults to 2)
sigmoid.c2.vector	Vector containing sigmoid c2 parameters for the six sigmoids functions. (defaults to c(28, 38.3, 44.7, 55.3, 61.3, 71.3))
dup.threshold.score	Limit value to decide if a CNV duplication can be filtered out or not. A CNV duplication can be filtered out if the total score computed from heterozygous variants in the CNV is equal or greater than dup.threshold.score. (defaults to 0.5)
ht.deletions.threshold	Minimum percentage of heterozygous variants falling in a CNV deletion to filter that CNV. (defaults to 30)
verbose	Whether to show information messages. (defaults to TRUE)
margin.pct	Variants in the CNV but close to the ends of the CNV will be ignored. margin.pct defines the percentage of CNV length, located at each CNV limit, where variants will be ignored. For example, for a CNV chr1:1000-2000 and a margin.pct value of 10, variants within chr1:1000-1100 and chr1:1900-2000 will be ignored.

Details

Checks all the variants (SNV and optionally INDELs) in each CNV present in cnvs.gr to decide whether a CNV can be filtered out or not. It returns an S3 object with 3 elments: cnvs, variantsForEachCNV and filterParameters. See return section for further details.

A CNV deletion can be filtered out if there is at least ht.deletions.threshold A CNV duplication can be filtered out if the score is >= dup.threshold.score after computing all heterozygous variants falling in the CNV.

If a CNV can be filtered out, then the value TRUE is set in the filter column of the cnvs element.

Value

A S3 object with 3 elements:

- cnvs: GRanges with the input CNVs and the meta-columns added during the call:

  - cnv.id: CNV id
  - filter: Set to TRUE if the CNV can be filtered out
  - n.total.variants: Number of variants in the CNV
  - n.hm.variants: Number of homozygous variants. They do not give any evidenced for confirming or discarding the CNV.
  - n.ht.discard.CNV: For a CNV duplication, number of heterozygous variants in that discard the CNV (those with a positive score)
  - n.ht.confirm.CNV: For a CNV duplication, number of heterozygous variants that confirm the CNV (those with a negative score)
  - ht.pct: Percentage of heterozygous variants for deletion CNVs
  - score: total score when computing all the variants scores
- variantsForEachCNV: named list where each name correspond to a CNV id and the value is a data.frame with all variants falling in that CNV
- filterParameters: input parameters used for filtering

Examples

```
# Load CNVs data
cnvs.file <- system.file("extdata", "DECoN.CNVcalls.csv", package = "CNVfilteR", mustWork = TRUE)
cnvs.gr <- loadCNVcalls(cnvs.file = cnvs.file, chr.column = "Chromosome", start.column = "Start", end.column = "End

# Load VCFs data
vcf.files <- c(system.file("extdata", "variants.sample1.vcf.gz", package = "CNVfilteR", mustWork = TRUE),
          system.file("extdata", "variants.sample2.vcf.gz", package = "CNVfilteR", mustWork = TRUE))
vcfs <- loadVCFs(vcf.files, cnvs.gr = cnvs.gr)

# Filter CNVs
results <- filterCNVs(cnvs.gr, vcfs)

# Check CNVs that can be filtered out
as.data.frame(results$cnvs[results$cnvs$filter == TRUE])
```

---

getVariantScore *getVariantScore*

Description

Returns score for a given allele frequency

Usage

```
getVariantScore(
  freq,
  expected.ht.mean,
  expected.dup.ht.mean1,
```

```
  expected.dup.ht.mean2,
  sigmoid.c1,
  sigmoid.c2.vector,
  sigmoid.int1,
  sigmoid.int2
)
```

Arguments

freq	Variant allele frequency
expected.ht.mean	Expected heterozygous SNV/indel allele frequency
expected.dup.ht.mean1	Expected heterozygous SNV/indel allele frequency when the variant IS NOT in the same allele than the CNV duplication call
expected.dup.ht.mean2	Expected heterozygous SNV/indel allele frequency when the variant IS in the same allele than the CNV duplication call
sigmoid.c1	Sigmoid c1 parameter
sigmoid.c2.vector	Vector containing sigmoid c2 parameters for the six sigmoids functions
sigmoid.int1	Sigmoid int 1
sigmoid.int2	Sigmoid int 2

Details

Returns a value between -1 and 1. If the allele frequency increases the evidence of discarding a CNV, then the score is positive. If the allele frequency decreases the evidence for discarding a CNV, the score is negative.

The model is based on the fuzzy logic and the score is calculated using sigmoids. See the vignette to get more details.

Value

variant score in the [-1, 1] range

---

loadCNVcalls *loadCNVcalls*

Description

Loads CNV calls from a csv/tsv file

Usage

```
loadCNVcalls(
  cnvs.file,
  chr.column,
  start.column,
  end.column,
  coord.column = NULL,
  cnv.column,
  sample.column,
  sample.name = NULL,
  gene.column = NULL,
  deletion = "deletion",
  duplication = "duplication",
  ignore.unexpected.rows = FALSE,
  sep = "\t",
  skip = 0,
  genome = "hg19",
  exclude.non.canonical.chrs = TRUE,
  check.names.cnvs.file = FALSE
)
```

Arguments

cnvs.file	Path to csv/tsv file containing the CNV calls.
chr.column	Which column stores the chr location of the CNV.
start.column	Which column stores the start location of the CNV.
end.column	Which column stores the end location of the CNV.
coord.column	CNV location in the chr:start-end format. Example: "1:538001-540000". If NULL, chr.column, start.column and end.column columns will be used. (Defaults to NULL)
cnv.column	Which column stores the type of CNV (deletion or duplication).
sample.column	Which column stores the sample name.
sample.name	Sample name for all CNVs defined in cnvs.file. If set, sample.column is ignored (Defaults to NULL)
gene.column	Which columns store the gene or genes affected (optional). (Defaults to NULL)
deletion	Text used in the cnv.column to represent deletion CNVs. Multiple values are also allowed, for example: c("CN0", "CN1"). (Defaults to "deletion")
duplication	Text used in the cnv.column to represent duplication CNVs. Multiple values are also allowed, for example: c("CN3", "CN4") (Defaults to "duplication")
ignore.unexpected.rows	Whether to ignore the rows which CNV cnv.column value is different to deletion or duplication values (Defaults to FALSE). It is useful for processing output from callers like LUMPY or Manta (they call also events that are not CNVs)
sep	Separator symbol to load the csv/tsv file. (Defaults to "\t")

skip — Number of rows that should be skipped when reading the csv/tsv file. (Defaults to 0)

genome — The name of the genome. (Defaults to "hg19")

exclude.non.canonical.chrs — Whether to exclude non canonical chromosomes (Defaults to TRUE)

check.names.cnvs.file — Whether to check cnvs.file names or not (Defaults to FALSE). If TRUE then column names in the cnvs.file are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by make.names) so that they are, and also to ensure that there are no duplicates

Details

Loads a csv/tsv file containing CNV calls, and transform it into a GRanges with cnv and sample metadata columns.

Value

A GRanges with a range per each CNV and the metadata columns:

- cnv: type of CNV, "duplication" or "deletion"
- sample: sample name

Returns NULL if cnvs.file has no CNVs

Examples

```
# Load CNVs data
cnvs.file <- system.file("extdata", "DECoN.CNVcalls.csv", package = "CNVfilteR", mustWork = TRUE)
cnvs.gr <- loadCNVcalls(cnvs.file = cnvs.file, chr.column = "Chromosome", start.column = "Start", end.column = "End
```

---

loadSNPsFromVCF *loadSNPsFromVCF*

Description

Loads SNPs (SNVs/indels) from a VCF file

Usage

```
loadSNPsFromVCF(
  vcf.file,
  vcf.source = NULL,
  ref.support.field = NULL,
  alt.support.field = NULL,
  list.support.field = NULL,
```

```
  regions.to.filter = NULL,
  genome = "hg19",
  exclude.non.canonical.chrs = TRUE,
  verbose = TRUE
)
```

Arguments

vcf.file	VCF file path
vcf.source	VCF source, i.e., the variant caller used to generate the VCF file. If set, the function will not try to recognize the source. (Defaults to NULL)
ref.support.field	Reference allele depth field. (Defaults to NULL)
alt.support.field	Alternative allele depth field. (Defaults to NULL)
list.support.field	Allele support field in a list format: reference allele, alternative allele. (Defaults to NULL)
regions.to.filter	The regions to which limit the VCF import. It can be used to speed up the import process. (Defaults to NULL)
genome	The name of the genome (Defaults to "hg19")
exclude.non.canonical.chrs	Whether to exclude non canonical chromosomes (Defaults to TRUE)
verbose	Whether to show information messages. (Defaults to TRUE)

Details

Given a VCF file path, the function recognizes the variant caller source to decide which fields should be used to calculate ref/alt support and allelic frequency (see `return`). Current supported variant callers are VarScan2, Strelka/Strelka2, freebayes, HaplotypeCaller, UnifiedGenotyper and Torrent Variant Caller.

Optionally, the fields where the data is stored can be manually set by using the parameters `ref.support.field`, `alt.support.field` and `list.support.field`

Requirement: a TabixFile (.tbi) should exists in the same directory of the VCF file.

Value

A list where names are sample names, and values are `GRanges` objects containing the variants for each sample, including the following metadata columns:

- `ref.support`: Reference allele depth field
- `alt.support`: Alternative allele depth field
- `alt.freq`: allelic frequency
- `total.depth`: total depth

Examples

```
vcf.file <- system.file("extdata", "variants.sample1.vcf.gz", package = "CNVfilteR", mustWork = TRUE)
vcf <- loadSNPsFromVCF(vcf.file)
```

---

loadVCFs *loadVCFs*

Description

Loads VCFs files

Usage

```
loadVCFs(
  vcf.files,
  sample.names = NULL,
  cnvs.gr,
  min.total.depth = 10,
  regions.to.exclude = NULL,
  vcf.source = NULL,
  ref.support.field = NULL,
  alt.support.field = NULL,
  list.support.field = NULL,
  homozygous.range = c(90, 100),
  heterozygous.range = c(28, 72),
  exclude.indels = TRUE,
  genome = "hg19",
  exclude.non.canonical.chrs = TRUE,
  verbose = TRUE
)
```

Arguments

vcf.files	vector of VCFs paths. Both .vcf and .vcf.gz extensions are allowed.
sample.names	Sample names vector containing sample names for each vcf.files. If NULL, sample name will be obtained from the VCF sample column. (Defaults to NULL)
cnvs.gr	GRanges object containg CNV calls. Call loadCNVcalls to obtain it. Only those variants in regions affected by CNVs will be loaded to speed up the load.
min.total.depth	Minimum total depth. Variants under this value will be excluded. (Defaults to 10)
regions.to.exclude	A GRanges object defining the regions for which the variants should be excluded. Useful for defining known difficult regions like pseudogenes where the allele frequency is not trustable. (Defaults to NULL)

`vcf.source` VCF source, i.e., the variant caller used to generate the VCF file. If set, the `loadSNPsFromVCF` function will not try to recognize the source. (Defaults to NULL)

`ref.support.field` Reference allele depth field. (Defaults to NULL)

`alt.support.field` Alternative allele depth field. (Defaults to NULL)

`list.support.field` Allele support field in a list format: reference allele, alternative allele. (Defaults to NULL)

`homozygous.range` Homozygous range. Variants not in the homozygous/heterozygous intervals will be excluded. (Defaults to `c(90, 100)`)

`heterozygous.range` Heterozygous range. Variants not in the homozygous/heterozygous intervals will be excluded. (Defaults to `c(28, 72)`)

`exclude.indels` Whether to exclude indels when loading the variants. TRUE is the recommended value given that indels frequency varies in a different way than SNVs. (Defaults to TRUE)

`genome` The name of the genome. (Defaults to "hg19")

`exclude.non.canonical.chrs` Whether to exclude non canonical chromosomes (Defaults to TRUE)

`verbose` Whether to show information messages. (Defaults to TRUE)

Details

Loads VCF files and computes alt allele frequency for each variant. It uses `loadSNPsFromVCF` function load the data and identify the correct VCF format for allele frequency computation.

If sample.names is not provided, the sample names included in the VCF itself will be used. Both single-sample and multi-sample VCFs are accepted, but when multi-sample VCFs are used, sample.names parameter must be NULL.

If vcf is not compressed with bgzip, the function compresses it and generates the .gz file. If .tbi file does not exist for a given VCF file, the function also generates it. All files are generated in a temporary folder.

Value

A list where names are the sample names, and values are the `GRanges` objects for each sample.

Note

Important: Compressed VCF must be compressed with [bgzip ("block gzip") from Samtools htslib](http://www.htslib.org/doc/bgzip.html) and not using the standard Gzip utility.

Examples

```
# Load CNVs data (required by loadVCFs to speed up the load process)
cnvs.file <- system.file("extdata", "DECoN.CNVcalls.csv", package = "CNVfilteR", mustWork = TRUE)
cnvs.gr <- loadCNVcalls(cnvs.file = cnvs.file, chr.column = "Chromosome", start.column = "Start", end.column = "End

# Load VCFs data
vcf.files <- c(system.file("extdata", "variants.sample1.vcf.gz", package = "CNVfilteR", mustWork = TRUE),
          system.file("extdata", "variants.sample2.vcf.gz", package = "CNVfilteR", mustWork = TRUE))
vcfs <- loadVCFs(vcf.files, cnvs.gr = cnvs.gr)
```

---

plotAllCNVs *plotAllCNVs*

Description

Plots all CNVs on chromosome ideograms

Usage

```
plotAllCNVs(cnvs.gr, genome = "hg19")
```

Arguments

cnvs.gr	GRanges containing al CNV definitions returned by `filterCNVs` or `loadCNVcalls` functions.
genome	The name of the genome. (Defaults to "hg19")

Details

Plots all CNVs defined at `cnvs.gr` on a view of horizontal ideograms representing all chromosomes.

Value

invisibly returns a `karyoplot` object

Examples

```
cnvs.file <- system.file("extdata", "DECoN.CNVcalls.2.csv", package = "CNVfilteR", mustWork = TRUE)
cnvs.gr <- loadCNVcalls(cnvs.file = cnvs.file, chr.column = "Chromosome", start.column = "Start", end.column = "End

# Plot all CNVs
plotAllCNVs(cnvs.gr)
```

plotScoringModel *plotVariantsForCNV*

Description

Plots scoring model used for CNV duplications

Usage

```
plotScoringModel(
  expected.ht.mean,
  expected.dup.ht.mean1,
  expected.dup.ht.mean2,
  sigmoid.c1,
  sigmoid.c2.vector
)
```

Arguments

expected.ht.mean	Expected heterozygous SNV/indel allele frequency
expected.dup.ht.mean1	Expected heterozygous SNV/indel allele frequency when the variant IS NOT in the same allele than the CNV duplication call
expected.dup.ht.mean2	Expected heterozygous SNV/indel allele frequency when the variant IS in the same allele than the CNV duplication call
sigmoid.c1	Sigmoid c1 parameter
sigmoid.c2.vector	Vector containing sigmoid c2 parameters for the six sigmoids functions

Value

nothing

Examples

```
# Load CNVs data
cnvs.file <- system.file("extdata", "DECoN.CNVcalls.csv", package = "CNVfilteR", mustWork = TRUE)
cnvs.gr <- loadCNVcalls(cnvs.file = cnvs.file, chr.column = "Chromosome", start.column = "Start", end.column = "End

# Load VCFs data
vcf.files <- c(system.file("extdata", "variants.sample1.vcf.gz", package = "CNVfilteR", mustWork = TRUE),
          system.file("extdata", "variants.sample2.vcf.gz", package = "CNVfilteR", mustWork = TRUE))
vcfs <- loadVCFs(vcf.files, cnvs.gr = cnvs.gr)

# Filter CNVs
```

```
results <- filterCNVs(cnvs.gr, vcfs)

# Plot scoring model for duplication CNVs
p <- results$filterParameters
plotScoringModel(expected.ht.mean = p$expected.ht.mean, expected.dup.ht.mean1 = p$expected.dup.ht.mean1,
            expected.dup.ht.mean2 = p$expected.dup.ht.mean2, sigmoid.c1 = p$sigmoid.c1, sigmoid.c2.vector = p$sig
```

---

plotVariantsForCNV *plotVariantsForCNV*

Description

Plots a CNV with all the variants in it

Usage

```
plotVariantsForCNV(
  cnvfilter.results,
  cnv.id,
  points.cex = 1,
  points.pch = 19,
  legend.x.pos = 0.08,
  legend.y.pos = 0.25,
  legend.cex = 0.8,
  legend.text.width = NULL,
  legend.show = TRUE,
  karyotype.cex = 1,
  cnv.label.cex = 1,
  x.axis.bases.cex = 0.7,
  x.axis.bases.digits = 5,
  y.axis.title.cex = 0.8,
  y.axis.label.cex = 0.8,
  cnv.zoom.margin = TRUE
)
```

Arguments

cnvfilter.results	S3 object returned by `filterCNVs` function
cnv.id	CNV id for which to plot variants
points.cex	Points cex (size). (Defaults to 1)
points.pch	Points pch (symbol). (Defaults to 19)
legend.x.pos	Legend x position. (Defaults to 0.08)
legend.y.pos	Legend y position. (Defaults to 0.25)
legend.cex	Legend cex. (Defaults to 0.8)

`legend.text.width`
: Legend text width (Defaults to NULL)

`legend.show`
: Whether to show the legend (Defaults to TRUE)

`karyotype.cex`
: karyotype cex: affects top title and chromosome text (at bottom). (Defaults to 1)

`cnv.label.cex`
: "CNV" text cex. (Defaults to 1)

`x.axis.bases.cex`
: X-axis bases position cex. (Defaults to 0.7)

`x.axis.bases.digits`
: X-axis bases position number of digits. (Defaults to 5)

`y.axis.title.cex`
: Y-axis title cex. (Defaults to 0.8)

`y.axis.label.cex`
: Y-axis labels cex. (Defaults to 0.8)

`cnv.zoom.margin`
: If TRUE, the zoom leaves an small margin at both sides of the CNV. False otherwise. (Defaults to TRUE)

Value

invisibly returns a `karyoplot` object

Examples

```
# Load CNVs data
cnvs.file <- system.file("extdata", "DECoN.CNVcalls.csv", package = "CNVfilteR", mustWork = TRUE)
cnvs.gr <- loadCNVcalls(cnvs.file = cnvs.file, chr.column = "Chromosome", start.column = "Start", end.column = "End

# Load VCFs data
vcf.files <- c(system.file("extdata", "variants.sample1.vcf.gz", package = "CNVfilteR", mustWork = TRUE),
          system.file("extdata", "variants.sample2.vcf.gz", package = "CNVfilteR", mustWork = TRUE))
vcfs <- loadVCFs(vcf.files, cnvs.gr = cnvs.gr)

# Filter CNVs
results <- filterCNVs(cnvs.gr, vcfs)

# Check CNVs that can be filtered out
as.data.frame(results$cnvs[results$cnvs$filter == TRUE])

# Plot one of them
plotVariantsForCNV(results, "3")
```

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