

Package: rabhit (via r-universe)

September 23, 2026

Type Package

Title Inference Tool for Antibody Haplotype

Version 0.4.0

Description Infers V-D-J haplotypes and gene deletions from AIRR-seq data for Ig and TR chains, based on J, D, or V genes as anchor, by adapting a Bayesian framework. It also calculates a Bayes factor, a number that indicates the certainty level of the inference, for each haplotyped gene. Citation: Gidoni, et al (2019) <[doi:10.1038/s41467-019-08489-3](https://doi.org/10.1038/s41467-019-08489-3)>. Peres and Gidoni, et al (2019) <[doi:10.1093/bioinformatics/btz481](https://doi.org/10.1093/bioinformatics/btz481)>.

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URL <https://github.com/ayeletperes/rabhit>,
<https://ayeletperes.github.io/rabhit/>

BugReports <https://github.com/ayeletperes/rabhit/issues>

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.onAttach	<i>.onAttach start message</i>
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Description

.onAttach start message

Usage

```
.onAttach(libname, pkgname)
```

Arguments

libname	defunct
pkgname	defunct

Value

```
invisible()
```

convertToASC	<i>Prepare AIRR-seq data and germline for haplotype inference with allele similarity clusters (ASC)</i>
--------------	---

Description

convertToASC converts IMGT-named V alleles to PigLET Allele Similarity Cluster (ASC) names and returns the pieces needed to run [createFullHaplotype](#) on the clustered data. ASCs collapse near-identical and duplicated IGHV alleles (for example *IGHV1-69* / *IGHV1-69D*) that are otherwise difficult to assign unambiguously, and provide a naming scheme compatible with OGRDB reference sets. It is a thin wrapper around the **piglet** package.

Usage

```
convertToASC(
  clip_db,
  germline,
  chain = c("IGH", "IGK", "IGL", "TRB"),
  allele_cluster_table = NULL,
  v_call = "v_call",
  ...
)
```

Arguments

clip_db	AIRR-seq repertoire data.frame.
germline	named vector of IMGT-gapped germline sequences for the V genes (e.g. HVGerm).
chain	the chain. One of "IGH", "IGK", "IGL" or "TRB".
allele_cluster_table	optional precomputed ASC table (a data.frame with iuis_allele and new_allele columns, as produced by <code>piglet::inferAlleleClusters()</code> or downloaded from OGRDB with <code>piglet::recentAlleleClusters()</code> / <code>piglet::extractASCTable()</code>). If NULL it is inferred from germline.
v_call	the column holding the V allele calls to convert. Default "v_call".
...	further arguments passed to <code>piglet::inferAlleleClusters()</code> when <code>allele_cluster_table</code> is inferred.

Details

The returned objects feed directly into the standard workflow:

```
asc <- convertToASC(clip_db, HVGERM, chain = "IGH")
hap <- createFullHaplotype(asc$clip_db, toHap_col = "v_call",
                           hapBy_col = "j_call", hapBy = "IGHJ6",
                           toHap_GERM = asc$germline, chain = "IGH")
plotHaplotype(hap, genes_order = asc$genes_order)
```

Allele similarity clustering is applied to the V genes only; D and J calls are left unchanged.

Value

a list with:

- clip_db - the input data with v_call converted to ASC names.
- germline - the ASC-named germline vector to pass as toHap_GERM.
- genes_order - an ASC gene order (derived from the chromosomal order in GENE.loc) to pass to the plotting functions.
- allele_cluster_table - the ASC table that was used.

See Also

[createFullHaplotype](#); the **piglet** package for the underlying clustering (inferAlleleClusters, assignAlleleClusters, germlineASC).

Examples

```
## Not run:
data(samples_db, HVGERM)
clip_db <- samples_db[samples_db$subject == "I5", ]
asc <- convertToASC(clip_db, HVGERM, chain = "IGH")
hap <- createFullHaplotype(asc$clip_db, toHap_col = "v_call",
                           hapBy_col = "j_call", hapBy = "IGHJ6",
                           toHap_GERM = asc$germline, chain = "IGH")
plotHaplotype(hap, genes_order = asc$genes_order)

## End(Not run)
```

createFullHaplotype *Anchor gene haplotype inference*

Description

The createFullHaplotype functions infers haplotype based on an anchor gene.

Usage

```
createFullHaplotype(
  clip_db,
  toHap_col = c("v_call", "d_call"),
  hapBy_col = "j_call",
  hapBy = "IGHJ6",
  toHap_GERM = NULL,
  relative_freq_priors = TRUE,
  kThreshDel = 3,
  rmPseudo = TRUE,
  deleted_genes = c(),
  nonReliable_Vgenes = c(),
  min_minor_fraction = 0.3,
  single_gene = TRUE,
  chain = c("IGH", "IGK", "IGL", "TRB")
)
```

Arguments

<code>clip_db</code>	a <code>data.frame</code> in AIRR format. See details.
<code>toHap_col</code>	a vector of column names for which a haplotype should be inferred. Default is <code>v_call</code> and <code>d_call</code>
<code>hapBy_col</code>	column name of the anchor gene. Default is <code>j_call</code>
<code>hapBy</code>	a string of the anchor gene name. Default is <code>IGHJ6</code> .
<code>toHap_GERM</code>	a vector of named nucleotide germline sequences matching the allele calls in <code>toHap_col</code> columns in <code>clip_db</code> .
<code>relative_freq_priors</code>	if <code>TRUE</code> , the priors for Bayesian inference are estimated from the relative frequencies in <code>clip_db</code> . Else, priors are set to <code>c(0.5, 0.5)</code> . Default is <code>TRUE</code>
<code>kThreshDel</code>	the minimum IK ($\log_{10}$ of the Bayes factor) to call a deletion. Default is 3.
<code>rmPseudo</code>	if <code>TRUE</code> non-functional and pseudo genes are removed. Default is <code>TRUE</code> .
<code>deleted_genes</code>	double chromosome deletion summary table. A <code>data.frame</code> created by <code>deletionsByBinom</code> .
<code>nonReliable_Vgenes</code>	a list of known non reliable gene assignments. A list created by <code>nonReliableVGenes</code> .
<code>min_minor_fraction</code>	the minimum minor allele fraction to be used as an anchor gene. Default is 0.3
<code>single_gene</code>	if to only consider genes from single assignment. If true then calls where genes appear with others are discarded. If false then the calls are separated and counted for all genes that appeared. Default is <code>True</code> .
<code>chain</code>	the IG/TR chain: <code>IGH,IGK,IGL,TRB</code> . Default is <code>IGH</code> .

Details

Function accepts a `data.frame` in AIRR format (<https://changeo.readthedocs.io/en/stable/standard.html>) containing the following columns:

- 'subject': The subject name
- 'v_call': V allele call(s) (in an IMGT format)
- 'd_call': D allele call(s) (in an IMGT format, only for heavy chains)
- 'j_call': J allele call(s) (in an IMGT format)

Value

A data.frame, in which each row is the haplotype inference summary of a gene from the column selected in toHap_col.

The output contains the following columns:

- subject: the subject name.
- gene: the gene name.
- Anchor gene allele 1: the haplotype inference for chromosome one. The column name is the anchor gene with the first allele.
- Anchor gene allele 2: the haplotype inference for chromosome two. The column name is the anchor gene with the second allele.
- alleles: allele calls for the gene.
- proirs_row: priors based on relative allele usage of the anchor gene.
- proirs_col: priors based on relative allele usage of the inferred gene.
- counts1: the appereance count on each chromosome of the first allele from alleles, the counts are seperated by a comma.
- k1: the Bayesian factor value for the first allele (from alleles) inference.
- counts2: the appereance count on each chromosome of the second allele from alleles, the counts are seperated by a comma.
- k2: the Bayesian factor value for the second allele (from alleles) inference.
- counts3: the appereance count on each chromosome of the third allele from alleles, the counts are seperated by a comma.
- k3: the Bayesian factor value for the third allele (from alleles) inference.
- counts4: the appereance count on each chromosome of the fourth allele from alleles, the counts are seperated by a comma.
- k4: the Bayesian factor value for the fourth allele (from alleles) inference.

Examples

```
# Load example data and germlines
data(samples_db, HVGERM, HDGERM)

# Selecting a single individual
clip_db = samples_db[samples_db$subject=='I5', ]

# Infering haplotype
haplo_db = createFullHaplotype(clip_db,toHap_col=c('v_call','d_call'),
hapBy_col='j_call',hapBy='IGHJ6',toHap_GERM=c(HVGERM,HDGERM))
```

createHaplotypeTable	<i>Create haplotype table</i>
----------------------	-------------------------------

Description

createHaplotypeTable Haplotype of a specific gene

Usage

```
createHaplotypeTable(  
  df,  
  HapByPriors = c(0.5, 0.5),  
  toHapByCol = TRUE,  
  toHapPriors = c(0.5, 0.5)  
)
```

Arguments

df	table of counts
HapByPriors	vector of frequencies of each of the anchor gene alleles
toHapByCol	logical, haplotype each chromosome separately to improve the aligner assignment
toHapPriors	vector of frequencies of the haplotyped gene alleles

Value

data frame with chromosomal associations of alleles of a specific gene

deletionHeatmap	<i>Graphical output of single chromosome deletions</i>
-----------------	--

Description

The deletionHeatmap function generates a graphical output of the single chromosome deletions in multiple samples.

Usage

```
deletionHeatmap(  
  hap_table,  
  chain = c("IGH", "IGK", "IGL", "TRB", "TRA"),  
  kThreshDel = 3,  
  genes_order = NULL,  
  html_output = FALSE  
)
```

Arguments

hap_table	haplotype summary table. See details.
chain	the IG chain: IGH,IGK,IGL. Default is IGH.
kThreshDel	the minimum lK (log10 of the Bayes factor) used in createFullHaplotype to call a deletion. Indicates the color for strong deletion. Default is 3.
genes_order	A vector of the genes by the desired order. Default is by GENE.loc
html_output	If TRUE, a html5 interactive graph is outputed instead of the normal plot. Default is FALSE

Details

A data.frame created by createFullHaplotype.

Value

A single chromosome deletion visualization.

Examples

```
# Plotting single chromosome deletion from haplotype inference
deletionHeatmap(samplesHaplotype)
```

deletionsByBinom	<i>Double chromosome deletion by relative gene usage</i>
------------------	--

Description

The deletionsByBinom function infers double chromosome deletion events by relative gene usage.

Usage

```
deletionsByBinom(
  clip_db,
  chain = c("IGH", "IGK", "IGL"),
  nonReliable_Vgenes = c(),
  genes_order = NULL
)
```

Arguments

clip_db	a data.frame in AIRR format. See details.
chain	the IG/TR chain: IGH,IGK,IGL,TRB. Default is IGH.
nonReliable_Vgenes	a list of known non reliable gene assignments. A list created by nonReliableVGenes.
genes_order	A vector of the genes by the desired order. Default is by GENE.loc

Details

The function accepts a `data.frame` in AIRR format (<https://changeo.readthedocs.io/en/stable/standard.html>) containing the following columns:

- 'subject': The subject name
- 'v_call': V allele call(s) (in an IMGT format)
- 'd_call': D allele call(s) (in an IMGT format, only for heavy chains)
- 'j_call': J allele call(s) (in an IMGT format)

Value

A `data.frame`, in which each row is the double chromosome deletion inference of a gene.

The output contains the following columns:

- subject: the subject name.
- gene: the gene call
- frac: the relative gene usage of the gene
- cutoff: the the cutoff of for the binomial test
- pval: the p-value of the binomial test
- deletion: if a double chromosome deletion event of a gene occurred.

Examples

```
# Load example data and germlines
data(samples_db)

# Selecting a single individual
clip_db = samples_db[samples_db$subject=='I5', ]
# Inferring haplotype
del_binom_df = deletionsByBinom(clip_db)
head(del_binom_df)
```

deletionsByVpooled	<i>Single chromosomal D or J gene deletions inferred by the V pooled method</i>
--------------------	---

Description

The `deletionsByVpooled` function infers single chromosomal deletion for D and J gene .

Usage

```
deletionsByVpooled(
  clip_db,
  chain = c("IGH", "IGK", "IGL"),
  deletion_col = c("d_call", "j_call"),
  count_thresh = 50,
  deleted_genes = "",
  min_minor_fraction = 0.3,
  kThreshDel = 3,
  nonReliable_Vgenes = c()
)
```

Arguments

<code>clip_db</code>	a <code>data.frame</code> in AIRR format. See details.
<code>chain</code>	the IG chain: IGH,IGK,IGL. Default is IGH.
<code>deletion_col</code>	a vector of column names for which single chromosome deletions should be inferred. Default is <code>j_call</code> and <code>d_call</code> .
<code>count_thresh</code>	integer, the minimum number of sequences mapped to a specific V gene to be included in the V pooled inference.
<code>deleted_genes</code>	double chromosome deletion summary table. A <code>data.frame</code> created by <code>deletionsByBinom</code> .
<code>min_minor_fraction</code>	the minimum minor allele fraction to be used as an anchor gene. Default is 0.3
<code>kThreshDel</code>	the minimum IK (log10 of the Bayes factor) to call a deletion. Default is 3.
<code>nonReliable_Vgenes</code>	a list of known non reliable gene assignments. A list created by <code>nonReliableVGenes</code> .

Details

The function accepts a `data.frame` in AIRR format (<https://changeo.readthedocs.io/en/stable/standard.html>) containing the following columns:

- 'subject': The subject name
- 'v_call': V allele call(s) (in an IMGT format)
- 'd_call': D allele call(s) (in an IMGT format, only for heavy chains)
- 'j_call': J allele call(s) (in an IMGT format)

Value

A `data.frame`, in which each row is the single chromosome deletion inference of a gene.

The output contains the following columns:

- subject: the subject name.
- gene: the gene call
- deletion: chromosome deletions inferred. Encoded 1 for deletion and 0 for no deletion.

- k: the Bayesian factor value for the deletion inference.
- counts: the appereance count of the gene on each chromosome, the counts are seperated by a comma.

Examples

```
data(samples_db)

# Infering V pooled deletions
del_db <- deletionsByVpooled(samples_db)
head(del_db)
```

GENE.loc	<i>Human Gene order on the chromosome</i>
----------	---

Description

A list of the chains genes order by their location on the chromosomes

Usage

```
GENE.loc
```

Format

A nested list with three enteries, each a vector of the IG chains (IGH, IGL, and IGK) genes ordered by location.

geneUsage	<i>Double chromosome deletion by relative gene usage</i>
-----------	--

Description

The geneUsage function calculates the relative gene usage.

Usage

```
geneUsage(
  clip_db,
  chain = c("IGH", "IGK", "IGL", "TRB"),
  genes_order = NULL,
  rmPseudo = TRUE
)
```

Arguments

<code>clip_db</code>	a <code>data.frame</code> in AIRR format. See details.
<code>chain</code>	the IG/TR chain: IGH,IGK,IGL,TRB. Default is IGH.
<code>genes_order</code>	A vector of the genes by the desired order. Default is by GENE.loc
<code>rmPseudo</code>	if TRUE non-functional and pseudo genes are removed. Default is TRUE.

Details

The function accepts a `data.frame` in AIRR format (<https://changeo.readthedocs.io/en/stable/standard.html>) containing the following columns:

- `'subject'`: The subject name
- `'v_call'`: V allele call(s) (in an IMGT format)
- `'d_call'`: D allele call(s) (in an IMGT format, only for heavy chains)
- `'j_call'`: J allele call(s) (in an IMGT format)

Value

A `data.frame`, in which each row is the relative gene usage value per individual.

The output contains the following columns:

- `subject`: the subject name.
- `gene`: the gene call
- `frac`: the relative gene usage of the gene

GERM

Human germlines

Description

A list of the germline genes from the human immunoglobulin loci

Usage

```
GERM
```

Format

Values correspond to IMGT-gaped nucleotide sequences (with nucleotides capitalized and gaps represented by '.').

hapDendo

Hierarchical clustering of haplotypes graphical output

Description

The hapDendo function generates a graphical output of an hierarchical clustering based on the Jaccard distance between multiple samples' haplotypes.

Usage

```
hapDendo(
  hap_table,
  chain = c("IGH", "IGK", "IGL", "TRB", "TRA"),
  genes_order = NULL,
  removeIGH = TRUE,
  mark_low_lk = TRUE,
  lk_cutoff = 1
)
```

Arguments

hap_table	haplotype summary table. See details.
chain	the IG/TR chain: IGH,IGK,IGL,TRB. Default is IGH.
genes_order	A vector of the genes by the desired order. Default is by GENE.loc
removeIGH	if TRUE, 'IGH'\IGK'\IGL' prefix is removed from gene names. Default is TRUE.
mark_low_lk	if TRUE, a texture is add for low IK values. Default is TRUE.
lk_cutoff	the IK cutoff value to be considered low for texture layer. Default is $IK < 1$.

Details

A data.frame created by createFullHaplotype.

Value

A multiple samples visualization of the distances between haplotypes.

Examples

```
# Plotting haplotype hierarchical clustering based on the Jaccard distance
hapDendo(samplesHaplotype)
```

hapHeatmap

*Graphical output of alleles division by chromosome***Description**

The hapHeatmap function generates a graphical output of the alleles per gene in multiple samples.

Usage

```
hapHeatmap(
  hap_table,
  chain = c("IGH", "IGK", "IGL", "TRB", "TRA"),
  genes_order = NULL,
  removeIGH = TRUE,
  lk_cutoff = 1,
  mark_low_lk = TRUE,
  size_annot = 1.5,
  color_y = NULL,
  order_subject = NULL,
  file = NULL,
  size_text = NULL,
  ylabel_size = 1
)
```

Arguments

hap_table	haplotype summary table. See details.
chain	the IG chain: IGH,IGK,IGL. Default is IGH.
genes_order	A vector of the genes by the desired order. Default is by GENE.loc
removeIGH	if TRUE, 'IGH'\`IGK'\`IGL'\`TRB' prefix is removed from gene names.
lk_cutoff	the IK cutoff value to be considered low for texture layer. Default is IK<1.
mark_low_lk	if TRUE, a texture is add for low IK values. Default is TRUE.
size_annot	size of bottom annotation text. Default is 1.5 .
color_y	named list of the colors for y axis labels.
order_subject	order subject by a vector.
file	file path for rendering the plot to pdf. If non is supplied than the plot is returned as object. Default is NULL.
size_text	text size for annotations.
ylabel_size	text size for y axis labels.

Details

A data.frame created by createFullHaplotype.

Value

A list with the following:

- 'p': heat-map visualization of the haplotype inference for multiple samples.
- 'width': Optimal width value for rendering plot.
- 'height': Optimal width value for rendering plot.

When a file is supplied the graph is also rendered to pdf.

Examples

```
# Plotting haplotpe heatmap
p <- hapHeatmap(samplesHaplotype)
p$p
```

HDGERM

Human IGHD germlines

Description

A character vector of all 37 human IGHD germline gene segment alleles in IMGT Gene-db release 2018-12-4.

Usage

HDGERM

Format

Values correspond to IMGT nuceltoide sequences.

References

Xochelli *et al.* (2014) Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukaemia. *Immunogenetics*. 67(1):61-6.

HJGERM

Human IGHJ germlines

Description

A character vector of all 13 human IGHJ germline gene segment alleles in IMGT Gene-db release 2018-12-4.

Usage

HJGERM

Format

Values correspond to IMGT nucleotide sequences.

References

Xochelli *et al.* (2014) Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukaemia. *Immunogenetics*. 67(1):61-6.

HVGERM

Human IGHV germlines

Description

A character vector of all 342 human IGHV germline gene segment alleles in IMGT Gene-db release 2018-12-4.

Usage

HVGERM

Format

Values correspond to IMGT-gapped nucleotide sequences (with nucleotides capitalized and gaps represented by '.').

References

Xochelli *et al.* (2014) Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukaemia. *Immunogenetics*. 67(1):61-6.

KJGERM*Human IGKJ germlines*

Description

A character vector of all 342 human IGKJ germline gene segment alleles in IMGT Gene-db release 2019-11-18.

Usage

KJGERM

Format

Values correspond to IMGT-gaped nuceltoide sequences (with nucleotides capitalized and gaps represented by '.').

KVGERM*Human IGKV germlines*

Description

A character vector of all 342 human IGKV germline gene segment alleles in IMGT Gene-db release 2019-11-18.

A character vector of all 342 human IGLV germline gene segment alleles in IMGT Gene-db release 2019-11-18.

Usage

KVGERM

LVGERM

Format

Values correspond to IMGT-gaped nuceltoide sequences (with nucleotides capitalized and gaps represented by '.').

Values correspond to IMGT-gaped nuceltoide sequences (with nucleotides capitalized and gaps represented by '.').

LJGERM	<i>Human IGLJ germlines</i>
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Description

A character vector of all 342 human IGLJ germline gene segment alleles in IMGT Gene-db release 2019-11-18.

Usage

LJGERM

Format

Values correspond to IMGT-gaped nuceltoide sequences (with nucleotides capitalized and gaps represented by '.').

nonReliableVGenes	<i>Detect non reliable gene assignment</i>
-------------------	--

Description

nonReliableVGenes Takes a data.frame in AIRR format and detect non reliable IGHV genes. A non reliable gene is when the ratio of the multiple assignments with a gene is below the threshold.

Usage

nonReliableVGenes(clip_db, thresh = 0.9, appearance = 0.01)

Arguments

clip_db	a data.frame in AIRR format. See details.
thresh	the threshold to consider non reliable gene. Default is 0.9
appearance	the minimum fraction of gene appearance to be considered for reliability check. Default is 0.01.

Details

The function accepts a data.frame in AIRR format (<https://changeo.readthedocs.io/en/stable/standard.html>) containing the following columns:

- 'subject': subject names
- 'v_call': V allele call(s) (in an IMGT format)

Value

a nested list of non reliable genes for all subject.

Examples

```
# Example IGHV call data frame
clip_db <- data.frame(subject=rep('S1',6),
  v_call=c('IGHV1-69*01','IGHV1-69*01','IGHV1-69*01,IGHV1-69*02',
    'IGHV4-59*01,IGHV4-61*01','IGHV4-59*01,IGHV4-31*02','IGHV4-59*01'))
# Detect non reliable genes
nonReliableVGenes(clip_db)
```

plotDeletionsByBinom *Graphical output of double chromosome deletions*

Description

The plotDeletionsByBinom function generates a graphical output of the double chromosome deletions in multiple samples.

Usage

```
plotDeletionsByBinom(
  GENE.usage.df,
  chain = c("IGH", "IGK", "IGL", "TRB", "TRA"),
  genes.low.cer = c("IGHV3-43", "IGHV3-20"),
  genes.dup = c("IGHD4-11", "IGHD5-18"),
  genes_order = NULL
)
```

Arguments

GENE.usage.df	double chromosome deletion summary table. See details.
chain	the IG chain: IGH,IGK,IGL. Default is IGH.
genes.low.cer	a vector of IGH genes known to be with low certantiny in the binomial test. Default is IGHV3-43 and IGHV3-20
genes.dup	a vector of IGH genes known to have a duplicated gene. Default is IGHD4-11 that his duplicate is IGHD4-4 and IGHD5-18 that his duplicate is IGHD5-5
genes_order	A vector of the genes by the desired order. Default is by GENE.loc

Details

A data.frame created by binom_test_deletion.

Value

A double chromosome deletion visualization.

Examples

```
# Load example data and germlines
data(samples_db)

# Infering haplotype
deletions_db = deletionsByBinom(samples_db);
plotDeletionsByBinom(deletions_db)
```

```
plotDeletionsByVpooled
```

Graphical output for single chromosome D or J gene deletions according to V pooled method

Description

The plotDeletionsByVpooled function generates a graphical output for single chromosome D or J gene deletions (for heavy chain only).

Usage

```
plotDeletionsByVpooled(
  del.df,
  chain = c("IGH", "IGK", "IGL", "TRB", "TRA"),
  K_ranges = c(3, 7)
)
```

Arguments

del.df	a data.frame created by deletionsByVpooled
chain	the IG chain: IGH,IGK,IGL. Default is IGH..
K_ranges	vector of one or two integers for log(K) certainty level thresholds

Details

A data.frame created by deletionsByVpooled.

Value

A single chromosome deletion visualization.

Examples

```
# Load example data and germlines
data(samples_db)
del_db <- deletionsByVpooled(samples_db)
plotDeletionsByVpooled(del_db)
```

plotHaplotype

Graphical output of an inferred haplotype

Description

The plotHaplotype functions visualizes an inferred haplotype.

Usage

```
plotHaplotype(
  hap_table,
  html_output = FALSE,
  genes_order = NULL,
  text_size = 14,
  removeIGH = TRUE,
  plotYaxis = TRUE,
  chain = c("IGH", "IGK", "IGL", "TRB"),
  dir,
  width = 15,
  height = 20
)
```

Arguments

hap_table	haplotype summary table. See details.
html_output	if TRUE, a html5 interactive graph is outputed. Default is FALSE.
genes_order	A vector of the genes by the desired order. Default is by GENE.loc
text_size	the size of graph labels. Default is 14 (pts).
removeIGH	if TRUE, 'IGH'\'IGK'\'IGL'\'TRB' prefix is removed from gene names.
plotYaxis	if TRUE, Y axis labels (gene names) are plotted on the middle and right plots. Default is TRUE.
chain	the Ig/TR chain: IGH,IGK,IGL,TRB. Default is IGH.
dir	The output folder for saving the haplotype map for multiple individuals.
width	width (in inches) of the multi-subject pdf output. Default is 15.
height	height (in inches) of the multi-subject pdf output. Default is 20.

Details

A data.frame in a haplotype format created by createFullHaplotype function.

Value

A haplotype map visualization. If more than one subject is visualized, a pdf is created. If html_output is TRUE, a folder named html_output is created with individual graphs.

Examples

```
# Selecting a single individual from the haplotype samples data
haplo_db = samplesHaplotype[samplesHaplotype$subject=='I5', ]

# plot haplotype
plotHaplotype(haplo_db)
```

 rabhit

The RAbHIT package

Description

The `rabhit` package provides a robust novel method for determining antibody heavy and light chain haplotypes by adapting a Bayesian framework. The key functions in `rabhit`, broken down by topic, are described below.

Haplotype and deletions inference

`rabhit` provides tools to infer haplotypes based on given anchor genes, deletion detection based on relative gene usage, pooling v genes, and a single anchor gene.

- [createFullHaplotype](#): Haplotypes inference and single chromosome deletions based on an anchor gene.
- [deletionsByVpooled](#): Single chromosomal deletion detection by pooling V genes.
- [deletionsByBinom](#): Double chromosomal deletion detection by relative gene usage.
- [geneUsage](#): Relative gene usage.
- [nonReliableVGenes](#): Non reliable gene assignment detection.

Haplotype and deletions visualization

Functions for visualization of the inferred haplotypes and deletions

- [plotHaplotype](#): Haplotype inference map.
- [deletionHeatmap](#): Single chromosome deletions heatmap.
- [hapHeatmap](#): Chromosome comparison of multiple samples.
- [hapDendo](#): Hierarchical clustering of multiple haplotypes based on Jaccard distance.
- [plotDeletionsByVpooled](#): V pooled based single chromosome deletions heatmap.
- [plotDeletionsByBinom](#): Double chromosome deletions heatmap.

References

1. Gidoni, M., Snir, O., Peres, A., Polak, P., Lindeman, I., Mikocziova, I., . . . Yaari, G. (2019). Mosaic deletion patterns of the human antibody heavy chain gene locus shown by Bayesian haplotyping. *Nature Communications*, 10(1). doi:10.1038/s41467-019-08489-3

readHaplotypeDb	<i>Read a Change-O tab-delimited database file</i>
-----------------	--

Description

readHaplotypeDb reads a tab-delimited haplotype file created by a createFullHaplotype into a data.frame. Based on readChangeoDb function from alakazam.

Usage

```
readHaplotypeDb(file)
```

Arguments

file	tab-delimited database file output by a Change-O tool.
------	--

Value

A data.frame of the haplotype file. Columns will be imported as is, except for the following columns which will be explicitly converted into character values:

- alleles
- subject

samples_db	<i>Example IGH human naive b-cell repertoire</i>
------------	--

Description

A data.frame of example IGH human naive b-cell repertoire data from five individuals (see references). Overall, the data set includes 6 samples. A single individual has two samples (Individual I5), one is short read sequences from BIOMED-2 protocol primers for framework 2 region (The sample is annotated I5_FR2).

Usage

```
samples_db
```

Format

A data.frame in Change-O format (<https://changeo.readthedocs.io/en/stable/standard.html>) containing the following columns:

- 'SUBJECT': subject names
- 'V_CALL': V allele call(s) (in an IMGT format)
- 'D_CALL': D allele call(s) (in an IMGT format, only for heavy chains)
- 'J_CALL': J allele call(s) (in an IMGT format)

References

Gidoni, Moriah, *et al.* Mosaic deletion patterns of the human antibody heavy chain gene locus shown by Bayesian haplotyping. *Nature Communications*. 10.1 (2019): 628.

samplesHaplotype	<i>Example haplotype inference results</i>
------------------	--

Description

A data.frame of example haplotype infrence results from [createFullHaplotype](#) after double chromosome deletion inference via [deletionsByBinom](#) and non reliable V genes detection via [nonReliableVGenes](#). Source data is a colletion of IGH human naive b-cell repertiore data from five individuals (see references). Overall, the data set includes 6 samples. A single individual has two samples (Individual I5), one is short read sequences from BIOMED-2 protocol primers for framework 2 region (The sample is annotated I5_FR2).

Usage

samplesHaplotype

Format

A data.frame, in which each row is the haplotype inference summary of a gene of an individual, from the column selected to prefrom the haplptype infrence on.

References

Gidoni, Moriah, *et al.* Mosaic deletion patterns of the human antibody heavy chain gene locus shown by Bayesian haplotyping. *Nature Communications*. 10.1 (2019): 628.

See Also

See [createFullHaplotype](#) for detailed column descriptions.

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