Package ‘clonotypeR’
January 31, 2017

Type Package
Title High throughput analysis of T cell antigen receptor sequences
Version 1.12.0
Date 2016-10-13
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Description High throughput analysis of T cell antigen receptor sequences The
genes encoding T cell receptors are created by somatic recombination, generating
an immense combination of V, (D) and J segments. Additional processes during
the recombination create extra sequence diversity between the V an J segments.
Collectively, this hyper-variable region is called the CDR3 loop. The purpose
of this package is to process and quantitatively analyse millions of V-CDR3-J
combination, called clonotypes, from multiple sequence libraries.

License file LICENSE
Imports methods
Suggests BiocGenerics, edgeR, knitr, pvclust, RUnit, vegan
VignetteBuilder knitr
biocViews Sequencing
URL http://clonotyper.branchable.com/
BugReports http://clonotyper.branchable.com/Bugs/
RoxygenNote 5.0.1
NeedsCompilation no

R topics documented:

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clonotype_table

Description

clonotypeR: High throughput analysis of T cell antigen receptor sequences

clonotype_table

Description

Create a table count of clonotypes or other features

Usage

clonotype_table(libs, feats = c("V", "pep", "J"), data,
    filter = (data$unproductive | data$ambiguous), minscore = 0,
    minqual = 1, sample = FALSE)

Arguments

libs A character vector containing the name of one or many libraries. Same names
must not appear twice. If no library names are provided, all the libraries present
in the clonotypes data frame will be used.

feats What to count. By default, it counts clonotypes, defined as c("V", "pep", "J").
But it can also count single features, such as the V or J segments.

data Data frame as loaded by read_clonotypes.

filter Logical vector to filter out clonotypes. By default it relies on the clonotypes
data frame to provide a “unproductive” column that indicates clonotypes with a
stop codon or a frame shift, and a “ambiguous” column that indicates clonotypes
where the DNA sequences has ambiguous (“N”) nucleotides.

minscore Minimum alignment score. Clonotypes with an alignment score lower than this
value are discarded.

minqual Minimum mapping quality. Clonotypes with a mapping quality lower than this
value are discarded.

sample Indicate the number of clonotypes to randomly sample from the library (no re-
placement). Default: no

Details

Using a clonotype data frame loaded with read_clonotypes, clonotype_table will create a ta-
ble counting how many times each clonotypes have been seen in each libraries. By default, the
unproductive rearrangements are filtered out.
Value

clonotype_table returns a data frame, where row names are features (clonotypes, segment names, ...), column names are libraries, and values are number of times each feature was found in each library.

See Also

read_clonotypes

Examples

# Read the package's example data
clonotypes <- read_clonotypes(system.file('extdata', 'clonotypes.txt.gz', package = "clonotypeR"))

# Inspect the alignment scores
hist(clonotypes$score)

# Count J segments
j <- clonotype_table(levels(clonotypes$lib), "J", data=clonotypes)

# Normalise counts in parts per million
J <- data.frame(prop.table(as.matrix(j),2) * 1000000)

common_clonotypes

Description

Reports clonotypes common between libraries.

Usage

common_clonotypes(group1, group2, mode, data)

## S4 method for signature 'character,missing,missing,data.frame'
common_clonotypes(group1, data)

## S4 method for signature 'character,character,missing,data.frame'
common_clonotypes(group1, group2, data)

## S4 method for signature 'missing,missing,ANY,data.frame'
common_clonotypes(mode = "count", data)

## S4 method for signature 'missing,missing,ANY,matrix'
common_clonotypes(mode, data)
common_clonotypes

Arguments

- group1: A character vector containing clonotype library names.
- group2: A character vector containing clonotype library names.
- mode: Only when producing a matrix of pairwise comparisons: “count” (default) or “abundance”, see below.
- data: A clonotype table where the data is stored.

Details

- When given one group of libraries, lists the clonotypes that have been observed at least in one library of that group. The returned list can be used to subset a data frame produced by `clonotype_table`.
- When given two groups of libraries, lists the clonotypes that have been observed at least in one library of each group. Groups can contain a single library, in which case the returned list is simply the clonotypes found in both libraries.
- When given a table of clonotypes, produces a matrix in which each cell reports quantitatively the overlap between each pair of libraries.

Value

- In “count” mode, each value in a matrix is the number of clonotypes seen in both of the two libraries considered. The matrix is therefore symmetric.
- In “abundance” mode, each value indicates, for a given pair of libraries, the cumulative abundance of the common clonotypes (seen in both libraries), calculated for the library indicated by the row. The matrix is therefore not symmetric. For instance, a pair of libraries A and B can have 100 sequences each in total, one clonotype in common, which is found 8 times in A, but 54 times in B.

Methods (by class)

- `group1 = character, group2 = missing, mode = missing, data = data.frame`: Reports clonotypes common between libraries.
- `group1 = character, group2 = character, mode = missing, data = data.frame`: Reports clonotypes common between libraries.
- `group1 = missing, group2 = missing, mode = ANY, data = data.frame`: Reports clonotypes common between libraries.
- `group1 = missing, group2 = missing, mode = ANY, data = matrix`: Reports clonotypes common between libraries.

See Also

- `clonotype_table`, `unique_clonotypes`

Examples

```r
# Load example data
clonotypes.long <- read_clonotypes(system.file("extdata", "clonotypes.txt.gz", package = "clonotypeR"))
clonotypes <- clonotype_table(levels(clonotypes.long$lib), data=clonotypes.long)
summary(clonotypes)

# List clonotypes found in library A, and B or C.
common_clonotypes(group1="A", group2=c("B","C"), data=clonotypes)
```
```r
# Count clonotypes found in library A, and B or C.
length(common_clonotypes(group1="A", group2=c("B","C"), data=clonotypes))

# Matrix of numbers of common clonotypes
common_clonotypes(data=clonotypes)

# Matrix of abundance of common clonotypes
common_clonotypes(data=clonotypes, mode="abundance")
```

---

**extdata**

*Extra data used to calculate ID numbers in Yassai et al.’s nomenclature.*

**Description**

Data frame derived from Table 1 of Yassai et al., 2009, to construct clonotype names.

**Details**

- **V_after_C**: sequence of the V segments after their conserved cystein.
- **J_before_FGxG**: sequence of the J segments before their conserved FGxG motif.
- **codon_ids**: data frame derived from Table 1 of Yassai et al., 2009, to construct clonotype names.

The `V_after_C` and `J_before_FGxG` tables are generated from the mouse reference data with the command: `make refresh-data` in the source repository of clonotypeR.

**Value**

- **codon_ids**:
  - **codon**: Nucleotide triplet.
  - **aminoacid**: Single-letter amino acid abbreviation (“O” for stop).
  - **id**: ID numbers assigned to the codons for each amino acids.

- **J_before_FGxG**:
  - **row name**: J segment name, for instance “TRAJ61”.
  - **sequence**: Sequence of the nucleic acids preceding the first codon of the conserved FGxG motif.

- **V_after_C**:
  - **row name**: V segment name, for instance “TRAV1”.
  - **sequence**: Sequence of the nucleic acids following the codon of the conserved cysteine.

**References**

is_unproductive

Description

Determines if clonotype sequences are productive.

Usage

is_unproductive(data)

Arguments

data

Data frame of clonotype sequences, or character vector describing a single clonotype, where the DNA sequence is available under the name “dna” and its translation available under the name “pep”. Clonotypes are marked unproductive if the length of their DNA sequence is not a multiple of 3, or if they contain a stop codon, as indicated by an asterisk in the translated sequence.

Details

ClonotypeR identifies V and J segments, isolates the DNA sequence between the conserved cystein and the FGxG motifs, and translates it. This function verifies that this sequence is in frame and has no stop codon.

Value

Logical vector, with one value per row in the original data.

See Also

read_clonotypes

Examples

clonotypes <- read_clonotypes(system.file('extdata', 'clonotypes.txt.gz', package = "clonotypeR"))
is_unproductive(clonotypes)
Description

List clonotypes found exclusively in one library.

Usage

private_clonotypes(..., data)

Arguments

... Library names.

data A clonotype table.

Value

A vector of clonotype names.

See Also

clonotype_table

Examples

clonotypes <- read_clonotypes(system.file('extdata', 'clonotypes.txt.gz', package = "clonotypeR"))
clonotypes <- clonotype_table(levels(clonotypes$lib), data=clonotypes)
private_clonotypes("C", data=clonotypes)

Description

Reads a clonotype_table and returns a data frame.

Usage

read_clonotypes(filename, scores = TRUE, ...)

Arguments

filename Path to the tabulation-delimited text file containing the extracted clonotypes.

scores Set to false to load legacy data that did not contain “score” and “mapq” columns.

... The rest of the arguments are passed to the read.table() function.
Details

Reads a clonotype_table in a TAB-separated or OSCT format, and returns a data frame that has eight columns, for library name, V and J segments names, sequence read identifier, DNA, sequence quality, aminoacid sequence of the CDR3 region, mark for unproductive recombinations, and mark for ambiguous sequences.

Value

lib       Library name (factor).
V         V segment name (factor).
J         J segment name (factor).
score     Alignment score (numeric).
mapq      Mapping quality (numeric). A sequence with a good alignment score will still have a low mapping quality if there are good alternative alignments to other V segments.
read      Sequence read identifier (character).
dna       DNA sequence of the CDR3 region (character).
qual      Quality values for the DNA sequence (character).
pep       Translation of the DNA sequence (character).
unproductive Flag indicating stop codons or frame shifts (logical).
ambiguous Flag indicating that the DNA sequences has ambiguous ("N") nucleotides (logical).

See Also

clonotype_table, is_unproductive, read.table, Order Switchable Column Table (OSCT, http://sourceforge.net/projects/osctf/)

Examples

clonotypes <- read_clonotypes(system.file( 'extdata', 'clonotypes.txt.gz' , package = "clonotypeR"))
yassai_identifier

Arguments

... One or more character vectors contain clonotype library names.
data The name of the clonotype_table where the data is stored.

Details

Finds all the clonotypes expressed in one or more libraries, and returns a vector where they are listed once. This vector can be used to subset a clonotype_table.

Value

Character vector of clonotype names. Their order follows the original row name order of the clonotype_table.

See Also

clonotype_table, common_clonotypes

Examples

# Load example data
clonotypes.long <- read_clonotypes(system.file("extdata", "clonotypes.txt.gz", package = "clonotypeR"))
clonotypes <- clonotype_table(levels(clonotypes.long$lib), data=clonotypes.long)
summary(clonotypes)

# List clonotypes found in library A.
unique_clonotypes("A", data=clonotypes)

# List clonotypes found in library A or B.
unique_clonotypes("A","B", data=clonotypes)

yassai_identifier yassai_identifier

Description

TCR clonotype identifier (Yassai et al.)

Usage

yassai_identifier(data, V_after_C, J_before_FGxG, long = FALSE)

## S4 method for signature 'character,data.frame,data.frame,ANY'
yassai_identifier(data, V_after_C, J_before_FGxG, long = FALSE)

## S4 method for signature 'ANY,missing,missing,ANY'
yassai_identifier(data, long)

## S4 method for signature 'data.frame,data.frame,data.frame,logical'
yassai_identifier(data, V_after_C, J_before_FGxG, long = FALSE)
**Arguments**

- **data**
  A data frame or a character vector containing a clonotype(s) with proper row or element names.

- **V_after_C** (optional)
  A data frame indicating the aminoacids following the conserved cysteine for each V segment.

- **J_before_FGxG** (optional)
  A data frame indicating the aminoacids preceding the conserved FGxG motif for each V segment.

- **long** (optional)
  Avoids identifier collisions by displaying the codons, and indicating the position of the V–J junction in ambiguous cases.

**Details**

The clonotype nomenclature defined by Yassai et al. in [http://dx.doi.org/10.1007/s00251-009-0383-x](http://dx.doi.org/10.1007/s00251-009-0383-x).

By default, `yassai_identifier()` assume mouse sequences and will load the V_after_C and J_before_FGxG tables distributed in this package. It is possible to provide alternative tables either by passing them directly as argument, or by installing them as `./inst/extdata/V_after_C.txt.gz` and `./inst/extdata/J_before_FGxG.txt.gz`.

Some clonotypes have a different DNA sequence but the same identifier following the original nomenclature (see below for examples). The ‘long’ mode was created to avoid these collisions. First, it displays all codons, instead of only the non-templated ones and their immediate neighbors. Second, for the clonotypes where all codons are identical to the V or J germline sequence, it indicates the position of the V–J junction in place of the codon IDs.

**Value**

The name (for instance sIRSSy.1456B19S1B27L11) consists of five segments:

1. CDR3 amino acid identifier (ex. sIRSSy), followed by a dot;
2. CDR3 nucleotide sequence identifier (ex. 1456);
3. variable (V) segment identifier (ex. BV19S1);
4. joining (J) segment identifier (ex. BJ2S7);
5. CDR3 length identifier (ex. L11).

**Methods (by class)**

- `data = character,V_after_C = data.frame,J_before_FGxG = data.frame,long = ANY: TCR clonotype identifier (Yassai et al.)`

- `data = ANY,V_after_C = missing,J_before_FGxG = missing,long = ANY: TCR clonotype identifier (Yassai et al.)`

- `data = data.frame,V_after_C = data.frame,J_before_FGxG = data.frame,long = logical: TCR clonotype identifier (Yassai et al.)`

**See Also**

`codon_ids, J_before_FGxG, V_after_C`
Examples

```r
clonotypes <- read_clonotypes(system.file('extdata', 'clonotypes.txt.gz', package = "clonotypeR"))
head(yassai_identifier(clonotypes))

# The following two clonotypes have a the same identifier, and are
disambiguated by using the long mode

yassai_identifier(c(V="TRAV14-1", J="TRAJ43", dna="GCAGCTATAAACAATGCCCCACGA", pep="AANNNAPR"))
# [1] "aAn.1A14-1A43L9"

yassai_identifier(c(V="TRAV14-1", J="TRAJ43", dna="GCAGCAGCTAAACAAATGCCCCACGA", pep="AAANNNAPR"))
# [1] "aAn.1A14-1A43L9"

yassai_identifier(c(V="TRAV14-1", J="TRAJ43", dna="GCAGCTATAAACAATGCCCCACGA", pep="AANNNAPR"), long=TRUE)
# [1] "aAnnnnapr.1A14-1A43L9"

yassai_identifier(c(V="TRAV14-1", J="TRAJ43", dna="GCAGCAGCTAAACAAATGCCCCACGA", pep="AAANNNAPR"), long=TRUE)
# [1] "aaAnnnnapr.1A14-1A43L9"

# The following two clonotypes would have the same identifier in long mode
# if the position of the V-J junction would not be indicated in place of the
# codon IDs.

yassai_identifier(c(V="TRAV14N-1", J="TRAJ56", dna="GCAGCTACTGGAGGGAATAATAAGCTGACT", pep="AATGGNNKLT"), long=TRUE)
# [1] "aatggnnklt.1A14N1A56L10"

yassai_identifier(c(V="TRAV14N-1", J="TRAJ56", dna="GCAGCAACTGGAGGGAATAATAAGCTGACT", pep="AATGGNNKLT"), long=TRUE)
# [1] "aatggnnklt.2A14N1A56L10"
```
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