

Package ‘immunotation’

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Type Package

Title Tools for working with diverse immune genes

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Description

MHC (major histocompatibility complex) molecules are cell surface complexes that present antigens to T cells. The repertoire of antigens presented in a given genetic background largely depends on the sequence of the encoded MHC molecules, and thus, in humans, on the highly variable HLA (human leukocyte antigen) genes of the hyperpolymorphic HLA locus. More than 28,000 different HLA alleles have been reported, with significant differences in allele frequencies between human populations worldwide. Reproducible and consistent annotation of HLA alleles in large-scale bioinformatics workflows remains challenging, because the available reference databases and software tools often use different HLA naming schemes. The package immunotation provides tools for consistent annotation of HLA genes in typical immunoinformatics workflows such as for example the prediction of MHC-presented peptides in different human donors. Converter functions that provide mappings between different HLA naming schemes are based on the MHC restriction ontology (MRO). The package also provides automated access to HLA alleles frequencies in worldwide human reference populations stored in the Allele Frequency Net Database.

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Contents

assemble_protein_complex	3
build_allele_group	3
check_geographics	4
check_hla_locus	4
check_hla_selection	5
check_population	5
check_sample_size	6
check_standard	6
create_encode_handle	7
decode_MAC	7
encode_MAC	8
extract_population_id	8
extract_population_info	9
extract_population_name	9
extract_sample_info	10
fetch_encoded_MAC	10
getURL	11
get_external_file	11
get_G_group	12
get_mhcpan_input	12
get_nb_pages	13
get_P_group	13
get_serotypes	14
get_valid_geographics	14
get_valid_organisms	15
human_protein_complex_table	15
load_mro	16
mro.obo	16
parse_allele_freq_html	16
parse_haplotype_freq_html	17
plot_allele_frequency	17
query_allele_frequencies	18
query_haplotype_frequencies	19
query_population_detail	20
read_complete_freq_table	20
read_population_detail	21
retrieve_chain_lookup_table	21
verify_parameters	22

Index

23

assemble_protein_complex	
	<i>Assemble protein complex</i>

Description

Assemble a table of MHC protein complexes for a given organism.

Usage

```
assemble_protein_complex(organism)
```

Arguments

organism	Organism for which the lookup should be built (e.g. "human", "mouse", ...). The list of valid organisms can be found using the function <code>get_valid_organisms</code>
----------	--

Value

a data frame with the MHC complexes annotated in MRO (only completely annotated complexes are returned)

Examples

```
assemble_protein_complex(organism = "mouse")
```

build_allele_group	<i>Building a list of alleles to cover</i>
--------------------	--

Description

build_allele_group e.g. A*01:01 -> A*01:01:01, A*01:01:02, A*01:01:03

Usage

```
build_allele_group(allele_selection)
```

Arguments

allele_selection	HLA allele for which the allele group should be built.
------------------	--

Value

list of alleles

Examples

```
build_allele_group("A*01:01")
```

check_geographics	<i>check_geographics, stops if input not adequate</i>
-------------------	---

Description

check_geographics, stops if input not adequate

Usage

```
check_geographics(country, region, ethnic)
```

Arguments

country	country used for allele frequency selection
region	geographical region used for allele frequency selection
ethnic	ethical origin used for allele frequency selection

Value

TRUE

check_hla_locus	<i>check_hla_locus, stops if input not adequate</i>
-----------------	---

Description

check_hla_locus, stops if input not adequate

Usage

```
check_hla_locus(hla_locus)
```

Arguments

hla_locus	locus of hla frequencies to query
-----------	-----------------------------------

Value

TRUE

check_hla_selection	<i>check_hla_selection, stops if input not adequate</i>
---------------------	---

Description

check_hla_selection, stops if input not adequate

Usage

```
check_hla_selection(hla_selection, query_type)
```

Arguments

hla_selection	HLA alleles used for selection
query_type	["allele" "haplotype"] type of AFND query

Value

TRUE

check_population	<i>check_population, stops if input not adequate</i>
------------------	--

Description

check_population, stops if input not adequate

Usage

```
check_population(hla_population)
```

Arguments

hla_population	population id
----------------	---------------

Value

TRUE

check_sample_size	<i>check_sample_size, stops if input not adequate</i>
-------------------	---

Description

check_sample_size, stops if input not adequate

Usage

check_sample_size(hla_sample_size_pattern, hla_sample_size)

Arguments

- hla_sample_size_pattern
one of "bigger_than", "equal", "less_than", "less_equal_than", "bigger_equal_than", "different"
- hla_sample_size
integer number used for population size

Value

TRUE

check_standard	<i>check_standard, stops if input not adequate</i>
----------------	--

Description

check_standard, stops if input not adequate

Usage

check_standard(standard)

Arguments

- standard
one of "a" - all, "s" - silver, "g" - gold

Value

TRUE

create_encode_handle	<i>create_encode_handle</i>
----------------------	-----------------------------

Description

create_encode_handle

Usage

create_encode_handle(allele_names)

Arguments

allele_names list of HLA alleles

Value

curl handle

decode_MAC	<i>Decode MAC</i>
------------	-------------------

Description

Decode a multiple allele code (MAC) into a list of HLA alleles. #' The National Marrow Donor Program (NMDP) uses [MAC](<https://bioinformatics.bethematchclinical.org/hla-resources/allele-codes/allele-code-lists/>) to facilitate the reporting and comparison of HLA alleles. MAC represent groups of HLA alleles and are useful when the HLA typing is ambiguous and does not allow to narrow down one single allele from a list of alleles.

Usage

decode_MAC(MAC)

Arguments

MAC multiple allele code (e.g. "A*01:ATJNV")

Value

list of HLA alleles

Examples

```
MAC <- "A*01:ATJNV"
decode_MAC(MAC)
```

encode_MAC

Encode MAC

Description

Encode a list of HLA alleles into multiple allele code (MAC). The National Marrow Donor Program (NMDP) uses [MAC](<https://bioinformatics.bethematchclinical.org/hla-resources/allele-codes/allele-code-lists/>) to facilitate the reporting and comparison of HLA alleles. MAC represent groups of HLA alleles and are useful when the HLA typing is ambiguous and does not allow to narrow down one single allele from a list of alleles.

Usage

```
encode_MAC(allele_list)
```

Arguments

allele_list list of HLA alleles (e.g. c("A*01:01:01", "A*02:01:01", "A*03:01"))

Value

encoded MAC

Examples

```
allele_list <- c("A*01:01:01", "A*02:01:01", "A*03:01")
encode_MAC(allele_list)
```

extract_population_id *extract_population_id*

Description

extract the population ids from the html result

Usage

```
extract_population_id(data)
```

Arguments

data html from AFND website

Value

population ids

extract_population_info
<i>extract_population_info</i>

Description

extract_population_info

Usage

extract_population_info(data)

Arguments

data html input page

Value

population information

extract_population_name
<i>extract_population_name</i>

Description

extract_population_name

Usage

extract_population_name(data)

Arguments

data html input page

Value

population name

extract_sample_info	<i>extract_sample_info</i>
---------------------	----------------------------

Description

extract_sample_info

Usage

extract_sample_info(data)

Arguments

data html input page

Value

sample information

fetch_encoded_MAC	<i>fetch_encoded_MAC</i>
-------------------	--------------------------

Description

fetch_encoded_MAC

Usage

fetch_encoded_MAC(handle)

Arguments

handle curl handle

Value

curl handle fetch

getURL	<i>getURL</i>
--------	---------------

Description

getURL

Usage

```
getURL(
  URL,
  N.TRIES = 2L,
  read_method = c("delim", "lines", "html"),
  skip = 0,
  delim = "\t",
  col_names = TRUE
)
```

Arguments

URL	Indicated the url that will be read
N.TRIES	Integer, how often should the function try to read the URL?
read_method	Method to be used for reading of URL content ("delim" -> readr::read_delim, "lines" -> readr::read_lines, "html" -> xml2::read_html)
skip	integer indicating how many lines to skip when reading URL
delim	pattern used for delim (passed to delim of read functions)
col_names	list of colnames to use

Value

returns a the content of the URL. The format of the return object depends on the read_method that was used.

get_external_file	<i>get_external_file</i>
-------------------	--------------------------

Description

get_external_file

Usage

```
get_external_file(file, skip = 0, delim = "\t", col_names = TRUE)
```

Arguments

file	Indicated the file that will be read
skip	integer indicating how many lines to skip when reading URL
delim	pattern used for delim (passed to delim of read functions)
col_names	list of colnames to use

Value

returns a the content of the file. The format of the return object depends on the read_method that was used.

get_G_group	<i>G groups</i>
-------------	-----------------

Description

Get the G groups for a list of HLA alleles. [G groups](http://hla.alleles.org/alleles/g_groups.html) are groups of HLA alleles that have identical nucleotide sequences across the exons encoding the peptide binding domains.

Usage

```
get_G_group(allele_list)
```

Arguments

allele_list List of alleles.

Value

Named list of G-groups the input alleles belong to.

Examples

```
allele_list <- c("DQB1*02:02:01", "DQB1*06:09:01")
get_G_group(allele_list)
```

get_mhcpan_input	<i>Get format for NetMHCpan tools</i>
------------------	---------------------------------------

Description

NetMHCpan tools for MHC-peptide binding prediction require HLA complex names in a specific format. get_mhcpan_input formats a list of HLA alleles into a list of NetMHC-formated complexes.

Usage

```
get_mhcpan_input(allele_list, mhc_class)
```

Arguments

allele_list list of HLA alleles (e.g. c("A*01:01:01", "B*27:01"))
 mhc_class ["MHC-I"|"MHC-II"] indicated which NetMHC you want to use.

Value

protein chain list as formatted for MHCpan input

Examples

```
allele_list <- c("A*01:01:01", "B*27:01")
get_mhcpan_input(allele_list, mhc_class = "MHC-I")
```

get_nb_pages	<i>get_nb_pages</i>
--------------	---------------------

Description

get_nb_pages

Usage

```
get_nb_pages(page_tbl)
```

Arguments

page_tbl html input page

Value

integer number of pages in the html input

get_P_group	<i>P groups</i>
-------------	-----------------

Description

Get the P groups for a list of HLA alleles. [P groups](http://hla.alleles.org/alleles/p_groups.html) are groups of HLA alleles that have identical protein sequences in the peptide binding domains.

Usage

```
get_P_group(allele_list)
```

Arguments

allele_list list of HLA alleles

Value

Named list of P-groups the input alleles belong to.

Examples

```
allele_list <- c("DQB1*02:02:01", "DQB1*06:09:01")
get_P_group(allele_list)
```

get_serotypes	<i>Serotypes</i>
---------------	------------------

Description

Get the serotypes of the MHC complexes encoded by a list of MHC alleles.

Usage

```
get_serotypes(allele_list, organism = "human", mhc_type)
```

Arguments

allele_list	List of allele
organism	Organism to be used for MRO lookup. If the organism does not match the given allele, a empty object is returned.
mhc_type	["MHC-I" or "MHC-II"] MHC class to use for MRO lookup.

Value

Named list of serotypes, which only contains complexes contained in the MRO. If no serotype is annotated for a given complex, the list element is NA.

Examples

```
allele_list <- c("A*01:01:01", "B*27:01")
get_serotypes(allele_list, mhc_type = "MHC-I")
```

get_valid_geographics	<i>get_valid_geographics</i>
-----------------------	------------------------------

Description

get a list of valid countries, regions and ethnic origins

Usage

```
get_valid_geographics()
```

Value

list of valid countries, regions and ethnic origin

get_valid_organisms	<i>get_valid_organisms</i>
---------------------	----------------------------

Description

get the list of organisms that are part of the MRO annotation

Usage

```
get_valid_organisms()
```

Value

list of organisms

Examples

```
get_valid_organisms()
```

human_protein_complex_table	<i>human_protein_complex_table</i>
-----------------------------	------------------------------------

Description

human_protein_complex_table

Usage

```
human_protein_complex_table
```

Format

An object of class data.frame with 12385 rows and 8 columns.

Details

human_protein_complex_table: human_protein_complex_table.

Examples

```
# The human protein complex table is available in the following
# exported variable
human_protein_complex_table
```

load_mro	<i>load_mro</i>
----------	-----------------

Description

load_mro

Usage

load_mro()

Value

MRO in ontology_index format

mro.obo	<i>MRO</i>
---------	------------

Description

mro.obo: MHC Restriction Ontology obo file.

Usage

mro.obo

Format

An object of class ontology_index of length 18.

parse_allele_freq_html	<i>parse_allele_freq_html</i>
------------------------	-------------------------------

Description

format the allele frequency table and select columns of interest

Usage

parse_allele_freq_html(allele_freq_table)

Arguments

allele_freq_table
allele frequency table parsed from AFND website

Value

allele_freq_table reformatted

```
parse_haplotype_freq_html
      parse_haplotype_freq_html
```

Description

format the haplotype frequency table and select columns of interest

Usage

```
parse_haplotype_freq_html(haplotype_freq_table)
```

Arguments

haplotype_freq_table
haplotype frequency table parsed from AFND website

Value

haplotype_freq_table reformatted

```
plot_allele_frequency Plotting allele frequencies
```

Description

plot_allele_frequency Generate a World map displaying the frequency of a given table of HLA alleles. Use the function [query_allele_frequencies](#) to generate a table with allele frequencies.

Usage

```
plot_allele_frequency(allele_frequency)
```

Arguments

allele_frequency
returned by [query_allele_frequencies](#)

Value

ggplot2 object displaying the allele frequencies on a world map.

Examples

```
# select frequency of given allele
sel_allele_freq <- query_allele_frequencies(hla_selection = "A*02:01",
hla_sample_size_pattern = "bigger_than",
hla_sample_size = 10000, standard="g")

plot_allele_frequency(sel_allele_freq)
```

```
query_allele_frequencies
```

Query allele frequencies

Description

Query allele frequencies

Usage

```
query_allele_frequencies(
  hla_locus = NA,
  hla_selection = NA,
  hla_population = NA,
  hla_country = NA,
  hla_region = NA,
  hla_ethnic = NA,
  hla_sample_size_pattern = NA,
  hla_sample_size = NA,
  standard = "a"
)
```

Arguments

hla_locus	HLA locus that will be used for filtering data. A, B, C, DPA1, DPB1, DQA1, DQB1, DRB1
hla_selection	Allele that will be used for filtering data. e.g. A*01:01
hla_population	Numeric identifier of the population that will be used for filtering. This identifier is defined by the Allele Frequency Net Database.
hla_country	Country of interest (e.g. Germany, France, ...).
hla_region	Geographic region of interest (e.g. Europe, North Africa, ...)
hla_ethnic	Ethnic origin of interest (e.g. Caucasoid, Siberian, ...)
hla_sample_size_pattern	Keyword used to define the filtering for a specific population size. e.g. "bigger_than", "equal", "less_than", "less_equal_than", "bigger_equal_than"
hla_sample_size	Integer number used to define the filtering for a specific population size, together with the hla_sample_size_pattern argument.
standard	Population standards, as defined in the package vignette. "g" - gold, "s" - silver, "a" - all

Value

data.frame object containing the result of the allele frequency query

Examples

```
# select frequencies of the A*02:01 allele,
# for gold standard population with more than 10,000 individuals
sel <- query_allele_frequencies(hla_selection = "A*02:01",
hla_sample_size_pattern = "bigger_than", hla_sample_size = 10000,
standard="g")
```

query_haplotype_frequencies

Query haplotype frequencies

Description

Query haplotype frequencies

Usage

```
query_haplotype_frequencies(
  hla_selection = NA,
  hla_population = NA,
  hla_country = NA,
  hla_region = NA,
  hla_ethnic = NA,
  hla_sample_size_pattern = NA,
  hla_sample_size = NA
)
```

Arguments

hla_selection	Alleles that will be used to build the haplotype query. One entry per locus. If no entry for a given locus, the function will search for haplotypes that do not include specifications for this locus. If any allele for a given locus should be considered, the list entry should be "A*" or other locus in same format.
hla_population	Numeric identifier of the population that will be used for filtering. This identifier is defined by the Allele Frequency Net Database.
hla_country	Country of interest (e.g. Germany, France, ...).
hla_region	Geographic region of interest (e.g. Europe, North Africa, ...)
hla_ethnic	Ethnic origin of interest (e.g. Caucasoid, Siberian, ...)
hla_sample_size_pattern	Keyword used to define the filtering for a specific population size. e.g. "bigger_than", "equal", "less_than", "less_equal_than", "bigger_equal_than"
hla_sample_size	Integer number used to define the filtering for a specific population size, together with the hla_sample_size_pattern argument.

Value

data.frame object containing the result of the allele frequency query

Examples

```
# works only for one haplotype at a time
query_haplotype_frequencies(hla_selection = c("A*02:01", "B*", "C*"),
hla_region = "Europe")
```

```
query_population_detail
```

Query population metainformation

Description

Query population metainformation

Usage

```
query_population_detail(population_ids)
```

Arguments

`population_ids` List of numeric identifiers of the population that will be used for filtering. The identifier is defined by the Allele Frequency Net Database.

Value

data.frame object containing the result of the population detail query

Examples

```
population_detail <- query_population_detail(0001986)
```

```
read_complete_freq_table
```

read_complete_freq_table

Description

read_complete_freq_table

Usage

```
read_complete_freq_table(url, type)
```

Arguments

`url` URL of the website containing frequency table
`type` ["allele"|"haplotype"]

Value

frequency table

`read_population_detail`*read_population_detail*

Description`read_population_detail`**Usage**`read_population_detail(url, population_id)`**Arguments**

<code>url</code>	url of the page containing population information
<code>population_id</code>	numeric population identifier

Value`population information`

`retrieve_chain_lookup_table`*Retrieve MHC chain lookup table*

Description`Retrieve MHC chain lookup table`**Usage**`retrieve_chain_lookup_table(organism)`**Arguments**

<code>organism</code>	name of organism (e.g. "human")
-----------------------	---------------------------------

Value`Table containing MHC chain information for the organism. It contains chain names, MHC restriction and protein sequence.`**Examples**`retrieve_chain_lookup_table("mouse")`

verify_parameters	<i>verify_parameters</i>
-------------------	--------------------------

Description

verify_parameters

Usage

```
verify_parameters(  
  hla_locus,  
  hla_selection,  
  hla_population,  
  hla_country,  
  hla_region,  
  hla_ethnic,  
  hla_sample_size_pattern,  
  hla_sample_size,  
  standard = "a",  
  query_type  
)
```

Arguments

- hla_locus locus of hla frequencies to query
- hla_selection HLA alleles used for selection
- hla_population population id
- hla_country country used for allele frequency selection
- hla_region geographical region used for allele frequency selection
- hla_ethnic ethical origin used for allele frequency selection
- hla_sample_size_pattern
 one of "bigger_than", "equal", "less_than", "less_equal_than", "bigger_equal_than", "different"
- hla_sample_size
 integer number used for population size
- standard one of "a" - all, "s" - silver, "g" - gold
- query_type "allele" or "haplotype"

Value

boolean to indicate, whether tests were passed

Index

* datasets

human_protein_complex_table, [15](#)

* internal

check_geographics, [4](#)
check_hla_locus, [4](#)
check_hla_selection, [5](#)
check_population, [5](#)
check_sample_size, [6](#)
check_standard, [6](#)
create_encode_handle, [7](#)
extract_population_id, [8](#)
extract_population_info, [9](#)
extract_population_name, [9](#)
extract_sample_info, [10](#)
fetch_encoded_MAC, [10](#)
get_external_file, [11](#)
get_nb_pages, [13](#)
get_valid_geographics, [14](#)
getURL, [11](#)
load_mro, [16](#)
mro.obo, [16](#)
parse_allele_freq_html, [16](#)
parse_haplotype_freq_html, [17](#)
read_complete_freq_table, [20](#)
read_population_detail, [21](#)
verify_parameters, [22](#)

assemble_protein_complex, [3](#)

build_allele_group, [3](#)

check_geographics, [4](#)
check_hla_locus, [4](#)
check_hla_selection, [5](#)
check_population, [5](#)
check_sample_size, [6](#)
check_standard, [6](#)
create_encode_handle, [7](#)

decode_MAC, [7](#)

encode_MAC, [8](#)
extract_population_id, [8](#)
extract_population_info, [9](#)
extract_population_name, [9](#)

extract_sample_info, [10](#)

fetch_encoded_MAC, [10](#)

get_external_file, [11](#)
get_G_group, [12](#)
get_mhcpan_input, [12](#)
get_nb_pages, [13](#)
get_P_group, [13](#)
get_serotypes, [14](#)
get_valid_geographics, [14](#)
get_valid_organisms, [15](#)
getURL, [11](#)

human_protein_complex_table, [15](#)

load_mro, [16](#)

mro.obo, [16](#)

parse_allele_freq_html, [16](#)
parse_haplotype_freq_html, [17](#)
plot_allele_frequency, [17](#)

query_allele_frequencies, [17](#), [18](#)
query_haplotype_frequencies, [19](#)
query_population_detail, [20](#)

read_complete_freq_table, [20](#)

read_population_detail, [21](#)

retrieve_chain_lookup_table, [21](#)

verify_parameters, [22](#)