Package ‘mhc nuggets’

October 13, 2022

Title Call MHCnuggets
Version 1.1
Maintainer Richèl J.C. Bilderbeek <richel@richelbilderbeek.nl>
Description MHCnuggets (<https://github.com/KarchinLab/mhc nuggets>) is a Python tool to predict MHC class I and MHC class II epitopes. This package allows one to call MHCnuggets from R.
License GPL-3
Imports rappdirs, reticulate, stringr, tibble
Suggests knitr, testthat, rmarkdown
Encoding UTF-8
LazyData true
RoxygenNote 7.1.1
URL https://github.com/richelbilderbeek/mhcnuggets/
BugReports https://github.com/richelbilderbeek/mhcnuggets
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are_mhcnuggets_names  Are these MHCnuggets names?

Description
Determine if an HLA haplotype name follow the name format that MHCnuggets uses internally

Usage
are_mhcnuggets_names(mhcs)

Arguments
mhcs  the MHC haplotype names

Value
a vector of booleans, TRUE for HLA haplotypes that follow the MHCnuggets naming convention

Examples
if (is_mhcnuggets_installed()) {
  are_mhcnuggets_names(get_mhc_1_haplotypes())
  are_mhcnuggets_names(get_mhc_2_haplotypes())
}

check_mhcnuggets_installation

Check if MHCnuggets is installed.

Description
Check if MHCnuggets is installed. Will stop if not.

Usage
check_mhcnuggets_installation(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments
folder_name  superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share
by default, as can be obtained by get_default_mhcnuggets_folder
mhcnuggets_url  URL to the MHCnuggets GitHub repository
**Details**

An MHCnuggets installation has two parts:

1. The installation of the Python package, for running the code
2. The download of the Python source code, which allows the use of example files

**Value**

Nothing.

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```r
if (is_mhcnuggets_installed()) {
    check_mhcnuggets_installation()
}
```

---

**check_mhcnuggets_options**

*Check the MHCnuggets options.*

---

**Description**

Check the MHCnuggets options. Will stop if the options are invalid.

**Usage**

```r
check_mhcnuggets_options(mhcnuggets_options)
```

**Arguments**

- `mhcnuggets_options` options to run MHCnuggets with, as can be created by `create_mhcnuggets_options`.

**Note**

An `mhcnuggets_options` created by `create_mhcnuggets_options` is always checked by `check_mhcnuggets_options`.

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```r
if (is_mhcnuggets_installed()) {
    check_mhcnuggets_options(create_test_mhcnuggets_options())
}
```
check_mhcnuggets_options_names

Check the names of the elements in an mhcnuggets_options list.

Description

Check the names of the elements in an mhcnuggets_options list. Will stop if an element is missing.

Usage

check_mhcnuggets_options_names(mhcnuggets_options)

Arguments

mhcnuggets_options

options to run MHCnuggets with, as can be created by create_mhcnuggets_options.

Author(s)

Richèl J.C. Bilderbeek

Examples

if (is_mhcnuggets_installed()) {
  check_mhcnuggets_options_names(
    create_test_mhcnuggets_options()
  )
}

check_mhc_class

Check the MHC class.

Description

Check the MHC class. Will stop if it is invalid.

Usage

check_mhc_class(mhc_class)

Arguments

mhc_class

MHC class. Must be I, II or NA. Use NA to let the class be deduced automatically.
create_mhcnuggets_options

Create a set of MHCnuggets options.

Description

Create a set of options to run MHCnuggets with.

Usage

create_mhcnuggets_options(
  mhc_class = NA,
  mhc, 
  ba_models = FALSE,
  verbose = FALSE,
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments

mhc_class MHC class. Must be I, II or NA. Use NA to let the class be deduced automatically
mhc the MHC haplotype name
ba_models Set to TRUE to use a pure BA model
verbose set to TRUE for more debug information
folder_name superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder
mhcnuggets_url URL to the MHCnuggets GitHub repository

Details

This function will give an error message if the arguments are invalid.
Value

an mhcnuggets_options

Note

an mhcnuggets_options created by create_mhcnuggets_options is always checked by check_mhcnuggets_options

Author(s)

Richèl J.C. Bilderbeek

See Also

use create_test_mhcnuggets_options to create an MHCnuggets object for testing

Examples

```r
if (is_mhcnuggets_installed()) {
    create_mhcnuggets_options(
        mhc = "HLA-A02:01"
    )
}
```

---

**create_temp_peptides_path**

Create a path to a non-existing temporary file

**Description**

Create a path to a non-existing temporary file

**Usage**

```r
create_temp_peptides_path(fileext = ".fasta")
```

**Arguments**

- `fileext` file extension

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```r
create_temp_peptides_path()
```
create_test_mhcnuggets_options

Create testing options for MHCnuggets

Description

Create a set of testing options to run MHCnuggets with. The most important setting is the use of a specific haplotype.

Usage

```r
create_test_mhcnuggets_options(
  mhc_class = NA,
  mhc = "HLA-A02:01",
  ba_models = FALSE,
  verbose = FALSE,
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)
```

Arguments

- `mhc_class`: MHC class. Must be I, II or NA. Use NA to let the class be deduced automatically.
- `mhc`: the MHC haplotype name
- `ba_models`: Set to TRUE to use a pure BA model
- `verbose`: set to TRUE for more debug information
- `folder_name`: superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by `get_default_mhcnuggets_folder`
- `mhcnuggets_url`: URL to the MHCnuggets GitHub repository

Author(s)

Richèl J.C. Bilderbeek

Examples

```r
if (is_mhcnuggets_installed()) {
  create_test_mhcnuggets_options()
}
```
null
**downgrade_pip**

protein_sequence  
protein sequence, in uppercase, for example FAMILYVW

verbose  
set to TRUE for more debug information

**Note**

This is an internal function, so it should be marked with @noRd. This is not done, as this will disallow all functions to find the documentation parameters

**Author(s)**

Richèl J.C. Bilderbeek

---

**Description**

Set the version of pip to a specific earlier version.

**Usage**

```r
downgrade_pip(version = "9.0.0")
```

**Arguments**

- `version`: pip version

**Value**

Nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

use `upgrade_pip` to set pip to the latest version. Use `set_pip_version` to install a specific version of pip

**Examples**

```r
## Not run:
if (is_pip_installed()) {
  downgrade_pip()
}
## End(Not run)
```
get_default_mhcnuggets_folder

Get the path to the folder where this package installs MHCnuggets by default

Description
Get the path to the folder where this package installs MHCnuggets by default

Usage
get_default_mhcnuggets_folder()

Value
the path to the folder where this package installs MHCnuggets by default

Author(s)
Richèl J.C. Bilderbeek

Examples
get_default_mhcnuggets_folder()

get_example_filename

Get the full path to an MHCnuggets example file

Usage
get_example_filename(
  filename = "test_peptides.peps",
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments
filename name of the example file, without the path
folder_name superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder
mhcnuggets_url URL to the MHCnuggets GitHub repository
get_example_filenames

Value
the full path to an MHCnuggets example file

Author(s)
Richèl J.C. Bilderbeek

See Also
use get_example_filenames to get all MHCnuggets example filenames

Examples
if (is_mhcnuggets_installed()) {
  get_example_filename("test_peptides.peps")
}

get_example_filenames  Get the full path to all MHCnuggets example files

Description
Get the full path to all MHCnuggets example files

Usage
get_example_filenames(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments
folder_name  superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder
mhcnuggets_url  URL to the MHCnuggets GitHub repository

Value
a character vector with all MHCnuggets example files

Author(s)
Richèl J.C. Bilderbeek

See Also
use get_example_filename to get the full path to a MHCnuggets example file
Examples

```r
if (is_mhcnuggets_installed()) {
  get_example_filenames()
}
```

---

**get_mhcnuggets_url**  
*Get the URL of the MHCnuggets source code*

**Description**

Get the URL of the MHCnuggets source code

**Usage**

```r
get_mhcnuggets_url()
```

**Value**

a string that is a URL

**Author(s)**

Richèl J.C. Bilderbeek

--

**get_mhcnuggets_version**  
*Get the MHCnuggets version*

**Description**

Get the MHCnuggets version

**Usage**

```r
get_mhcnuggets_version(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)
```
Arguments

folder_name superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by `get_default_mhcnuggets_folder`

mhcnuggets_url URL to the MHCnuggets GitHub repository

Value

a string that is a version, for example 2.3.2

Author(s)

Richèl J.C. Bilderbeek

Examples

```r
if (is_mhcnuggets_installed()) {
  get_mhcnuggets_version()
}
```

---

get_mhc_1_haplotypes Get all the MHC-I haplotypes

---

Description

Get all the MHC-I haplotypes that MHCnuggets has been trained upon.

Usage

```r
get_mhc_1_haplotypes(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)
```

Value

a character vector with haplotype names in MHCnuggets format

Author(s)

Richèl J.C. Bilderbeek
get_mhc_2_haplotypes

Examples

if (is_mhcnuggets_installed()) {
  get_mhc_2_haplotypes()
}

get_mhc_2_haplotypes  Get all the MHC-II haplotypes

Description

Get all the MHC-II haplotypes that MHChnuggets has been trained upon.

Usage

get_mhc_2_haplotypes(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments

folder_name  superfolder of MHChnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder

mhcnuggets_url  URL to the MHChnuggets GitHub repository

Value

a character vector with haplotype names in MHChnuggets format

Author(s)

Richèl J.C. Bilderbeek

Examples

if (is_mhcnuggets_installed()) {
  get_mhc_2_haplotypes()
}
get_pip_version

*Get the version of pip*

**Description**

Get the version of pip

**Usage**

```r
get_pip_version()
```

**Value**

a string that is a version, for example 20.2

**Author(s)**

Richôté J.C. Bilderbeek

**Examples**

```r
if (is_pip_installed()) {
  get_pip_version()
}
```

get_python_package_versions

*Get the version of all Python packages*

**Description**

Get the version of all Python packages

**Usage**

```r
get_python_package_versions()
```

**Value**

a tibble with two columns: (1) package, the name of the package, for example absl-py, (2) version, the version of that package, for example 0.9.0

**Author(s)**

Richôté J.C. Bilderbeek
get_trained_mhc_1_haplotypes

Examples

```r
if (rappdirs::app_dir()$os != "win" && is_pip_installed()) {
  get_python_package_versions()
}
```

Description

Get all the MHC-I haplotypes that have been trained on a model

Usage

```r
get_trained_mhc_1_haplotypes(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)
```

Arguments

- `folder_name` superfolder of MHChnuggets. The name of the superfolder is `/home/[user_name]/.local/share` by default, as can be obtained by `get_default_mhcnuggets_folder`
- `mhcnuggets_url` URL to the MHChnuggets GitHub repository

Value

- a character vector with haplotype names in MHChnuggets format

Author(s)

Richèl J.C. Bilderbeek

Examples

```r
if (is_mhcnuggets_installed()) {
  get_trained_mhc_1_haplotypes()
}
```
get_trained_mhc_2_haplotypes

Get all the MHC-II haplotypes that have been trained on a model

Description
Get all the MHC-II haplotypes that have been trained on a model

Usage
get_trained_mhc_2_haplotypes(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments
folder_name superfolder of MHChnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder
mhcnuggets_url URL to the MHChnuggets GitHub repository

Value
a character vector with haplotype names in MHChnuggets format

Author(s)
Richèl J.C. Bilderbeek

Examples
if (is_mhcnuggets_installed()) {
  get_trained_mhc_2_haplotypes()
}

install_mhcnuggets

Install the MHChnuggets Python package.

Description
Install the MHChnuggets Python package.
install_pip

Usage

install_pip()

Value

Nothing

Author(s)

Richèl J.C. Bilderbeek

install_mhcnuggets

Usage

install_mhcnuggets(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)

Arguments

folder_name superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder

mhcnuggets_url URL to the MHCnuggets GitHub repository

Value

Nothing

Author(s)

Richèl J.C. Bilderbeek

Examples

## Not run:
install_mhcnuggets()

## End(Not run)
is_mhcnuggets_installed

Check if MHCnuggets is installed

### Description

Check if MHCnuggets is installed

### Usage

```r
is_mhcnuggets_installed(
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)
```

### Arguments

- `folder_name` superfolder of MHCnuggets. The name of the superfolder is `/home/[user_name]/.local/share` by default, as can be obtained by `get_default_mhcnuggets_folder`
- `mhcnuggets_url` URL to the MHCnuggets GitHub repository

### Value

TRUE if MHCnuggets is installed

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```r
is_mhcnuggets_installed()
```
is_mhcnuggets_name  Is this an MHCnuggets name?

Description
Determine if an HLA haplotype name follow the name format that MHCnuggets uses internally

Usage
is_mhcnuggets_name(mhc)

Arguments
mhc  the MHC haplotype name

Value
TRUE if the name follows the MHCnuggets naming convention

Examples
# The official name is not the name format used by MHCnuggets
is_mhcnuggets_name("HLA-A*01:01")

# MHCnuggets uses names without the asterisk
is_mhcnuggets_name("HLA-A01:01")

is_mhcnuggets_options  Is this a mhcnuggets_options?

Description
Determine if the MHCnuggets options is valid.

Usage
is_mhcnuggets_options(mhcnuggets_options)

Arguments
mhcnuggets_options  options to run MHCnuggets with, as can be created by create_mhcnuggets_options.

Value
TRUE if this a valid set of MHCnuggets options
**is_on_appveyor**

Determines if the environment is AppVeyor

**Usage**

```r
is_on_appveyor()
```

**Value**

TRUE if run on AppVeyor, FALSE otherwise

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```r
is_on_appveyor()
```

---

**is_on_ci**

Determines if the environment is a continuous integration service

**Usage**

```r
is_on_ci()
```

**Value**

TRUE if run on AppVeyor or Travis CI, FALSE otherwise

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```r
is_on_ci()
```
**is_on_travis**

**Author(s)**
Richèl J.C. Bilderbeek

**Examples**

```r
is_on_ci()
```

---

**is_on_travis**

*Determine if the environment is Travis CI*

**Description**

Determines if the environment is Travis CI

**Usage**

```r
is_on_travis()
```

**Value**

TRUE if run on Travis CI, FALSE otherwise

**Author(s)**
Richèl J.C. Bilderbeek

**Examples**

```r
is_on_travis()
```

---

**is_pip_installed**

*Determine if pip is installed*

**Description**

Determine if pip is installed

**Usage**

```r
is_pip_installed()
```

**Value**

TRUE if pip is installed, FALSE otherwise
Author(s)

Richèl J.C. Bilderbeek

Examples

```r
is_pip_installed()
```

| mhcnuggetsr | mhcnuggetsr: estimate the topology of membrane proteins |

Description

Proteins reside in either the cell plasma or in the cell membrane. A membrane protein goes through the membrane at least once. There are multiple ways to span this hydrophobic layer. One common structure is the transmembrane (alpha) helix (TMH). Given the amino acid sequence of a membrane protein, this package predicts which parts of the protein are TMHs

Author(s)

Richèl J.C. Bilderbeek

Examples

```r
if (is_mhcnuggets_installed()) {
    peptides_path <- get_example_filename("test_peptides.peps")
    mhc_1_haplotype <- "HLA-A02:01"
    mhcnuggets_options <- create_mhcnuggets_options(
        mhc = mhc_1_haplotype
    )
    predict_ic50_from_file(
        peptides_path = peptides_path,
        mhcnuggets_options = mhcnuggets_options
    )
}
```
Create a mhcnuggetsr report, to be used when reporting bugs

Usage

mhcnuggetsr_report(
    folder_name = get_default_mhcnuggets_folder(),
    mhcnuggets_url = get_mhcnuggets_url()
)

Arguments

folder_name superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder

mhcnuggets_url URL to the MHCnuggets GitHub repository

Author(s)

Richèl J.C. Bilderbeek

Examples

## Not run:

mhcnuggetsr_report()

## End(Not run)

Self-test the package

Usage

mhcnuggetsr_self_test(mhcnuggets_options = create_test_mhcnuggets_options())

Arguments

mhcnuggets_options options to run MHCnuggets with, as can be created by create_mhcnuggets_options.
predict_ic50

Predict the IC50 for peptides.

Description

Predict the half maximal inhibitory concentration (aka IC50) (in nM) for one or more peptides. Each peptide must be 15 amino acids at most (use predict_ic50s to predict the IC50s for longer peptides)

Usage

predict_ic50(
  mhcnuggets_options,
  peptides,
  peptides_path = create_temp_peptides_path()
)

Arguments

mhcnuggets_options
  options to run MHCnuggets with, as can be created by create_mhcnuggets_options.

peptides
  one of more peptide sequences

peptides_path
  the path to the peptides

Value

a tibble with two columns: (1) peptide, which holds the peptide sequence, and (2) ic50, which holds the predicted IC50

Note

this function uses a temporary file, because MHCnuggets reads its input from file. This temporary file is deleted after this function passed successfully.

Author(s)

Richèl J.C. Bilderbeek
Examples

```r
if (is_mhcnuggets_installed()) {

    peptides <- c("AIAACAMLLV", "ALVCYIVMPV", "ALEPRKEIDV")
    mhc_1 haplotype <- "HLA-A02:01"

    mhcnuggets_options <- create_mhcnuggets_options(
        mhc = mhc_1 haplotype
    )

    predict_ic50(
        peptides = peptides,
        mhcnuggets_options = mhcnuggets_options
    )
}
```

---

**predict_ic50s**

**Description**

Predict the half maximal inhibitory concentrations (aka IC50s) (in nM) of all possible n-mers within a peptide

**Usage**

```r
predict_ic50s(
    protein_sequence,
    peptide_length,
    mhcnuggets_options,
    peptides_path = create_temp_peptides_path()
)
```

**Arguments**

- `protein_sequence`: protein sequence, in uppercase, for example FAMILYVW
- `peptide_length`: length of a peptide, in number of amino acids
- `mhcnuggets_options`: options to run MHCnuggets with, as can be created by `create_mhcnuggets_options`
- `peptides_path`: the path to the peptides
predict_ic50_from_file

Value

A tibble with columns:

- peptide the peptide fragment, each of length peptide_length
- ic50 the predicted IC50 (in nM)

Author(s)

Richèl J.C. Bilderbeek

Examples

```r
if (is_mhcnuggets_installed()) {
  mhcnuggets_options <- create_mhcnuggets_options(  
    mhc = "HLA-A02:01"
  )

  predict_ic50s(  
    protein_sequence = "AIAACAMLLVCCCCCC",  
    peptide_length = 13,  
    mhcnuggets_options = mhcnuggets_options
  )
}
```

---

**predict_ic50_from_file**

*Predict the half maximal inhibitory concentration (aka IC50) (in nM) for one or more peptides as saved in a file. Each peptide must be 15 amino acids at most (use predict_ic50s to predict the IC50s for longer peptides)*

**Usage**

```r
predict_ic50_from_file(  
  mhcnuggets_options,  
  peptides_path,  
  mhcnuggets_output_filename = mhcnuggetsr::create_temp_peptides_path(fileext = ".csv")
)
```
set_is_mhcnuggets_installed

Arguments

mhcnuggets_options
  options to run MHCnuggets with, as can be created by create_mhcnuggets_options.

peptides_path
  the path to the peptides

mhcnuggets_output_filename
  path to a temporary file to write the MHCnuggets results to. This file will be
  deleted at the end of the function if it passes successfully.

Author(s)

Richèl J.C. Bilderbeek

Examples

if (is_mhcnuggets_installed()) {
  peptides_path <- get_example_filename("test_peptides.peps")
  mhc_1_haplotype <- "HLA-A02:01"
  mhcnuggets_options <- create_mhcnuggets_options(
    mhc = mhc_1_haplotype
  )
  predict_ic50_from_file(
    peptides_path = peptides_path,
    mhcnuggets_options = mhcnuggets_options
  )
}

set_is_mhcnuggets_installed

  Set the MHCnuggets installation state to the desired one

Description

Set the MHCnuggets installation state to the desired one

Usage

set_is_mhcnuggets_installed(
  is_installed,
  verbose = FALSE,
  folder_name = get_default_mhcnuggets_folder(),
  mhcnuggets_url = get_mhcnuggets_url()
)
set_pip_version

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>is_installed</td>
<td>the desired installation state. Must be TRUE or FALSE</td>
</tr>
<tr>
<td>verbose</td>
<td>set to TRUE for more debug information</td>
</tr>
<tr>
<td>folder_name</td>
<td>superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by <code>get_default_mhcnuggets_folder</code></td>
</tr>
<tr>
<td>mhcnuggets_url</td>
<td>URL to the MHCnuggets GitHub repository</td>
</tr>
</tbody>
</table>

Value

Nothing

Author(s)

Richèl J.C. Bilderbeek

Description

Set the version of pip to a specific version, by installing that version.

Usage

`set_pip_version(version)`

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>version</td>
<td>pip version</td>
</tr>
</tbody>
</table>

Value

Nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

use `upgrade_pip` to set pip to the latest version. Use `downgrade_pip` to set pip to a specific earlier version.
to_mhcnuggets_name

Examples

```r
## Not run:
if (is_pip_installed()) {
  set_pip_version("19.0")
}
```

## End(Not run)

---

to_mhcnuggets_name  Convert a standard haplotype name to the MHCnuggets name

Description

Convert a standard haplotype name to the MHCnuggets name. Will stop if this conversion fails.

Usage

```r
to_mhcnuggets_name(mhc)
```

Arguments

- `mhc`: the MHC haplotype name

Value

the MHCnuggets name for the haplotype

Author(s)

Richèl J.C. Bilderbeek

Examples

```r
to_mhcnuggets_name("HLA-A*01:01")
```
to_mhcnuggets_names

Convert one or more standard haplotype name to the MHCnuggets names

Description

Convert one or more standard haplotype names to the MHCnuggets names. Will stop if this conversion fails.

Usage

to_mhcnuggets_names(mhcs)

Arguments

mhcs the MHC haplotype names

Value

the MHCnuggets names for the haplotypes

Author(s)

Richèl J.C. Bilderbeek

Examples

to_mhcnuggets_names("HLA-A*01:01")

uninstall_mhcnuggets

Uninstall the MHCnuggets Python package.

Description

Uninstall the MHCnuggets Python package.

Usage

uninstall_mhcnuggets(
    folder_name = get_default_mhcnuggets_folder(),
    mhcnuggets_url = get_mhcnuggets_url()
)
Arguments

folder_name  superfolder of MHCnuggets. The name of the superfolder is /home/[user_name]/.local/share by default, as can be obtained by get_default_mhcnuggets_folder

mhcnuggets_url  URL to the MHCnuggets GitHub repository

Author(s)

Richèl J.C. Bilderbeek

---

uninstall_pip  

Install pip.

Description

Install pip.

Usage

uninstall_pip()

Value

Nothing

Author(s)

Richèl J.C. Bilderbeek

Examples

## Not run:

uninstall_pip()

## End(Not run)
**upgrade_pip**

Upgrade pip.

### Description
Upgrade pip.

### Usage
`upgrade_pip()`

### Value
Nothing

### Author(s)
Richèl J.C. Bilderbeek

### See Also
Use `downgrade_pip` to set pip to an earlier version. Use `set_pip_version` to install a specific version of pip.

### Examples
```r
## Not run:
install_pip()
```

## End(Not run)
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