Package ‘mhcнуggetsr’

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Title Call MHCnuggets
Version 1.1
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Description MHCnuggets (<https://github.com/KarchinLab/mhcнуggets>) 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
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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

`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

Value
Nothing.

Author(s)
Richèl J.C. Bilderbeek

Examples
check_mhc_class("I")
check_mhc_class("II")
check_mhc_class(NA)

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.
create_temp_peptides_path

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

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

create_temp_peptides_path(fileext = ".fasta")

Arguments

fileext file extension

Author(s)

Richèl J.C. Bilderbeek

Examples

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()
}
```
This function does nothing. It is intended to inherit the documentation of the parameters from.

Usage

```r
default_params_doc(
  ba_models,
  folder_name,
  mhc,
  mhcs,
  mhc_class,
  mhcnuggets_options,
  mhcnuggets_url,
  n_aas,
  peptide,
  peptides,
  peptide_length,
  peptides_path,
  protein_sequence,
  verbose
)
```

Arguments

- **ba_models** : Set to TRUE to use a pure BA model
- **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`
- **mhc** : the MHC haplotype name
- **mhcs** : the MHC haplotype names
- **mhc_class** : MHC class. Must be I, II or NA. Use NA to let the class be deduced automatically
- **mhcnuggets_options** : options to run MHCnuggets with, as can be created by `create_mhcnuggets_options`
- **mhcnuggets_url** : URL to the MHCnuggets GitHub repository
- **n_aas** : number of amino acids
- **peptide** : one peptide sequence
- **peptides** : one of more peptide sequences
- **peptide_length** : length of a peptide, in number of amino acids
- **peptides_path** : the path to the peptides
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

downgrade_pip  Downgrade pip.

Description
Set the version of pip to a specific earlier version.

Usage
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
## 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

Description
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
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
```r
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
```r
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
get_mhcnuggets_url

Examples
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
get_mhcnuggets_url()

Value
a string that is a URL

Author(s)
Richèl J.C. Bilderbeek

Examples
get_mhcnuggets_url()

get_mhcnuggets_version
Get the MHcnuggets version

Description
Get the MHcnuggets version

Usage
get_mhcnuggets_version(
    folder_name = get_default_mhcnuggets_folder(),
    mhcnuggets_url = get_mhcnuggets_url()
)
get_mhc_1_haplotypes

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

  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

  get_mhc_1_haplotypes(
    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 haplotype names in MHCnuggets format

Author(s)

  Richèl J.C. Bilderbeek
get_mhc_2_haplotypes

Examples

```r
if (is_mhcnuggets_installed()) {
  get_mhc_2_haplotypes()
}
```

Description

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

Usage

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

Arguments

- `folder_name` superfolder of MHCluggets. 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 MHCluggets GitHub repository

Value

- a character vector with haplotype names in MHCluggets format

Author(s)

Richèl J.C. Bilderbeek

Examples

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

*Description*
Get the version of pip

*Usage*
get_pip_version()

*Value*
a string that is a version, for example 20.2

*Author(s)*
Richèl J.C. Bilderbeek

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

get_python_package_versions

*Description*
Get the version of all Python packages

*Usage*
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)*
Richèl J.C. Bilderbeek
get_trained_mhc_1_haplotypes

Examples

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

get_trained_mhc_1_haplotypes

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

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_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)

install_pip

Install pip.

Description

Install pip.

Usage

install_pip()

Value

Nothing

Author(s)

Richèl J.C. Bilderbeek
is_mhcnuggets_installed

Check if MHCnuggets is installed

Description

Check if MHCnuggets is installed

Usage

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

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.
Author(s)  
Richèl J.C. Bilderbeek

Examples  
```r  
if (is_mhcnuggets_installed()) {  
is_mhcnuggets_options(create_test_mhcnuggets_options())  
}  
```

---

**is_on_appveyor**  
*Determine if the environment is AppVeyor*

Description  
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**  
*Determine if the environment is a continuous integration service*

Description  
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
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

---

**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

**Description**
Create a `mhcnuggetsr` report, to be used when reporting bugs

**Usage**
```r
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**
```r
## Not run:
mhcnuggetsr_report()

## End(Not run)
```

Self-test the package

**Description**
Self-test the package

**Usage**
```r
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

Author(s)
Richêl J.C. Bilderbeek

Examples
if (is_mhcnuggets_installed()) {
    mhcnuggetsr_self_test()
}

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)
Richêl J.C. Bilderbeek
predict_ic50s

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

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

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
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

if (is_mhcnuggets_installed()) {

mhcnuggets_options <- create_mhcnuggets_options(
    mhc = "HLA-A02:01"
)

predict_ic50s(
    protein_sequence = "AIAACAMLLVCCCCC",
    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

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**

- `is_installed` the desired installation state. Must be **TRUE** or **FALSE**
- `verbose` set to **TRUE** for more debug information
- `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_mhchnuggets_folder`
- `mhchnuggets_url` URL to the MHChnuggets GitHub repository

**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**

- `version` pip version

**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.
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()
)
install_pip

Arguments

folder_name superfolder of MHCanuggets. 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 MHCanuggets GitHub repository

Author(s)

Richél J.C. Bilderbeek

Description

Install pip.

Usage

uninstall_pip()

Value

Nothing

Author(s)

Richél J.C. Bilderbeek

Examples

## Not run:
uninstall_pip()

## End(Not run)
upgrade_pip

Uograde pip.

Description

Uograde 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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