

Package ‘mycobacrV’

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Type Package

Title Integrative immunoinformatics for Mycobacterial diseases in R platform

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Author Deepika Kulshreshtha, Rupanjali Chaudhuri, Dr. S. Ramachandran

Maintainer Dr. S. Ramachandran<ramu@igib.in>

Description The mycobacrV package contains utilities to provide detailed information for B cell and T cell epitopes for predicted adhesins from various servers such as ABCpred, Bcepred, Bimas, Propred, NetMHC and IEDB. Please refer to the URL below for more information.

Depends R (>= 2.15), methods

Collate 'iedb_consensus_mhci_nmer.R' 'abcpred_nmer.R' 'algpred.R'
'allermatch.R' 'bcepred_nmer.R' 'bimas_nmer.R' 'filter.firstlayer.R' 'iedb_arb_mhcii_nmer.R'
'iedb_consensus_mhcii_nmer.R' 'netmhcNN_nmer.R'
'netmhcWT_nmer.R' 'propred_nmer.R' 'iedb_arb_mhci_nmer.R' 'zzz.R'

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abcpred_nmer

Epitope prediction from ABCpred server

Description

abcpred_nmer is a method to get information of epitopes from ABCPred server

Usage

```
abcpred_nmer(epi_length)
```

Arguments

epi_length A character vector of epitope length

Details

This function takes epitope length as input into epi_length object. ABCPred server provide epitopes by selecting window size of epitope length such as 10, 12, 14, 16, 18, 20. Therefore epi_length should be given as "10mer".

Value

abcpred_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope that shows orthologs of H37Rv containing that epitope

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: abcpred_nmer("10mer")##Here abcpred_nmer will provide conservation of epitope
```

algpred*Filter Allergic/Non Allergic proteins using output of Algpred*

Description

algpred is a function to filter allergic and non allergic proteins of an organism using output of Algpred

Usage

```
algpred(xz, organism, ginumber, prediction)
```

Arguments

xz	Object containing tabular output from Algpred
organism	A character vector specifying name of species present in second column of xz
ginumber	A numeric vector specifying ginumber of protein for a species for which allergic property is to be predicted
prediction	A character vector specifying "Allergen" or "Non Allergen"

Details

This function takes tabular output of Algpred in xz as input. Using arguments organism, ginumber and prediction algpred() filters xz. Default value for ginumber is "ALL" and for prediction is "Non Allergen"

Value

A file of filtered proteins named "filtered_algpred.txt" using the given arguments.

Author(s)

Deepika Kulshreshtha

See Also

[allermatch](#)

Examples

```
## Not run: algpred(xz,organism="Mycobacterium abscessus ATCC 19977")
```

allermatch

Filter Allergic/Non Allergic proteins using output of Allermatch

Description

allermatch is a function to filter allergic and non allergic proteins of an organism using output of Allermatch

Usage

```
allermatch(xz, organism, ginumber, prediction)
```

Arguments

xz	Object containing tabular output from Allermatch
organism	A character vector specifying name of species present in second column of xz
ginumber	A numeric vector specifying ginumber of protein for a species for which allergic property is to be predicted
prediction	A character vector specifying "Allergen" or "Non Allergen"

Details

This function takes tabular output of Allermatch in xz as input. Using arguments organism, ginumber and prediction allermatch() filters xz. Default value for ginumber is "ALL" and for prediction is "Non Allergen"

Value

A file of filtered proteins named "filtered_allermatch.txt" using the given arguments.

Author(s)

Deepika Kulshreshtha

See Also

[algpred](#)

Examples

```
## Not run: allermatch(xz,organism="Mycobacterium abscessus ATCC 19977")
```

bcepred_nmer

Epitope prediction from Bcepred server

Description

bcepred_nmer is a method to get information of epitopes from Bcepred server

Usage

```
bcepred_nmer(clas)
```

Arguments

clas A character vector for server name

Details

This function takes server name "bcepred" as input into clas object. Bcepred server provides epitopes of different length.

Value

bcepred_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: bcepred_nmer("bcepred") ##Here bcepred_nmer will provide conservation of epitope
```

`bimas_nmer`*Epitope prediction from Bimas server*

Description

`bimas_nmer` is a method to get information of epitopes from Bimas server

Usage

```
bimas_nmer(epi_length)
```

Arguments

`epi_length` A character vector of epitope length

Details

This function takes epitope length as input into `epi_length` object. Bimas server provide epitopes by selecting window size of epitope length such as 8, 9 and 10. Therefore `epi_length` should be given as "10mer".

Value

`bimas_nmer()` will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: bimas_nmer("10mer") ## Here bimas_nmer will provide conservation of epitopes of
```

`filter.firstlayer` *Filter first layer data*

Description

`filter.firstlayer` is a function to filter first layer data

Usage

```
filter.firstlayer(xz, organism, ginumber, spaanscore, subcelllocal, tmhelices, H
```

Arguments

xz	object containing first layer data table
organism	A character vector specifying species name
ginumber	A numeric vector specifying ginumber
spaanscore	A numeric vector specifying SPAAN score
subcelllocal	A character vector specifying location of the protein
tmhelices	A numeric vector specifying number of TM helix
Hrefhits	A character vector specifying non similarity to Human Reference Proteins

Details

This function filters the first layer data according to "motif and topology", "subcellular location" and "homology". Default value for ginumber,spaanscore,subcelllocal,tmhelices and Hrefhits is "ALL", >0.6, "Extracellular OR Cellwall", <2 and "No Hits found"

Value

A file of filtered proteins named "filtered_firstlayer.txt" using the given arguments

Author(s)

Deepika Kulshreshtha, Rupanjali Chaudhuri, Dr. S. Ramachandran

Examples

```
## Not run: filter.firstlayer(xz,organism="Mycobacterium abscessus ATCC 19977")
```

iedb_arb_mhcii_nmer

Epitope conservation prediction for MHCII using IEDB-ARB server information

Description

iedb_arb_mhcii_nmer is a method to predict conservation of epitopes among orthologs for MHCII using IEDB-ARB server data

Usage

```
iedb_arb_mhcii_nmer(clas)
```

Arguments

clas	A character vector for server name
------	------------------------------------

Details

This function takes server name "IEDB_arbMHCII" as input into clas object. IEDB-ARB server provides epitopes of different length.

Value

iedb_arb_mhcii_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: iedb_arb_mhcii_nmer("IEDB_arbMHCII")##Here IEDB_arb_mhcii_nmer will provide c
```

iedb_arb_mhci_nmer *Epitope conservation prediction for MHCI using IEDB-ARB server information*

Description

iedb_arb_mhci_nmer is a method to predict conservation of epitopes among orthologs for MHCI using IEDB-ARB server data

Usage

```
iedb_arb_mhci_nmer(clas)
```

Arguments

clas A character vector for server name

Details

This function takes server name "IEDB_arb_mhci" as input into clas object. IEDB-ARB server provides epitopes of different length.

Value

iedb_arb_mhci_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: iedb_arb_mhci_nmer("IEDB_arb_mhci")##Here IEDB_arb_mhci_nmer will provide con
```

```
iedb_consensus_mhcii_nmer
```

Epitope conservation prediction for MHCII using IEDB-consensus information

Description

`iedb_consensus_mhcii_nmer` is a method to predict conservation of epitopes among orthologs for MHCII using IEDB-consensus server data

Usage

```
iedb_consensus_mhcii_nmer (clas)
```

Arguments

`clas` A character vector for server name

Details

This function takes server name "IEDB_consensusMHCII" as input into `clas` object. IEDB-consensus provides epitopes of different length.

Value

`iedb_consensus_mhcii_nmer()` will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: iedb_consensus_mhcii_nmer("IEDB_consensusMHCII")##Here IEDB_consensus_mhcii_n
```

```
iedb_consensus_mhci_nmer
```

Epitope conservation prediction for MHCI using IEDB-consensus information

Description

`iedb_consensus_mhci_nmer` is a method to predict conservation of epitopes among orthologs for MHCI using IEDB-consensus server data

Usage

```
iedb_consensus_mhci_nmer (epi_length)
```


Arguments

epi_length A character vector of epitope length

Details

This function takes epitope length as input into epi_length object. IEDB server provides epitopes by selecting window size of epitope length such as 8, 9, 10. Therefore epi_length should be given as "10mer".

Value

iedb_consensus_mhci_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: iedb_consensus_mhci_nmer("10mer") ## Here IEDB_consensus_mhci_nmer will provide
```

netmhcNN_nmer	<i>Epitope conservation prediction from NetMHC server 3.0 using artificial neural networks (ANNs)</i>
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Description

netmhcNN_nmer is a method to conservation of epitopes among orthologs from NetMHC server 3.0 using artificial neural networks (ANNs)

Usage

```
netmhcNN_nmer(epi_length)
```

Arguments

epi_length A character vector of epitope length

Details

This function takes epitope length as input into epi_length object. NetMHC server 3.0 provides epitopes by selecting window size of epitope length such as 8mer, 9mer, 10mer, 11mer. Therefore epi_length should be given as "10mer".

Value

netmhcNN_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: netmhcNN_nmer("10mer") ##Here netmhcNN_nmer will provide conservation of epitope
```

netmhcWT_nmer	<i>Epitope conservation prediction from NetMHC server 3.0 using weight matrices</i>
---------------	---

Description

netmhcWT_nmer is a method to conservation of epitopes among orthologs from NetMHC server 3.0 using weight matrices

Usage

```
netmhcWT_nmer(epi_length)
```

Arguments

epi_length A character vector of epitope length

Details

This function takes epitope length as input into epi_length object. NetMHC server 3.0 provides epitopes by selecting window size of epitope length such as 8mer, 9mer, 10mer, 11mer. Therefore epi_length should be given as "10mer".

Value

netmhcWT_nmer() will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: netmhcWT_nmer("10mer") ##Here netmhcWT_nmer will provide conservation of epitope
```

`propred_nmer`*Epitope conservation prediction from Propred server*

Description

`propred_nmer` is a method to conservation of epitopes among orthologs from Propred server

Usage

```
propred_nmer(epi_length)
```

Arguments

`epi_length` A character vector of epitope length

Details

This function takes epitope length as input into `epi_length` object. Propred server provide epitopes by selecting window size of epitope length such as 10, 12, 14, 16, 18, 20. Therefore `epi_length` should be given as "10mer".

Value

`propred_nmer()` will write two files in the working directory. One file contains the information of epitope and the other file contains metadata for epitope showing orthologs of H37Rv

Author(s)

Deepika Kulshreshtha

Examples

```
## Not run: propred_nmer("9mer") ## Here propred_nmer will provide conservation of epitopes
```

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