Package: AmyloGram (via r-universe)

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Type Package

Title Prediction of Amyloid Proteins

Version 1.2

LazyData TRUE

Date 2018-10-10

Description Predicts amyloid proteins using random forests trained on the n-gram encoded peptides. The implemented algorithm can be accessed from both the command line and shiny-based GUI.

License GPL-3

URL https://github.com/michbur/AmyloGram

BugReports https://github.com/michbur/AmyloGram/issues

RoxygenNote 6.1.1

Encoding UTF-8

Depends R (>= 3.0.0)

Imports biogram, ranger, seqinr, shiny

Suggests dplyr, DT, markdown, shinythemes

Repository https://michbur.r-universe.dev

RemoteUrl https://github.com/michbur/amylogram

RemoteRef HEAD

RemoteSha a69da65aa7dd27dba3b6cffde1569c559cb5576f

Contents

`AmyloGram-package` *Prediction of amyloids*

Description

Amyloids are proteins associated with the number of clinical disorders (e.g., Alzheimer's, Creutzfeldt-Jakob's and Huntington's diseases). Despite their diversity, all amyloid proteins can undergo aggregation initiated by 6- to 15-residue segments called hot spots. Henceforth, amyloids form unique, zipper-like beta-structures, which are often harmful. To find the patterns defining the hot spots, we developed our novel predictor of amyloidogenicity AmyloGram, based on random forests.

Details

AmyloGram is available as R function (`predict.ag_model`) or shiny GUI (`AmyloGram_gui`).

The package is enriched with the benchmark data set `pep424`.

Author(s)

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References

Burdukiewicz MJ, Sobczyk P, Roediger S, Duda-Madej A, Mackiewicz P, Kotulska M. (2017) *Amyloidogenic motifs revealed by n-gram analysis*. Scientific Reports 7 https://doi.org/10.1038/s41598-017-13210-9

`AmyloGram_gui` *AmyloGram Graphical User Interface*

Description

Launches graphical user interface that predicts presence of amyloids.

Usage

```
AmyloGram_gui()
```

Warning

Any ad-blocking software may cause malfunctions.

AmyloGram_model *Random forest model of amyloid proteins*

Description

Random forest grown using the `ranger` package with additional information.

Format

A list of length three: random forest, a vector of important n-grams and the best-performing encoding.

See Also

`ranger`

is_protein *Protein test*

Description

Checks if an object is a protein (contains letters from one-letter amino acid code).

Usage

```
is_protein(object)
```

Arguments

`object`	`character` vector where each elemenents represent one amino acid.

Value

`TRUE` or `FALSE`.

pep424 *pep424 data set*

Description

Benchmark dataset for PASTA 2.0. 5 sequences shorter than 6 amino acids (1% of the original dataset) were removed.

Usage

```
pep424
```

Format

a list of 424 peptides (class SeqFastaAA).

Source

Walsh, I., Seno, F., Tosatto, S.C.E., and Trovato, A. (2014). *PASTA 2.0: an improved server for protein aggregation prediction*. Nucleic Acids Research gku399.

predict.ag_model *Predict amyloids*

Description

Recognizes amyloids using AmyloGram algorithm.

Usage

```
## S3 method for class 'ag_model'
predict(object, newdata, ...)
```

Arguments

object	ag_model object.
newdata	list of sequences (for example as given by read.fasta).
...	further arguments passed to or from other methods.

Examples

```
data(AmyloGram_model)
data(pep424)
predict(AmyloGram_model, pep424[c(4, 10)])
```

print.ag_model *Print AmyloGram object*

Description

Prints ag_model objects.

Usage

```
## S3 method for class 'ag_model'
print(x, ...)
```

Arguments

x	ag_model object.
...	further arguments passed to or from other methods.

Examples

```
data(AmyloGram_model)
print(AmyloGram_model)
```

print.ag_prediction *Print AmyloGram prediction*

Description

Prints ag_prediction objects.

Usage

```
## S3 method for class 'ag_prediction'
print(x, ...)
```

Arguments

x	ag_prediction object.
...	further arguments passed to or from other methods.

Examples

```
data(AmyloGram_model)
data(pep424)
pred <- predict(AmyloGram_model, pep424[c(4, 10)])
print(pred)
```

read_txt *Read sequences from .txt file*

Description

Read sequence data saved in text file.

Usage

```
read_txt(connection)
```

Arguments

connection	a connection to the text (.txt) file.

Details

The input file should contain one or more amino acid sequences separated by empty line(s).

Value

a list of sequences. Each element has class SeqFastaAA. If connection contains no characters, function prompts warning and returns NULL.

spec_sens *Specificity/sensitivity balance*

Description

Sensitivity, specificity and Matthew's Correlation Coefficient of AmyloGram for different cutoffs computed on pep424 dataset.

Usage

```
spec_sens
```

Format

a data frame with four columns and 99 rows.

Source

Walsh, I., Seno, F., Tosatto, S.C.E., and Trovato, A. (2014). *PASTA 2.0: an improved server for protein aggregation prediction*. Nucleic Acids Research gku399.

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