

# Package ‘AmyloGram’

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**Type** Package

**Title** Prediction of Amyloid Proteins

**Version** 1.1

**LazyData** TRUE

**Date** 2017-10-11

**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** 6.0.1

**Depends** R (>= 3.0.0)

**Imports** biogram, ranger, seqinr, shiny

**Repository** CRAN

**NeedsCompilation** no

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AmyloGram-package	<i>Prediction of amyloids</i>
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## 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>

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AmyloGram_gui	<i>AmyloGram Graphical User Interface</i>
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## Description

Launches graphical user interface that predicts presence of amyloids.

## Usage

```
AmyloGram_gui()
```

## Warning

Any ad-blocking software may cause malfunctions.

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AmyloGram_model	<i>Random forest model of amyloid proteins</i>
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**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](#)

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is_protein	<i>Protein test</i>
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**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 elements represent one amino acid.

**Value**

TRUE or FALSE.

pep424

*pep424 data set*

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**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.

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predict.ag\_model

*Predict amyloids*

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**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 <a href="#">read.fasta</a> ).
...	further arguments passed to or from other methods.

**Examples**

```
data(AmyloGram_model)  
data(pep424)  
predict(AmyloGram_model, pep424[17])
```

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print.ag_model	<i>Print AmyloGram object</i>
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**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)
```

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read_txt	<i>Read sequences from .txt file</i>
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**Description**

Read sequence data saved in text file.

**Usage**

```
read_txt(connection)
```

**Arguments**

connection	a <a href="#">connection</a> to the text (.txt) file.
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**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.

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spec_sens	<i>Specificity/sensitivity balance</i>
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**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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