

# Package: AmpGram (via r-universe)

August 20, 2024

**Type** Package

**Title** Prediction of Antimicrobial Peptides

**Version** 1.1

**LazyData** TRUE

**Date** 2022-03-01

**Description** Predicts antimicrobial peptides using random forests trained on the n-gram encoded peptides (10.3390/ijms21124310). The implemented algorithm can be accessed from both the command line and shiny-based GUI. The AmpGram model is too large for CRAN and it has to be downloaded separately from the repository: <<https://github.com/michbur/AmpGramModel>>.

**License** GPL-3

**URL** <https://github.com/michbur/AmpGram>

**BugReports** <https://github.com/michbur/AmpGram/issues>

**Encoding** UTF-8

**Depends** R (>= 3.5.0)

**Imports** biogram, devtools, pbapply, ranger, shiny, stringi

**Suggests** DT, ggplot2, pander, rmarkdown, shinythemes, spelling

**RoxygenNote** 7.1.0

**Language** en-US

**Repository** <https://michbur.r-universe.dev>

**RemoteUrl** <https://github.com/michbur/ampgram>

**RemoteRef** HEAD

**RemoteSha** b04c301e15bf4dad0ea61675e5d0defae509cca2

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AmpGram-package      *Prediction of antimicrobial peptides*

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## Description

Antimicrobial peptides (AMPs) are ancient and evolutionarily conserved molecules widespread in all living organisms that participate in host defence and/or microbial competition. Due to their positive charge, hydrophobicity and amphipathicity, they preferentially disrupt negatively-charged bacterial membranes. AMPs are considered an important alternative to traditional antibiotics, especially in times when the latter are drastically losing their effectiveness. Therefore, efficient computational tools for AMP prediction are essential to identify the best AMP candidates without undertaking expensive experimental studies. AmpGram is our novel tool for predicting AMPs based on the stacked random forests and n-gram analysis, able to successfully predict antimicrobial peptides in proteomes.

## Details

AmpGram is available as R function ([predict.ampgram\\_model](#)) or shiny GUI ([AmpGram\\_gui](#)).

AmpGram requires the external package, AmpGramModel, which contains models necessary to perform the prediction. The model can be installed using [install\\_AmpGramModel](#)

## Author(s)

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## References

Burdukiewicz M, Sidorczuk K, Rafacz D, Pietluch F, Chilimoniuk J, Roediger S, Gagat P. (2020) *AmpGram: a proteome screening tool for prediction and design of antimicrobial peptides*. (submitted)

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`AmpGram_gui`*AmpGram Graphical User Interface*

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**Description**

Launches graphical user interface that predicts presence of antimicrobial peptides.

**Usage**

```
AmpGram_gui()
```

**Value**

No return value, called for side effects.

**Warning**

Any ad-blocking software may cause malfunctions.

**See Also**

[runApp](#)

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`AmpGram_predictions`*Prediction of antimicrobial peptides*

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**Description**

Predictions made with the AmpGram methods.

**Format**

A list of length three: random forest for 10-mer analysis, random forest for predictions of AMPs, and a vector of important n-grams.

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`get_AMPs`*Get putative antimicrobial peptides*

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**Description**

Function gets sequences recognized as antimicrobial peptides and returns as data.frame.

**Usage**

```
get_AMPs(x)
```

**Arguments**

`x` AmpGram predictions for a single protein

**Value**

a data.frame with sequences recognized as antimicrobial peptides (AMPs). It consists of two columns:

**putative\_AMP** amino acid sequence of a 10-mer (subsequence of an analyzed peptide) predicted as AMP.

**prob** Probability with which a 10-mer is recognized as AMP.

**Examples**

```
data(AmpGram_predictions)
get_AMPs(AmpGram_predictions[[2]])
```

---

`install_AmpGramModel` *Install AmpGramModel package containing model for AMP prediction*

---

**Description**

Installs AmpGramModel package containing model required for prediction of antimicrobial peptides. Due to large size of our model and file size limit on CRAN, it needs to be stored in the external repository. See readme for more information or in case of installation problems.

**Usage**

```
install_AmpGramModel()
```

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pred2df	<i>Convert predictions to data.frame Return predictions as data.frame</i>
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**Description**

Convert predictions to data.frame Return predictions as data.frame

**Usage**

```
pred2df(x)
```

**Arguments**

x results of prediction as produced by [predict.ampgram\\_model](#)

**Value**

a data.frame with two columns and number of rows corresponding to the number of peptides/proteins in the results of prediction. Columns contain following information:

**seq\_name** Name of an analyzed sequence

**probability** Probability that a protein/peptide possesses antimicrobial activity. It assumes values from 0 (non-AMP) to 1 (AMP).

Row names contain sequence name and decision if a peptide/protein is classified as AMP (TRUE) or non-AMP (FALSE).

**Examples**

```
data(AmpGram_predictions)
pred2df(AmpGram_predictions)
```

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predict.ampgram_model	<i>Predict antimicrobial peptides</i>
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**Description**

Recognizes antimicrobial peptides using the AmpGram algorithm.

**Usage**

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

**Arguments**

object	ampgram_model object.
newdata	list of sequences (for example as given by <a href="#">read_fasta</a> or <a href="#">read_txt</a> ).
...	further arguments passed to or from other methods.

**Details**

AmpGram requires the external package, AmpGramModel, which contains models necessary to perform the prediction. The model can be installed using [install\\_AmpGramModel](#).

Predictions for each protein are stored in objects of class `single_ampgram_pred`. It consists of three elements:

**seq** Character vector of amino acid sequence of an analyzed peptide/protein

**all\_mers\_pred** Numeric vector of predictions for each 10-mer (subsequence of 10 amino acids) of a sequence. Prediction value indicates probability that a 10-mer possesses antimicrobial activity and ranges from 0 (non-AMP) to 1 (AMP).

**single\_prot\_pred** Named numeric vector of a single prediction value for a whole peptide/protein. Its value corresponds to the probability that a peptide/protein exhibits antimicrobial activity. It assumes name TRUE if probability is equal or greater than 0.5, i.e. peptide/protein is classified as antimicrobial (AMP), and FALSE if probability is less than 0.5, i.e. peptide/protein is classified as non-antimicrobial (non-AMP).

**Value**

list of objects of class `single_ampgram_pred`. Each object of this class contains analyzed sequence, values of predictions for 10-mers and result of the prediction for the whole peptide/protein.

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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 [connection](#) to the text (.txt) file.

**Details**

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

*read\_txt*

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**Value**

a list of sequences.

**Examples**

```
(sequences <- read_txt(system.file("AmpGram/protos.txt", package = "AmpGram")))
```

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