

AmyloGram: a novel predictor of amyloidogenicity

Michał Burdukiewicz¹, Piotr Sobczyk², Stefan Rödiger³, Paweł Mackiewicz¹ and Małgorzata Kotulska⁴

¹University of Wrocław, Department of Genomics,

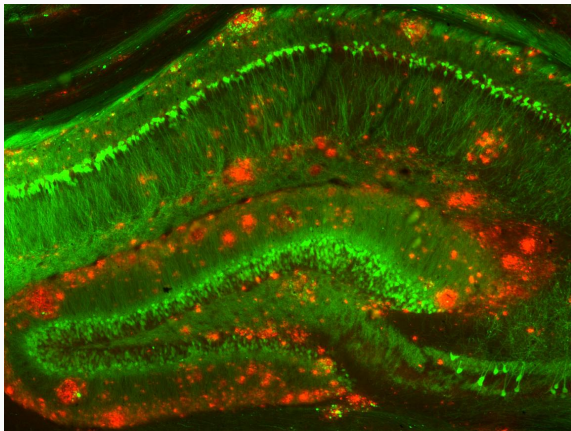
²Wrocław University of Science and Technology, Faculty of Pure and Applied Mathematics,

³Brandenburg University of Technology Cottbus-Senftenberg, Institute of Biotechnology,

⁴Wrocław University of Science and Technology, Department of Biomedical Engineering

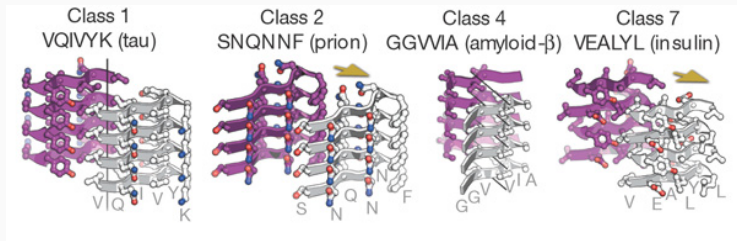
Amyloids

Proteins associated with various neurodegenerative disorders (e.g., Alzheimer's, Parkinson's, Creutzfeldt-Jakob's diseases) creating harmful aggregates.



Amyloid aggregates (red) around neurons (green). Strittmatter Laboratory, Yale University

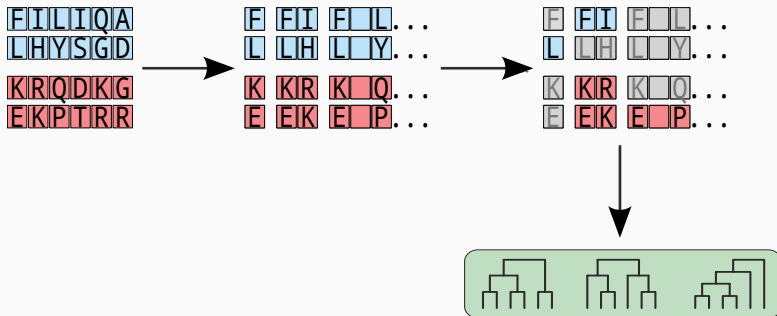
The aggregation of amyloids is initiated by 6- to 15-residue segments called hot spots, diverse subsequences that form unique zipper-like β -structures.



Sawaya et al. (2007)

Amyloidogenic motifs

Which motifs (continuous or gapped subsequences of amino acids) are associated with amyloidogenicity?



Quick Permutation Test

Informative n-grams are usually selected using permutation tests.

During a permutation test we shuffle randomly class labels and compute a defined statistic (e.g. information gain). Values of statistic for permuted data are compared with the value of statistic for original data.

$$\text{p-value} = \frac{N_{T_P > T_R}}{N}$$

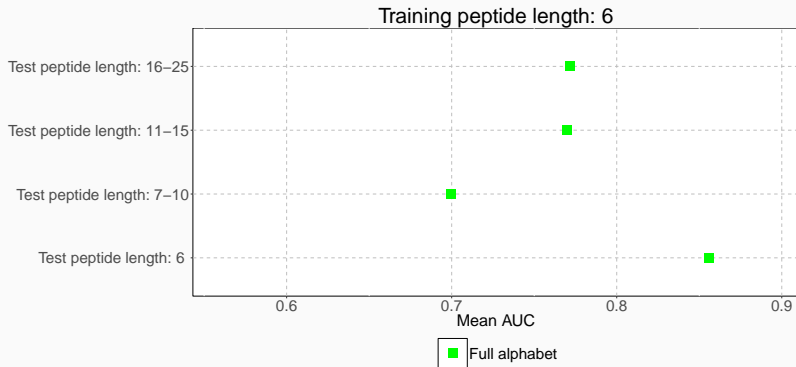
$N_{T_P > T_R}$: number of cases, where T_P (permuted test statistic) has more extreme values than T_R (test statistic for original data).

N : number of permutations.

Quick Permutation Test is a fast alternative to permutation tests for n-gram data. It also allows precise estimation of p-value.

QuiPT is available as part of the **biogram** R package.

Cross-validation



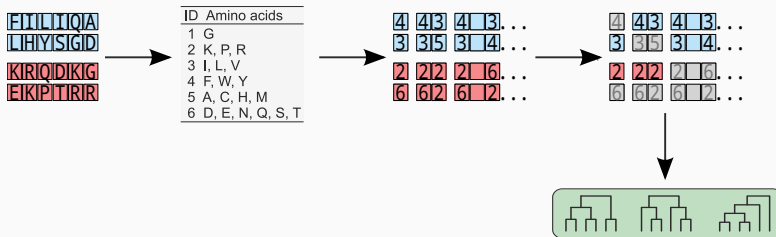
Reduced amino acid alphabets

Does amyloidogenicity depend on the exact sequence of amino acids?

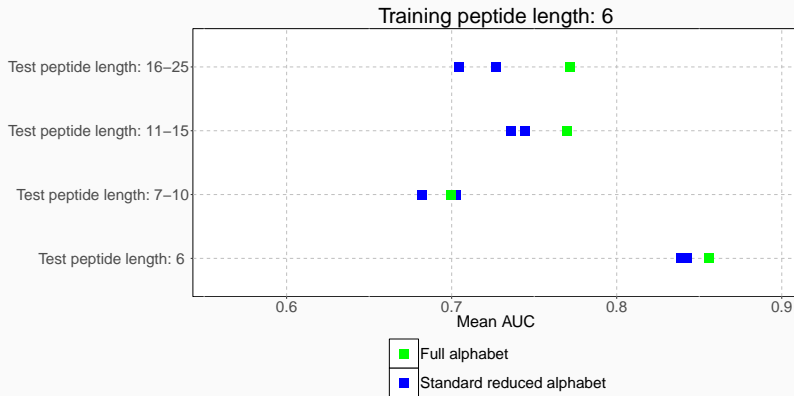
Standard reduced amino acid alphabets

To date, several reduced amino acid alphabets have been proposed, which have been applied to (among others) protein folding and protein structure prediction (Kosiol et al., 2004; Melo and Marti-Renom, 2006).

Standard reduced amino acid alphabets



Cross-validation

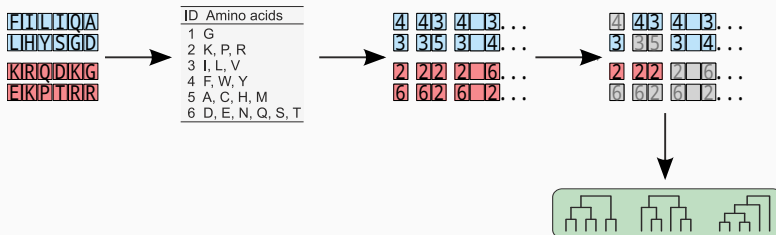


Standard reduced amino acid alphabets do not enhance discrimination between amyloidogenic and non-amyloidogenic proteins.

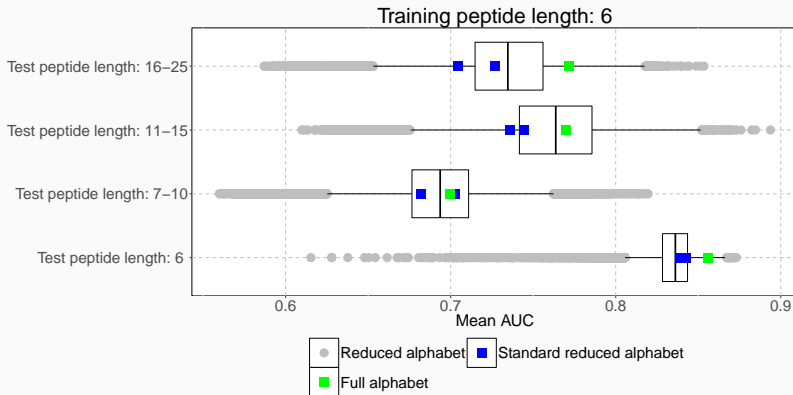
Novel reduced amino acid alphabets

- 17 measures handpicked from AAIndex database:
 - size of residues,
 - hydrophobicity,
 - solvent surface area,
 - frequency in β -sheets,
 - contactivity.
- 524 284 amino acid reduced alphabets with different level of amino acid alphabet reduction (three to six amino acid groups).

Novel reduced amino acid alphabets

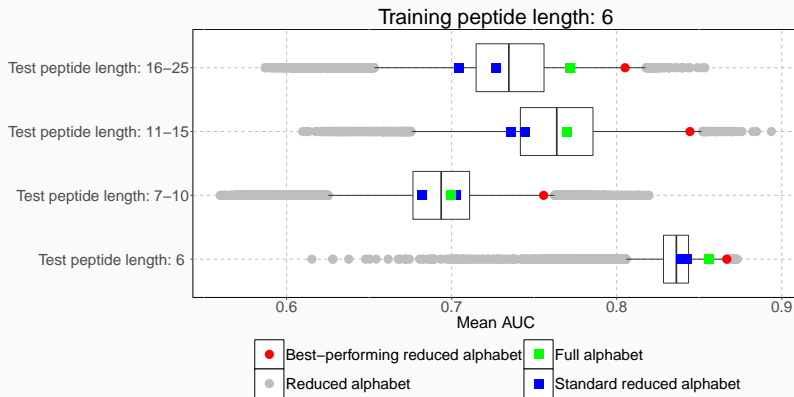


Cross-validation



Hinges of boxes correspond to the 0.25 and 0.75 quartiles. The bar inside the box represents the median. The gray circles correspond to the reduced alphabets with the AUC outside the 0.95 confidence interval.

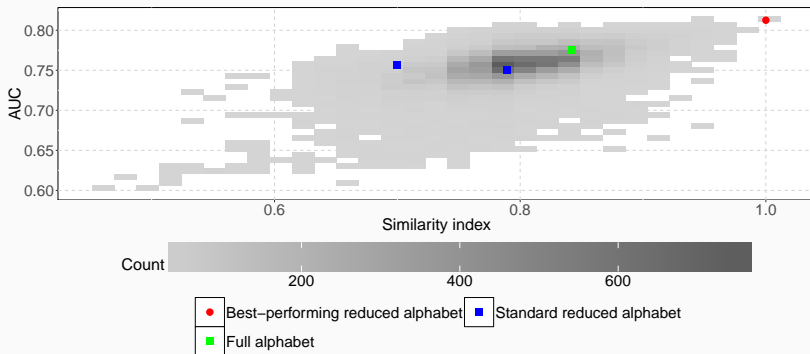
Cross-validation



The best-performing reduced amino acid alphabet has the highest prediction rank in all test categories.

Is the best-performing reduced amino alphabet associated with amyloidogenicity?

Similarity index

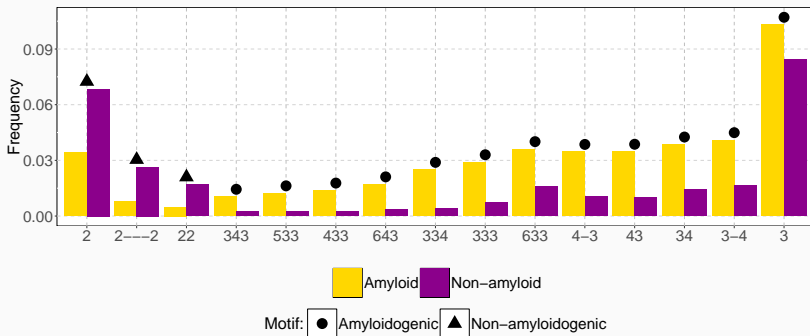


Similarity index (Stephenson and Freeland, 2013) measures the similarity between two reduced alphabets (1 - identical, 0, totally dissimilar).

Knowledge-discovery

Are informative n-grams found by QuiPT associated with amyloidogenicity?

Informative n-grams



Out of 65 the most informative n-grams, 15 (23%) were also found in the motifs validated experimentally (Paz and Serrano, 2004).

Amino acid properties used to create the best-performing amino acid alphabet reveal the role of amino acid flexibility in the creation of amyloid aggregate.

Benchmark and summary

Is performance of the AmyloGram, the classifier based on the best-performing reduced amino acid alphabet, also adequate on the independent dataset?

Waltz2 benchmark!!!

Benchmark results

Classifier	AUC	MCC
AmyloGram	0.8972	0.6307
PASTA 2.0(Walsh et al., 2014)	0.8550	0.4291
FoldAmyloid (Garbuzynskiy et al., 2010)	0.7351	0.4526
APPNN (Família et al., 2015)	0.8343	0.5823

The predictor based on the best-performing alphabet, called AmyloGram, was benchmarked against the most popular tools for the detection of amyloid peptides using an external data set *pep424*.

Summary

We identified a group of reduced amino acid alphabets which capture properties of amyloids.

Our algorithm was also capable of extracting n-gram associated with amyloidogenicity, partially confirming experimental results.

Our software is available as a web-server:

`smorfland.uni.wroc.pl/amylogram`.

n-gram analysis workflow is implemented in the R package

biogram: <https://cran.r-project.org/package=biogram>.

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References

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