Reviewer’s report

Title: Encodings and models for antimicrobial peptide classification for multi-resistant pathogens

Version: 0 Date: 01 Feb 2019

Reviewer: Richard Röttger

Reviewer’s report:

=== General Comments ===

The manuscript reviews methods for the numerical encoding of amino acid sequences in order to serve as input for subsequent machine learning approaches. The application focus of the review is on the training of machine learning algorithms for identifying active Antimicrobial peptides (AMPs). The authors split the encoding methods broadly into sequence vs. structural encodings; thereafter they discuss encodings not falling in either of these categories, like encodings based on deep learning. All encodings are evaluated based on their density and information preservation and summarized in tables. Overall, the paper is very thorough, exhaustive and well written.

=== Specific Comments ===

* Even though the paper is very thorough, the different criteria for classifying the different methods with respect to density and information is not transparent. When is a method classified as ++ compared to +.

* In my opinion, the paper would benefit from a user guide: In what circumstances would the authors recommend what method and why; are there combinations of particular machine learning tools and encodings which work particular well or should be avoided.

Level of interest
Please indicate how interesting you found the manuscript:

An article of importance in its field

Quality of written English
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Acceptable

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