

Review of: "Functional classification and validation of yeast prenylation motifs using machine learning and genetic reporters"

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In this study, the authors used machine learning and yeast genetic data to develop methods (SVM-ESM-1b) for predicting the prenylation potential of 8000 Cxxx sequences within the yeast system, and demonstrated that machine learning can be developed into a useful tool to prediction prenylation and cleavage events associated with CaaX proteins. However, the data of *in vivo* methods were insufficient to support their conclusion due to the small number of samples, such as "For these 12 Cxxx sequences, Freq correctly predicted 10, SVM-ESM-1b correctly predicted 9, and PrePS correctly predicted 4 (Table 4, Fig 4B)." and "for the combined set of 31 sequences evaluated, SVM correctly predicted 81% (25/31), Freq correctly identified 77% (24/31), and PrePS correctly predicted 61% (19/31)". There's no significant difference between the models of SVM and Freq. Besides, there are some other problems need to be improved:

1. It's better for authors to demonstrate concisely the advantages of SVM-ESM-1b for prenylation and cleavage predictions compared to other methods in Abstract.
2. The markers in the left of Fig S1 were out of alignment with the bands.