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Prediction of protein subcellular localization with oversampling approach and Chou's general PseAAC

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## Highlights

- We combined oversampling method with SVM to deal with the protein subcellular localization of unbalanced data sets.
- Results of SVM by Jackknife tests show that oversampling methods have successfully decrease the imbalance of data sets.

• The excellent overall accuracy indicates that the feature representation and selection capture useful information of protein sequence.

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