

Protein Classification By feature extraction

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Aim : The goal of this assignment is to provide an automated system that is able to classify proteins (Amino Acid sequences) into four classes each being a subcellular locations : **[Cytosolic, Secreted, Nuclear, Mitochondrial]**

Improvements: In order to improve the results of the classifier, deepening the feature extraction method seems to be the way to go. Another method would be to use neural network techniques.

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Currently, There is a growing need for fully automated methods to analyse amino acids sequences. One of the process that need to be automated is **the identification of the protein's subcellular location**. This problem can be splitted into two sub problems :

- Although these methods usually yields better results than the methods presented before, the results obtained are far harder to interpret as these systems behave as "**black boxes**" and it's quite difficult to interpret what was *learned*.

2 Approach

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row3	row3	row3	row3
row4	row4	row4	row4

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Fig. 1. Caption, caption.

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3.2 Test1

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4 Discussion

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5 Conclusion

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Acknowledgements

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