

Bioinformatics

Protein Classification By feature extraction

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Abstract

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]

Results: Using a *Random Forest Classifer* we manage to reache a **67% cross-validation accuracy**. **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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1 Introduction

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:

- feature extraction: the goal of this task is to choose the features that
 would allow an efficient classification, to be more precise, the chosen
 features should allow to easily seperate the sequences into classes
 or groups which will then be matched with the various subcellular
 locations
- **clasffication:** once the features obtained, it is then necessary to choose a fitting classification algorithm that will use the various features selected as a *vector representation* of each sequence that will then be fed to the classification algorithm during both training and testing.

It is however, possible to avoid splitting the problem into two subproblems by using methods that have been designed to classify sequences of variables lengths such as:

- HMM
- Recurrent neural networks & Seq2Seq Models
- 1D Convolutional Neural Networks

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

Therefore, The first approach was used in order to ease the analysis of the results and the task was splitted into a **feature-extraction** task and **classification** task

2 Approach

3 Methods

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2 Sample et al.

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4 Sample et al.

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4 Discussion

5 Conclusion

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