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ABSTRACT

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1 INTRODUCTION

The role of a machine learning framework is to learn the association between the inputs and the outputs in a training set. After this association is learnt, the model is used to predict the output of the unseen inputs. When addressing regression problems, a feature that is usually neglected by most frameworks is the certainty of the prediction. While most frameworks can predict an output for a given input, they do not provide the user with notion of how certain the framework is regarding this prediction. Inclusion of such notion can highly benefit many machine tasks by removing false positives that the method is uncertain about the decisions it has made. To address this problem, we will employ Gaussian Process (GP) framework? to predict peptide retention time. We will show, how the property in assigning certainty to the predictions provide a ground for removing more faulty predictions. Moreover, we will argue how this framework can provide us with a model with significantly higher performance compared to previously used frameworks for solving the retention time prediction task.

2 APPROACH

The task of retention time prediction, focuses on determining the retention time of a peptide given its amino acid sequence. To obtain a robust model for solving this task, one needs to address the following problems. Most machine learning frameworks require the inputs to come from a vector space. To map the peptide into a vector space by extracting biologically meaningful features ?, collecting

general statistical entities collected from the sequences? or using different kernels such as spectrum kernel? or string kernel?. Once the feature vectors are calculated, a machine learning framework should be selected for solving the prediction problem. The choice this method can highly affect the quality of the prediction. For example in?, the authors have chosen Support Vector Regression (SVR) framework? to solve the regression problem.

In this paper, we throughly analyze the retention time prediction problem from the machine learning perspective. First, we will look at different methods that can be used for mapping the peptide sequences into vector spaces. In this process, our aim is to determine the pros and cons of different feature extraction techniques in association with large data analysis. Second, we will look at Gaussian Process (GP)? as more sophisticated framework for solving the prediction task and compare its performance with the widely used SVR framework. We will also analyze how varying the size of the training set can affect the performance of both models.

3 METHODS

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4 DISCUSSION

5 CONCLUSION

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