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ORIGINAL ARTICLE

Type-2 fuzzy support vector machine model for conformational epitope prediction

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Abstract

Identifying and predicting epitopes by experimental approaches is a time-consuming and expensive procedure. As a result, computational methods have been explored as a faster and more cost-effective alternative. Nevertheless, existing computational methods encounter difficulties in achieving accuracy due to the presence of data ambiguity. The type-1 fuzzy set may effectively manage the uncertainty present in data. Nevertheless, it lacks the ability to effectively manage uncertainty in the data's relationship. This research proposes a model that combines a type-2 fuzzy set with a support vector machine to handle ambiguity in data relationships to enhance the accuracy of predicting conformational epitopes. The results obtained from the proposed method demonstrated a substantial enhancement in accuracy when compared to earlier methods in the prediction of conformational epitopes.

Keywords Epitope · Scoring function · Support vector machine · Type 2 fuzzy set

1 Introduction

An epitope is a specific location within the structure of an antigen that has the ability to elicit an immune response when it interacts with an antibody. Following the binding of the epitope to the antibody molecule, a sequence of immunological processes might occur, ultimately resulting in the production of antibodies and memory cells. Memory cells are crucial components of the immune system as they enable the recognition and subsequent defeat of the same pathogen upon future encounters. Antigens are external substances that the body encounters from the surroundings. They typically provoke an immune response by stimulating the synthesis of specific proteins known as immunoglobulins, which are antibodies (Runte et al. 2019). These proteins move through bodily fluids and function upon encountering an antigen by binding to it, neutralizing its effects, and thus preventing immunological activation. When antibodies bind to epitopes, these epitopes can be classified into two categories: linear (continuous) or conformational (discontinuous) (Sharif et al. 2019). Computational advancements within the recent past in biology and bioinformatics have significantly enhanced the ability to predict epitopes (Guarra and Colombo 2023). With techniques such as machine learning, structural modeling, and high-throughput sequencing, it is now possible to identify potential epitopes with accuracy

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