

MHC binding peptide prediction models: New approach for vaccine development

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The prediction of peptides which are presented by the restricting major histocompatibility complex (MHC) molecules is a crucial problem in immunology. In silico methods for the prediction of antigenic peptides binding to MHC class molecules play an increasingly important role in the identification of T-cell epitopes. Statistical and machine learning methods in particular are widely used to score candidate binders based on their similarity with known binders and non-binders. The genes coding for the MHC molecules, however are highly polymorphic, and statistical methods have difficulties building models for alleles with few known binders. In this context, recent work has demonstrated the utility of leveraging information across alleles to improve the performance of the prediction. The aim of our method is to build each and every known MHC class allele, a model to predict whether or not candidate peptides can bind to it. Our method must then learn the binding predictive models from the training set. The most relevant measure of a prediction model's accuracy is how well it performs on novel peptide sequences that are dissimilar to those used to fit the model. A model with a large number of parameters, such as most peptide-MHC binding prediction models, can potentially overfit the data so that its accuracy is good on the training set but poor on unrelated peptide sequences. Cross-validation is one procedure that can be used to estimate the accuracy of the prediction model for novel data.

Biography

Virendra Gomase [BPharma, MSc, MPhil, PhD] did his PhD in Computer Science from Department of Computer Science and IT, Dr. B.A.M. University, Aurangabad, India. He has authored more than 15 books. He has published more than 300 international and national peer reviewed journals research papers having Impact Factor. He presented more than 200 articles in international and national conferences, seminars. His research included work on Bioinformatics, Machine Learning, Computational Intelligence, Immunoproteomics, Toxicoproteomics. He is serving as member of more than 60 scientific societies. He is serving as an editorial member of several reputed journals.

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