## MHC binding prediction with a novel hierarchical kernel

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Antigenic peptides presented to T cells by MHC molecules are essential for T or B cells to proliferate and eventually differentiate into effector cells or memory cells. Hence, the MHC–peptide interaction is essential for activating adaptive immune response. MHC binding prediction is an active research area since experimental identification is costly and time consuming. Reliable predictors are demanded to understand the vertebrate adaptive immune process as well as identify potential vaccine candidates. Here we describe a novel hierarchical kernel on strings and the kernel is used in learning machines to predict binding affinities of peptides to MHC molecules. The kernel is also used to define a distance on an HLA-DR allele set based on which a clustering analysis precisely recovers the serotype classifications assigned by the World Health Organization.