An Integrative Computational Pipeline for Detection of Tumor Epitopes in Cancer Patients

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Abstract : Genomics-based personalized medicine is a promising approach to fight aggressive tumors based on patient's specific tumor mutation and expression profiles. A remarkable case is, dendritic cell-based immunotherapy, in which tumor epitopes targeting patient's specific mutations are used to design a vaccine that helps in stimulating cytotoxic T cell mediated anticancer immunity. Here we present a computational pipeline for epitope-based personalized cancer vaccines using patient-specific haplotype and cancer mutation profiles. In the workflow proposed, we analyze Whole Exome Sequencing and RNA Sequencing patient data to detect patient-specific mutations and their expression level. Epitopes including the tumor mutations are computationally predicted using patient's haplotype and filtered based on their expression level, binding affinity, and immunogenicity. We calculate binding energy for each filtered major histocompatibility complex (MHC)-peptide complex using docking studies, and use this feature to select good epitope candidates further.