Computational Methods for Identification of T Cell Neoepitopes in Tumors

Cancer immunotherapy has experienced several major breakthroughs in the past decade. Most recently, technical advances in next-generation sequencing methods have enabled discovery of tumor-specific mutations leading to protective T cell neoepitopes. Many of the successes are enabled by computational methods, which facilitate processing of raw data, mapping of mutations, and prediction of neoepitopes. In this book chapter, we provide an overview of the computational tasks related to the identification of neoepitopes, propose specific tools and best practices, and discuss strengths, weaknesses, and future challenges.