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.

General information
State: Published
Organisations: Disease Intelligence and Molecular Evolution, Immunoinformatics and Machine Learning, Department of Bio and Health Informatics, Cancer Genomics
Contributors: Jurtz, V. I., Olsen, L. R.
Pages: 157-172
Publication date: 2019

Host publication information
Title of host publication: Cancer Bioinformatics
Volume: 1878
Publisher: Springer
ISBN (Electronic): 978-1-4939-8868-6
(Methods in Molecular Biology).
Keywords: Cancer immunotherapy, Epitope prediction, Next-generation sequencing, Nonsynonymous mutations
DOIs: 10.1007/978-1-4939-8868-6_9
Source: FindIt
Source-ID: 2441217663
Research output: Research - peer-review » Book chapter – Annual report year: 2019