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A bioinformatics framework for personalized detection of tumor neoepitopes

Tanushree Jaitly

University of Erlangen-Nuremberg, Germany

In tailor-made therapeutic cancer vaccines, individual patient's genomics and transcriptomics tumor profiling is used to optimize the design of the therapy. In case of dendritic cell-based immunotherapy, tumor epitopes targeting patient's specific mutations are selected and loaded on mature dendritic cells to stimulate cytotoxic T cell mediated anticancer immunity. Here, we present a bioinformatics framework for detection of patient specific tumor neoepitopes using patient's genomics and transcriptomics profile. In the framework proposed, whole exome sequencing data from patient's tumor material are analyzed to identify tumor mutations. This information is combined with patient's haplotype information to predict tumor neoepitopes. Tumor transcriptomics data are used to predict expression of the mutations. Next, tumor peptides are classified and ranked based on their tumor and peptide

features using machine learning methods. Lastly, docking and molecular dynamics simulations are used to select the most promising tumor neoepitopes for vaccination. This computational workflow allows personalized selection of tumor neoepitopes for cancer immunotherapy. We illustrate the use of the method in a cutaneous melanoma patient.

Speaker Biography

Tanushree Jaitly is a doctoral candidate working on bioinformatics applied to dendritic cell based cancer immunotherapy. She is developing computational pipelines for high-throughput data-based (genomic and transcriptomics data) prediction of tumor neoepitopes under the supervision of Prof Dr Julio Vera-González and Prof Dr Leila Taher at Friedrich-Alexander-University Erlangen-Nuremberg, Germany. Her interests are on next generation sequencing data analysis, cancer immunotherapy, 3D docking and simulation and machine learning methods.

e: Tanushree.jaitly@uk-erlangen.de

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