INSTITUTE for COMPUTATIONAL MEDICINE

Distinguished Seminar Series Fall 2023

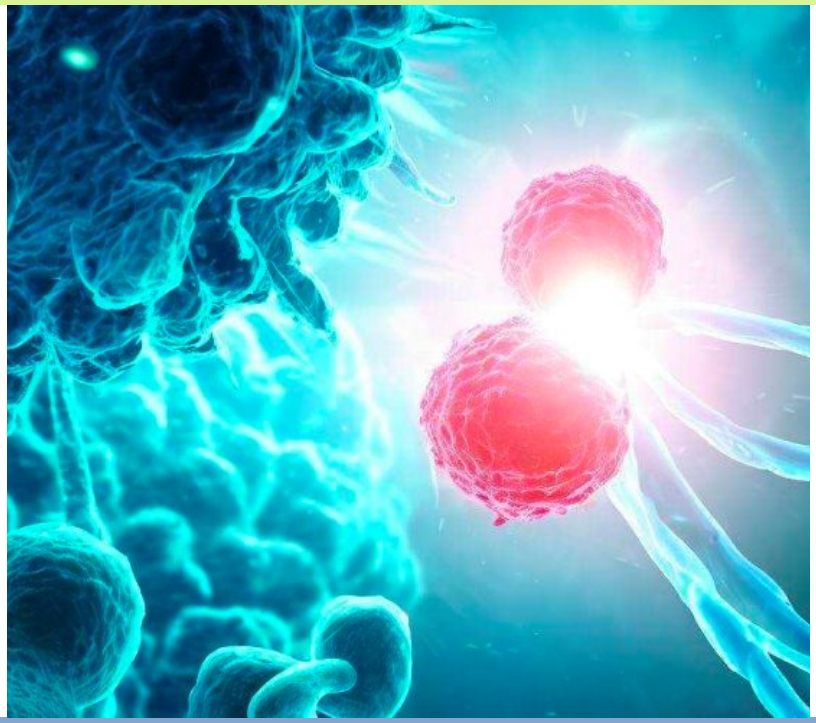
Predicting Immunogenic Neoepitopes in Cancer

Rachel Karchin, PhD

Professor, Biomedical Engineering, Oncology, and Computer Science

Academic Program Co-Director, Biomedical Engineering PhD Program

Johns Hopkins University



Identifying neoepitopes that elicit an adaptive immune response is a major bottleneck to developing personalized cancer vaccines. Experimental validation of candidate neoepitopes is extremely resource intensive and the vast majority of candidates are non-immunogenic, creating a needle-in-a-haystack problem. Here we address this challenge, presenting computational methods for predicting class I major histocompatibility complex (MHC-I) epitopes and identifying immunogenic neoepitopes with improved precision. The BigMHC method comprises an ensemble of seven pan-allelic deep neural networks trained on peptide-MHC eluted ligand data from mass spectrometry assays and transfer learned on data from assays of antigen-specific immune response. Compared with four state-of-the-art classifiers, BigMHC significantly improves the prediction of epitope presentation on a test set of 45,409 MHC ligands among 900,592 random negatives (area under the receiver operating characteristic = 0.9733; area under the precision-recall curve = 0.8779). After transfer learning on immunogenicity data, BigMHC yields significantly higher precision than seven state-of-the-art models in identifying immunogenic neoepitopes, making BigMHC effective in clinical settings.

Tuesday, December 5, 2023 @ 4:00PM ET in Clark 110

Live Webcast: https://wse.zoom.us/j/94073678803

JOHNS HOPKINS UNIVERSITY