Department of
BIOMEDICAL ENGINEERING
THE UNIVERSITY OF UTAH

Predicting Immunogenic Neoepitopes in Cancers

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11:45 am – SMBB Auditorium (2650)

Hosted by Orly Alter, Ph.D.
Sorenson Molecular Biotechnology Building (USTAR Bldg) – 2nd Floor

Bio: Rachel Karchin, Ph.D. is Professor in the Department of Biomedical Engineering at Johns Hopkins University. She received a Ph.D. in Computer Science from the University of California, Santa Cruz in 2003, spent three years as a postdoctoral fellow in the Department of Biopharmaceutical Sciences at University of California, San Francisco, and joined the Hopkins faculty in 2006. Dr. Karchin has a joint appointment in the Department of Oncology, a secondary appointment in the Department of Computer Science, and is a core member of the Institute for Computational Medicine at the Whiting School of Engineering.

Her lab develops algorithms and tools to interpret and model molecular sequence data, with a focus on how tumors evolve and how they interact with the immune system. In 2017, she was inducted into the College of Fellows of the American Institute for Medical and Biological Engineering for her contributions to translational computational biology.

Abstract: Identifying neoepitopes that elicit an adaptive immune response is a major bottleneck to developing personalized cancer vaccines and engineered T cell therapies. 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.

Website: karchinlab.org