Machine Learning Methods for Protein Design

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Abstract

I will cover recent work from my lab on machine learning methods for protein design, with a focus towards protein therapeutics. Our methods cover solutions to protein-protein and protein-peptide docking, sequence and backbone design as well as applications to antibodies and Zinc Fingers. We incorporate modern machine learning methods such as graph neural networks and diffusion models.

Bio

Philip M. Kim is a Professor at the University of Toronto with appointments in the Donnelly Centre, the Department of Molecular Genetics and the Department of Computer Science. He leads a research laboratory that integrates machine learning and wet/experimental methods for the development of novel protein and peptide therapeutics. He authored over 70 publications, 8 invention disclosures and 6 patent applications and has been a co-founder, consultant and member of the scientific advisory board of various biotechnology companies. Before setting up his lab in 2009, he was a postdoctoral fellow at Yale University and an associate with McKinsey & Co. He holds a Ph.D. from the Artificial Intelligence Laboratory and Department of Chemistry at the Massachusetts Institute of Technology and a B.S. in Biochemistry and Physics from the University of Tuebingen.