Deep learning for protein-RNA interactions

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Abstract:
Protein-RNA binding, mediated through both RNA sequence and structure, plays vital role in many cellular processes, including neurodegenerative diseases. Modeling the sequence and structure binding preferences of an RNA-binding protein is a key computational challenge. Accurate models will enable prediction of new interactions and better understanding of the binding mechanism.

In the talk, I will describe a new deep learning based approach to learn RNA sequence and structure binding preferences from large biological datasets. I will present results of our algorithm outperforming the state of the art, both in vitro and in vivo. I will give examples of the biological insights we can gain by applying our neural networks to largest datasets of protein-RNA interactions. I will conclude with open questions and a discussion on the success of deep learning in computational biology.

No biological background is assumed.

Bio: Yaron is a senior lecturer at the School of Electrical and Computer Engineering, BGU. He spent his post-doctoral training at CSAIL, MIT and Simons Institute, UC Berkeley. Previously, he received his Ph.D and M.Sc degrees from CS and EE, TAU, respectively. Yaron completed his bachelor’s degree in computer science and electrical engineering at TAU.

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