Colloquium №102

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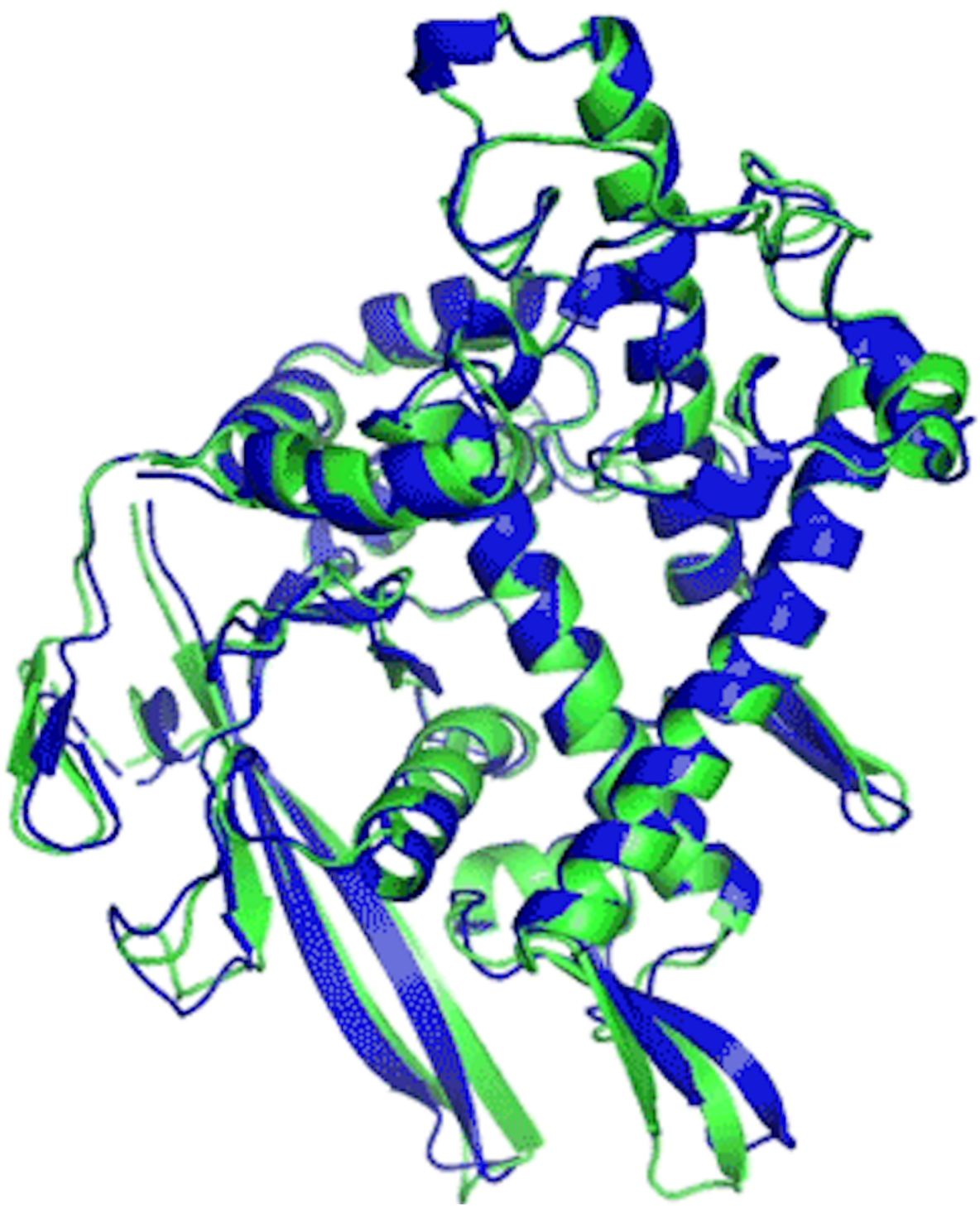
Online

Highly accurate protein structure prediction with AlphaFold

Speaker: Anna Potapenko, DeepMind



Abstract

Predicting a protein's structure from its primary sequence has been a grand challenge in biology for the past 50 years, holding the promise to bridge the gap between the pace of genomics discovery and resulting structural characterization. In this talk, we will describe work at DeepMind to develop AlphaFold, a new deep learning-based system for structure prediction that achieves high accuracy across a wide range of targets. We demonstrated our system in the 14th biennial Critical Assessment of Protein Structure Prediction (CASP14) across a wide range of difficult targets, where the assessors judged our predictions to be at an accuracy "competitive with experiment" for approximately 2/3rds of proteins. The talk will cover both the underlying machine learning ideas and the implications for biological research.

Registration link

HSE University
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