

# Junior Investigator – Advanced Biomedical Computation (ABC) Series

**Monday, November 2, 4:00 – 5:00 PM (EST)**

Zoom link (wait room protected)

<https://mit.zoom.us/j/93883153770>



**Mohammed AlQuraishi, PhD**  
Assistant Professor, Columbia University

**“Machine-learned molecular models for a  
bottom-up systems biology”**

The advent of a new modeling paradigm known as ‘differentiable programming’ makes possible bespoke machine-learned models of biological phenomena that are partly learned from data and partly informed by human-derived biophysical knowledge. In this talk I will describe three instantiations of this approach for predicting protein structure, protein-protein interactions, and protein function. Using these models, we have begun to uncover a combinatorial grammar underlying signal transducing proteins in metazoa. This grammar describes how modular protein interaction domains and their cognate binding sites combine to form units of functional logic that are widely reused throughout signaling networks. I will also describe how machine-learned models enable us to predict the effects of disease-causing mutations on the wiring of these signaling networks in human cancers. Looking ahead, I will conclude by considering the short and long-term prospects of integrating molecular models in a bottom-up fashion to assemble increasingly more accurate representations of biological systems that facilitate a principled and mechanistic approach to systems biology and precision medicine.

ABC Series Organized by the Division of Computational Pathology

<https://comp-path.bwh.harvard.edu/>

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