Reconstructing SARS-COV-2 Response Pathways

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SARS-CoV-2 is known to primarily impact cells via two viral entry factors, ACE2 and TMPRSS2. However, much less is currently known about virus activity within cells. We used computational methods based on probabilistic graphical models to integrate several recent SARS-CoV-2 interaction and expression datasets with general protein-protein and protein-DNA interaction datasets. The reconstructed models display the pathways viral proteins use to drive expression in human cells and the pathways the cell uses to respond to the infection. Intersecting key proteins on these pathways with expression data from underlying conditions shown to increase mortality from SARS-CoV-2, and with knockout and phosphorylation data, identifies a few potential targets for treating cells to reduce viral loads.

Ziv Bar-Joseph is the FORE Systems Professor of Computational Biology and Machine Learning at Carnegie Mellon University. His work focuses on the development of machine learning methods for the analysis, modeling, and visualization of time series high throughput biological data. Dr. Bar-Joseph is the recipient of the Overton Prize, an NSF CAREER Award, and several conference Best Paper awards. He is currently leading the Computational Tools Center for the National Institutes of Health Human BioMolecular Atlas Program (HuBMAP). He has served on the advisory board of several national efforts including the National Institute for Allergy and Infectious Diseases Systems Biology Program. Software tools developed by his group are widely used for the analysis of genomics data.