Understanding genetic networks with Compressive Biology

Recent technological developments have made it possible to study genetic networks at unprecedented scale. In methods like Perturb-Seq, pooled CRISPR screens are combined with rich single cell molecular profiles as phenotypes to measure the effect of perturbations in tens of thousands of single cells. However, the capability of these methods is still dramatically limited; performing a genome-wide Perturb-Seq screen, for instance, would be ~1,000x larger than what has been demonstrated to date. More fundamentally, measuring the effect of combinatorial perturbations – which may be necessary to study functional redundancy – will be limited by the number of cells that can be grown, even if technological capabilities rapidly improve. In this talk, I introduce a new framework, Compressive Biology, to address these challenges. Compressive Biology has three foundational principles: (1) high-dimensional cellular systems can be organized into a compact, modular representation; (2) when genes are co-regulated and organized into response modules, measurements (e.g. a gene expression profile) can be compressed at the time of data collection; (3) when genes co-regulate their targets and are organized into functional modules, experiments (e.g. genetic perturbations) can be compressed. I discuss the mathematical theory underlying these principles, and practical applications to efficiently study genetic networks with composite measurements and composite experiments.

Bio:

Brian Cleary is a PhD student at MIT in the labs of Aviv Regev and Eric Lander. His work focuses on using mathematical principles, most notably compressed sensing, to describe and apply new modalities of experimentation in biology. Prior to coming to MIT, Brian founded a company developing Natural Language Processing technology, and worked in options and algorithmic trading. He is a graduate of the California Institute of Technology, with B.S. degrees in Biology and Finance.