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TITLE: A next generation connectivity map using the L1000 platform

ABSTRACT: The Connectivity Map seeks to identify functional relationships between genes, drugs and disease states by virtue of common gene expression signatures. Unfortunately, the high cost of commercial gene expression microarrays and even RNA sequencing makes a genome-scale resource cost-prohibitive. We invented L1000, a new approach to gene expression profiling based on a reduced representation of the transcriptome. We then developed a high-throughput platform at the Broad Institute, which brings together L1000 and extensive laboratory automation. In this talk, I will describe the L1000 platform and generation of over 1M profiles. I will describe analytical methodologies that utilize these data to discover mechanism of action of small molecules, functionally annotate genetic variants of disease genes, and inform clinical trials. These datasets and tools for their analysis are available at https://clue.io.