Multichannel microformulators for massively parallel machine learning and automated design of biological experiments[1] JOHN WIKSWO, Vanderbilt Univ, ADITYA KOLLI, HARISH SHANKARAN, MATTHEW WAGONER, JEROME METTETAL, AstraZeneca, RONALD REISERER, GREGORY GERKEN, CLAYTON BRITT, DAVID SCHAFFER, Vanderbilt Univ — Genetic, proteomic, and metabolic networks describing biological signaling can have 10^2 to 10^3 nodes. Transcriptomics and mass spectrometry can quantify 10^4 different dynamical experimental variables recorded from *in vitro* experiments with a time resolution approaching 1 s. It is difficult to infer metabolic and signaling models from such massive data sets, and it is unlikely that causality can be determined simply from observed temporal correlations. There is a need to design and apply specific system perturbations, which will be difficult to perform manually with 10 to 10^2 externally controlled variables. Machine learning and optimal experimental design can select an experiment that best discriminates between multiple conflicting models, but a remaining problem is to control in real time multiple variables in the form of concentrations of growth factors, toxins, nutrients and other signaling molecules. With time-division multiplexing, a microfluidic MicroFormulator (μF) can create in real time complex mixtures of reagents in volumes suitable for biological experiments. Initial 96-channel μF implementations control the exposure profile of cells in a 96-well plate to different temporal profiles of drugs; future experiments will include challenge compounds.

John Wikswo
Vanderbilt Univ

Date submitted: 08 Nov 2016   Electronic form version 1.4