Lecture 16: Assessing drug efficacy at the single cell level

I. Introduction and overview
   A. nanomedical treatment at the single cell level requires evaluation at the single cell level
   B. for evaluation purposes, does structure reveal function?
   C. the difficulty of anything but simple functional assays
   D. the need for assays which at least show correlation to functional activity

II. Quantitative single cell measurements of one or more proteins per cell by flow and image/confocal cytometry
   A. cell surface measures of protein expression on live, single cells
   B. high-throughput flow cytometric screening of bioactive compounds
   C. challenges of measuring protein expression inside fixed, single cells
   D. when location is important 2D or 3D imaging is required to get spatial location of proteins inside cells

III. Quantitative multiparameter phospho-specific flow cytometry
   A. attempts to measure "functional proteins" by detecting phosphorylation
   B. example of phospho-specific, multiparameter flow cytometry
   C. example of measuring single cell gene silencing by phospho-specific flow cytometry

IV. Quantitative measures of gene expression – the promises and the realities
   A. is gene expression at the single cell level really possible?
   B. is it even useful to measure a single gene's changes?
   C. gene arrays of purified cell subpopulations
   D. RNA amplification techniques to attempt to perform single cell gene arrays

References


Szansiszlo, P. Gene Expression Microarray Analysis of Small, Purified Cell Subsets. University of Texas Medical Branch, Galveston, TX April, 2007 (mentor: Dr. Leary)