

Pat Brown's lab

A major theme of research in my lab is developing and applying experimental and analytical methods to systematically study global gene expression patterns, using them both to provide detailed molecular pictures of the physiology and behavior of cells and tissues, and to investigate the logic and mechanisms of biological regulation. We also look for opportunities to study human biology and human disease, and try to find practical ways to improve detection diagnosis and treatment of diseases.

Exploring and mapping the gene expression programs of the yeast and human genomes.

- systematic approach to post-transcriptional regulation: how extensive is the regulation of the localization, translation and degradation of mRNA's, what is the global organization of this regulatory system and what are the mechanisms.
- developing computational methods for finding and visualizing features and relationships in very large (10^7 - 10^8 measurements) systematic bodies of gene expression and
- developing computational tools for high-throughput analysis of cell and tissue imaging data.

Gene expression patterns as windows on physiology and architecture of yeast and humans.

- fine local differentiation of cells and cell-cell interactions in normal and diseased tissues.
- spatial and functional compartmentalization of mRNA transcripts
- innate responses to infection, stress and injury
- host-pathogen interactions in viral and bacterial infections

Exploring and mapping the microbial ecosystems in and on the human body.

- microarrays for detection, identification and quantitation of microbes.
- what bugs live in and on us? How and why do they vary over time and between individuals? What relationship do they have to health and disease?

Clinical applications.

- high-dimensional characterization of molecular variation in blood, urine, etc. and its diagnostic potential.
- new ways to detect, diagnose, and predict the behavior of cancers.
- strategies for therapy based on molecular profiles of diseases.
- global characterization of the human T-cell repertoire using protein microarrays.