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1989	A.B. cum laude in Mathematics, Harvard College, Cambridge, MA
1996	MA. Ph.D. in Biophysics, Harvard University, Cambridge, MA
1996–present	Postdoctoral Fellow, Department of Genetics. Stanford University School of Medicine. Stanford, CA

Honors

1990–1994	National Science Foundation Predoctoral Fellowship
1997–1999	Postdoctoral Fellowship in Computational Molecular Biology, Alfred E. Sloan Foundation, Department of Energy

Making biological sense of genome-wide expression data

Microarrays generate a lot of data. In our lab alone, on the order of 20 million measurements have been made of the expression level of a single gene in a single condition, in viruses, bacteria, yeast and humans. As the technology spreads, orders of magnitude more data will be generated. A key challenge in transforming this wealth of information into meaningful biological insights is the development and distribution of analytical tools to explore and analyse the data. I will describe a number of such tools and present their application to two experimental systems: transcriptional regulation in yeast and the molecular diversity of human tumours.

Using thousands of DNA microarrays containing essentially all of the open reading frames from the yeast Saccharomyces cerevisiae, members of our lab have monitored gene expression during many important biological processes and conditions. We have applied and developed many analytical methods for discovering underlying order in this data. I will present many of the intriguing properties of transcriptional regulation revealed by these methods. I will also compare and contrast many methods that are in use or have been proposed. I will also describe methods we are developing for combining genome-wide expression data with genome sequence information to further our understanding of the nature and logic of transcriptional regulation in this important model organism, including methods for identifying potential cis-regulatory sequences and the proteins that bind them.

Many researchers have grasped the potential of microarray-based methods to improve the diagnosis and treatment of disease. We have focused on using gene expression profiling to develop improved and, we hope, clinically relevant methods for classifying human tumours. Much of the clinically important variation among tumours is dictated by the genetic program of the tumour cells. Thus, we expect to discover systematic differences in molecular properties of tumours that will correlate with differences in the biology of the tumours by conducting genome-scale molecular characterizations of human tumours. I will describe a gene expression survey of human tumour cell lines, as well as initial results from examinations of clinical samples of breast and lymphoid malignancies. I will focus on the methods we have used to analyse data from these experiments, what these analyses have taught us and what analytical issues we are likely to face as we move toward large-scale surveys of human tumours.

Slides from my talk will be made available (http://bronzino.stanford.edu/Talks). All software discussed is also available (http://www.microarrays.org/software).