David J. Lockhart, Ph.D.

Affymetrix, Inc.
3380 Central Expressway
Santa Clara, California 95051,
USA

Novartis Institute for Functional Genomics,
3115 Merryfield Row, Suite 200
San Diego, California 92121,
USA

1983	Westmont College, Summa cum laude
1990	Ph.D., Stanford University, Chemistry (Biophysical)
1989–1993	Postdoctoral Research, Whitehead Institute for Biomedical Research, MIT Department of Biology
1993–1995	Staff Scientist, Affymetrix
1996–1997	Senior Scientist, Affymetrix
1997–1998	Director of Genomics Research, Affymetrix
1998–1999	Vice President, Genomics Research, Affymetrix
1999–present	Genomics Advisor, Affymetrix
1999–present	Director of Genomics, Novartis Institute for Functional Genomics

Honors

1986–1987	Franklin Veatch Fellowship, Stanford University
1990–1993	Postdoctoral Fellowship, Damon Runyon – Walter Winchell Cancer Research Fund

Genomics, genes, tags, SNPs, drugs and chips

The power and usefulness of nucleic acid arrays stem from their ability to interrogate extremely complex mixtures of DNA and RNA, and to effectively count molecules in a highly parallel fashion. Counting molecules in complex mixtures of cDNA or RNA is obviously what needs to be done for gene expression monitoring (or 'expression profiling'), and both oligonucleotide and cDNA arrays have been put to good use for this purpose. For these types of measurements, it is important that the counting be consistent and at least semi-quantitative, and that the readout be as accurate, sensitive and specific as possible so that researchers can use the minimum number of cells, the fewest sample manipulations, detect the rarest mRNAs and keep the false positive rate to an absolute minimum. It is also important that these methods be robust and efficient so that they can be used when many experimental measurements are required (for example, extended time courses, multi-tissue comparisons and population studies), and can be incorporated into relatively high-throughput screens for chemical activities and interesting cellular phenotypes.

But beyond measurements of mRNA levels and expression changes, oligonucleotide arrays of various designs have been used successfully to search genes and other regions for sequence variations (for example SNPs), to genotype SNPs, to scan whole genomes for genetic markers (in yeast), to scan whole genomes for somatic-cell genetic changes (for example LOH events) that may be associated with tumour progression, to read out the results of genetic screens or selections, to count bar-coded yeast cells following parallel competitive growth, to read out the results of multiplexed, bar-coded DNA extension reactions and to investigate protein-DNA interactions with arrays of double-stranded DNA. It seems the list of possibilities will continue to grow rapidly as more people take advantage of the power and versatility of small arrays containing large numbers of specifically chosen oligonucleotides.