

Introduction to DNA Microarray Technologies

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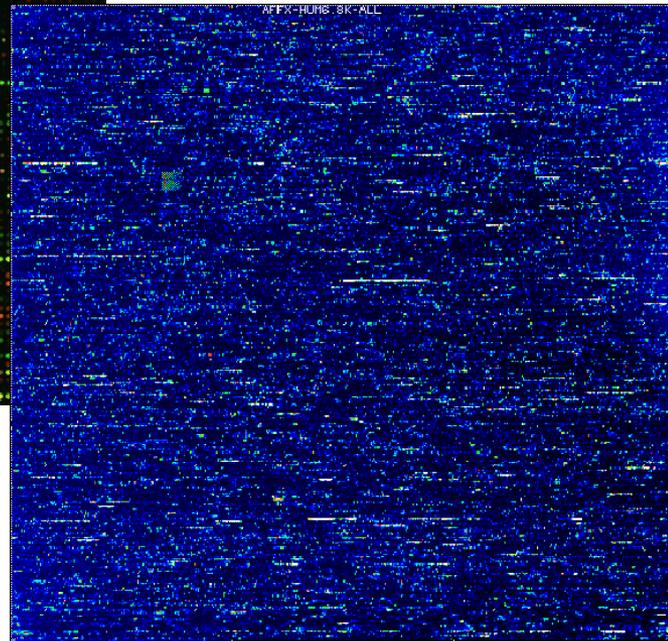
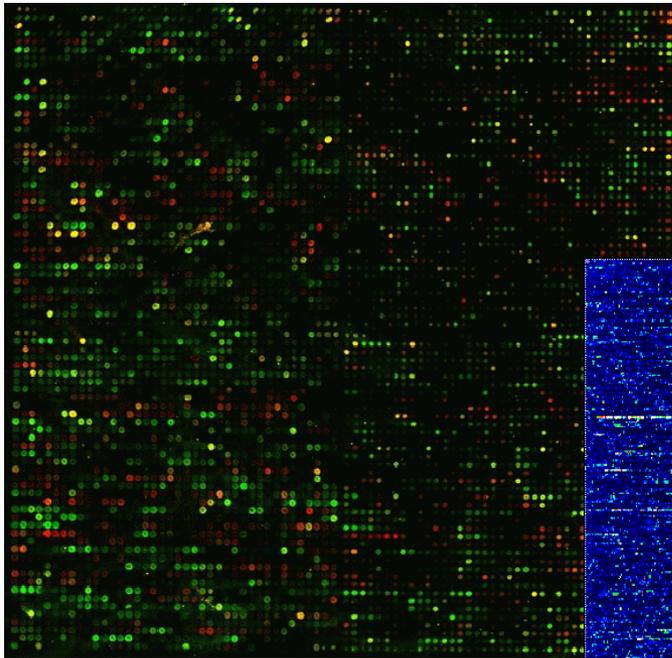
Bioconductor Short Course

Winter 2002

Outline

- Basic principles
- Spotted DNA microarrays
- Affymetrix oligonucleotide chips

DNA microarrays



DNA microarrays

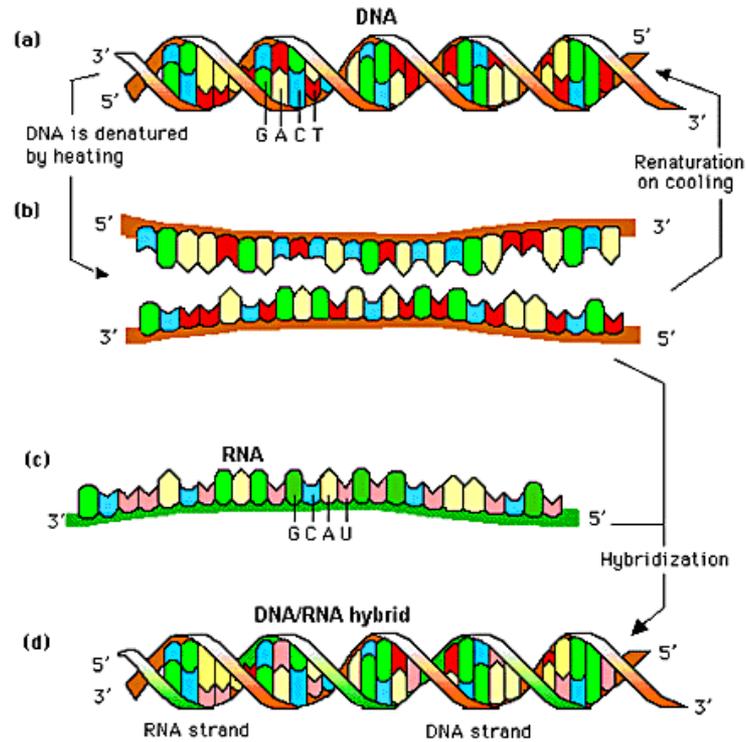
DNA microarrays rely on the hybridization properties of nucleic acids to monitor DNA or RNA abundance on a genomic scale in different types of cells.

The ancestor of cDNA microarrays: the Northern blot.

Hybridization

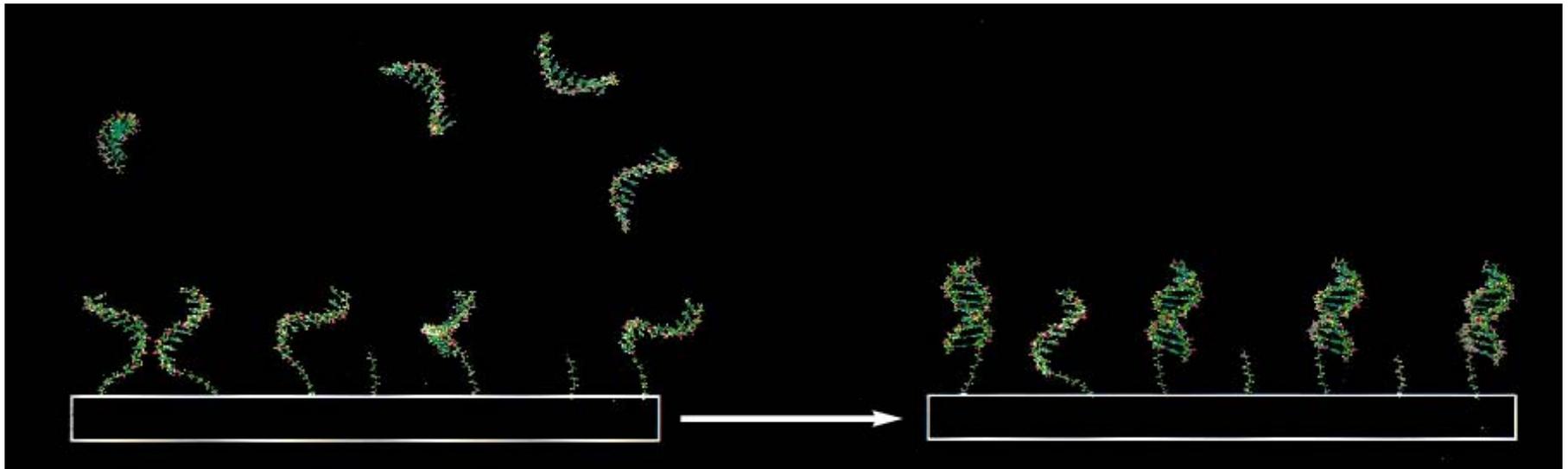
- **Hybridization** refers to the **annealing** of two nucleic acid strands following the base-pairing rules.
- Nucleic acid strands in a duplex can be separated, or **denatured**, by heating to destroy the hydrogen bonds.

Hybridization



Nucleic Acid Hybridization

Hybridization



Gene expression assays

The main types of gene expression assays:

- Serial analysis of gene expression (SAGE);
- Short oligonucleotide arrays (Affymetrix);
- Long oligonucleotide arrays (Agilent Inkjet);
- Fibre optic arrays (Illumina);
- Spotted cDNA arrays (Brown/Botstein).

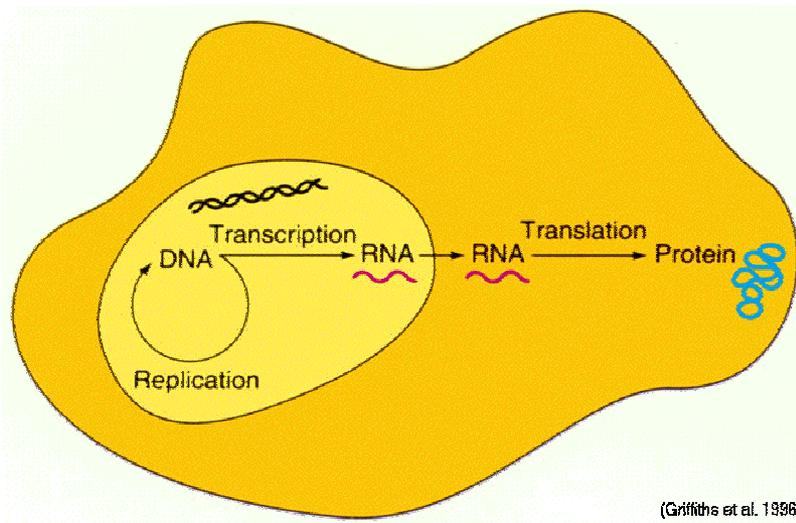
Applications of microarrays

- Measuring transcript abundance (cDNA arrays);
- Genotyping;
- Estimating DNA copy number (CGH);
- Determining identity by descent (GMS);
- Measuring mRNA decay rates;
- Identifying protein binding sites;
- Determining sub-cellular localization of gene products;
- ...

Applications of microarrays

- **Cancer research:** Molecular characterization of tumors on a genomic scale
 - more reliable diagnosis and effective treatment of cancer.
- **Immunology:** Study of host genomic responses to bacterial infections.
- ...

Transcriptome



- mRNA or transcript levels sensitively reflect the state of a cell.
- Measuring protein levels (translation) would be more direct but more difficult.

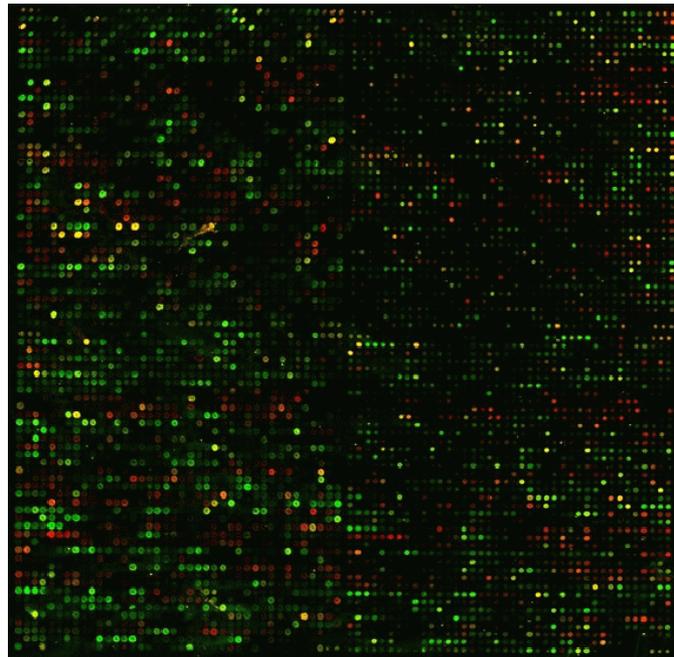
Transcriptome

- The **transcriptome** reflects
 - Tissue source: cell type, organ.
 - Tissue activity and state:
 - Stage of development, growth, death.
 - Cell cycle.
 - Disease vs. healthy.
 - Response to therapy, stress.

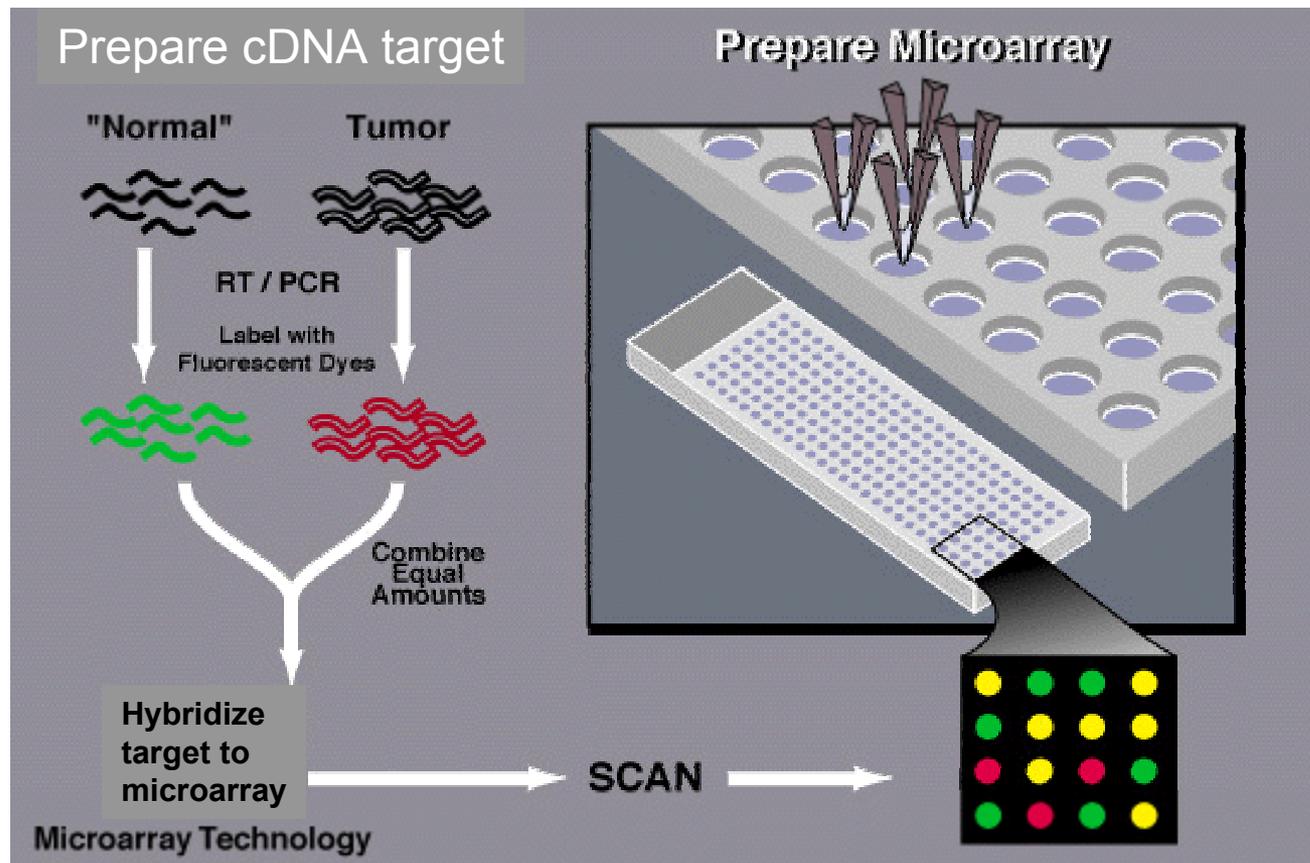
Applications of microarrays

- Compare mRNA (transcript) levels in different types of cells, i.e., vary
 - Tissue: liver vs. brain;
 - Treatment: drugs A, B, and C;
 - State: tumor vs. non-tumor, development;
 - Organism: different yeast strains;
 - Timepoint;
 - etc.

Spotted DNA microarrays



Spotted DNA microarrays



Spotted DNA microarrays

- The **relative abundance** of a spotted DNA sequence in two DNA or RNA samples may be assessed by monitoring the **differential hybridization** of these two samples to the sequence on the array.
- **Probes**: DNA sequences spotted on the array, immobile substrate.
- **Targets**: Nucleic acid samples hybridized to the array, mobile substrate.

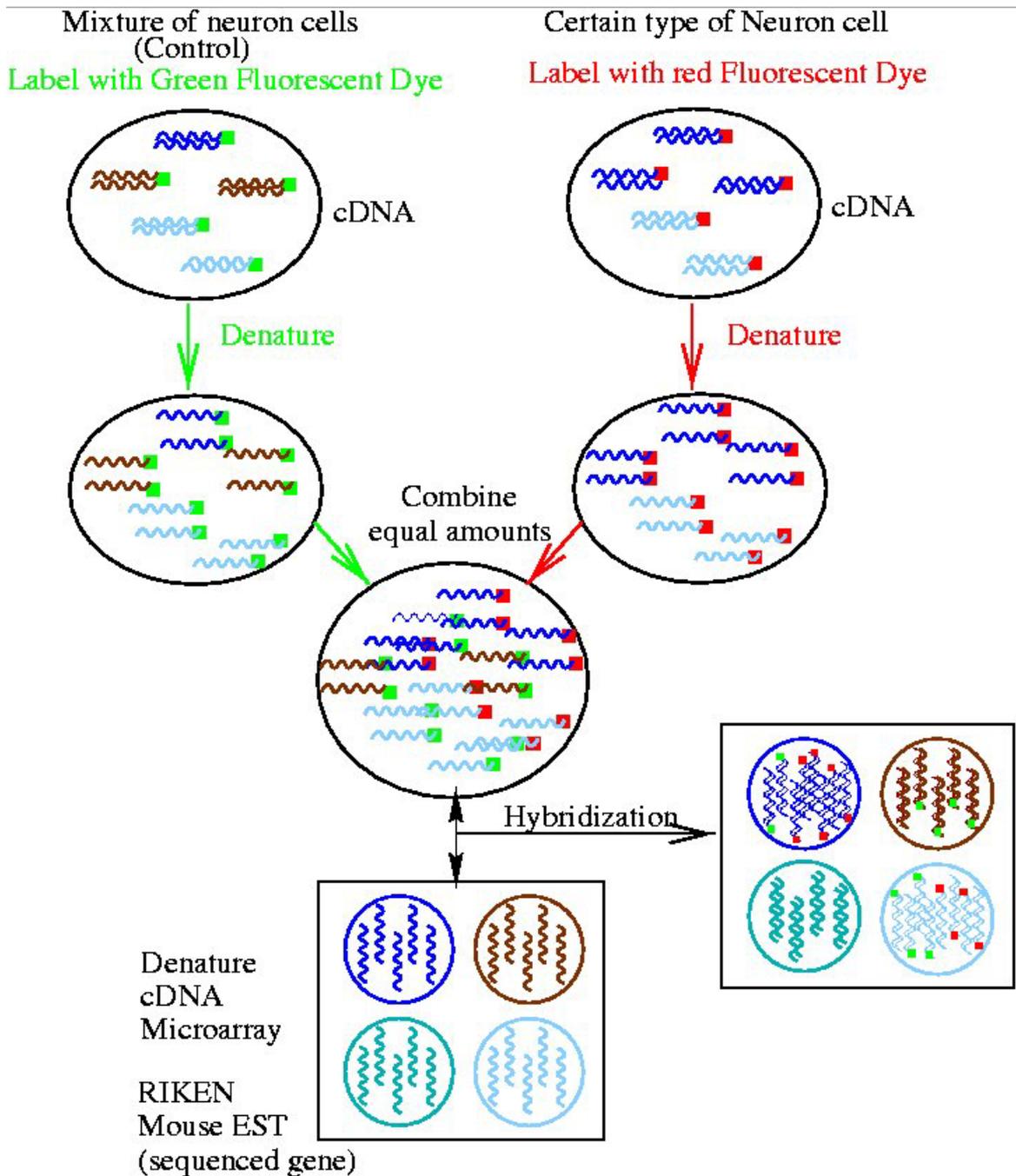
Spotted DNA microarrays

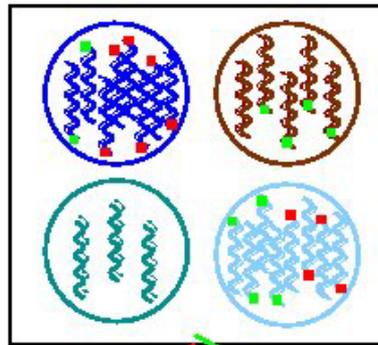
- The **ratio** of the red and green fluorescence intensities for each spot is indicative of the relative abundance of the corresponding DNA probe in the two nucleic acid target samples.

Spotted DNA microarrays

$$M = \log_2 R/G = \log_2 R - \log_2 G$$

- **M < 0**, gene is over-expressed in green-labeled sample compared to red-labeled sample.
- **M = 0**, gene is equally expressed in both samples.
- **M > 0**, gene is over-expressed in red-labeled sample compared to green-labeled sample.





Scan for Red
Wavelength

Scan for Green
Wavelength

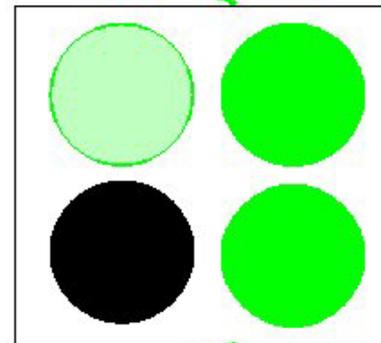
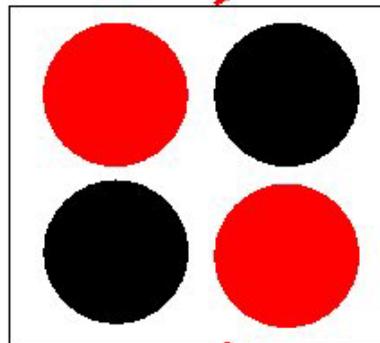
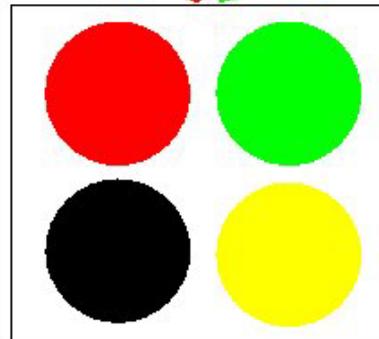
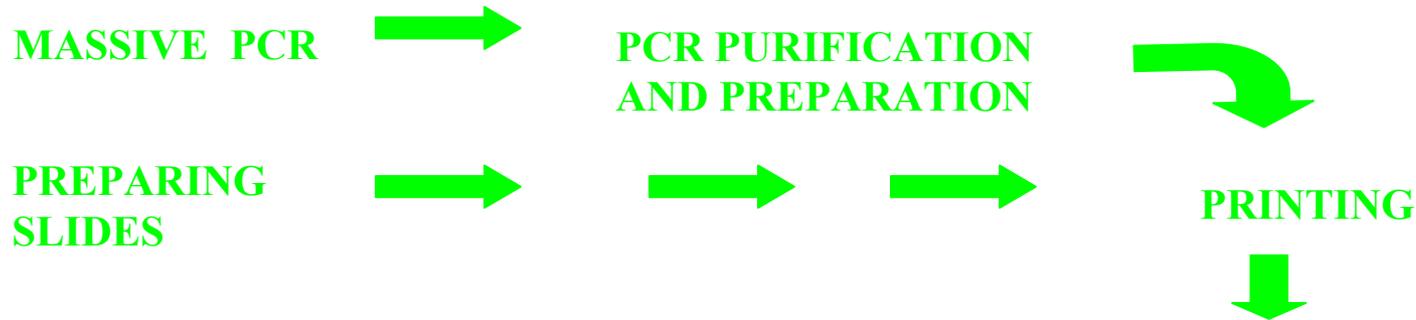


Image Programs
ScanAlyze

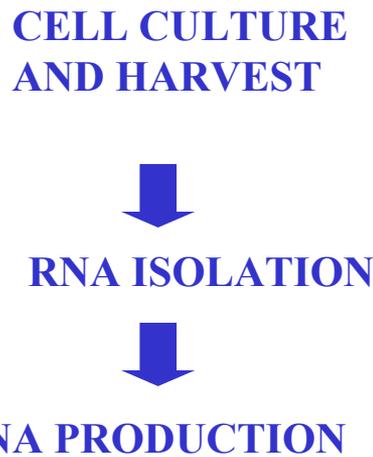


The process

Building the microarray:



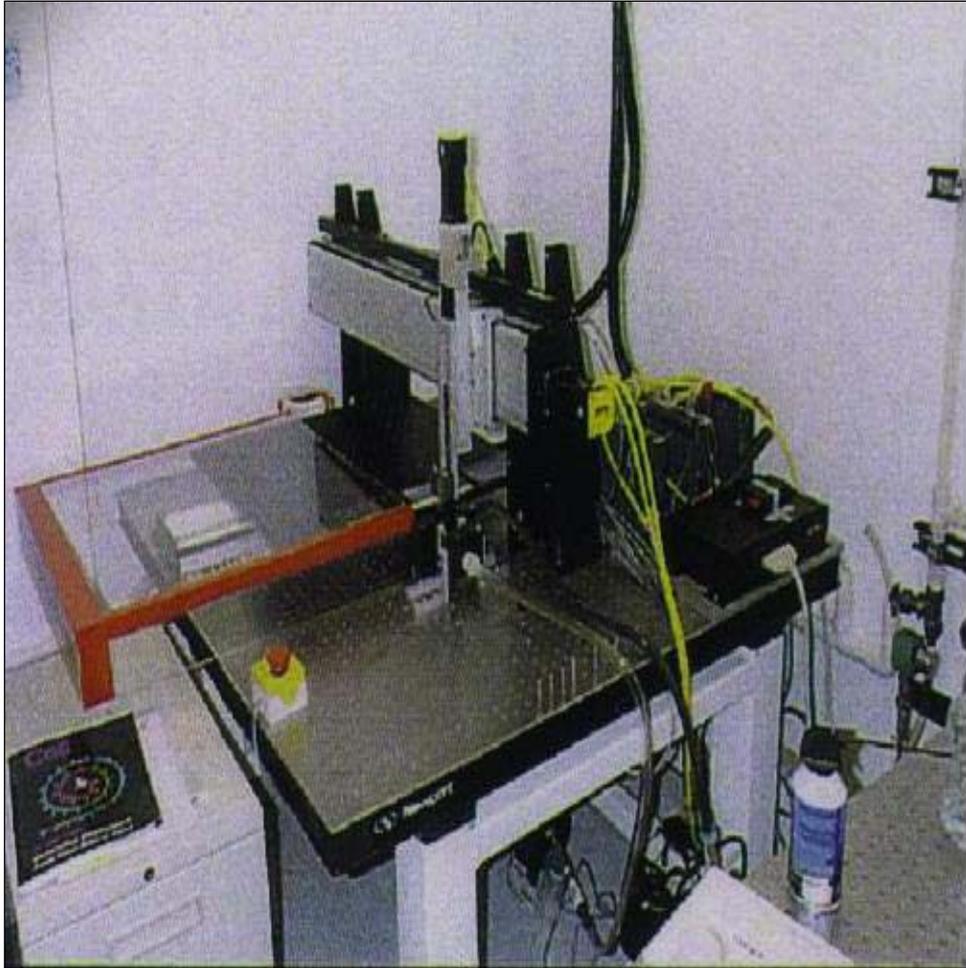
RNA preparation:



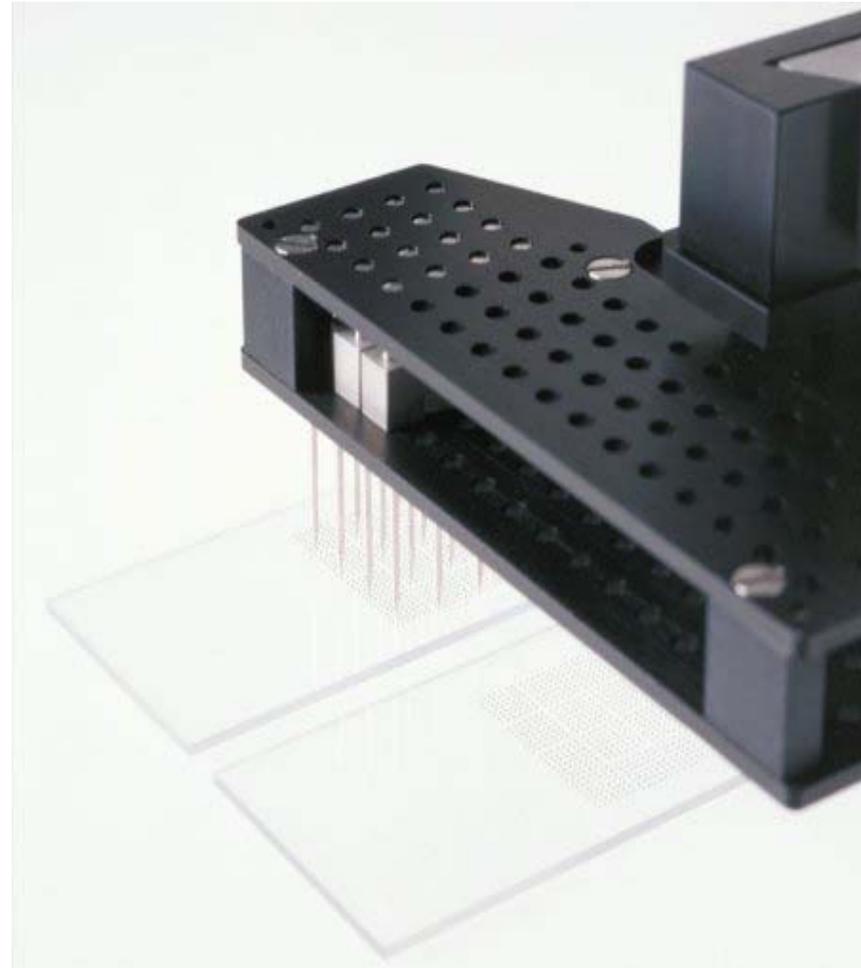
Hybing the array:



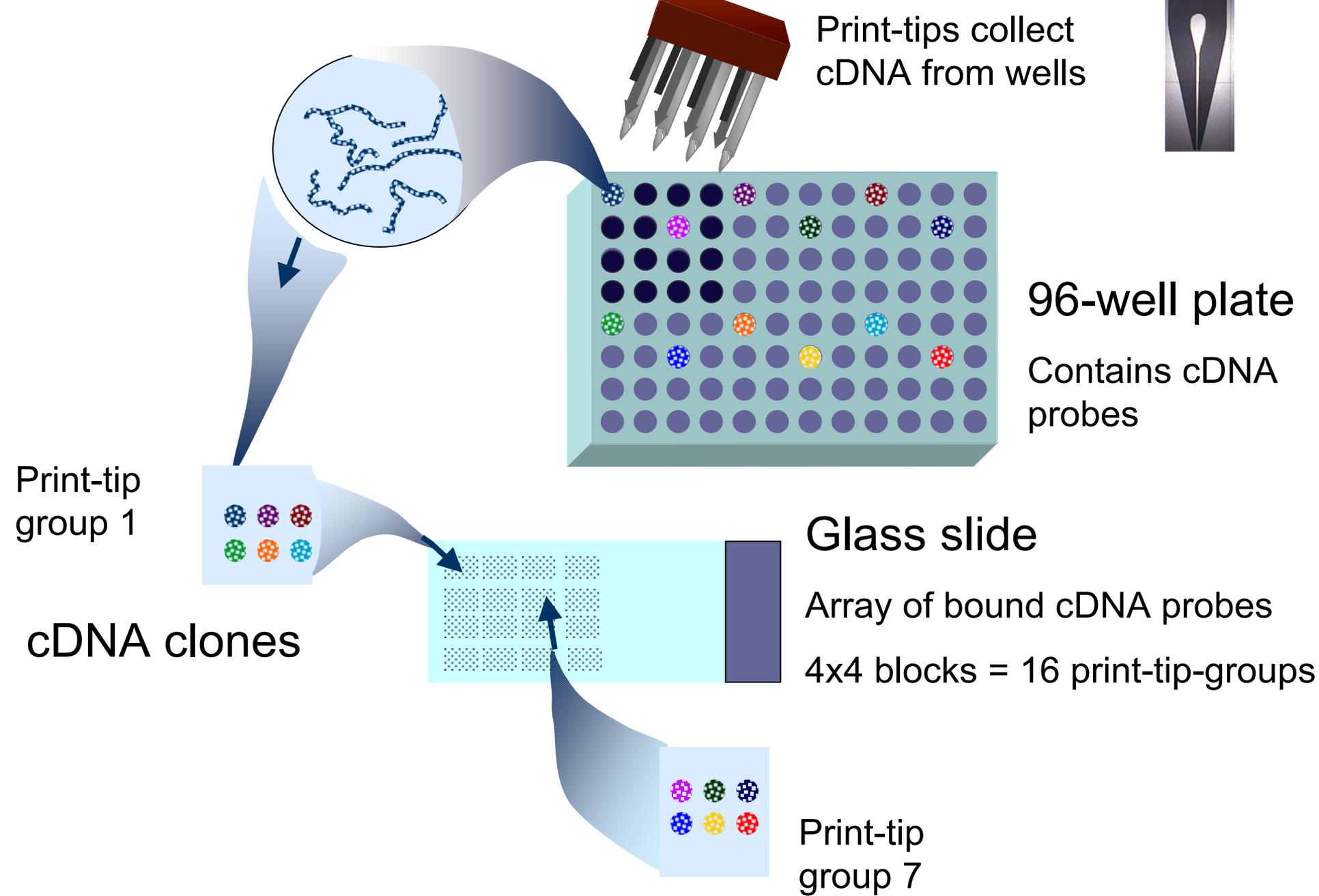
The arrayer



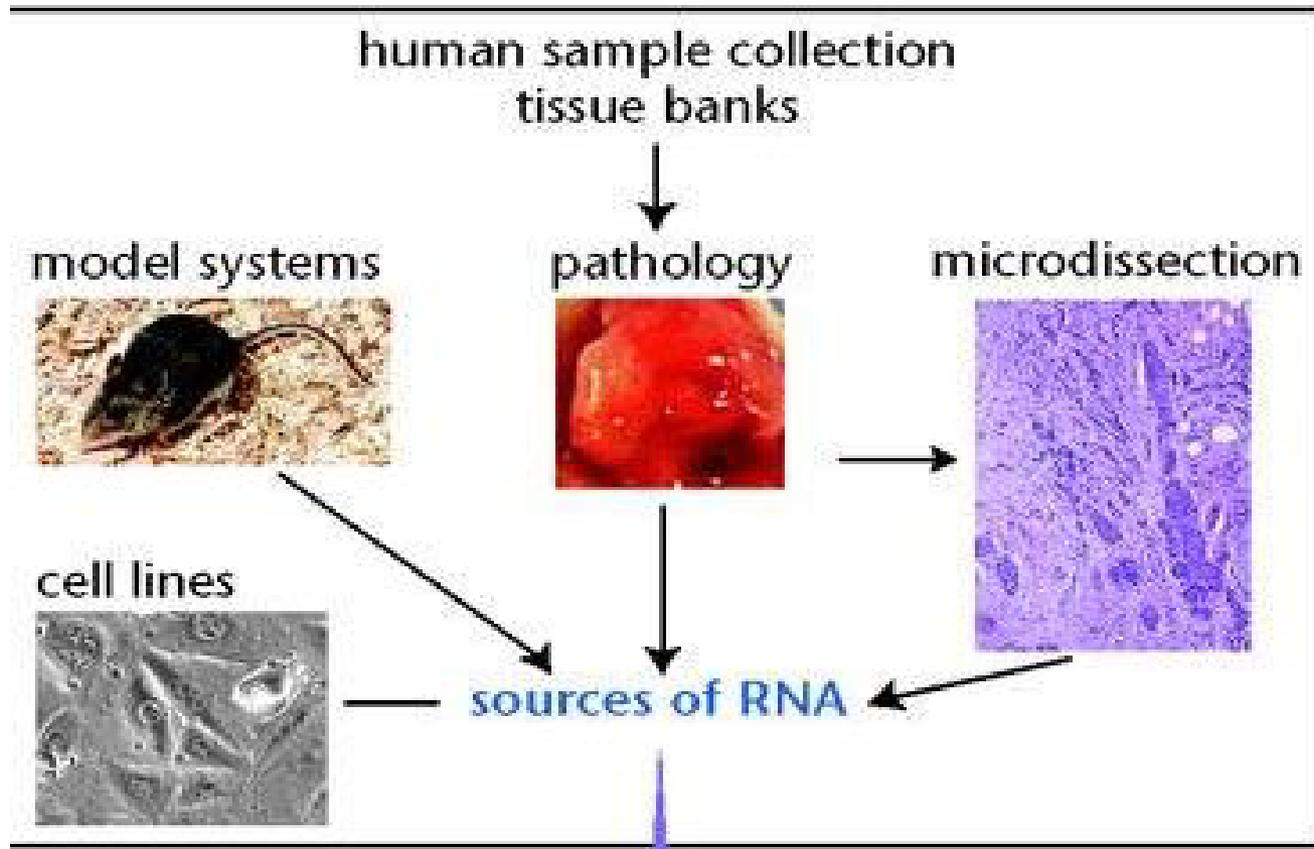
Ngai Lab arrayer, UC Berkeley



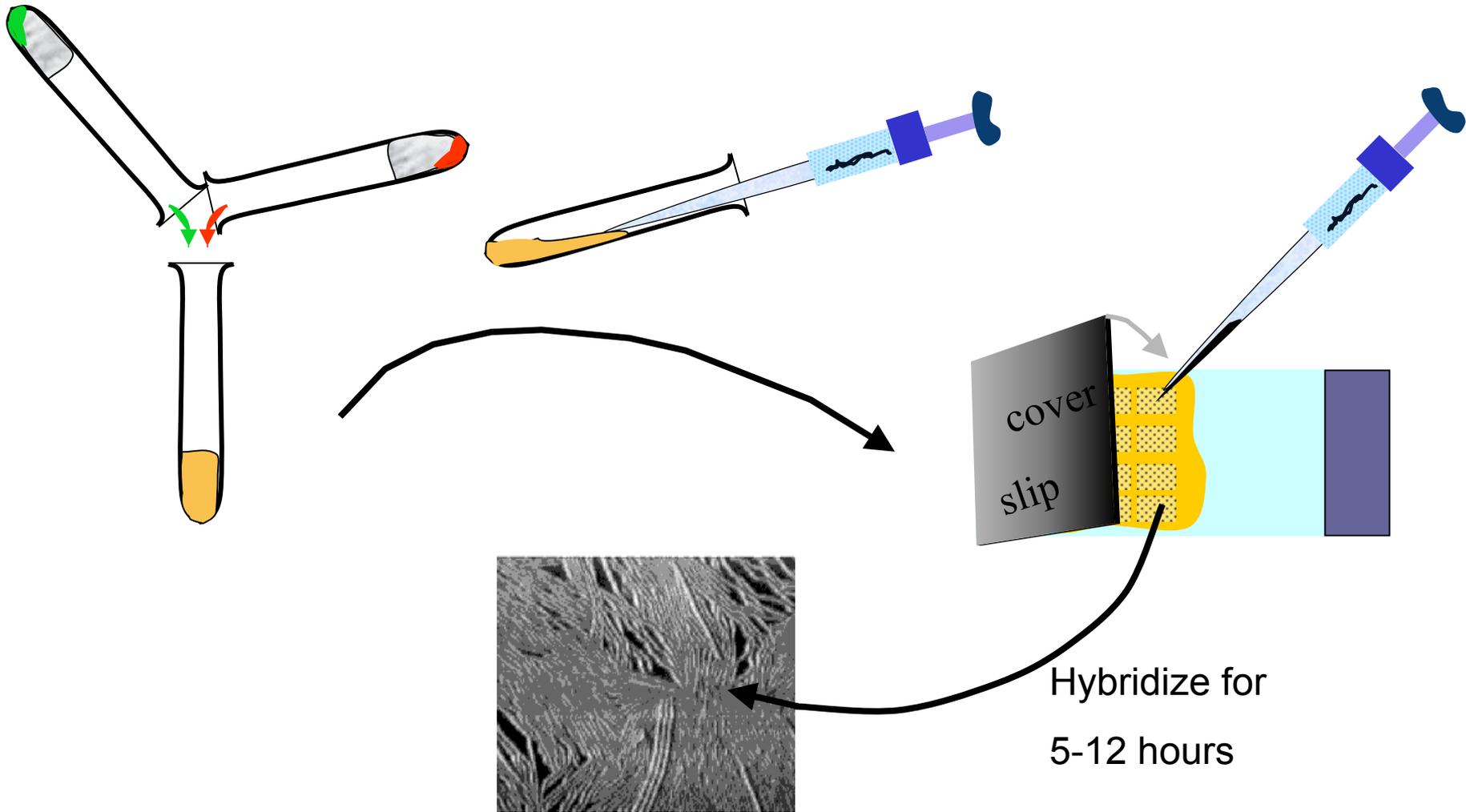
Print-head



Sample preparation

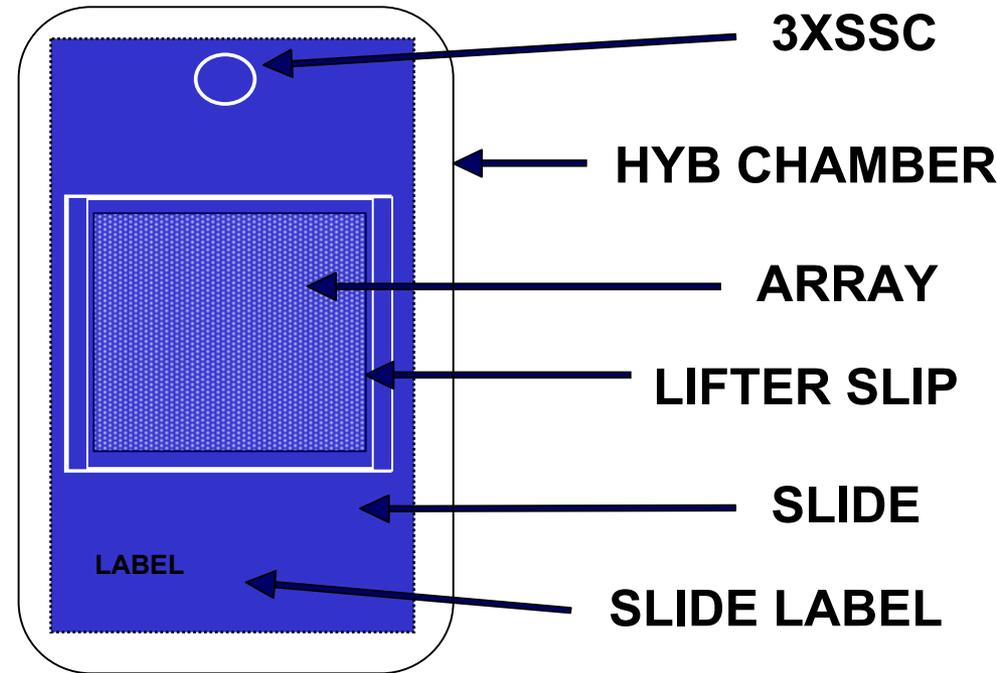


Hybridization



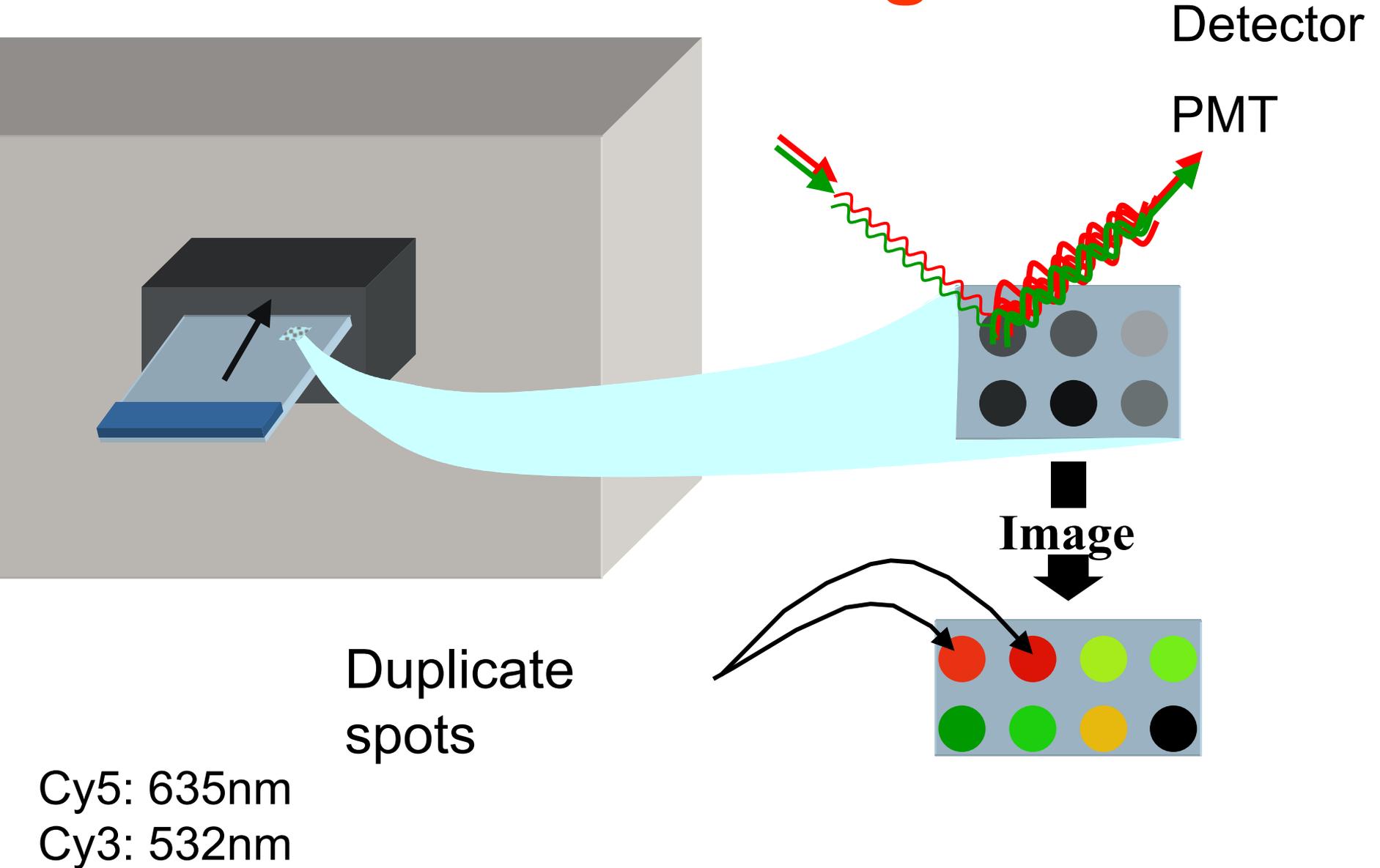
Binding of cDNA target samples to cDNA probes on the slide

Hybridization chamber

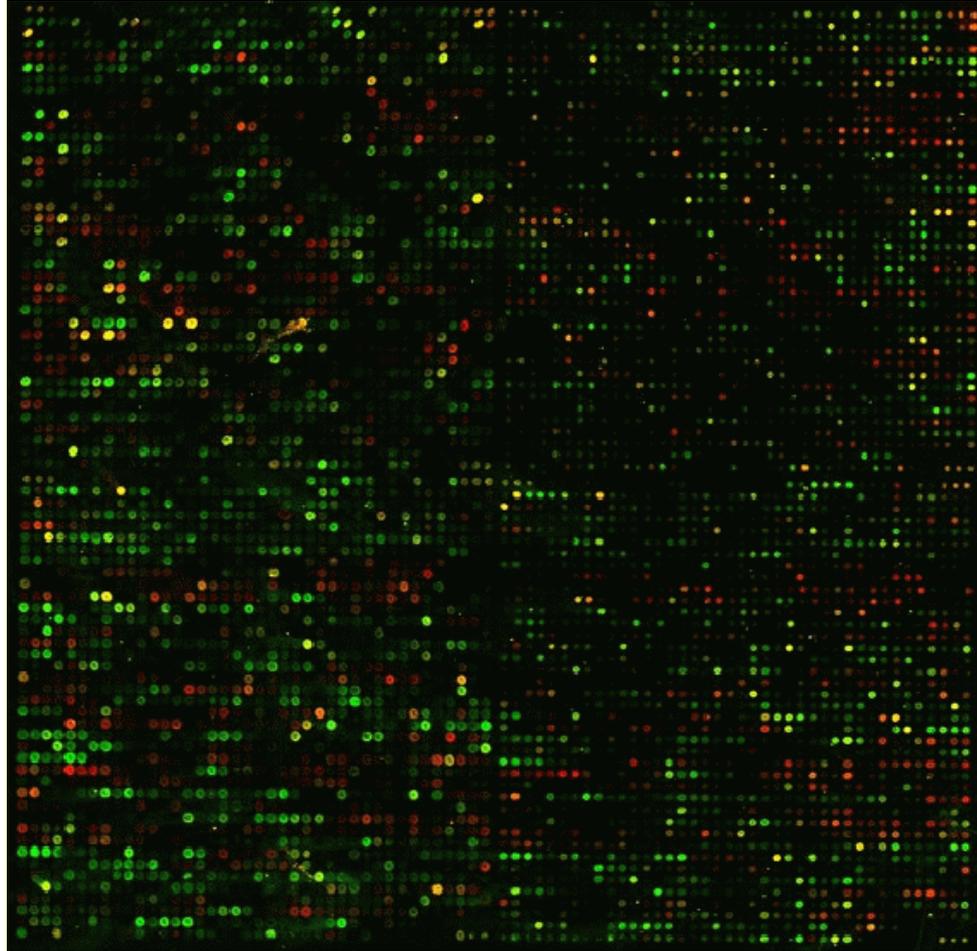


- Humidity
- Temperature
- Formamide
(Lowers the Tmp)

Scanning



RGB overlay of Cy3 and Cy5 images



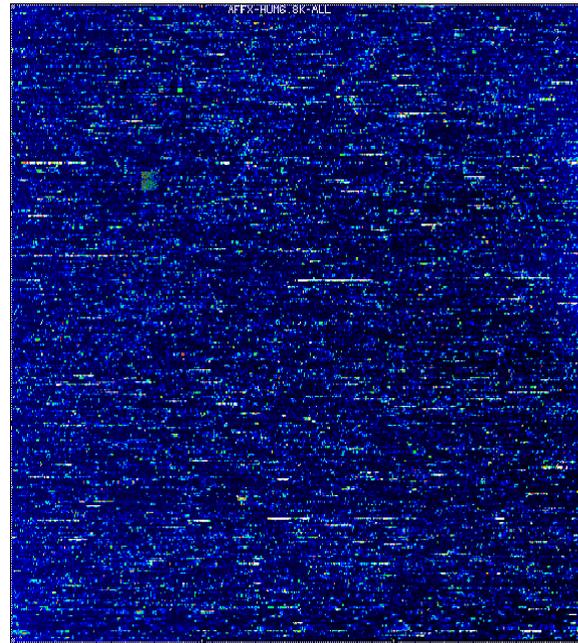
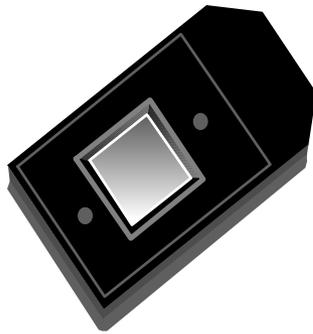
Raw data

- Pairs of 16-bit TIFFs, one for each dye.
- E.g. Human cDNA arrays:
 - ~43K spots;
 - ~ 20Mb per channel;
 - ~ 2,000 x 5,500 pixels per image;
 - spot separation: ~ 136 μ m.
- For a “typical” array, the spot area has
 - mean = 43 pixels,
 - med = 32 pixels,
 - SD = 26 pixels.

Animation

<http://www.bio.davidson.edu/courses/genomics/chip/chip.html>

Oligonucleotide chips



Terminology

- Each gene or portion of a gene is represented by 16 to 20 oligonucleotides of 25 base-pairs.
- **Probe**: an oligonucleotide of 25 base-pairs, i.e., a 25-mer.
- **Perfect match (PM)**: A 25-mer complementary to a reference sequence of interest (e.g., part of a gene).
- **Mismatch (MM)**: same as PM but with a single homomeric base change for the middle (13th) base (transversion purine \leftrightarrow pyrimidine, G \leftrightarrow C, A \leftrightarrow T) .
- **Probe-pair**: a (PM,MM) pair.
- **Probe-pair set**: a collection of probe-pairs (16 to 20) related to a common gene or fraction of a gene.
- **Affy ID**: an identifier for a probe-pair set.
- The purpose of the MM probe design is to measure non-specific binding and background noise.

Probe-pair set

GeneChip® Expression Array Design

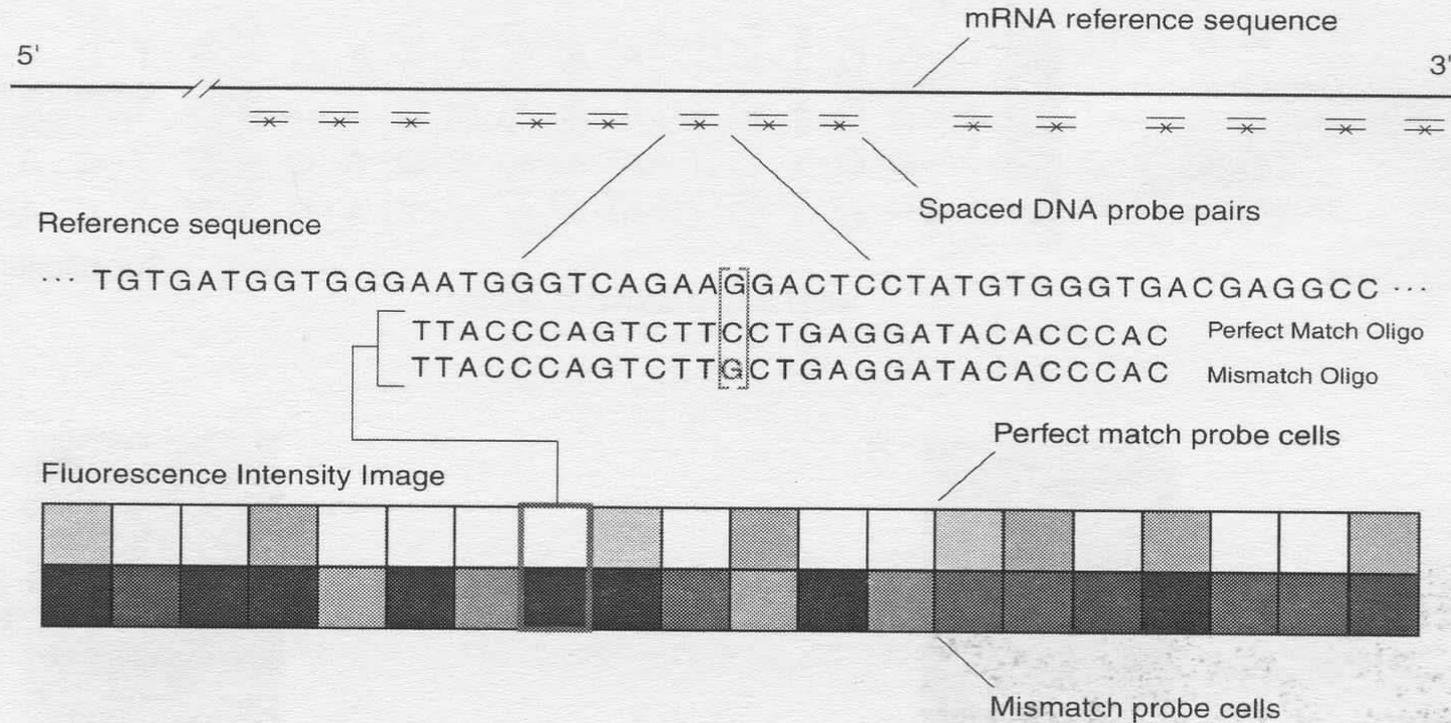


Figure 1-3 Expression tiling strategy

Spotted vs. Affymetrix arrays

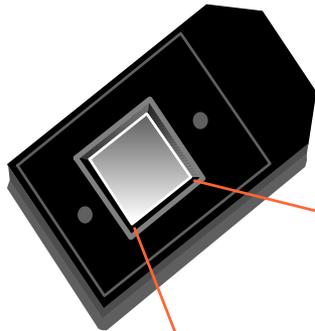
Spotted arrays

Affymetrix arrays

One probe per gene	16 – 20 probe-pairs per gene
Probes of varying length	Probes are 25-mers
Two target samples per array	One target sample per array

Oligonucleotide chips

GeneChip Probe Array



1.28cm

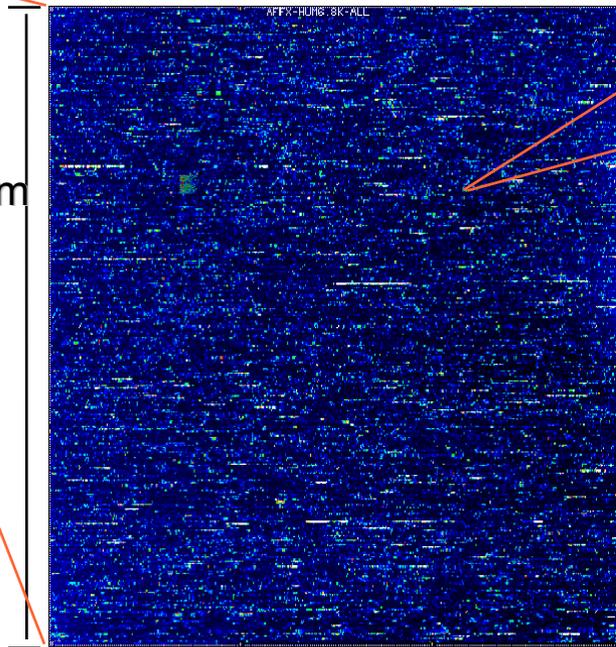
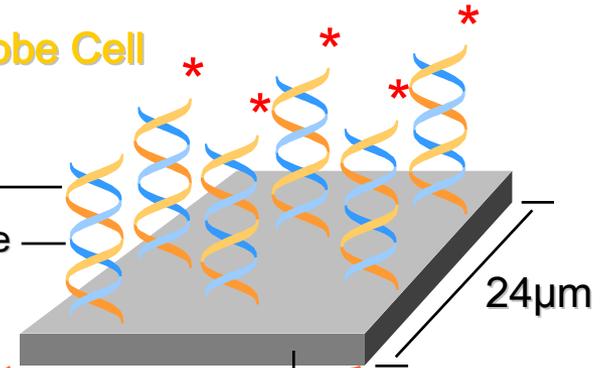


Image of Hybridized Probe Array

Hybridized Probe Cell

Single stranded,
labeled RNA target
Oligonucleotide probe



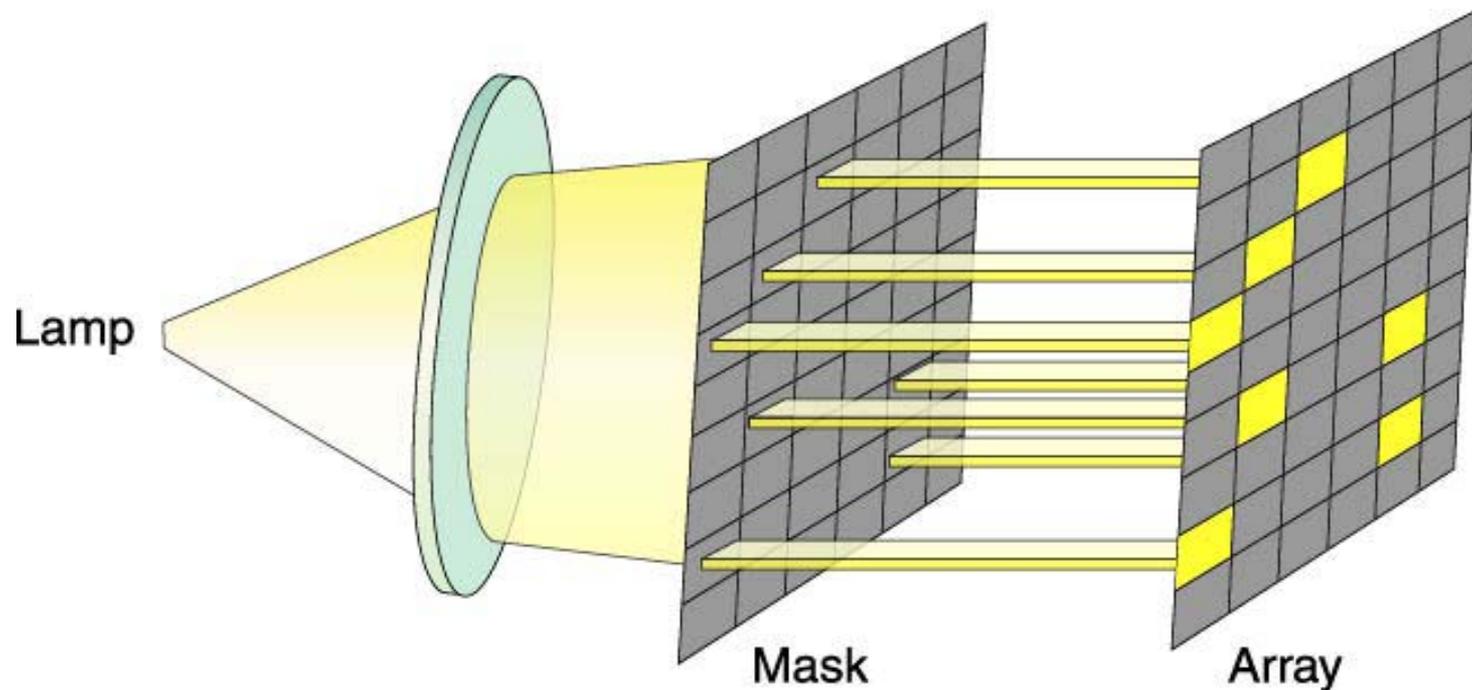
Millions of copies of a specific
oligonucleotide probe

>200,000 different
complementary probes

Oligonucleotide chips

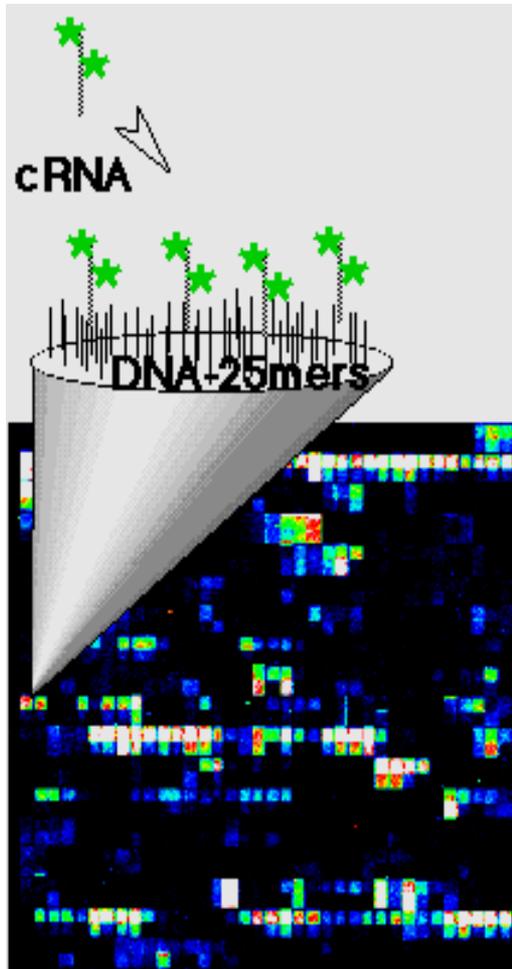
- The probes are synthesized *in situ*, using combinatorial chemistry and photolithography.
- **Probe cells** are square-shaped features on the chip containing millions of copies of a single 25-mer probe. Sides are 18-50 microns.

Oligonucleotide chips



The manufacturing of GeneChip® probe arrays is a combination of photolithography and combinational chemistry.

Image analysis

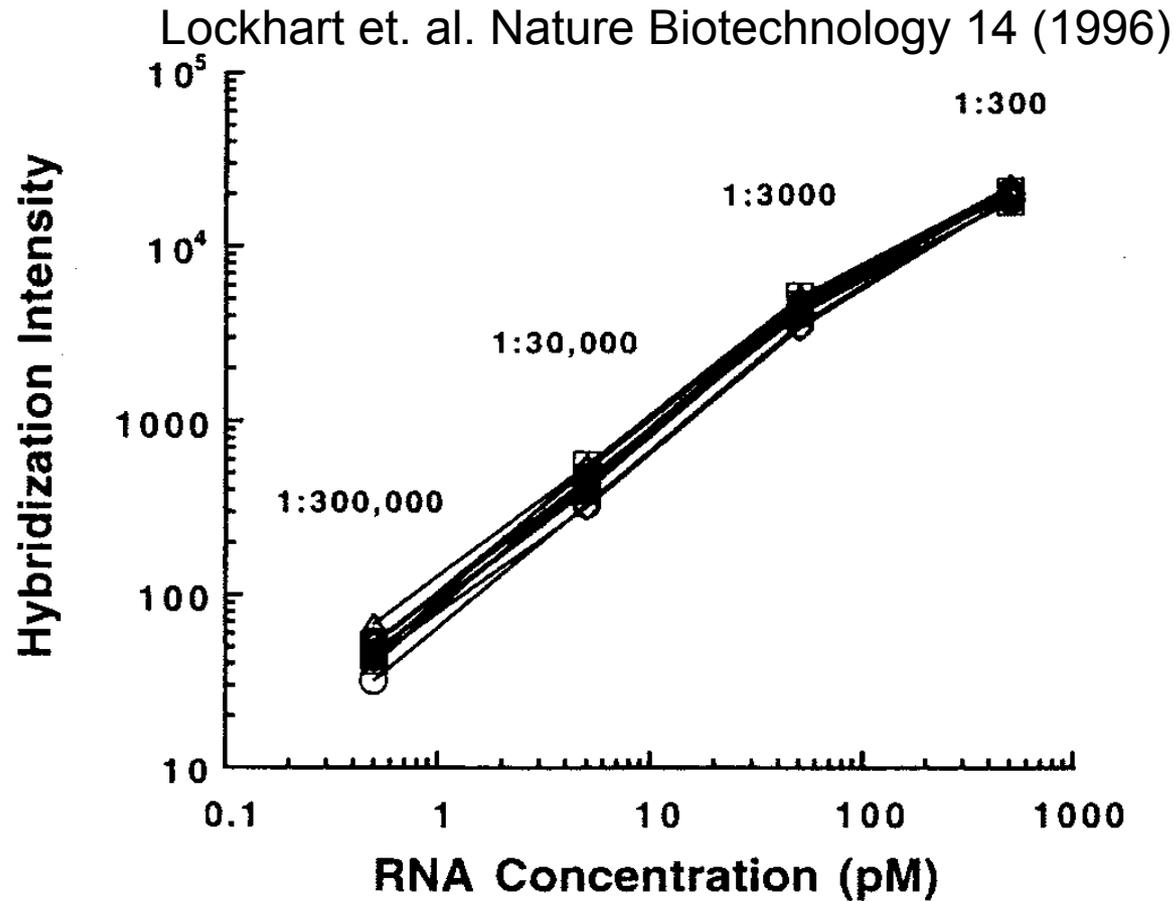


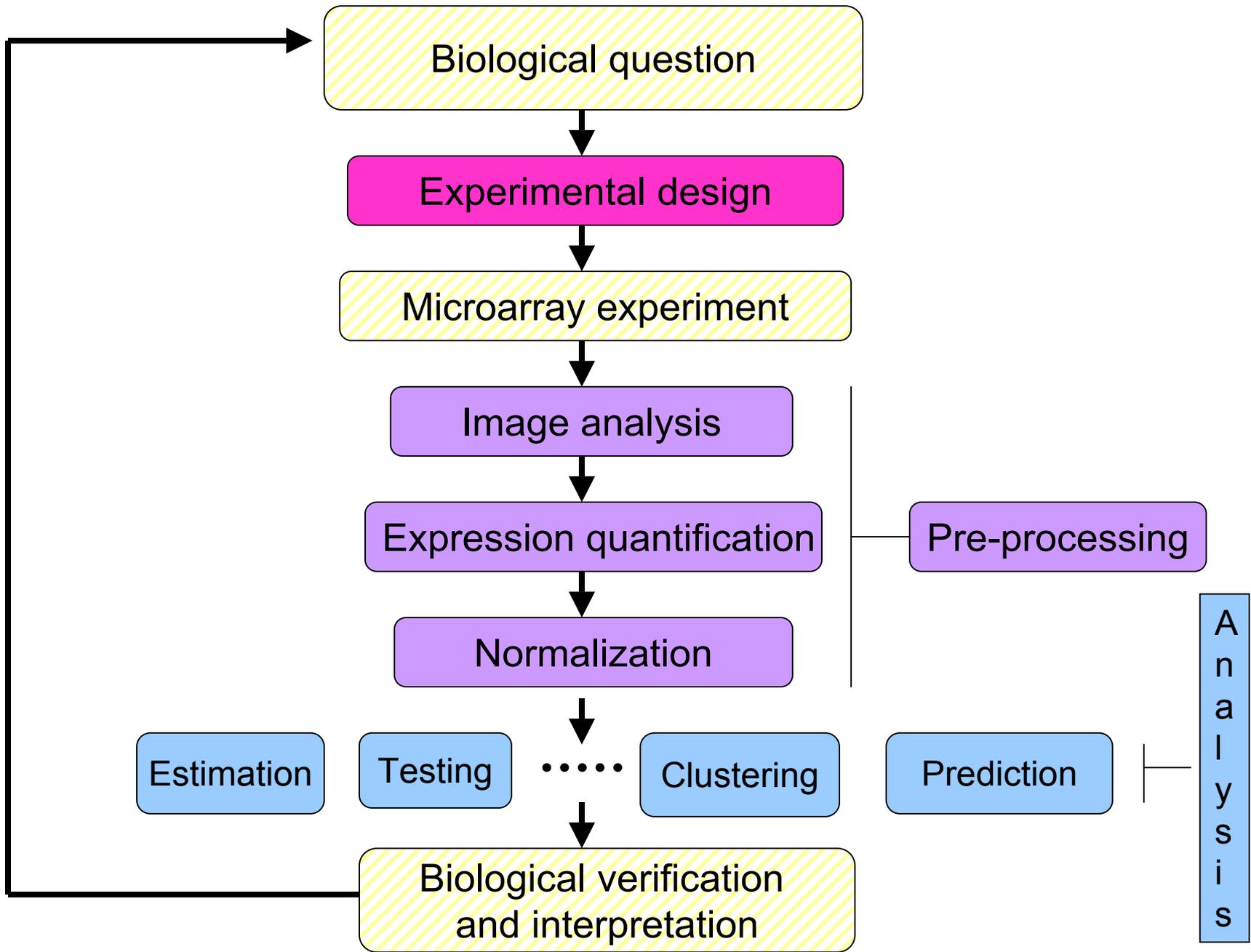
- About 100 pixels per probe cell.
- These intensities are combined to form one number representing the expression level for the probe cell oligo.
- → CEL file with PM or MM intensity for each cell.

Expression measures

- Most expression measures are based on differences of **PM-MM**.
- The intention is to correct for background and non-specific binding.
- E.g. *MarrayArray Suite*[®] (MAS) v. 4.0 uses Average Difference Intensity (ADI) or
AvDiff = average of PM-MM.
- Problem: MM may also measure signal.
- More on this in lecture *Pre-processing DNA Microarray Data*.

What is the evidence?





Statistical computing

Everywhere ...

- Statistical design and analysis:
 - image analysis, normalization, estimation, testing, clustering, prediction, etc.
- Integration of experimental metadata with biological metadata from WWW-resources
 - gene annotation (GenBank, LocusLink);
 - literature (PubMed);
 - graphical (pathways, chromosome maps).

Integration of experimental and biological metadata

- Expression, sequence, structure, annotation, literature.
- Integration will depend on our using a common language and will rely on database methodology as well as statistical analyses.
- This area is largely unexplored.

WWW resources

- **Complete guide to “microarraying”**

<http://cmgm.stanford.edu/pbrown/mguide/>

<http://www.microarrays.org>

- Parts and assembly instructions for printer and scanner;
- Protocols for sample prep;
- Software;
- Forum, etc.

- **cDNA microarray animation**

<http://www.bio.davidson.edu/courses/genomics/chip/chip.html>

- **Affymetrix**

<http://www.affymetrix.com>

Next ...

Pre-processing DNA Microarray Data

- Spotted DNA microarrays
 - Image analysis;
 - Normalization.
- Affymetrix oligonucleotide chips
 - Image analysis;
 - Normalization;
 - Expression measures.