

Scanning Microarrays: Current Challenges and Future Directions

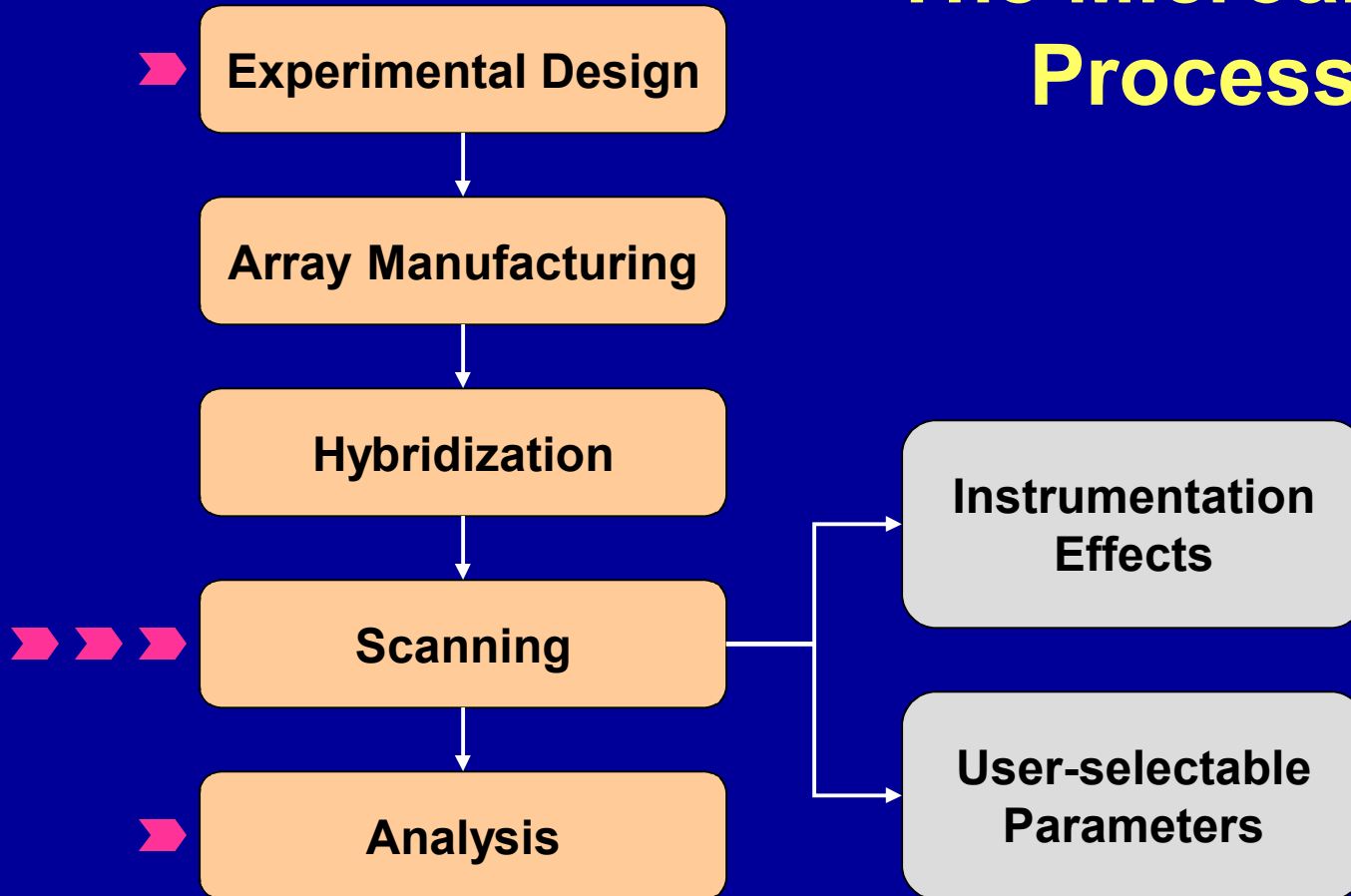
**Jerilyn A. Timlin, David M. Haaland,
Michael B. Sinclair, Rachel Noek
Sandia National Laboratories***

* Sandia is a multiprogram laboratory operated by Sandia Corporation,
a Lockheed Martin Company, for the United States Department of
Energy's National Nuclear Security Administration under contract DE-
AC04-94AL85000

Presentation Overview

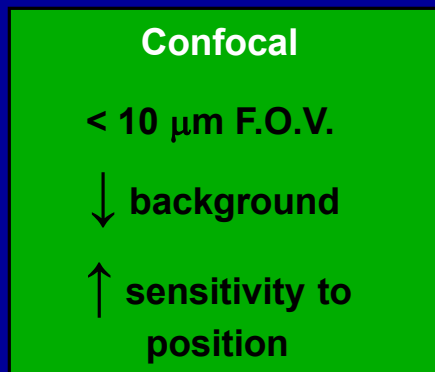
- Introduction
- Current challenges
 - User
 - Slide handling
 - Display
 - Resolution, averaging
 - PMT settings
 - Instrument
 - Signal contamination, bias
 - Use of calibration slides
- Complimenting technology ... spectral imaging

The Microarray Process

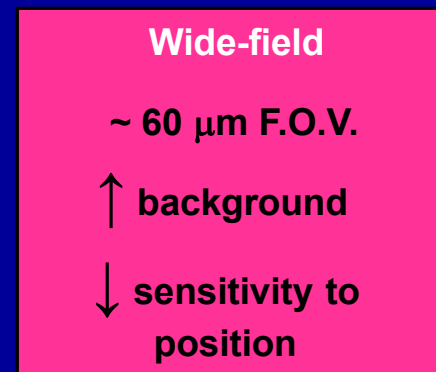


User-Selectable Parameters – Array Handling

- Fingerprints, dust contaminate signal
- Light and ozone decrease signal
- Positioning:
 - Face-up vs. Face down
 - Scanner matters



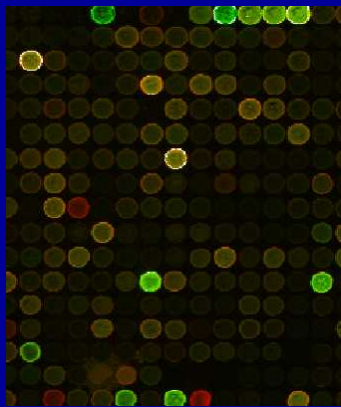
VS.



User- Selectable Parameters – Image Display

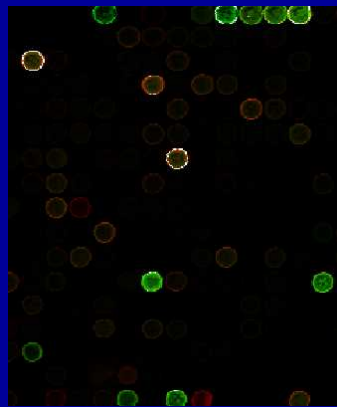
16-bit data → 8-bit display

Compression

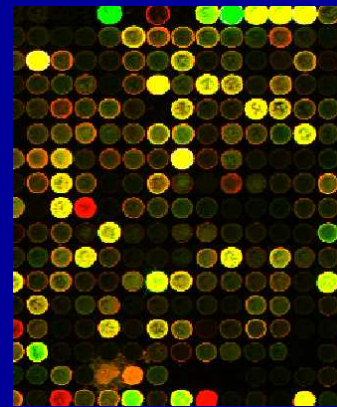


Sq Root Transform
0 - 65535

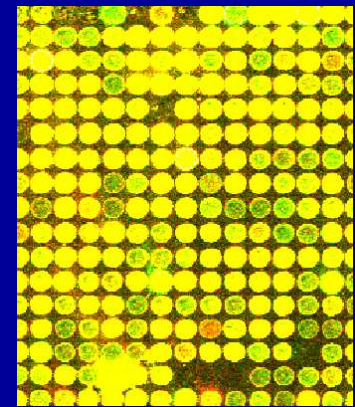
Reduction



High
256 - 65535



Middle
16 - 4096



Low
0 - 255

User- Selectable Parameters – Getting Signal

- Pixel dwell time
- Spatial resolution
- Signal averaging
- Laser power
- PMT gain

User- Selectable Parameters – Getting Signal

On-the-fly PMT Gain Optimizing – not Advantageous?

Measurement Model

$$Y_{ijk} = \mu_i + \alpha_j + \beta_{k(j)} + \varepsilon_{ijk}$$

Y_{ijk} = Log2(R/G) measurement of i^{th} gene (k^{th} rep within j^{th} culture)

i = gene label

j = culture label

k = rep (withinculture) label

μ_i = overall average of i^{th} gene

α_j = global effect of j^{th} culture (across all genes)

$\beta_{k(j)}$ = global effect of k^{th} rep within j^{th} culture (across all genes)

ε_{ijk} = specific effect of i^{th} gene (k^{th} rep within j^{th} culture)

PMT Settings Adjusted

$$\hat{\sigma}_{\alpha} = .575 \text{ (2 dof)}$$

$$\hat{\sigma}_{\beta} = .179 \text{ (3 dof)}$$

PMT Settings Constant

$$\hat{\sigma}_{\alpha} = .081 \text{ (2 dof)}$$

$$\hat{\sigma}_{\beta} = .090 \text{ (3 dof)}$$

Instrumentation Effects – Scanner Bias/ Stability

- Bias to one channel can arise from:

- Dye hybridization
- Contaminating signal *
- PMTs *

Solutions? Transforms,
Spectral imaging

- Stability

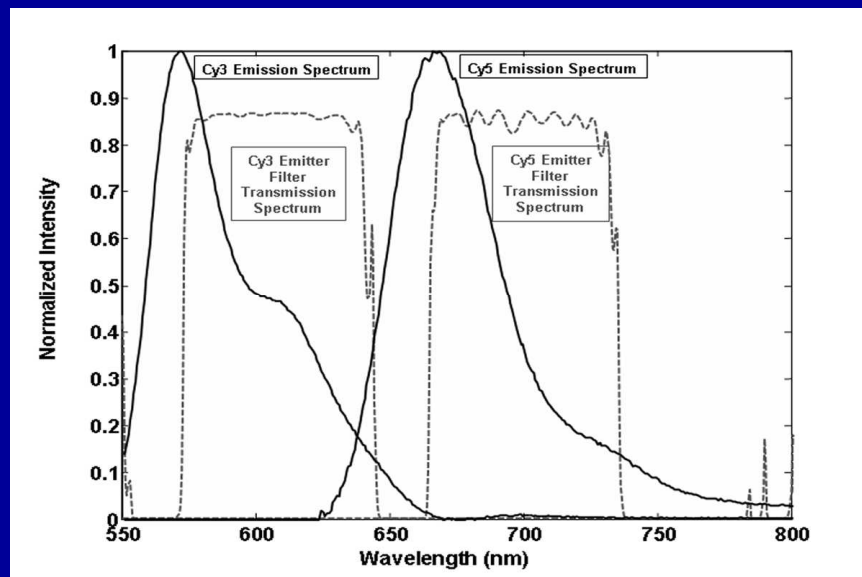
- Lasers
- PMTs
- Optics
- Scanning devices

Instrument stability
needs to be thoroughly
checked on a regular
basis → standards

Example...

Instrumentation Effects – Signal Contamination

- Signal from something other than dye of interest gets detected in a channel
- Spectral crosstalk, contaminating fluorescence, stray light, etc.
- Background methods assume approximation from signal around spot – a rarity
- Even low absolute intensities lead to normalization, ratio errors

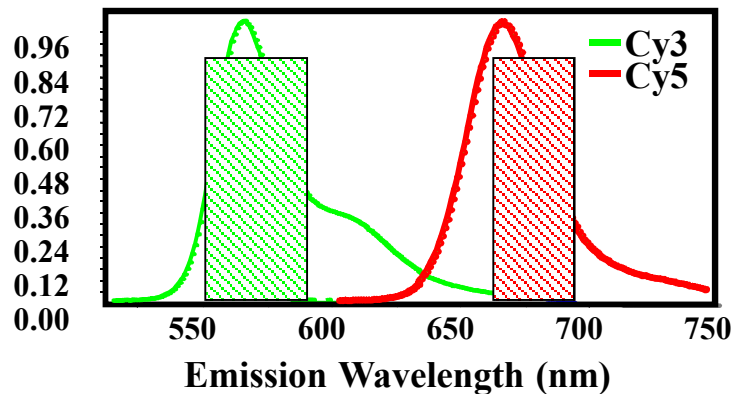


Alternative Scanning Technologies

- **Surface Plasmon Resonance (SPR)**
- **Resonance Light Scattering (RLS)**
- **Hyperspectral Scanning (HSS)**

Technology Comparison

Filter-based Scanner



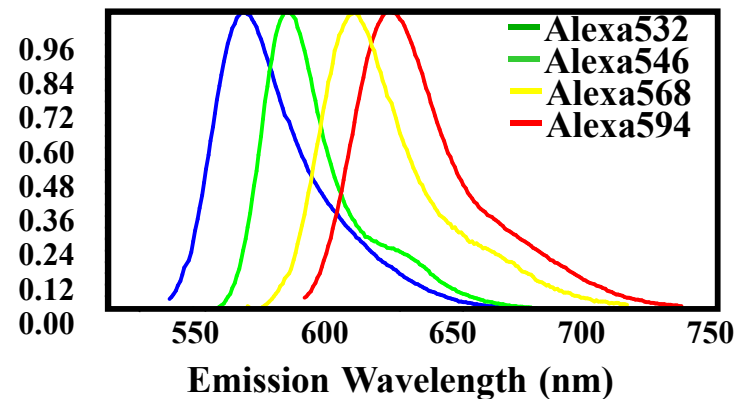
Univariate

Collect all photons within a wavelength region

Require well-separated emissions and ONE laser/label

Limited in practice to 2/3 labels

Hyperspectral Scanner



Multivariate

Collects an entire emission spectrum at each pixel

Excites multiple, overlapping dyes with ONE laser

Have shown separation of 4+

The key to HSS is Multivariate Analysis

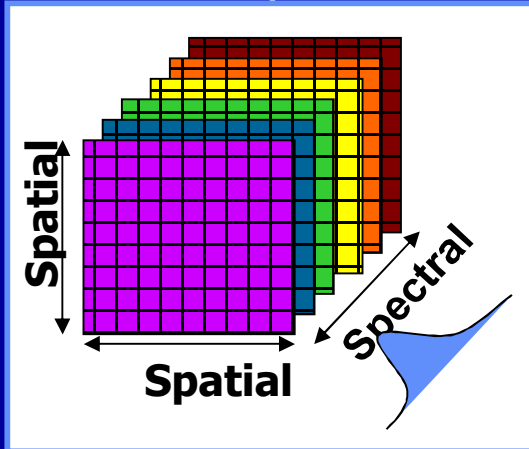
Advantages of HSS & Multivariate Data Analysis

Discover & quantify all emitting species in a sample simultaneously

- Increased sensitivity
- Extended dynamic range
- Improved background/interference correction
- Improved accuracy , reliability , & quantitation
- Increase throughput – multiple overlapping dyes

Hyperspectral Image Cube & Analysis

Each pixel of the image contains the entire emission spectrum 540-900 nm



Preprocess

Initial Estimates

MCR

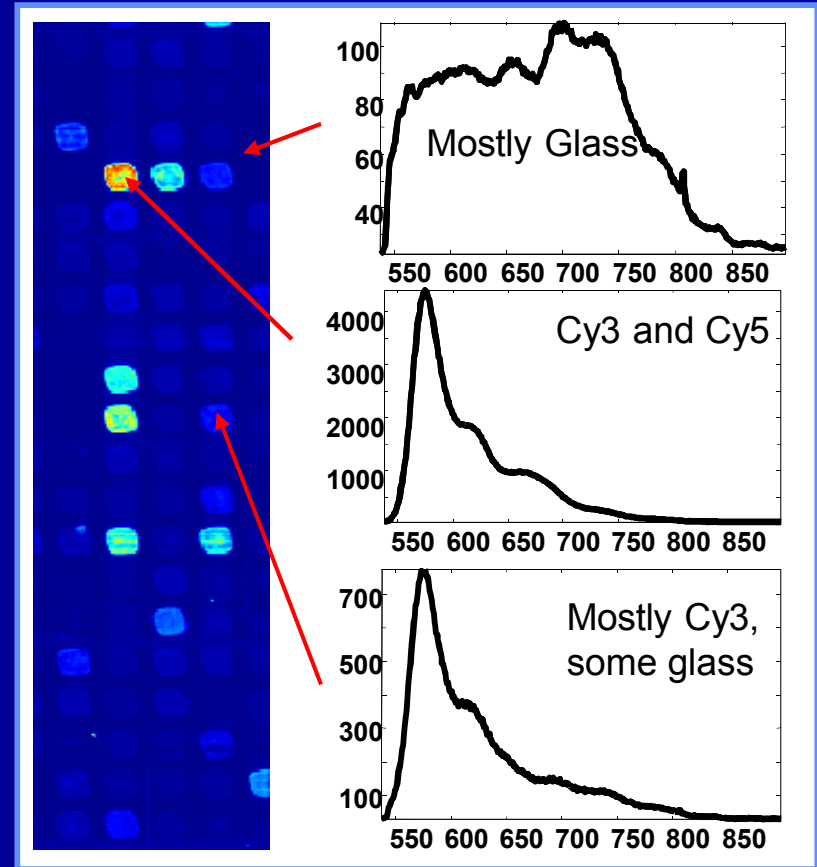
Spectral
Components

WHAT?

Concentration
Maps

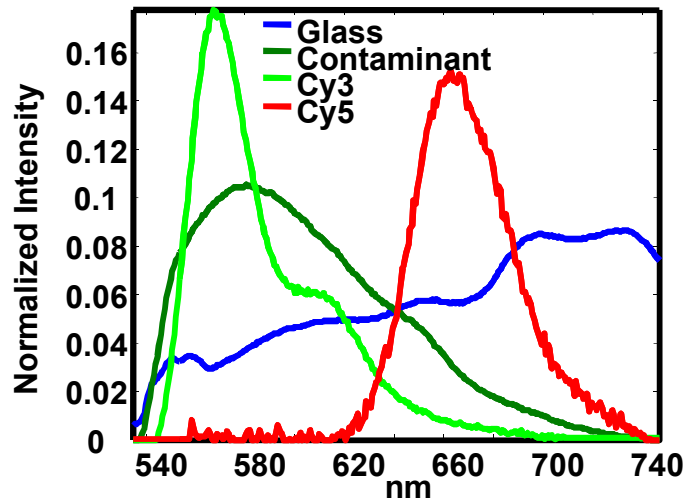
WHERE?
HOW MUCH?

A peek at the raw data...

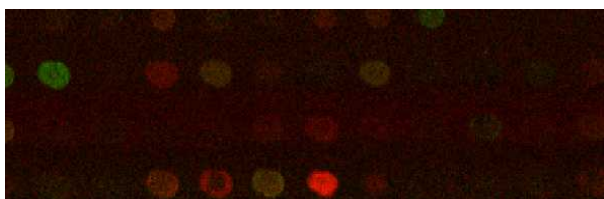
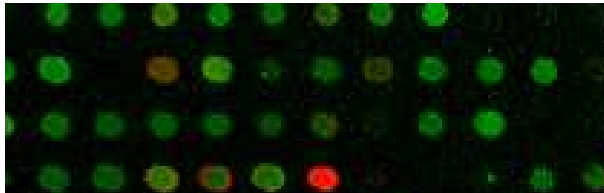


HSS Helps Understand Problems with Arrays

a. Contamination

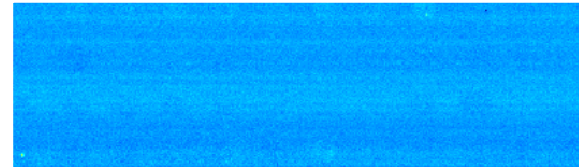


Commercial Scanner
Contaminated Red/Green Ratio

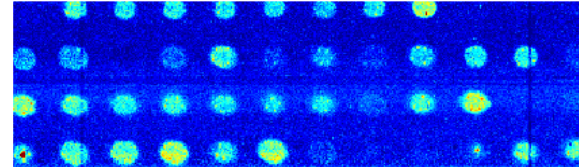


Hyperspectral Scanner
Accurate Cy5/Cy3 Ratio

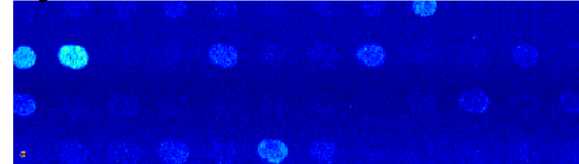
Glass



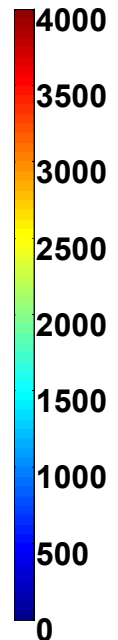
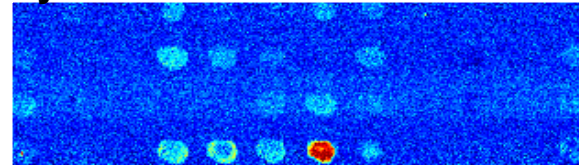
Contaminant



Cy3

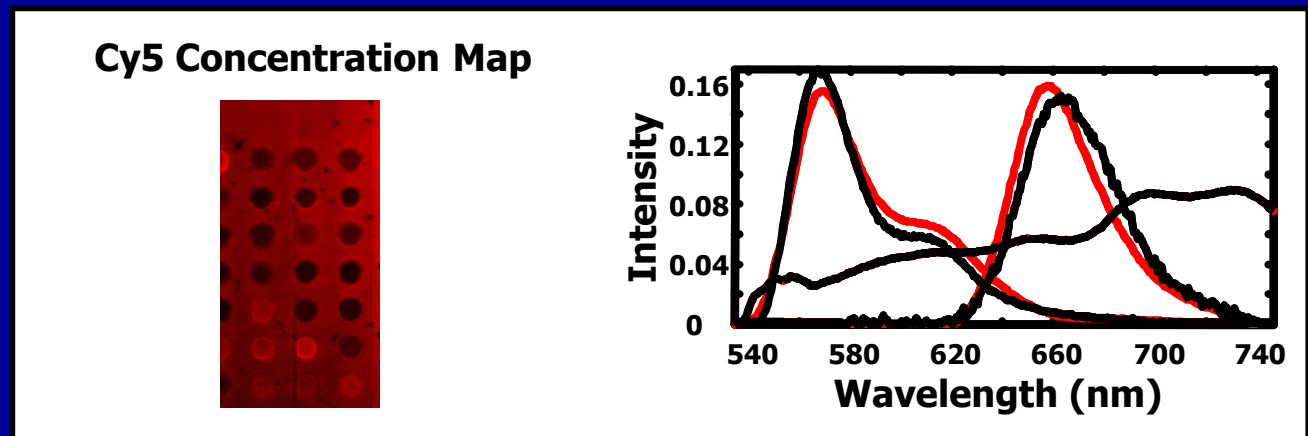


Cy5



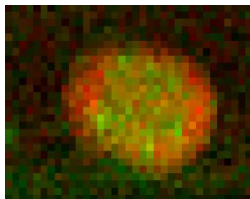
HSS Helps Understand Problems with Arrays

b. Black holes – non-specific binding



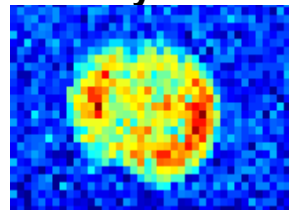
c. Dye separation?

R/G Ratio Image



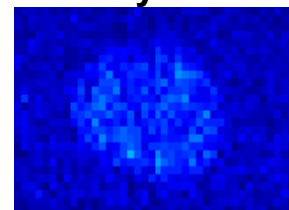
Hyperspectral Scanner Concentration Maps

Cy5



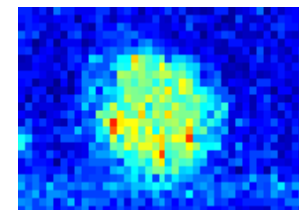
22 pixels across

Cy3



22 pixels across

Contaminant

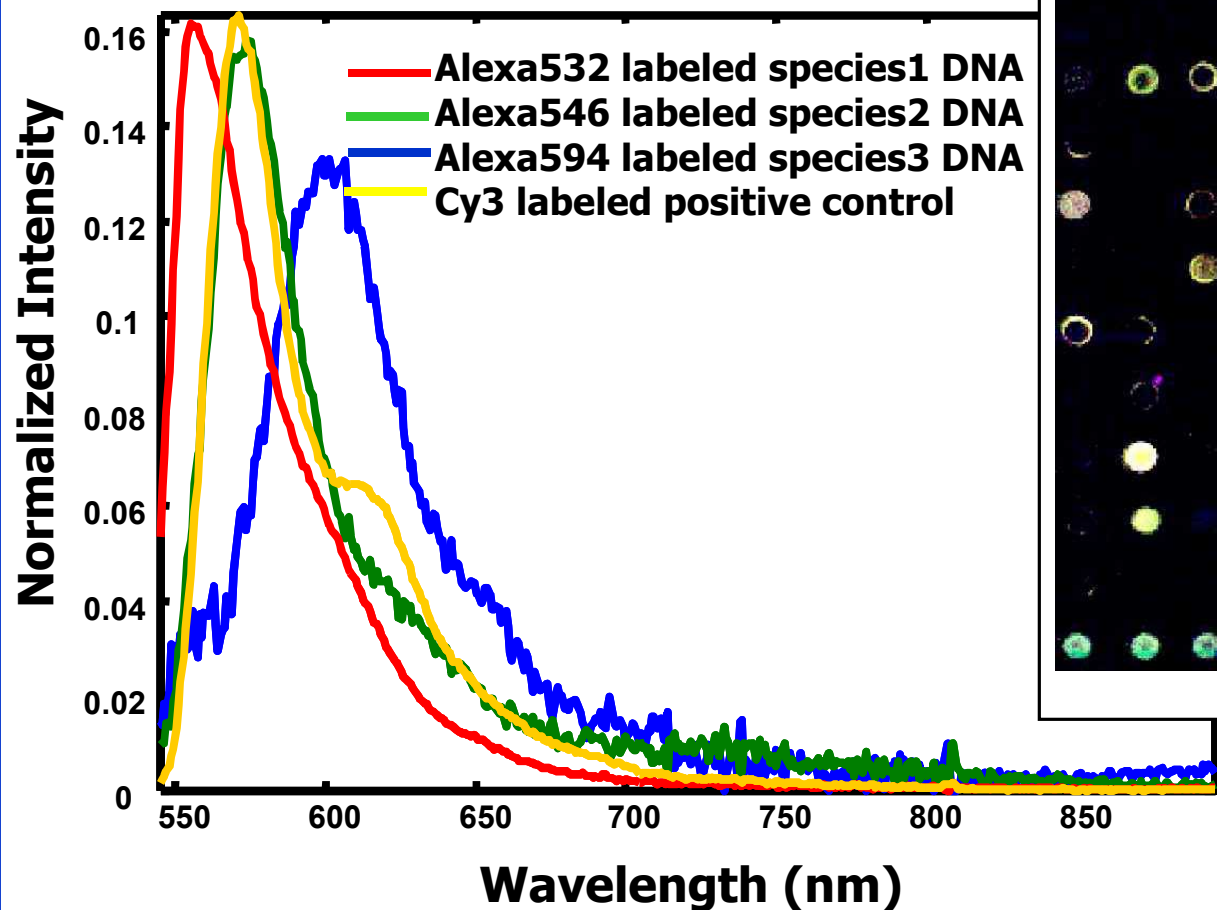


17 pixels across

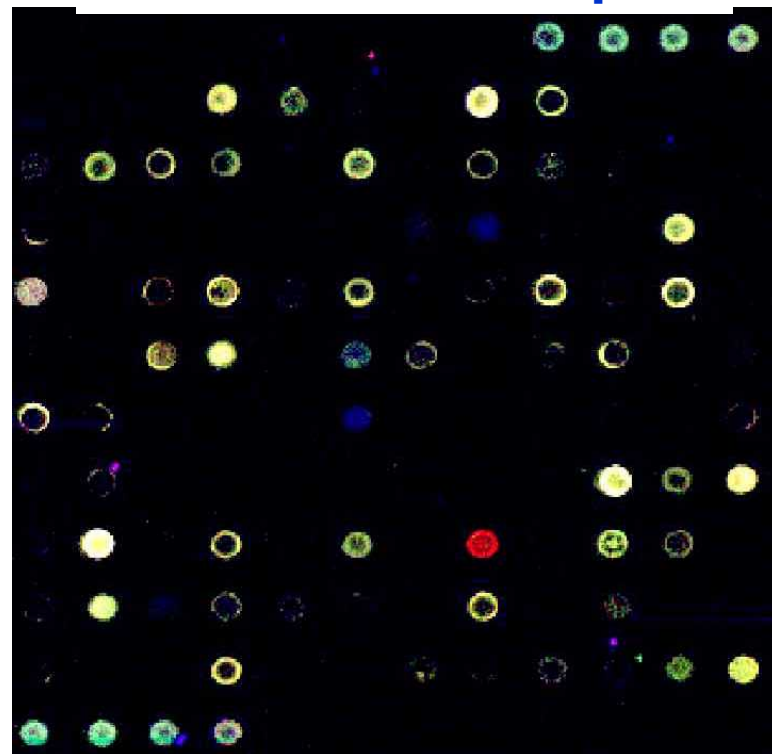
Contaminant spot is smaller in diameter than Cy5 and Cy3, gives appearance of brighter green in center, but hyperspectral data reveals it is not Cy3

Multiple Green Dyes – More Multiplexing

**MCR Generated
Pure Component Spectra**



**RGB Image of Alexa Dye
Concentration Maps**



In Summary

- **Optimal performance realized when sources of variation are understood, controlled, minimized...**
- **Scanning/Scanner is a critical part of the microarray process and should not be overlooked**
 - Instrument
 - User settings
 - Special considerations for large scale studies
- **Emerging scanner technologies, like HSS, can compliment traditional scanning methods**
 - Dye specific bias
 - Background, contaminant emissions
 - Increase multiplexing

Acknowledgments

- **Statistical analysis, exp design**
 - *Edward V. Thomas, SNL*
- **Software / algorithm development at SNL**
 - *Howland D. T. Jones*
 - *David M. Haaland*
 - *Michael R. Keenan*
 - *Paul G. Kotula*
 - *David K. Melgaard*
 - *Greg Poulter*
 - *Mark H. VanBentham*
- **Microarray collaborations**
 - *David Bencic, Ronglin Wang (US EPA)*
 - *Brian Palenik (Scripps)*
 - *Ian Paulsen (TIGR)*
 - *Maggie Werner-Washburne (UNM)*
 - *Cheryl Willman (UNM CTC)*

\$ Sandia Laboratory Directed Research and Development (LDRD) Program

\$ NIH

\$ US EPA

\$ This work was funded in part by the US DOE's Genomes to Life program under project, "Carbon Sequestration in *Synechococcus* Sp.: From Molecular Machines to Hierarchical Modeling,"

\$ Some experiments provided by the Keck-UNM Genomics Resource, a facility supported by the WM Keck Foundation, the State of NM, the UNM Cancer Research and Treatment Center, and the NM Center for Environmental Health Sciences."

References

- Thomas, EV, et. al., “*Statistical Analysis of Microarray Data with Replicated Spots: A Case Study with Synechococcus WH8102,*” 2007, submitted
- Timlin, JA, et. al., “*Hyperspectral microarray scanning: impact on the accuracy and reliability of gene expression data,*” *BMC Genomics*, 2005, 6:72.
- Sinclair, MB, et. al., “*Design, construction, characterization of a hyperspectral microarray scanner*”, *Applied Optics*, 2004, 43, 2079-2089.
- Martinez, MJ, et. al, “*Identification and removal of contaminating fluorescence from commercial and in-house printed DNA microarrays*” *Nucleic Acid Research*, 2003, 31:4, e18.
- Haaland DM, et. al. “*Multivariate curve resolution for hyperspectral image analysis: applications to microarray technology,*” *Spectral Imaging: Instrumentation, Applications, and Analysis*, 2003; 4959: 55-66.