

# Scanning Microarrays: Current Challenges and Future Directions

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

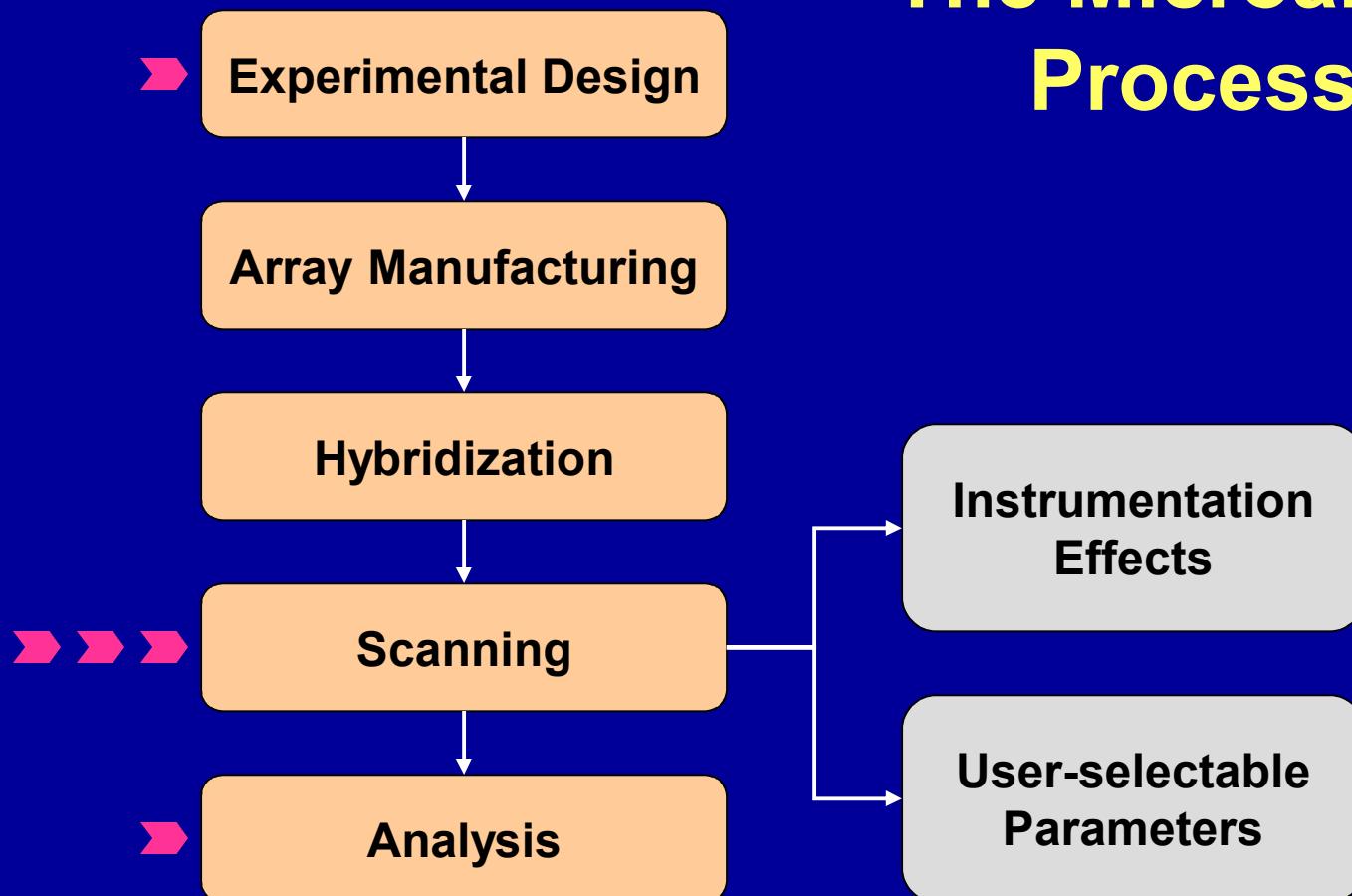
**\* Sandia is a multiprogram laboratory operated by Sandia Corporation,  
a Lockheed Martin Company, for the United States Department of  
Energy's National Nuclear Security Administration under contract DE-  
AC04-94AL85000**

# 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

Confocal

< 10  $\mu\text{m}$  F.O.V.

↓ background

↑ sensitivity to position

VS.

Wide-field

~ 60  $\mu\text{m}$  F.O.V.

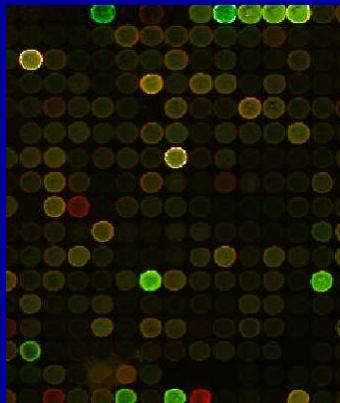
↑ background

↓ sensitivity to position

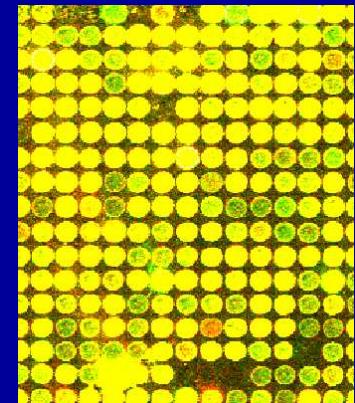
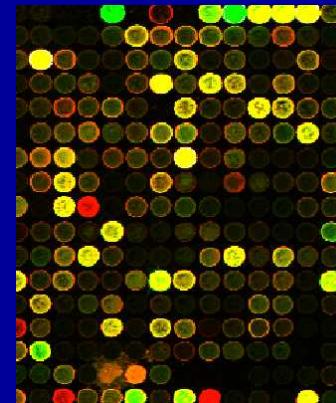
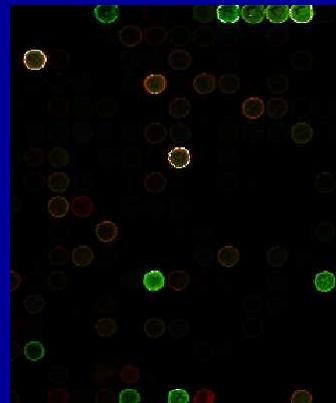
# User- Selectable Parameters – Image Display

16-bit data → 8-bit display

## Compression



## Reduction



Sq Root Transform  
0 - 65535

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

$\mu_i$  = overall average of  $i^{th}$  gene

$\alpha_j$  = 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)

$\varepsilon_{ijk}$  = 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 \*
- Stability
  - Lasers
  - PMTs
  - Optics
  - Scanning devices

Solutions? Transforms,  
Spectral imaging

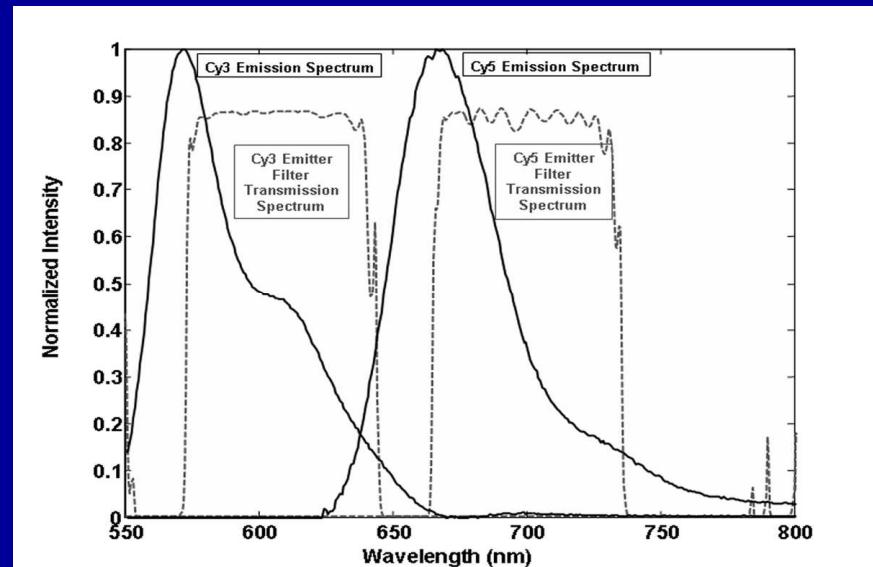
Instrument stability  
needs to be thoroughly  
checked on a regular  
basis → standards

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



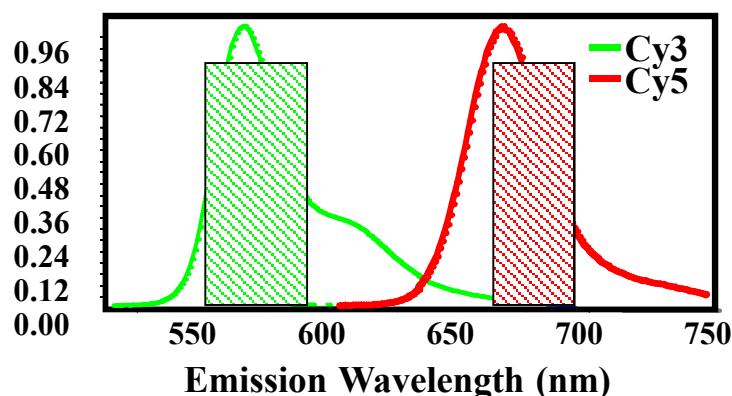
# Alternative Scanning Technologies

---

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

# Technology Comparison

## Filter-based Scanner



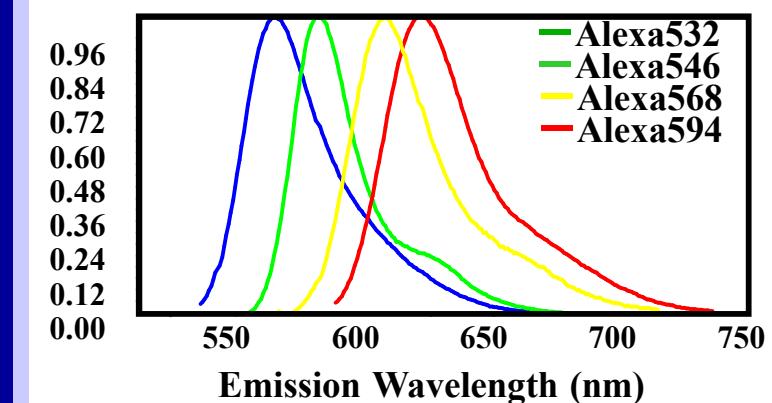
### Univariate

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

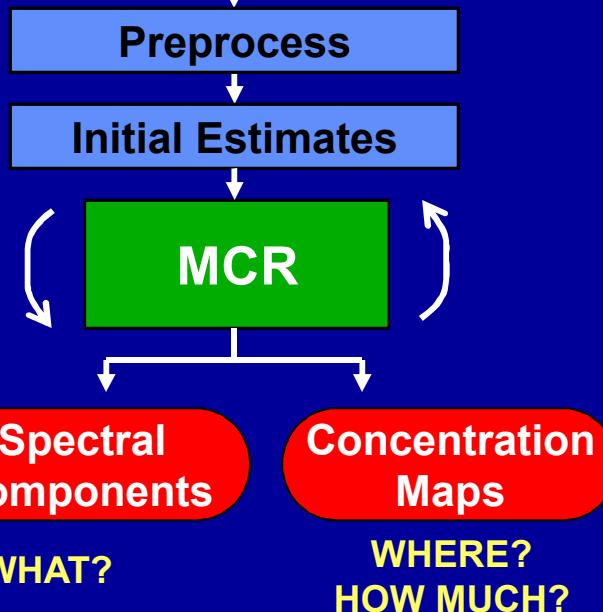
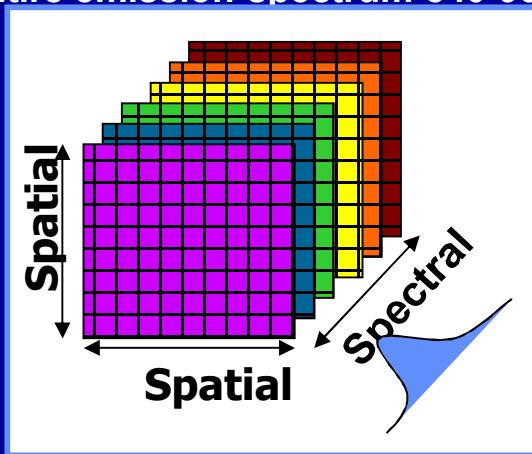
---

**Discover & quantify all emitting species in a sample simultaneously**

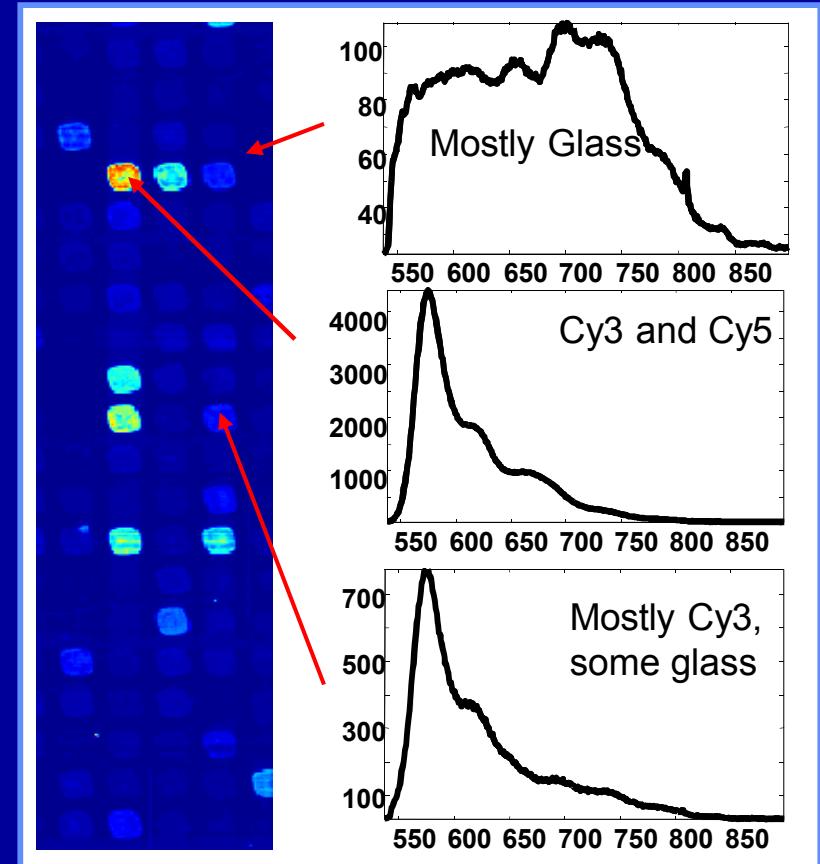
- Increased sensitivity
- Extended dynamic range
- Improved background/interference correction
- Improved accuracy , reliability , & quantitation
- Increase throughput – multiple overlapping dyes

# Hyperspectral Image Cube & Analysis

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

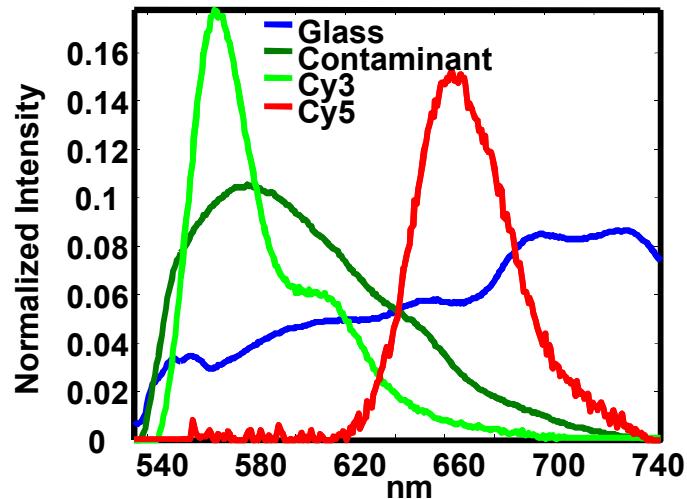


A peek at the raw data...

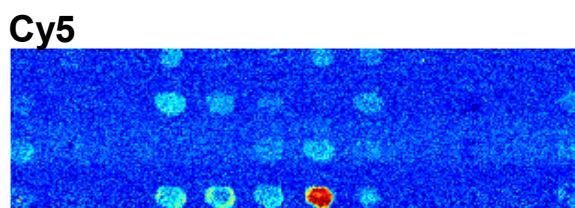
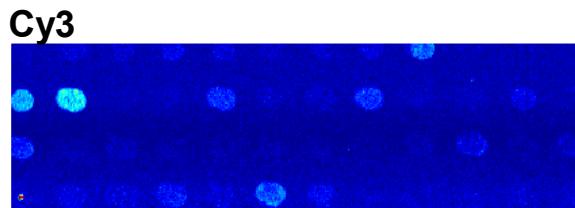
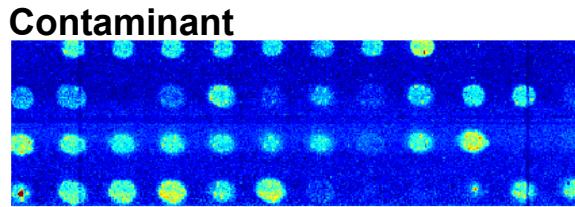
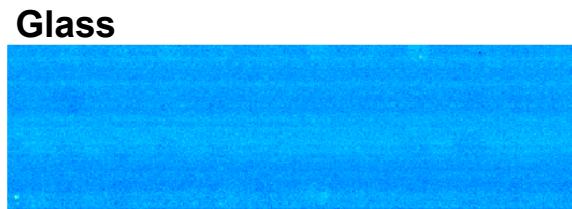
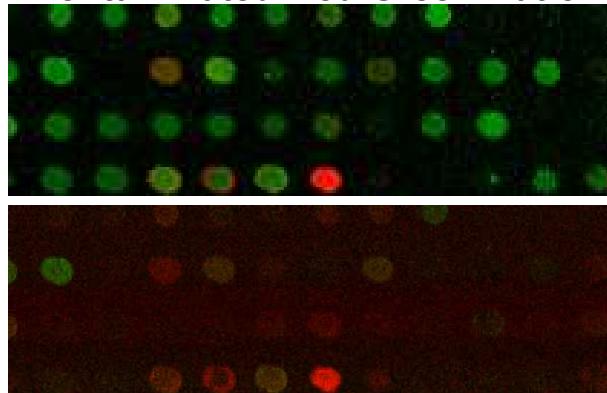


# HSS Helps Understand Problems with Arrays

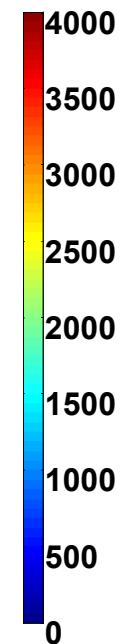
## a. Contamination



Commercial Scanner  
Contaminated Red/Green Ratio

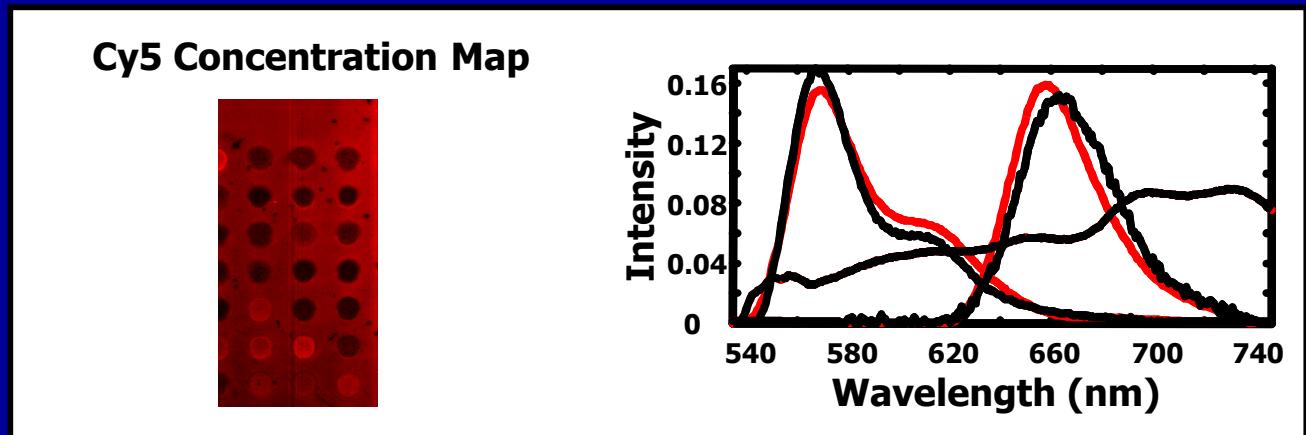


Hyperspectral Scanner  
Accurate Cy5/Cy3 Ratio

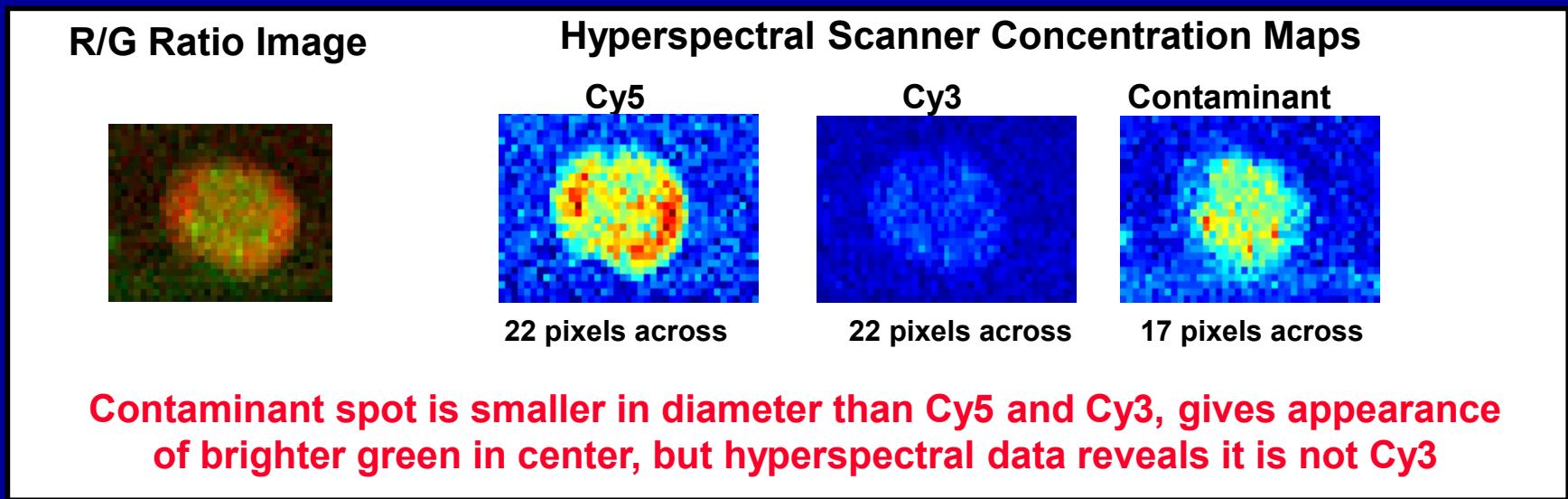


# HSS Helps Understand Problems with Arrays

## b. Black holes – non-specific binding



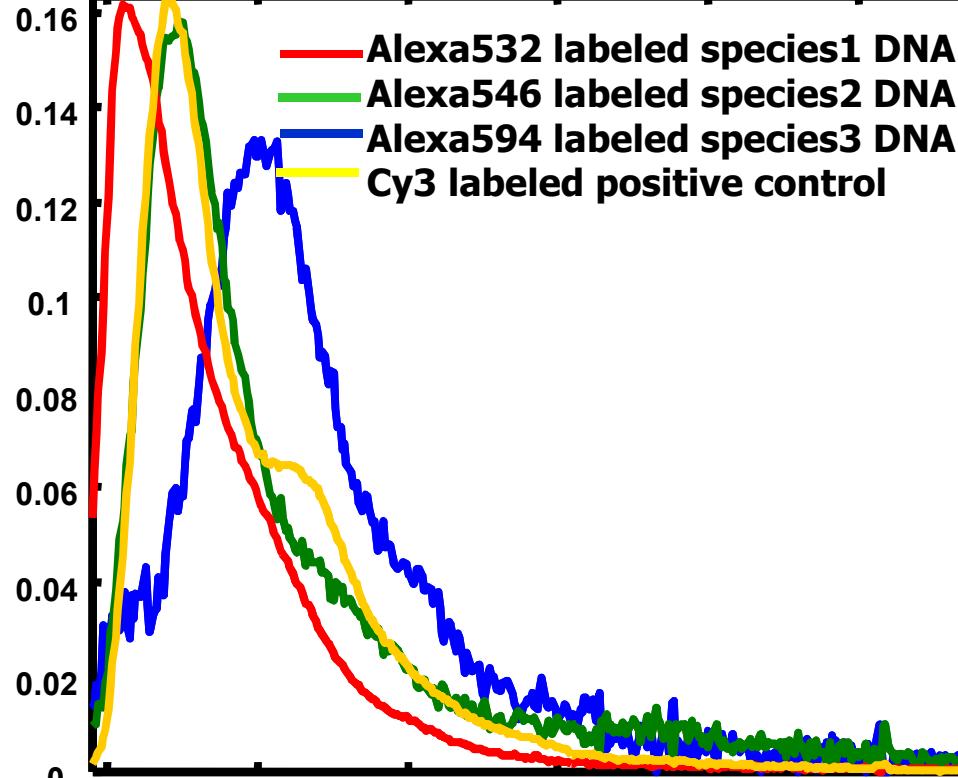
## c. Dye separation?



# Multiple Green Dyes – More Multiplexing

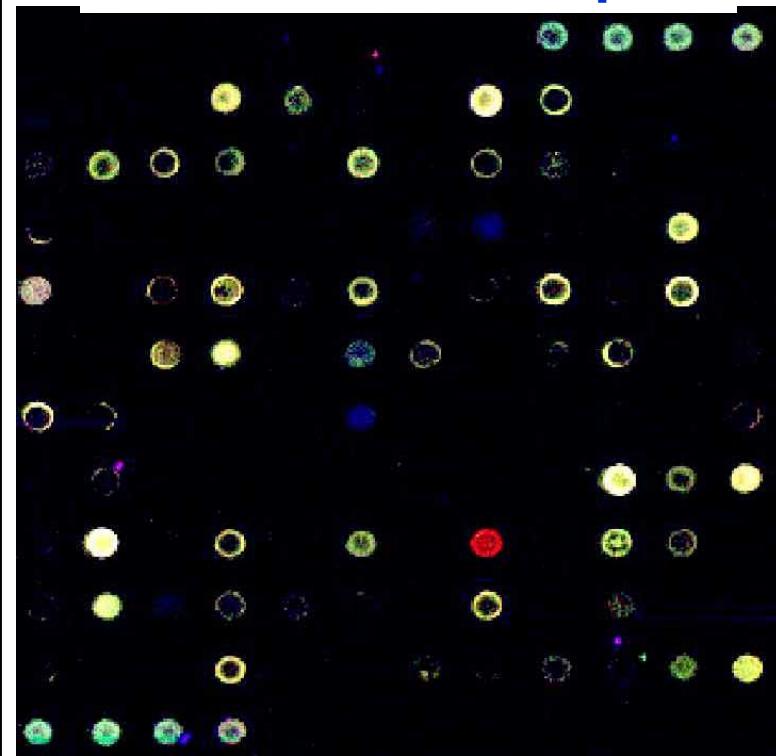
## MCR Generated Pure Component Spectra

Normalized Intensity



Wavelength (nm)

## 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. VanBenthem*
- **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.