

Monday
27. November 06

Microarray: Quality Control, Normalization and Design

Tim Beißbarth

Deutsches Krebsforschungszentrum

Molecular Genome Analysis

Bioinformatics

Heidelberg, INF 580
t.beissbarth@dkfz.de

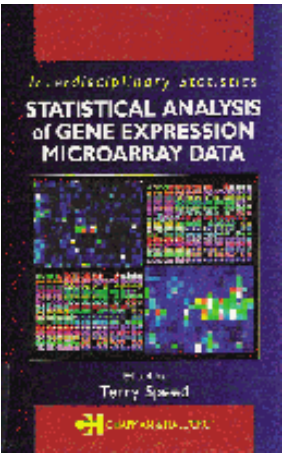


Overview

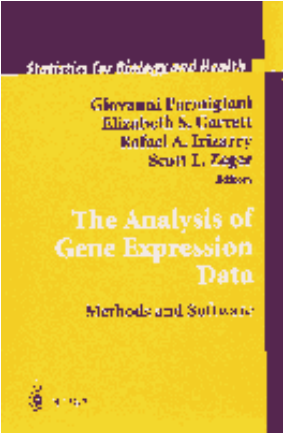
- Introduction to microarray technologies
- Image Processing:
Spot Identification, Spot/Background quantification, Quality Measures
- Normalization:
Scaling, Quantile, Lowess, vsn
- Experimental Design:
Comparison of typical Designs
- Affy Issues

Books

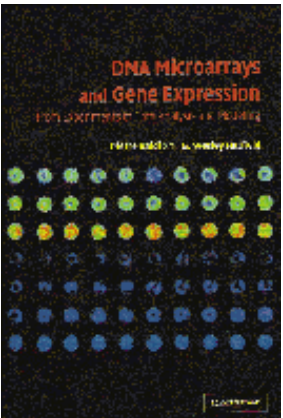
- Terry Speed, „Statistical Analysis of Gene Expression Microarray Data“. Chapman & Hall/CRC



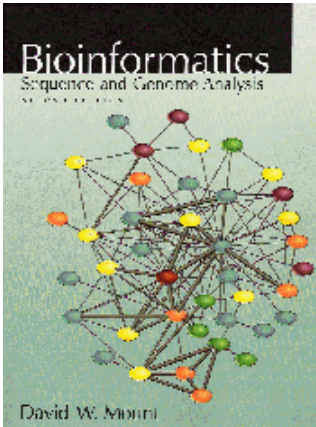
- Giovanni Parmigiani et al, „The Analysis of Gene Expression Data“, Springer



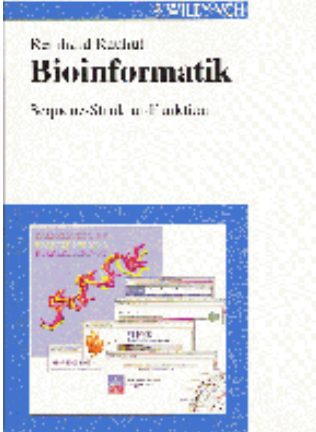
- Pierre Baldi & G. Wesley Hatfield, „DNA Microarrays and Gene Expression“, Cambridge



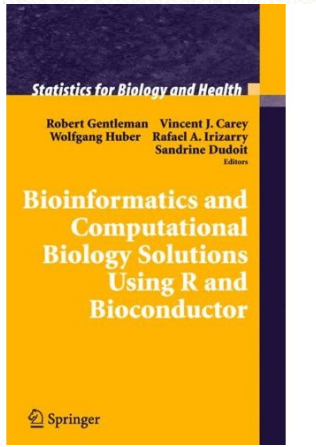
- David W. Mount, „Bioinformatics“, Cold Spring Harbor



- Reinhard Rauhut, „Bioinformatik“, Wiley-VCH



- Gentleman, Carey, Huber, „Bioinformatics and Computational Biology Solutions Using R and Bioconductor“, Springer

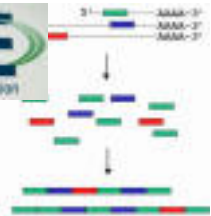


Online

- NGFN Course „Practical DNA Microarray Analysis“:
<http://compdiag.molgen.mpg.de/lectures.shtml>
- Lectures Terry Speed, Berkeley:
<http://www.stat.berkeley.edu/users/terry/Classes/>
- R/Bioconductor Dokumentation (Vignetten):
<http://www.bioconductor.org>
- Google, Pubmed, Wikipedia

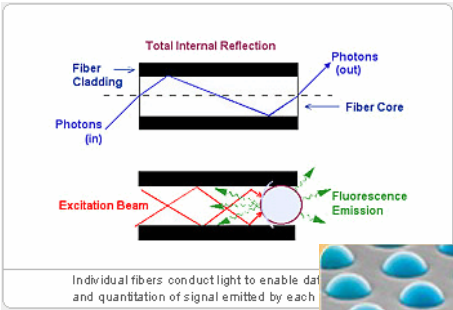


SAGE

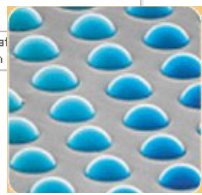


1975: Southern Blotting Technology (Edward Southern)

2003: Illumina Bead Arrays



Illumina Bead Array

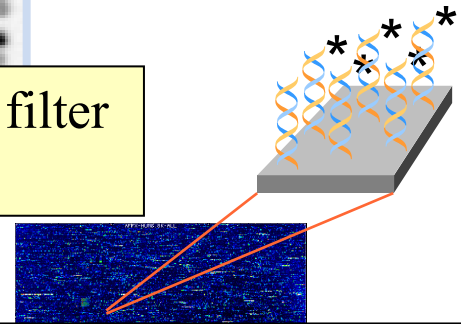


1991: First high-density Nylon filter Arrays (Lennon, Lehrach)

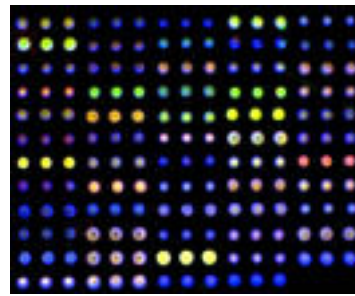
Different Technologies for Measuring Gene Expression

1996: Affymetrix Genechip Technology (Lockhart et al.)

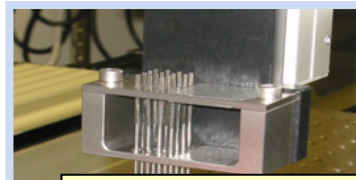
GeneChip Affymetrix



Agilent: Long oligo Ink Jet

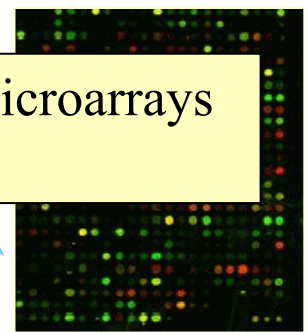


CGH



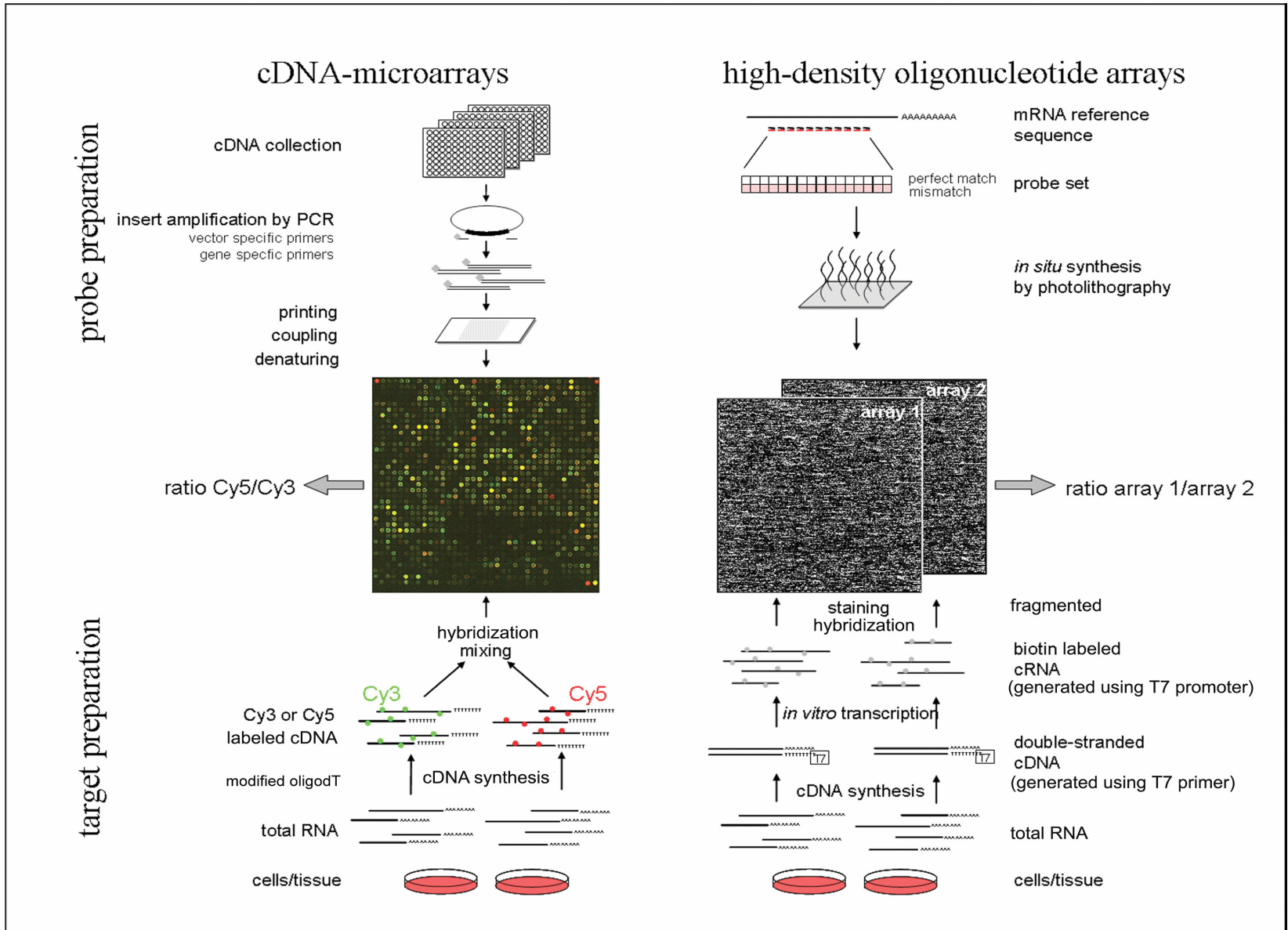
cDNA microarray

1995: cDNA-Microarrays (Schena et al.)



cDNA and Affymetrix (short, 25 bp) Oligo Technologies.

Long Oligos (60-75 bp) are used similar to cDNA.



Experimental Cycle

Biological question
(hypothesis-driven or explorative)

Experimental design

To call in the statistician after the experiment is done may be no more than asking him to perform a post-mortem examination: he may be able to say what the experiment died of.

Ronald Fisher

Pass

Normalization

Analysis

Estimation Testing ... Clustering Discrimination

Biological verification and interpretation

Gene-expression-data

gene expression-data for **G** genes and **n** hybridisations.
Genes times arrays data-matrix:

		mRNA Samples					
		sample1	sample2	sample3	sample4	sample5	...
Gene	1	0.46	0.30	0.80	1.51	0.90	...
	2	-0.10	0.49	0.24	0.06	0.46	...
	3	0.15	0.74	0.04	0.10	0.20	...
	4	-0.45	-1.03	-0.79	-0.56	-0.32	...
	5	-0.06	1.06	1.35	1.09	-1.09	...

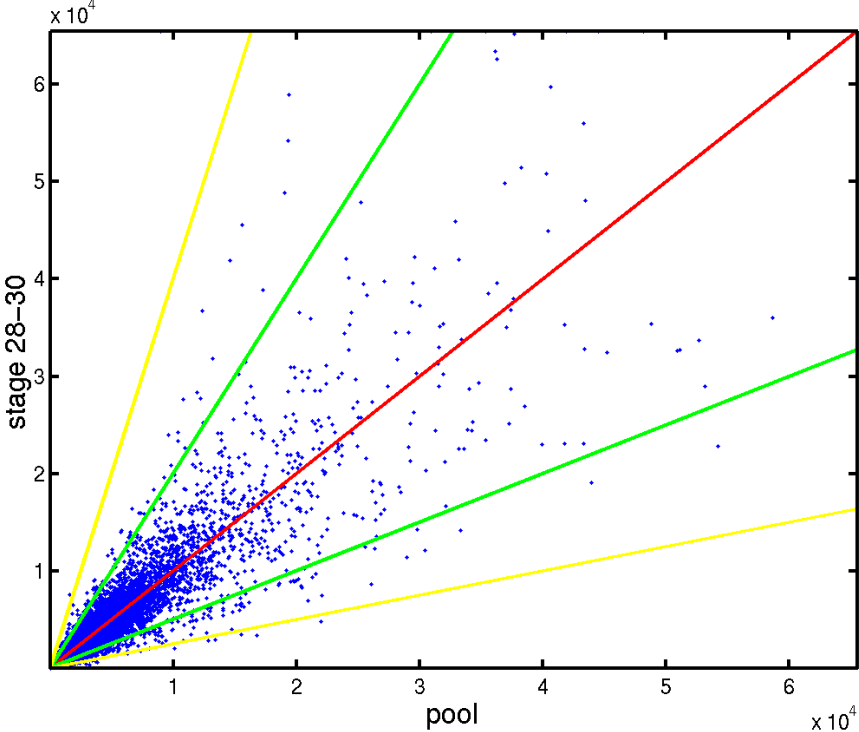
gene-expression level or ratio for gene i in mRNA sample j

M = { $\text{Log}_2(\text{red intensity} / \text{green intensity})$
Function (PM, MM) of MAS, dchip or RMA

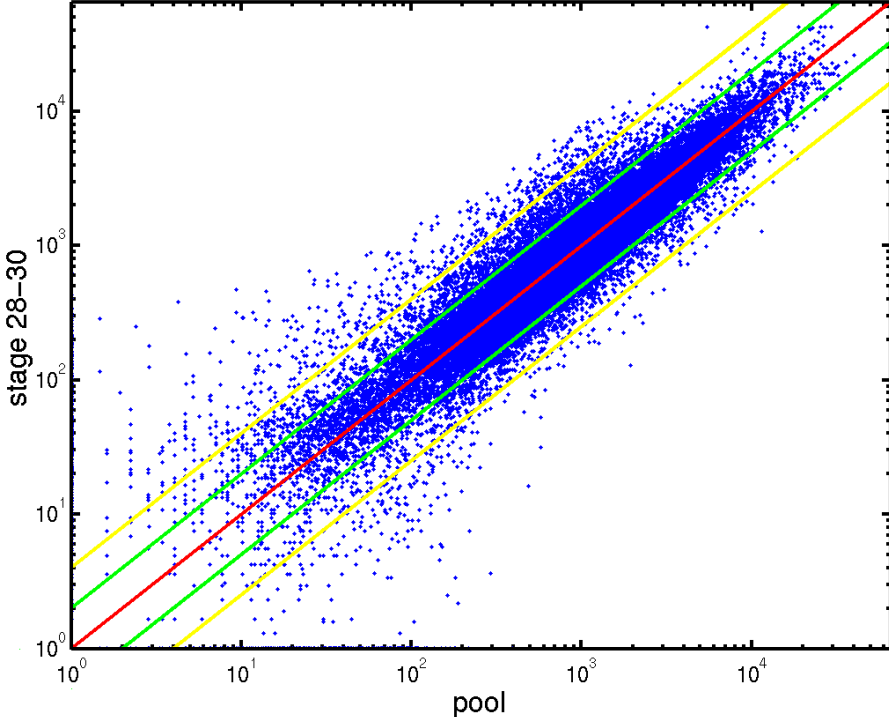
A = { average: $\log_2(\text{red intensity})$, $\log_2(\text{green intensity})$
Function (PM, MM) of MAS, dchip or RMA

Scatterplot

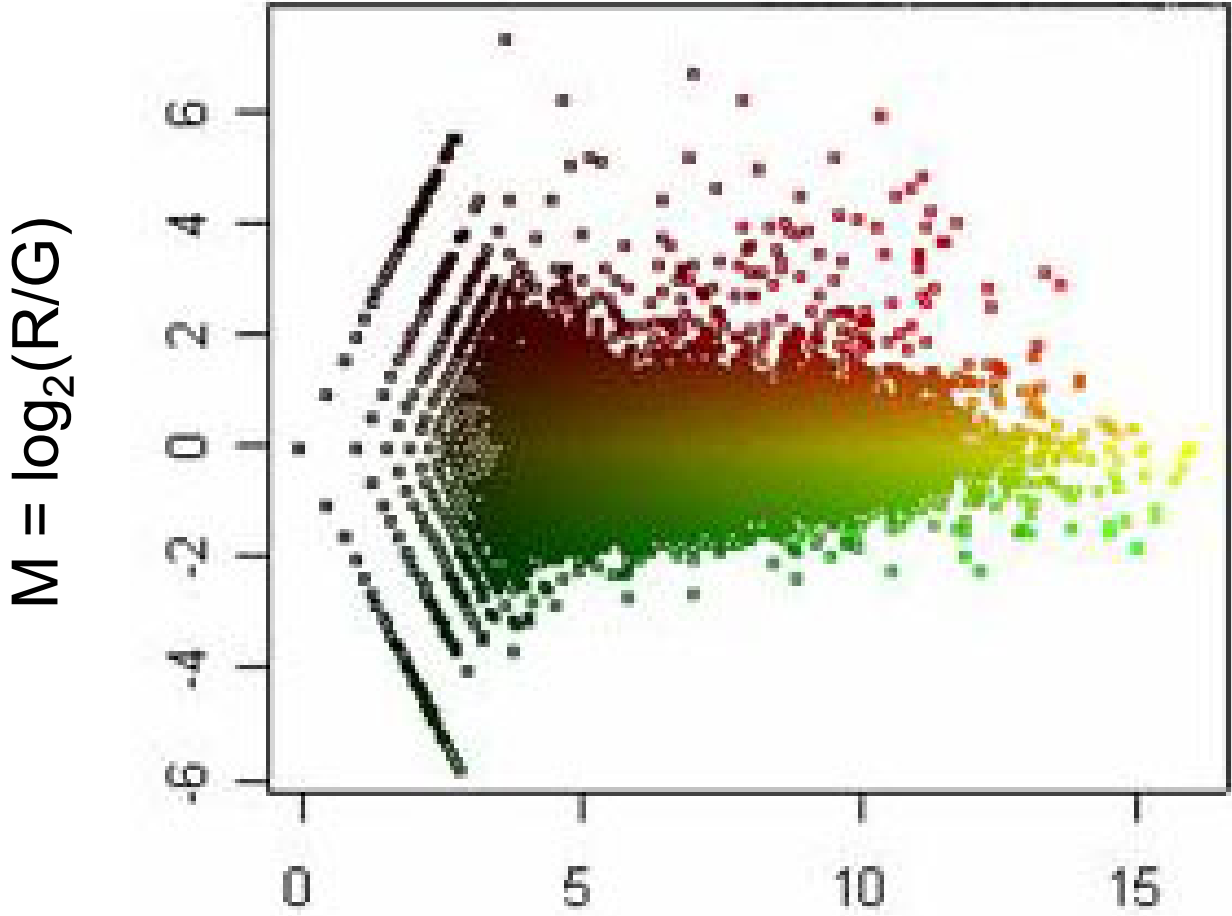
Data



Data (log scale)



MA Plot



$$A = 1/2 \log_2(RG)$$

Sources of Variation

- Variance and Bias
- Different Sources of Variation
- Measuring foreground and background signal
- Control quality at different levels

Raw data are not mRNA concentrations

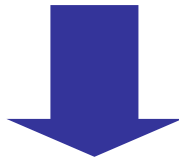
- tissue contamination
- RNA degradation
- amplification efficiency
- reverse transcription efficiency
- Hybridization efficiency and specificity
- clone identification and mapping
- PCR yield, contamination
- spotting efficiency
- DNA support binding
- other array manufacturing related issues
- image segmentation
- signal quantification
- “background” correction

Sources of Variation for Microarray-Data

- amount of RNA in biopsy
- efficiency of:
 - RNA extraction
 - reverse transcription
 - labeling
 - photodetection
- PCR yield
- DNA quality
- spotting efficiency, spot size
- cross-/unspecific hybridization
- stray signal

Systematic

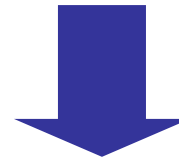
- similar effect on many measurements
- corrections can be estimated from data



Normalization

Stochastic

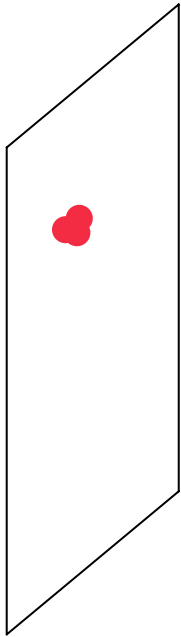
- Effects, on single spots
- random effects cannot be estimated, „noise“



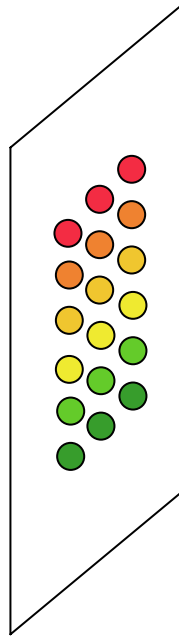
Error model

Quality control: Noise and reliable signal

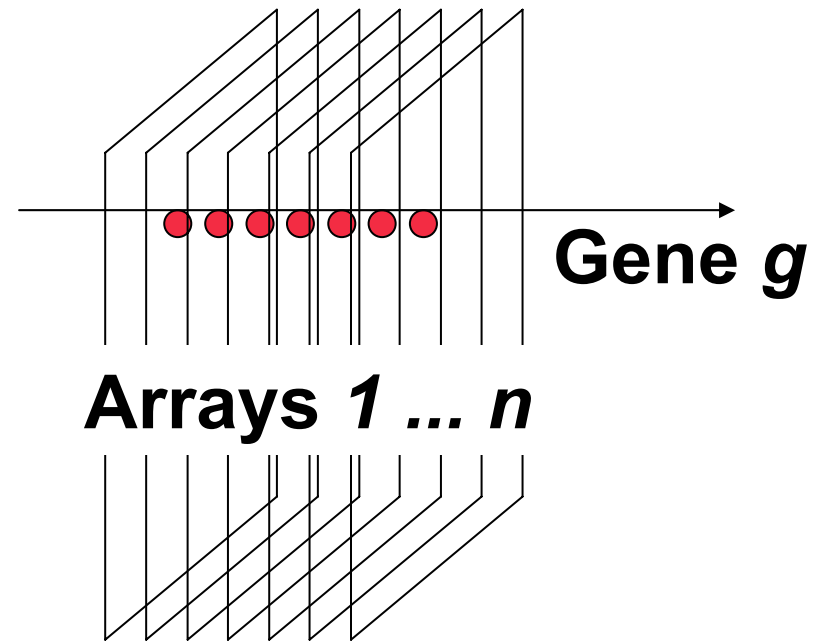
Probe level



Array level



Gene level



Probe level: quality of the expression measurement of one spot on one particular array

Array level: quality of the expression measurement on one particular glass slide

Gene level: quality of the expression measurement of one probe across all arrays

Probe-level quality control

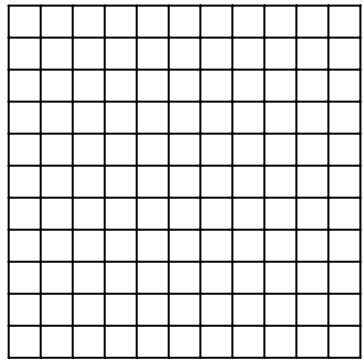
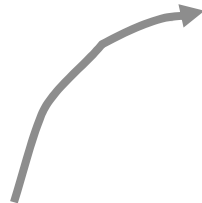
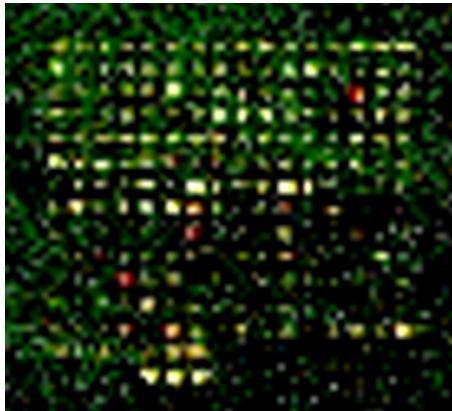
- Individual spots printed on the slide
- Sources:
 - faulty printing, uneven distribution, contamination with debris, magnitude of signal relative to noise, poorly measured spots;
- Visual inspection:
 - hairs, dust, scratches, air bubbles, dark regions, regions with haze
- Spot quality:
 - *Brightness*: foreground/background ratio
 - *Uniformity*: variation in pixel intensities and ratios of intensities within a spot
 - *Morphology*: area, perimeter, circularity.
 - *Spot Size*: number of foreground pixels
- Action:
 - set measurements to NA (missing values)
 - local normalization procedures which account for regional idiosyncrasies.
 - use weights for measurements to indicate reliability in later analysis.

Image Analysis – Spot Identification

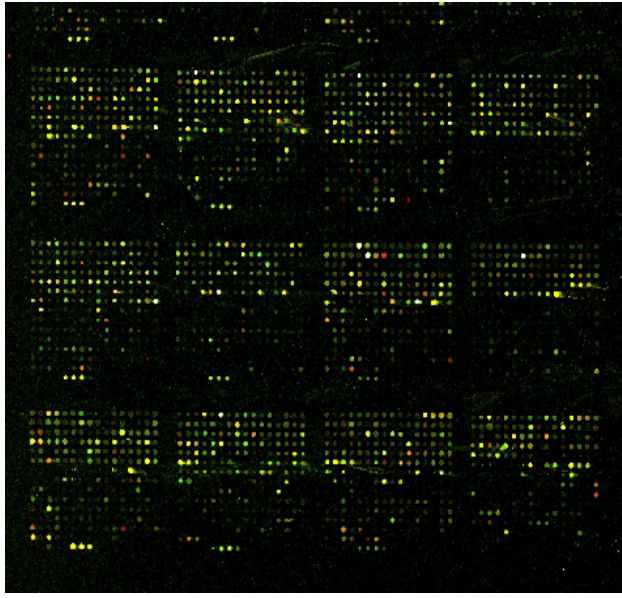
- The grid structure is provided by the manufacturer or generated individually for custom-made microarrays (e.g. GAL-files)
- The grid is overlaid by hand or automatically onto the image (beware of column/row displacement errors!)

Columns

Rows



Blocks



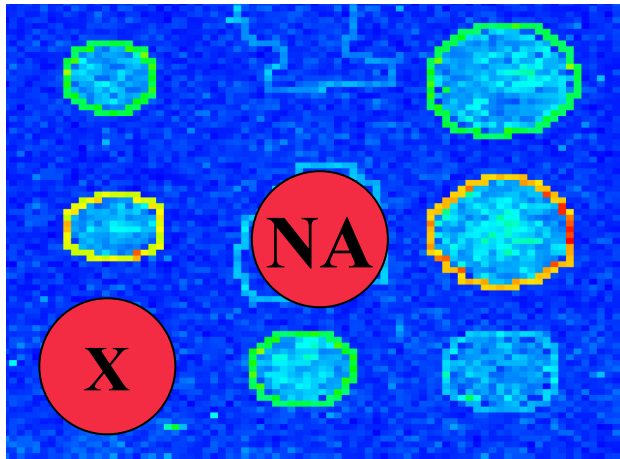
	A	B	C	D	E
1	ATF	1.0			
2	22	5			
3	Type=GenePix ArrayList V1.0				
4	Supplier=Company X				
5	ArrayName=MouseApoptosisProteins 4000				
6	ArrayRevision=2.7				
7	URL= http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=Protein&list_uids=11139671				
8	BlockCount=16				
9	Block1= 100, 100, 150, 24, 180, 17, 180				
10	Block2= 4600, 100, 150, 24, 180, 17, 180				
11	Block3= 9100, 100, 150, 24, 180, 17, 180				
12	Block4= 13600, 100, 150, 24, 180, 17, 180				
13	Block5= 100, 4600, 150, 24, 180, 17, 180				
14	Block6= 4600, 4600, 150, 24, 180, 17, 180				
15	Block7= 9100, 4600, 150, 24, 180, 17, 180				
16	Block8= 13600, 4600, 150, 24, 180, 17, 180				
17	Block9= 100, 9100, 150, 24, 180, 17, 180				
18	Block10= 4600, 9100, 150, 24, 180, 17, 180				
19	Block11= 9100, 9100, 150, 24, 180, 17, 180				
20	Block12= 13600, 9100, 150, 24, 180, 17, 180				
21	Block13= 100, 13600, 150, 24, 180, 17, 180				
22	Block14= 4600, 13600, 150, 24, 180, 17, 180				
23	Block15= 9100, 13600, 150, 24, 180, 17, 180				
24	Block16= 13600, 13600, 150, 24, 180, 17, 180				
25	Block	Column	Row	Name	ID
26	1	1	1	MAP-1	11139671
27	1	2	1	bad protein	1083224
28	1	3	1	bcl2-like	6753170
29	1	4	1	interleukin-1	2137456
30	1	5	1	caspase 6	6753286



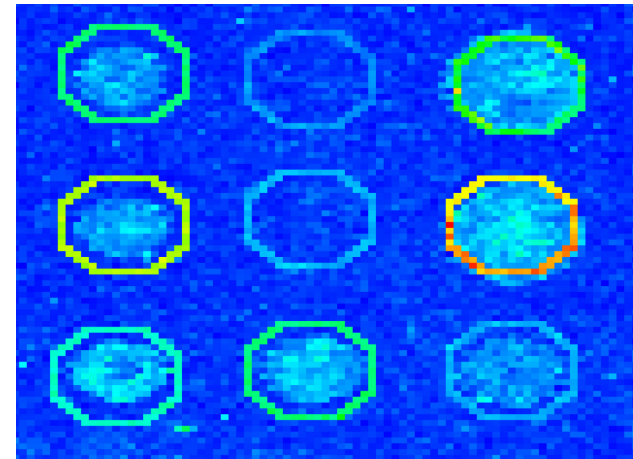
GAL-file contains Clone-IDs and defines their position on the grid

Spot Identification

- Individual spots are recognized, size and shape might be adjusted per spot (automatically fine adjustments by hand).
- Additional manual flagging of bad (X) or non-present (NA) spots



poor spot quality



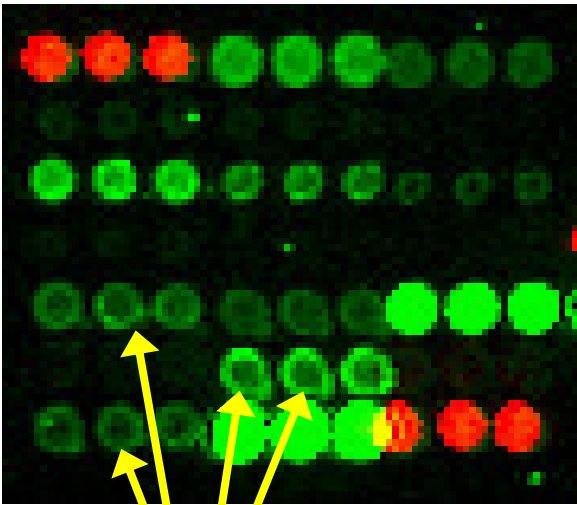
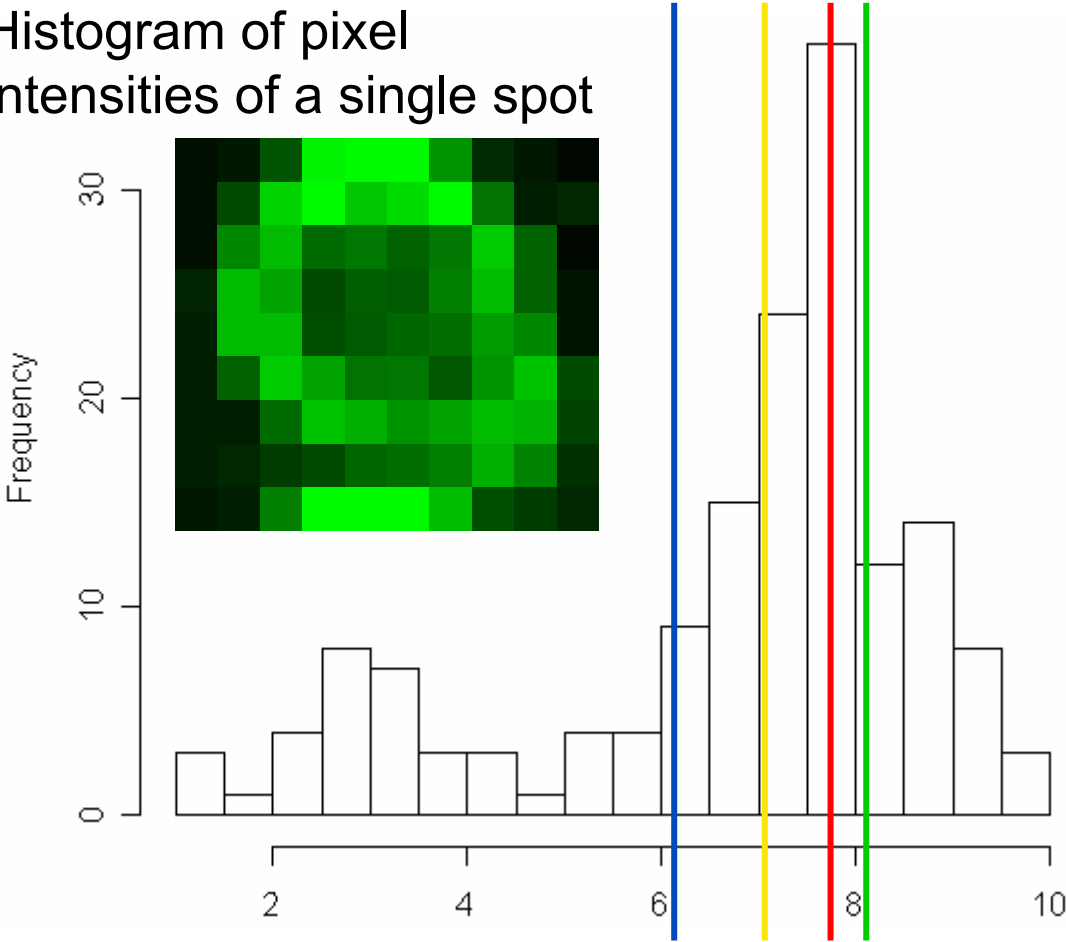
good spot quality

Different Spot identification methods: Fixed circles, circles with variable size, arbitrary spot shape (morphological opening)

Spot identification

- The signal of the spots is quantified.

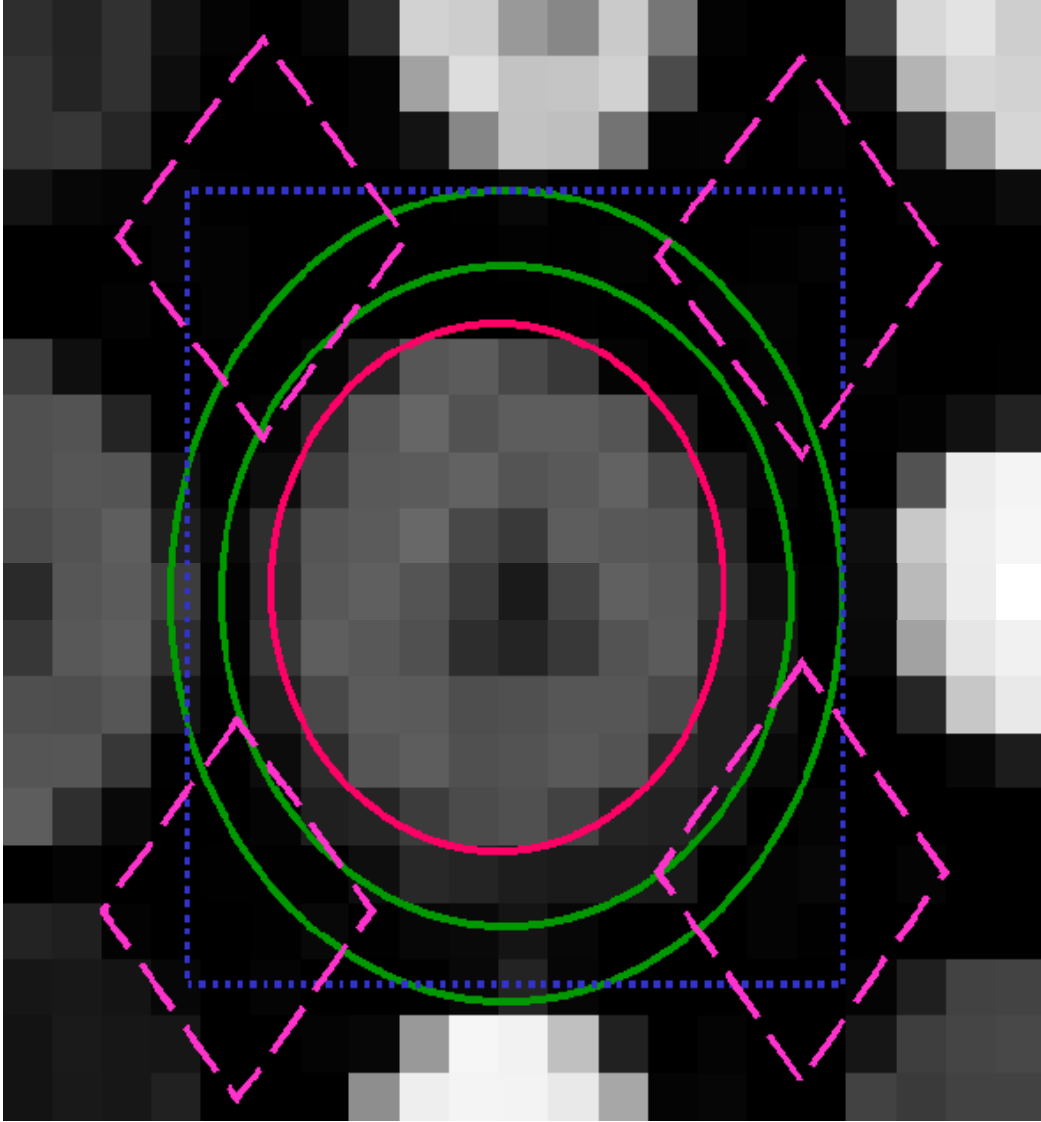
Histogram of pixel intensities of a single spot



„Donuts“

Mean / Median / Mode / 75% quantile

Different Regions around the spot are quantified to measure local background.



GenePix

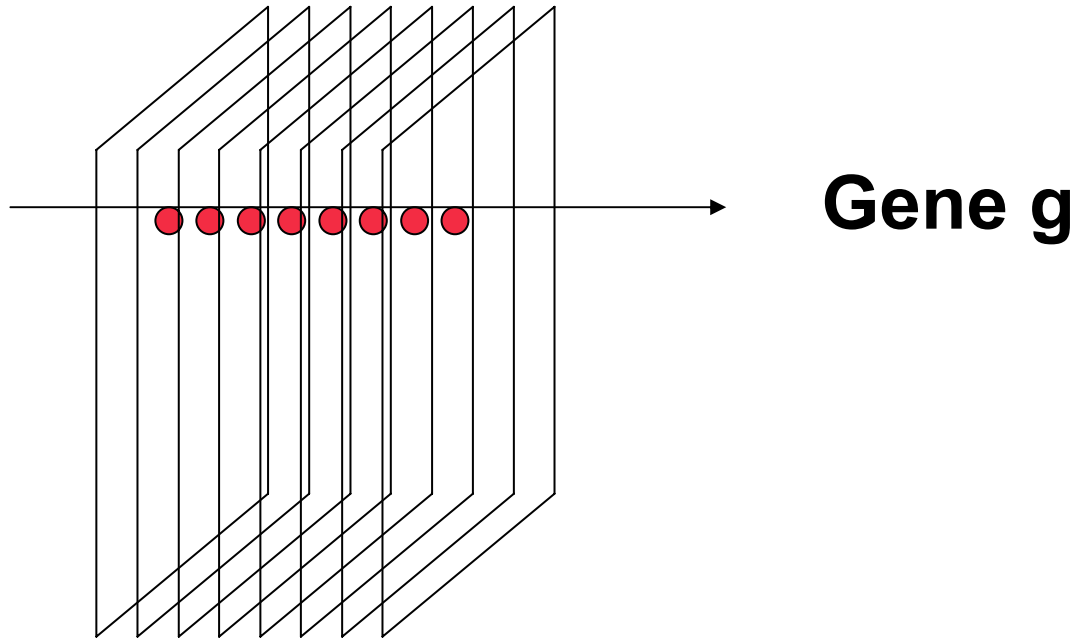
QuantArray

ScanAlyse

Array-level quality control

- Problems:
 - array fabrication defect
 - problem with RNA extraction
 - failed labeling reaction
 - poor hybridization conditions
 - faulty scanner
- Quality measures:
 - Percentage of spots with no signal (~30% excluded spots)
 - Range of intensities
 - $(\text{Av. Foreground})/(\text{Av. Background}) > 3$ in both channels
 - Distribution of spot signal area
 - Amount of adjustment needed: signals have to substantially changed to make slides comparable.

Gene-level quality control



- Poor hybridization in the reference channel may introduce bias on the fold-change

Gene-level quality control: Poor Hybridization and Printing

- Some probes will not hybridize well to the target RNA
- Printing problems such that all spots of a given inventory well have poor quality.
- A well may be of bad quality – contamination
- Genes with a consistently low signal in the reference channel are suspicious: Median of the background adjusted signal $< 200^*$

**or other appropriate choice*

Gene-level quality control: Probe quality control based on duplicated spots

- Printing different probes that target the same gene or printing multiple copies of the same probe.
- Mean squared difference of \log_2 ratios between spot r and s :

$$\text{MSDLR} = \sum (x_{jr} - x_{js})^2 / J \quad \text{sum over arrays } j = 1, \dots, J$$

recommended threshold to assess disagreement: $\text{MSDLR} > 1$

- Disagreement between copies: printing problems, contamination, mislabeling. Not easy if there are only 2 or 3 slides.
- Jenssen et al (2002) Nucleic Acid Res, 30: 3235-3244. Theoretical background

Swirl Data

- Experiment to study early development in zebrafish.
- Swirl mutant vs. wild-type zebrafish.
- Two sets of dye-swap experiments.
- Microarray containing 8448 cDNA probes
- 768 control spots (negative, positive, normalization)
- printed using 4x4 print-tips, each grid contains a 22x24 Spot matrix

R Console

```
> library(marray)
> data(swirl)
> ll()

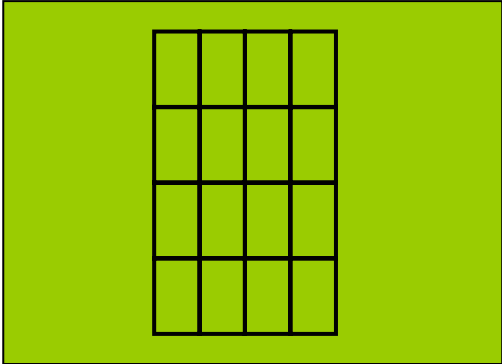
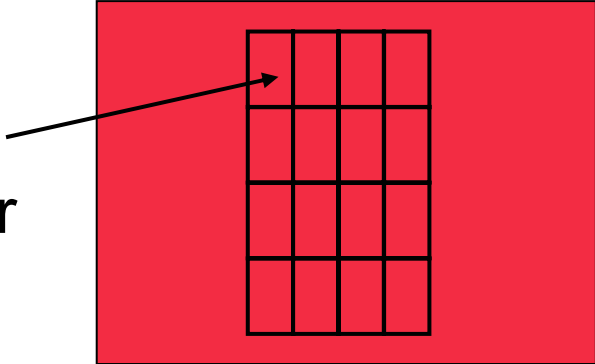
  member class      mode  dimension
1  swirl  marrayRaw list    c(8448,4)
```

Swirl Data

MT - R
WT - G

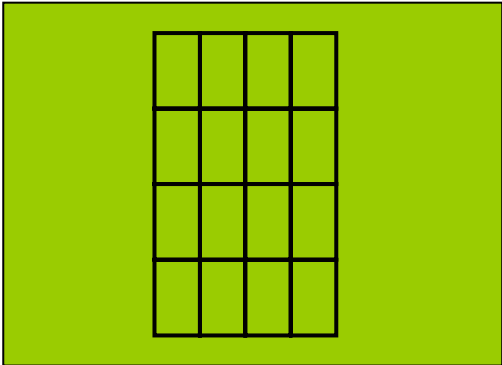
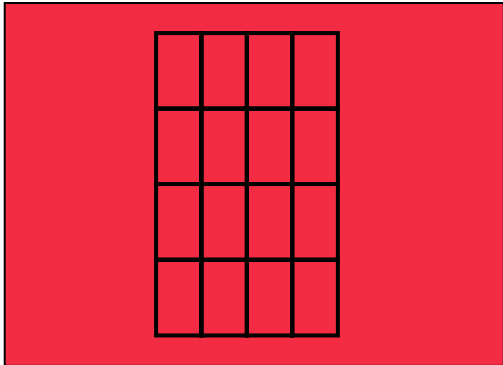
MT - G
WT - R

24 x 22
spots per
print-tip



Hybr. I

technical,
biological
variability



Hybr. II

Visual inspection

4 x 4 sectors

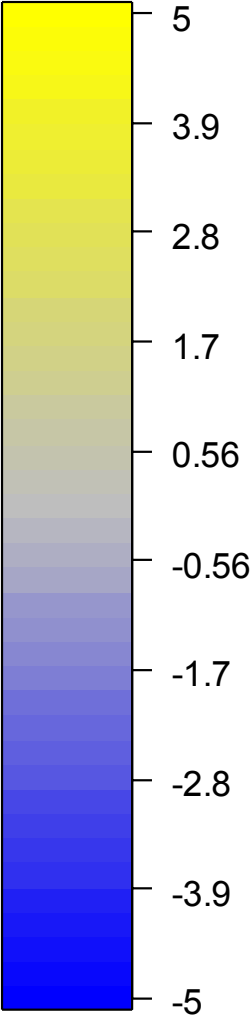
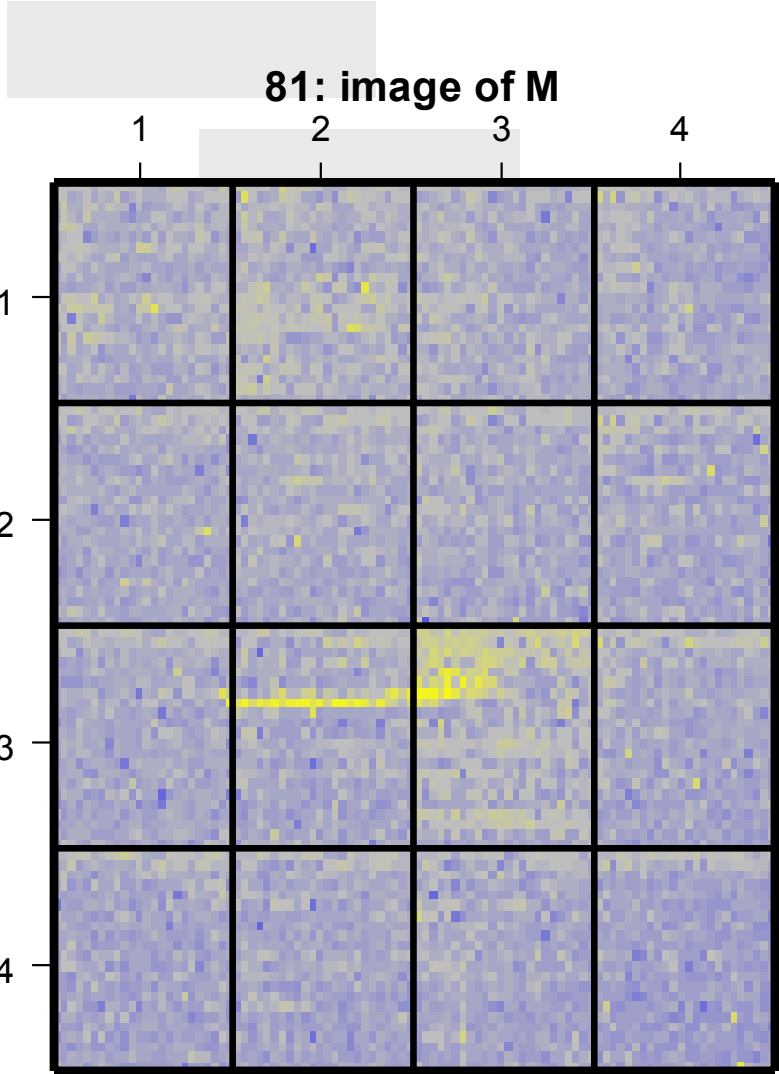
Sector:

24 rows

22 columns

8448 spots

Mean signal intensity



```
R R Console  
  
> image(swirl[,1])
```

Visual inspection – Foreground and Background intensities

R Console

```

> Gcol <- maPalette(
  low = "white",
  high = "green",
  k = 50)

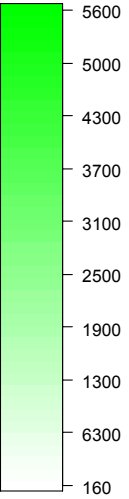
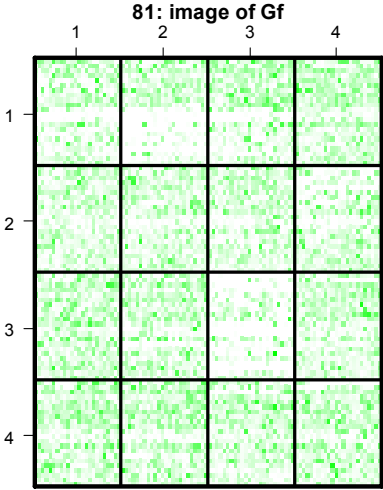
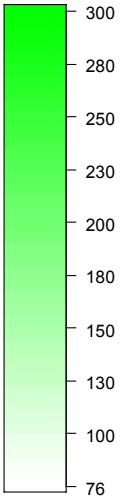
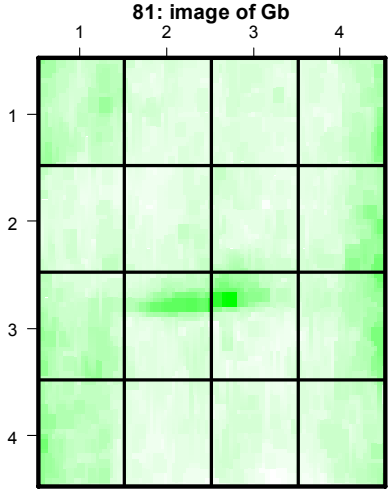
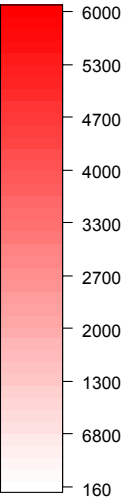
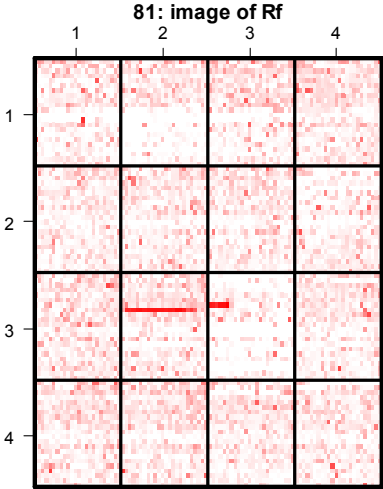
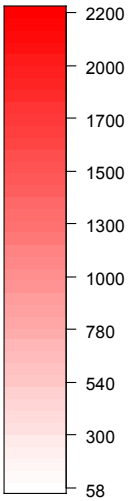
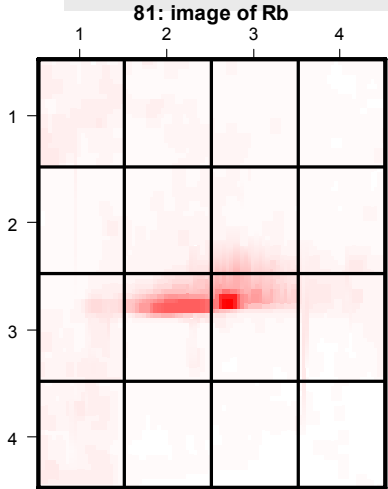
> Rcol <- maPalette(
  low = "white",
  high = "red",
  k = 50)

> image(swirl[,1]
  xvar="maRb",
  col=Rcol)

> image(swirl[,1]
  xvar="maRf",
  col=Rcol)

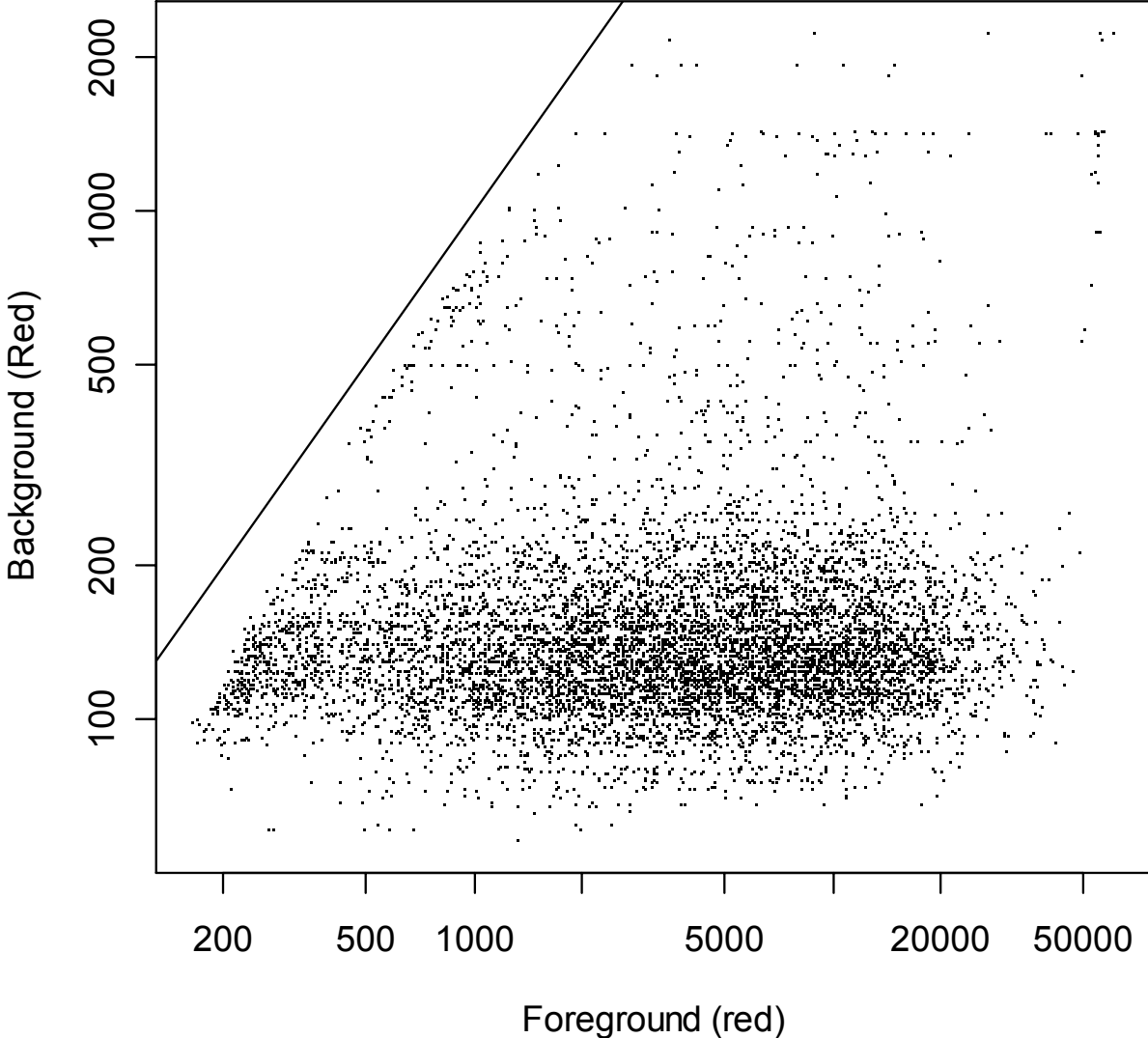
> image(swirl[,1]
  xvar="maGb",
  col=Gcol)

> image(swirl[,1]
  xvar="maGf",
  col=Gcol)
  
```



Foreground versus Background intensities

swirl.1.spot

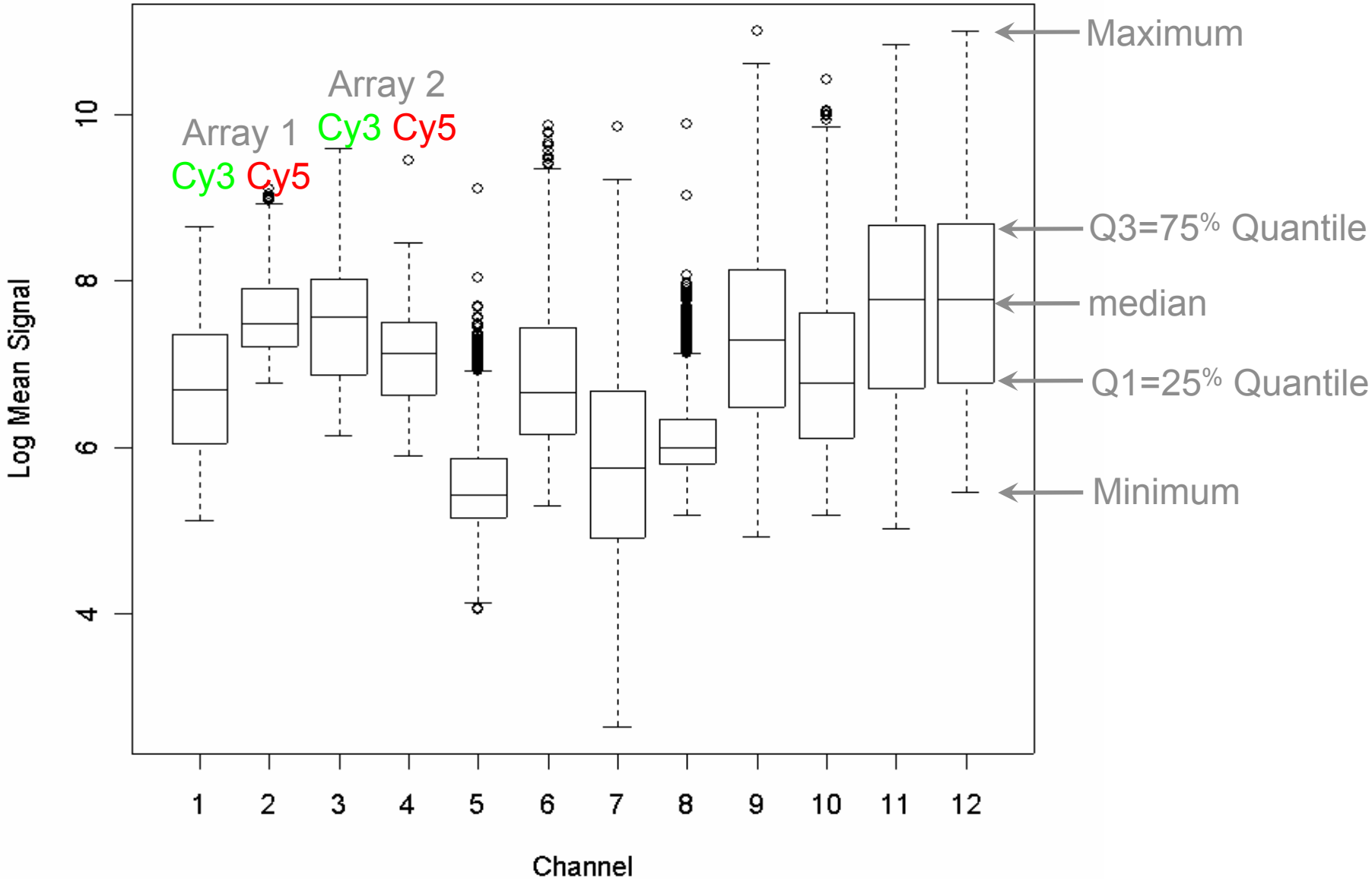


```
R R Console
> plot(
  maRf(swirl[,1]),
  maRb(swirl[,1]),
  log="xy")
> abline(0,1)
```

Normalization Methods:

- Scale normalization
- Quantile normalization
- Lowess normalization
- Variance stabilization

Displaying Variability of Microarray-Data



Normalization via rescaling

- Location and scale are basic statistical concepts for data description:

Location

normalization: corrects for spatial or dye bias

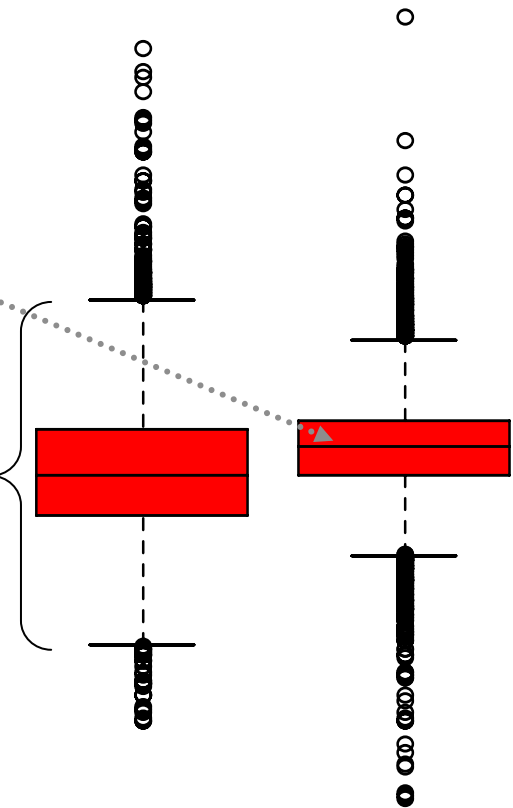
Scale

normalization: homogenizes the variability across arrays

Normalized log-intensity ratios are given by

$$M_{\text{norm}} = (M\text{-location}) / \text{scale}$$

“Location and scale of different MA measurements should be (approximately) the same.”



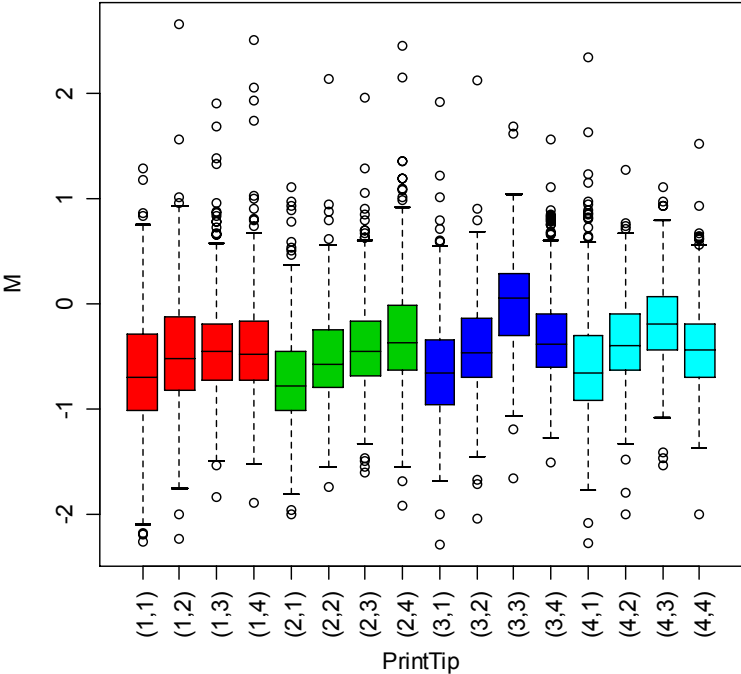
boxplots

Normalizing the Hybridization-Intensities

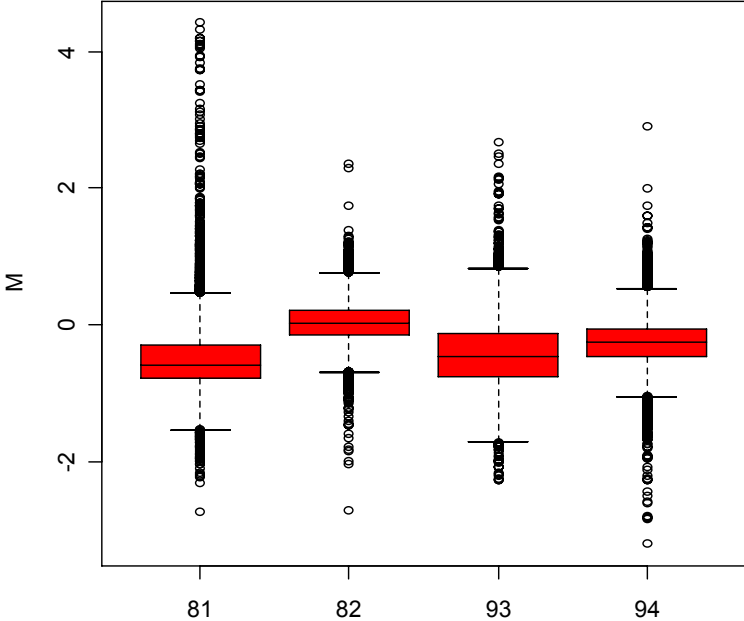
- Background Correction
 - Local Background → Image Analysis
 - Global Background → e.g. 5% Quantile
- Robust estimation of a “rescaling” Factor, e.g. *Median of Differences* based on
 - the majority of genes
 - Housekeeping genes
 - *Spiked* in control genes
- There are many other normalization methods!
Other methods:
 - Lowess (aka loess)
 - Quantile
 - VSN

marray – Swirl Data: Pre Normalization

Swirl array 93: pre-norm



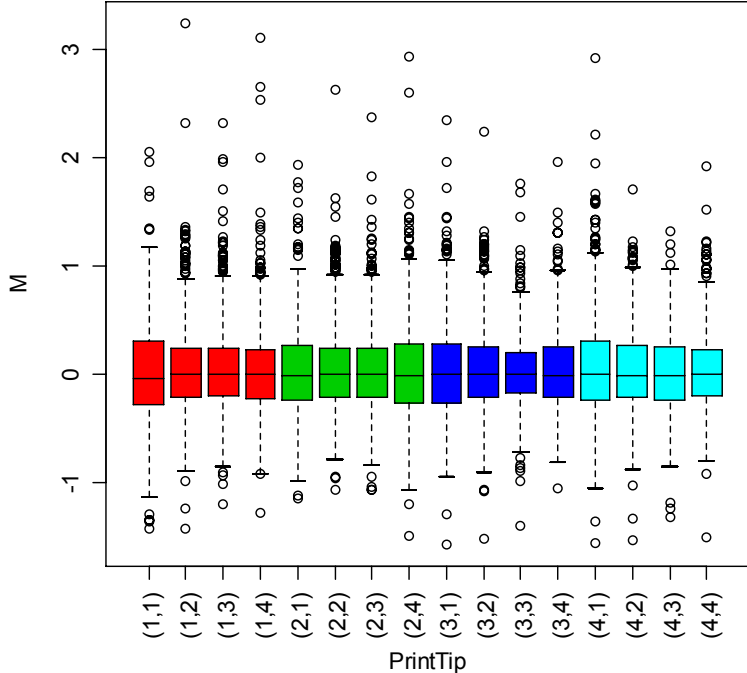
Swirl arrays: pre-normalization



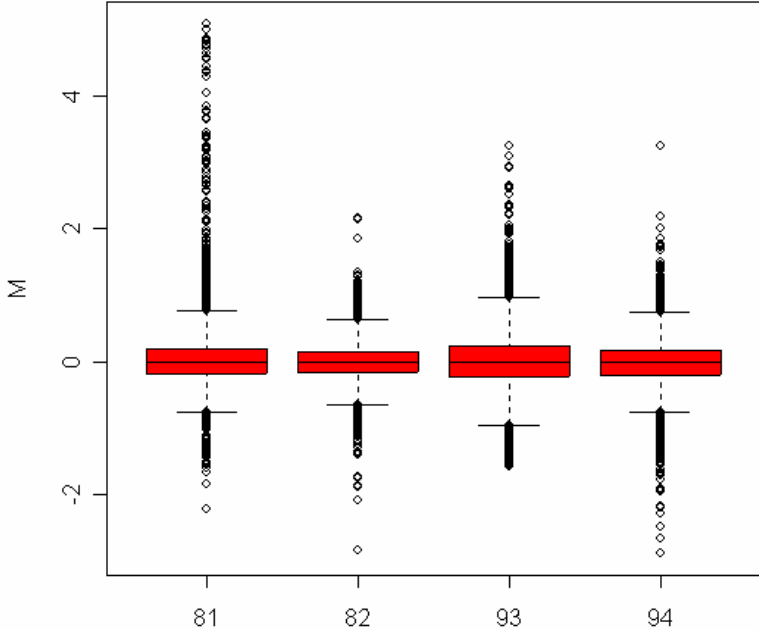
```
R Console  
  
> boxplot(swirl[, 3], xvar = "maPrintTip", yvar = "maM")  
> boxplot(swirl, yvar = "maM")
```

marray – Swirl Data: Post Normalization

Swirl array 93: post-norm

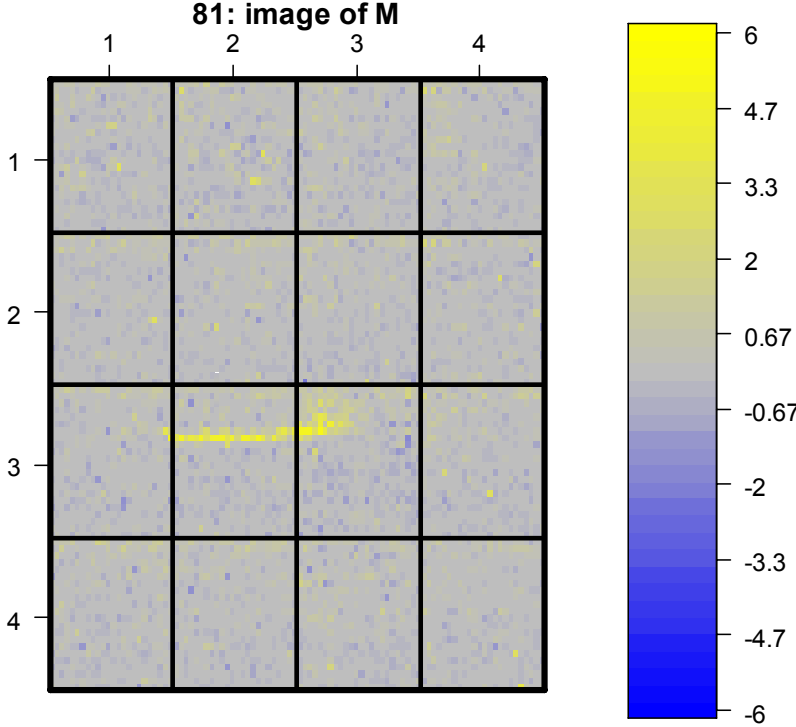
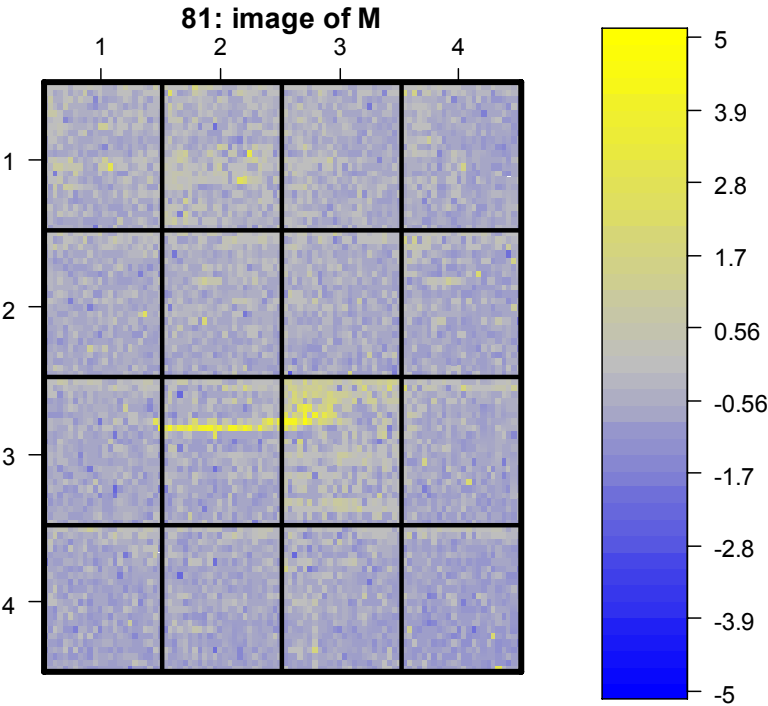


Swirl arrays: post-normalization



```
R R Console
> swirl.norm <- maNorm(swirl, norm = "p")
> boxplot(swirl.norm[, 3], xvar = "maPrintTip", yvar = "maM")
> boxplot(swirl.norm, yvar = "maM")
```

Swirl Data – M values, raw versus normalized



Normalization procedure was not able to remove scratch

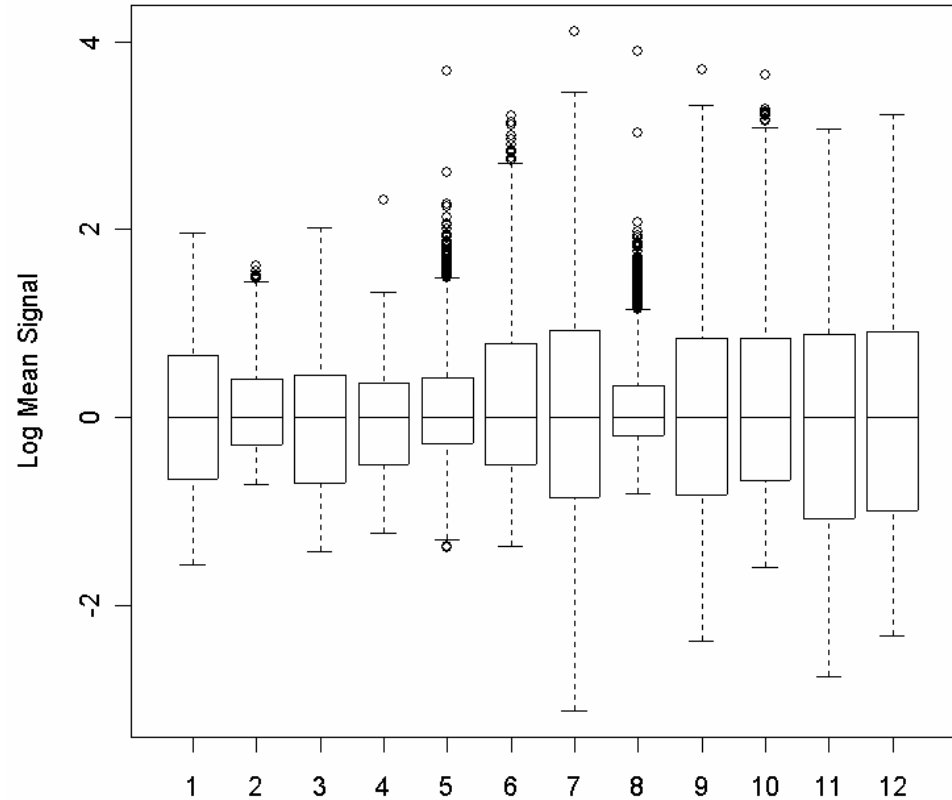
```
R R Console  
> image(swirl[,1])  
> image(swirl.norm[,1])
```

Median-centering

- One of the simplest strategies is to bring all „Centers“ of the array data to the same level.
- Assumption, the majority of genes or the center should not change between conditions.
- the Median is used as a robust measure.

divide all
expression
measurements of
each array by the
Median.

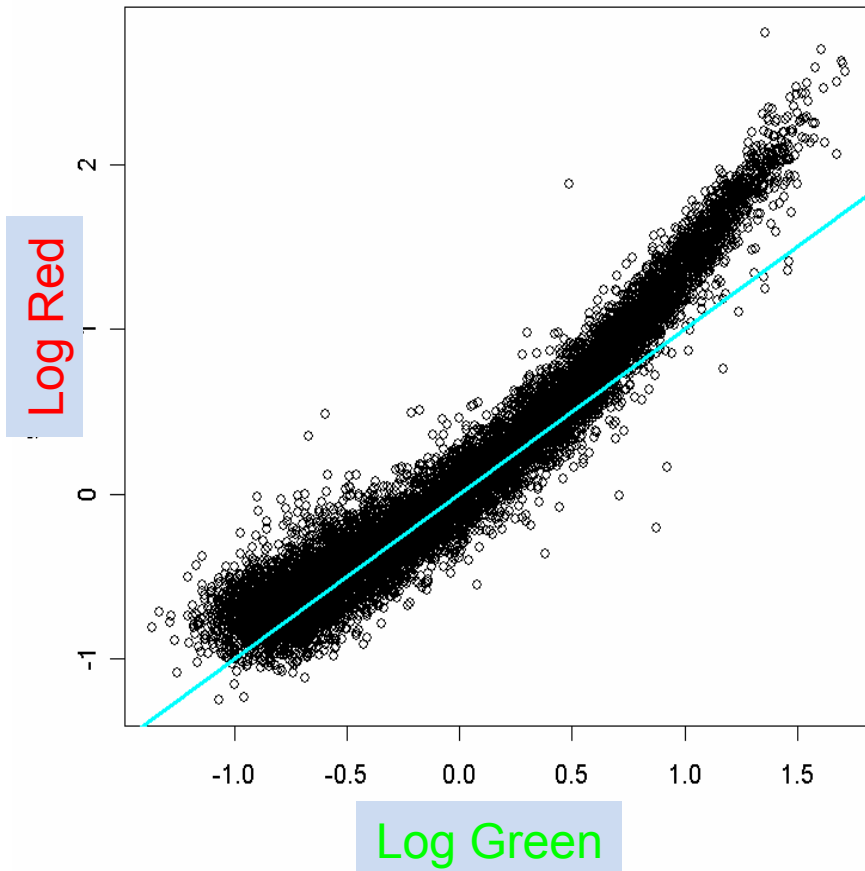
Log Signal, centered at 0



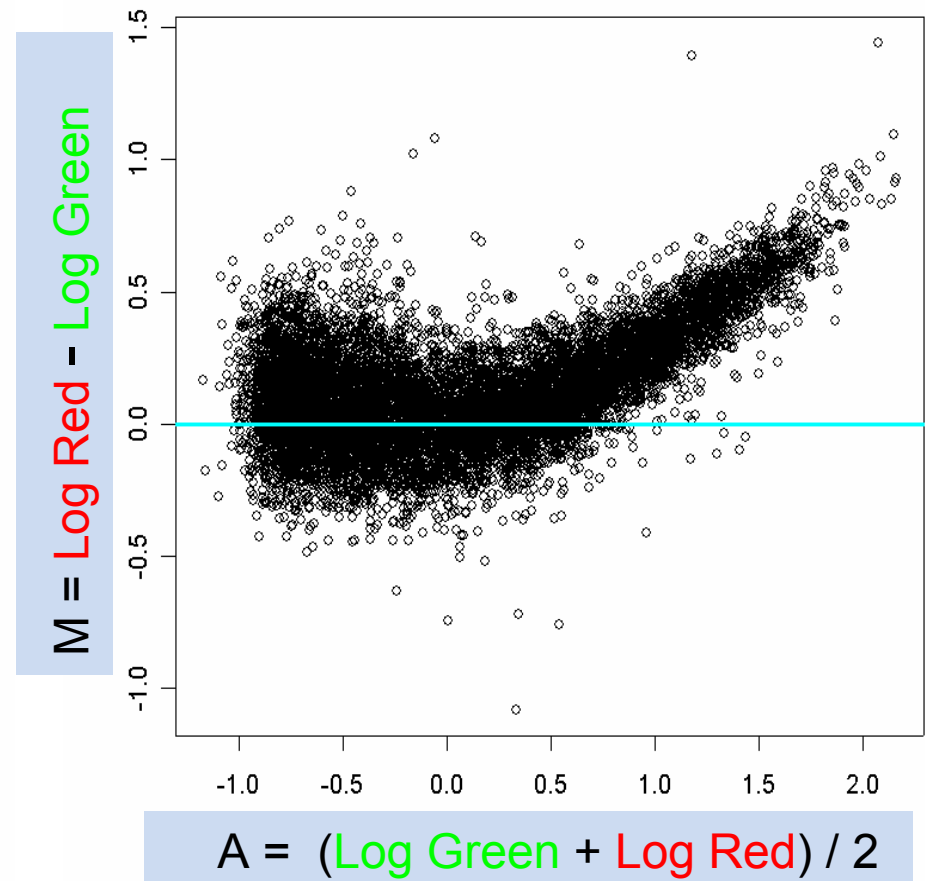
Problems with Median-Centering

Median-Centering is a **global Method**. It does not adjust for local effects, intensity dependent effects, print-tip effects, etc.

Scatterplot of log-Signals
after Median-centering



M-A Plot of the same data



Lo(w)ess Normalization

Assumption: There is an intensity-dependent bias of the fold change,

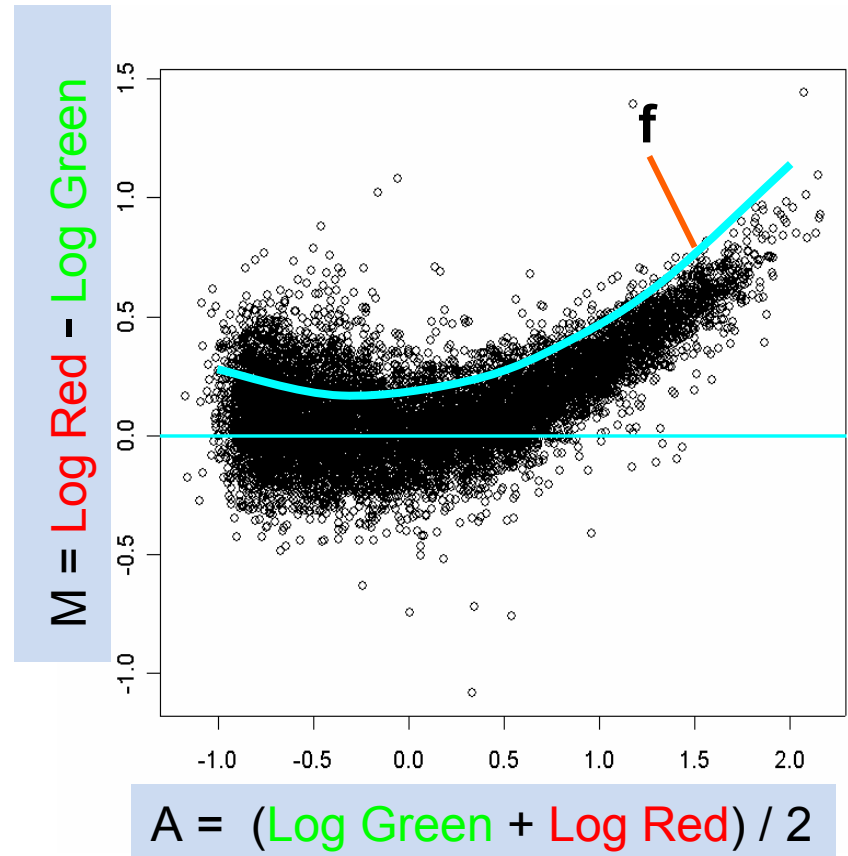
$$M = f(A)$$

and hence $y_j = f(x_j) + \delta_j$
where δ_j is the “true” log fold change for gene j . The true fold change distribution is approximately a zero-symmetric normal distribution.

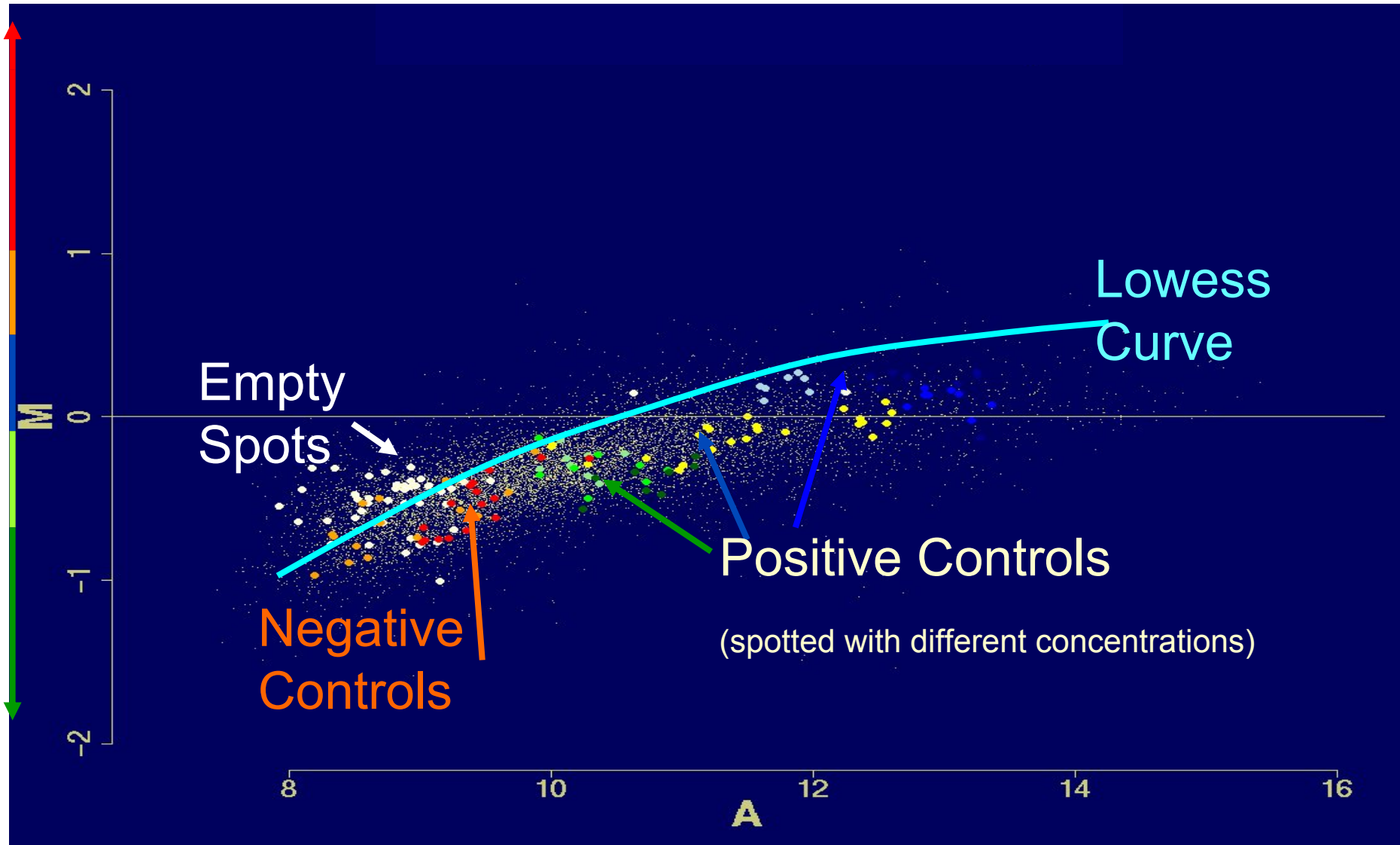
Task: Find f , replace y_j by $y_j - f(x_j)$.

The **idea of local regression** is that f can be estimated locally at a point x by a simple (and easy-to-fit) function f_x . For each point x , we then estimate f by

$$\hat{f}(x) = f_x(x)$$



Lowess Normalization

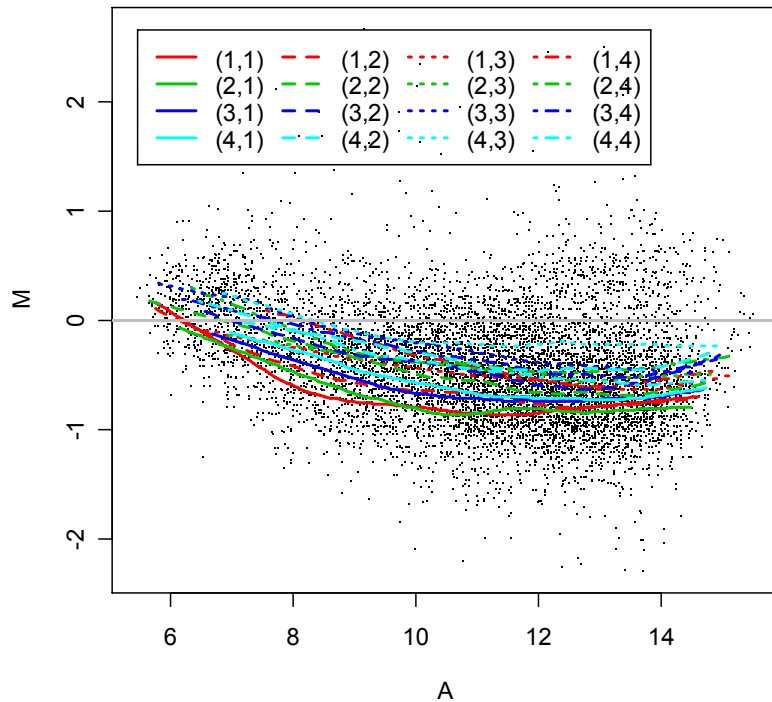


$$M = \log R/G = \log R - \log G$$

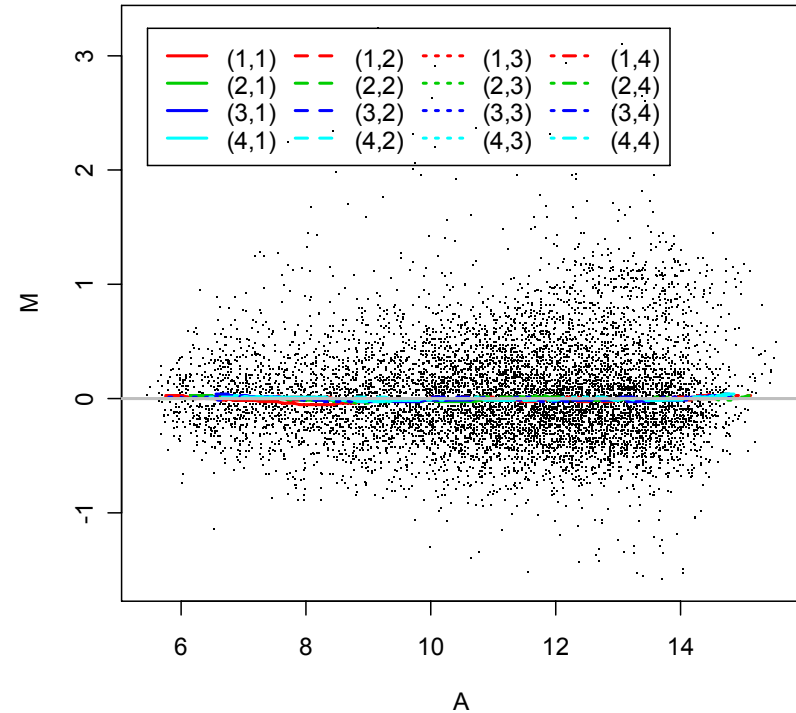
$$A = (\log R + \log G) / 2$$

marray – Swirl Data: Print-tip lowess Normalization

Swirl array 93: pre-norm MA-Plot



Swirl array 93: post-norm MA-Plot



R Console

```
> plot(swirl[, 3], xvar = "maA", yvar = "maM",  
      zvar = "maPrintTip")  
  
> plot(swirl.norm[, 3], xvar = "maA", yvar = "maM",  
      zvar = "maPrintTip")
```

Non-parametric smoother: loess, lowess, local regression line, generalizes the concept of moving average.

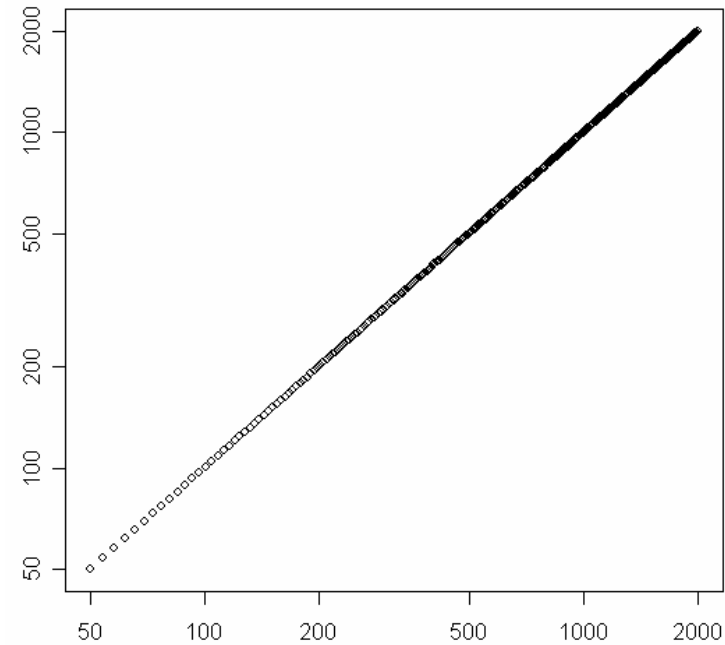
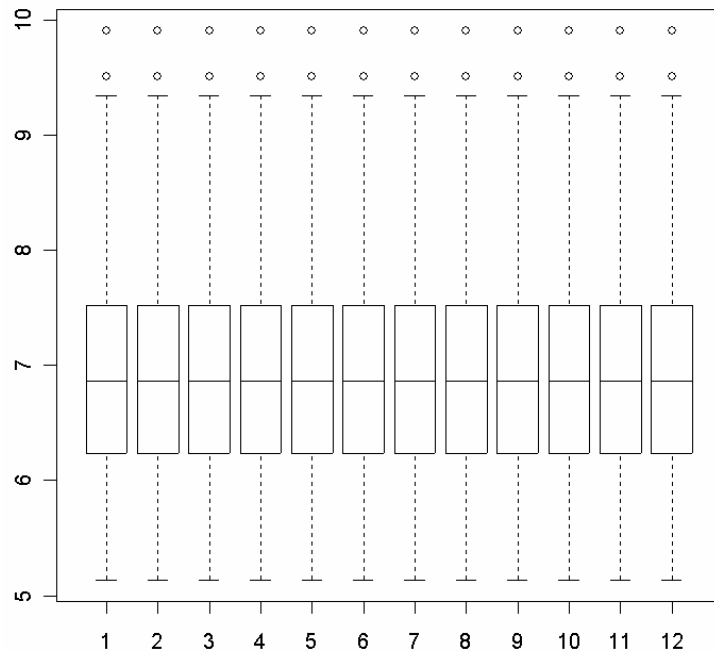
Quantile Normalization

The basic idea of Quantile-Normalization is very simple:

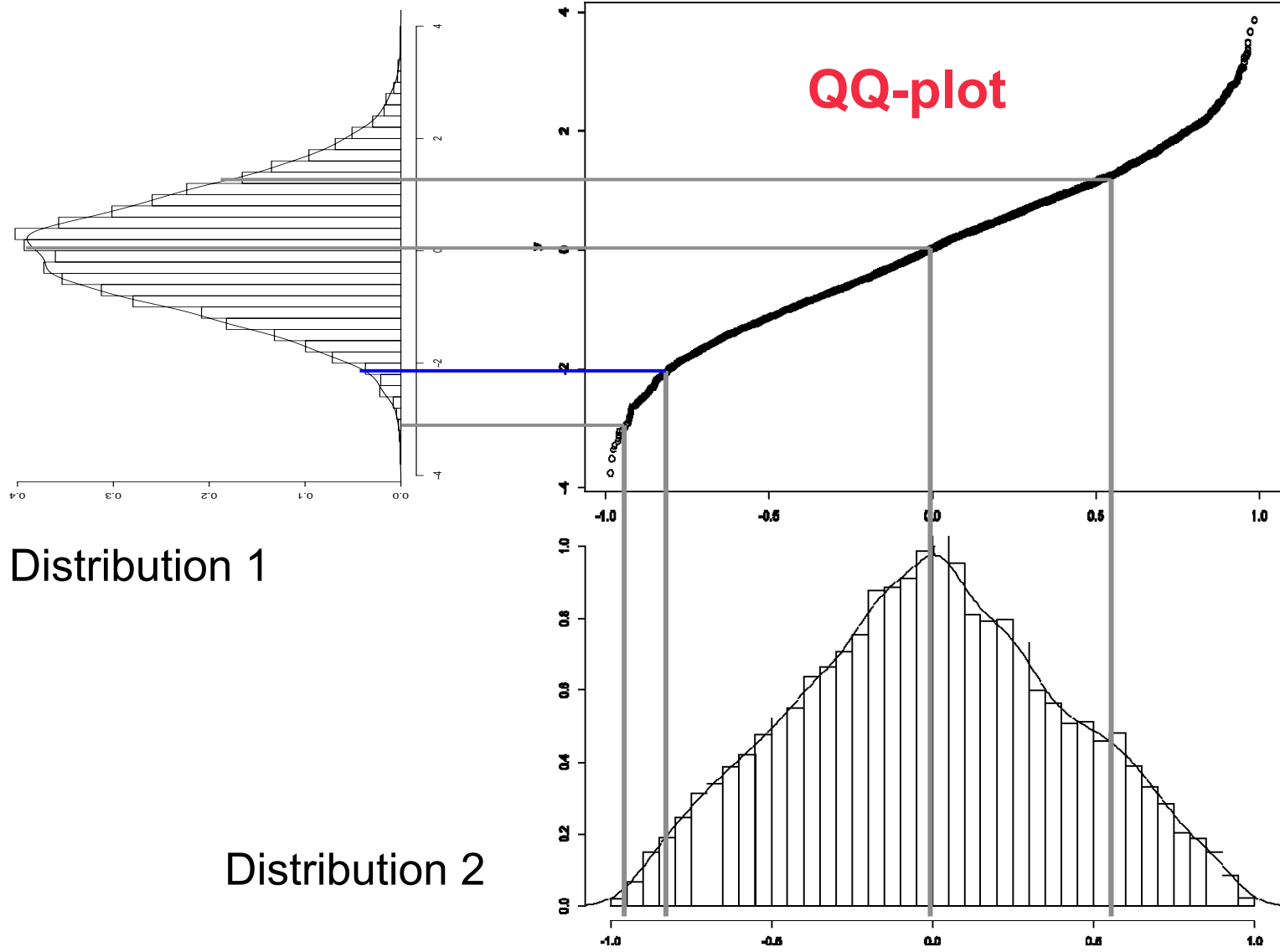
„The Histograms of all Slides are made identical“

Tightens the idea of Median-Centering. Not only the 50%-Quantile is adjusted, but *all* Quantiles.

Boxplot and QQ-plot after Quantile normalization



Quantile Normalization



Distribution 1

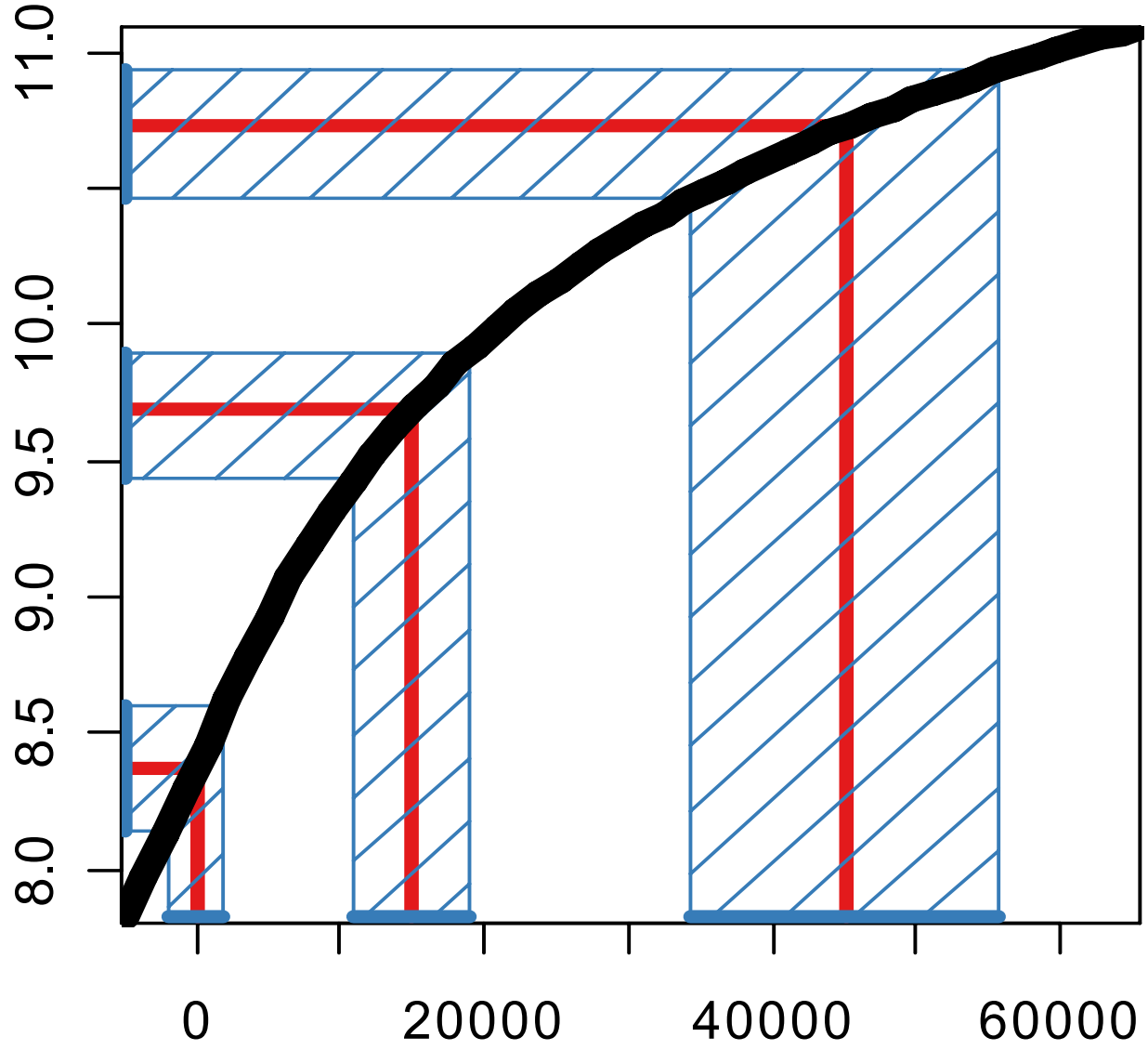
Distribution 2

VSN: model and theory

- Huber et al. (2002) *Bioinformatics*, 18:S96–S104
- Model for measured probe intensity
Rocke DM, Durbin B (2001) *Journal of Computational Biology*, 8:557–569
- log-transformation is replaced by a transformation (arcsinh) based on theoretical grounds.
- Estimation of transformation parameters (location, scale) based on ML paradigm and numerically solved by a least trimmed sum of squares regression.
- vsn-normalized data behaves close to the normal distribution

variance stabilizing transformations

Transformed Scale - $f(x)$



Original Scale - x

variance stabilizing transformations

$$f(x) = \int \frac{1}{\sqrt{v(u)}} du$$

1.) constant variance ('additive') $v(u) = s^2 \Rightarrow f \propto u$

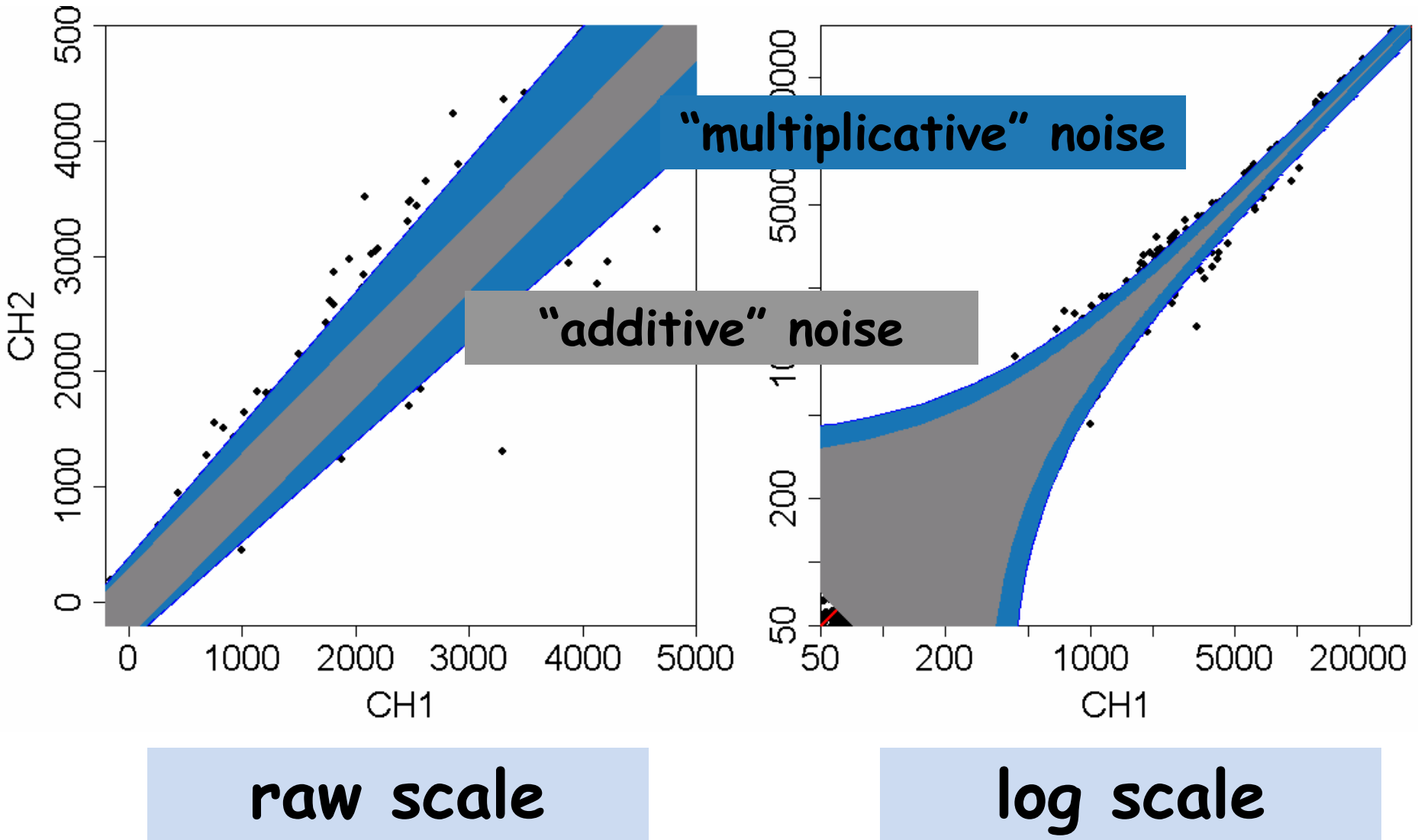
2.) constant CV ('multiplicative') $v(u) \propto u^2 \Rightarrow f \propto \log u$

3.) offset $v(u) \propto (u + u_0)^2 \Rightarrow f \propto \log(u + u_0)$

4.) additive and multiplicative

$$v(u) \propto (u + u_0)^2 + s^2 \Rightarrow f \propto \operatorname{arsinh} \frac{u + u_0}{s}$$

The two-component model



B. Durbin, D. Rocke, JCB 2001

Fitting of an error model

measured intensity = offset + gain × true abundance

$$y_{ik} = a_{ik} + b_{ik} x_k$$

$$a_{ik} = a_i + \varepsilon_{ik}$$

a_i per-sample offset

$$\varepsilon_{ik} \sim N(0, b_i^2 s_1^2)$$

“additive noise”

$$b_{ik} = b_i b_k \exp(\eta_{ik})$$

b_i per-sample
normalization factor

b_k sequence-wise
probe efficiency

$$\eta_{ik} \sim N(0, s_2^2)$$

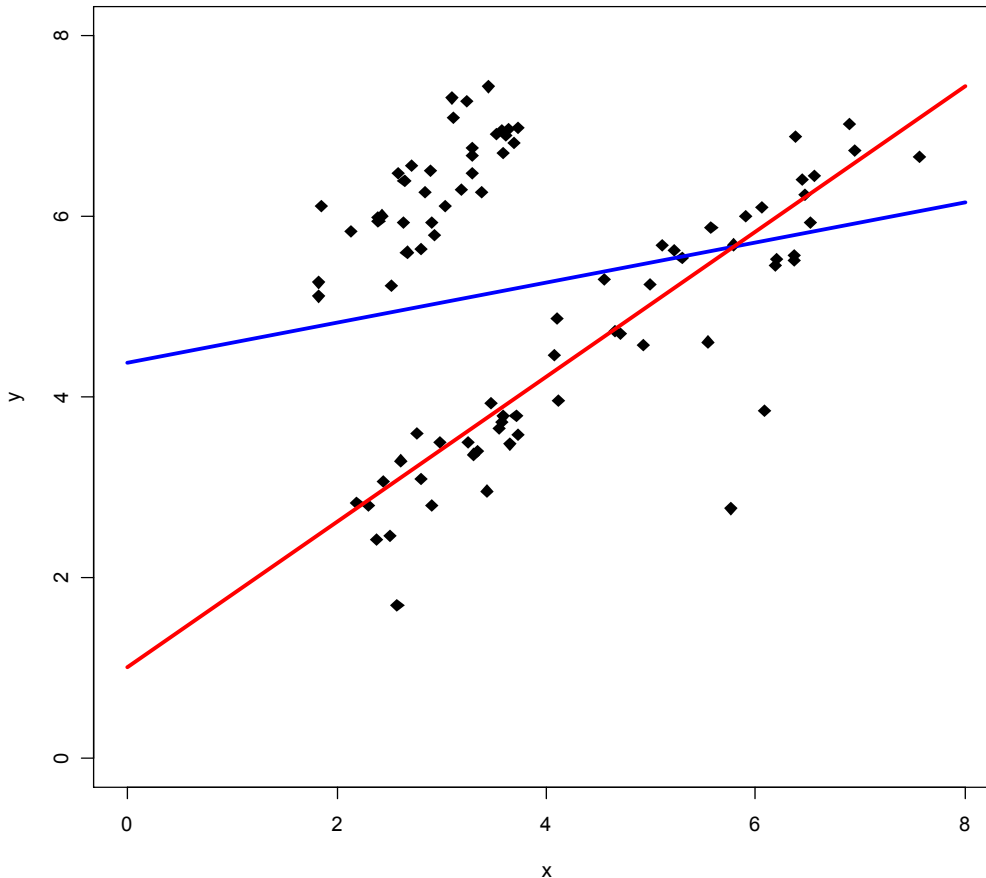
“multiplicative noise”

Parameter-Estimation

$$\operatorname{arsinh} \frac{y_{ki} - a_i}{b_i} = \mu_k + \varepsilon_{ki}, \quad \varepsilon_{ki} \sim N(0, c^2)$$

- maximum likelihood estimator: straightforward - but sensitive to deviations from normality
- model holds for genes that are unchanged; differentially transcribed genes act as outliers.
- robust variant of ML estimator, à la Least Trimmed Sum of Squares regression.
- works as long as <50% of genes are differentially transcribed

Least trimmed sum of squares regression



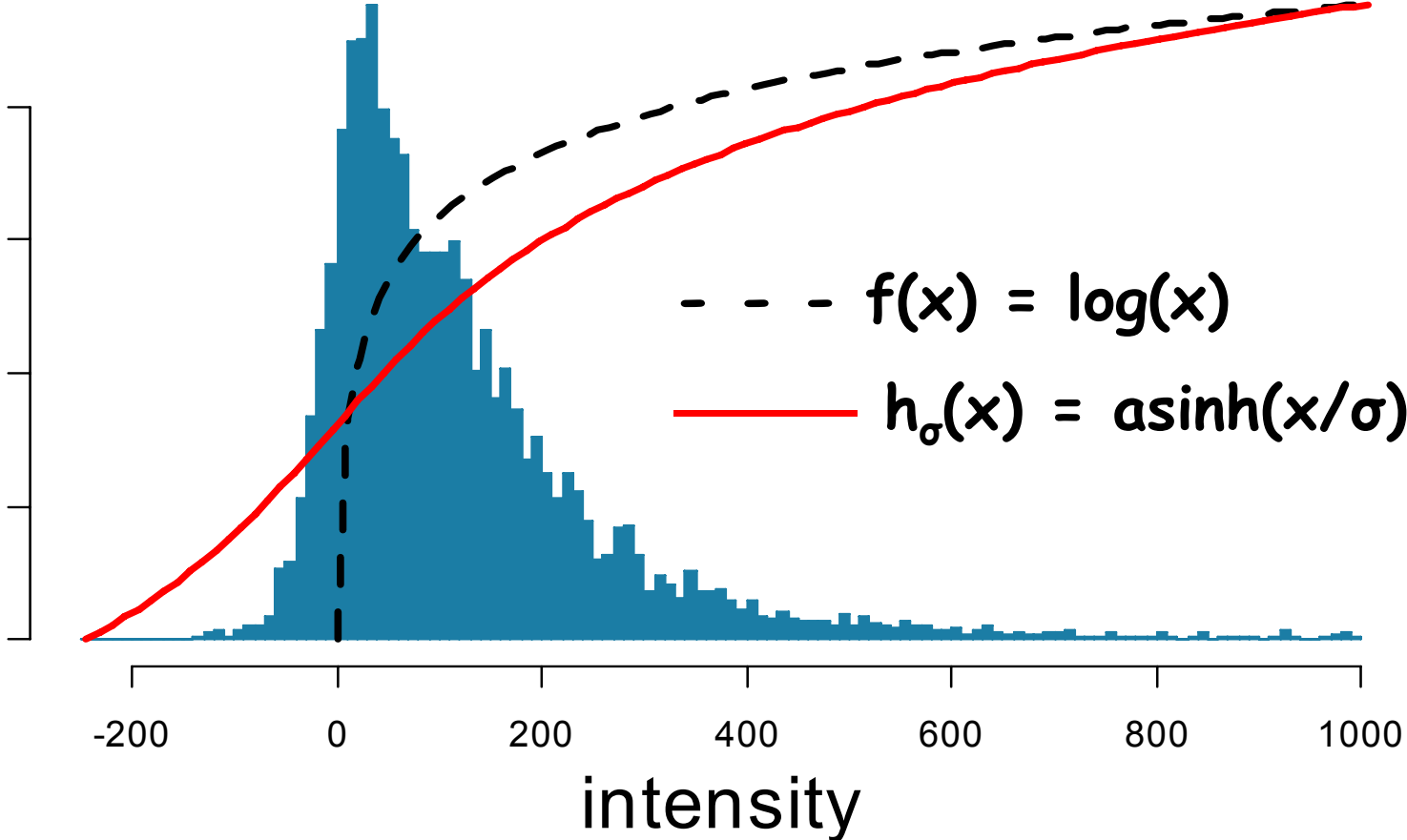
- least sum of squares
- **least trimmed sum of squares**

minimize

$$\sum_{i=1}^{n/2} (y_{(i)} - \mathcal{A}(x_{(i)}))^2$$

P. Rousseeuw, 1980s

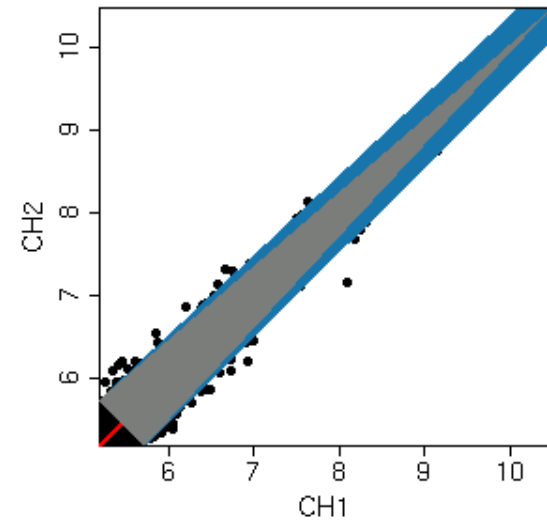
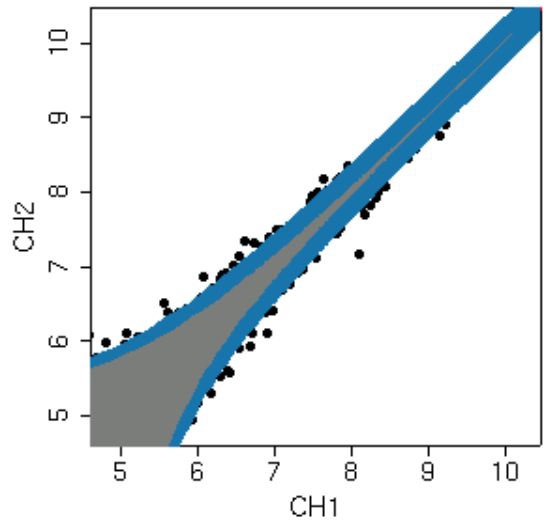
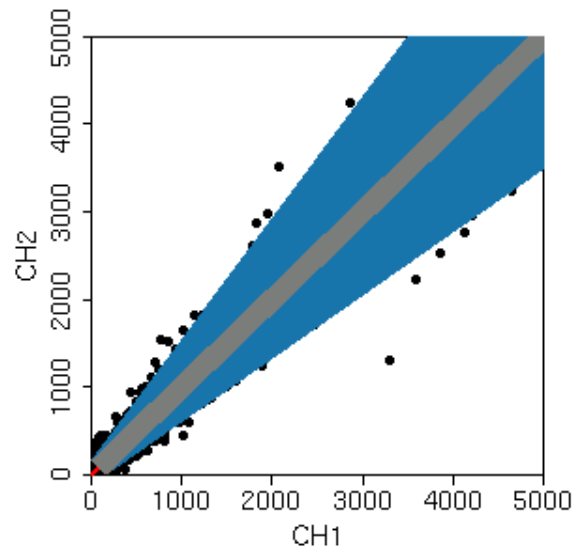
The „glog“-Transformation



$$\text{arsinh}(x) = \log(x + \sqrt{x^2 + 1})$$

$$\lim_{x \rightarrow \infty} (\text{asinh}(x) - \log(x)) \longrightarrow \log(2)$$

The „glog“-Transformation

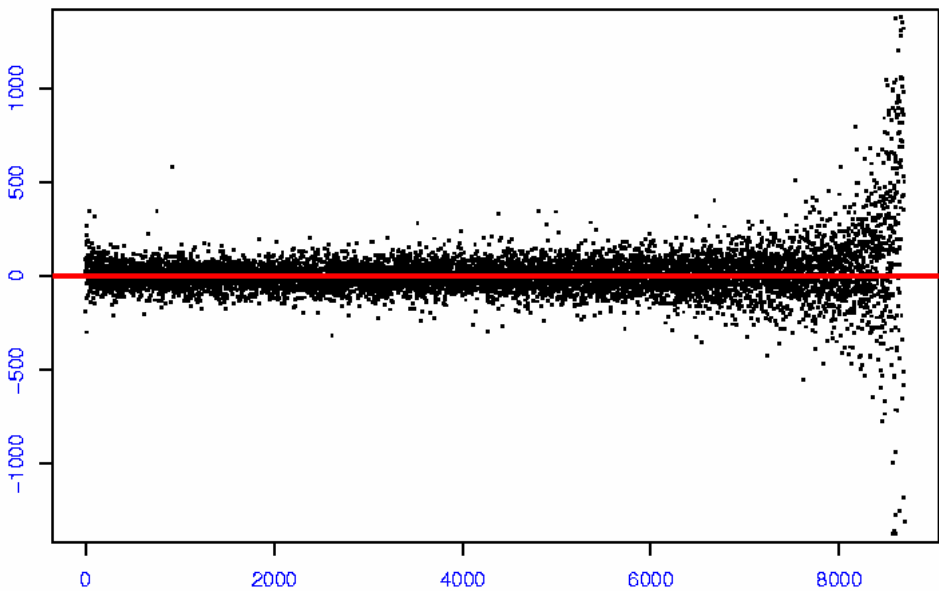


Variance:

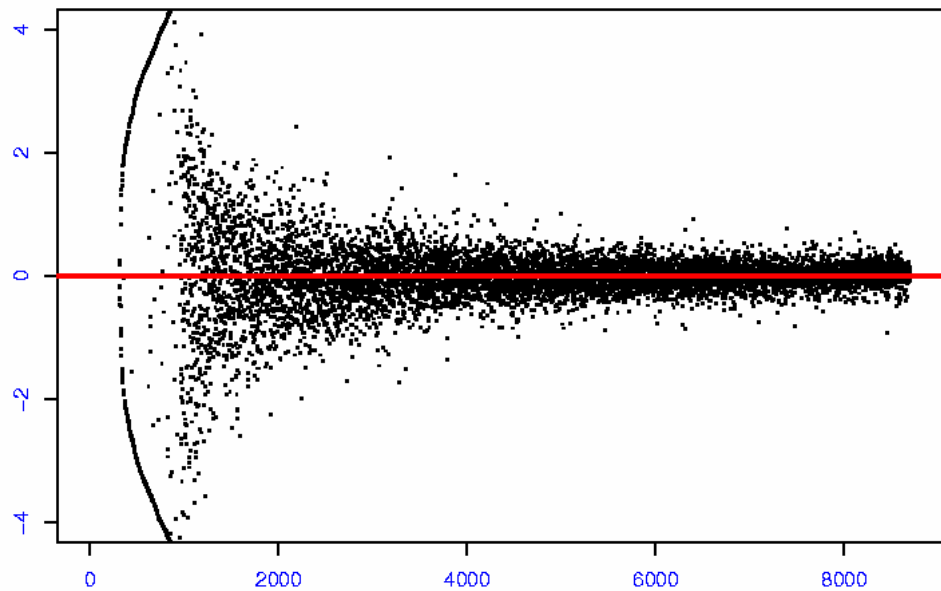
-  Additive component
-  multiplicative component

P. Munson, 2001
D. Rocke & B. Durbin, ISMB 2002
W. Huber et al., ISMB 2002

a) Δy

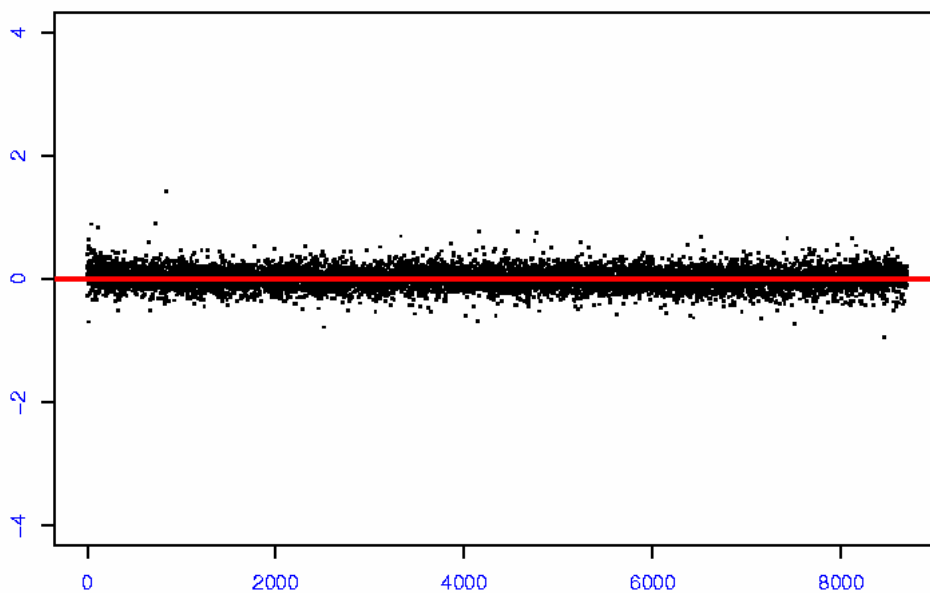


b) $\Delta \log(y)$



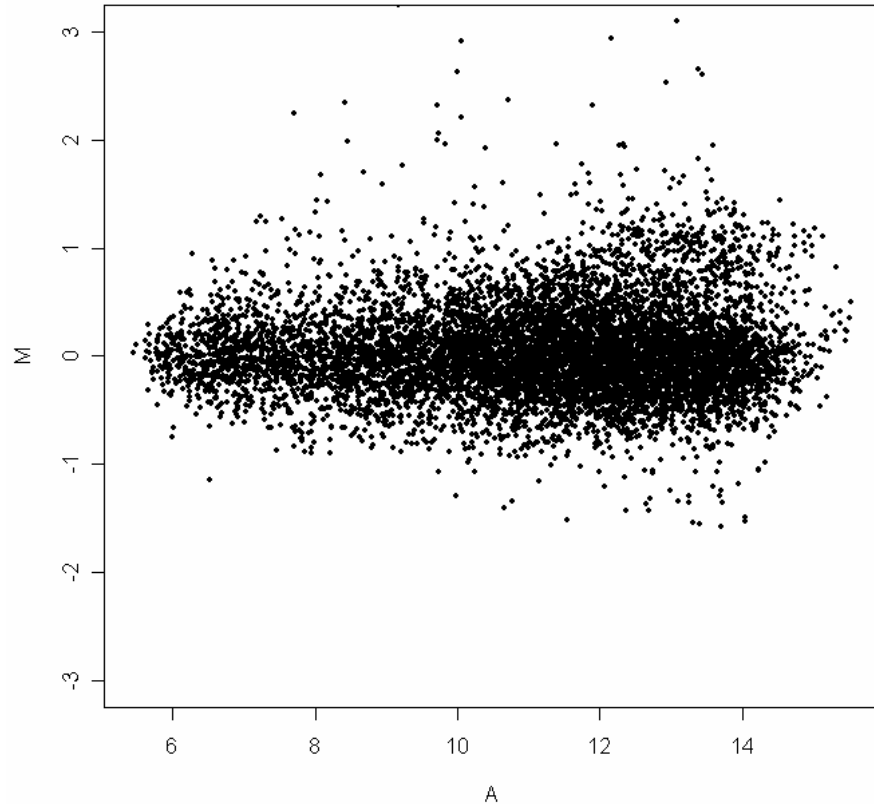
c) $\Delta h(y)$

difference red-green
rank(average)

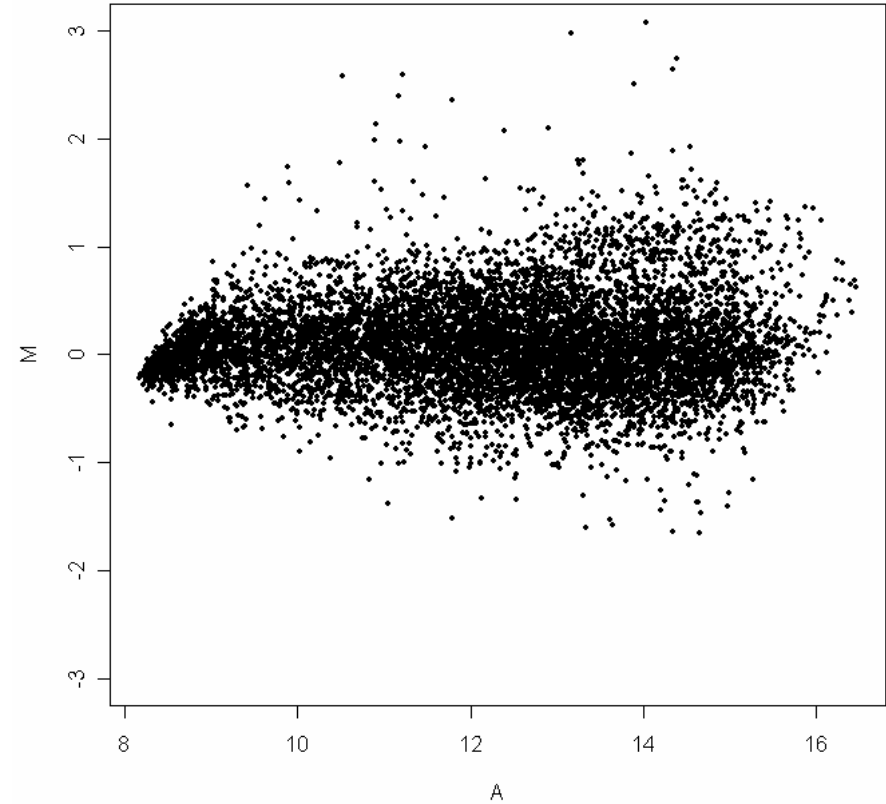


Swirl Data: Lowess versus VSN

Swirl array 93: lowess normalization



Swirl array 93: vsn normalization



R Console

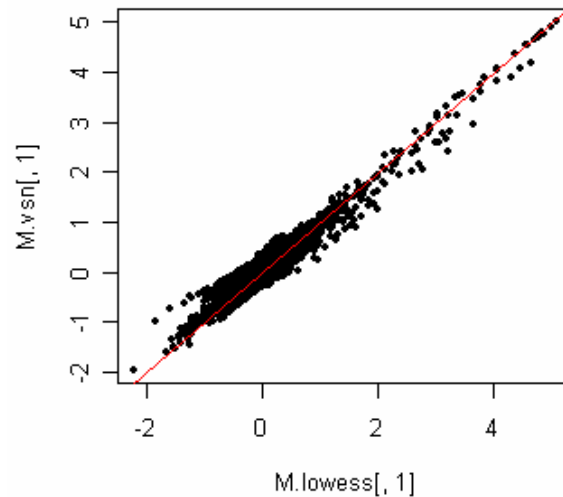
```
> plot(maA(swirl.norm[,3]), maM(swirl.norm[,3]), ylim=c(-3,3))
> library(vsn); library(limma);
> A.vsn<-log2(exp(exprs(swirl.vsn[,6])+exprs(swirl.vsn[,5])))/2
> M.vsn<-log2(exp(exprs(swirl.vsn[,6])-exprs(swirl.vsn[,5]))))
> plot(A.vsn, M.vsn, ylim=c(-3,3))
```


Swirl: LOWESS versus VSN

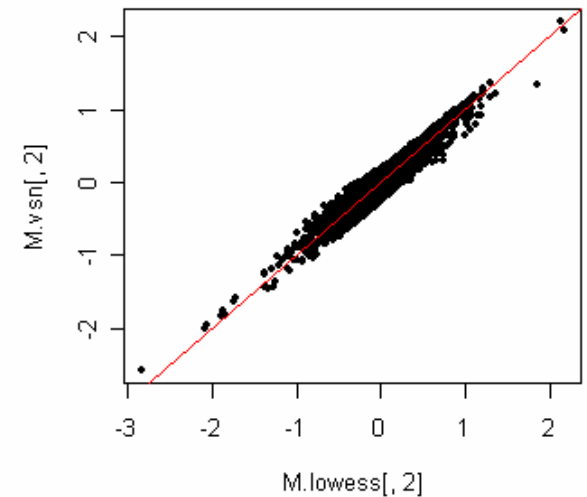
R Console

```
> M.lowess<-maM(swirl.norm)
> M.vsn<-log2(exp(exprs(
  swirl.vsn[,c(2,4,6,8)])-
  exprs(swirl.vsn[,c(1,3,5,7)]
  )))
> par(mfrow=c(2,2))
> plot(M.lowess[,1],
       M.vsn[,1], pch=20)
> abline(0,1, col="red")
> plot(M.lowess[,1],
       M.vsn[,1], pch=20)
> abline(0,1, col="red")
> plot(M.lowess[,1],
       M.vsn[,1], pch=20)
> abline(0,1, col="red")
> plot(M.lowess[,1],
       M.vsn[,1], pch=20)
> abline(0,1, col="red")
```

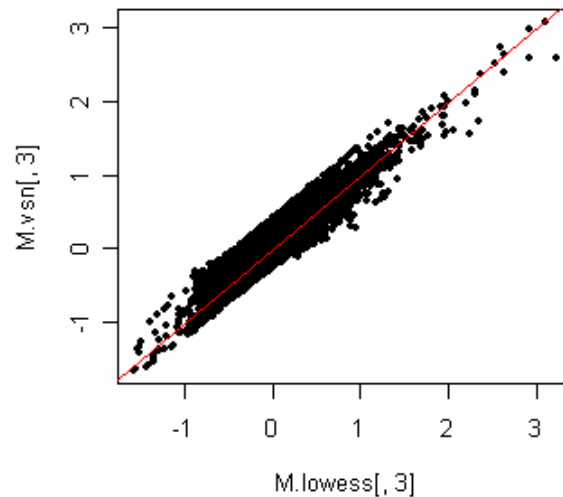
Swirl 83



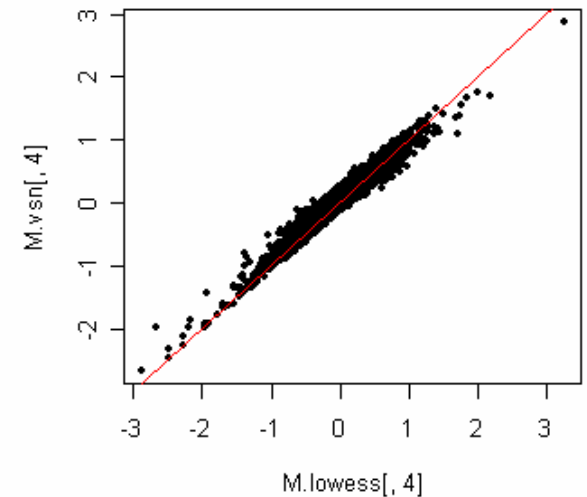
Swirl 84



Swirl 93



Swirl 94



Summary

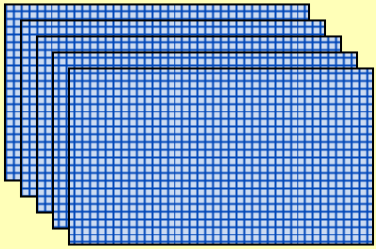
- What makes a good measurement: Precision and Unbiasedness
- Need to normalize.
- Normalization is not something trivial, has many practical and theoretical implications which need to be considered.
- What is the best way to normalize?
- How dependent is the result of your analysis from the normalization procedure?

Experimental Design:

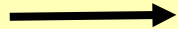
- Different levels of replication
- Pooling vs. non pooling
- different strategies to pair hybridization targets on cDNA arrays
- direct vs. indirect comparisons

Two main aspects of array design

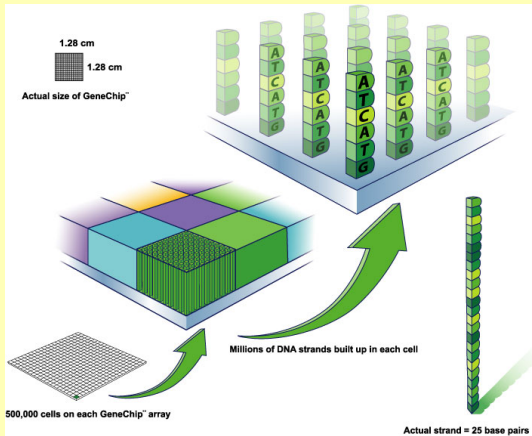
Design of the array



Arrayed Library
(96 or 384-well plates of bacterial glycerol stocks)

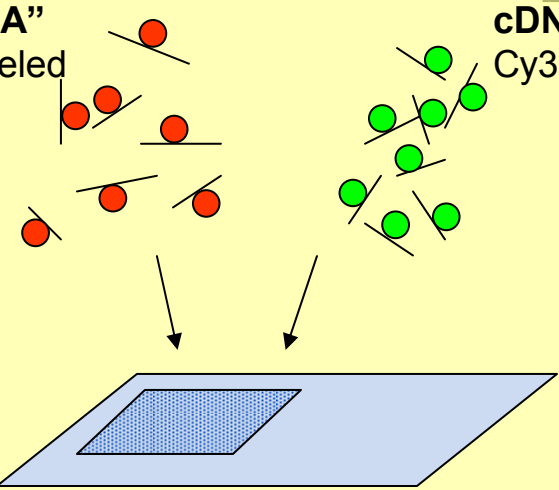


Spot as microarray on glass slides



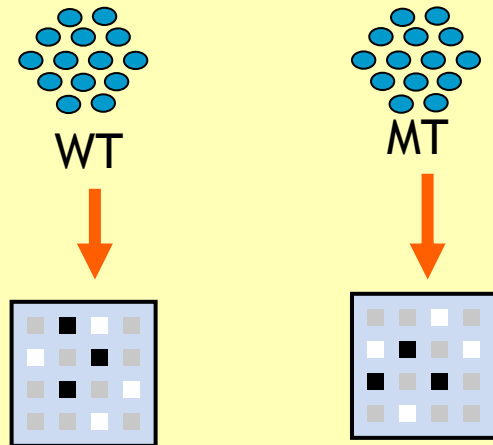
Allocation of mRNA samples to the slides

cDNA cDNA "A" Cy5 labeled cDNA "B" Cy3 labeled



Hybridization

affy

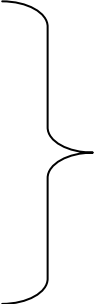


Some aspects of design

2. Allocation of samples to the slides

A Types of Samples

- Replication – technical, biological.
- Pooled vs individual samples.
- Pooled vs amplification samples.



This relates to both Affymetrix and two color spotted array.

B Different design layout

- Scientific aim of the experiment.
- Robustness.
- Extensibility.
- Efficiency.

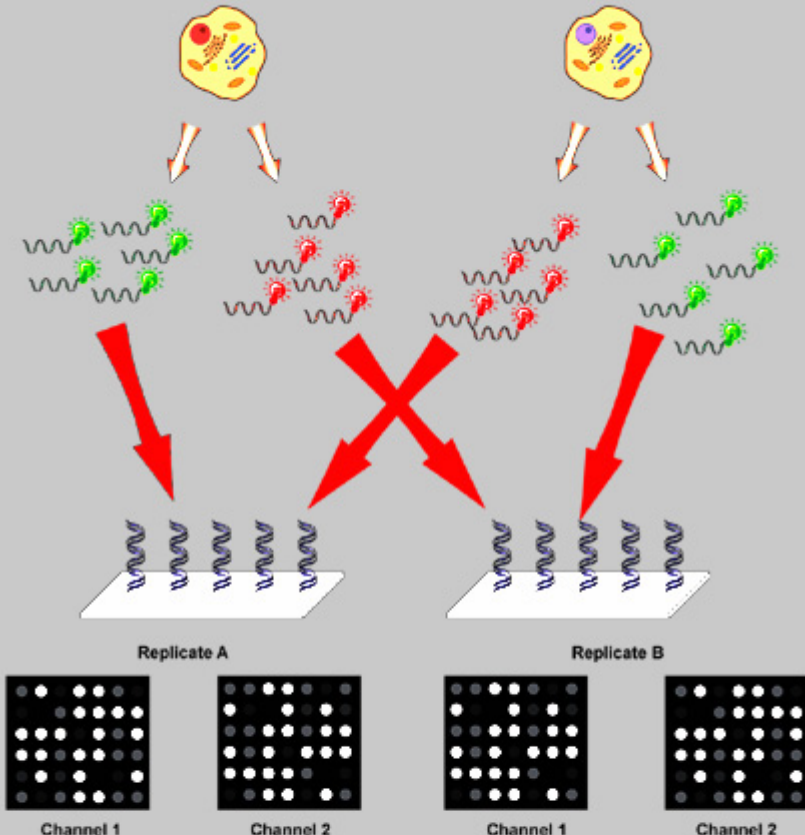
Taking physical limitations or cost into consideration:

- the number of slides.
- the amount of material.

Design of a Dye-Swap Experiment

- Repeats are essential to control the quality of an experiment.
- One example for Replicates is the Dye-Swap, i.e. Replicates with the same mRNA Pool but with swapped labels.
- Dye-Swap shows whether there is a dye-bias in the Experiment.

Figure 1B



- Data Processing Steps:**
1. Image Segmentation and Analysis
 2. Data Filtering
 3. Data Normalization
 4. Ratio Calculation

Replicate A

Gene Name	Ratio (Ch1/Ch2)	Log Ratio $\log_2(\text{Ch1/Ch2})$
A	2	1
B	0.5	-1
C	1	0
D	4	2

Assess normalization with array deviation calculation

Replicate B

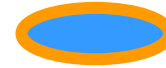
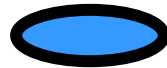
Gene Name	Ratio (Ch1/Ch2)	Log Ratio $\log_2(\text{Ch1/Ch2})$
A	0.5	-1
B	2	1
C	1	0
D	0.25	-4

Preparing mRNA samples:

Mouse model
Dissection of
tissue



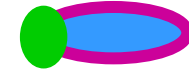
RNA
Isolation



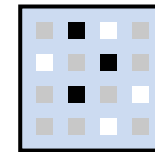
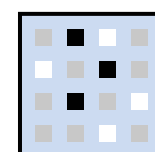
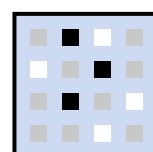
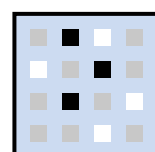
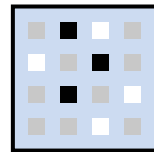
Amplification



Probe
labelling



Hybridization



Preparing mRNA samples:

Mouse model
Dissection of
tissue



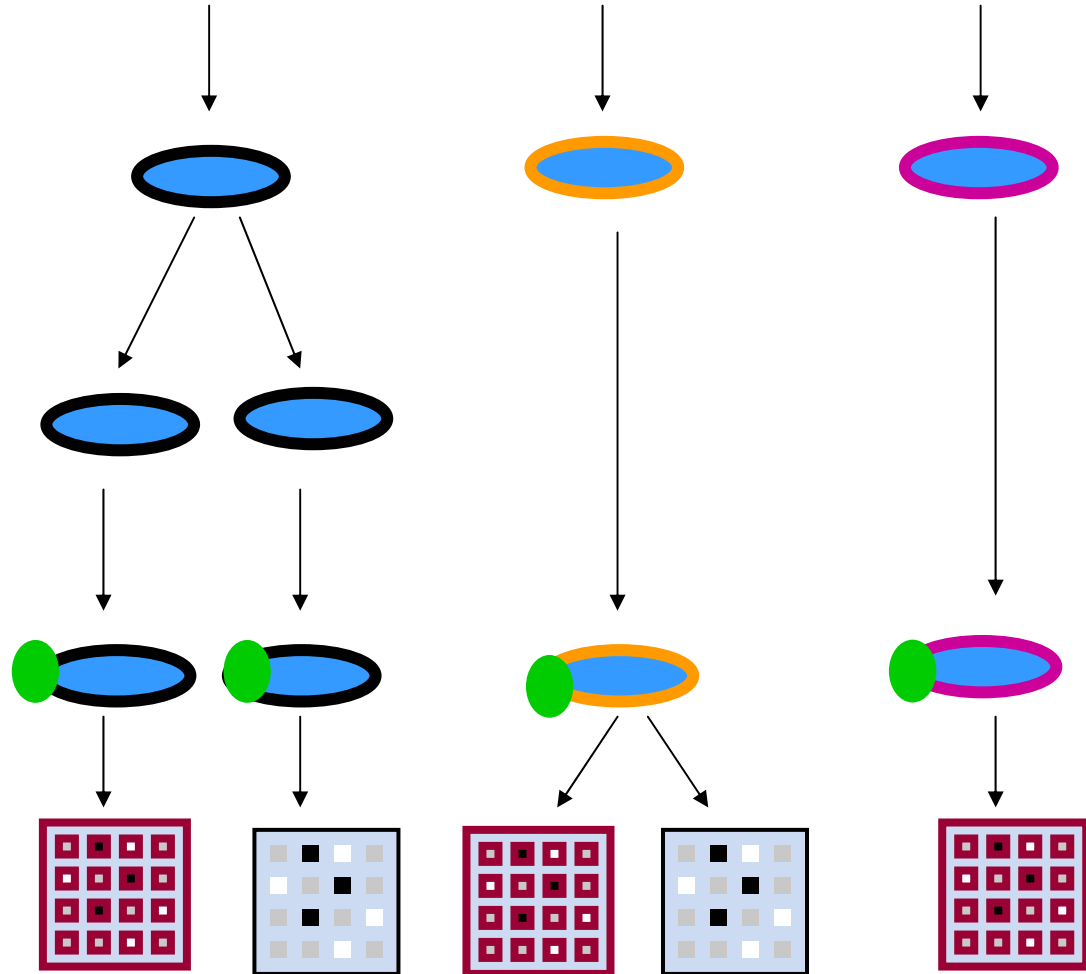
Biological Replicates

RNA
Isolation

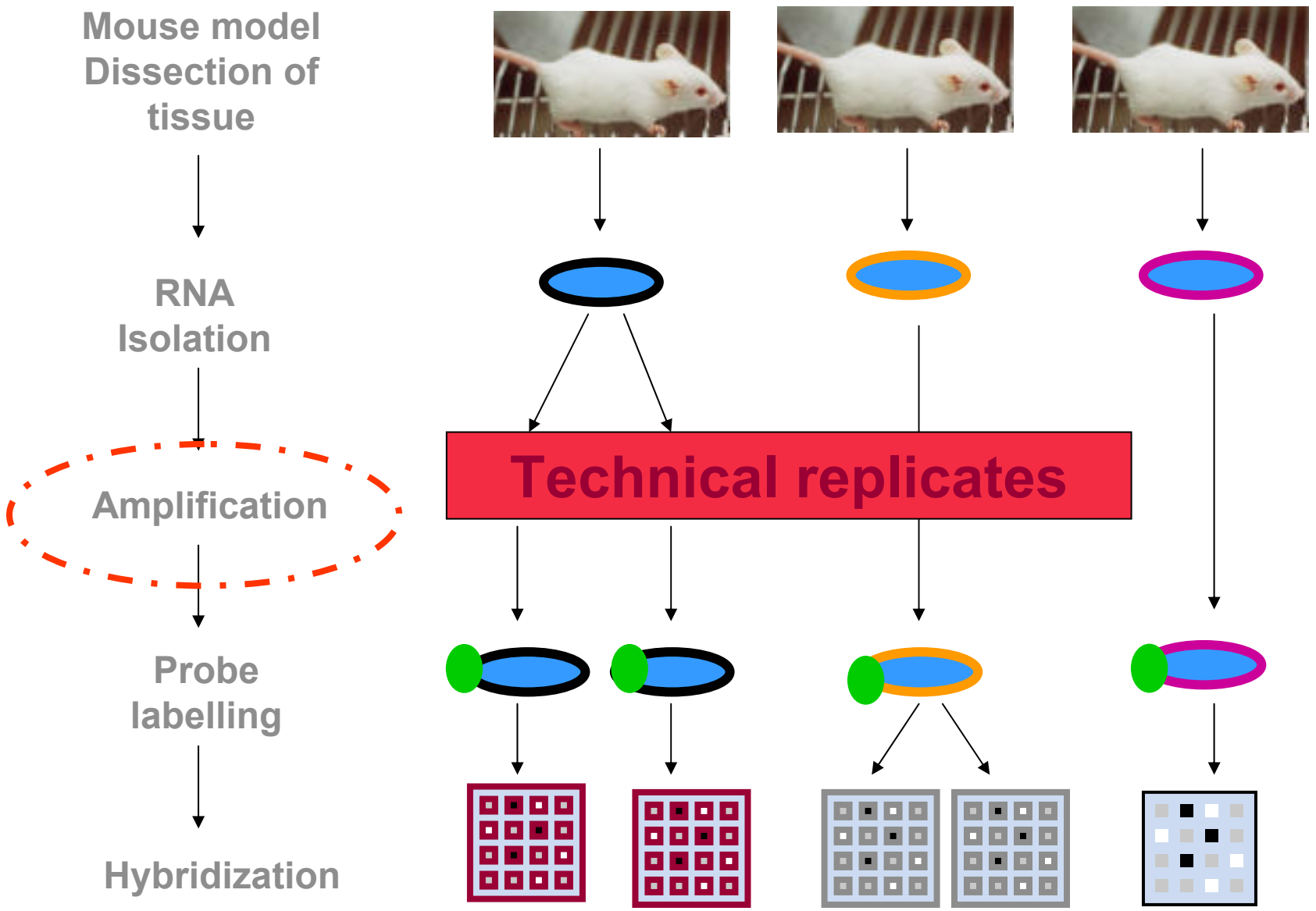
Amplification

Probe
labelling

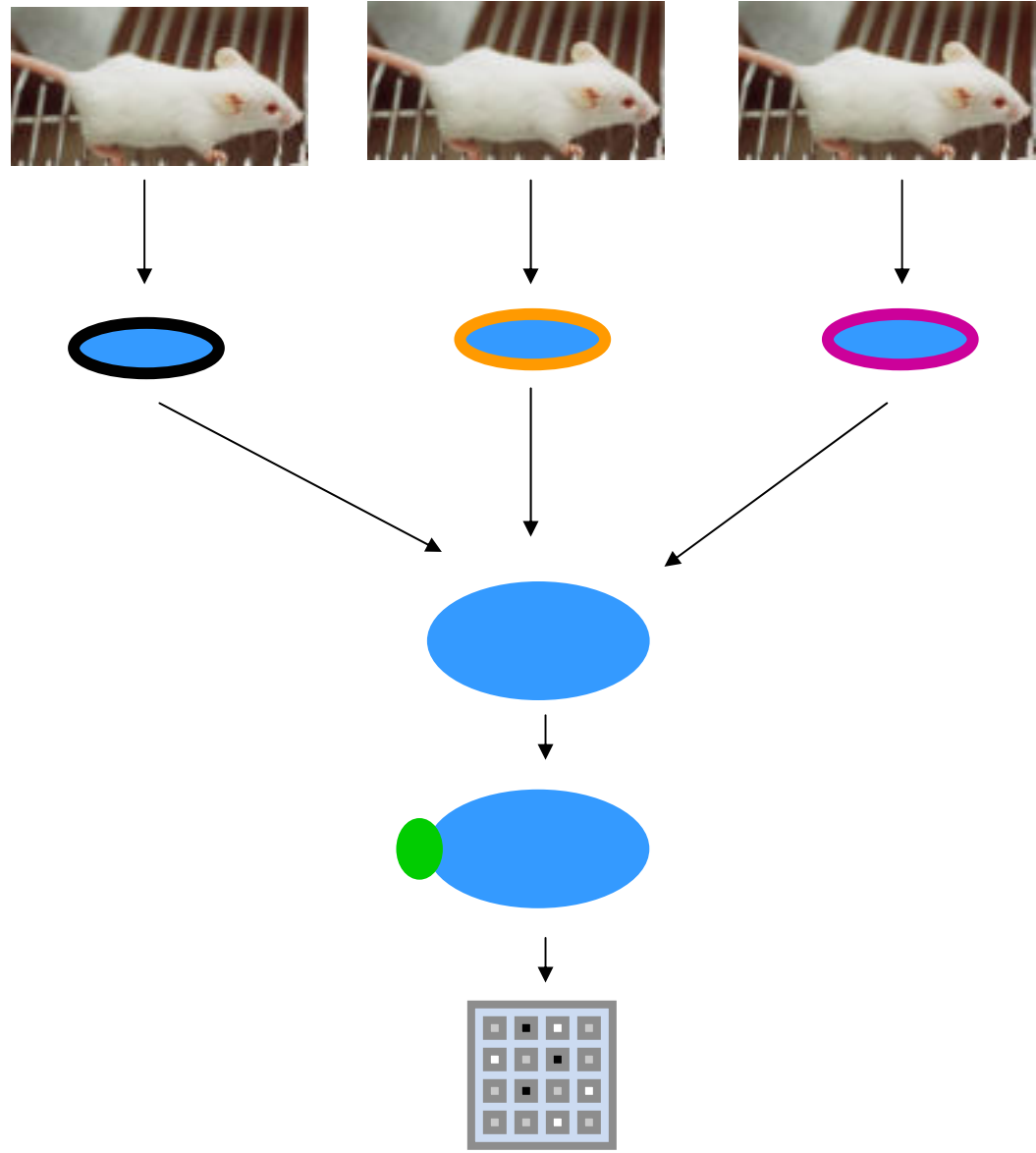
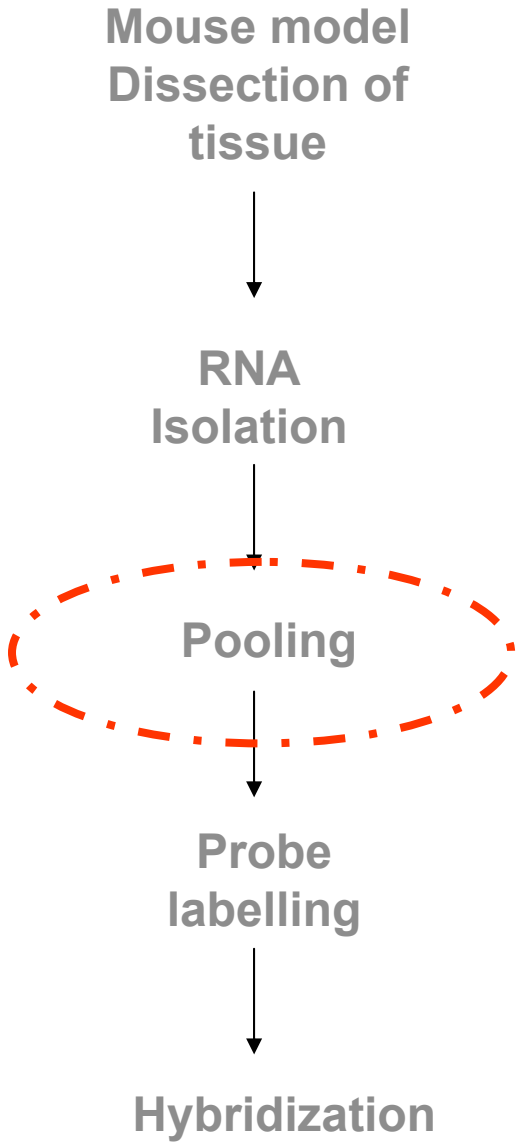
Hybridization



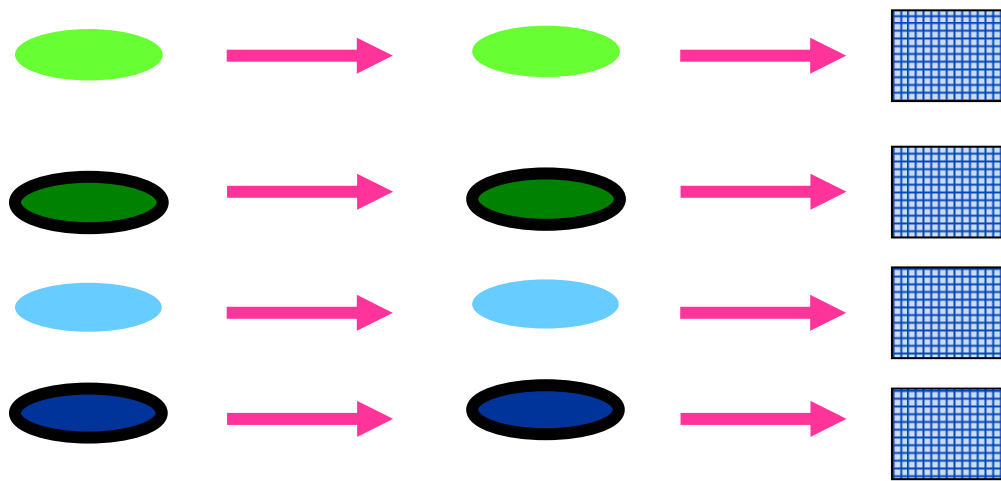
Preparing mRNA samples:



Pooling: looking at very small amount of tissues

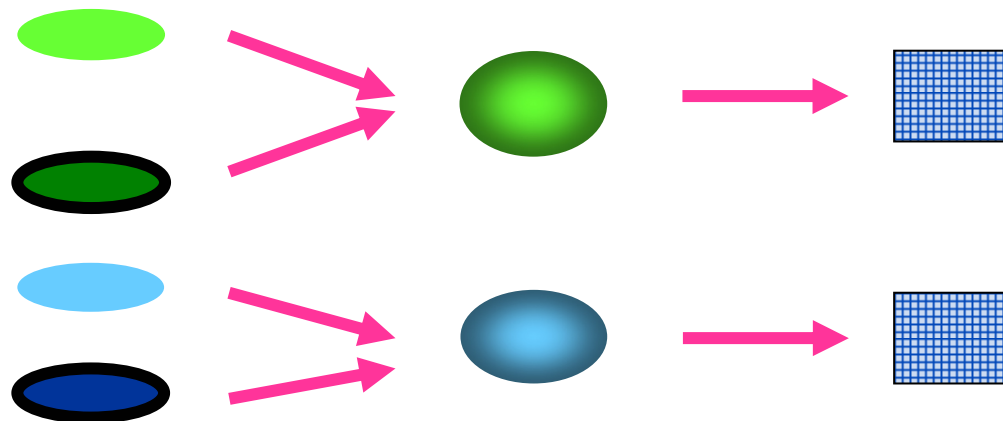


Design 1



Pooled vs Individual samples

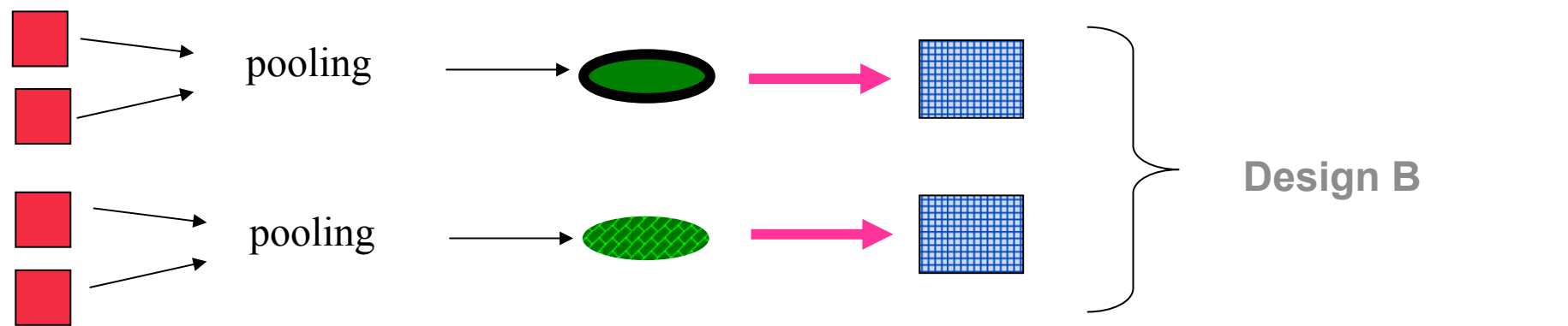
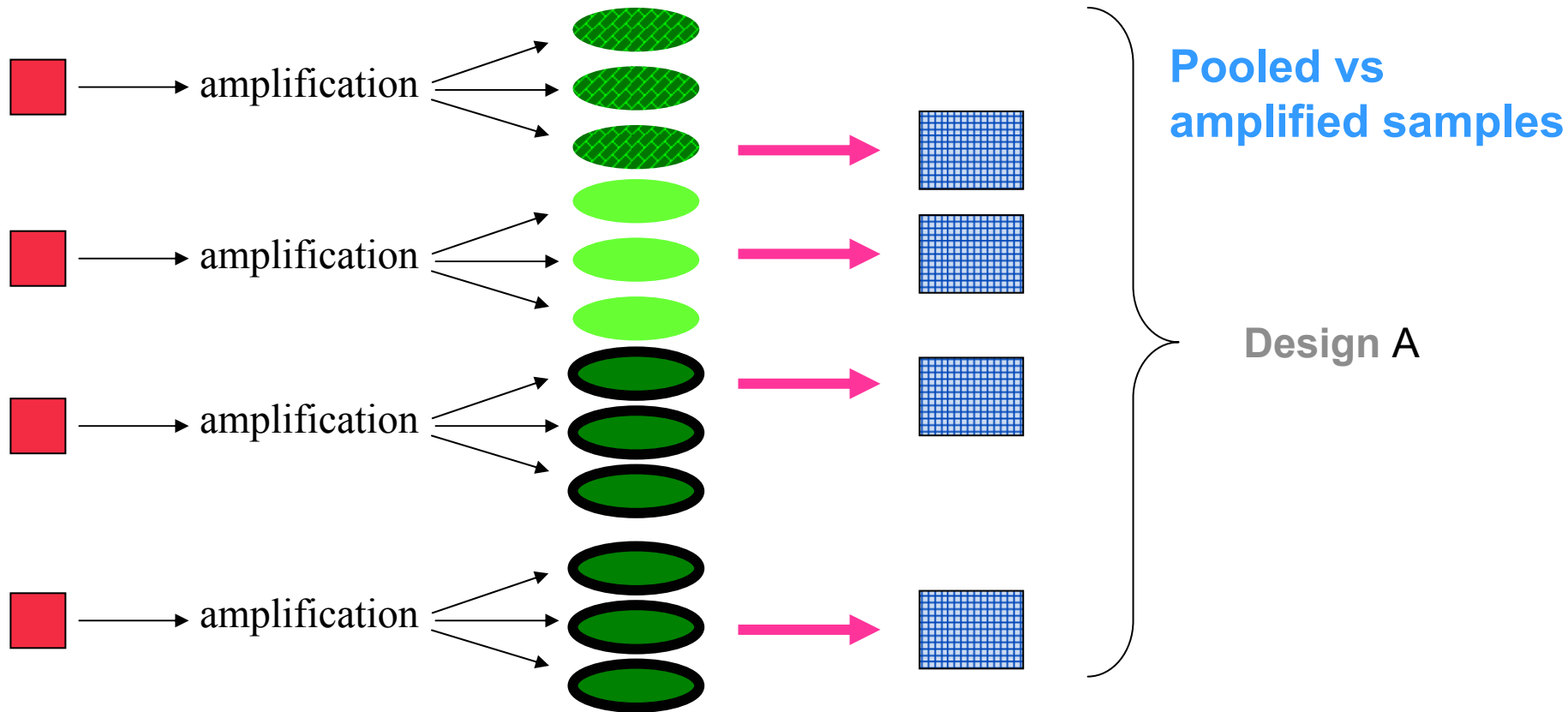
Design 2



Taken from
Kendzioriski etl al (2003)

Pooled versus Individual samples

- Pooling is seen as “biological averaging”.
- Trade off between
 - Cost of performing a hybridization.
 - Cost of the mRNA samples.
- Case 1: Cost of mRNA samples \ll Cost per hybridization
Pooling can assist reducing the number of hybridizations.
- Case 2: Cost of mRNA samples \gg Cost per hybridization
Hybridize every sample on an individual array to get the maximum amount of information.
- **References:**
 - Han, E.-S., Wu, Y., Bolstad, B., and Speed, T. P. (2003). A study of the effects of pooling on gene expression estimates using high density oligonucleotide array data. Department of Biological Science, University of Tulsa, February 2003.
 - Kendzierski, C.M., Y. Zhang, H. Lan, and A.D. Attie. (2003). The efficiency of mRNA pooling in microarray experiments. *Biostatistics* **4**, 465-477. 7/2003
 - Xuejun Peng, Constance L Wood, Eric M Blalock, Kuey Chu Chen, Philip W Landfield, Arnold J Stromberg (2003). Statistical implications of pooling RNA samples for microarray experiments. *BMC Bioinformatics* **4**:26. 6/2003



Original samples

Amplified samples

Pooled vs Amplified samples

- In the cases where we **do not** have enough material from one biological sample to perform one array (chip) hybridizations. Pooling or Amplification are necessary.
- Amplification
 - Introduces more noise.
 - Non-linear amplification (??), different genes amplified at different rate.
 - Able to perform more hybridizations.
- Pooling
 - Less replicates hybridizations.

Some aspects of design

2. Allocation of samples to the slides

A Types of Samples

- Replication – technical, biological.
- Pooled vs individual samples.
- Pooled vs amplification samples.

B Different design layout

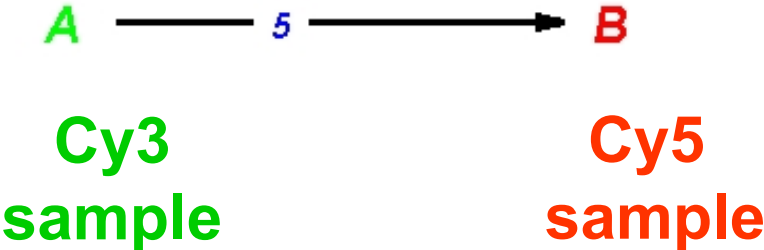
- Scientific aim of the experiment.
- Robustness.
- Extensibility.
- Efficiency.

Taking physical limitation or cost into consideration:

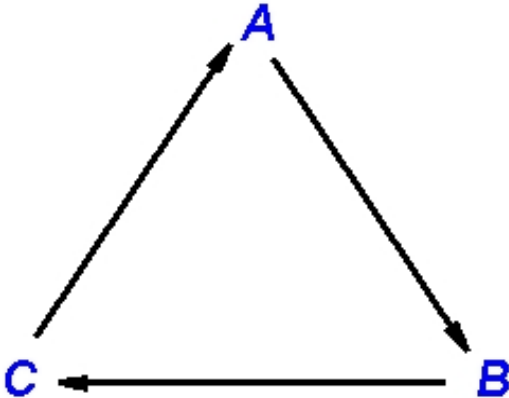
- the number of slides.
- the amount of material.

Graphical representation

Vertices: mRNA samples;
Edges: hybridization;
Direction: dye assignment.



(a)



(b)

Graphical representation

- The structure of the graph determines which effects can be estimated and the **precision** of the estimates.
 - Two mRNA samples can be compared only if there is a **path** joining the corresponding two vertices.
 - The precision of the estimated contrast then depends on the **number of paths** joining the two vertices and is inversely related to the **length of the paths**.
- Direct comparisons **within slides** yield more precise estimates than indirect ones between slides.

The simplest design question: Direct versus indirect comparisons

Two samples (A vs B)
e.g. KO vs. WT or mutant vs. WT

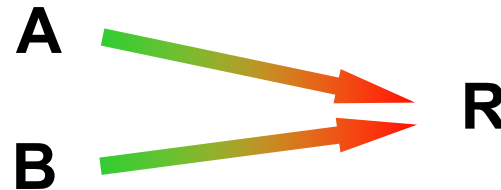
Direct



average ($\log (A/B)$)

$$\sigma^2 / 2$$

Indirect



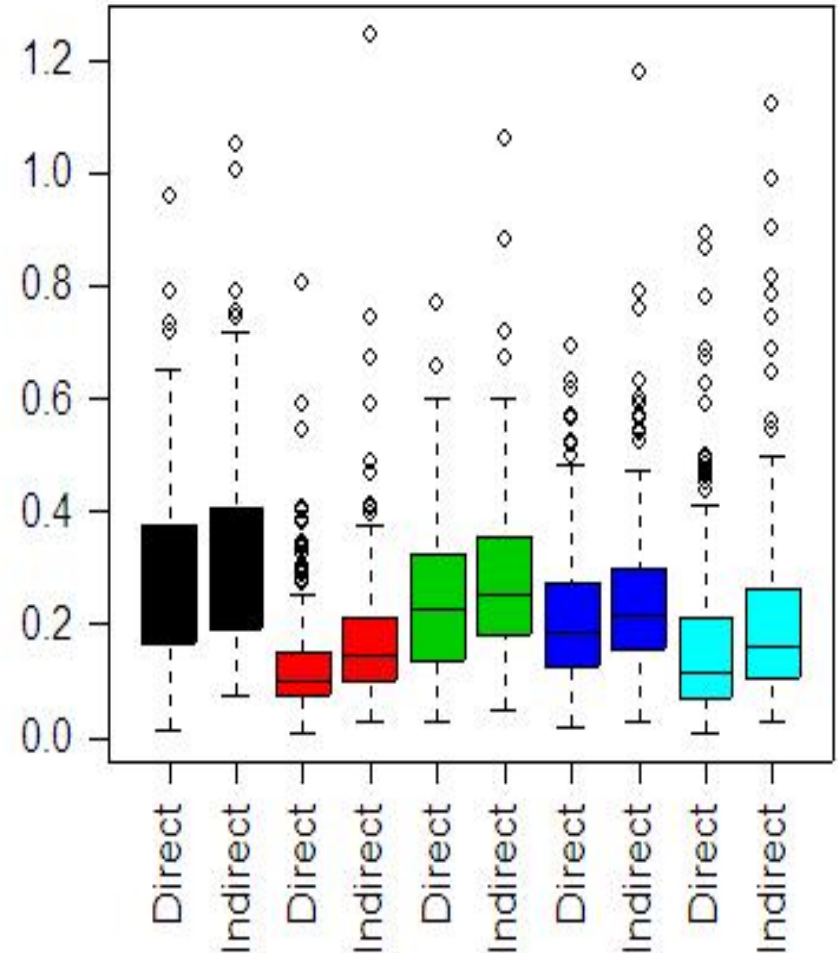
$\log (A / R) - \log (B / R)$

$$2\sigma^2$$

These calculations assume independence of replicates: the reality is not so simple.

Experimental results

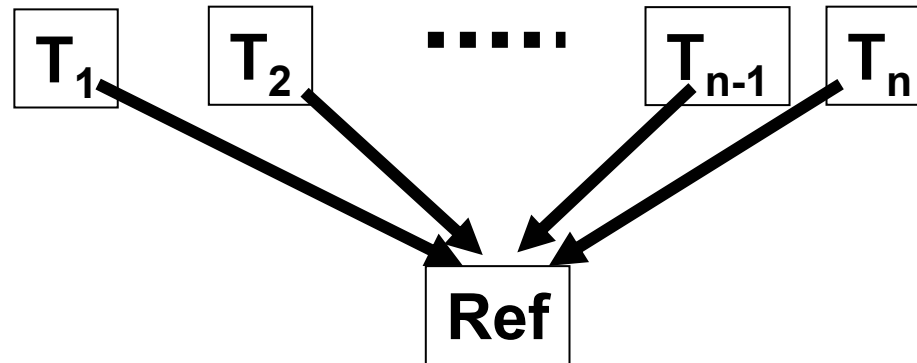
- 5 sets of experiments with similar structure.
- Compare (Y axis)
 - A) SE for aveM_{mt}
 - B) SE for $\text{aveM}_{\text{mt}} - \text{aveM}_{\text{wt}}$
- Theoretical ratio of (A / B) is 1.6
- Experimental observation is 1.1 to 1.4.



Experimental design

- Create **highly correlated reference samples** to overcome inefficiency in common reference design.
- Not advocating the use of technical replicates in place of biological replicates for samples of interest.
- Efficiency can be measured in terms of different quantities
 - number of slides or hybridizations;
 - units of biological material, e.g. amount of mRNA for one channel.
- In addition to experimental constraints, design decisions should be guided by the knowledge of which effects are of greater interest to the investigator.
E.g. which main effects, which interactions.
- The experimenter should thus decide on the comparisons for which he wants the most precision and these should be made **within slides** to the extent possible.

Common reference design



- Experiment for which the common reference design is appropriate
 - Meaningful biological control (C)** Identify genes that responded differently / similarly across two or more treatments relative to control.
 - Large scale comparison.** To discover tumor subtypes when you have many different tumor samples.
- Advantages:
 - Ease of interpretation.
 - Extensibility - extend current study or to compare the results from current study to other array projects.

Design choices in time series		t vs t+1			t vs t+2			
		T1T2	T2T3	T3T4	T1T3	T2T4	T1T4	Ave
N=3	A) T1 as common reference 	1	2	2	1	2	1	1.5
	B) Direct Hybridization 	1	1	1	2	2	3	1.67
N=4	C) Common reference 	2	2	2	2	2	2	2
	D) T1 as common ref + more 	.67	.67	1.67	.67	1.67	1	1.06
	E) Direct hybridization choice 1 	.75	.75	.75	1	1	.75	.83
	F) Direct Hybridization choice 2 	1	.75	1	.75	.75	.75	.83

References

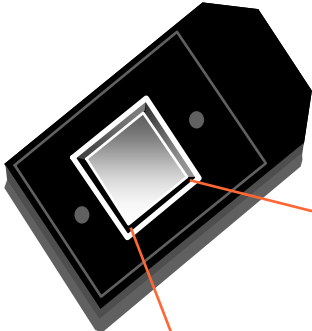
- T. P. Speed and Y. H Yang (2002). Direct versus indirect designs for cDNA microarray experiments. *Sankhya : The Indian Journal of Statistics*, Vol. 64, Series A, Pt. 3, pp 706-720
- Y.H. Yang and T. P. Speed (2003). Design and analysis of comparative microarray Experiments In T. P Speed (ed) **Statistical analysis of gene expression microarray data**, Chapman & Hall.
- R. Simon, M. D. Radmacher and K. Dobbin (2002). **Design of studies using DNA microarrays**. *Genetic Epidemiology* 23:21-36.
- F. Bretz, J. Landgrebe and E. Brunner (2003). **Efficient design and analysis of two color factorial microarray experiments**. *Biostatistics*.
- G. Churchill (2003). **Fundamentals of experimental design for cDNA microarrays**. *Nature genetics review* 32:490-495.
- G. Smyth, J. Michaud and H. Scott (2003) **Use of within-array replicate spots for assessing differential expression in microarray experiments**. Technical Report In WEHI.
- Glonek, G. F. V., and Solomon, P. J. (2002). Factorial and time course designs for cDNA microarray experiments. Technical Report, Department of Applied Mathematics, University of Adelaide. 10/2002

Monday
27. November 06

Affy Chips: PM versus MM and summary information

Affymetrix GeneChips zusammengefasst

GeneChip Probe Array



1.28cm

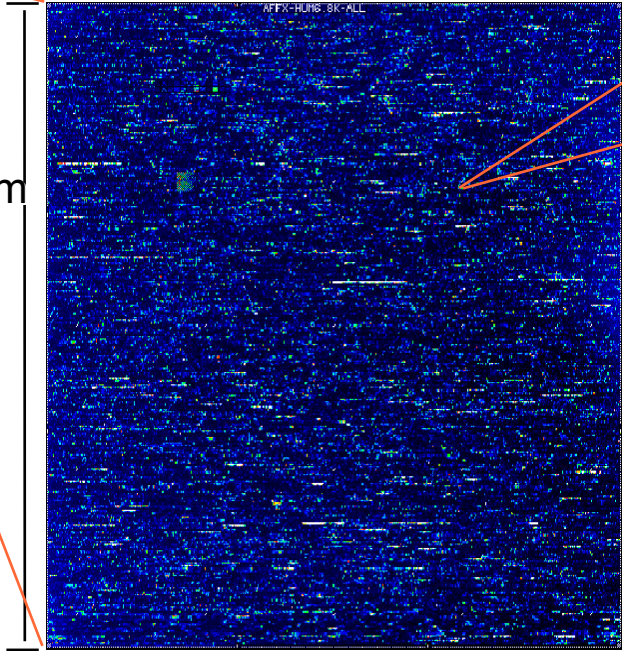
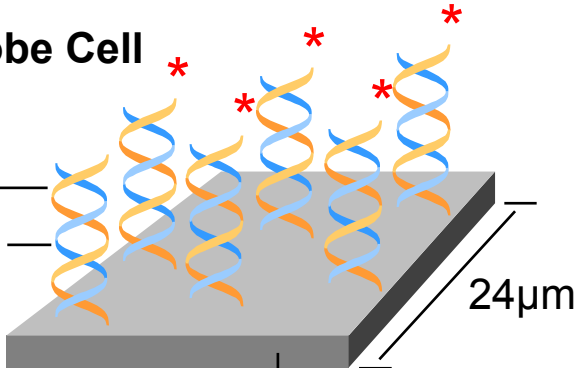


Image of Hybridized Probe Array

Hybridized Probe Cell

Single stranded, labeled RNA target
Oligonucleotide probe



Millions of copies of a specific oligonucleotide probe synthesized in situ ("grown")

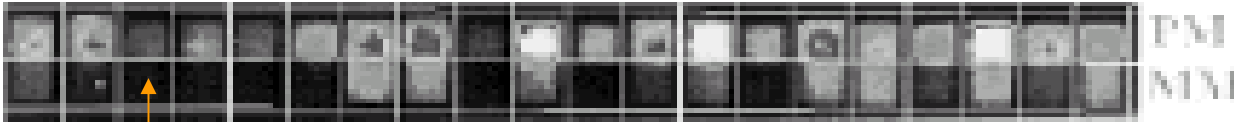
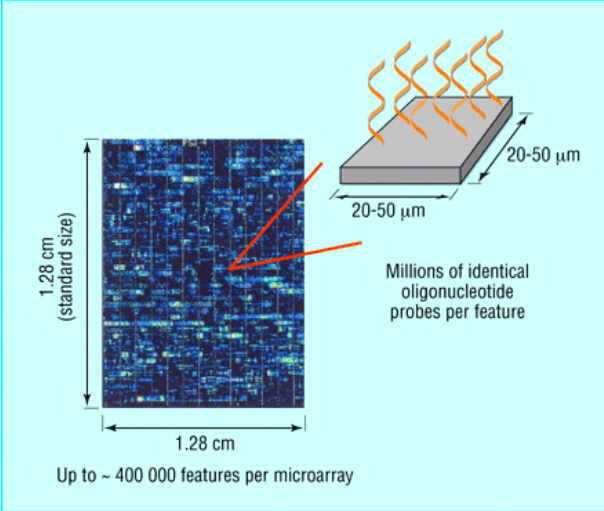
>200,000 different complementary probes

Affymetrix technology



16-20 probe pairs per gene

PM: ATGAGCTGTACCAATGCCAACCTGG
 MM: ATGAGCTGTACCTATGCCAACCTGG



64 pixels; Signal intensity is upper quartile of the 36 inner pixels

16-20 probe pairs: HG-U95a
 11 probe pairs: HG-U133

Stored in CEL file

Affymetrix expression measures

- PM_{ijg} , MM_{ijg} = Intensity for perfect match and mismatch probe j for gene g in chip i .
 - $i = 1, \dots, n$ one to hundreds of chips
 - $j = 1, \dots, J$ usually 16 or 20 probe pairs
 - $g = 1, \dots, G$ 8...20,000 probe sets.
- **Tasks:**
 - **calibrate** (normalize) the measurements from different chips (samples)
 - **summarize** for each probe set the probe level data, i.e., 20 PM and MM pairs, into a single **expression measure**.
 - **compare** between chips (samples) for detecting differential expression.

Low – level -Analysis

- Preprocessing signals: background correction, normalization, PM-adjustment, summarization.
- Normalization on probe or probe set level?
- Which probes / probe sets used for normalization
- How to treat PM and MM levels?

Normalization – complete data methods

- Quantile normalization:
Make the distribution of probe intensities the same for all arrays.
 $F_{i,\text{normalised}}(x) = F_{\text{global}}^{-1}(F_i(x))$ (Q-Q-Plot)
- Robust quantile normalization
- Cyclic loess (MA plots of two arrays for log-transformed signals and loess)
- VSN

What is the best approach? Look at criteria provided by the affycomp procedure.

*Cope LM, Irizarry RM, Jaffee H, Wu Z, Speed TP, **A Benchmark for Affymetrix GeneChip Expression Measures**, *Bioinformatics*, 2004, 20:323-31*

expression measures: MAS 4.0

Affymetrix GeneChip MAS 4.0 software uses **AvDiff**, a trimmed mean:

$$AvDiff = \frac{1}{\# J} \sum_{j \in J} (PM_j - MM_j)$$

- sort $d_j = PM_j - MM_j$
- exclude highest and lowest value
- $J :=$ those pairs within 3 standard deviations of the average

Expression measures MAS 5.0

Instead of MM, use "repaired" version CT

$$\begin{aligned} \text{CT} &= \text{MM} && \text{if } \text{MM} < \text{PM} \\ &= \text{PM} / \text{"typical log-ratio"} && \text{if } \text{MM} \geq \text{PM} \end{aligned}$$

"Signal" =

Tukey.Biweight (log(PM-CT))

(... \approx median)

Tukey Biweight: $B(x) = (1 - (x/c)^2)^2$ if $|x| < c$, 0 otherwise

Expression measures: Li & Wong

dChip fits a model for each gene

$$PM_{ij} - MM_{ij} = \theta_i \phi_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \propto N(0, \sigma^2)$$

where

- θ_i : **expression index** for gene i
- ϕ_j : **probe sensitivity**

Maximum likelihood estimate of MBEI is used as expression measure of the gene in chip i .

Need at least 10 or 20 chips.

Current version works with PMs only.

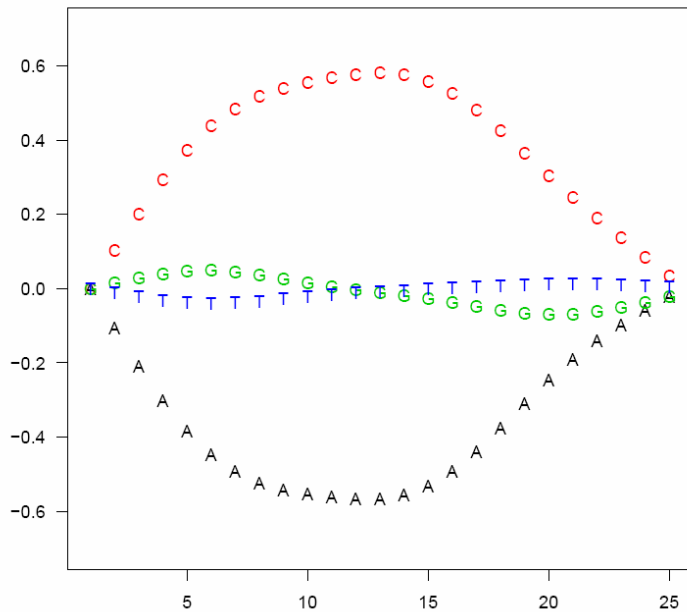
Expression measures

RMA: Irizarry et al. (2002)

- o Estimate one **global background** value $b = \text{mode}(MM)$. No probe-specific background!
- o Assume: $PM = s_{\text{true}} + b$
Estimate $s \geq 0$ from PM and b as a conditional expectation $E[s_{\text{true}} | PM, b]$.
- o Use $\log_2(s)$.
- o Nonparametric nonlinear calibration ('quantile normalization') across a set of chips.

Expression Measures: GC-RMA: Wu, Irizarry et al, 2004

- Uses a stochastic model for background adjustment that uses probe sequence information.



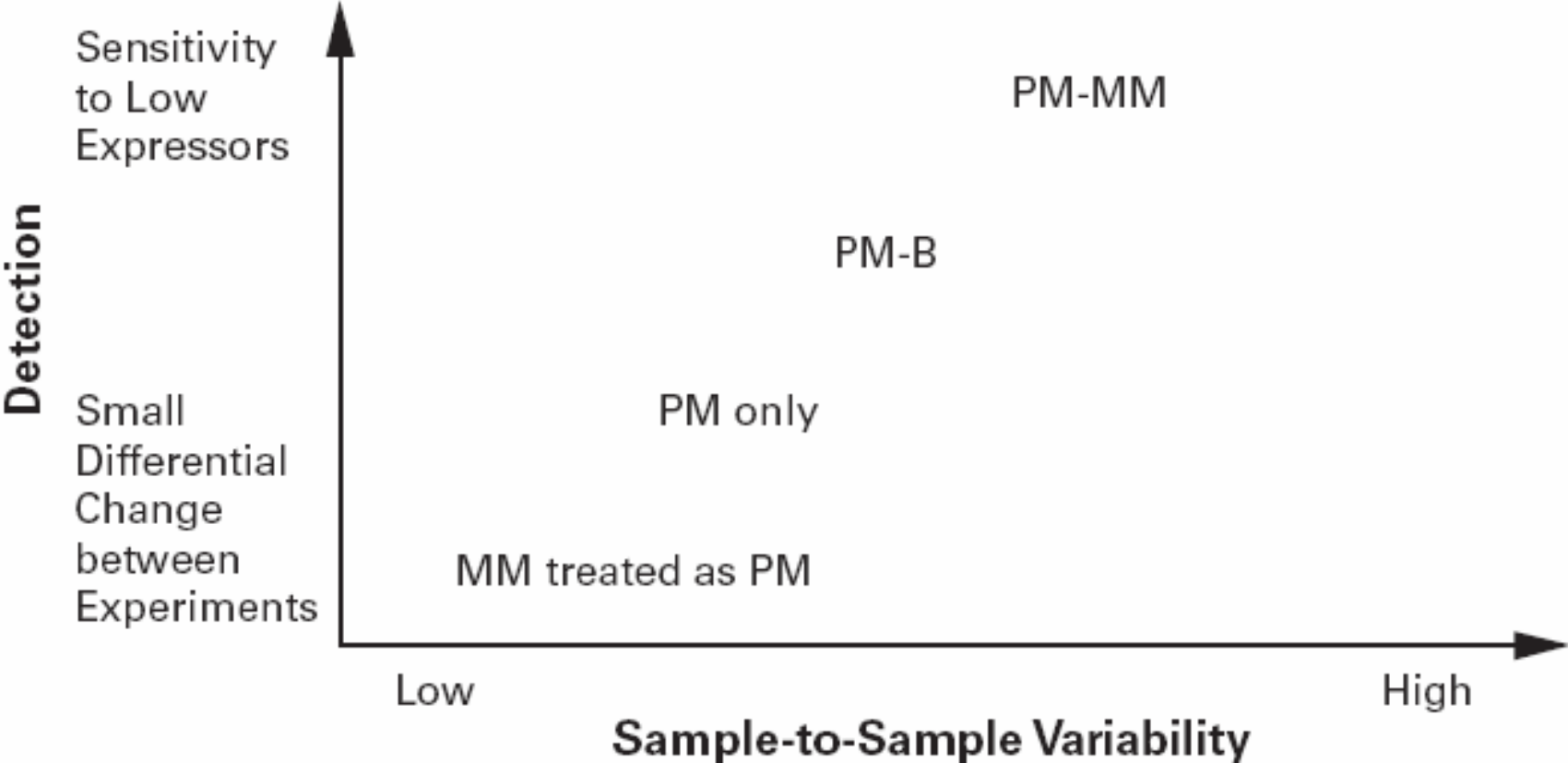
The effect of base A in position k , $\mu_A; k$, is plotted against k . Similarly for the other three bases.

$$PM = O_{PM} + N_{PM} + S$$

$$MM = O_{MM} + N_{MM} + \phi S.$$

Here O represents optical noise, N represents NSB noise and S is a quantity proportional to RNA expression (the quantity of interest). The parameter $0 < \phi < 1$ accounts for the fact that for some probe-pairs the MM detects signal.

Expression Measures: PLIER - Probe Logarithmic Intensity Error Estimation

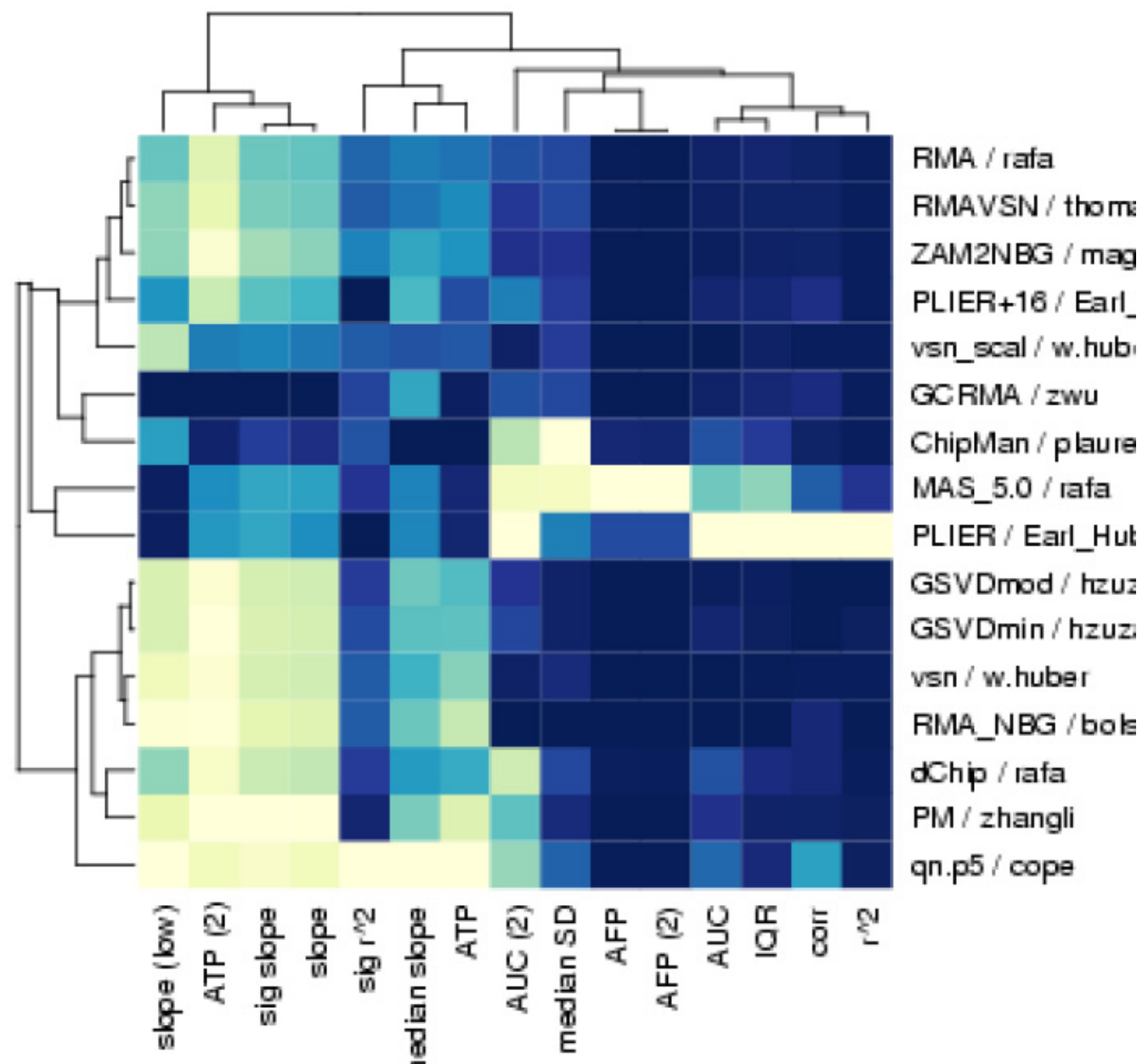


Arguments against the use of $d = PM-MM$

- Difference is more variable. Is there a gain in bias to compensate for the loss of precision?
- MM detects signal as well as PM
- PM / MM results in a bias.
- Subtraction of MM is not strong enough to remove probe effects, nothing is gained by subtraction

affycomp results

good



bad

Acknowledgements – Slides borrowed from

- **Achim Tresch**
- **Wolfgang Huber**
- **Ulrich Mansmann**
- **Terry Speed**
- **Jean Yang**
- **Benedikt Brors**
- **Anja von Heydebreck**
- **Rainer König**