Affy Chips: Cel-file versus summary information

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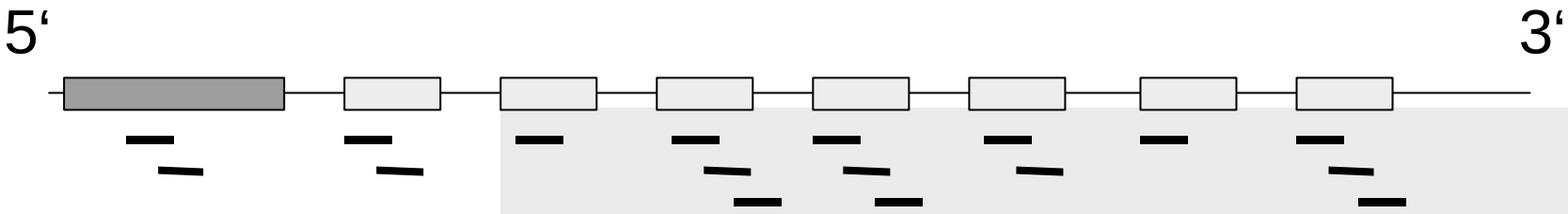
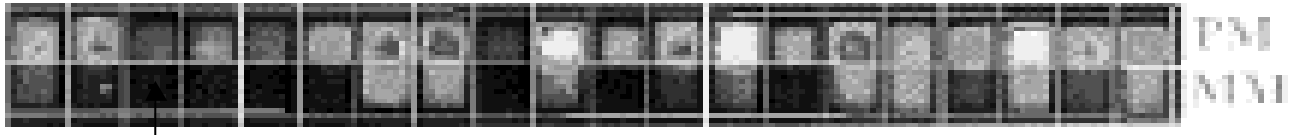
Affymetrix technology



16-20 *probe pairs* per gene

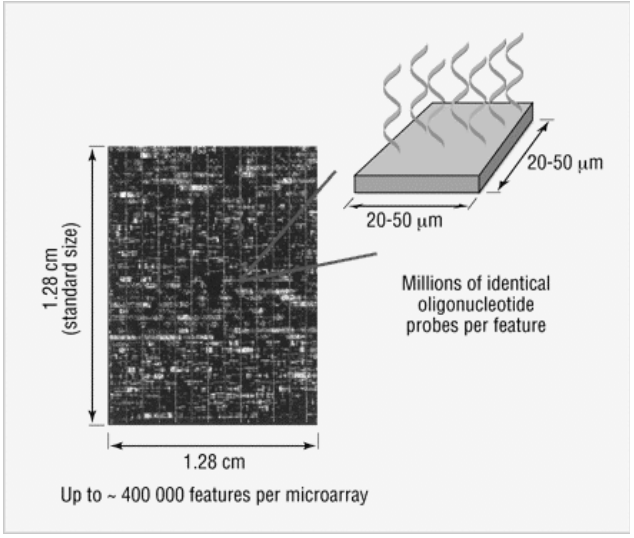
PM: ATGAGCTGTACCAATGCCAACCTGG
MM: ATGAGCTGTACCTATGCCAACCTGG



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



Low – level -Analysis

- Preprocessing signals: background correction, normalization, PM-adjustment, summarization.
- Witt E, McClure J (2004) Statistics for Microarray: design, analysis, and inference, Chichester, John Wiley & Sons
- Noise and Bias
- Differences in sample preparation, variation during mRNA extraction and isolation
- Manuifacturing of the array: variation in hybridization efficiency, abundance
- Normalization on probe or probe set level?
- Which probes / probe sets used for normalization
- How to treat PM and MM levels?
- Linear or non-linear normalization?

Expression measures based on d = PM-MM

- AvDiff

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

A contains only probes with d not an outlyer

- Li & Wong (dChip)

$Pm_{ij} - Mm_{ij} = \theta_i \varphi_j + \varepsilon_{ij}$ $\quad \varepsilon_{ij} \sim N(0, \sigma^2)$

MLE for θ_i gives expression measure

- MAS5

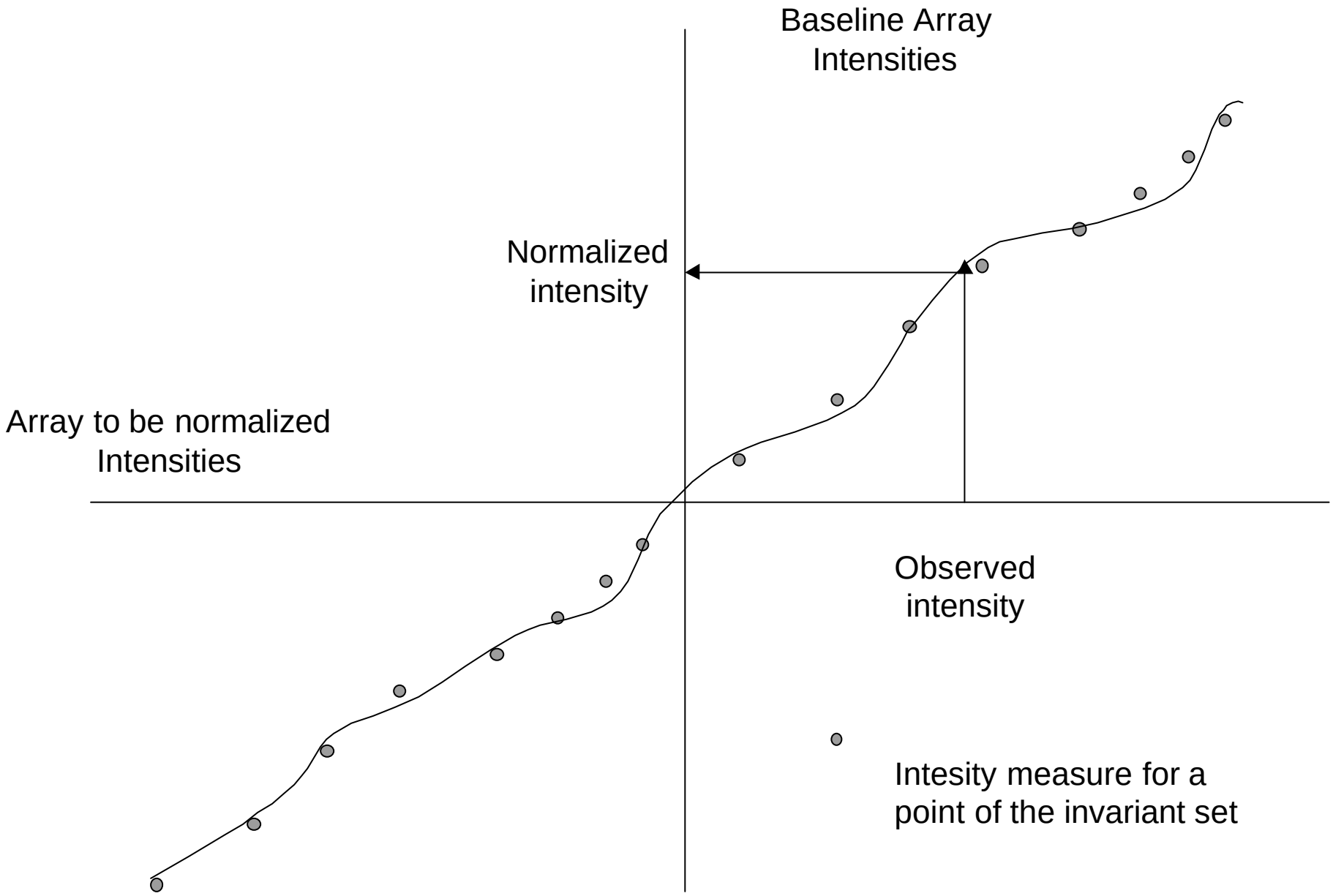
signal = Tuckey Biweight[$PM_j - CT_j$]

$CT_j = \min(MM_j, PM_j)$

Normalization – Baseline Array

- **Scaling:**
  First array is baseline: m_{base} mean intensity of baseline array, m_i (i=1,…,n) mean intensity of array i, scale factor for array i: $\beta_i = m_{base} / m_i$.
  Normalized intensity an array i: $x_{i,norm} = x_i \cdot \beta_i$.
  Two options: apply normalisation to probes or after summarization to probe set measures.

- **Invariant set:**
  PM probe values are used only.
  Probes which are not differentially expressed (unknown). It is assumed that PM probe signals which not differentially expressed in two arrays have similar intensity ranks (r).
  Point's proportion rank difference (PRD): $|(r_{k,i}-r_{k,base})|(\#probes)$
  Small $PRD_{k,i}$ (<0.003, 0.007), iclude probe into invariant set, cycle through all arrays, use invariant set to create array specific calibration curve by running median.


Baseline Array
Intensities
Normalized
intensity
Array to be normalized
Intensities
Observed
intensity
Intesity measure for a
point of the invariant set

Normalization – complete data methods

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

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

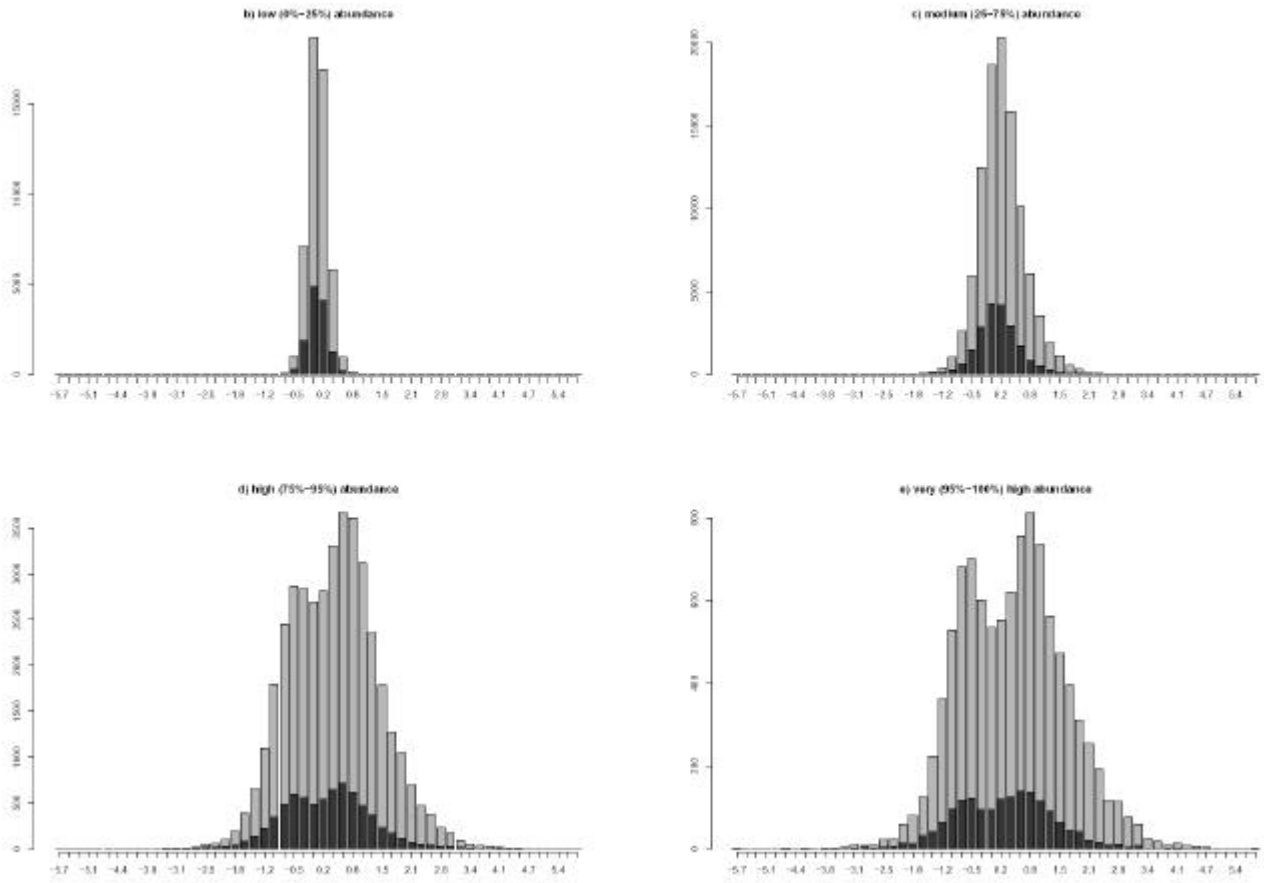
Cope LM, Irizarry RM, Jaffee H, Wu Z, Speed TP, ***A Benchmark for Affymetrix GeneChip Expression Measures,***
Bioinformatics, 2004, 20:323-31

How to approach the quantification of gene expression:Three data sets to learn from

- **Mouse Data Set (A)**
  5 MG-U74A GeneChip® arrays, 20% of the probe pairs were incorrectly sequenced, measurements read for these probes are entirely due to non-specific binding
- **Spike-In Data Set (B)**
  11 control cRNAs were spiked-in at different concentrations
- **Dilution Data Set (C)**
  Human liver tissues were hybridised to HG-U95A in a range of proportions and dilutions.

Feature of probe level data

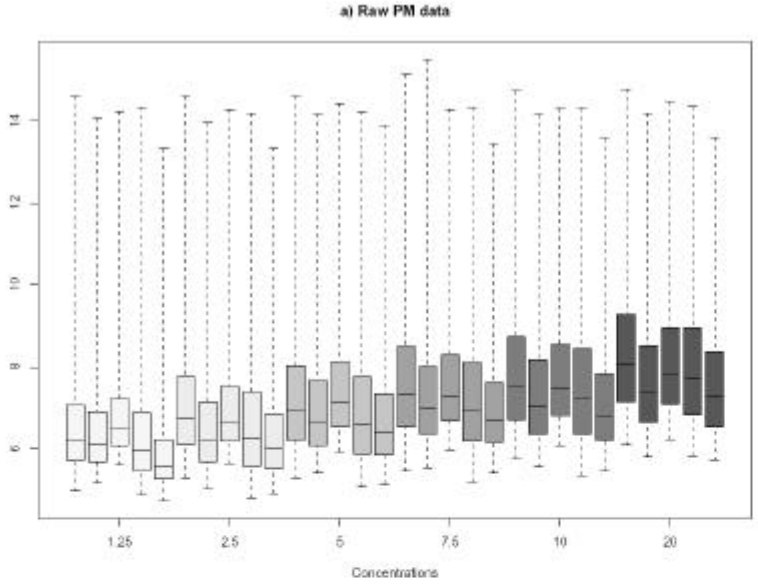
- MM grows with PM
- Many MM >> PM
- log scale stabilises variance

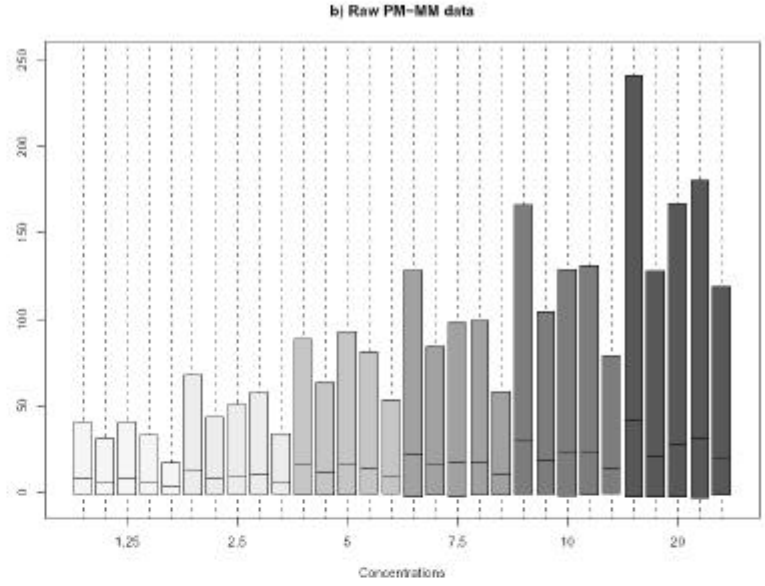


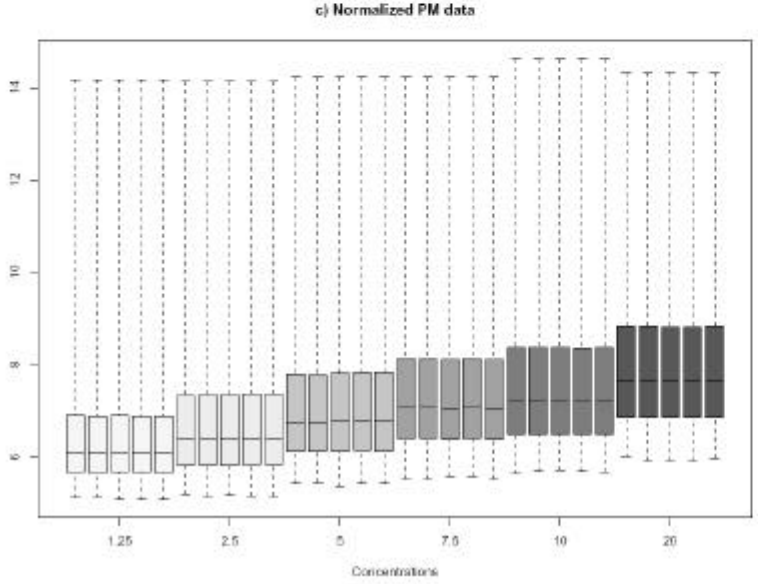
$M = \log_2(PM/MM)$

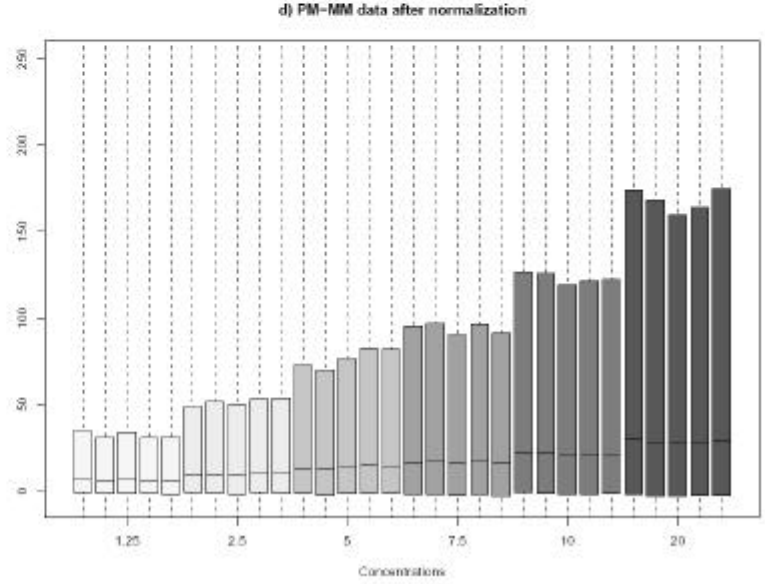
$A = 0.5 \cdot \log_2(PM \cdot MM)$ abundance

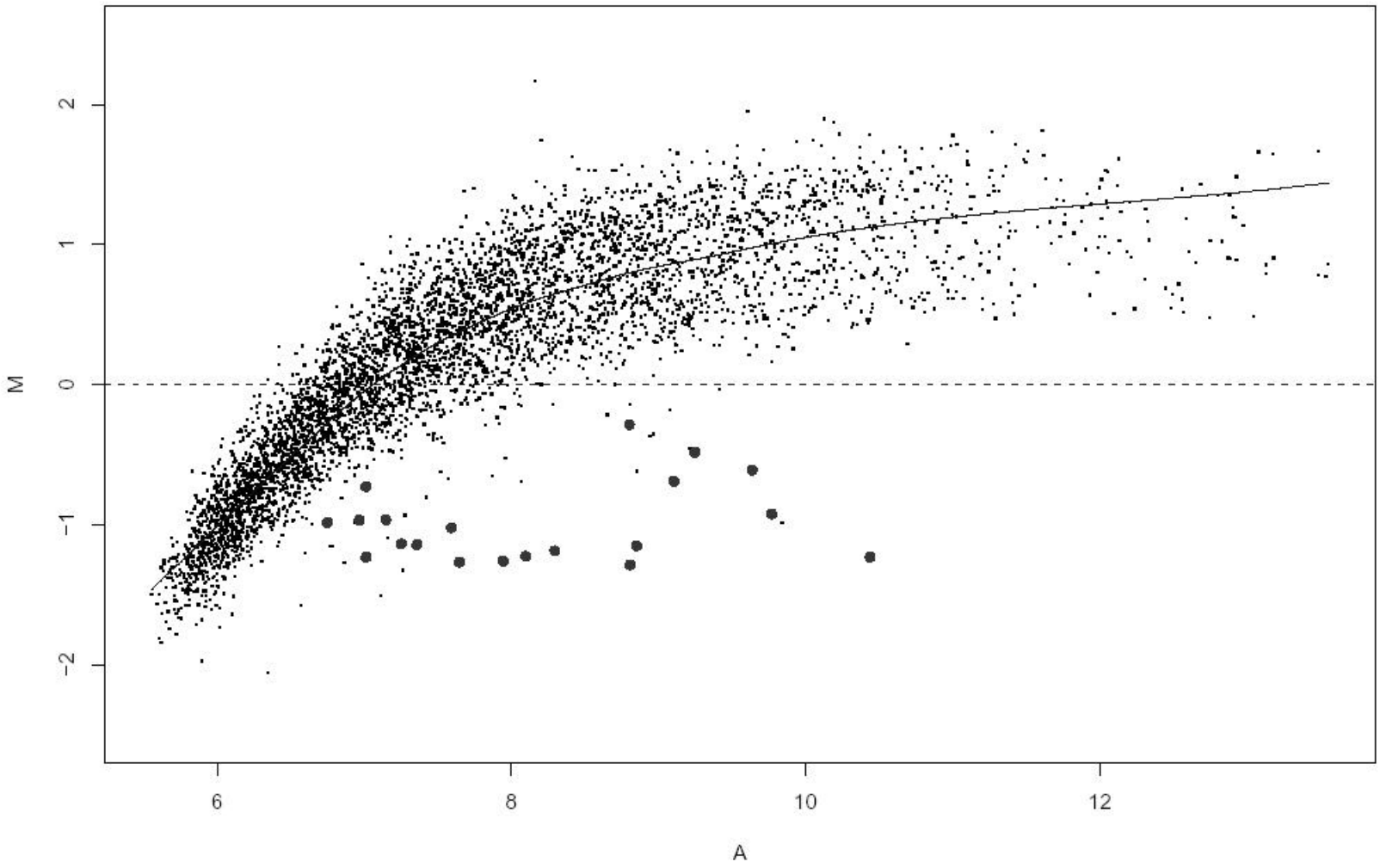
Dilution data









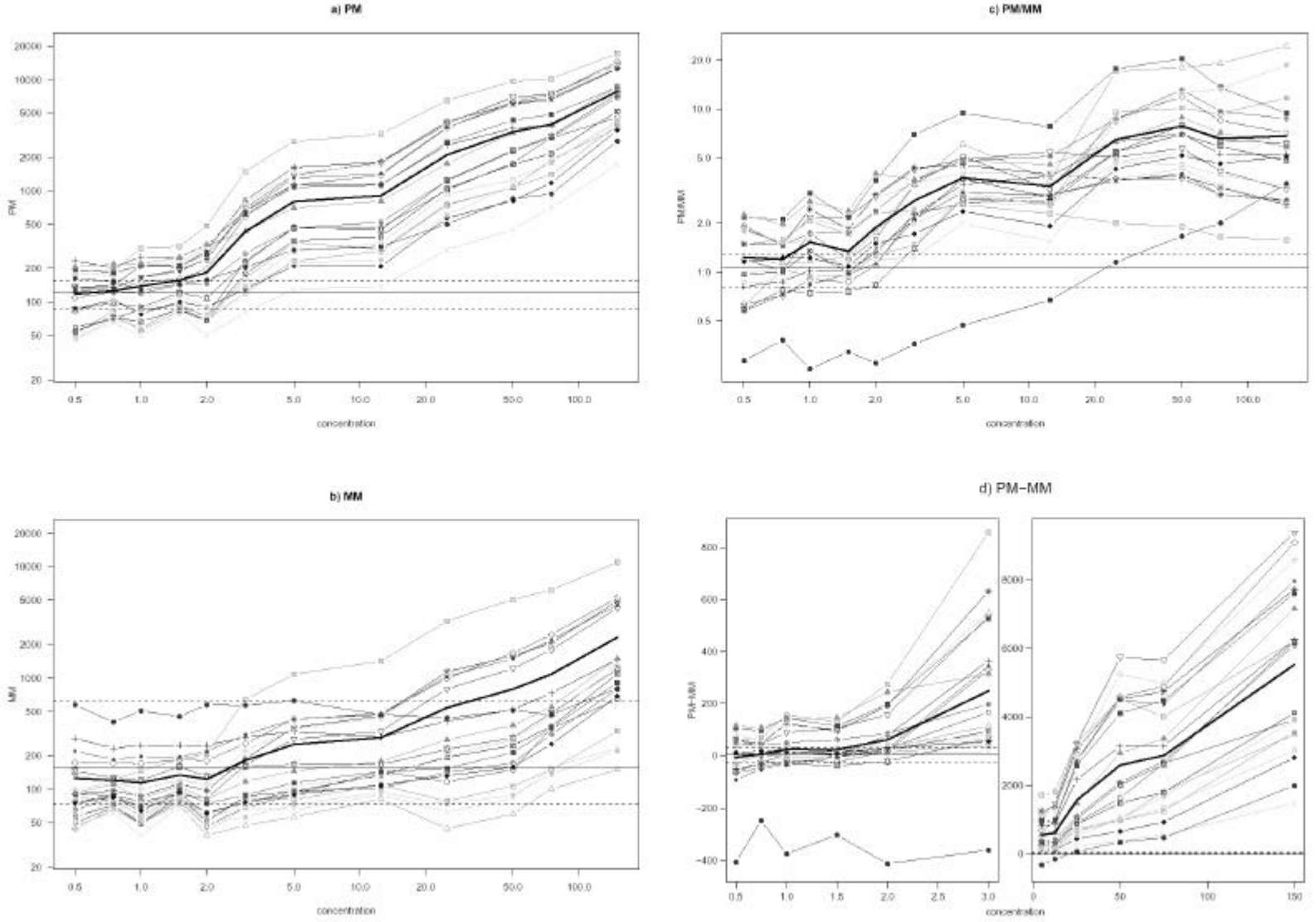


$M = \log_2(PM_1 / PM_2)$ $A = 0.5 \cdot \log_2(PM_1 \cdot PM_2)$

Bland-Altman plots

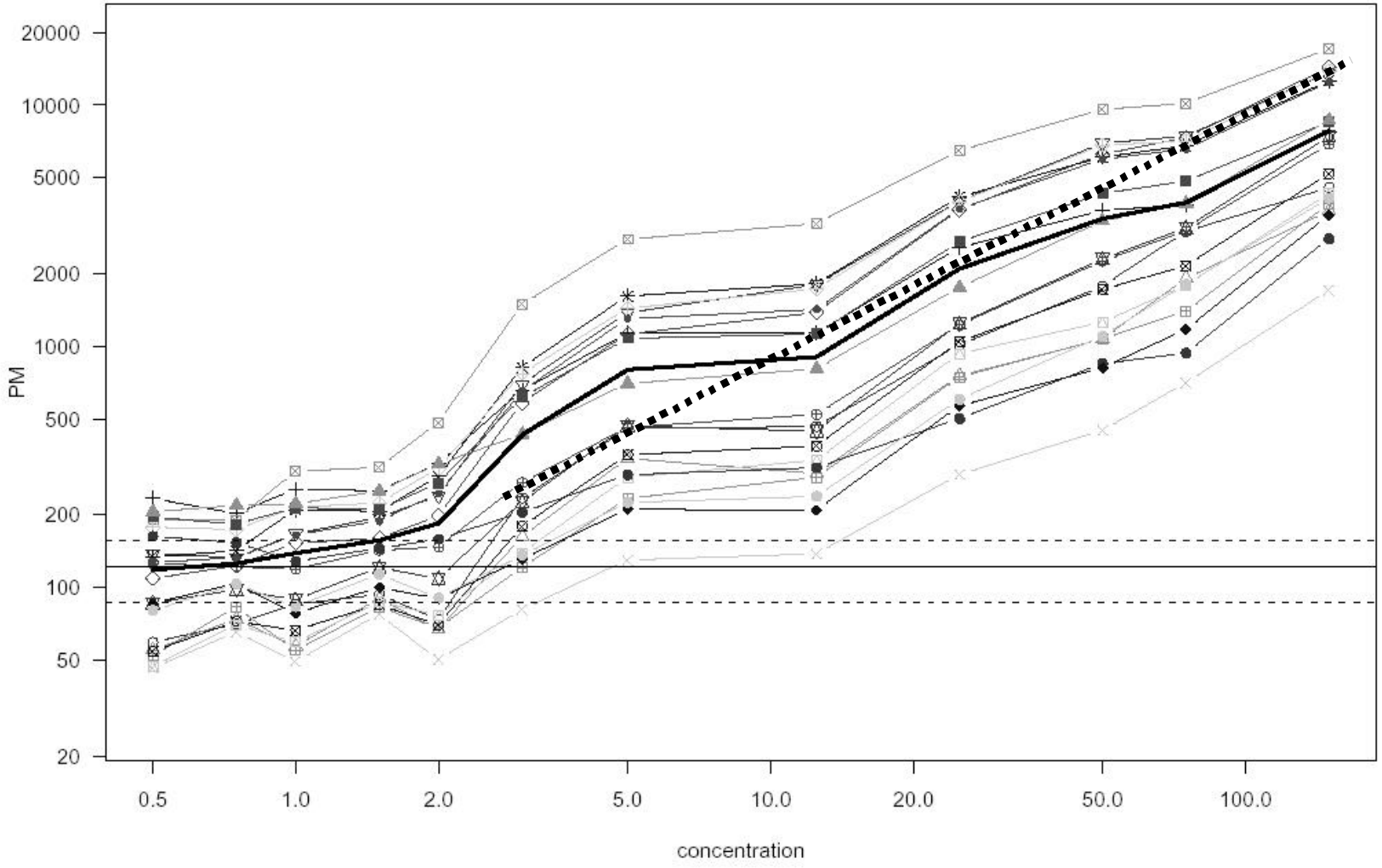
Arguments against the use of d = PM-MM

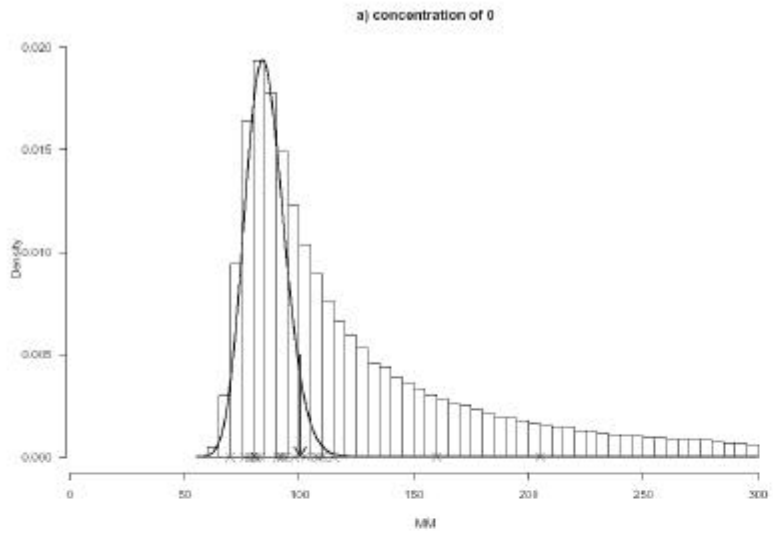
- Difference is more variable. Is there a gain in bias to compensate for the loss of precision?
- MM detects signal as well as PM
- PM / MM results in a bias.
- Subtraction of MM is not strong enough to remove probe effects, nothing is gained by subtraction

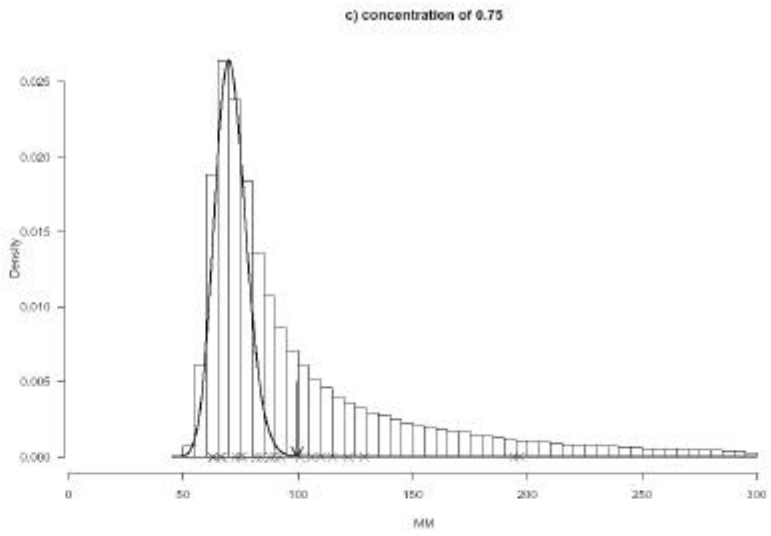

a) PM
PM
concentration
c) PM/MM
PM/MM
concentration
b) MM
MM
concentration
d) PM−MM
PM−MM
concentration

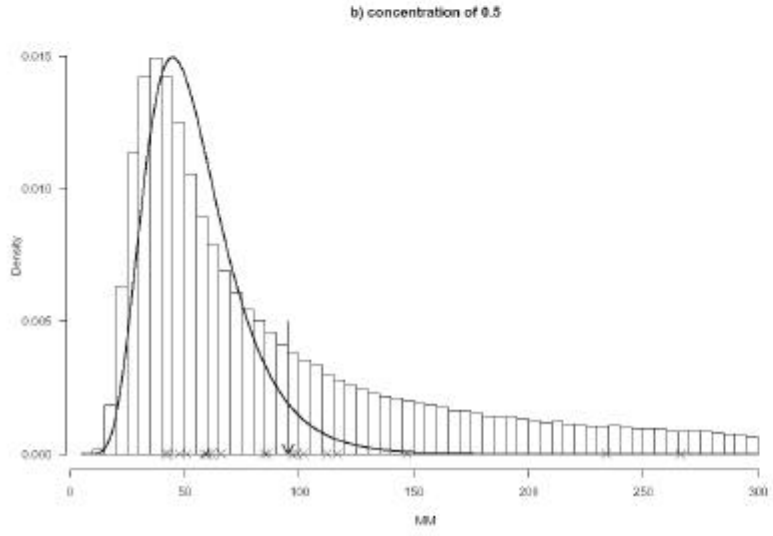
Expression measure based on PM only

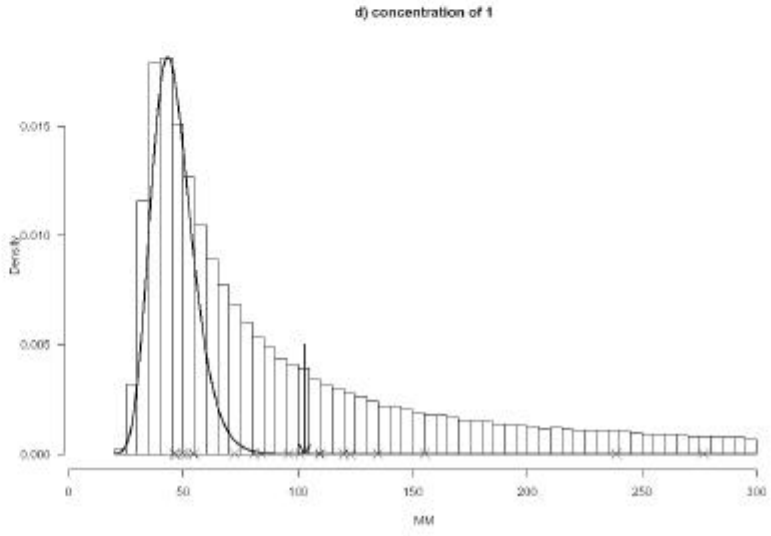
- Use PM values but correct for unspecific binding and background (optical) noise.
  For small signals uncorrected values may give misleading results: $\log_2(100+2s)-\log_2(100+s)$ versus $\log_2(2s)-\log_2(s)$
- $PM_{ijn} = bg_{ijn} + s_{ijn}$
- Basic idea:
  Correct by $PM_{ijn} - b_i$ with $\log_2(b_i)$ equal to the mode of $\log_2(MM)$
- Advanced idea:
  $B(PM_{ijn}) = E[s_{ijn} | PM_{ijn}]$ with s_{ijn} exponential and bg_{ijn} normally distributed. This problem has an explicit solution and gives a closed form transformation B.


20000
10000
5000
2000
1000
500
200
100
50
20
PM
0.5
1.0
2.0
5.0
10.0
20.0
50.0
100.0
concentration


a) concentration of 0
Density
MM


c) concentration of 0.75
Density
MM


b) concentration of 0.5
Density
MM


d) concentration of 1
Density
MM

The RMA procedure

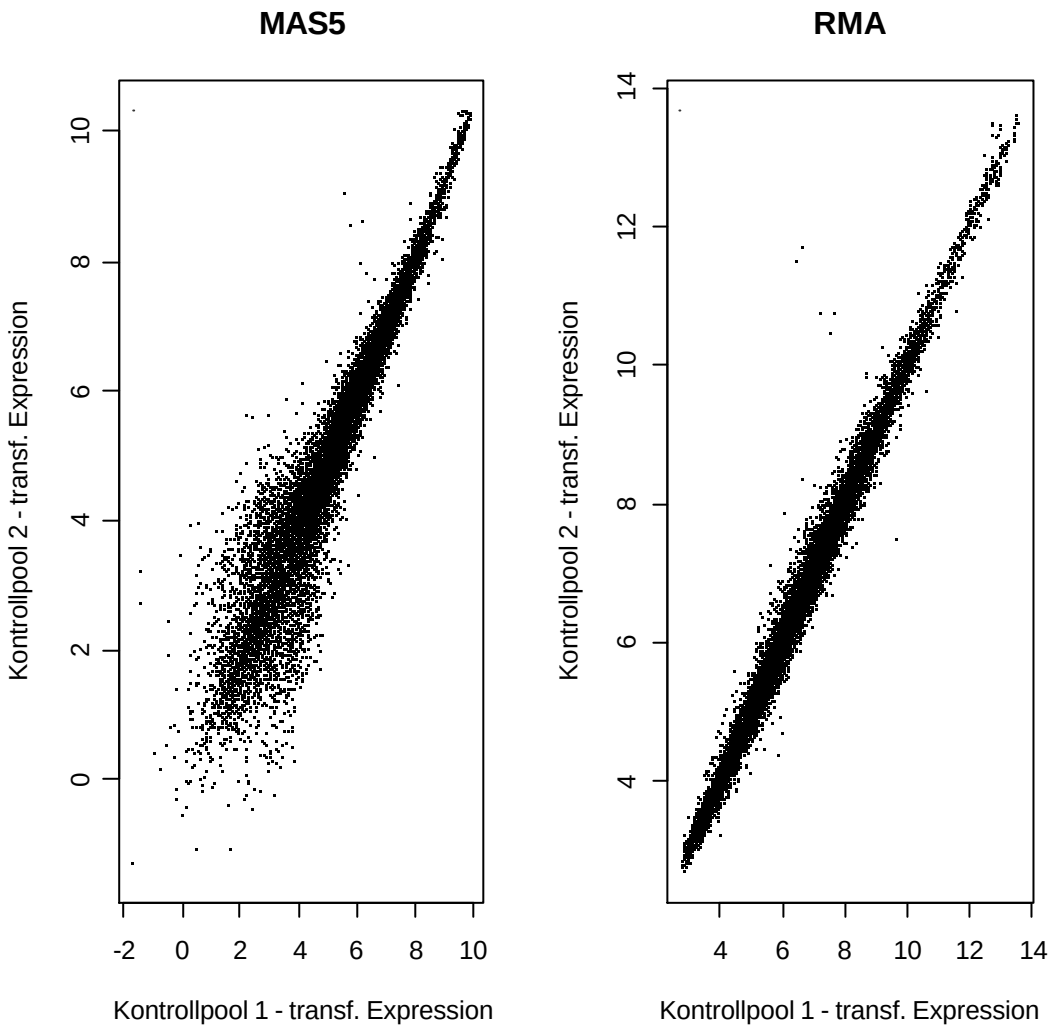
- Robust multi-array average
- Background corrections for array using transformation B
- Normalise the arrays by using quantile normalisation
- Use the background adjusted, normalised, log-transformed PM intensities (Y) and follow a linear model:

$$Y_{ijn} = \mu_{in} + \alpha_{jn} + \varepsilon_{ijn}$$

where α_{jn} is the probe affinity, $\Sigma\, \alpha_{jn} = 0$ for all n
μ_{in} is the log scale expression level
ε_{ijn} is an error with mean 0

Irizarry et al. (2002) www.biostat.jhsph.edu/~rirzarr/affy

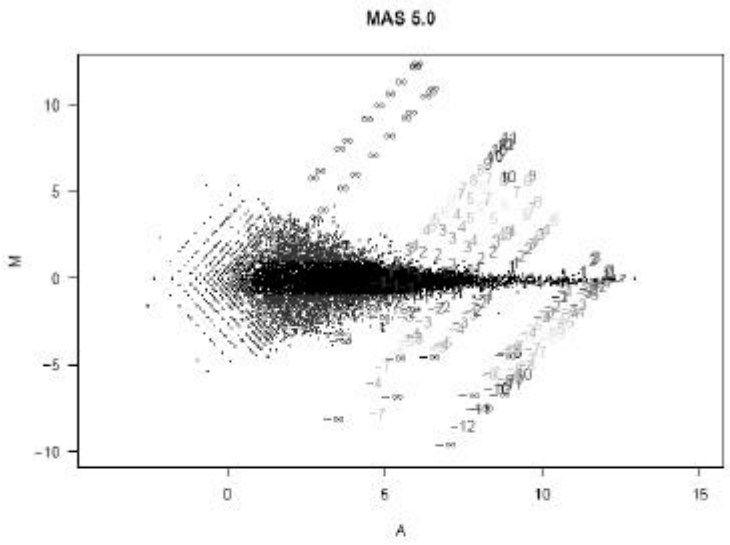
Example LPS: *Expression Summaries*

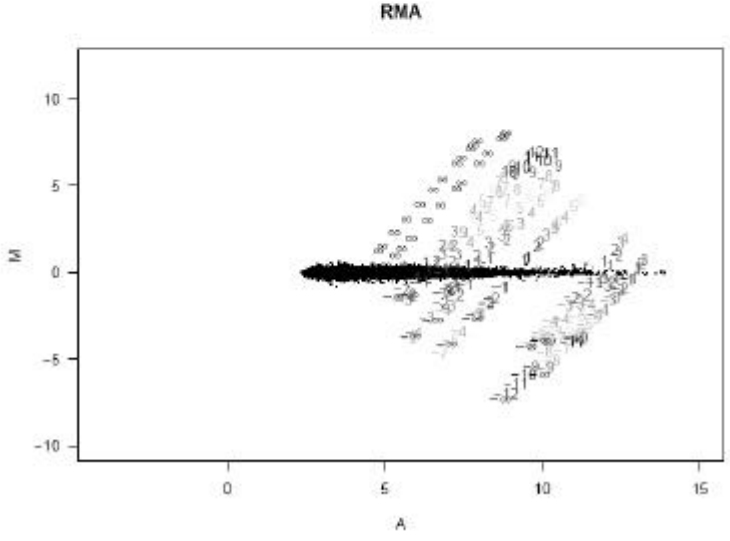


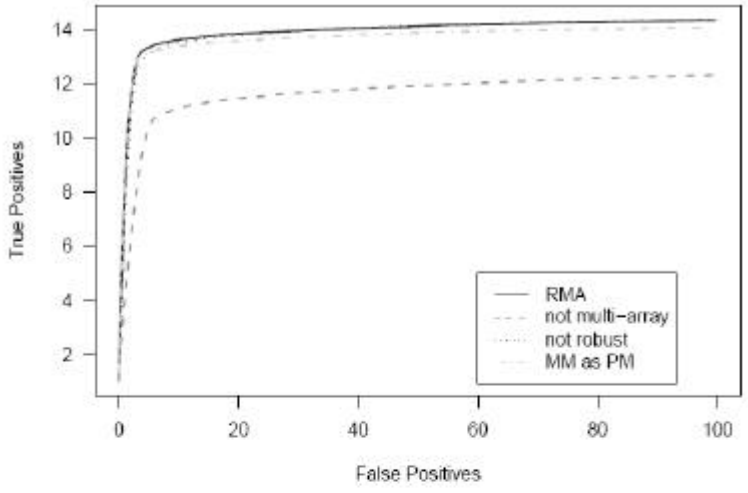
AffyComp

- Graphical tool to evaluate summaries of Affymetrix probe level data.
- Plots and summary statistics
- Comparison of competing expression measures
- Selection of methods suitable for a specific investigation
- Use of benchmark data sets

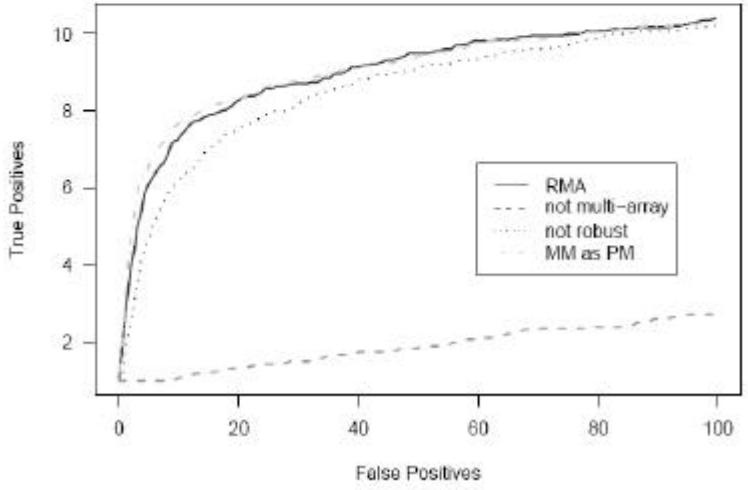
What makes a good expression measure: leads to good and precise answers to a research question.


MAS 5.0
M
A


RMA
M
A


True Positives
False Positives
RMA
not multi-array
not robust
MM as PM

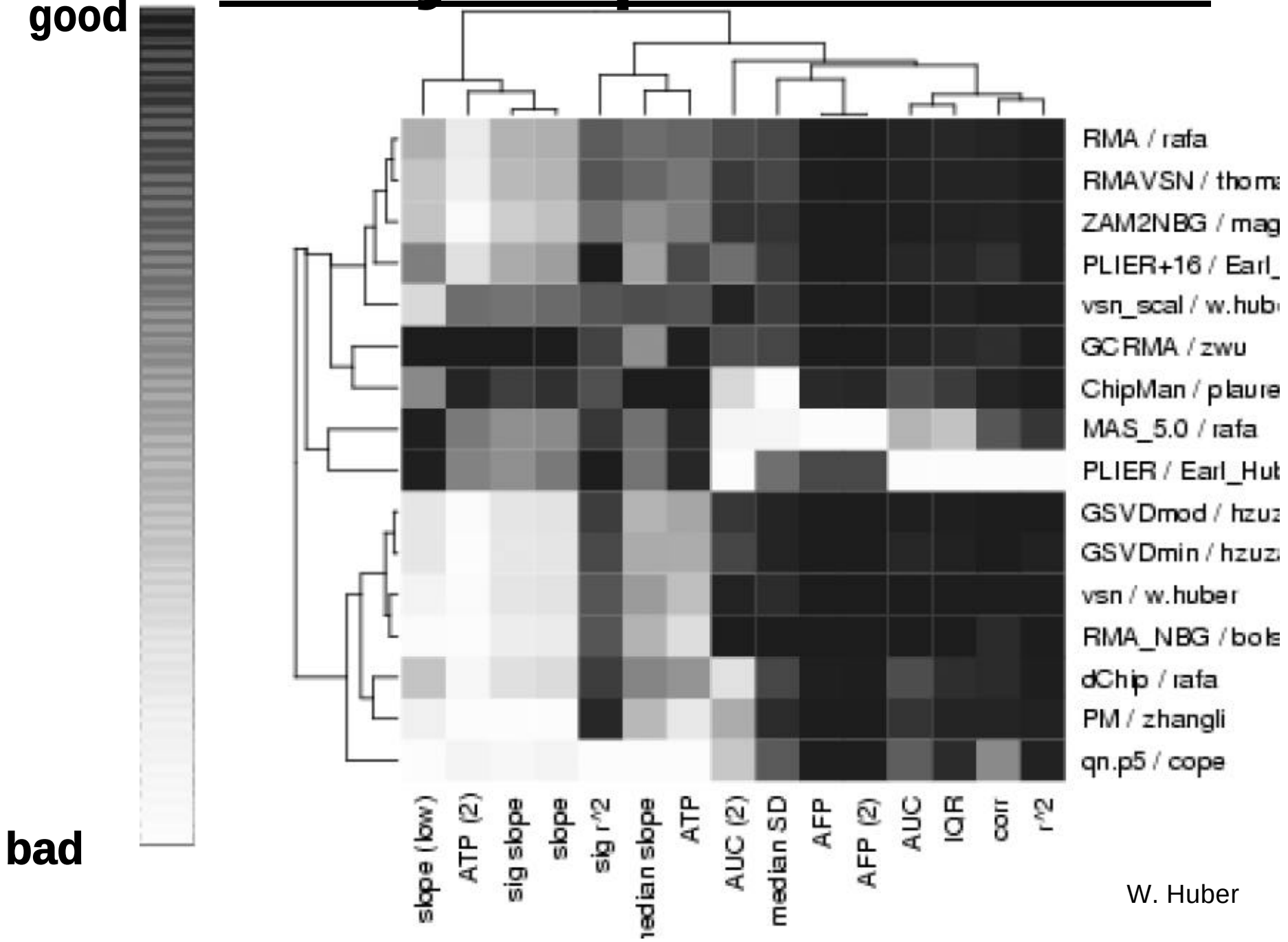
b) FC=2


True Positives
False Positives
RMA
not multi-array
not robust
MM as PM

> affycompTable(rma.assessment, mas5.assessment)

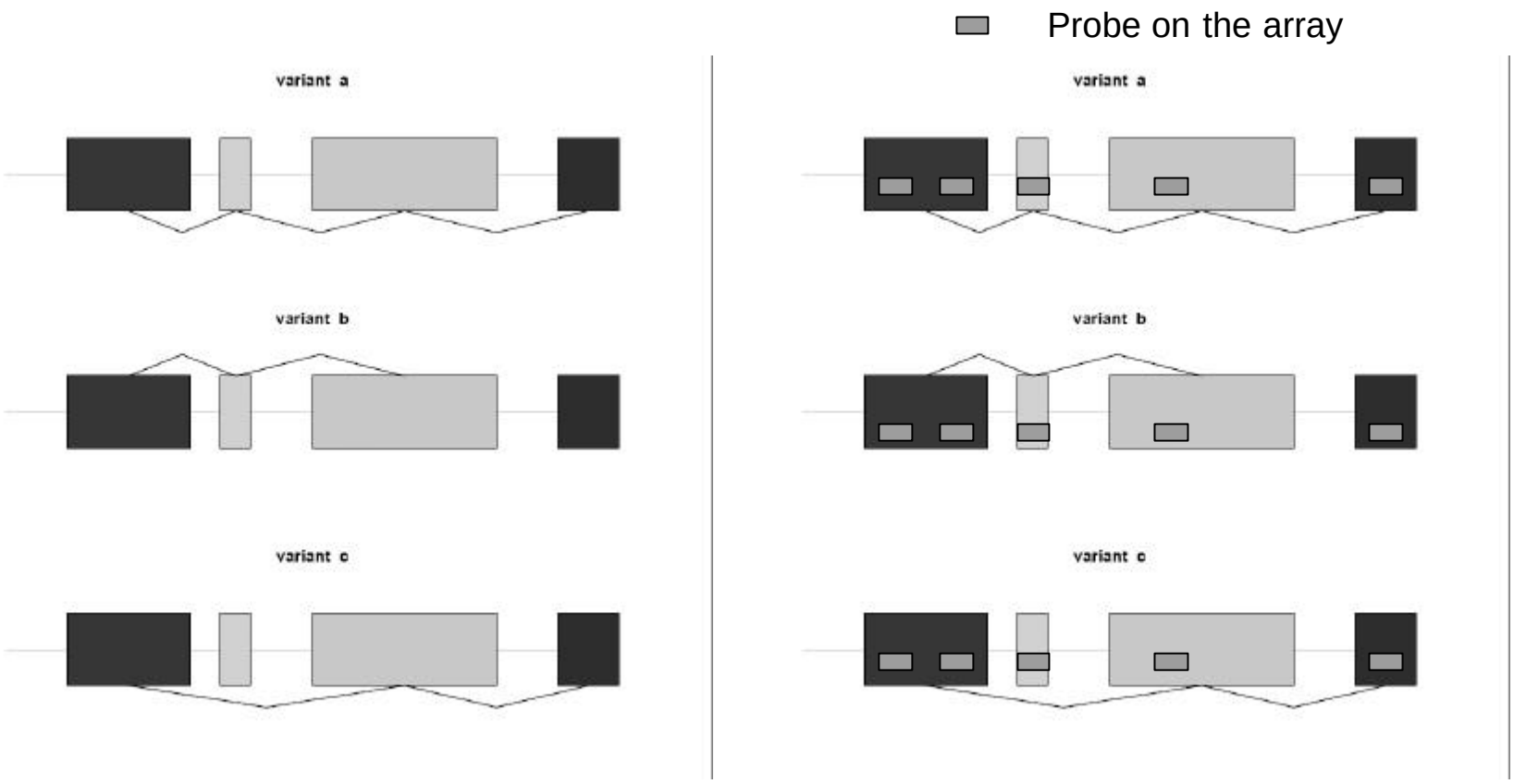
	RMA	MAS.5.0	whatsgood	Figure
Median SD	0.08811999	2.920239e-01	0	2
R2	0.99420626	8.890008e-01	1	2
1.25v20 corr	0.93645083	7.297434e-01	1	3
2-fold discrepancy	21.00000000	1.226000e+03	0	3
3-fold discrepancy	0.00000000	3.320000e+02	0	3
Signal detect slope	0.62537111	7.058227e-01	1	4a
Signal detect R2	0.80414899	8.565416e-01	1	4a
Median slope	0.86631340	8.474941e-01	1	4b
AUC (FP<100)	0.82066051	3.557341e-01	1	5a
AFP, call if fc>2	15.84156379	3.108992e+03	0	5a
ATP, call if fc>2	11.97942387	1.281893e+01	16	5a
FC=2, AUC (FP<100)	0.54261364	6.508575e-02	1	5b
FC=2, AFP, call if fc>2	1.00000000	3.072179e+03	0	5b
FC=2, ATP, call if fc>2	1.71428571	3.714286e+00	16	5b
IQR	0.30801579	2.655135e+00	0	6
Obs-intended-fc slope	0.61209902	6.932507e-01	1	6a
Obs-(low)int-fc slope	0.35950904	6.471881e-01	1	6b

u affycomp results (28 Sep 2003)



W. Huber

Alternative Splicing



A popular representation of splice variants shows exons as boxes, linked by broken lines to show which exons are skipped and which ones are not for the splice variants.

Alternative Splicing

hgu95av2probe {hgu95av2probe}

R Documentation

Probe sequence for microarrays of type hgu95av2.

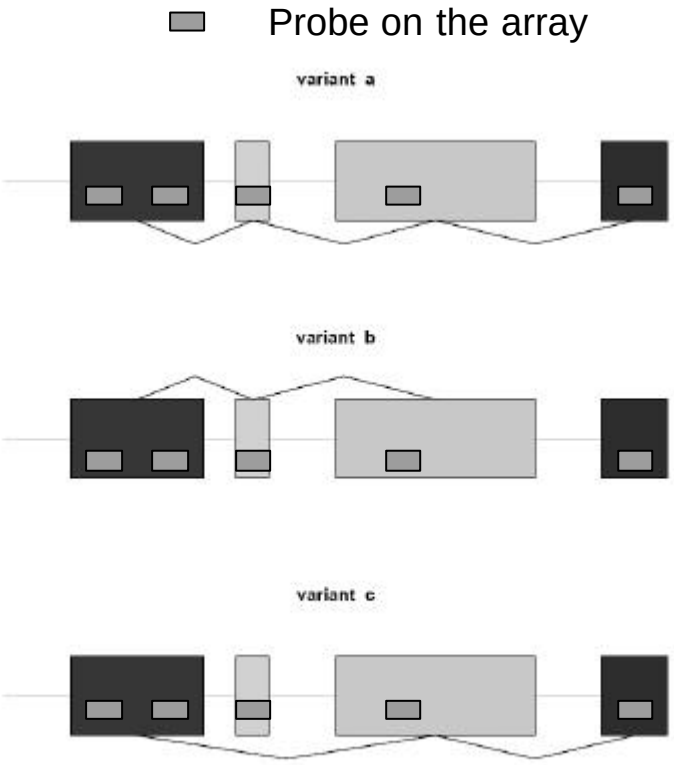
Description: This data object was automatically created by the package matchprobes version 0.8.3.

Usage: data(hgu95av2probe)

Format: A data frame with 199084 rows and 6 columns, as follows.

sequence	character probe sequence
x	integer, x-coordinate on the array
y	integer, y-coordinate on the array
Probe.Set.Name	character, Affymetrix Probe Set Name
Probe.Interrogation.Position	integer, Probe Interrogation Position
Target.Strandedness	factor, Target Strandedness

Alternative Splicing



Expression measurement

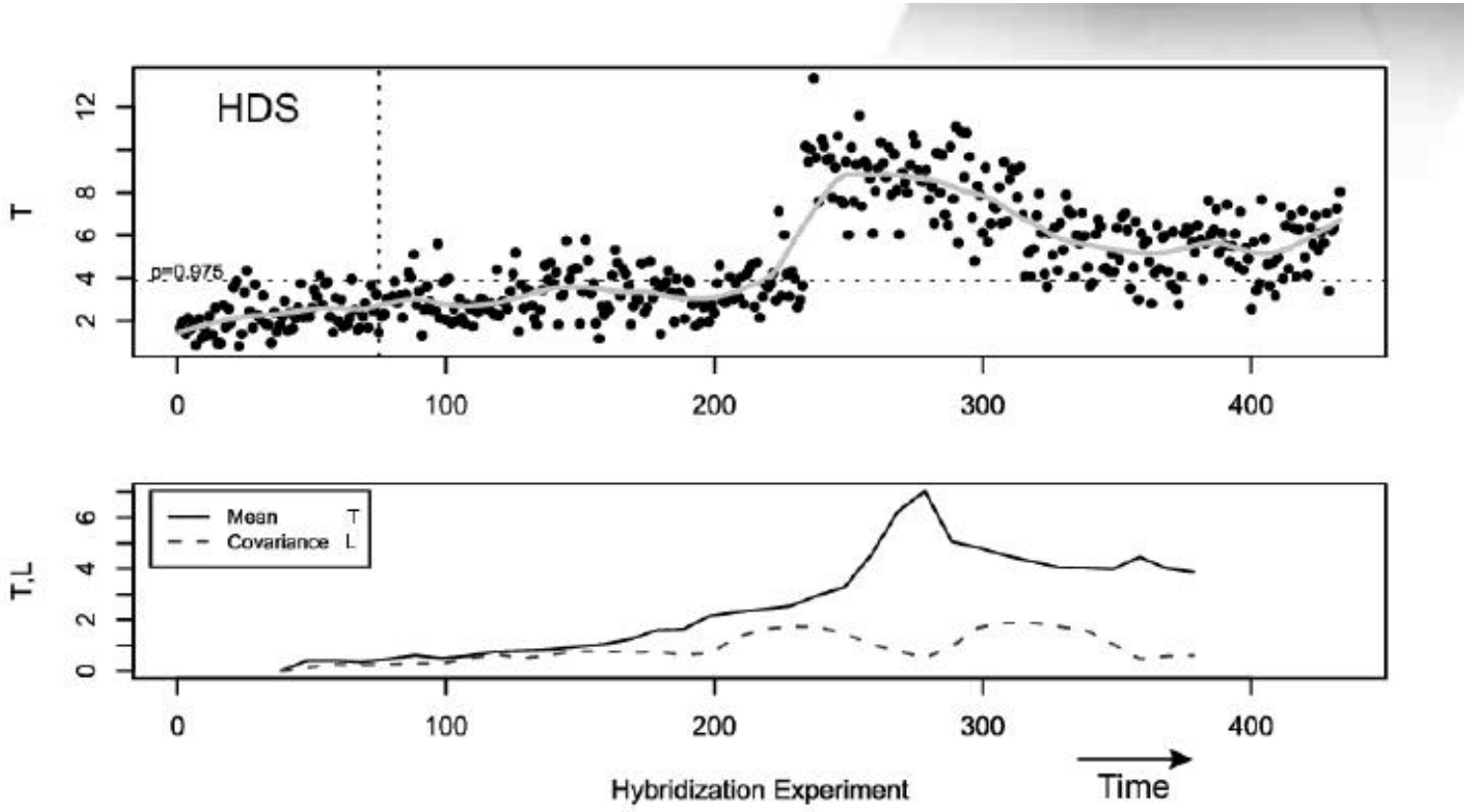
P_1	P_2	P_3	P_4	P_5	
H	H	H	H	H	V_a
H	H	H	H	L	V_b
H	L	H	H	H	V_c

Techniques from Discriminant Analysis help to calculate discriminatory scores to identify a certain variant with an array.

Process Control for large scale experiments

- Model F. et al. (2002) Bioinformatics, 18:S155-163
- HDS: historical data set, variables of a process for some time under perfect working conditions. CDS: current data set.
- How far is the current state of the process away from the perfect state?
- Distance measure: Hotelling's $T^2 = (m-\mu)^t S^{-1} (m-\mu)^t$
  parameter μ and S estimated from the HDS
- Additional tasks:
  1. outlier treatment with robust Principle Component Analysis (rPCA)
     The estimates μ and S are not robust against outliers
  2. For fewer arrays than number of gene expression, the sample covariance matrix S is singular and not invertible.
     PCA is used to reduce dimensionality of the measurement space.
- Calculate an upper control limit to initiate interventions in the ongoing process.
- In order to see whether an observed change in T^2 comes from a simple translation, it is of interest to compare the two sample covariances between HDS and CDS.
  A LRT for different covariances is used, calculates statistic L (H_0: L=0)

Process Control for large scale experiments



T^2 control chart of ALL/AML study. Over the course of the experiment a total of 46 oligomeres for 35 different CpG positins had to be re-synthesized.

They all talked at once, their voices insistent and contradictory and impatient, making of unreality a possibility, then a probability, than an incontrovertible fact, as people will when their desires become words.

Willian Faulkner, *The sound and the fury*, 1929