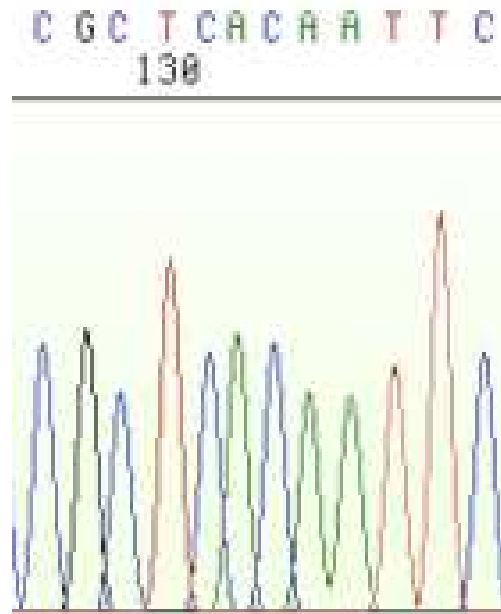


Toxicogenomics, human risk assessment and possible regulatory uses

Timothy W Gant

20 plus years of 'omics

- Omics has been with us for 20 years plus starting with early metabolomics by NMR and leading into transcriptomics in the late 20th century building on the back of the development of the 96 well capillary sequencer giving rise to clone availability and later the genome sequence (draft 2001; complete 2003).



The Chipping Forecast I

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perspective

Experimental manipulations will also need to be rigorously controlled. Responses to microenvironment (for example, the position of a culture dish in an incubator or the time of day at which an assay is performed) pose a special risk of misleading global expression studies, in which one is fishing through 100,000 genes to find the small subset that vary. It is well known among *aficionados* that comparison of the 'same' experiment performed a few weeks apart reveals considerably wider variation than seen when a single sample is tested by repeated hybridization.

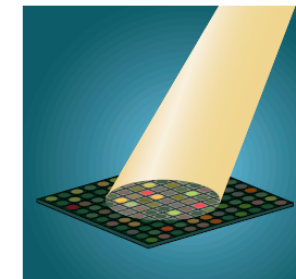
Microarray technology is a powerful tool for studying gene expression. It allows researchers to measure the expression levels of thousands of genes simultaneously. This is done by hybridizing a sample of RNA to a microarray, which is a chip containing thousands of small spots of DNA. The spots are then scanned, and the intensity of the signal is measured. This allows researchers to identify genes that are up-regulated or down-regulated in a particular condition.

The greatest challenge, however, is analytical. The first expression profiling experiments involved comparing just two samples, with the aim of identifying those genes whose expression levels

extended its dominion: it has domesticated the Megabase and will tame the Gigabase in the not-too-distant future.

The next great challenge is to discern the underlying order. The Periodic Table summarized chemical propensities in its rows and

columns (owing to the actual capital cost of setting up an arraying facility or the amortized capital costs reflected in the purchase price of arrays). Still, these problems are likely to be solved by economies of scale, free-market competition and time—just as



Bob Crimi

The Chipping Forecast II (2002)

Jorewora

Biology's century: just the beginning for microarrays

doi:10.1038/ng1026

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biology. Scientists are conducting profiling studies that may lead to the use of microarrays in personalized medicine, in molecular diagnosis of disease and in predicting drug efficacy and toxicity in different individuals. **Just imagine the opportunities to learn even more using this technology!**

At times like this, scientists require the utmost flexibility and support from the technologies that they use and from the companies with whom they work. Agilent's vision is to provide scien-

in different individuals. **Just imagine the opportunities to learn even more using this technology!**

At times like this, scientists require the utmost flexibility and support from the technologies that they use and from the companies with whom they work. Agilent's vision is to provide scien-

and services that we provide to help scientists in their research.

Agilent Technologies is proud to sponsor this special supplement of *Nature Genetics*. We salute the spirit of innovation that has exemplified the past 50 years of genetic research and look forward to supporting you for the next 50.

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CHRIS VAN INGEN

Agilent Technologies, Life Sciences & Chemical Analysis
395 Page Mill Road

Genomics in regulatory use

Regulatory Toxicology and Pharmacology xxx (2017) 1–13



Contents lists available at ScienceDirect

Regulatory Toxicology and Pharmacology

journal homepage: www.elsevier.com/locate/yrtph



The challenge of the application of 'omics technologies in chemicals risk assessment: Background and outlook

Ursula G. Sauer^a, Lize Deferme^b, Laura Gribaldo^c, Jörg Hackermüller^d, Tewes Tralau^e, Ben van Ravenzwaay^f, Carole Yauk^g, Alan Poole^h, Weida Tongⁱ, Timothy W. Gant^{j,*}

^a Scientific Consultancy – Animal Welfare, Germany

^b ExxonMobil Petroleum and Chemical, Belgium

^c European Commission, Joint Research Centre, European Reference Laboratory for Alternatives to Animal Testing (EURL ECVAM), Italy

^d Department of Molecular Systems Biology, Helmholtz Centre for Environmental Research - UFZ, Germany

^e Department of Chemical and Product Safety, German Federal Institute of Risk Assessment (BfR), Germany

^f BASF SE, Germany

^g Environmental Health Science and Research Bureau, Health Canada, Canada

^h European Centre for Ecotoxicology and Toxicology of Chemicals (ECETOC), Belgium

ⁱ National Center for Toxicological Research (NCTR), U.S. Food and Drug Administration (FDA), USA

^j Centre for Radiation, Chemical and Environmental Effects (CRCE), Harwell Science and Innovation Campus, Public Health England (PHE), UK

How is omics applied in regulation?

Table 1

Summary of responses from the written inquiry: Chemical companies' experiences with the regulatory use of 'omics technologies.

Respondent	Regulatory use of 'omics?	If yes: For which purpose? If no: Why not?	Regulatory acceptance of 'omics data?	Technical comments
A	Yes, transcript-omics.	MoA categorisation for hepatocarcinogenesis; classification based on data similarity by the hierarchical clustering method.	Under consideration.	Procedure conducted in accordance with Affymetrix or Agilent protocols.
B	No.	Results not sufficiently reliable to ensure worker protection; 'omics data do not satisfy REACH provisions.		'Omics technologies must deliver reliable endpoint-relevant results, which can be used for the derivation of Derived No Effect Levels or Predicted No Effect Concentrations and for C&L.
C	Yes, but not in REACH dossiers.	'Omics were applied to support occupational exposure limits.		Data generation is not controlled; the outcome is too experimental condition-specific to be meaningful; it is difficult to correlate 'omics data to actual adverse effects and to determine human relevance.
D	Yes, Next Generation Sequencing, transcript-omics.	For internal decision making and as supporting data for all crop protection products. A few situations where full 'omics data were used for regulatory submission – to elucidate very complex MoAs.	Differently: (1) To help support a MoA and determine relevance, or lack thereof, to humans; (2) To derive NOAEL; (3) One case: 2-year cancer bioassay waived based upon MoA and gene expression data.	
E	Yes, but not in REACH dossiers	Pesticide registrations. For important commodity chemicals, research studies using 'omics approaches have been applied for product stewardship and for establishing MoAs.		

There has never been inclusion of 'omics data in a REACH submission

EHCA report of 2016 on New Approach Methodologies

ECHA stated in its progress report 2015 (published in 2016), that experience has shown that different advanced techniques such as new approach methodologies [that include 'omics methodologies] are not used in many registration dossiers... This lack of use may be an indication that industry does not consider these NAMs to be sufficiently developed (ECHA, 2016).

Applications and issues?

- Omics data is sometimes generated with chemical actives; eg: Pesticides and biocides. Data analysis typically follows 'that recommended by the manufacturer'.
- Omics data has never been used to support a submission under REACH
- Some use in establishing MoA particularly for pesticides and for product stewardship
- **There are no consistent methods applied to the analysis of omics data**
- Used internally for decision making
- If omics output could be standardised then there are opportunities for greater use in chemical grouping and read across as well as the assessment of modes of action.

Research verses regulation?

Research allows for:

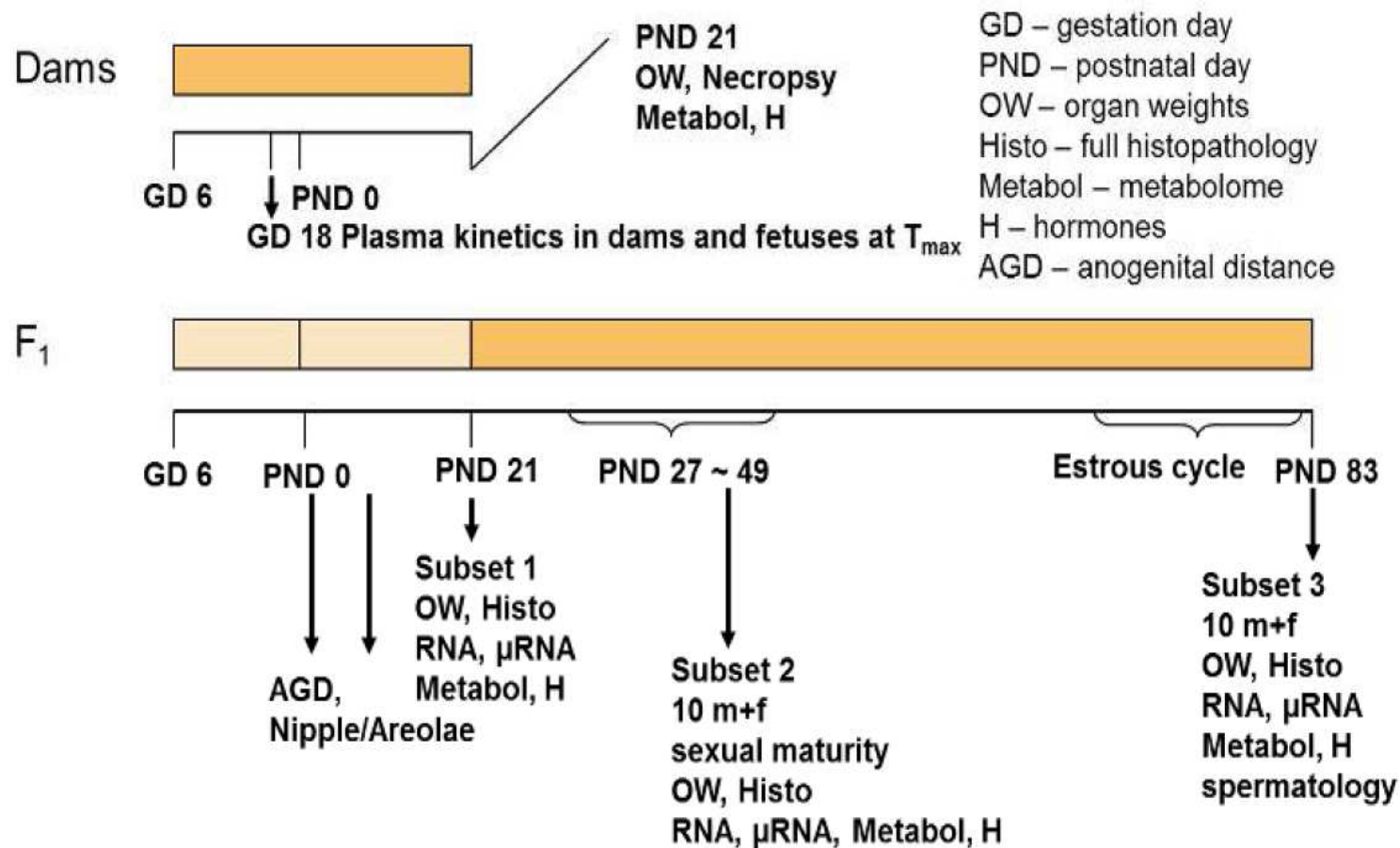
- Individuality in approach
- Peer review of methods
- Justification of choices made
- Repetition and verification

Regulatory use requires:

- Common methods and acceptance thereof
- Consistency and reproducibility between laboratories
- Proprietary independence

Exemplar: The Data Issue: EMSG56

The year is late 2014 - EUROTOX



Data mass

Doses

Flutamide – 0.0025, 0.25 and 2.5 mg/kg/day

Prochloraz – 0.01, 5 and 30 mg/kg/day

Vinclozolin – 0.005, 4 and 20 mg/kg/day

Controls – no compound

X

Time points

PND0

PND30-40

PND83

X

Replicates

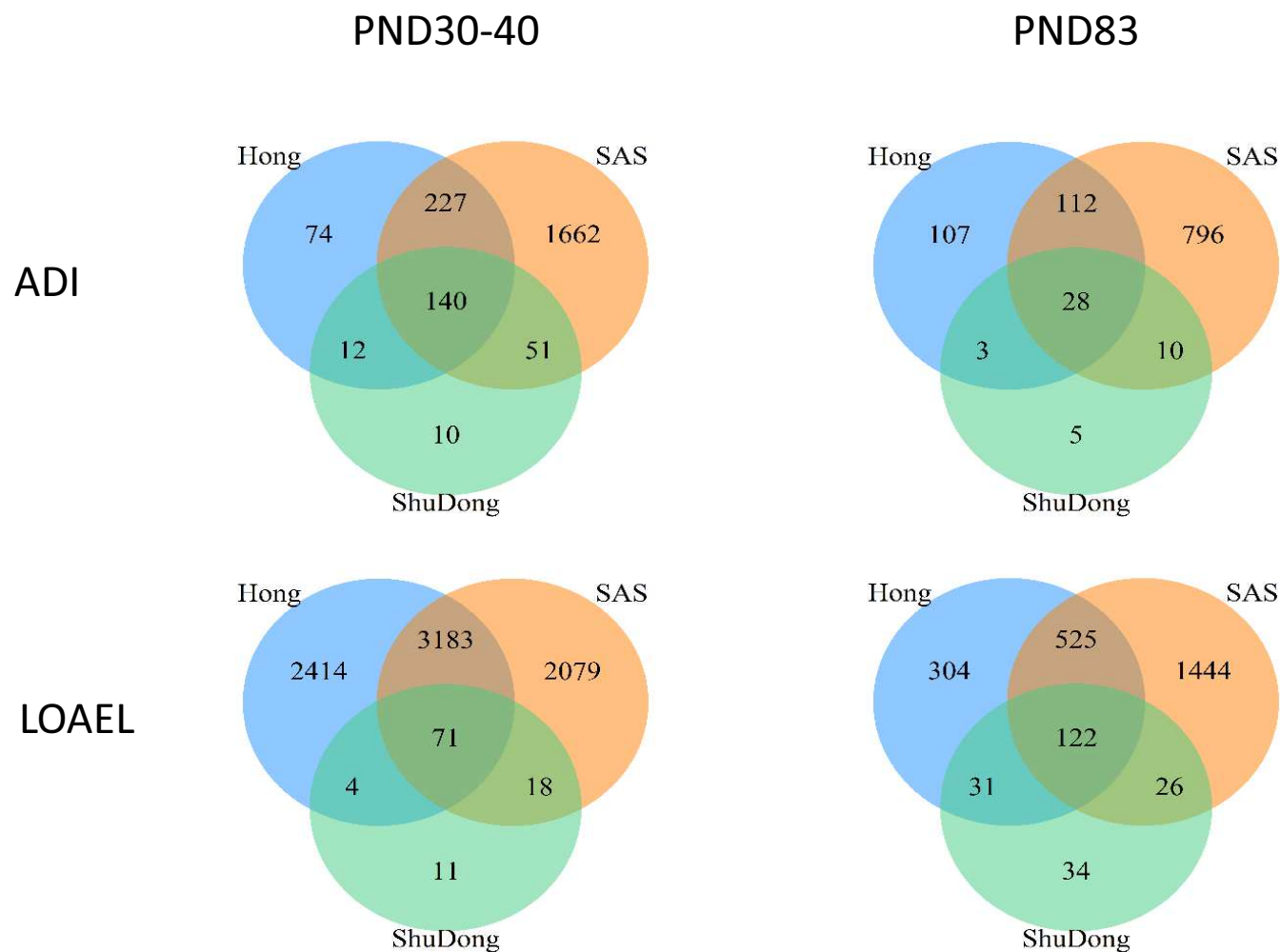
4

120 data sets of 62976
data points per data
set giving 7.56 million
data points total

EMSG 56

- Searched for a standard, regulatory accepted method for undertaking the bioinformatic analysis of large data sets
- There were no such methods published – OECD does not have a test guideline or a guidance document; MAQC had dealt with data generation but not data processing
- So the data was sent to four houses with specific instructions on how to process the data
- And what did they do.....?

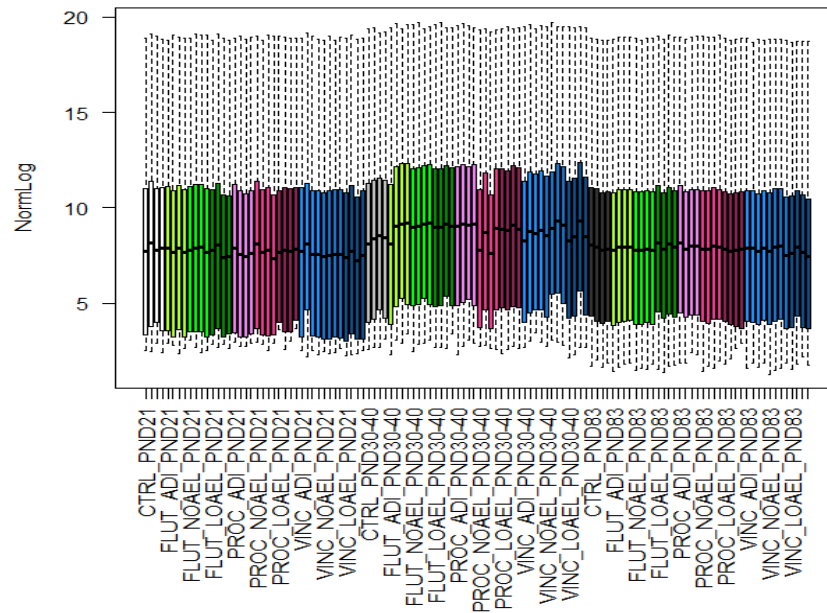
Analysis by three groups – January 2016



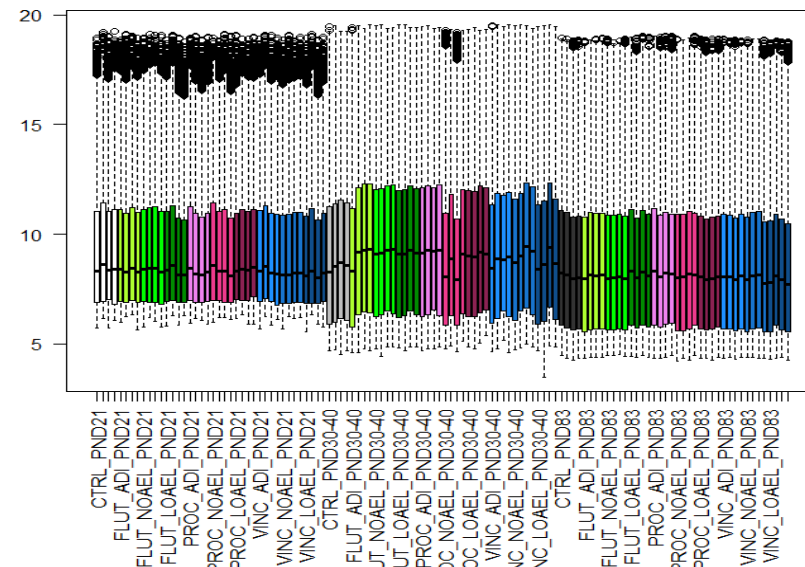


Issue 1 – raw data type

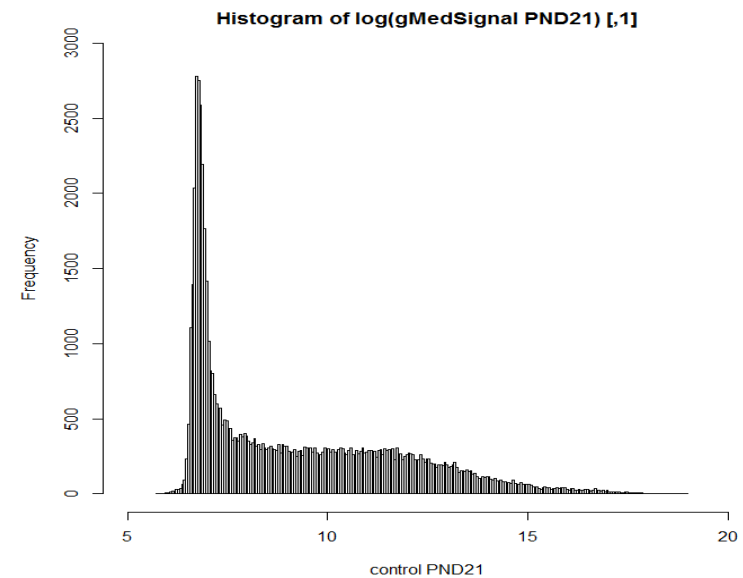
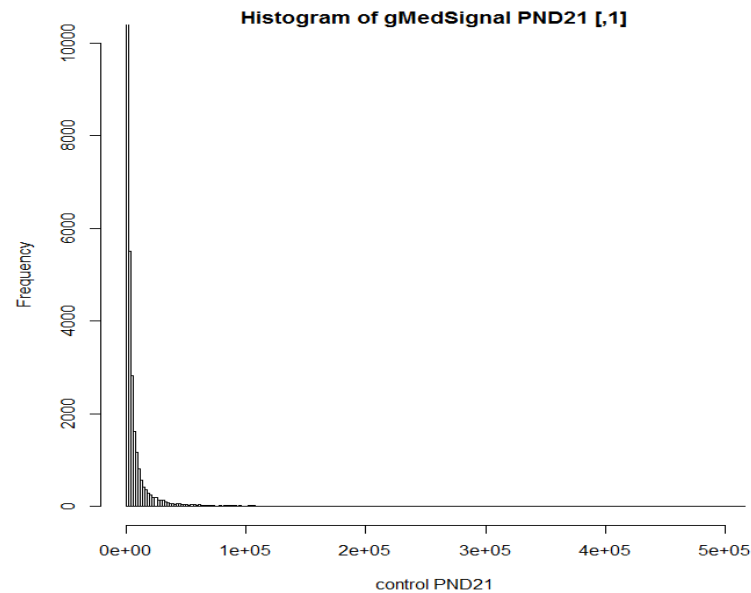
gProcessedData



gMedianData



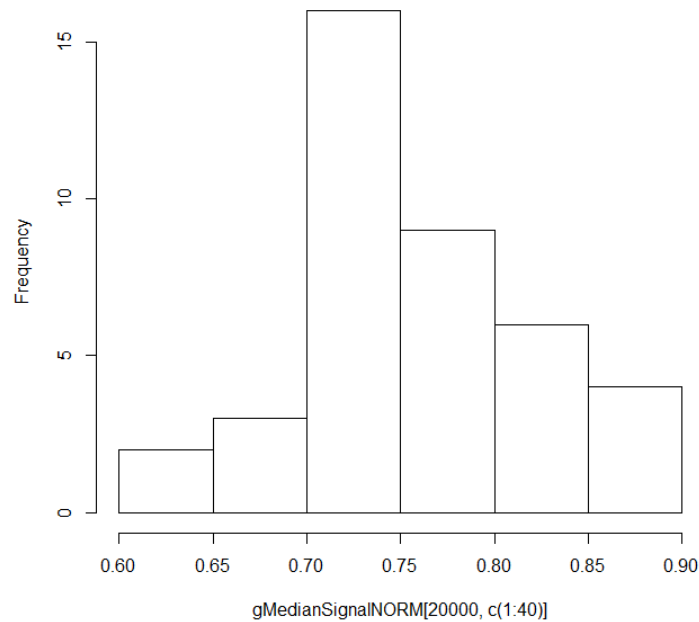
Issue 2 – Logs and normality



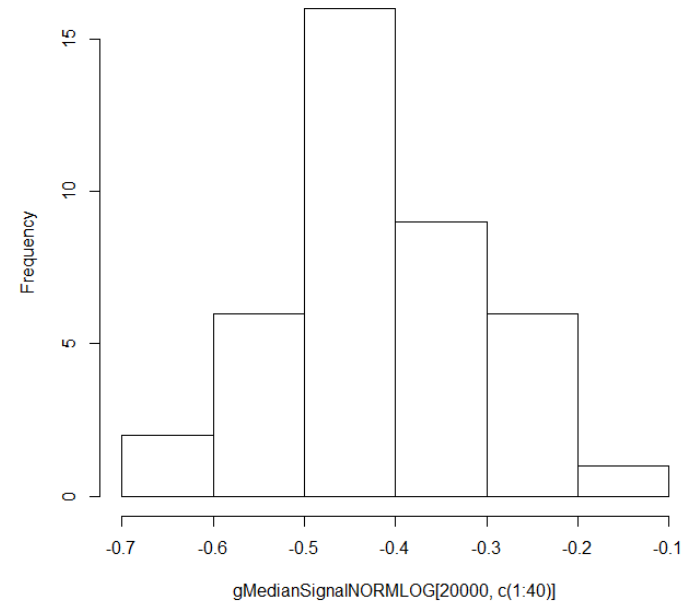


Normality: for pairwise comparisons

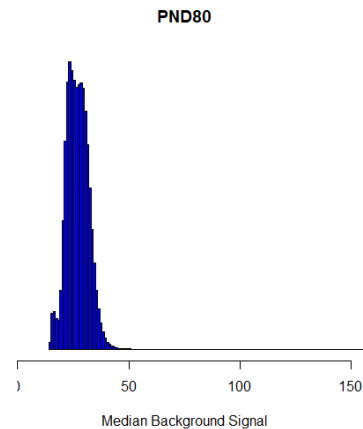
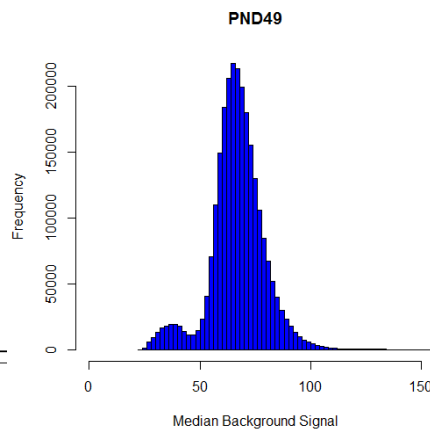
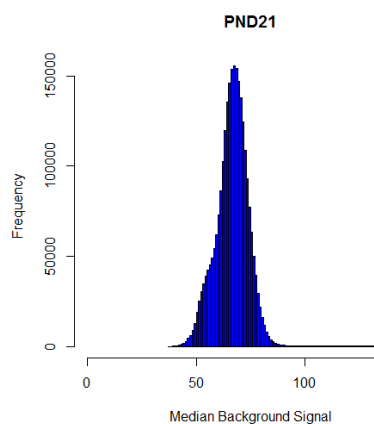
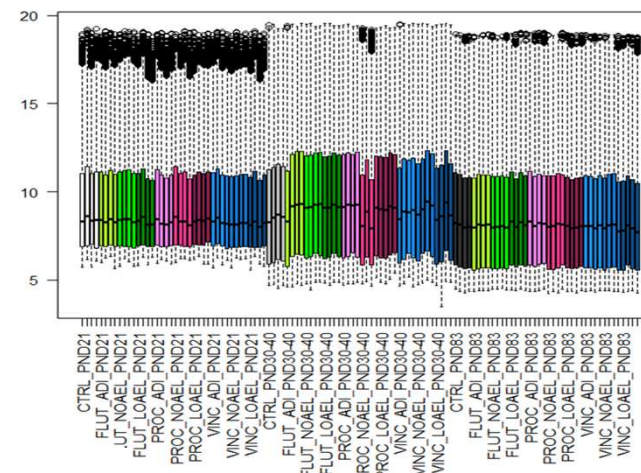
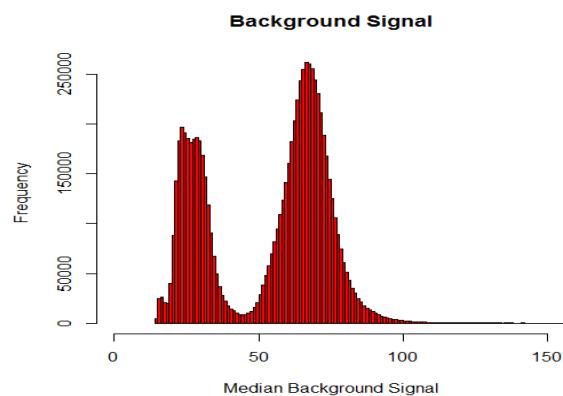
Histogram of gMedianSignalNORM[20000, c(1:40)]



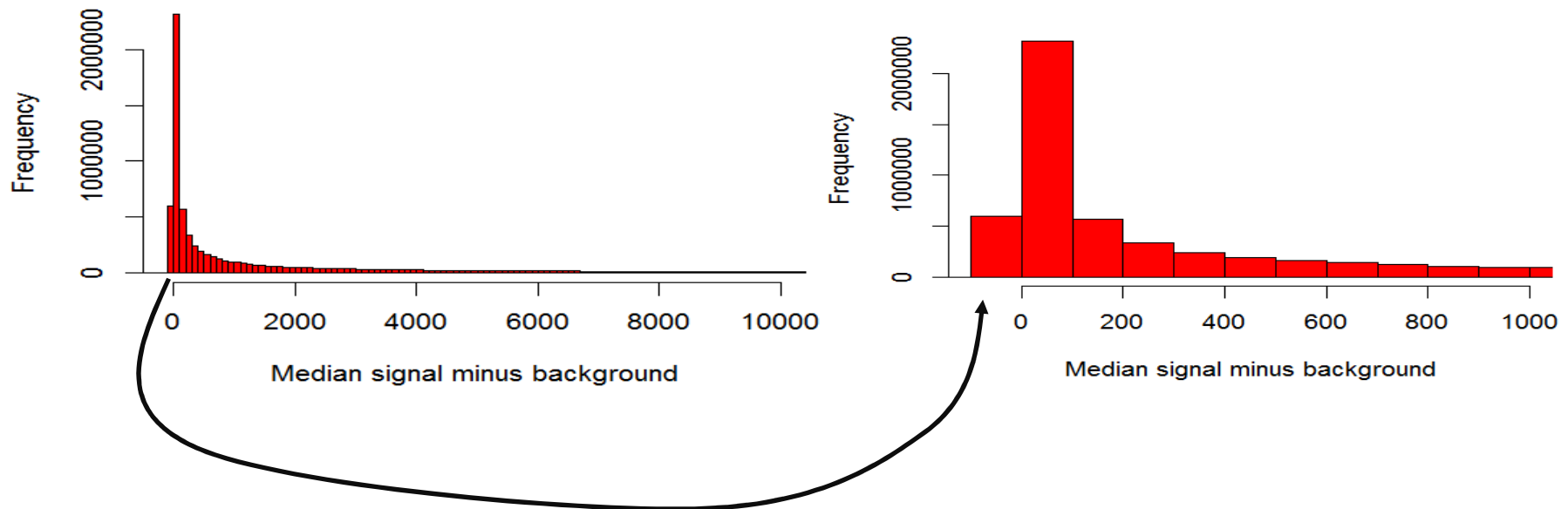
Histogram of gMedianSignalNORMLOG[20000, c(1:40)]



Issue 3 – Background subtraction – yes or no?



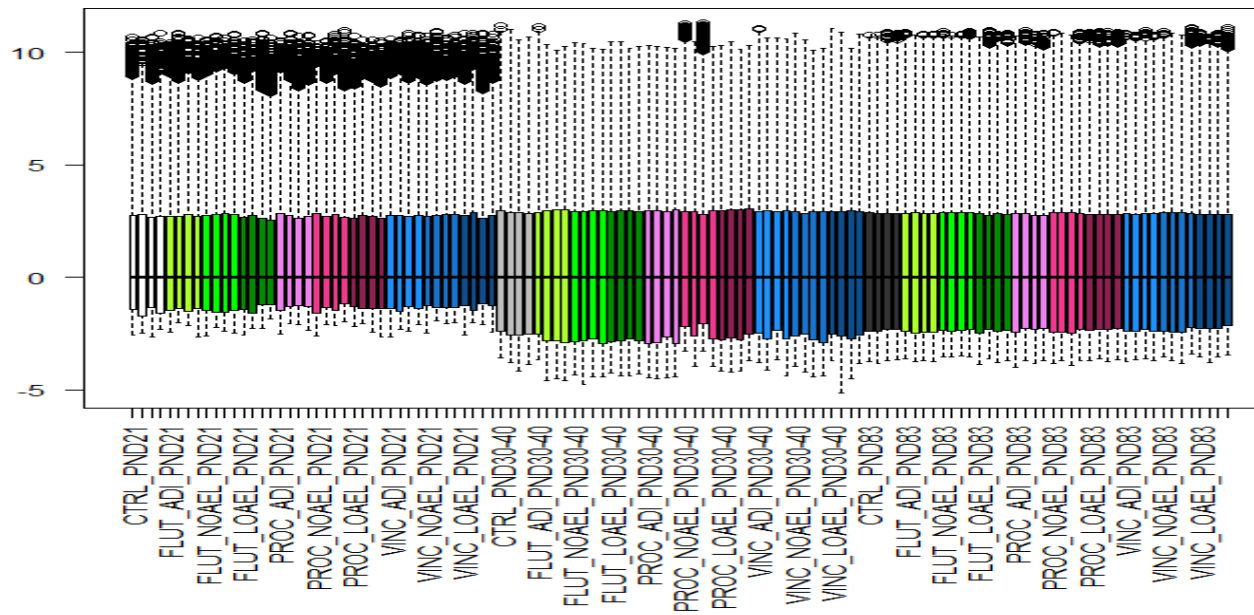
Issue 3 – background subtraction



Some signals go below zero because the background is not being measured within the hybridisation area but in the area surrounding and these can be different.

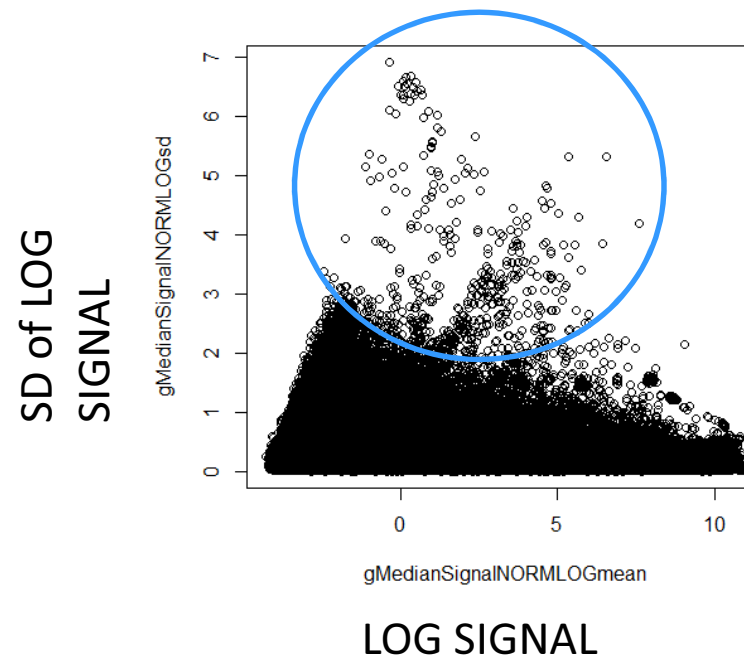
Issue 4 - Normalization

- Median centering
- LOWESS
- RMA (commonly used in Affymetrix)
- Within sample and across samples



Issue 5 – Low signal strength

Greater variation in measurement is associated with a lower signal strength



Values are the mean of the four biological replicates for each time and dose.

Combinations in data analysis

- Image processing
- Background handling
- Transformation
- Normalization
- Gene selection
- Classification
- Biological interpretation
-

>10 million combinations

Based on estimation by Dr. Russ Wolfinger (SAS Institute Inc.)
The 4th MAQC Project Meeting, Feb. 3-4, 2006, Boston, MA

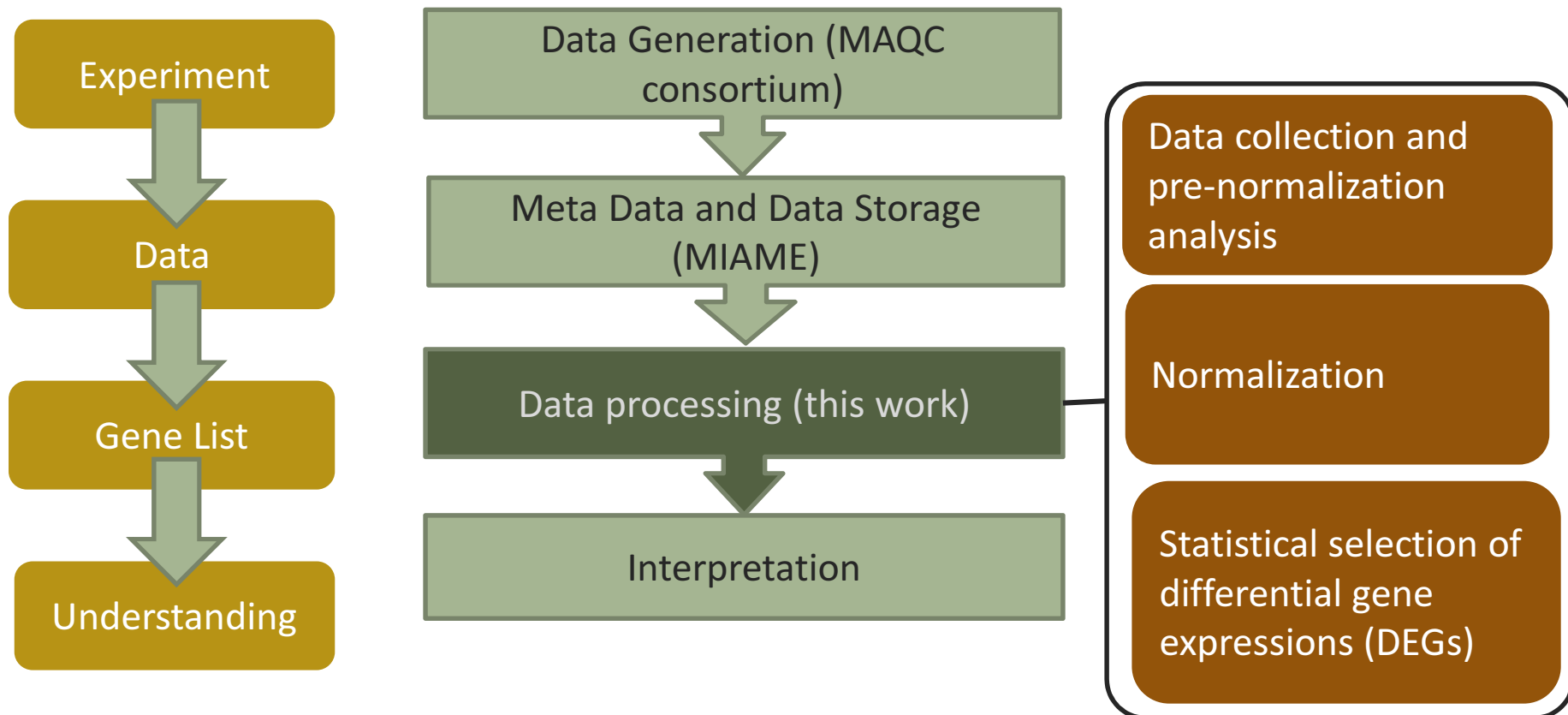
ECETOC

- 6th March 2015 a group convened to look at the data issues from EMSG56 and consider the development of protocols.
- From this a larger group convened July 7-8, 2015 under the auspices of ECETOC to look at the processes of getting from raw data to processed list of differential gene expressions (DEGs).

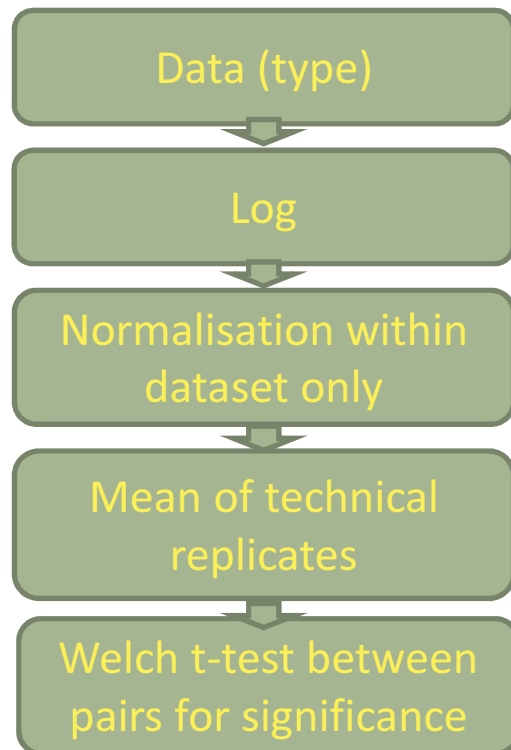


Process control in 'omic assessments

July 2015 in Brussels



Outcomes of the July 2015 meeting



How to recognise outlier data sets?

How to deal with low signal strength?

Background subtraction?

Type of normalisation and why not between data sets?

Welch (deals with unequal variance better than Students t-test)

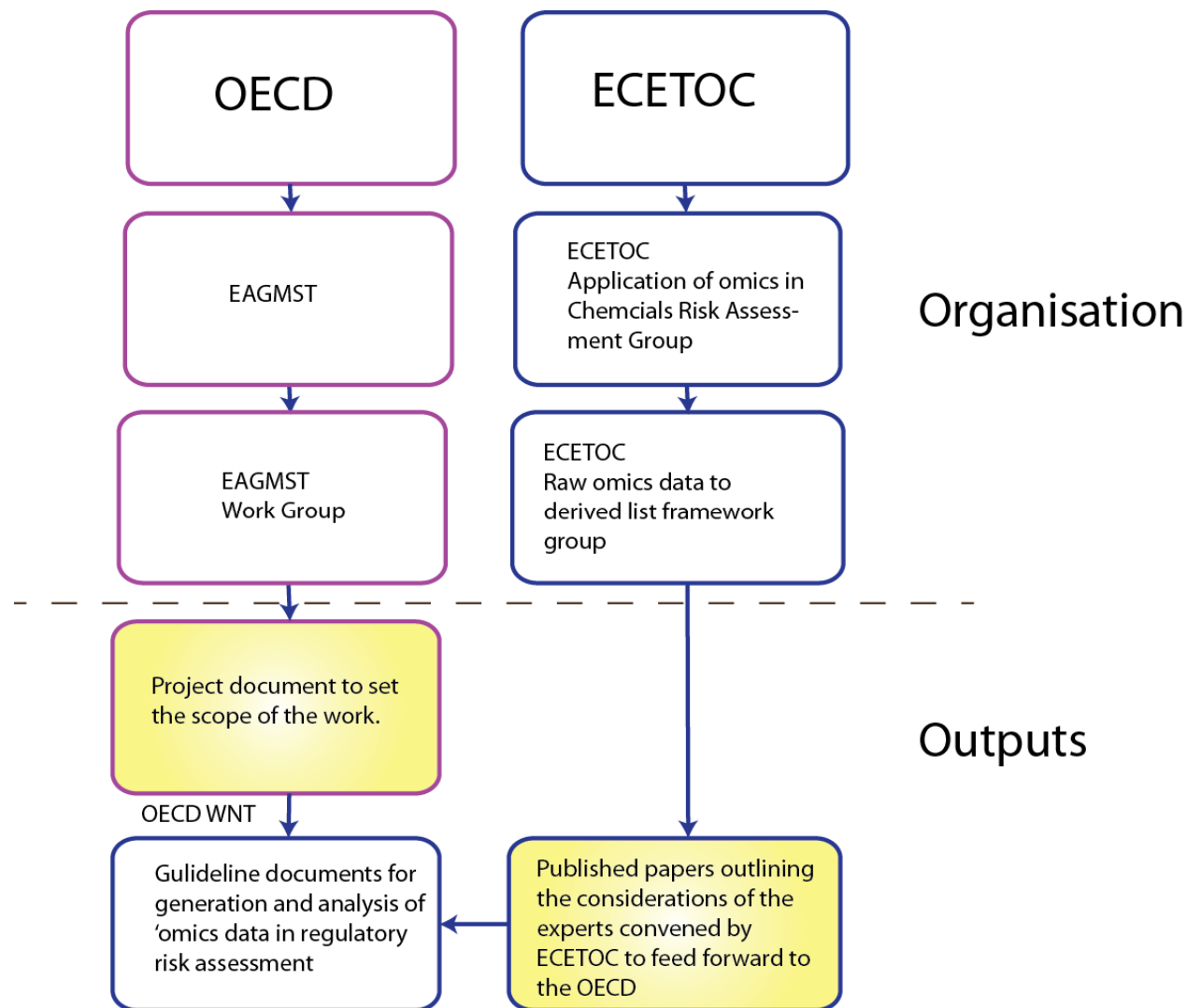
A fold change of 1.5 and p value of $p < 0.05$ should be used as a cut-off

A reference baseline analysis to act as a denominator for comparison of all other analysis methods

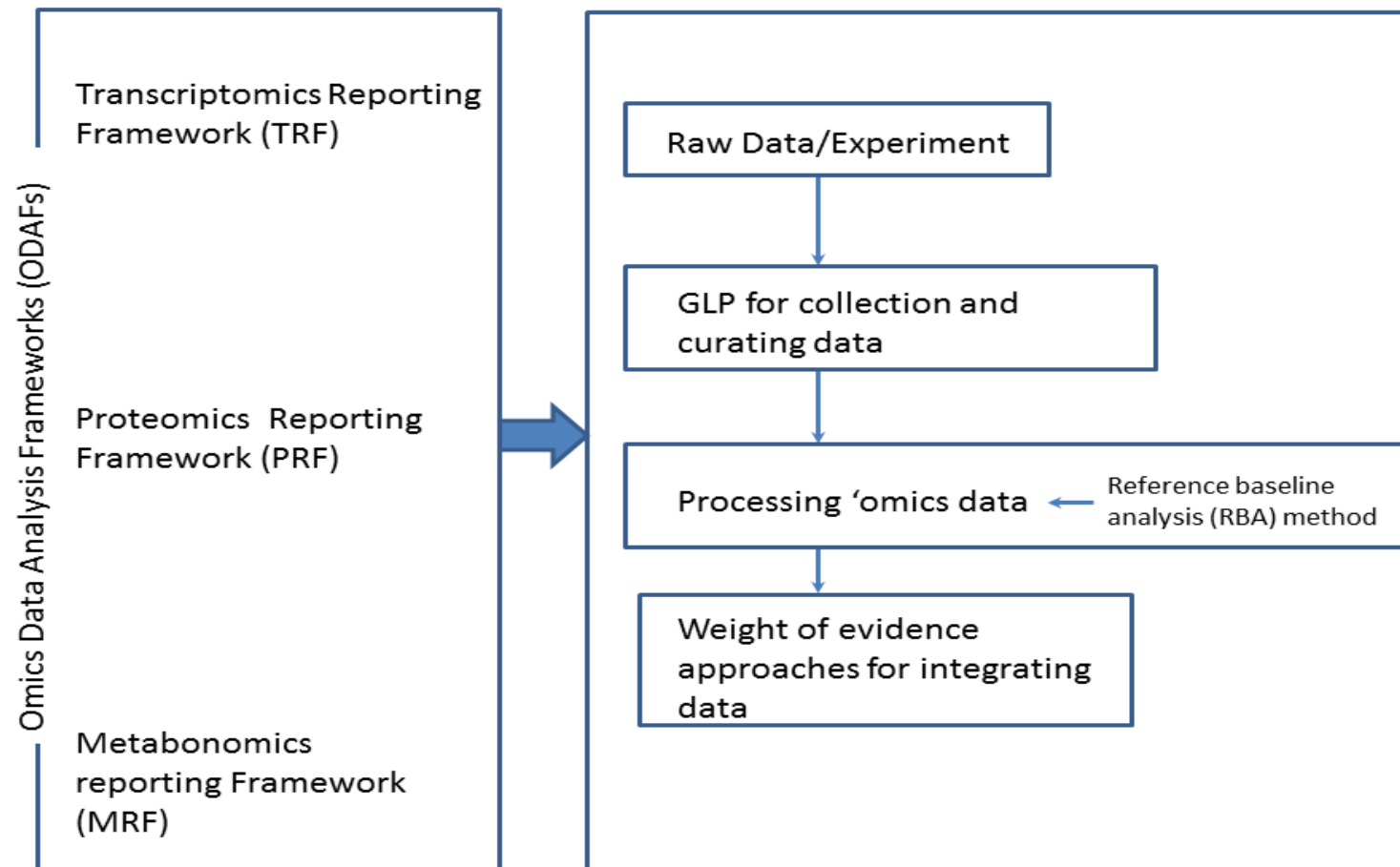
(Extended Advisory Group on Molecular Screening and Toxicogenomics)

- Work from the 2015 workshops presented to the OECD EAGMST meeting in June 2016 (Gant) and agreed for a draft standard project submission form (SPSF) for submission at the December 2016 EAGMST meeting
- Further ECETOC workshop held in Madrid in October 10-12, 2016 led to the development of the concept of 'omics reporting frameworks of which one is the transcriptomics reporting framework. The work to this point is being published in 5 papers currently in press or published with *Regulatory Toxicology and Pharmacology*
- December 2016 – EAGMST acceptance of the SPSF informal agreement to include a project within the EAGMST workplan pending acceptance at the June 2017 meeting
- June 2017 – Acceptance of the project by EAGMST for a series of guidance documents on the three main 'omics to be presented to the OECD Working Group of the National Coordinators for the Test Guidelines Programme (WNT)
- October 2017 – Progress occurring with Transcriptomics and Metabolomics project submission form for the OECD WNT – proteomics is not being pursued at the current time

OECD/ECETOC workstreams



The frameworks – work in progress



Conference presentations

- 2015 - workshop outcomes presented at the EUROTOX meeting - **Porto**
- 2016 – ECHA meeting on NAMS - **Helsinki**
- 2016 – SETAC meeting - **Brussels**

(Following this meeting Metabolomics came on board leading to the MERIT project)

- 2017 – SOT - **Baltimore**

Where could omics potentially be used in regulation (not exhaustive)

- Classification and labelling (C&L) of substances, for example as part of a tiered testing strategy.
- Weight-of-evidence (WoE) approaches to elucidate the MoA of the substance under investigation.
- Substantiation of chemical similarity for read-across Determination of points-of-departure (PoDs) for hazard assessment.
- Demonstration of species-specific effects and human health relevance (or absence thereof).
- Read across for grouping and hazard identification
- Reduction, Refinement and Replacement.
- Epigenetic assessment for historical exposure

Thanks

- Wenjun Bao
- Mohamed Bonahmed
- Tim Ebbels
- Karma Fussell
- Madeleine Laffont
- Alan Poole
- David Rouquie
- Steffen Schneider
- Leming Shi
- Tokuo Sukata
- Kayo Sumida
- Weida Tong
- Shu-Dong Zhang
- Hervé Seitz - CNRS France
- Matthew Martin – USEPA
- Miriam Jacobs (OCED WNT for the UK)
- Ursula Sauer
- Rusty Thomas (USFDA)
- Carole Yauk – Health Canada
- Mark Viant