

Microarray quality control exchange experiment
 Jakob Hedegaard, University of Aarhus

EADGENE European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety

Genomics for Animal Health: Outlook for the Future
 13- 14th October 2009, Muséum National d'Histoire Naturelle, Paris, France

Microarray quality control exchange experiment

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EADGENE Exchange - 2008

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EADGENE The QC experiment

Quality and reproducibility of the results from DNA microarrays

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BMC Genomics

Research article
Learning from microarray interlaboratory studies: measures of precision for gene expression
 David I. Ducever¹, Wendell D Jones², Laura H Reid³ and Marc Salis¹

The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements

MAQC Consortium*

See the full results, the introduction of microarray technology has had a profound impact on gene expression research. The production of studies with increasing or decreasing reproducibility directly affected cross-platform microarray studies. The MAQC project was initiated to address these concerns, as well as other performance and data analysis issues. Collaborative data on the MAQC project have been deposited into public databases and generated a number of publications using a variety of alternative based and alternative technology platforms. We now describe the experimental design and data analysis efforts behind the MAQC project. See the introduction of microarray technology at <http://dx.doi.org/10.1186/1471-2107-9-102>

Reproducibility of microarray data: a further analysis of quality control (MAQC) data
 James I Chen^{1,2}, Hanyu Minn Hsuah¹, Robert R DeJonghamp¹, and Chen-An Tsai¹

Proceedings
Cross-platform comparability of microarray technology: Intra-platform consistency and appropriate data analysis procedures are essential
 Leming Shi^{1,2}, Weida Tong¹, Hong Fang¹, Uwe Scher¹, Jing H Hao¹, Raj K Puri¹, Felix W Frueh¹, Federico M Goodkaid¹, Lei Guo¹, Zhenqiang Su¹, Tao Han¹, Jar Ro

BMC Proceedings

Gene expression
Ratio adjustment and calibration scheme for gene-wise investigation of reproducibility of differentially expressed genes in normalization to enhance microarray inter-study predict DNA microarrays through statistical simulation
 Chunrong Chang¹, Hai Shen¹, Ch Song¹, Junhua Luo¹ and George G. Tse
 Xiaohui Fan^{1,2}, Leming Shi¹, Hong Fang¹, Stephen Harris¹, Roger Perkins¹

BIOINFORMATICS ORIGINAL PAPER
 doi:10.1093/bioinformatics/btp188

Gene expression
The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies
 Leming Shi¹, Wendell D Jones², Roderick V Vincent³, Stephen C Harris¹, Roger C Perkins⁴, Federico M Goodkaid¹, Lei Guo¹, Lisa I Croser¹, Cecile Boyen¹, Hong Fang¹, Feng Qian¹, Shaohi Amur¹, Wenjun Bao¹, Canlin C Barbacid¹, Vincent Berthelot¹, Xianxi Megan Cao¹, Tao Ming Chu¹, Patrick J Collins¹, Xiao-hui Fan^{1,2}, Felix W Frueh¹, James C Fusco¹, Xu Guo¹, Jing Han¹, Demir Herman¹, Huixiao Hong¹, Ernes S Kawasaki¹, Quan-Zhen Liu¹, Yaling Luo¹, Yunqing Ma¹, Hain Mei¹, Ron L Peterson¹, Raj K Puri¹, Richard Shippy¹, Zhenqiang Su¹

EADGENE The QC experiment

This study:

- Samples of biological relevance
- Lab-specific protocols

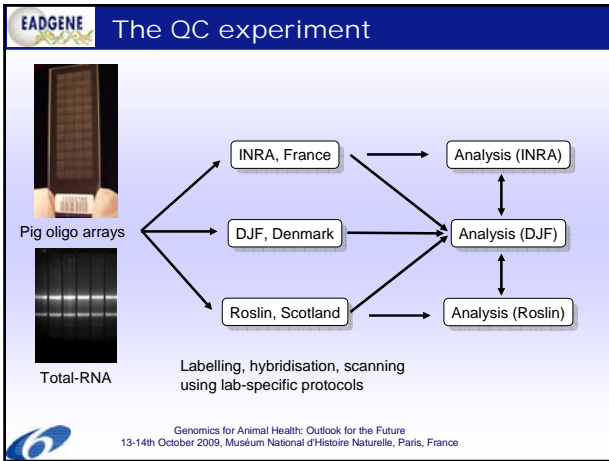
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EADGENE The QC experiment

- Liver sampled 14-18 hours after challenge
- Common reference design (15 arrays)

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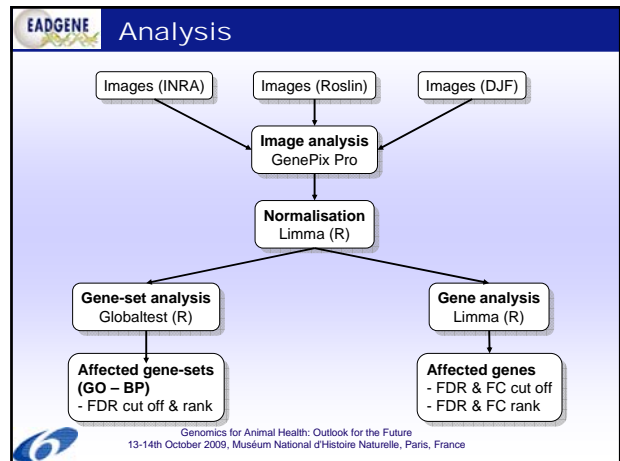
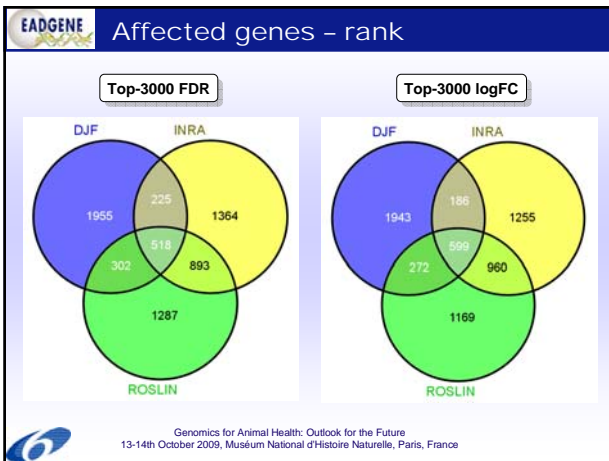
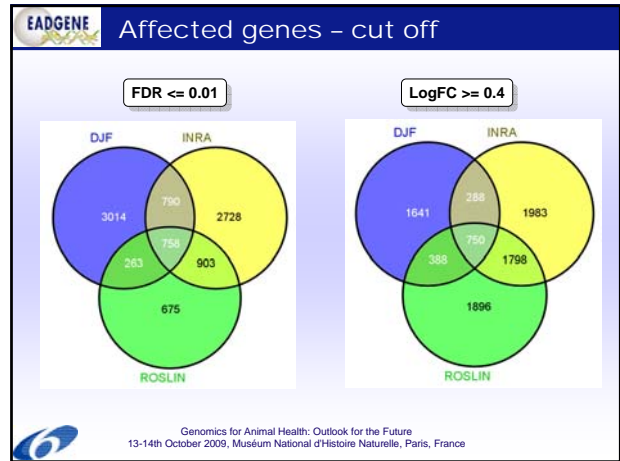
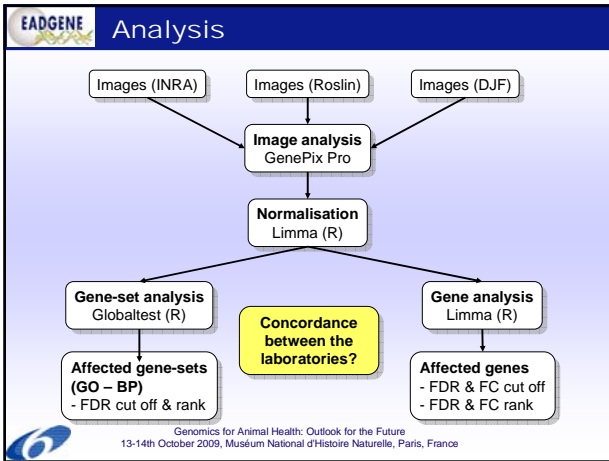
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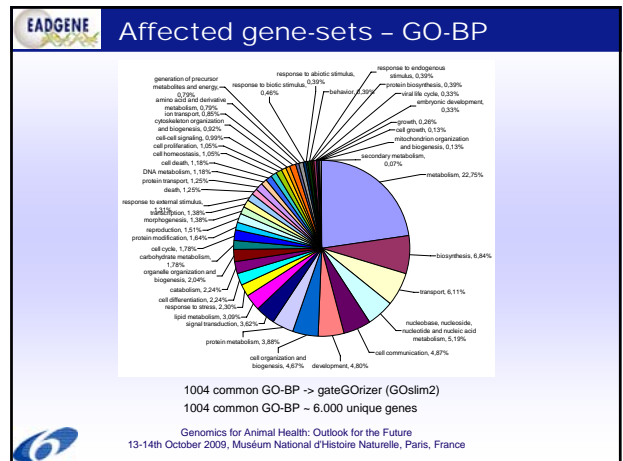
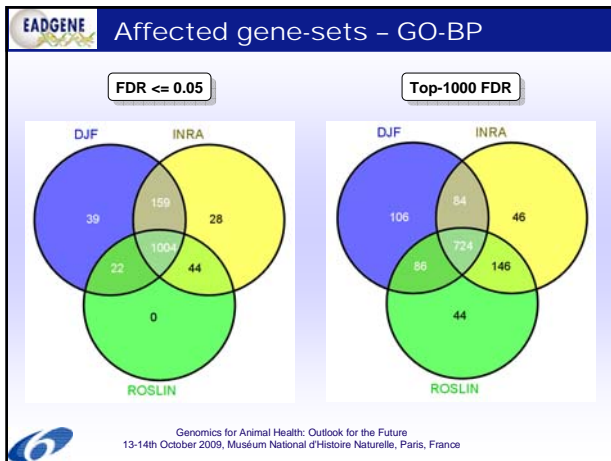
The QC experiment

| Laboratory | Labelling | Dyes | Hybridisation | Scanner |
|------------|--------------------------|----------------------|-----------------|----------------------|
| INRA | Indirectly labelled aRNA | Cy3, Cy5 | Nimblegen 4-bay | Genepix 4000B |
| Roslin | Indirectly labelled cDNA | Cy3, Cy5 | Gene TAC | Genepix 4200AL |
| DJF | Directly labelled cDNA | Alexa 647, Alexa-555 | Discovery XT | ScanArray Express HT |

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Conclusions

- Results from DNA microarrays are “reproducible”....
- Affected genes are less reproducible
- Affected gene-sets are very reproducible

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The future? NGS...

Potential information:

- Gene expression profiling
- Gene discovery
- Alternative splicing variants
- Rare transcripts
- Full length cDNA
- UTRs
- SNP analysis
- Annotation of genomes
-

Potential challenges:

- improving methods
- data handling
- data analysis
- reproducibility?
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