



HANDS ON WORKSHOP ON ADVANCED MICROARRAY TECHNIQUES

January 30-31, 2006,
Department of Microbiology and Cell Biology,
Indian Institute of Science, Bangalore



About the Workshop:

This workshop aims at providing advanced training to the participants on RNA QC, Labeling, Hybridization and Analysis of Microarray data. The participants will learn how to obtain high quality data and efficiently analyze the Microarray data. The training will help to address issues most often faced by users of Microarrays like reliability, reproducibility and deriving biological meaning from the large amounts of data generated. Professionals from Agilent Technologies and Genotypic will provide the training, share tips and answer your questions. The workshop will use Agilent's Microarrays and Labeling reagents, Bioanalyzer for RNA QC, Genespring Data Analysis software and Biological interpretation using Genotypic's tools Arrayaid and Biointerpreter. Participants will be briefly trained in MS Excel and Access.

Program 1: Workshop in Microarray Technology (2 days inclusive of data analysis)

Bring a pair of RNA, do the labeling and hybridization and take back high quality data and interpretations.

Program 2: Microarray Data Analysis training (1 day)

Bring raw data sets and take back statistical and biological significances and publication quality reports.

Who should participate?

This workshop is meant for participants with prior hands on experience in Microarray technology aiming to enhance the quality of the generated data and perform efficient data analysis. To ensure that participants obtain complete benefit from this workshop, only ten participants each will be selected for the hybridization workshop and Analysis training. Due to limitation in bench space only one participant from an Institution / Microarray facility will be selected. Selected Applicants will be notified by 30th December 2005. The participants are requested to bring their own RNA samples. A high density Microarray slide from Agilent technologies and the necessary reagents will be provided to each of the Program 1 participants. A computer with the required software will be available for each participant.

Visit www.genotypic.co.in/workshop/ for workshop Program details and Registration form

Last Date for registration - 24th December 2005

Unable to attend the workshop? Register to get Free Electronic version of the workshop handbook with protocols, analysis manuals and reports at www.genotypic.co.in/workshop/handbook/

Workshop Sponsor



Agilent Technologies

Benefits to the participants:

- ✍ Learn to obtain reproducible High quality images and data (visit www.genotypic.co.in/images.htm for examples).
- ✍ Maximize the value of the data by efficient statistical and biological analysis.
- ✍ Automate and Speed up QC and analysis using cutting edge tools.
- ✍ Don't miss the obvious and the hidden significance in the differentially regulated genes.

Program 1 Workshop in Microarray Technology (2 days)

Day 1:

- 1a. Microarray work flow presentation
- 1b. Synthesis of ds cDNA from total RNA*
- 1c. Amplification and Labeling with Cy3 and Cy5
- 1d. Quantification of labeled probes by Nano Drop spectrophotometer
- 1e. QC of labeled probes using Bioanalyzer
- 1f. Hybridization to Microarray slides.

*The RNA from participants will undergo Bioanalyzer QC prior to the start of the workshop.

Day 2:

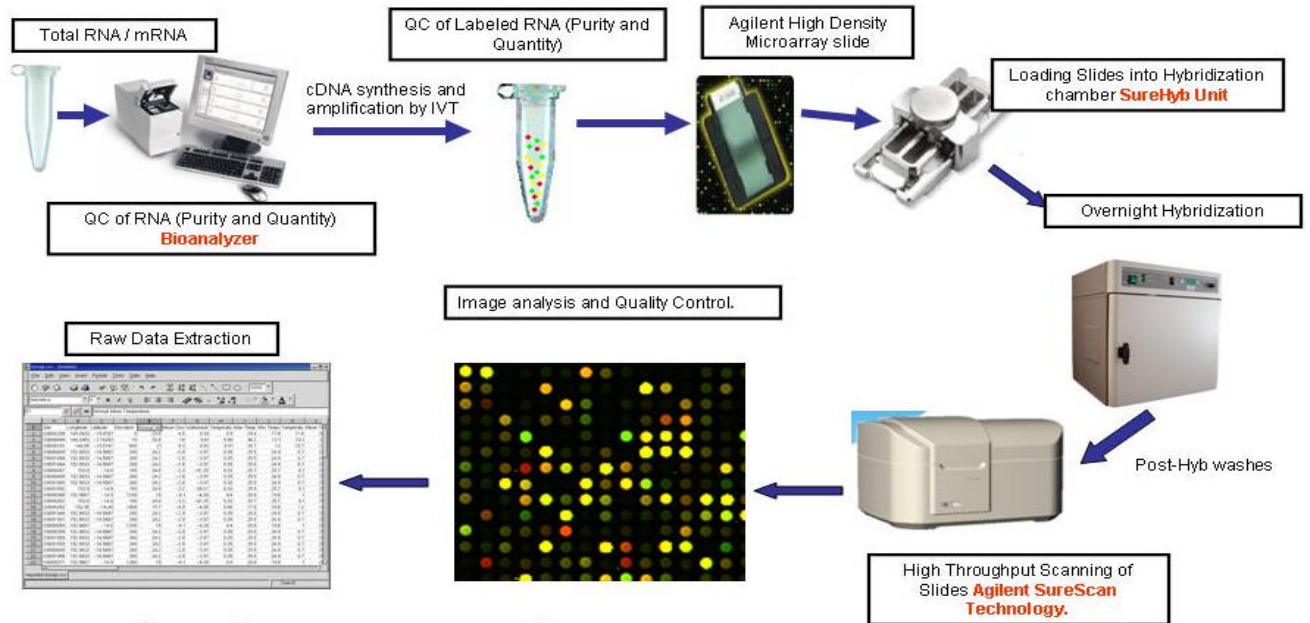
- 2a. Post hybridization washing and Drying
- 2b. Scanning using Agilent Scanner.
- 2c. QC of hybridization and Image and extraction of data.
- 2d. Raw data QC
- 2e. Finding the best Normalization method using Normalization Wizard and QC using Spot checker.
- 2f. Sorting differentially regulated genes into different groups.
- 2g. Automated QC of the ratios by replicate gene analysis
- 2h. Statistical Analysis and advanced data Analysis using Genspring GX software
- 2i. Biological Analysis using Biointerpreter, ArrayAid and GeneSpring GX
- 2j. Generating Reports.

Program 2 Analysis Workshop (30 January 2005): Participants will start from step 2C on 30th Jan

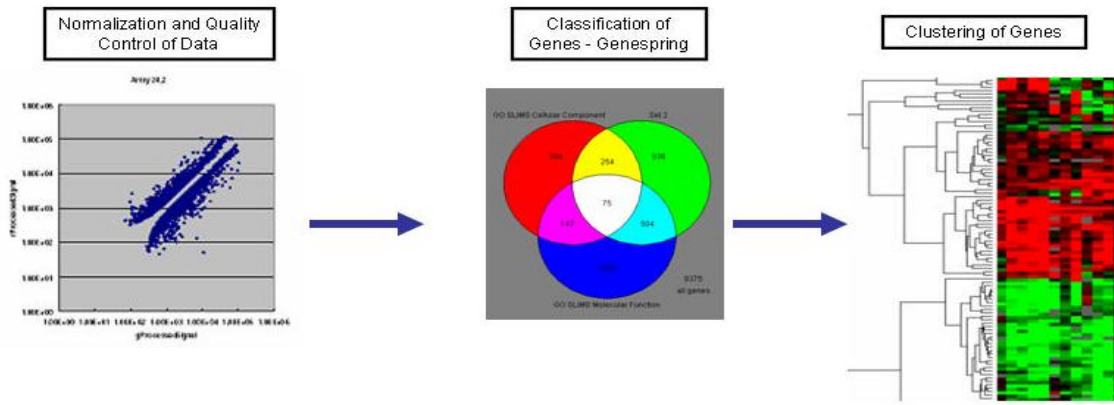
2006

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Microarray workflow – Program 1



Program 2 starts here



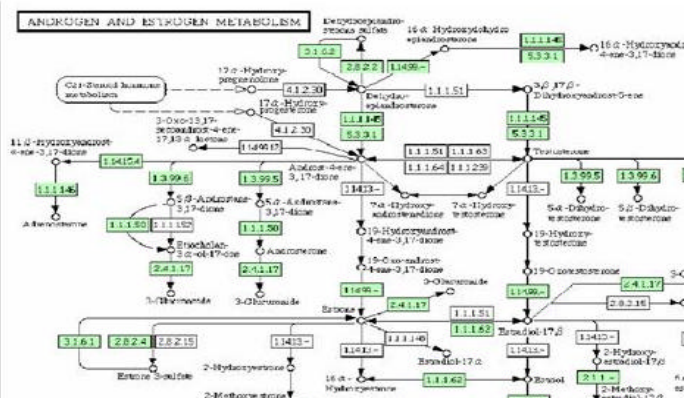
Functional Annotation of Differentials from Literature Curated Information

Gene Expression Data						
Experiment Condition	Red-Up	Green-Down	Blue-Both	Up	Down	Both
<input type="checkbox"/> Heat / Cold Shock	█			1	0	0
<input type="checkbox"/> Other stress	█	█		2	0	0
<input type="checkbox"/> Drug	█	█	█	3	1	0
<input type="checkbox"/> Chemical	█	█	█	5	1	1
<input type="checkbox"/> Knockout / Mutation	█	█	█	2	1	0
<input type="checkbox"/> Saline	█			1	0	0

Gene Expression based Annotation of Differentials from Literature Curated Information

Significant Functions		
<input type="checkbox"/>	Aerobic	4/20
<input type="checkbox"/>	Energy	6/20
<input type="checkbox"/>	Fatty Acid Metabolism	5/20
<input type="checkbox"/>	Glucose	4/20
<input type="checkbox"/>	Lipid Metabolism	6/20
<input checked="" type="checkbox"/>	Metabolism	15/20
<input type="checkbox"/>	Transport	8/20

Pathway Centric Analysis



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Workshop Co-Host: Prof. Parag Sadhale, MCB, IISc