



## **Analysis of microarray gene expression data using R/BioC and web tools**

Organised by MolMed & MGC  
11th edition, Erasmus MC, June 20-24, 2011  
Vs 110506

### **Course organizers and website**

**Program: Dr. Judith Boer**

Pediatric Oncology, Erasmus MC-Sophia Children's Hospital, and Human Genetics, Leiden University Medical Center, [j.m.boer@erasmusmc.nl](mailto:j.m.boer@erasmusmc.nl)

**Coordination: Dr. Frank van Vliet**

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**Website: [www.molmed.nl](http://www.molmed.nl)**

### **Speakers and moderators**

- Judith Boer, Department of Pediatric Oncology, Erasmus MC-Sophia Children's Hospital, Rotterdam and Center for Human and Clinical Genetics, Leiden University Medical Center
- Andrew Stubbs and Elizabeth McClellan, Department of Bioinformatics, Erasmus MC, Rotterdam
- Paul Eilers & Dimitris Rizopoulos, Dept. of Biostatistics, Erasmus MC, Rotterdam
- Johan de Rooi, Department of Bioinformatics and Department of Biostatistics, Erasmus MC, Rotterdam
- Kristina Hettne & Herman van Haagen, Biosemantics Group, Erasmus MC, Rotterdam & LUMC, Leiden
- Monique den Boer & Leila Mohammadi Khankahdani, Department of Pediatric Oncology, Erasmus MC-Sophia Children's Hospital, Rotterdam
- Maarten van Iterson, Center for Human and Clinical Genetics, Leiden University Medical Center
- Jelle Goeman and Ramin Monajemi, Dept. Medical Statistics and Bioinformatics, Leiden University Medical Center
- Renée de Menezes, Department of Epidemiology and Biostatistics, VUmc, Amsterdam
- Hinrich Göhlmann, Bioinformatics Team of Johnson & Johnson Pharmaceutical Research & Development, a division of Janssen, Beerse, Belgium
- Marcel Reinders, Information and Communication Theory Group, TU Delft
- Peter van Baarlen, Guido Hooiveld, Mark Boekschoten, Wageningen University
- Software: Dr. Mirjam van den Hout-van Vroonhoven & Sylvia de Does, Department of Bioinformatics, Erasmus MC

**Location:** Erasmus MC, Computer room **COO-5**.

### **Target group**

The course is tailored for biological and clinical researchers whose research involves experiments that generate gene expression data. The course focuses on microarray data, but some concepts may be applicable to next-generation sequencing gene expression data, or other types of genomics data measured on microarrays. Most of the speakers (and therefore examples) have a biomedical background.

## **Pre-requisites for participants**

Participants need to know what a microarray experiment is, and have their own expression profiling data. They have preferably followed an introduction to R course; alternatively they have practiced the "Getting started in R" practical prior to the course. Basic statistical concepts including mean, variance, standard deviation, probability distributions, t-test, p-value, correlation, and linear regression are assumed known. These are typically seen during basic statistics courses. **Please fill in the online registration form (free text at the bottom):**

- **do you have basis R knowledge (yes/no); if yes, please indicate how you acquired this knowledge: basic R course/ other...;**
- **do you have gene expression data to analyse yes/no, if yes: which platform? Affymetrix/ Illumina microarrays/ Agilent/ other: .....**

## **Format**

The course is intensive, and covers the basic concepts and methods required for microarray expression analysis. Presentations are followed by hands-on computer sessions to directly apply and get more insight in the analysis methods. One afternoon is dedicated to the analysis of a new data set, allowing the students to refresh and extend their analysis skill. After the course, the Presentations, practicals and test data will remain available for future reference. Software packages used are mostly freeware, including the statistical software R, Bioconductor, Cytoscape and web tools. The only commercial tool used is Spotfire.

## **Learning objectives**

1. The participant has insight in the issues involved in good experimental design, including power to detect differential expression.
2. The participant knows and can perform analysis steps in microarray data analysis, visually present and judge the results for:
  - quality control and preprocessing,
  - finding differentially expressed genes,
  - cluster analysis,
  - classification analysis,
  - pathway testing.
3. The participant has insight in the different algorithms and options available to perform an analysis, and can make an informed choice.
4. The participant knows the pitfalls of existing analyses and is able to critically judge the statistical analysis of microarray expression data performed by others.

## **Registration, deadline, admittance, sponsored places & related courses**

The total number of participants is limited to 40. Deadline for registration is Wednesday June 1<sup>st</sup>, 9 a.m. **When more than 40 students register before this deadline, the organisers will make a selection and admit the students with own data and experience in R.** Please note that to this aim you must fill in the online registration form (free text at the bottom):

- do you have basis R knowledge (yes/no); if yes, please indicate how you acquired this knowledge: basic R course/ other...;
- do you have gene expression data to analyse yes/no, if yes: which platform? Affymetrix/ Illumina microarrays/ Agilent/ other: .....

**Important: 5 Special places are reserved for participants from NBIC and 5 from CMSB.** NBIC and CMSB sponsor these places. This sponsoring can be applied for in the open text field on the bottom of the registration form. These applicants will be evaluated equally as the other registrants.

**LUMC will organize a basic course in R** from 6-8 June; see: [www.boerhaavenet.nl](http://www.boerhaavenet.nl); preference for registrations from LUMC. **MolMed (Erasmus MC) organized several of these courses**, the next one is open for registration ([www.molmed.nl](http://www.molmed.nl)) and will be planned the coming months.

## Programme

<b>Day 1</b>	<b>Monday June 20: Design and Preprocessing Room: COO-5</b>	
	<b>Moderator : Judith Boer</b>	
9:15	Welcome coffee and registration	
9:45	Short introduction to data sets and tools	Judith Boer
10:00	Experimental design: Think before you start	Judith Boer
11:00	Coffee	
11:15	Preprocessing and quality control	Hinrich Göhlmann
12:30	Lunch <b>outside, opposite to Coffee Corner</b>	
13:30	Normalization	Judith Boer
14:15	Introduction to R and Bioconductor	Judith Boer
14:30	Coffee	
14:45	Practical: Normalization and quality control in R	Judith Boer, Elizabeth McClellan, Hinrich Göhlmann <i>till 16:00</i> ; Dimitris Rizopoulos, Johan de Rooi
17:00	End day 1	

<b>Day 2</b>	<b>Tuesday June 21: Gene testing and Clustering Room: COO-5</b>	
	<b>Moderator: Renée de Menezes</b>	
8:45	Welcome coffee	
9:00	Finding differentially expressed genes	Renée de Menezes
10:15	Coffee	
10:30	Practical: Finding differentially expressed genes in R	Renée de Menezes, Elizabeth McClellan, Johan de Rooi
12:30	Lunch <b>(in Ae 4.06, NB Room COO-5 occupied)</b>	
13:30	Hierarchical and K-means clustering	Marcel Reinders
14:30	Coffee	
14:45	Cluster validation and principal component analysis	Marcel Reinders
15:45	Practical: Clustering using Spotfire	Marcel Reinders, Jan Bot, Erik van den Akker
17:00	End day 2	

<b>Day 3</b>	<b>Wednesday June 22: Classification and Gene set testing</b>	
	<b>Room: COO-5</b>	
	<b>Moderator: Paul Eilers</b>	
8:45	Welcome coffee	
9:00	Classification and PAM	Paul Eilers
10:30	Coffee	
10:45	Practical: Classification using PAM	Paul Eilers, Johan de Rooi
12:30	Lunch in Ae 4.06	
13:30	Testing groups of genes	Jelle Goeman
14:30	Coffee	
14:45	Practical: Testing groups of genes	Jelle Goeman, Ramin Monajemi
17:00	End day 3	

<b>Day 4</b>	<b>Thursday June 23: Power and Practise</b>	
	<b>Room: Ae 4.06 (9:30-13:00), COO-5 (from 13:00)</b>	
	<b>Moderator: Judith Boer</b>	
9:15	Welcome coffee	
9:30	Power and sample size estimation	Maarten van Iterson
10:15	Coffee	
10:30	Gene expression profiling; from computer to bedside	Monique den Boer
12:00	Lunch in Ae 4.06	
13:00	Practical: Sample size estimation	Maarten van Iterson, Elizabeth McClellan, Judith Boer
14:00	Coffee	
14:15	Assignment: Data analysis of ALL samples	Judith Boer, Leila Mohammadi Khankahdani, Elizabeth McClellan, Maarten van Iterson
15:45	Coffee	
16:00	Assignment: Data analysis of ALL samples, continued	Judith Boer, Leila Mohammadi Khankahdani, Elizabeth McClellan, Maarten van Iterson
17:30	End day 4	

<b>Day 5</b>	<b>Friday June 24: Databases and Pathways</b>	
	<b>Room: COO-5</b>	
	<b>Moderator: Andrew Stubbs</b>	
8:45	Welcome coffee	
9:00	Interpretation of gene lists	Kristina Hettne/Herman v Haagen
9:45	Databases and pathway analysis	Andrew Stubbs
10:30	Coffee	
11:00	Practical: Interpretation of gene lists Anni and DAVID; Databases and pathway analysis	Kristina Hettne/ Herman van Haagen; Andrew Stubbs
12:30	Lunch in Ae 4.06	
13:30	Presentation Cytoscape	Peter van Baarlen
15:45	Coffee	
16:00	Practical Cytoscape	Peter van Baarlen, Guido Hooiveld, Mark Boekschoten
17:00	End day 5: hand in evaluation form & badge!	

## **Attendance fees**

Course tuition for non-commercial participants is **€ 600**. Discounts are handled as followed:

- Participants from the postgraduate schools MolMed, MGC and other participating organisations (NBIC *t.b.c.*, CMSB *confirmed*) get a discount of **100%** (tuition = **€0**).
- Other Erasmus MC participants get a discount of **50%** (tuition = **€300**).
- PhD students, Master's students and Post docs, regardless of institution, get a discount of **50%** (tuition = **€300**).

The course is considered an entirety, and participants are encouraged to attend all parts of the course. No discounts are given for participants who chose not to participate in a portion of the course.

If these financial requirements pose a problem, please contact Frank van Vliet, managing director of the Erasmus Postgraduate School Mol Med, at: [f.vanvliet@erasmusmc.nl](mailto:f.vanvliet@erasmusmc.nl).

## **Invoices**

Fees should only be paid after receipt of an INVOICE. Shortly after your registration you will receive the INVOICE by mail. Payment should be transferred to account: 43.47.01.408 / Erasmus MC, (IBAN code bank: NL86ANBA0434701408; SWIFT code bank: ABNANL2A), with the invoice number noted. Late registrations may also pay in cash upon arrival.

## **Cancellations**

**Cancellation is possible up to one week before the start** of the Course. Later cancellation will not be accepted, but you are allowed to send a substitute.

## **Commercial participants & sponsors**

Companies are invited to inquire about commercial participant tuition fees and about sponsoring.

**We thank our sponsors:**



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