



Transcriptomics (28-30 Jan 2008)



DAY1 (afternoon)

Introduction

You will learn about different microarray applications,
Microarray technology: how is the field evolving?
High throughput sequencing techniques - digital
expression

Data storage

ArrayExpress

HANDS ON: ArrayExpress

DAY2 (morning)

Designing a microarray experiment

You will learn about: Experimental design; The statistics behind microarray;
Hypothesis testing; Array quality metrics; Normalisation; Introduction to
limma

HANDS ON: array quality, limma

DAY2 (afternoon)

Data analysis I

Overview of the principles and
methods for differentially expressed
genes identification: t-test; ANOVA;
False Discovery Rate; more on limma

*HANDS ON: Expression Profiler &
Bioconductor*

DAY3 (morning)

Data analysis II

Looking for biological patterns in the
data: Clustering; Principal Component
Analysis (PCA); Meta analysis; Gene set
analysis;

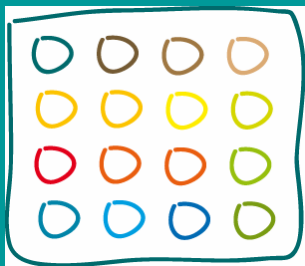
*HANDS ON: Expression Profiler &
Bioconductor*

DAY3 (afternoon)

Link to other EBI resources for gene
set analysis

Go & REACTOME





Transcriptomics course @ EBI (28-30 Jan 2008)

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The EMBL-EBI maintains the world's most comprehensive range of molecular databases. This course provides an introduction to Transcriptomics incorporating and using the related EBI resources and practicals, trainer-guided demonstration of when, why and how to use them.

Some of the trainers involved:



Gabriella Rustici is a research scientist in the Microarray Informatics group at the EBI and her research focuses on meta-analysis of microarray datasets. She is also involved in training activities and applies her experience to provide hands-on training in several resources including ArrayExpress and Expression Profiler.

David Croft is a bioinformatician and has been giving talks and training for the Reactome project since 2005. He is also involved in maintaining and updating the Reactome website. Prior to joining the EBI, he spent seven years in industry, designing bioinformatics and cheminformatics applications.

