



Data Analysis Workshop

An introductory course to GeneChip® Exon 1.0 ST and NGS microRNA data analysis

Further Information

For more information, please contact the course organizer:
Prof. Raffaele A. Calogero
Bioinformatics and Genomics
Unit, Molecular Biotechnology
Center, Via Nizza 52, 10126,
Torino Italy.
Tel. ++39 0116706457
Fax ++39 0116706487
Mobile ++39 3333827080
email:
raffaele.calogero@unito.it

Teaching Format

This course will include a series of theoretical sessions followed by practical exercises. This course will utilize open-source software. All software and hardware will be provided by the B&G.

Aims and Objectives

At the end of the course you will be able to:

- ✓ understand the importance of experimental design in order to ask sensible biological questions
- ✓ assess the quality of your data
- ✓ perform normalization and reformatting procedures
- ✓ complete basic statistical tests on GeneChip® Exon 1.0 ST array data and Next Generation Sequencing (NGS) data
- ✓ annotate and interpret your data and perform integration between gene-level expression and microRNA differential expression data.
- ✓ understand some of the problems encountered when analyzing data

Audience

This course is suitable for biologists who are new to exon arrays as well to Next Generation Sequencing technology. Additionally if you have analyzed gene expression data from Affymetrix® GeneChip® 3'IVT expression arrays and would now like to do projects using Exon 1.0 ST arrays, then this workshop will enable you to do data analysis at both the gene-level and exon-level. Knowledge of statistics is not necessary prior to attending the course.

Course Description

Tools for microarray and NGS data analysis

The course is based on the use of Affymetrix and Bioconductor open-source software solutions. However, R coding skill is not required since all the analyses are performed using oneChannelGUI, a graphical interface to Bioconductor tools, designed for life scientists who are not familiar with R language.

Experimental design

This section of the course discusses several criteria and principles of experiment design as well as related problems. Questions such as how many replicates one needs to detect differential gene/microRNA expression or alternative splicing events are addressed.

Quality control

This section will focus on Exon 1.0 ST array quality controls. Approaches to check the quality of raw microarray data will be presented as well as approaches to identify array artifacts. Approaches to experimental replicates will also be considered. All approaches will be practically tested on real data provided during the practical training sessions.

Normalization and data reformatting

This section concentrates on data preparation issues. The effect of normalization techniques on gene/exon-level analysis will be described. microRNA's NGS primary mapping tools will be described and their output

Instructor Credentials

Raffaele Calogero is

Associate Professor at Turin University and the P.I. of the Bioinformatics and Genomics unit. The Bioinformatics and Genomics unit (B&Gu) is a core facility to support researchers in multiplatform microarray experimental design, analysis and mining. Since 2002 he has led theoretical/practical training courses on microarray data analysis. In 2005 he was part of the training team at EMBO Practical Course on Functional Genomics (Milan, Italy) and in 2006 he led the Bioconductor training at MUGEN Gene Expression Profiling and Bioinformatics Course (Milan, Italy). In 2006-2007 he has taught in a series of Affymetrix pilot data analysis training courses in Europe/USA/Asia.

Remo Sanges has a Ph.D. in Computational Biology. He completed his Ph.D. in the Ensembl group at the EBI. Actually he is a researcher at Stazione Zoologica Anton Dohrn of Naples.

Francesca Cordero is a researcher of B&Gu. She has a degree in Biological Sciences and a PhD in Informatics.

Alessandro Davassi is the Affymetrix Field Application Specialist for Italy, responsible for training and technical support on all Affymetrix platforms. He has a wealth of experience in Bioinformatics and Data Analysis in several fields such as Forensic Science and Population Genetics.

will be reformatted to be uploaded in oneChannelGUI. Normalization and data reformatting will be applied to real data by the students.

Basic Statistics

This part will provide the biologist with a general overview on issues closely related to Exon 1.0 ST microarrays and NGS data. The purpose is to give only as much information as needed to be able to make an informed choice during the subsequent data analysis. The aim of the training module is to put things in the perspective of someone who analyzes gene/exon-level microarray data as well as NGS data, rather than offer a full treatment of the respective statistical notions and techniques. No previous statistical knowledge is assumed.

Selecting differentially regulated genes/microRNAs

This portion presents several methods used to select differentially regulated genes/microRNAs in comparative experiments. The advantages and disadvantages of all methods are discussed in detail.

Selecting alternative splicing events

This portion presents several approaches to identify alternative splicing events in a two group experiment. The advantages and disadvantages of all methods are discussed in detail.

Multiple testing

This section discusses issues related to the fact that microarrays interrogate a very large number of genes/exons simultaneously and its consequences regarding data analysis. This is a crucial aspect that changes the nature of the data analysis techniques used. Yet, this aspect is often neglected, although issues related to multiple testing can easily invalidate otherwise well-conceived experiments.

Biological interpretation

This session will deal with the relationship existing between microRNAs differential expression and their effects on putative target genes. The limits of bioinformatics identification of microRNAs gene-targets will be addressed as well as the improvement that can be obtained integrating gene expression data.

Practical sessions

The course is structured to provide practical analysis skill to the students. Datasets will be provided by B&Gu although students are welcome to bring their own data. Data provided by the organizers are based on cell lines experiments.

Dates Times and Locations

The GeneChip®Exon 1.0 ST & microRNA data analysis will last three full days, in February 2011.

Day 1 23rd February 9:30 – 17:00

Day 2 24th February 9.30 – 18:00

20:30 – 22.:00 Social dinner sponsored by B&Gu and Affymetrix

Day 3 25th February 10:00 – 17:30

Course Costs

The cost of the course is 600 Euros and includes all required materials, coffee breaks, lunches and the social dinner at Adriano Mesa restaurant (via Principe Amedeo 57 I - 10060 Frossasco)

AGENDA

DAY ONE			
09:30	10:00	Registration	
10:00	10:15	Course Introduction	RAC
10:15	11:15	Exon 1.0 ST arrays structure and QC with Expression Console (T)	AD
11:15	11:35	Break	
11:35	13:30	Exon 1.0 ST arrays structure and QC with Expression Console (E)	AD
13:00	14:00	Lunch	
14:00	15:00	oneChannelGUI introduction, data loading and normalization (T)	RAC
15:00	16:00	QC and data filtering at gene/exon-level (T)	RAC
16:00	16:15	Break	
16:15	17:00	Statistical detection and annotation at gene/exon-level(T)	RAC
DAY TWO			
09:30	10:30	Statistical detection and annotation at gene/exon-level (T)	RAC
10:30	11:00	Gene/Exon-level exercise session (E)	RAC/RS/FC
11:00	11:30	Break	
11:30	13:00	Gene/Exon-level exercise session (E)	RAC/RS/FC
13:00	14:00	Lunch	
14:00	16:00	Gene/Exon-level exercise session (E)	RAC/RS/FC
16:00	16:30	Break	
16:30	18:00	NGS primary mapping tools (T)	FC
	18:00	Back to Hotel	
	19:30	Bus pick-up at Piazza Carlo Felice	
20:30	22:30	Social dinner (sponsored by B&Gu and Affymetrix)	
DAY THREE			
09:30	10:30	microRNA secondary data analysis on oneChannelGUI	RAC
10:30	11:00	Break	
11:00	12:00	Statistical analysis of NGS data (T)	RAC
12:00	13:00	microRNA gene target detection (T)	RAC
13:00	14:00	Lunch	
14:00	15:30	microRNA exercise session (E).	RAC/RS/FC
15:30	16:00	Break	
16:00	17:00	microRNA exercise session (E).	RAC/RS/FC
17:00	17:30	End of the course	

(T: Theory; E: Exercises; RAC: Raffaele A. Calogero; RS: Remo Sanges; FC:

Venue Details

Aula Seminari, Centro di Biotecnologie Molecolari (MBC), Via Nizza 52 Torino, 10126 Italy.

Tel. ++39 0116706457

Fax ++39 0116706487

Mobile ++39 3333827080

email:

raffaele.calogero@unito.it

Travel Information

By Air (Torino Airport):

Torino International Airport receives flights from all of Europe

(<http://www.aeroporto.torino.it/IT/voli/default.php>). A taxi is approximately 40 Euros from the terminals to MBC (http://www.mbcunito.it/how_to_reach.php).

By train (Porta Nuova station):

Torino can be reached by train (<http://www.ferroviedellostatunito.it/>). A taxi is approximately 10 Euros from the station to the MBC.

By Car

See directions at:

http://www.mbcunito.it/how_to_reach.php

Meals and

Accommodation

Lunch and coffee breaks will be provided on all days for the duration of the course. In addition there will be a group dinner for all course attendees on 24th February 2011.

Participants will need to organize their own accommodation. You will be provided with hotel suggestion after course registration..

Francesca Cordero; AD: Alessandro Davassi)

How to Register

Course Registration

The course is limited to 15 participants.

Please complete the registration at

www.bioinformatica.unito.it/exon.array.course.html before **1st February 2011**

Once you have received confirmation of the availability of your seat, you will need to make a bank transfer of **600 Euros** to the course registration account:

Code for Italy

BANCA SELLA SPA

Agenzia di Rosta , Via Rivoli, 63 (TO) Italy

IBAN: IT 78 Z 03268 31260 052843266940

International code:

BBAN: Z 03268 31260 052843266940

When you specify the reason of this money transfer, please indicate:

EXONS2011

Please, send a proof of money transfer via email

(raffaele.calogero@unito.it) or fax (+39 0116706487)

Organized by:

UNIVERSITÀ
DEGLI STUDI
DI TORINO
ALMA UNIVERSITAS
TAURINENSIS



Sponsored by:

