RNA-seq Workshop

An introductory course to RNA-seq

(Torino 17th-19th March 2015)

Further Information

For more information, please contact the course organizer:

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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&Gu.

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
- ✓ complete basic statistical tests on 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 Next Generation Sequencing technology. Knowledge of statistics is not necessary prior to attending the course.

Course Description

Tools for RNA-seq data analysis

The course is based on the use of 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. Furthermore, RNAseq and miRNAseq analysis will be also performed using the apps available in BaseSpace (https://basespace.illumina.com/home/index)

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 RNA-seq quality controls. Approaches to check the quality of raw data will be presented as well as approaches to identify sequencing bias. Approaches to experimental replicates will also be considered. All approaches will be practically tested on real data provided during the practical training sessions.

Basic Statistics

This part will provide the biologist with a general overview on issues closely related to RNA-seq 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 RNA-seq data, rather than offer a full treatment of the respective statistical notions and techniques. No previous statistical knowledge is assumed.

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/RNA-seq experimental design, analysis and mining. Since 2002 he has led theoretical/practical training courses on microarray data analysis. Since 2008 he is part of the training team of the EMBL Whole transcriptome data analysis course (Heidelberg,DE)

Francesca Cordero is a researcher at Dept. of Computer Science, University of Torino. She has a degree in Biological Sciences and a PhD in Informatics. She is involved in NGS tools development.

Matteo Carrara is a Ph D student in Complex Systems in Life Sciences, University of Torino. Since 2011 he was part of the team of the Whole transcriptome data analysis course (Heidelberg, DE) and of various RNA-seq courses organized by B&Gu in 2012.

Chiara Del fiume is Marketing Technical Specialist Italy and Spain at Illumina

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 approaches to identify alternative splicing events in a two groups experiment. The advantages and disadvantages of all methods are discussed in detail.

Detecting fused transcripts

The discovery of novel gene fusions can lead to a better comprehension of cancer progression and development. RNAseq, has opened many opportunities for the identification of this class of genomic alterations, leading to the discovery of novel chimeric transcripts in melanomas, breast cancers and lymphomas. Nowadays, various computational approaches have been developed for the detection of chimeric transcripts. The advantages and disadvantages of these methods are discussed in detail.

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 skills to the students. Datasets will be provided by B&Gu. Data provided by the organizers are based on cell lines experiments.

Dates Times and Locations

The RNA-seq workshop will last two and half days, in March 2015.

Day 1 17th March 9:30 – 18:00
Day 2 18th March 9:30 – 18:00
20:30 – 22.:00 Social dinner sponsored by B&Gu
Day 3 19th March 10:00-16:00

Course Costs

The cost of the course is 500 Euros (**max 20 persons**)
A booklet with all presentations, coffee breaks, lunches and the social dinner are provided as part of the course.

AGENDA

DAY ONE			
08:30	08:45	Registration	
08:45	09:00	Course Introduction	RAC
09:00	10:00	About RNA-seq Illumina technology (T)	LS
10:00	11:00	RNA-seq libraries preparation (T)	CD
11:00	11:30	Coffe break.	
11:30	12:00	NGS primary mapping tools (T)	FC
12:00	12:30	mRNA-seq data analysis tools (T)	FC
12:30	13:00	About alternative splicing analysis with RNA-seq (T)	FC
13:00	14:00	Lunch	
14:00	14:30	mRNA-seq Fusion-detection approaches (T)	RAC
14:30	15:00	miRNA-seq data analysis pipe-line (T)	RAC
15.00	15.30	miRNA-seq: microRNA data analysis on oneChannelGUI (T) and on BaseSpace	RAC
15:30	16:30	microRNA exercise session (E)	
16:30	17:00	Coffe break	
17:00	18:00	microRNA gene target detection	RAC

DAY TWO			
09:30	10:30	microRNA exercise session (E)	
10:30	11:00	RNA-seq with oneChannelGUI (T) and BaseSpace	RAC
11:00	11:30	RNA-seq with oneChannelGUI/BaseSpace and differential gene expression (E)	
11:30	12:00	Break	
12:00	13:00	RNA-seq with oneChannelGUI gene fusion detection (E)	RAC
13:00	14:00	Lunch	
14:00	17:30	RNA-seq with oneChannelGUI exercises alternative splicing analysis (E)	
20:30:	22:00	Social dinner	

DAY TWO		
10:00	13:00	Free exercises
13:00	14:00	Lunch
14:00	15:45	Free exercises
:	16:00	Final remarks and Departure

(T: Theory; E: Exercises; RAC: Raffaele A. Calogero; FC: Francesca Cordero; CD: Chiara Delfiume)

Venue Details

Aula Seminari, Centro di Biotecnologie Molecolari (MBC), Via Nizza 52 Torino, 10126 Italy.
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Fax ++39 0112366457
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Travel Information

By Air (Torino Airport):

Torino International Airport receives flights from all of Europe (http://www.aeroportoditorino.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.ferroviedellostato.it/). Take underground, direction Lingotto, get out at Nizza station. MBC is 100 meters from the station.

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 18th March 2015. Participants will need to organize their own accommodation. You will be provided with hotel suggestion after course registration..

How to Register

Course Registration

The course is limited to 20 participants.
Please complete the registration at
www.bioinformatica.unito.it/RNAseq.course.html before **1st March 2015**
Once you have received confirmation of the availability of your seat, you can:

- make a credit card payment through the BITS online payment form: www.bioinformatics.it/index.php?mod=bitpos
  The 'Motivation' must be: RNAseq2015 <name surname> BITS member YES/NO
  In case you are a BITS member you are eligible to a 10% discount, i.e. 450 Euros

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  Take note of the code that is returned at the end of the procedure. This code is in the format BITS-NNNN, where NNNN is a four digit number

- pay the registration fee via bank transfer 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 credit card/money transfer, please indicate: **RNAseq2015**
Please, send a proof of credit card (i.e. BITS-NNNN code)/money transfer via email (raffaele.calogero@unito.it) or fax (++39 0112366457)

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