



Basic Next Generation Sequencing (NGS) procedures

15-16-17 giugno 2015

Sede: Università dell'Insubria, Via Alberto da Giussano 12, Busto Arsizio, Aula informatica
Orario delle lezioni: 9.30-16.30

Le lezioni sono a numero chiuso poiché si svolgono in aula informatica in parallelo ad esercitazioni pratiche.

Docenti: Cristina Cheroni, Riccardo Rossi, Istituto Nazionale di Genetica Molecolare - INGM, Milano

I giorno

- Introduction & overview of NGS (RNA and DNA sequencing)
- Sequencing technologies and platforms (3 generations, methods, main actors)
- Introduction to R and command line interface
- Basic R (*practical session*)

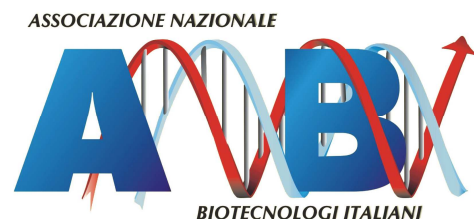
II giorno

- NGS data format (FASTA, FASTQ, SAM, BAM, GTF)
- RNASeq Analysis Workflow (Quality Control, Alignment, Gene expression quantification, Differential expression analysis)
- Software frameworks: NGS "basic toolkits" (Galaxy, Genepatterns)
- 101 on the interactive platform Galaxy (*practical session*)
- RNASeq Analysis Workflow in Galaxy (*practical session*)

III giorno

- RNASeq Analysis Workflow in R: Cummerbund and DeSeq2 (*practical session*)
- Exome sequencing workflow (alignment, SNP calling)
- ChIPSeq workflow - *optional* - (Alignment, Peak calling, downstream analyses)

Con il Patrocinio di:



CV docenti

Riccardo Lorenzo Rossi, PhD. Head of Computational Biology and Data Analysis, Fondazione Istituto Nazionale di Genetica Molecolare (INGM), Milano.

Riccardo L. Rossi graduated in biological sciences at the University of Milan with a thesis on budding yeast cell cycle, working on glucose mediated cell cycle regulation. He then obtained his PhD in Industrial Biotechnology at the University of Milano-Bicocca with a thesis on innovative flow cytometry-based multiparametric detection methods applied to budding yeast research and then working on systems biology approaches to cell cycle regulation. During a two year post doc period spent at the Department of Biochemistry of the University of Washington in Seattle, USA, he deepened his knowledge on metabolic transcriptional regulation of budding yeast.

Back in Italy in 2008, Riccardo moved to INGM where he approached molecular immunology, working on microRNA mediated regulatory transcriptional networks in human lymphocytes. He specialized in microRNA research, medium and high throughput gene and microRNA expression; he authored papers and an international patent on microRNAs as regulators and biomarkers. He currently coordinates a group of computational biologists and informaticians working on high throughput data - mainly transcriptomics, arrays and ngs - generated in the Institute; he and his colleagues are involved in an effort of introducing computational techniques in the realm of biological and clinical data trying to efficiently integrate them.

Cristina Cheroni, PhD. Bioinformatician, Computational Biology and Data Analysis Unit, Fondazione Istituto Nazionale di Genetica Molecolare (INGM), Milano.

Cristina Cheroni graduated in Pharmaceutical Biotechnology in 2002 at the University of Milan, discussing a thesis on alterations of the protein SOD1 in the neurodegenerative disorder amyotrophic lateral sclerosis. She completed the PhD in Life and Biomolecular Sciences in 2008 at Mario Negri Institute of Pharmacological Research (Milano, Italy), as sponsoring establishment of the Open University of London. The PhD project, conducted in the laboratory of Molecular Neurobiology, was focused on mechanisms of protein aggregation and ubiquitin-proteasome dysfunction in neurodegeneration.

Since 2008 she has been working at INGM, applying molecular biology and computational biology tools to study host and virus genetic variability in Hepatitis C Virus infection; she has been involved in the production and bioinformatics analysis of experimental data such as single nucleotide polymorphisms, copy number variations, mRNA and microRNA profiling, RNASeq profiling of the transcriptome. From 2012 she has joined the Computational Biology and Data Analysis Unit, focusing on the analysis of -omics datasets deriving from high-throughput platforms, especially Next Generation Sequencing technology (RNASeq for both coding and non-coding RNAs).

Come arrivare

In treno: raggiungere le stazioni di Busto Arsizio (da Milano Porta Garibaldi o Passante Ferroviario) o Busto Arsizio Nord (da Novara, Milano Cadorna, Milano Bovisa, Milano Centrale o Milano Porta Garibaldi).

Orari consultabili su <http://www.fsitaliane.it/>. Seguire le indicazioni della mappa; A: Stazione Busto Arsizio; B: sede della scuola; C: Stazione Busto Arsizio Nord.

In auto: uscire a Busto Arsizio (A8) o Marcallo Mesero (A4, poi superstrada per Malpensa e uscita Vanzaghello) e raggiungere il parcheggio di Piazzale dei Bersaglieri (non disponibile il giovedì e il sabato). Coordinate GPS 45.607621, 8.857178.

In aereo: per chi vola a Milano Linate è consigliabile raggiungere Milano Centrale e seguire le indicazioni per chi viaggia in treno. Percorrenza 65 minuti circa.

È consigliabile volare su Milano Malpensa e prendere il Malpensa Express dal Terminal 1 e scendere a Busto Arsizio Nord. Orari consultabili su www.trenord.it/. Percorrenza 9 minuti.



Indicazioni per il pernottamento:

A 10-15 minuti a piedi:

Hotel Ortensia (***) <http://www.hotelhortensia.it/>

Albergo Mazzini (**) 0331-631715 <http://www.paginegialle.it/albmazzini>

Raggiungibili solo con mezzo proprio:

Hotel MO.OM (****) <http://www.moomhotel.com/>

Hotel Pineta (****) <http://pineta.lerobinie.com/>

Modalità di partecipazione

Entro il 18 maggio 2015	Dopo il 18 maggio 2015
€ 280 +IVA*	€ 350 +IVA*

***In caso di esenzione IVA, allegare documentazione.**

Informazioni, [CONDIZIONI GENERALI](#) e modulo di iscrizione: www.afinubria.org.

Pagamento da effettuare con bonifico bancario **dopo la conferma dell'attivazione del corso** da parte della Segreteria Organizzativa:

Codice IBAN **IT23X0558450233000000000229**

CIN X

Beneficiario: D'Urso & Fanali S.r.l. - AFInubria

Causale: Nome Cognome Corso NGS giugno 2015

Segreteria scientifica e organizzativa:

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<http://www.afinubria.org>

