

COST workshop – Bari 2013

NGS and non-coding RNA Data Analysis

Programme

day 1 -17 April

09:00 – 09:20		Registration
09:20 – 09:30	Andreas Gisel , CNR – ITB, Bari Chair: Pasquale Saldarelli CNR – IVV, Bari	Welcome
09:30 – 10:10	Tamas Dalmay University of East Anglia, United Kingdom	Reducing ligation bias during sRNA library preparation
10:10 – 10:50	Jan Fiedler Medizinische Hochschule Hannover, Germany	Regulatory RNAs in the cardiovascular system
10:50 – 11:20	Coffee Break	
11:20 – 12:00	Jozsef Burgyan , Agricultural Biotechnology Center, Godollo, Hungary	Small RNAs in plant virus interaction
12:00 – 12:40	Alessandra Romanelli University of Naples “Federico II” and IC CNR Bari, Italy	PNA: applications and perspectives
12:40 – 14:30	Chair: Francesco Di Serio CNR – IVV, Bari	Lunch
14:30 – 15:10	Ricardo Flores UPV-CSIC, Valencia, Spain	Genesis and effects of the small RNAs derived from the minimal non-coding replicons: the viroids
15:10 – 15:30	David Dobnik National Institute of Biology, Slovenia	Small RNAs in potato-PVY interaction
15:30 – 16:10	Mick Watson ARK-Genomics, The Roslin Institute, United Kingdom	Bioinformatic analysis of small RNA data reveals novel biological insights
16:10 – 16:40		Coffee Break
16:40 – 17:20	Sébastien Pfeffer University of Strasbourg, France	microRNAs as key regulators in mammalian host-virus interactions
17:20 – 18:00	Noam Shomron Tel Aviv University, Israel	Information stored in small RNAs
20:00		Social Dinner

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day 2 -18 April

Presentations on bioinformatics approaches in ncRNA data analysis

09:00 – 09:10	Andreas Gisel CNR – ITB, Bari Chair: Domenica D’Elia CNR – ITB, Bari	Introduction
09:10 – 09:40	Graziano Pesole IBBE – CNR, Bari, Italy	High-throughput investigation of RNA editing in Amiotrophic Lateral Sclerosis
09:40 – 10:10	Marc Friedlander Centre for Genomic Regulation, Barcelona, Spain	Prediction and profiling of miRNAs from sRNA-seq data
10:10 – 10:40	Thomas J Hardcastle University of Cambridge, United Kingdom	Analyses of high-throughput sequencing data of siRNAs
10:40 – 11:10	Alfredo Pulvirenti University of Catania, Italy	Computational techniques for RNA-based gene regulation: Artificial miRNA design, miRNA targeting, miRNA Knowledge bases, and A-to-I RNA Editing
11:10 – 11:40		Coffee Break
11:40 – 12:10	Antonio Marco University of Manchester, United Kingdom	On the origin of microRNA clusters
12:10 – 12:40	Flavio Licciulli ITB – CNR, Bari, Italy	Database resources for ncRNA
12:40 – 14:00		Lunch
14:00 – 14:30	Artemis Hatzigeorgiou University of Thessaly, Greece	MiRNA targets in coding and non-coding genes characterised through NGS
14:30 – 17:30		Discussion sessions between biologists and bioinformaticians Creation of a ‘ncRNA network’

During the discussion session we will split in different groups. The groups should discuss the following topics:

- Interaction biologist – bioinformatician for the design of biological NGS experiments
- NGS Data analysis for the discovery of new ncRNAs – biological and bioinformatic point of view
- NGS Data analysis for ncRNA target search - biological and bioinformatic point of view
- Biological interpretation of NGS ncRNA data
- Development of NGS ncRNA data analysis workflows

The discussion should be summarized in a short text and presented to the whole workshop.

14:30 – 15:00 introduction and forming groups

15:00 – 16:00 discussion

16:00 – 16:30 coffee break

16:30 – 17:00 presentation of group discussions

17:00 – 18:00 final discussion and perspectives for the creation of the **ncRNA network** and conclusions