

Firenze, 18 Ottobre 2013 – Ex presidenza della Facoltà di Medicina

# Seconda giornata Toscana di Bioinformatica e Systems Biology

9:00 Registration and poster hang up

9:30 Opening remarks

Session 1: ALGORITHMS AND TOOLS

10:00 **StreamingTrim 1.0: a Java software for dynamic trimming of 16SrRNA sequence data from metagenetic studies**

Giovanni Bacci<sup>1,2</sup>, Marco Bazzicalupo<sup>1</sup>, Anna Benedetti<sup>2</sup>, Alessio Mengoni<sup>1\*</sup>

<sup>1</sup> Department of Biology, University of Florence (Combo – Florence Computational Biology Group).

<sup>2</sup> Agricultural Research Council /Research Centre for the Soil-Plant System (CRA-RPS)

10:30 **On efficient algorithms for the single individual haplotyping problem**

Loredana M. Genovese, Filippo Geraci, Marco Pellegrini

Istituto di Informatica e Telematica, CNR, Pisa

11:00 **Mobilomics in yeast**

Giulia Menconi

Dipartimento di Informatica, Università di Pisa

11:30–11:45 **Coffee Break**

11:45 **EXCAVATOR: detecting copy number variants from whole-exome sequencing data.**

Alberto Magi<sup>1</sup>, Lorenzo Tattini<sup>1</sup>, Romina D'Aurizio<sup>2</sup>, Gian Franco Gensini<sup>1</sup>.

<sup>1</sup> Dipartimento di Medicina Sperimentale e Clinica, Università di Firenze.

<sup>2</sup> Istituto di Informatica e Telematica, CNR, Pisa.

Session 2: MODELING

12:15 **Stochastic models in biology**

Duccio Fanelli e Francesca Di Patti

Dipartimento di Fisica e Astronomia, Università di Firenze

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**12:45 Identification of a branching process model for adaptive immune response**

Alessandro Boianelli, Elena Pettini, Gennaro Prota, Donata Medaglini, Antonio Vicino

Dip. di Ingegneria dell'Informazione e Scienze Matematiche, Università di Siena  
Dipartimento di Biotecnologie Mediche, Università di Siena

**13:15 – 14:30 Lunch**

Session 3: Cancer Applications

**14:30 Two topics of ongoing research in Pisa: identification of pathway components and model-based cancer therapies**

Paolo Milazzo

Dipartimento di Informatica, Università di Pisa

**15:00 Role of microRNAs–Transcription Factors Gene Regulatory Networks dynamics in the onset and progression of human genetic tumors: the neuroendocrine MEN1 syndrome as a model**

Ettore Luzi

Laboratory of Neuroendocrine Complex Diseases Center on Endocrine Hereditary Tumors, AOUC,  
Department of Surgery and Translational Medicine , University of Firenze

Session 4: Proteins

**15:30 Different protein folds require different amino acid composition of their cores**

Davide Alocci, Andrea Bernini, Pasquale Lista, Andrea Santarelli, Ottavia Spiga, Edoardo Morandi and Neri Niccolai

Department of Biotechnology, Chemistry and Pharmacy, University of Siena

**16:00 A gateway for the determination of the 3D structure of biological macromolecules**

Lucio Ferella, Andrea Giachetti, Antonio Rosato

Magnetic Resonance Center (CERM), University of Florence

**16:30–17:00 Coffee Break**

**17:00 Round Table: La bioinformatica in Toscana: Presente e Futuro**

**18:00 Closing Remarks**