

Workshop **Gruppo SIB Biologia Computazionale e dei Sistemi**

Bologna, 9 Luglio 2019
Laboratorio di Biocomputing, via San Giacomo 9/2, Bologna

Con la collaborazione di:
**Centro Interdipartimentale “Luigi Galvani” per Studi Integrati di Bioinformatica,
Biofisica e Biocomplexità - Università di Bologna**

- 10:15 – 10:30 Apertura: Pier Luigi Martelli
- 10:30 – 10:50 Allegra Via (IBPM CNR, Roma)
Open data, open software and reproducible research
- 10:50 – 11:10 Riccardo Percudani (Università di Parma)
From sequence to function and vice versa
- 11:10 – 11:30 Castrense Savojardo (Università di Bologna)
Inferring protein localization from sequence
- 11:30 – 11:50 *Coffee Break*
- 11:50 – 12:10 Veronica Morea (IBPM CNR, Roma)
Automation of the procedure to identify key-structural and functional residues in homologous protein structures
- 12:10 – 12:30 Giovanni Minervini (Università di Padova)
Insights into the molecular features of the von Hippel-Lindau like protein
- 12:30 – 12:50 Anna Marabotti (Università di Salerno)
Dealing with inborn error of metabolism to predict structural and functional features associated to protein variant
- 12:50 – 13:10 Marco Necci (Università di Padova)
DisProt: The database of protein disorder
- 13:10 – 14:20 Pranzo
- 14:20 – 14:40 Fabio Polticelli (Università Roma Tre)
Fragment-based ligand-protein contact statistics: application to docking simulation
- 14:40 – 15:00 Luana Licata (Università Tor Vergata, Roma)
Mint, Signor, Disnor
- 15:00 – 15:20 Marco Vanoni (Università Milano Bicocca)
Multi-scale modeling of cell growth and cell cycle in budding yeast
- 15:20 – 15:40 Davide Maspero (Università Milano Bicocca)
Integration of single cell transcriptomics data into metabolic models
- 15:40 – 16:00 *Coffee Break*
- 16:00 – 16:20 Marzia Di Filippo (Università Milano Bicocca)
*Computational pipeline for the semi-automatic reconstruction of the genome-scale metabolic model of the stress-tolerant hybrid yeast *Zygosaccharomyces parvii**
- 16:20 – 16:40 Francesco Raimondi (IEO, Milano)
Decoding and recoding onco-GPCR signaling by exploiting G-protein coupling information
- 16:40 – 17:00 Pasquale Palumbo (IASI CNR, Roma)
Noise propagation in enzymatic reaction networks