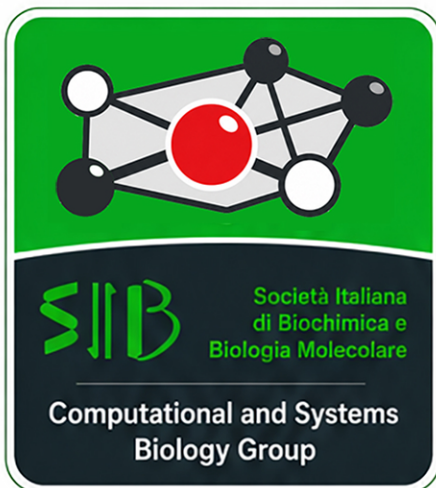




MEETING

OF THE COMPUTATIONAL AND SYSTEMS BIOLOGY GROUP

SIB BOLOGNA



OPENING REMARKS

10:00 – 10:10 | (CHAIR/ORGANIZER)

Welcome and Introduction to the Meeting

SESSION 1: SYSTEMS BIOLOGY, METABOLIC & CLINICAL TRANSLATION

Chair: Lara Console

TIME	SPEAKER	TITLE
10:10 – 10:25	Matteo Turati (University of Milano Bicocca)	Stability-Aware Parameter Identification for Generalized Lotka-Volterra Models
10:25 – 10:40	Pasquale Palumbo (University of Milano Bicocca)	Expanding the iMeGroCy Framework: Dynamic Nutrient Responses, Ribosome Biogenesis Modules, and Mammalian Cell Modeling
10:40 – 10:55	Bruno Giovanni Galuzzi (CNR, Milan)	Unveiling Spatial and Pathway-Level Metabolic Programs in Cancer Through Transcriptome-Guided Flux Analysis
10:55 – 11:10	Anna Visibelli (University of Siena)	Quantifying the Functional Gap in Alkaptonuria Through Machine Learning and Clinical Data Integration



COFFEE BREAK: 11:10 – 11:40 (30 minutes)

SESSION 2: MOLECULAR MECHANISMS, DYNAMICS & METABOLIC MODELING

Chair: Giulia Babbi

TIME	SPEAKER	TITLE
11:40 – 11:55	Alfonso Trezza (University of Siena)	Architecture and Dynamics of a Supramolecular Oxygen Transport System in Human Homogentisate 1,2-Dioxygenase
11:55 – 12:10	Miriana Quaranta (Sapienza University of Rome)	SLC25A38 Preferentially Transports Pyridoxal 5'-Phosphate over Glycine: A Computational Study
12:10 – 12:25	Lara Console (University of Calabria)	A Combined Computational Modeling and Proteoliposome Nanotechnology to Accelerate Ligand Discovery for Solute Carrier Transporters
12:25 – 12:40	Giovanni Merici (University of Parma)	Integrating Coevolutionary Analysis, Structural Prediction, and Molecular Dynamics for Complex Discovery
12:40 – 12:55	Davide Bianchi (University of Milan)	Computational Dissection of the Cooperative Effects of Fc Glycosylation and Light Chain Isotype on IgG1::FcγRIIIa Recognition



LUNCH BREAK: 13:00 – 14:00 (60 minutes)

SESSION 3: STRUCTURAL BIOINFORMATICS & PREDICTIVE TOOLS

Chair: Maria Cristina Aspromonte

TIME	SPEAKER	TITLE
14:00 – 14:15	Matteo Manfredi (University of Bologna)	Alpha&ESMhFolds: An Updated Database for the Comparison and Functional Annotation of Predicted Structural Models for the Human Proteome
14:15 – 14:30	Veronica Morea (CNR, Rome)	A Consensus-Based Framework for the Identification of Structurally Conserved Protein Regions
14:30 – 14:45	Damiano Parrone (Sapienza University of Rome)	A Prediction Tool for the Inference of Rare Misfolding Variants Responsive to Pharmacological Chaperones
14:45 – 15:00	Alessandra Robello (Sapienza University of Rome)	Computational Framework for the Design of Second-Generation Pharmacochaperones Targeting Allosteric Pockets
15:00 – 15:15	Sol Clara Begue (University of Padova)	Towards RING 5.0: An Updated Tool for the Analysis of Protein Structures Through Residue Interaction Networks



COFFEE BREAK: 15:15 – 15:45 (30 minutes)

SESSION 4: GENE AND VARIANT PRIORITIZATION FOR GENOME INTERPRETATION

Chair: Alfonso Trezza

TIME	SPEAKER	TITLE
15:45 – 16:00	Alessia Pinto (University of Tor Vergata)	Complex Genotype-Phenotype Correlations in Autism Spectrum Disorder: A Systems Biology Approach
16:00 – 16:15	Chiara Rivi (University of Bologna)	Mapping the Neurodevelopmental Disorder Gene Landscape: From Data Integration to Multi-Ontology Candidate Prioritization
16:15 – 16:30	Maria Cristina Aspromonte (University of Padova)	Localized Missense Constraint Reveals Functional Regions in Intrinsically Disordered Proteins Associated with Neurodevelopmental Disorders
16:30 – 16:45	Giulia Babbi (University of Bologna)	Bioinformatic Sweeties: A Suite of User-Friendly Bioinformatic Tools for Characterizing Proteins and Their Variants



CLOSING REMARKS

16:45 – 16:55 | (CHAIR/ORGANIZER)

Summary and Closing of the Meeting



JUNE
16
2026



10:00 – 17:00



ACCADEMIA
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