

27 June

08:00 - 9:00	Registration and poster hang-up
09:00 - 10:30	Workshop - Bioinformatics for unraveling brain complexity (part I) LINK
10:30 - 11:00	Coffee break - Poster session
11:00 - 12:30	Workshop - Bioinformatics for unraveling brain complexity (part II)
12:30 - 12:45	CINI InfoLife Presentation
12:45 - 13:50	Lunch - Poster session - Registration
13:50 - 14:15	Opening remarks - Raffaele Calogero , President of BITS - Roberto Giacobazzi , Pro-rector of University of Verona

Session 1 - Multi-omics data analysis and integration

chair(s) TBD

14:15 - 15:00	BITS-Preparata Lecture - Giorgio Valle Bioinformatics and Informational Biology: two different cakes from the same basic ingredients
15:00 - 15:45	ChiaraDamiani Knowledge-based multi-omics data integration to unveil the many facets of metabolic variation and regulation FedericaChiappori Host-gut microbiota cross-talk in autism via microbiota, mycobiota and small ncRNAs EttoreMosca Integrative analysis of multiple omics and interactomes to find key mechanisms underlying disease activity in the early phases of Multiple Sclerosis
15:45 - 16:00	RSG-Italia Presentation
16:00 - 16:30	Invited Talk - Vincenzo Bronte Novel therapeutics: from cancer to severe Covid-19
16:30 - 17:00	Coffee break - Poster Session
17:00 - 19:00	BITS members meeting
19:30	YOUNG BITS Event

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Session 2 - Molecular Evolution analysis

chair(s) TBD

09:00 - 09:45	Invited speaker - Esti Yeger-Lotem Predicting molecular mechanisms of hereditary diseases by using their tissue-specific manifestation
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09:45 - 10:30 DavideMarnetto
Ancestral genomic contributions to complex traits in contemporary Europeans

FerdinandoFiumara
Amino acid repeat length co-evolution in neural proteins

Pier FedericoGherardini
Identification of RNA modules in human lncRNAs

10:30 - 11:00 Coffee break - Poster Session

Session 3 - Algorithms for Bioinformatics

chair(s) TBD

11:00 - 11:30 Invited Talk - **Massimo Delledonne**
De novo genome assembly across multiple species

11:30 - 12:45 BenedettoPolimeni
IRescue: single cell uncertainty-aware quantification of transposable elements expression

GiorgioValentini
Right Normalized Laplacian improves the performance of Node2Vec embedding for edge prediction in STRING PPI Graphs

AtzeniRossano
A novel affordable and reliable framework for accurate detection and comprehensive analysis of somatic mutations in cancer.

AndreasGisel
3-Tag RNA-sequencing

Zahrasadat Alavikakhki
Metabolite identification in tandem MS untargeted metabolomics studies

12:45 - 13:00 Presentation of BITS 2023

13:00 - 14:15 Lunch - Poster session - Registration

Session 4 - Computational transcriptomics and RNA data analysis

chair(s) TBD

14:15 - 15:00 Invited Speaker - **Francesco Iorio**
Optimisation and drug-discovery oriented analyses of CRISPR screens

15:00 - 15:15 SIBIM Presentation

15:15 - 16:30 LorenzoFranchitti
A computational pipeline for functional analysis of alternative splicing events

SimoneAvesani
A new space-based method for downstream analysis of spatial transcriptomics data

ValentinaLorenzi
Not all fetal gonadal macrophages are alike: a tale of three phenotypes

LuigiMansi
REDIportal: the RNA editing comprehensive catalog

DanieleMercatelli
Detection of pan-cancer surface protein biomarkers via a network-based approach on transcriptomics data

Session 5 - Drug and therapies discovery

16:30 - 17:00	Coffee break - Poster Session
17:00 - 17:30	Invited Talk - Aldo Scarpa The International Cancer Genome Consortium
17:30 - 18:00	SimonePernice GreatNector: a new perspective on personalized drug therapy for MS patients
	DeborahGiordano Molecular docking simulations for the screening of putative ligands of SARS-CoV-2 proteins
18:00 - 19:30	Social Activities
20:00	Social Dinner

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Session 6 - Metagenomics

chair(s) TBD

09:00 - 09:45	Invited Speaker - Erik Garrison Genomes from many frames of reference
09:45- 10:30	GrazianoPesole New challenges in shotgun metagenomics with kMetaShot
	MatteoComin Refined Classification of Metagenomic Long reads with Overlap Graphs
	MatteoCalgaro benchdamic: benchmarking of differential abundance methods for microbiome data
10:30 - 11:00	Coffee break - Poster Session

Session 7 - Artificial intelligence in biology and medicine

chair(s) TBD

11:00 - 12:30	<p>Mikele Milia Simulate personalized tumor microenvironment evolution through a hybrid Multi-Agent Spatio-Temporal model informed by sequencing data</p> <p>Silvia Cascianelli Machine learning to discover genes predictive of RAS-mutated cases in mutational profiles of colorectal cancer patients</p> <p>Monica Bianchini Drug side-effect prediction with Graph Neural Networks</p> <p>Marco Cappellato From microbial community model to interaction networks</p> <p>Enrico Blanzieri The direction of causation: inferring directed relationships by post-processing causal gene networks discovered from omics data.</p> <p>Vincenzo Bonnici A systematic evaluation of computational tools for gene-oriented pangenome detection in fragmented genomes.</p>
12:30 - 13:00	Invited Talk - Carlo Combi
13:00 - 14:00	Lunch - Poster session
14:00 - 14:30	Invited Speaker - Anna Monreale Explainable AI for healthcare

Young BITS-RSG Symposium

chair(s) TBD

14:30 - 17:00	<p>Young BITS-RSG Symposium</p> <p>LINK</p>
17:00 - 17:30	Coffee break - Poster Session
17:30 - 19:00	CINI InfoLife Meeting