Program

27 June

08:00 - 09:00	Registration

Workshop - Bioinformatics for unraveling brain complexity
chair(s) **N. Vitulo, A. Giorgetti**

09:00 - 10:30	Workshop - Bioinformatics for unraveling brain complexity (part I)[link](link)
10:30 - 11:00	Coffee break - Poster session
11:00 - 12:00	Workshop - Bioinformatics for unraveling brain complexity (part II)
12:00 - 12:15	CINI InfoLife Presentation
12:15 - 13:45	Lunch - Poster session - Registration
13:45 - 14:15	Opening remarks - **Raffaele Calogero**, President of BITS - **Roberto Giacobazzi**, Pro-rector of University of Verona
14:15 - 15:00	**Giorgio Valle** BITS-PREPARATA LECTURE *Bioinformatics and Informational Biology: two different cakes from the same basic ingredients*

Metagenomics
chair(s) **TBD**

15:00	Matteo Calgaro *benchdamic: benchmarking of differential abundance methods for microbiome data*
15:15	Matteo Comin *Refined Classification of Metagenomic Long reads with Overlap Graphs*
15:30	Graziano Pesole *New challenges in shotgun metagenomics with kMetaShot*
15:45 - 16:00	RSG-Italia Presentation
16:00 - 16:30	**Vincenzo Bronte** INVITED TALK *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

28 June

09:00 - 09:45	**Esti Yeger-Lotem** INVITED SPEAKER

Predicting molecular mechanisms of hereditary diseases by using their tissue-specific manifestation

Molecular Evolution analysis
chair(s) **TBD**

09:45	Davide Marnetto *Ancestral genomic contributions to complex traits in contemporary Europeans*
10:00	Ferdinando Fiumara *Amino acid repeat length co-evolution in neural proteins*
10:15	Pier Federico Gherardini *Identification of RNA modules in human lncRNAs*
10:30 - 11:00	Coffee break - Poster Session
11:00 - 11:30	**Massimo Delledonne** INVITED TALK *De novo genome assembly across multiple species*

Algorithms for Bioinformatics
chair(s) **TBD**

11:30	Benedetto Polimeni *IRescue: single cell uncertainty-aware quantification of transposable elements expression*
11:45	Giorgio Valentini *Right Normalized Laplacian improves the performance of Node2Vec embedding for edge prediction in STRING PPI Graphs*
12:00	Rossano Atzeni *A novel affordable and reliable framework for accurate detection and comprehensive analysis of somatic mutations in cancer.*
12:15	Andreas Gisel *3'-Tag RNA-sequencing*
12:30	Zahrasadat Alavikakhki *Metabolite identification in tandem MS untargeted metabolomics studies*
12:45 - 13:00	Presentation of BITS 2023
13:00 - 13:15	SIBIM Presentation
13:15 - 14:30	Lunch - Poster session - Registration
14:30 - 15:15	**Francesco Iorio** INVITED SPEAKER *Optimisation and drug-discovery oriented analyses of CRISPR screens*

Computational transcriptomics and RNA data analysis
chair(s)

15:15	Lorenzo Franchitti *A computational pipeline for functional analysis of alternative splicing events*
15:30	Simone Avesani

	A new space-based method for downstream analysis of spatial transcriptomics data
15:45	Valentina Lorenzi
	Not all fetal gonadal macrophages are alike: a tale of three phenotypes
16:00	Luigi Mansi
	REDIportal: the RNA editing comprehensive catalog
16:15	Daniele Mercatelli
	Detection of pan-cancer surface protein biomarkers via a network-based approach on transcriptomics data
16:30 - 17:00	Coffee break - Poster Session
17:00 - 17:30	**Aldo Scarpa** INVITED TALK
	The International Cancer Genome Consortium

Drug and therapies discovery
chair(s) **TBD**

17:30	Simone Pernice
	GreatNector: a new perspective on personalized drug therapy for MS patients
17:45	Deborah Giordano
	Molecular docking simulations for the screening of putative ligands of SARS-CoV-2 proteins
18:00 - 19:30	Social Activities
20:00	Social Dinner

29 June

09:00 - 09:45	**Erik Garrison** INVITED SPEAKER
	Genomes from many frames of reference

Multi-omics data analysis and integration
chair(s) **TBD**

09:45	Federica Chiappori
	Host–gut microbiota cross-talk in autism via microbiota, mycobiota and small ncRNAs
10:00	Ettore Mosca
	Integrative analysis of multiple omics and interactomes to find key mechanisms underlying disease activity in the early phases of Multiple Sclerosis
10:15	Chiara Damiani
	Knowledge-based multi-omics data integration to unveil the many facets of metabolic variation and regulation
10:30 - 11:00	Coffee break - Poster Session

Artificial intelligence in biology and medicine
chair(s) **TBD**

11:00	**Mikele Milia**
	Simulate personalized tumor microenvironment evolution through a hybrid Multi-Agent Spatio-Temporal model informed by sequencing data
11:15	**Silvia Cascianelli**
	Machine learning to discover genes predictive of RAS-mutated cases in mutational profiles of colorectal cancer patients
11:30	**Monica Bianchini**
	Drug side-effect prediction with Graph Neural Networks
11:45	**Marco Cappellato**
	From microbial community model to interaction networks
12:00	**Enrico Blanzieri**
	The direction of causation: inferring directed relationships by post-processing causal gene networks discovered from omics data.
12:15	**Manuel Mangoni**
	A systematic evaluation of computational tools for gene-oriented pangenome detection in fragmented genomes.
12:30 - 13:00	**Carlo Combi** INVITED TALK
	Challenges and data-oriented perspectives in explainable AI in Medicine
13:00 - 14:00	Lunch - Poster session
14:00 - 14:30	**Anna Monreale** INVITED SPEAKER
	Explainable AI for healthcare
14:30 - 14:45	Closing remarks

Young BITS-RSG Symposium
chair(s) **TBD**

14:45 - 17:15	Young BITS-RSG Symposium [link](#)
17:15 - 17:45	Coffee break - Poster Session
17:45 - 19:00	CINI InfoLife Meeting