

# BITS2023 Poster List

21-23 June 2023, Bari

Session	Position	ID	Topic	Name	Surname	Title
1	1	626	Algorithms for Bioinformatics	marianna	milano	MultiLoaL- A New Local Alignment Algorithm for Multilayer Networks
1	2	628	Algorithms for Bioinformatics	Rossano	Atzeni	VariantAlert: a web service to notify updates in genetic variant annotations
1	3	632	Algorithms for Bioinformatics	Pietro	Cinaglia	Serverless computing for parallel alignment of RNA-Seq reads
1	4	640	Algorithms for Bioinformatics	Fabio	Lauria	Ribosome positioning at single nucleotide resolution with riboWaltz: the case of Spinal Muscular Atrophy
1	5	642	Algorithms for Bioinformatics	Giulia	Calia	LEAF: a machine learning approach to predict effector proteins in Candidatus Phytoplasma
1	6	646	Algorithms for Bioinformatics	Lorraine	Ayad	Seedability: Optimising alignment parameters for sensitive sequence comparison
1	7	669	Algorithms for Bioinformatics	Giacomo	Baruzzo	mopo16Sweb: a cloud-based app for multi-objective optimization of bacterial 16S PCR primers
1	8	686	Algorithms for Bioinformatics	Adriano	Fonzino	Detecting C-to-U RNA editing by direct RNA sequencing
1	9	696	Algorithms for Bioinformatics	Giulio	Caravagna	A Bayesian model to deconvolve mutational signatures in a semi-supervised way.
1	10	707	Algorithms for Bioinformatics	Giulia	Calia	MOOnSTER: a novel method to identify and score clusters of motifs in protein sequences (CLUMPs) based on amino acids physicochemical properties
1	11	712	Algorithms for Bioinformatics	Giovanni	Micale	MUTClass: a mutation-based system to robustly classify cancer patients
1	12	715	Algorithms for Bioinformatics	GRAZIA	GARGANO	An NMF-based approach to identify differentially expressed genes in microarray and RNA-seq data
1	13	723	Bioimaging	Matteo	Gravina	Radiogenomic Framework to Predict Mutational Status of KRAS and EGFR from Computed Tomography Scans of Lung Adenocarcinoma
1	14	693	Food & Nutrition	Lorella	Bottino	Towards a nutritional profile of individuals: nutritional, metabolic and nutrigenomic data, and related bioinformatic methods
1	15	655	Genomics, transcriptomics, epigenomics and epitranscriptomics	Ugo	Ala	Small-RNA molecules regulatory network and their role as genomic biomarkers for Vitamin D3 response in patients with Covid-19 and Inflammatory Bowel Disease.
1	16	668	Genomics, transcriptomics, epigenomics and epitranscriptomics	Silvia	Rotunno	Identification of Arundo donax L. microRNAs and their targets using high-throughput sequencing and degradome analysis
1	17	672	Genomics, transcriptomics, epigenomics and epitranscriptomics	Letizia	Messa	Computer-based approaches for the identification of new biomarkers and treatment of neurodegenerative disorders
1	18	678	Genomics, transcriptomics, epigenomics and epitranscriptomics	Pasquale Luca	Curci	Transcriptional reprogramming during biostimulant-plant-pathogen interaction
1	19	705	Genomics, transcriptomics, epigenomics and epitranscriptomics	Sharon Natasha	Cox	Development of a workflow for the identification of mito-nuclear variants in Amyotrophic Lateral Sclerosis patients from Whole Genome and Exome Sequencing data
1	20	706	Genomics, transcriptomics, epigenomics and epitranscriptomics	Ilenia	Urso	Optimizing Cas9 Targeted Sequencing for the Identification of Unknown Integration Sites
1	21	710	Genomics, transcriptomics, epigenomics and epitranscriptomics	Roberta	Zeloni	Unraveling the Neandertal impact on brain morphology through multivariate regression
1	22	716	Genomics, transcriptomics, epigenomics and epitranscriptomics	Davide	Marnetto	Prehistoric ancestries consistently associated to the complex trait landscape in European Biobanks
1	23	726	Genomics, transcriptomics, epigenomics and epitranscriptomics	Donato	Magista'	Comparative genomic analysis and secretome profiling of Penicillium species isolated from cured meat products
1	24	721	Proteomics	Gabriele	Tomè	ProTN: an integrative pipeline for extensive analysis of proteomics data from Mass Spectrometry
1	25	641	Structural Bioinformatics	Anna	Marabotti	The importance of glycans in the interaction between the human CD147 receptor and the meningococcal Tfp: a computational study
1	26	657	Structural Bioinformatics	Marin	Matic	Dissecting the sequence and structure determinants of GPCR - Gprotein selectivity via structural bioinformatics and machine learning
1	27	660	Structural Bioinformatics	Anna	Marabotti	The effects of the galactosemia-associated variant p.Q188R on global structural features and activity of GALT enzyme investigated by molecular dynamics simulations
1	28	663	Structural Bioinformatics	Alessandro	Ricci	Role of SL1, SL2 (5UTR) in Sars coronavirus 2 RNA translation
1	29	709	Structural Bioinformatics	Tommaso	Mazza	Pyntacle-MD: Harnessing the Power of Parallel Computing for Large-Scale Network Analysis of Molecular Dynamics Simulations
1	30	714	Structural Bioinformatics	Romina	Oliva	Nanobody-Protein Antigen Interfaces: Deriving and Analysing a Representative Dataset
4	34	749	Structural Bioinformatics	Paolo	Milazzo	In-silico study of amino acid mutations on protein-ligand interactions
1	32	720	Structural Bioinformatics	Federica	Chiappori	Effect of disease-linked mutations on long-chain fatty acid Acyl-CoA dehydrogenases, ACAD9 and VLCAD, structures
1	33	689	Systems Biology	Alice	Chiodi	Quantification of intra-cellular and inter-cellular cross-talks: case studies on breast cancer.
1	34	701	Systems Biology	Francesca	Cordero	From small to Great: a new computational workflow for data analysis and modelization
1	35	718	Systems Biology	Simone	Tomè	Gene co-expression network analysis for identifying cell populations in RNA-seq patient derived xenografts
1	36	725	Systems Biology	Toma	Tebaldi	Towards the discovery of causal relationships among the entire human genome: the expanded network of SARS-CoV-2 host interactors
1	37	727	Algorithms for Bioinformatics	Sachithra Kalhari	Yaddehige	An Innovative Tool for the Analysis and Interpretation of Genomic Content and Information Metrics from GBFF Files
2	1	629	Artificial Intelligence for Bioinformatics	Vincenzo	Bonnici	A machine learning approach to predict bacterial phenotypic patterns by means of fragment length distribution fingerprints
2	2	670	Artificial Intelligence for Bioinformatics	Carolina	Testa	Non-Negative Matrix Tri-Factorization based method for the Inference of Synthetically Lethal Pairs involving Metastatic Genes
2	3	688	Artificial Intelligence for Bioinformatics	Pier Luigi	Martelli	Deep Learning and protein embedding at the Bologna Biocomputing Group
2	4	700	Artificial Intelligence for Bioinformatics	Sofia	Mongardi	Adapting feature selection in gene expression-based classification for higher biological interpretability
2	5	703	Artificial Intelligence for Bioinformatics	Silvia	Cascianelli	Machine learning for multi-label subtyping: a key to dissecting intra-tumor heterogeneity at the bulk sample level.
2	6	724	Artificial Intelligence for Bioinformatics	Vitoantonio	Bevilacqua	Explainable Artificial Intelligence revealing novel prognostic genes to predict early progressors of Diffuse Large B-Cell Lymphoma from a set of 1075 patients
2	7	638	Biological data management	Giorgia	Mazzotti	CLsquared: a CLeaning and CLustering tool for viral genomic data
2	8	665	Biological data management	Andrea	Manconi	The infrastructure supporting the Italian node of BBMRI-ERIC (BBMRI.it)
2	9	713	Biological data management	Giuseppe	Defazio	Exome sequencing data management and variant filtering in azoospermic and testicular germ cell tumor patients
2	10	644	Computational RNA biology	Ivan	Molineris	3plex enables deep computational investigation of triplex forming lncRNAs
2	11	674	Computational RNA biology	Simone	Avesani	A novel pipeline for the detection and reconstruction of circular RNAs post-transcriptional regulatory interaction networks
2	12	681	Computational RNA biology	Barbara	Puccio	A pipeline proposal for RNA-seq data analysis
2	13	704	Computational RNA biology	Alessandro	Palma	Integration of transcriptomic data to dissect the role of long non coding RNAs in amyotrophic lateral sclerosis
2	14	711	Computational RNA biology	Christian	Ramirez Amarilla	SnoMatchR: Identification of Candidate snoRNAs for Newly-Discovered 2-O-methylations
2	15	647	Metagenomics and metatranscriptomics	Giuseppe	Defazio	The healthy control landscape of the human gut microbiota by using ITS1 DNA metabarcoding data

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2	16	648	Metagenomics and metatranscriptomics	Renaud	Van Damme	MUFFIN 2.0, a metagenomics and metatranscriptomics pipeline for Nanopore and Illumina data.
2	17	673	Metagenomics and metatranscriptomics	Davide	Corà	A comparison of two metagenomics pipelines for the identification of expressed species involved in the gut dysbiosis from a mouse model of Alzheimers disease
2	18	684	Metagenomics and metatranscriptomics	Bruno	Fosso	Unsupervised investigation of the relationship among respiratory microbiome and Sars-Cov-2 infection.
2	19	685	Metagenomics and metatranscriptomics	Francesca	De Leo	LIMS and cloud computing for running state of the art and reproducible NGS protocols
2	20	699	Metagenomics and metatranscriptomics	Samuele	Cancellieri	Investigating the genetic basis of the oral microbiome composition and function
2	21	722	Metagenomics and metatranscriptomics	Giacomo	Baruzzo	From microbial ground truth network simulation to inference method benchmark
2	22	708	Molecular Evolution	Yari	Cerruti	A Population Genetics perspective on the regulatory function of transposable elements in the human genome
2	23	633	Multi-omics data analysis and integration	Gionmattia	Carancini	RiboSeq.Org Data Portal: unified access to processed and standardised ribosome profiling data and metainformation
2	24	634	Multi-omics data analysis and integration	Mingming	Lu	TWAS Atlas: a curated knowledgebase of transcriptome-wide association studies
2	25	636	Multi-omics data analysis and integration	Massimo	Guazzini	INTEVINE: Multi-omics data integration to decode the interaction between soil and grapevine
2	26	656	Multi-omics data analysis and integration	Dario	Righelli	Differential Accessible Regions analysis of single-cell 10X Genomics multiome data
2	27	664	Multi-omics data analysis and integration	Barbara	Di Camillo	Data-driven meta-simulation of realistic tumoral samples
2	28	695	Multi-omics data analysis and integration	Alfredo	Pulvirenti	tRFUniverse: a comprehensive resource for the interactive analyses of tRNA-derived ncRNAs in human cancer
2	29	697	Multi-omics data analysis and integration	Romina	Appierdo	A Feature-based Meta-analysis Approach to Unravel the Pathophysiological Landscape of Autoimmune Diseases
2	30	630	Translational Bioinformatics	Matteo	Pallocca	The ACC-Reporter: a Clinical Bioinformatics Framework for Multicentric Genomics-Driven Clinical Trials
2	31	692	Translational Bioinformatics	Simona	De Summa	A routinely-applicable tool to identify Consensus Molecular Subtypes in colon cancer
2	32	637	Young BITS-RSG-InfoLife Symposium	Daniel	Puttini	Extension of the statistical and computational framework COTAN to compute a new similarity index per cell pair in scRNA-Seq data
2	33	667	Young BITS-RSG-InfoLife Symposium	Graziano	Pesole	Prediction of the gut microbiome health through a machine-learning based integrative omics data analysis.
2	34	682	Young BITS-RSG-InfoLife Symposium	Laura	Fiorenza	Transcriptional analysis of the synergism between simvastatin and valproic acid with chemotherapy in metastatic pancreatic adenocarcinoma
2	35	717	Young BITS-RSG-InfoLife Symposium	Elena	Abbatangelo	Transcriptomic analysis of natural killer (iNKT) and T lymphocytes CAR-T cells obtained by different interleukin treatments
2	36	729	Translational Bioinformatics	Claudio	Isella	Multi-label transcriptional classification of colorectal cancer reflects tumor cell population heterogeneity
2	37	728	Single-cell data analysis	Federico	Giorgi	Alcohol-intoxicated mouse models of Alzheimers disease under the single-celloscope: towards histologically accurate understanding of neurocognitive impairment.
2	38	679	Machine Learning applications for microbiome data analysis	Pierfrancesco	Novielli	Explainable Artificial Intelligence (XAI) for Microbiome Data Analysis in Colorectal Cancer Diagnosis