Giacomo Baruzzo, Ph.D.

Curriculum Vitae

Department of Information Engineering
Università Degli Studi di Padova
Via Gradenigo 6/b
35131, Padova, Italy

Email: giacomo.baruzzo@unipd.it
Website: https://www.dei.unipd.it/~baruzzog/

Summary

My scientific activity is in the bioinformatics and computational biology domain, and my research is aimed at developing efficient algorithms, methods and software for the preprocessing, mining, analysis and interpretation of biological data from high-throughput sequencing technologies (omics data).

I'm currently Assistant Professor (RTT, SSD IINF-05/A) at the Department of Information Engineering of the University of Padova, where I am the senior researcher in the *SysBioBig - Systems Biology and Bioinformatics Group* lead by Prof. Barbara Di Camillo.

During my Ph.D. I spent a semester studying at the University of Pennsylvania, being visiting PhD student in the bioinformatics group led by Prof. Gregory Grant, working on algorithms and methods for sequence alignment (NGS read alignment). During my PostDoc, I had a short mobility period at the Faculty of Computer and Information Science, University of Ljubljana, working on missing data imputation (zero-imputation of single cell transcriptomic data) in Prof. Blaž Zupan research group.

During my research activity, I have been involved in several national (e.g. PNRR, PON, FISA) and international (e.g. Horizon Europe, REACT-EU) research projects in the field of bioinformatics, computational biology and high performance computing. I've also been awarded a research grant in support of innovative and excellent research projects (Italian B senior research grant) for my individual research project "*Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems*" at the Department of Information Engineering, University of Padova.

I have authored 20 scientific articles published in international peer-reviewed journals (19 research articles and 1 commentary article). I've also promoted my research in 25 national and international scientific events through 56 conference contributions (27 abstract+poster, 6 abstract+poster+oral, 17 abstract+oral, 5 shortarticle+oral, 1 article+oral). I've delivered 11 oral presentations at national and international conferences, and I have been invited as speaker at one international workshop. Reported here are the main bibliometric performance indicators of my scientific output (data from Google Scholar, Scopus and Web of Science WOS, April 1, 2025):

- Citations: 907 (Google Scholar), 512 (Scopus), 460 (WoS)
- H-index: 11 (Google Scholar), 9 (Scopus), 9 (WoS)

I've been involved in the organization of 14 national and international scientific events (conferences, workshops and tutorials) serving in different roles (e.g. session chair, organizing committee co-chair / member, scientific committee co-chair / member, program committee member). I've been awarded of the best talk award at MSCX 2023, best paper awards at PDP 2025 (HPCMS track), and I was selected for travel fellowship at BITS 2023.

I constantly perform peer-review activities for scientific journals and conferences. I served as a reviewer for 13 different international peer-review journals and 6 different national and international conferences. I served as proceeding editor for an IEEE conference and as Guest Editor for BMC Medical Informatics and Decision Making. I'm currently serving as Guest Editor of 2 international journal special issues (Spinger Lecture Notes In Bioinformatics, BMC Bioinformatics).

I am co-founder and co-director of the CINI Young-InfoLife group, and associate member of the Italian Bioinformatics Society (BITS).
I am involved in University of Padova third mission' actions mainly to through contracts with private and public institutions (2 contracts of more than 6 months each), and dissemination activities (e.g. scientific divulgation event with private enterprises, recording of science pills about how computer science can be used to understand and model biological processes).

My educational activities at the University of Padova includes teaching activities in PhD Program, Master Degree courses (Italian disciplinary scientific areas SSD IINF-05/A, INFO-01/A, IBIO-01/A, most with responsibility of the course) and II level University Master. I've served as supervisor or co-supervisor for 9 PhD students (PhD Course in Information Engineering: 4 completed, 5 ongoing), 19 Master Degree students' thesis (Computer Engineering, Bioengineering and Molecular Biology) and 7 Bachelor Degree students' thesis (Information Engineering and Biomedical Engineering) at the University of Padova.

Education

January 2014-
December 2016

PhD in Information Engineering

Ph.D. Course in Information Engineering, XXIX series

Department of Information Engineering, University of Padova, Padova, Italy.

Thesis: "Improving the RNA-Seq analysis pipeline: read alignment and expression level quantification".

Advisor: Prof. Barbara Di Camillo

Research area: Bioinformatics on high-throughput sequencing data (RNA-Seq)

October 2011-
October 2013

Master degree in Computer Engineering, 110/110

Department of Information Engineering, University of Padova, Padova, Italy.

Thesis: "A maximum likelihood approach to genome assembly."

Advisor: Prof. Gianfranco Bilardi

Research area: Parallel computing, High Performance Computing, Bioinformatics on high-throughput sequencing data (DNA-Seq)

October 2008-
September 2011

Bachelor degree in Information Engineering, 100/110

Department of Information Engineering, University of Padova, Padova, Italy.

September 2003-
June 2008

Maturità tecnico-scientifica indirizzo informatica, 100 e lode

Istituto Tecnico Industriale Statale "F. Severi", Padova, Italy

Research experiences and academic appointments

March 2025-Present
Assistant Professor (Ricercatori Legge 240/10 - t.det. RTT IINF-05/A)
Department of Information Engineering, University of Padova, Padova, Italy.
Research area: Bioinformatics, data mining and computational modeling on omics data

January 2022-March 2025
Postdoctoral research fellow (Ricercatori Legge 240/10 - t.det. tipo A)
Department of Information Engineering, University of Padova, Padova, Italy.
Research project: *“Environmental Antimicrobial Resistance Load Tackling via Intelligent Systems (EARLIeSt)". REACT EU–PON “Ricerca e Innovazione 2014-2020” - DM 1062/2021*
Research area: Bioinformatics, data mining and computational modeling on omics data

November 2020-December 2021
Senior postdoctoral researcher
Department of Information Engineering, University of Padova, Padova, Italy.
Research project: *“Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems”*
Research area: Bioinformatics, data mining and computational modeling on omics data
Supervisor: Prof. Barbara Di Camillo

October 2017-October 2020
Junior postdoctoral researcher
Department of Information Engineering, University of Padova, Padova, Italy.
Research project: DEI PROACTIVE 2017 – Single Cell "*From Single-Cell to Multi-Cells Information Systems Analysis*"
Research area: Bioinformatics, data mining and computational modeling on omics data
Supervisor: Prof. Barbara Di Camillo

March 2019-April 2019
Visiting postdoctoral researcher
Bioinformatics Laboratory, Faculty of Computer and Information Science, University of Ljubljana, Ljubljana, Slovenia.
Research project: 1° Session of the Italian – Slovenian Joint Commission on Scientific and Technological Cooperation. *“Computational and data visualization approaches to mining of large-scale data in single-cell genomics”*
Research area: Bioinformatics and data preprocessing for omics data
Temporary advisor: Prof. Blaž Zupan

January 2017-September 2017
Junior postdoctoral researcher
Department of Information Engineering, University of Padova, Padova, Italy.
Research project: BIOBIG - “*Analisi di Big Data in Bioinformatica*”
Research area: Bioinformatics and data mining applied to omics data
Supervisor: Prof. Barbara Di Camillo

June 2015-December 2015
Visiting Ph.D. student
Bioinformatics group, Institute for Translational Medicine and Therapeutics, University of Pennsylvania, Philadelphia, USA.
Research area: Bioinformatics and sequence alignment applied to omics data
Temporary advisor: Prof. Gregory R. Grant

Funding from competitive grant programs

~ 50.000 € (including taxes)

24 months research grant (*Assegno di ricerca Senior Tipo B*) Nov 2020 – Oct 2022
“Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems”
Department of Information Engineering, University of Padova, Padova, Italy.

~ 60.000 € (including taxes)

24+12 months research grant (*Assegno di ricerca Tipo A*) Oct 2017 – Sep 2020
DEI PROACTIVE 2017 "*From Single-Cell to Multi-Cells Information Systems Analysis*"
Department of Information Engineering, University of Padova, Padova, Italy.

~ 25.500 € (including taxes)

16 months research grant (*Assegno di ricerca Tipo A*) Jan 2017 – Apr 2018
Actual length: 9 months (~14.400 € including taxes) Jan 2017 – Sep 2017
BIOBIG - “*Analisi di Big Data in Bioinformatica*”,
Department of Information Engineering, University of Padova, Padova, Italy.

~ 45.000 € (including taxes)

Fully-funded 3-years PhD scholarship (*Borsa di Ateneo*) Jan 2014 – Dec 2016
Ph.D. Course in Information Engineering, XXIX series
Department of Information Engineering, University of Padova, Padova, Italy.

Funding from contracts

9.600 €

Contract with “CORIS - Consorzio per la Ricerca Sanitaria“ (Regione Veneto) 2022/23

Project: “Enhancement of contact tracing by strengthening the role of the Prevention Departments in the area, even relating to condition of greater susceptibility to adverse consequences of the infection (behavioural risk factors, chronic deseases and multi-morbidity, odl age, etc..)”. Centro Nazionale per la prevezione e il controllo delle malattie – Ministero della salute; 3.250.000 € funded project.

Contract activities: design and implementation of an informatics platform for contract tracing and the related software documentation

Role: contract PI, supervision of a research fellow. Contract length: 6 months

12.000 € + VAT

Contract with “Fondazione Malattie del Sangue Onlus” 2022/23

Project: “Studio di geni candidati nel rischio di progressione di pazienti IgM MGUS in Waldenström's Macroglobulinemia e analisi di geni e pathways di pazienti con leucemia mieloide cronica alla diagnosi e dopo terapia con nilotinib”.

Contract activities: design and implementation of reproducible bioinformatics analysis and data mining pipelines for microarray data

Role: contract co-PI. Contract length: 12 months

Fellowships, Prizes and Awards

Best paper award

At **33rd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing** (PDP 2025), 12-14 March 2025, Torino, Italy. Article title: *“quickSparseM: a library for memory- and time-efficient computation on large, sparse matrices with application to omics data”*. Best paper of the track *High Performance Computing in Modelling and Simulation.*

Best talk award

At 8th **Mediterranean School of Complex Networks** (MSCX 2023), 25-30 June 2023, Catania, Italy. Talk title: *“Bioinformatics for complex biological systems: unraveling cell-cell and bacterial interactions”*

Best performing teams (3°rd place)

At “*Metagenomics Diagnosis for Inflammatory Bowel Disease Challenge (MEDIC) – sub challenge 2*” for the bioinformatic pre-processing and classification/prediction of Inflammatory Bowel Disease status from metagenomic sequencing data, **sbv IMPROVER Computational Challenge series 2019-2020** [data mining and machine learning challenge]

Travel Fellowship

19th Annual Meeting of the Bioinformatics Italian Society (BITS) 2023

Participation to funded research projects

2024-present **PNRR D.M. 630/2024 project “*Computational methods and network science approaches to infer and analyze bacteria interactions from microbiome sequencing data*” founded by PNRR (Missione 4, componente 2 “Dalla Ricerca all'Impresa” – Investimento 3.3)**

Role: Principal Investigator, Scientific Coordinator.

2024-present **Horizon Europe project “HetERogeneous sEmantic Data integratIon for the guT-bRain interplaY” funded by European Union (grant no. 101137074).** Principal investigator: Gianmaria Silvello, Manfredo Aztori, University of Padova.

Role: Collaborator.

2023-present **PNRR Centro Nazionale di Ricerca in High Performance Computing, Big Data e Quantum Computing (Project no. CN00000013 – CN1).**

Role: External collaborator.

2023-present **European Regional Development Fund (ERDF) project “*CONVECS – ComuNità Veneta per il Calcolo Scientifico*” funded by European Union / Regione Veneto FESR 2021-2027.** Principal Investigator: University of Padova.

Role: Head of the “Teaching and HPC community” committee, member of the “Access policies and co-financing” committee, member of the “Focus Group HPC”, member of the “Expert Group HPC”, grant proposal co-writer.

2022-present **PON “Ricerca e Innovazione 2014-2020” (DM 1062/2021) project “*Environmental Antimicrobial Resistance Load Tackling via Intelligent Systems (EARLIeSt)*" funded by REACT EU.** Principal Investigator: Barbara Di Camillo, University of Padova.

Role: Lead researcher.

2020-2022 **Senior Research Grant (Assegno di ricerca Senior - Tipo B): “*Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems*” funded by Department of Information Engineering, University of Padova.**

Role: Principal investigator, lead researcher, grant proposal writer.

2018-2020 **1° Session of the Italian – Slovenian Joint Commission on Scientific and Technological Cooperation: “*Computational and data visualization approaches to mining of large-scale data in single-cell genomics*” funded by Italian Ministry of Foreign Affairs and International Cooperation and Slovenian Ministry of Education, Science and Sport.** Principal investigator: Blaž Zupan, University of Ljubljana, and Barbara Di Camillo, University of Padova.

Role: Collaborator.

2017-2020 **Proactive Project Grant (C92F17003530005): “*From Single-Cell to Multi-Cells Information Systems Analysis*” funded by Department of Information Engineering, University of Padova.** Principal investigator: Barbara Di Camillo, University of Padova.

Role: Collaborator, grant proposal co-writer.

2017-present **Ateneo Strategic Research Infrastructure Grant: “*CAPRI: Calcolo ad Alte Prestazioni per la Ricerca e l’Innovazione*” funded by University of Padova.** Principal investigator: Barbara Di Camillo, University of Padova.

Role: Member of the Management committee, member of the Technical committee, collaborator, grant proposal co-writer.

2017-2018 **“*BioBIG – Analisi di Big Data in Bioinformatica*” funded by Department of Information Engineering, University of Padova.** Principal investigator: Barbara Di Camillo, University of Padova.

Role: Collaborator.

Research activities

2022-present

Computational modelling of cancer-specific variants and simulation of sequencing data

The aim of this project is to simulate realistic tumoral samples (mutated genomes and the corresponding sequencing reads), to be used in the assessment of variant calling software. The developed simulator (MOV&RSim) can simulate biological aspects (e.g., variant characteristics, clonality, contamination) and technical noise (e.g., sequencing errors, coverage, base qualities) typical of real data, learning such characteristics from the existing sequencing data and cancer samples databases. MOV&RSim has been implemented R, Python, and C and released as Docker container.

Role: contributed to the design of the simulation framework and software; co-coordination of the project.

Related research project: *National Center for HPC, BIG DATA AND QUANTUM COMPUTING (CN00000013)*

Scientific output: [C28][C31][C42][C45]

2019-present

Bioinformatics methods for the analysis of cell-cell communication from scRNA-seq data

The focus of this project is developing novel bioinformatics methods to infer cell-cell communication from large scale single cell RNA-seq data. The developed method (scSeqComm) uses statistical modeling and network science tools (e.g. Personalized Page Rank algorithm) to robustly identify intercellular signaling, quantify intracellular communication and automatically annotate the ongoing biological processes. The tool is developed in R/C++ and it uses a shared memory programming model to support parallel execution and reduce the memory footprint. The tool provides also interactive dashboard for results filtering and visualization.

Role: writing of the research proposal (Senior grant - Type B); lead the design and implementation of the methodology and the software; co-coordination of project activities.

Related research projects: *"Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems"* (PI: Giacomo Baruzzo) and "*DEI PROACTIVE 2017*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J12] [J18] [C15] [C16] [C19] [C24] [C29] [C30] [C32] [C35] [C38] [C40] [C41] [C43] [C46] [C47] [C54]

2019-present

Simulation and identification of bacterial interaction graphs from 16S metagenomic data

The focus of this project is studying reverse engineering (network inference) methods to infer biological networks from metagenomics data. First, a complete review of current state of the art methodologies for inferring microbial community networks from 16S data was conducted, including approaches for cross-sectional and longitudinal studies. Bioinformatics methods based on pairwise metrics, network topology, regression, probability theory, and (Bayesian) graphical model were reviewed. Moreover, the available approaches to simulate synthetic microbial community networks and the main assessment metrics were described. A novel Python simulation framework to generate in-silico bacterial network based on resource consumption/competition and *Microbial Consumer Resource Model* (MiCRM) has been developed in the N2SIMBA package (released also as Docker container).

Role: review of network inference approaches, network simulation procedures and assessment metrics; support to the development of the simulation framework; co-coordination of project activities.

Related research projects: *"Environmental Antimicrobial Resistance Load Tackling via Intelligent Systems (EARLIeSt)"* (PI: Giacomo Baruzzo) and "*tRajectoriEs of baCtErial NeTwoRks from hEalthy to disease state and back (RECENTRE)*" (PI: Barbara Di Camillo, University of Padova).

Scientific output: [J8] [C18] [C21] [C26] [C34] [C35] [C44] [C48] [C50] [C53] [C55]

Other: one co-supervised **PhD Thesis in Information Engineering** (M. Cappellato, XXXV series)

2018-present

Computational tools for missing data imputation in single cell RNA sequencing data

The focus of this project is creating joint research activity between Italian and Slovenian research groups. The research topic of this project is the development of computational and data visualization tools for the analysis of large-scale single cell data. More specifically, the project is focused on bioinformatics methods for missing data imputation (zero-imputation) in single cell RNA-seq data.

Role: co-writing of the research proposal; temporary mobility actions defined by the project; study and assessment of zero-imputation (missing data) methods for single cell data.

Related research project: "*Computational and data visualization approaches to mining of large-scale data in single-cell genomics - 1° Session of the Italian – Slovenian Joint Commission on Scientific and Technological Cooperation. Priority area: Information and Communication Technology*" (PI: Blaž Zupan, University of Ljubljana, and Barbara Di Camillo, University of Padova) and "*DEI PROACTIVE 2017*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: G. Baruzzo and P. Poličar, M. Stražar, P. Godec, A. Kovačič, B. Di Camillo, B. Zupan, "*Computational Approaches for Single-Cell RNA-seq Data Imputation*" (manuscript under preparation)

2018-2023

Simulation of cancer progression and tumor microenvironment using a multi agent model

The aim of this project is the development of a simulation model of the spatio-temporal interaction of cancer cells and immune system cells. A multi-agent based spatio-temporal model has been used as core model, for its ability to simulate complex systems of different types of cells, stochastic behavior, and interaction among cells. Partial differential equations are used to model nutrients diffusion from vessels within the tissue. A Python/Fortran software has been implemented (released also as Docker container), which provides a graphics interface emulating histological images of the tumor evolution.

Role: design of the multi-agent based spatio-temporal model; contribution to software development.

Related research project: *"Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems"* (PI: Giacomo Baruzzo) and "*DEI PROACTIVE 2017*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J15] [C8] [C10] [C20] [C23] [C27] [C36]

2017-present Bioinformatics methods for the preprocessing and analysis of 16S metagenomic data

The aims of this project are the development of an accurate modelling/simulation of 16S count data, the assessment of current bioinformatics preprocessing/analysis pipelines, and the development of new computational methods for the mining of omics data. The developed simulation model uses an innovative Gamma-Multivariate Hypergeometric modelling, able to capture the high level of sparsity typical of 16S data, and it was implemented in the R/C++ package metaSPARSim. Data produced by the proposed simulator were used to assess the performance of i) 35 bioinformatics preprocessing pipelines, investigating for the first time ever the role of missing data imputation in 16S data analysis, and ii) 9 biomarker discovery methods (i.e. differential abundance methods).

Role: definition of simulation model; contribution to the design and implementation of the simulation software; contribution to the definition and implementation of missing data imputation pipelines and assessment metrics; contribution to the definition of the benchmarking framework for biomarker discovery methods.

Related research project: "*Environmental Antimicrobial Resistance Load Tackling via Intelligent Systems (EARLIeSt)*" (PI: Giacomo Baruzzo) and "*DEI PROACTIVE 2017*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J7] [J13] [J14] [C13] [C14] [C17] [C22] [C25] [C37]

Other: two co-supervised **PhD Thesis in Information Engineering** (I. Patuzzi, XXXI series; M. Cappellato, XXXV series)

2017-present Multi-objective optimization of primer sequences

The aim of this project is to develop automated methods to design and update bacterial 16S primers sequences, able to consider new sequencing technologies with different sequence (read) length and growing available information about different bacterial species from public databases. The developed method exploited a multi-objective optimization technique, and it was implemented in a multithreading C++ bioinformatics tool. The multi-objective optimization tools was also extended to handle ITS1 sequences, through the design and development of a web-based Galaxy bioinformatics enviroment. The developed web platform included several DNA metabarcoding computationl analysis pipelines and tools, and it integrated high quality ITS1 sequences from existing databases in a FAIR-compliant way.

Role: contribution to the definition of the multi-objective optimization algorithm; contribution to the design and implementation of the software; implementation of the C++ multithreading version; extension of the multi-objective optimization framework to handle ITS1 sequencing primers; contribution to the integration of the developed method into the web-based Galaxy cloud enviroment.

Related research project: "*BIOBIG*" (PI: Barbara Di Camillo, University of Padova), "*LIFEWATCH*"(FP7); "*ELIXIR-EXCELERATE*"(H2020) (PI: Monica Santamaria, CNR)

Scientific output: [J4] [J10] [C33] [C39]

2019-2023 Machine learning techniques for the diagnosis of Inflammatory Bowel Disease from metagenomics data

The project is aimed to investigate the diagnostic potential of metagenomics data to classify patients with Inflammatory Bowel Disease, Ulcerative Colitis, Crohn's Disease and healthy subjects. Several bioinformatics preprocessing approaches, feature selection techniques (i.e. Randomized Logistic Regression and Recursive Feature Elimination) and classification models (i.e. Support Vector Machine, Random Forest and Adaboost) were tested and combined to predict subject labels. The proposed approach was submitted to the *Metagenomics Diagnosis for Inflammatory Bowel Disease Challenge* (sbv IMPROVER 2019-2020).

Role: design of bioinformatics pre-processing pipeline for metagenomic data; contribution to the feature selection and classification steps.

Scientific output: [J17]

Other: Best performing teams (3°rd place) at "*Metagenomics Diagnosis for Inflammatory Bowel Disease Challenge (MEDIC) – sub challenge 2*", sbv IMPROVER Computational Challenge series 2019-2020

2018-2023 Simulation of cancer progression and tumor microenvironment using a multi agent model

The aim of this project is the development of a simulation model of the spatio-temporal interaction of cancer cells and immune system cells. A multi-agent based spatio-temporal model has been used as core model, for its ability to simulate complex systems of different types of cells, stochastic behavior, and interaction among cells. Partial differential equations are used to model nutrients diffusion from vessels within the tissue. A Python/Fortran software has been implemented (released also as Docker container), which provides a graphics interface emulating histological images of the tumor evolution.

Role: design of the multi-agent based spatio-temporal model; contribution to software development.

Related research project: *"Development of single cell RNA-seq bioinformatics methods and tools to study cell-cell communication and spatio-temporal evolution of multi-cells systems"* (PI: Giacomo Baruzzo) and "*DEI PROACTIVE*

2017" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J15] [C8] [C10] [C20] [C23] [C27] [C36]

2018-2021

Bioinformatics pipelines for the analysis of Chronic myeloid leukemia patients' data

The aim of this project is the identification of important genes and signal pathways involved in the treatment of Chronic myeloid leukemia (CML) with Nilotinib. In this project, 87 CML patients were enrolled from 15 centers in Italy, monitoring their gene expression changes induced by the Nilotinib treatment. The developed bioinformatics pipeline included the following steps: quality control, denoising, batch effect removal, biomarker discovery.

Role: design and implementation of ad-hoc bioinformatics analysis pipeline for patient data.

Related research project: "*PhilosoPhi34 study - EudraCT: 2012-005062-34*" (PI: Alessandra Trojani and Ester Pungolino, Division of Hematology, ASST Grande Ospedale Metropolitano Niguarda, Milano, Italy)

Scientific output: [J5] [J11] [JA1] [JA2] [JA3]

2018-2020

2-Dimensional spatial mapping of cells from single-cell sequencing data

The aim of this project is the development of computational methods for the spatial mapping of single-cell RNA-seq data. The developed computational method exploits a reverse engineering approach and a linear regression model to identify the most informative features in the dataset, and then exploits a data quantization approach together with a similarity measure (i.e. cosine similarity) between scRNA-seq data and in situ data to perform the mapping. The proposed method was also submitted to the 2018 DREAM "Single Cell Transcriptomics Challenge".

Role: definition of the 2D spatial mapping algorithm; design and implementation of the software.

Related research project: "*DEI PROACTIVE 2017*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J9]

2018-2020

Single cells RNA-seq compositional count data modeling and simulation

The aim of this research project is the development of novel scRNA-seq count data modelling and its implementation into count matrix simulators. The developed simulation model uses an innovative Gamma-Multivariate Hypergeometric modelling, able to describe both the biological and technical variability typical of scRNA-seq data, including data sparsity and compositionality. The simulation model has been implemented in a R/C++ package (SPARSim) and compared with state-of-the-art scRNA-seq data simulators, showing comparable or better simulation accuracy and lower computational burden.

Role: definition of the simulation model; design and implementation of the software; definition of assessment metrics.

Related research project: "*DEI PROACTIVE 2017*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J6] [C5] [C6] [C7] [C9] [C11] [C12]

2017

Computational methods for marker genes discovery in single-cell RNA-seq data

The aim of this project was the identification of robust bioinformatics differential expression (DE) analysis methods on single cell RNA-seq data. Several statistical frameworks (generalized linear hurdle model, generalized additive model, Negative Binomial – Poisson Mixture model, Cramér-von Mises, likelihood ratio test, Kolmogorov-Smirnov test and Anderson-Darling) were evaluated on real and simulated data.

Role: definition of assessment metrics and identification of test datasets; design and implementation of the bioinformatics analysis.

Related research project: "*BIOBIG*" (PI: Barbara Di Camillo, University of Padova)

Scientific output: [J2] [C4]

2014-2017

Sequence alignment methods for RNA-seq data (NGS read) and their impact on bioinformatics analyses accuracy

The aim of this project was to perform a comprehensive assessment of splice aware (i.e. long gap) sequence alignment methods and provide useful suggestion for the development of novel alignment algorithm and heuristics, and the development of robust analysis pipelines. A total of 14 read aligners were assessed on synthetic data from *H.sapiens* and *P.falciparum* genome, collecting several assessment metrics and statistics. The assessment framework was also extended to splice unaware alignment methods, including the study of the effects on the accuracy of common downstream analysis such as gene expression level quantification. A total of 4 Burrow Wheeler Transform - based aligners were assessed on synthetic data from *S.Cerevisiae*. For each of four alignment pipelines, expression level quantification accuracy was measured using several assessment metrics, on both real and simulated data. Finally, the combined effect of different bioinformatics analysis pipelines, including RNA-seq read alignment, and sequencing platforms (Illumina and Ion Torrent) was investigated to study how they affect the accuracy of a common downstream analysis such as differential gene expression.

Role: study of aligners algorithms and data structures; definition of alignment procedures; investigation of alignment parameters; development of alignment scripts; definition of assessment scenarios; analysis of alignment results; definition expression level quantification metrics; analysis of expression level quantification results.

Principal Investigator: Gregory Grant, University of Pennsylvania; Barbara Di Camillo, University of Padova

Scientific output: [J1] [J3] [J16] [JC1] [C1] [C2] [C3]

Other: PhD Thesis G. Baruzzo, “*Improving the RNA-Seq analysis pipeline: read alignment and expression level quantification*”, **PhD Course in Information Engineering, XXIX series**, Department of Information Engineering, University of Padova

Institutional and management activities

2023-present

CONVECS (COmuNità Veneta per il Calcolo Scientifico)

The aim of this project is to support research and innovation in the Veneto region through the acquisition and management of a High Performance Computing (HPC) infrastructure at regional scale for the development of advanced computational models and analytics, encouraging synergies across research institutions, and developing a HPC community in the Veneto region. The consortium includes the University of Padova (leader), the National Institute of Nuclear Physics (INFN – Padova and Legnaro), the University of Verona, the Ca’ Foscari University of Venice, and Università IUAV di Venezia.

Role: co-writing of the research proposal (definition of the user community and science cases, definition of the HPC infrastructure characteristics, definition of the access policy and estimation of budget); lead of the “Teaching and HPC community” committee; member of the following commitees: “Access policies and co-financing”, “Focus Group HPC” and “Expert Group HPC”.

Related research project: *ComuNità Veneta per il Calcolo Scientifico (CONVECS) - FESR 2021-2017* [Budget: 16M€]

Output: CONVECS HPC infrastructure (https://convecs.it/)

2022-present

CINI Young-InfoLife

The CINI Young-InfoLife group was founded in 2022 and it aims to provide a platform for students, PhD candidates, and young researchers in the field of computer science and computer engineering who are involved in the topics covered by the CINI (Consorzio Interuniversitario Nazionale di Informatica) National InfoLife Laboratory. CINI Young-InfoLife fosters networking and training for its members through various initiatives, including organizing events and conferences, delivering courses and seminars, sharing opportunities (theses, projects, conferences, job positions, etc.), disseminating scientific content, and more. In the highly interdisciplinary field of bioinformatics, CINI Young-InfoLife stands out from similar initiatives due to its strong methodological and computational focus. Currently, the CINI Young InfoLife laboratory has almost 80 members from 29 Italian Universities and Research Institutions.

Role: co-founder and co-director of the CINI Young-InfoLife group; coordination and management of laboratory activities (networking, training, dissemination, research)

Output: CINI Young InfoLife laboratory (https://younginfolife.github.io/)

2017-present

CAPRI (Calcolo Avanzato Per la Ricerca e l’Innovazione)

The aim of this project is the acquisition and management of a High Performance Computing (HPC) infrastructure for the students and researchers of the University of Padova, together with the spread of HPC in research and innovation. The project is supported by 16 Departments of the University of Padova (including the Department of Information Engineering) and the National Institute of Nuclear Physics (INFN – Padova and Legnaro).

Role: co-writing of the research proposal (definition of the user community and science cases, definition of the HPC infrastructure characteristics, definition of the access policy and estimation of budget); member of the Management committee; member of the Technical committee; organization of training courses for users and PhD students.

Related research project: CAPRI (Calcolo Avanzato Per la Ricerca e l’Innovazione) – Bando Infrastrutture Strategiche di ricerca 2017, University of Padova [Budget: 330K€]

Output: CAPRI HPC infrastructure (https://capri.dei.unipd.it/)

Membership

Member	Association for Computing Machinery (ACM)
Member	Institute of Electrical and Electronics Engineers (IEEE)
Member	International Society of Computational Biology (ISCB)
Associate Member	Bioinformatics Italian Society (BITS)
Co-founder and co-director	Young-InfoLife group, InfoLife National Laboratory of CINI

Articles summary and bibliometrics (April 1, 2025)

Number of articles in international peer-reviewed journals	20 (19 research articles, 1 commentary article)
Number of conference contributions	56 (1 full-article +oral, 5 short-article +oral, 27 abstract+poster, 6 abstract+poster+oral, 17 abstract+oral)
Total number of journal articles citations	including self-citations: • 512 (Scopus) • 460 (WoS) • 907 (Google Scholar) excluding self-citations: • 500 (Scopus) • 448 (WoS) • 895 (Google Scholar)
Citations sources (not exhaustive list)	Bioinformatics, BMC Bioinformatics, Briefings in Bioinformatics, Bioinformatics Advances, PLOS ONE Computational Biology, Journal of Computational Biology, Computational and Structural Biotechnology Journal, NAR Genomics and Bioinformatics, Genome Biology, Nucleic Acids Research, Scientific Reports, Cell Systems, Cell Reports, Cell Steam Cell, Science, Nature, Nature Biotechnology, Nature Methods, Nature Communications, Nature Protocols, Nature Reviews Molecular Cell Biology, Nature Review Materials, Nature Review Genetics, Nature Immunology, PLOS ONE, GigaScience, IEEE/ACM conference proceedings, IEEE Journal of Biomedical and Health Informatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Lecture Notes in Computer Science, International Journal of Foundations of Computer Science, International Journal of Parallel Computing, International Journal of Parallel Programming, Computers in Biology and Medicine, Knowledge-Based Systems, Neural Computing and Applications
h-index	• 9 (Scopus) • 9 (WoS) • 11 (Google Scholar)
Scopus ID	57192312589
WoS ID	AAE-5962-2022
Google Scholar ID	hSVdrbwAAAAJ
ORCID ID	0000-0001-6129-5007

Submitted or under review contributions

Journal article — M. Baldan, G. Baruzzo, A. Rossato, M. Cappellato, B. Di Camillo, *"N2SIMBA: from Network topology to SIMulation of interactions and BActerial abundance, using microbial consumer resource model"*
BMC Bioinformatics / BMC Supplements [2° review round, minor revision – May 11, 2024]

Journal article — G. Cesaro, G. Baruzzo, G. Tussardi, B. Di Camillo, *"Differential cellular communication inference framework for large-scale single-cell RNA-sequencing data"*
NAR Genomics and Bioinformatics [1° review round: February 21, 2025]

Scientific publications in international peer-reviewed journals/conferences

Journal article [J1]

G. Baruzzo and K. Hayer, E. Ji Kim, B. Di Camillo, G. Fitzgerald, G. Grant, *"Simulation-based comprehensive benchmarking of RNA-seq aligners"*
Nature Methods, Dec 2016, 14(2):135–139. (DOI: 10.1038/nmeth.4106) [Scimago Q1]
Contributions: conceptualization; literature review; methodology; software; data analysis and interpretation; manuscript writing
Main computer science contributions: definition of sequence alignment procedures; investigation of alignment parameters; development of alignment scripts; definition of sequence alignment assessment metrics

Journal article [J2]

A. Dal Molin, G. Baruzzo, B. Di Camillo, *"Single-cell RNA-sequencing: assessment of differential expression analysis methods"*
Frontiers in Genetics, May 2017, 8:62. (DOI: 10.3389/fgene.2017.00062) [Scimago Q1]
Contributions: literature review; methodology; data analysis and interpretation; manuscript writing
Main computer science contributions: definition of method's assessment metrics; design and implementation of the bioinformatics analysis.

Journal article [J3]

N. Lahens, E. Ricciotti, O. Smirnova, E. Toorens, E. Ji Kim, G. Baruzzo, K. Hayer, T. Ganguly, J. Schug, G. Grant, *"A comparison of Illumina and Ion Torrent sequencing platforms in the context of differential gene expression"*
BMC Genomics, Aug 2017, 18(1):602. (DOI: 10.1186/s12864-017-4011-0) [Scimago Q1]
Contributions: software; data analysis and interpretation
Main computer science contributions: definition of sequence alignment procedures; investigation of alignment parameters; development of alignment scripts; definition of sequence alignment assessment metrics

Journal article [J4]

F. Sambo, F. Finotello, E. Lavezzo, G. Baruzzo, G. Masi, E. Peta, M. Falda, S. Toppo, L. Barzon, B. Di Camillo, *"Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene"*
BMC Bioinformatics, Sep 2018, 19(1):343. (DOI: 10.1186/s12859-018-2360-6) [Scimago Q1]
Contributions: methodology; software; manuscript writing
Main computer science contributions: support the definition of multi-objective optimization framework; C++ software co-development; C++ multithreading implementation

Journal article [J5]

A. Trojani, E. Pungolino, A. Dal Molin, M. Lodola, G. Rossi, M. D'adda, A. Perego, C. Elena, M. Turrini, L. Borin, C. Bucelli, S. Malato, M. C. Carraro, F. Spina, M. L. Latargia, S. Artale, P. Spedini, M. Anghilieri, B. Di Camillo, G. Baruzzo, G. De Canal, A. Iurlo, E. Morra, R. Cairoli, *"Nilotinib interferes with cell cycle, ABC transporters and JAK-STAT signaling pathway in CD34+/lin- cells of patients with chronic phase chronic myeloid leukemia after 12 months of treatment"*
PLOS ONE, July 2019, 17(4):e0218444. (DOI: 10.1371/journal.pone.0218444) [Scimago Q1]
Contributions: data curation; formal analysis; methodology; software; manuscript writing
Main computer science contributions: design and implementation of ad-hoc analysis pipeline (denoising, batch effect removal, biomarker discovery)

Journal article [J6]

G. Baruzzo, I. Patuzzi, B. Di Camillo, *"SPARSim single cell: a count data simulator for scRNA-seq data"*
Bioinformatics, Oct 2019, 36(5): 1468-1475. (DOI: 10.1093/bioinformatics/btz752) [Scimago Q1]
Contributions: project design; conceptualization; literature review; formal analysis; methodology; software; data analysis and interpretation; manuscript writing
Main computer science contributions: definition of the Gamma-Multivariate Hypergeometric simulation model; design and implementation of the R/C++ software; definition of assessment metrics

Journal article [J7]

I. Patuzzi, G. Baruzzo, C. Losasso, A. Ricci, B. Di Camillo, *"metaSPARSim: a 16S rRNA gene sequencing count data simulator"*
BMC Bioinformatics, Nov 2019, 20(9): 1-13. (DOI: 10.1186/s12859-019-2882-6) [Scimago Q1]
Contributions: conceptualization; methodology; software; manuscript writing
Main computer science contributions: support the definition of the Gamma-Multivariate Hypergeometric simulation model; design and implementation of the R/C++ software; definition of assessment metrics

Journal article [J8]

M. Cappellato, G. Baruzzo, I. Patuzzi, B. Di Camillo, *"Modelling Microbial Community Networks: Methods and Tools"*
Current Genomics, Aug 2020, 22(4): 267-290 (DOI: 10.2174/1389202921999200905133146) [Scimago Q3]
Contributions: conceptualization; manuscript writing
Main computer science contributions: review of reverse engineering (graph inference) methods

Journal article [J9]

J. Tanevski, T. Nguyen, B. Truong, N. Karaiskos, M.E. Ahsen, X. Zhang, C. Shu, K. Xu, X. Liang, Y. Hu, H. VV Pham, L. Xiaomei, T.D. Le, A.L. Tarca, G. Bhatti, R. Romero, N. Karathanasis, P. Loher, Y. Chen, Z. Ouyang, D. Mao, Y. Zhang, M. Zand, J. Ruan, C. Hafemeister, P. Qiu, D. Tran, T. Nguyen, A. Gabor, T. Yu, J. Guinney, E. Glaab, R. Krause, P. Banda, DREAM SCTC Consortium, G. Stolovitzky, N. Rajewsky, J. Saez-Rodriguez, P. Meyer, *"Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data"*
Life Science Alliance, Sep 2020, 3(11). (DOI: 10.26508/lsa.202000867) [Scimago Q1]

Contributions: methodology; manuscript review

Main computer science contributions: definition of the 2D spatial mapping algorithm; design and implementation of the software.

Journal article [J10]

M. Tangaro, G. Defazio, B. Fosso, V.F. Licciulli, G. Grillo, G. Donvito, E. Lavezzo, G. Baruzzo, G. Pesole, and M. Santamaria, *"ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy"*

Bioinformatics, Jun 2021, 37(22): 4253-4254. (DOI: 10.1093/bioinformatics/btab431) [Scimago Q1]

Contributions: methodology; manuscript review

Main computer science contributions: extension of the multi-objective optimization framework to ITS data; support the integration of the C++ software in the cloud-based platform.

Journal article [J11]

E. Pungolino, M. D'Adda, G. De Canal, A. Trojani, A. Perego, C. Elena, F. Lunghi, M. Turrini, L. Borin, A. Iurlo, M. La Targia, M.C. Carraro, F. Spina, S. Artale, M. Anghilieri, A. Molteni, M. Caramella, G. Baruzzo, M. Nichelatti, B. Di Camillo, R. Cairoli, *"Nilotinib induced Bone Marrow CD34+/lin-Ph+ cells early clearance in newly diagnosed CP-Chronic Myeloid Leukemia: final report of the PhilosoPhi34 study"*

European Journal of Haematology, Jun 2021. (DOI: 10.1111/ejh.13680) [Scimago Q1]

Contributions: data curation; manuscript review

Main computer science contributions: design and implementation of ad-hoc analysis pipeline (denoising, batch effect removal, biomarker discovery)

Journal article [J12]

G. Baruzzo, G. Cesaro, B. Di Camillo, *"Identify, quantify and characterize cellular communication from single cell RNA sequencing data with scSeqComm"*

Bioinformatics, Jan 2022, 38(7):1920–1929. (DOI: 10.1093/bioinformatics/btac036) [Scimago Q1]

Contributions: project design; conceptualization; literature review; formal analysis; methodology; software; data analysis and interpretation; manuscript writing

Main computer science contributions: definition of the fuzzy AND score for intercellular signaling; definition of the graph-based (Personalized Page Rank) score for intracellular signaling; design and implementation of the R/C++ software

Journal article [J13]

G. Baruzzo and I. Patuzzi, B. Di Camillo, "*Beware to ignore the rare: how imputing zero-values can improve the quality of 16S rRNA gene studies results*"

BMC Bioinformatics, Jan 2022, 22(15). (DOI: 10.1186/s12859-022-04587-0) [Scimago Q1]

Contributions: conceptualization; formal analysis; software; data analysis and interpretation; manuscript writing

Main computer science contributions: investigation of missing data imputation techniques on 16S omics data; definition of missing data imputation evaluation metrics; design and implementation of bioinformatics preprocessing pipelines

Journal article [J14]

M. Cappellato, G. Baruzzo, B. Di Camillo, "*Investigating differential abundance methods in microbiome data: a benchmark study*",

PLOS Computational Biology, Sep 2022, 18(9). (DOI: 10.1371/journal.pcbi.1010467) [Scimago Q1]

Contributions: conceptualization; methodology; manuscript writing

Main computer science contributions: design of simulated data; definition of assessment metrics

Journal article [J15]

G. Cesaro and M. Milia, G. Baruzzo, G. Finco, F. Morandini, A. Lazzarini, P. Alotto, N.F. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *"MAST: a hybrid Multi-Agent Spatio-Temporal model of tumor microenvironment informed using a data-driven approach"*

Bioinformatics Advances, Dec 2022, 2(1). (DOI: 10.1093/bioadv/vbac092) [Scimago Q1]

Contributions: project design; conceptualization; methodology; software; manuscript writing

Main computer science contributions: design of the multi-agent based spatio-temporal model; contribution to design and implementation of the Python/Fortran software

Journal article [J16]

G. Baruzzo, A. Serafini, F. Finotello, T. Sanavia, F. Boldrin, E. Lavezzo, L. Barzon, S. Toppo, R. Provvedi, R. Manganelli, B. Di Camillo, *"Role of the extracytoplasmic function sigma factor SigE in the stringent response of Mycobacterium tuberculosis"*

Microbiology Spectrum, Mar 2023, 11(2). (DOI: 10.1128/spectrum.02944-22) [Scimago Q1]

Contributions: conceptualization; formal analysis; methodology; software; data analysis and interpretation; manuscript writing

Main computer science contributions: design and implementation of ad-hoc analysis pipeline (sequence alignment, expression level quantification, denoising, clustering of time series data, biomarker discovery)

Journal article [J17]

L. Khachatryan, Y. Xiang, A. Ivanov, E. Glaab, G. Graham, I. Granata, M. Giordano, L. Maddalena, M. Piccirillo, I. Manipur, G. Baruzzo, M. Cappellato, B. Avot, A. Stan, J. Battey, G. Lo Sasso, S. Boue, N.V. Ivanov, M.C. Peitsch, J. Hoeng, L. Falquet, B. Di Camillo, M. Guarracino, V. Ulyantsev, N. Sierro, C. Poussin, *"Results and Lessons Learned from the sbv IMPROVER Metagenomics Diagnostics for Inflammatory Bowel Disease Challenge"*

Scientific Reports, April 2023, 13:6303. (DOI: 10.1038/s41598-023-33050-0) [Scimago Q1]

Contributions: conceptualization; methodology; data analysis; manuscript review

Main computer science contributions: design of bioinformatics pre-processing pipeline for metagenomic data; contribution to the feature selection and classification steps.

Journal article

O. Gagliano, F. Panariello, C. Luni, A. Grimaldi, S. Angiolillo, W. Qin, A. Manfredi, P. Annunziata, S. Slovin, L. Vaccaro, S. Riccardo, V. Bouche, M. Dionisi, M. Salvi, S. Martewicz, M. Hu, M. Cui, H. Stuart, C. Laterza, G. Baruzzo, G. Schiebinger, B. Di Camillo, D. Cacchiarelli, N. Elvassore, *"Cellular population dynamics shape*

[J18] *the route to human pluripotency"*
Nature Communication, May 2023, 14(1):2829. (DOI: 10.1038/s41467-023-37270-w) [Scimago Q1]
Contributions: methodology; software; data analysis
Main computer science contributions: extension of the (scSeqComm) method/software

Journal article [J19]
G.M. Di Liberto, A. Nidiffer, M.J. Crosse, N. Zuk, S. Haro, G. Cantisani, M.M. Winchester, A. Igoe, R. McCrann, S. Chandra, E.C. Lalor, G. Baruzzo, *"A standardised open science framework for sharing and re-analysing neural data acquired to continuous stimuli"*
Neurons, Behavior, Data analysis, and Theory , Oct 2024 (DOI: 10.51628/001c.124867)
Contributions: conceptualization; manuscript review
Main computer science contributions: open science roles (infrastructure, data and software) in bioinformatics

Conf. article [CA1]
G Baruzzo, G. Cesaro, B. Di Camillo, *"quickSparseM: a library for memory- and time-efficient computation on large, sparse matrices with application to omics data"*
Proceedings of 33rd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP 2025), IEEE Computer Society Digital Library, March 2025
Contributions: conceptualization; literature review; formal analysis; methodology; software; data analysis and interpretation; manuscript writing and reviewing; project design, supervision and coordination; funding acquisition
Main computer science contributions: design of parallel algorithm and code for memory- and time-efficient computation on large, sparse matrices; implementation of an R/C++/OpenMP package

Commentary article [JC1]
G. Baruzzo, K. Hayer, E. Ji Kim, B. Di Camillo, G. Fitzgerald, G. Grant, *"Comprehensive Benchmarking of RNA-Seq Aligners Indicates Large Variation in Performance"* in *"Principles of Systems Biology, No. 13".*
Cell Systems, Jan 2017, 4(1):3–6. (DOI: 10.1016/j.cels.2017.01.006) [Scimago Q1]
Contributions: conceptualization, manuscript writing

Journal abstract [JA1]
A. Trojani, E. Pungolino, G. Rossi, M. D'adda, M. Lodola, A. Dal Molin, G. Baruzzo, A. Perego, M. Turrini, C. Elena, L. M. Borin, A. Iurlo, S. Malato, F. Spina, M. L. Latarglia, P. Spedini, S. Artale, M. Anghilieri, M. C. Carraro, C. Bucelli, G. De Canal, E. Morra, R. Cairoli, *"Nilotinib Deregulates Cell Cycle Checkpoints, ABC Transporters Genes and JAK-STAT Signaling Pathway of CD34+/Lin-Cells in Chronic-Phase Chronic Myeloid Leukemia (CP-CML) Patients after 12 Months of Treatment."*
Blood, Nov 2018, 132(Suppl 1):5122. (DOI: 10.1182/blood-2018-99-112188) [Scimago Q1]

Journal abstract [JA2]
A. Trojani, E. Pungolino, G. Rossi, M. D'adda, L. E. Bossi, G. Baruzzo, B. Di Camillo, A. Perego, M. Turrini, C. Elena, L. M. Borin, A. Iurlo, S. Malato, F. Spina, M. L. Latargia, P. Spedini, S. Artale, M. Anghilieri, M. C. Carraro, C. Bucelli, G. De Canal, E. Morra, R. Cairoli, "*Progressive Down Regulation of JAK-STAT, Cell Cycle, and ABC Transporter Genes in CD34+/Lin- Cells of Chronic-Phase Chronic Myeloid Leukemia (CP-CML) Patients at Diagnosis Vs. 12 Months of Nilotinib Treatment Vs. Healthy Subjects*"
Blood, Nov 2019, 134(Supp 1):5034. (DOI: 10.1182/blood-2019-125595) [Scimago Q1]

Journal abstract [JA3]
A. Trojani, E. Pungolino, A. Dal Molin, L.E. Bossi, G. Rossi, M. D'Adda, A. Perego, C. Elena, M. Turrini, L. Borin, C. Bucelli, S. Malato, M.C. Carraro, F. Spina, M.L. Latargia, S. Artale, P. Spedini, M. Anghilieri, B. Di Camillo, G. Baruzzo, G. De Canal, A. Iurlo, E. Morra, R. Cairoli, *"Identification of mirna and target genes in the transcriptome analysis of CD34+/lin-cells of patients with chronic myeloid leukemia in the chronic phase after 12 months of nilotinib therapy."*
Haematologica, Oct 2019, 104(s2):144 [Scimago Q1]

National and international conference contributions

[C1] Abstract/poster: G. Baruzzo, F. Finotello, E. Lavezzo, A. Serafini, R. Provvedi, S. Toppo, L. Barzon, R. Manganelli, B. Di Camillo, *"Benchmarking RNA-seq mapping strategies for paired-end reads"* at **Network Tools and Applications for Biology (NETTAB) 2014**

[C2] Abstract/poster: N. Lahens, E. Ricciotti, O. Smirnova, E. Toorens, E. Ji Kim, G. Baruzzo, K. Hayer, T. Ganguly, J. Schug, G. Grant, *"A comparison of Illumina and Ion Torrent platforms in a study of differential gene expression"* at **Intelligent Systems for Molecular Biology (ISMB) 2016**

[C3] Abstract/poster: G. Baruzzo, K. Hayer, E. J. Kim, B. Di Camillo, G. Grant, *"Benchmark Analysis of RNA-Seq Aligners"* at **Intelligent Systems for Molecular Biology (ISMB) 2016**

[C4] Abstract/poster: A. Dal Molin, G. Baruzzo, B. Di Camillo, *"Evaluation of differential expression analysis methods for single-cell RNA-sequencing"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2017**

[C5] Abstract w/ oral presentation: I. Patuzzi and G. Baruzzo, A. Ricci, C. Losasso, B. Di Camillo, *"SPARSim: taking account of data sparsity in single cell and 16S rRNA gene sequencing"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2018**

[C6] Abstract/poster: A. Dal Molin, G. Baruzzo, I. Patuzzi, B. Di Camillo, *“Exploring single-cell RNA-seq data: a survey on sparsity and multimodality”* at **European Conference on Computational Biology (ECCB) 2018**

[C7] Abstract/poster: G. Baruzzo, I. Patuzzi, B. Di Camillo, *“SPARSim Single Cell: a count data simulator for single cell RNA-seq data”* at **RECOMB/ISCB Conference on Regulatory & Systems Genomics 2018**

[C8] Abstract/poster: G. Baruzzo, G. Finco, F. Morandini, P. Alotto, B. Di Camillo, *“MAST: a Multi-Agent based Spatio-Temporal model of the interaction between immune system and tumor growth”* at **RECOMB/ISCB Conference on Regulatory & Systems Genomics 2018**

[C9] Abstract/poster w/ oral presentation: G. Baruzzo, I. Patuzzi, B. Di Camillo, *“SPARSim Single Cell: a count data simulator for single cell RNA-seq data”* at **3rd Annual MAQC Society Conference 2019**

[C10] Abstract/poster w/ oral presentation: G. Baruzzo, G. Finco, F. Morandini, P. Alotto, B. Di Camillo, *“MAST: a Multi-Agent based Spatio-Temporal model of the interaction between immune system and tumor growth”* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2019**

[C11] Abstract/poster: G. Baruzzo, I. Patuzzi, B. Di Camillo, *“SPARSim Single Cell: a count data simulator for single cell RNA-seq data”* at **Conference on Intelligent Systems for Molecular Biology (ISMB) and European Conference on Computational Biology (ECCB) 2019**

[C12] Abstract w/ oral presentation: G. Baruzzo, I. Patuzzi, B. Di Camillo, *“Reliable simulation of count data for single cell RNA sequencing”* at **Network Tools and Applications for Biology (NETTAB) and Bioinformatics and Computational Biology Conference (BBCC) 2019**

[C13] Abstract w/ oral presentation: G. Baruzzo, I. Patuzzi, B. Di Camillo, *“Zero-imputation in 16S rRNA gene studies: do we need it?”* at **Bioinformatics and Computational Biology Conference (BBCC) 2020**

[C14] Abstract/poster: M. Cappellato, G. Baruzzo, B. Di Camillo, *“Investigating differential abundance methods in microbiome data: a benchmark study”* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2021**

[C15] Abstract w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *“scSeqComm: a bioinformatic tool to identify, quantify and characterize cellular communication from single cell RNA sequencing data”* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2021**

[C16] Abstract w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *“Analyze cellular communication from single cell RNA sequencing data with scSeqComm”* at **Bioinformatics and Computational Biology Conference (BBCC) 2021**

[C17] Abstract w/ oral presentation: M. Cappellato, G. Baruzzo, B. Di Camillo, *“Comprehensive assessment of microbiome differential abundance tools”* at **Bioinformatics and Computational Biology Conference (BBCC) 2021**

[C18] Abstract w/ oral presentation: A. Rossato, M. Cappellato, N Nikiloska, G. Baruzzo, B. Di Camillo, *“From microbial community model to interaction networks”* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2022**

[C19] Abstract/poster: G. Cesaro, G. Baruzzo, B. Di Camillo, *“Differential cellular communication analysis from single cell RNA sequencing data with scSeqComm”* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2022**

[C20] Abstract w/ oral presentation: G. Cesaro, M. Milia, G. Baruzzo, P. Alotto, NF. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *“Simulate personalized tumor microenvironment evolution through a hybrid Multi-Agent Spatio-Temporal model informed by sequencing data”* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2022**

[C21] Abstract/poster: A. Rossato, M. Cappellato, N. Nikoloska, G. Baruzzo, B. Di Camillo, *“Simulation of ground truth interaction networks from microbial community model”* at **21st European Conference of Computational Biology (ECCB) 2022**

[C22] Abstract/poster: M. Cappellato, G. Baruzzo, B. Di Camillo, *“Differential Abundance analysis of microbiome data: which tool and how to choose it?”* at **21st European Conference of Computational Biology (ECCB) 2022**

[C23] Abstract/poster: M. Milia, G. Cesaro, G. Baruzzo, G. Finco, F. Morandini, A. Lazzarini, P. Alotto, N.F. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *“Tumor microenvironment evolution simulated through a hybrid Multi-Agent Spatio-Temporal model informed using sequencing data”* at **21st European Conference of Computational Biology (ECCB) 2022**

[C24] Abstract/poster: G. Cesaro, G. Baruzzo, B. Di Camillo, *“Analysis of differential cellular communication from single cell RNA-seq data with scSeqComm”* at **21st European Conference of Computational Biology (ECCB) 2022**

[C25] Abstract/poster: M. Cappellato, M. Bellato, G. Baruzzo, S. Facchin, L. Barzon, V. Besutti, P. Brun, S. Del Favero, L. Schenato, E.V. Savarino, I. Castagliuolo, B. Di Camillo, *"Temporal changes in microbiome composition after FMT in subject with Clostridioides difficile infection: a network perspective"* at **21st European Conference of Computational Biology (ECCB) 2022**

[C26] Abstract/poster: A. Rossato, M. Cappellato, G. Baruzzo, B. Di Camillo, *"Simulation of ground truth interaction networks from microbial community model"* at **Bioinformatics and Computational Biology Conference (BBCC) 2022**

[C27] Abstract/poster: G. Cesaro, M. Milia, G. Baruzzo, P. Alotto, N.F. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *"Simulate tumor microenvironment evolution from sequencing data through a hybrid Multi-Agent Spatio-Temporal model"* at **Bioinformatics and Computational Biology Conference (BBCC) 2022**

[C28] Abstract/poster: E. Hazizaj, F. Longhin, G. Baruzzo, B. Di Camillo, *"Somatic read simulators: how to build a realistic gold standard using data from well-annotated cancer databases"* at **Bioinformatics and Computational Biology Conference (BBCC) 2022**

[C29] Abstract w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Differential cellular communication analysis across multi-condition and multi-patient scRNA-seq data"* at **Bioinformatics and Computational Biology Conference (BBCC) 2022**

[C30] Abstract/poster w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Cellular communication analysis of large-scale single-cell RNA sequencing data"* at **byteMAL 2023**

[C31] Abstract/poster: F. Longhin, E. Hazizaj, G. Baruzzo, B. Di Camillo, *"Data-driven meta-simulation of realistic tumoral samples"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2023**

[C32] Abstract w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"CClens: effective and efficient differential cellular communication analysis of large-scale single-cell RNA sequencing data"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2023**

[C33] Abstract/poster: M. Milia, N. Ferro, B. Di Camillo, G. Baruzzo, *"mopo16Sweb: a cloud-based app for multi-objective optimization of bacterial 16S PCR primers"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2023**

[C34] Abstract/poster: M. Baldan, A. Rossato, M. Bellato, G. Baruzzo, B. Di Camillo, *"From microbial ground truth network simulation to inference method benchmark"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2023**

[C35] Abstract w/ oral presentation: G. Baruzzo *"Bioinformatics for complex biological systems: unraveling cell-cell and bacterial interactions"* at **8th Mediterranean School of Complex Networks (MSCX 2023)**

[C36] Abstract/poster w/ oral presentation: G. Cesaro, M. Milia, G. Baruzzo, P. Alotto, N.F. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *"Modeling the tumor microenvironment with a hybrid Multi-Agent Spatio-Temporal model fed with sequencing data"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C37] Abstract/poster w/ oral presentation: M. Cappellato, G. Baruzzo, B. Di Camillo, *"Comprehensive benchmarking of differential abundance methods in microbiome data"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C38] Abstract w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Interactive and effective visualization framework for interpreting and exploring cellular communication data"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C39] Abstract/poster: M. Milia, N. Ferro, B. Di Camillo, G. Baruzzo, *"mopo16Sweb: A webapp for multi-objective optimization of 16S rRNA primers sequences on the cloud"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C40] Abstract/poster w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *"scSeqComm: a statistical and network-based framework to infer inter- and intra-cellular communication from single-cell RNA sequencing data"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C41] Abstract/poster: G. Cesaro, J.S. Nagai, A. Chiodi, V. Klöker, N. Gnoato, E. Mosca, I. Costa, E. Calura, B. Di Camillo, G. Baruzzo, *"Shedding light on cellular communication analysis: the present and the future"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C42] Abstract/poster: F. Longhin, E. Hazizaj, G. Baruzzo, B. Di Camillo, *"Comprehensive review of tumoral sample simulators: building a realistic gold standard for somatic variant calling validation"* at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

[C43] Abstract w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"CClens: a cellular communication workflow for large-scale single-cell RNA sequencing data"* at **19th ISCB Student Council Symposium (SCS 2023)**

[C44] Short article w/ oral presentation: M. Baldan, G. Baruzzo, B. Di Camillo, *"N2BPC: an algorithmic approach from Networks to Bacteria's metabolite Production and Consumption"* at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**

[C45] Short article w/ oral presentation: F. Longhin, E. Hazizaj, G. Baruzzo, B. Di Camillo, *"Leveraging on somatic sample simulators for realistic data-driven generation of tumoral genomes"* at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**

[C46] Short article w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Differential cellular communication analysis from large-scale single-cell RNA sequencing data"* at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**

[C47] Abstract w/ oral presentation: G. Tussardi, G. Cesaro, B. Di Camillo, G. Baruzzo , *"Interactive exploration of cell-cell communication results from single-cell RNA sequencing data through a webapp"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2024**

[C48] Abstract w/ oral presentation: P. Mariotto, M. Baldan, B. Di Camillo, G. Baruzzo, *"Limitations of the co-occurrence-based approach in the inference of microbiota interaction networks"* at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2024**

[C49] Short article w/ oral presentation: M. Milia, G. Baruzzo, B. Di Camillo, *"Network-Based Cross-Entropy Approach for Continuous Genotype-Phenotype Association Analysis"* at **19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)**

[C50] Short article w/ oral presentation: P. Mariotto, M. Baldan, B. Di Camillo, G. Baruzzo, *"Comprehensive benchmarking of network inference methods for 16S rDNA-Seq data"* at **19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)**

[C51] Abstract/poster: M. Andriolo, G. Baruzzo, B. Di Camillo, *"Using Archetypal Analysis for scRNAseq data clustering and trajectory identification"* at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**

[C52] Abstract/poster: M. Milia, G. Baruzzo, B. Di Camillo, *"INTERACT: A novel approach for continuous Genotype-Phenotype association analysis"* at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**

[C53] Abstract/poster: P. Mariotto, M. Baldan, B. Di Camillo, G. Baruzzo, *"Inferring microbial ecological networks from metagenomics data, when should we trust the results?"* at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**

[C54] Abstract w/ oral presentation: G. Tussardi, G. Cesaro, B. Di Camillo, G. Baruzzo, *"Addressing the Biological Interpretation of High-Dimensional Cell-Cell Communication Data from Single Cell Transcriptomics Through an Interactive Web Application"* at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**

[C55] Abstract w/ oral presentation: M. Baldan, G. Baruzzo, A. Rossato, M. Cappellato, B. Di Camillo, *"Simulation of bacteria interaction networks: from topology to species abundances"* at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**

[C56] Full article w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *"quickSparseM: a library for memory- and time-efficient computation on large, sparse matrices with application to omics data"* at **33rd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP) 2025**

Oral presentations and invited speaker

Invited seminar

at **ITMAT Bioinformatics, Institute for Translational Medicine and Therapeutics, University of Pennsylvania,** Philadelphia, USA, May 3, 2018
G. Baruzzo (speaker), "*Working with RNA sequencing data: challenges and strategies for data analysis*"

Conference oral presentation	at **15th Annual Meeting of the Bioinformatics Italian Society (BITS) 2018**, Turin, Italy, June 28, 2018 I. Patuzzi and G. Baruzzo (speaker), A. Ricci, C. Losasso, B. Di Camillo, *"SPARSim: taking account of data sparsity in single cell and 16S rRNA gene sequencing"*
Conference oral presentation	at **3rd Annual MAQC Society Conference,** Riva del Garda, Italy, April 9, 2019 G. Baruzzo (speaker), I. Patuzzi, B. Di Camillo, "*SPARSim Single Cell: a count data simulator for single cell RNA-seq data*"
Conference oral presentation	at **16th Annual Meeting of the Bioinformatics Italian Society (BITS) 2019,** Palermo, Italy, June 27, 2019 G. Baruzzo, G. Finco, F. Morandini, P. Alotto, B. Di Camillo (speaker), *"MAST: a Multi-Agent based Spatio-Temporal model of the interaction between immune system and tumor growth"*
Conference oral presentation	at **Network Tools and Applications for Biology (NETTAB) & Bioinformatics and Computational Biology Conference (BBCC) 2019 Meeting,** Fisciano, Italy, November 13, 2019 G. Baruzzo (speaker), I. Patuzzi, B. Di Camillo, "*Reliable simulation of count data for single cell RNA sequencing*"
Conference oral presentation	at **Bioinformatics and Computational Biology Conference (BBCC) 2020 Meeting, (**virtual conference), November 18, 2020 G. Baruzzo (speaker), I. Patuzzi, B. Di Camillo, *"Zero-imputation in 16S rRNA gene studies: do we need it?"*
Conference oral presentation	at **17th Annual Meeting of the Bioinformatics Italian Society (BITS)**, (virtual conference), July 2, 2021 G. Baruzzo (speaker), G. Cesaro, B. Di Camillo, *"scSeqComm: a bioinformatic tool to identify, quantify and characterize cellular communication from single cell RNA sequencing data"*
Conference oral presentation	at **Bioinformatics and Computational Biology Conference (BBCC) 2021 Meeting**, (virtual conference), December 2, 2021 G. Baruzzo (speaker), G. Cesaro, B. Di Camillo, *"Analyze cellular communication from single cell RNA sequencing data with scSeqComm"*
Conference oral presentation	at **Bioinformatics and Computational Biology Conference (BBCC) 2021 Meeting**, (virtual conference), December 2, 2021 M. Cappellato (speaker), G. Baruzzo, B. Di Camillo, *"Comprehensive assessment of microbiome differential abundance tools"*
Conference oral presentation	at **18th Annual Meeting of the Bioinformatics Italian Society (BITS)**, Verona, Italy, June 29, 2022 A. Rossato, M. Cappellato (speaker), N. Nikiloska, G. Baruzzo, B. Di Camillo, *"From microbial community model to interaction networks"*
Conference oral presentation	at **18th Annual Meeting of the Bioinformatics Italian Society (BITS)**, Verona, Italy, June 29, 2022 G. Cesaro, M. Milia (speaker), G. Baruzzo, P. Alotto, NF. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *"Simulate personalized tumor microenvironment evolution through a hybrid Multi-Agent Spatio-Temporal model informed by sequencing data"*
Invited talk	at **Cognition and Natural Sensory Processing Workshop 2022 (CNSP 2022)**, (virtual conference), July 20, 2022 G. Baruzzo (speaker), *"Data standardisation and sharing - A lesson from bioinformatics"*
Conference oral presentation	at **Bioinformatics and Computational Biology Conference (BBCC) 2022**, (virtual conference), December 14, 2022 G. Cesaro (speaker), G. Baruzzo, B. Di Camillo, *"Differential cellular communication analysis across multi-condition and multi-patient scRNA-seq data"*
Conference oral presentation	at **byteMAL 2023**, Aachen, Germany, May 23, 2023 G. Cesaro (speaker), G. Baruzzo, B. Di Camillo, *"Cellular communication analysis of large-scale single-cell RNA sequencing data"*
Conference oral presentation	at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2023**, Bari, Italy, June 22, 2023 G. Cesaro (speaker), G. Baruzzo, B. Di Camillo, *"CClens: effective and efficient differential cellular communication analysis of large-scale single-cell RNA sequencing data"*
Oral presentation	at **8th Mediterranean School of Complex Networks (MSCX 2023)**, Catania, Italy, June 26, 2023 G. Baruzzo (speaker), *"Bioinformatics for complex biological systems: unraveling cell-cell and bacterial interactions"*
Conference oral presentation	at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**, Lyon, France, July 27, 2023 G. Cesaro, M. Milia (speaker), G. Baruzzo, P. Alotto, N.F. da Cunha Carvalho de Miranda, Z. Trajanoski, F. Finotello, B. Di Camillo, *"Modeling the tumor microenvironment with a hybrid Multi-Agent Spatio-Temporal model fed with sequencing data"*

Conference oral presentation	at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**, Lyon, France, July 25, 2023 M. Cappellato, G. Baruzzo (speaker), B. Di Camillo, *“Comprehensive benchmarking of differential abundance methods in microbiome data”*
Conference oral presentation	at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**, Lyon, France, July 25, 2023 G. Cesaro (speaker), G. Baruzzo, B. Di Camillo, *“Interactive and effective visualization framework for interpreting and exploring cellular communication data”*
Conference oral presentation	at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**, Lyon, France, July 24, 2023 G. Baruzzo (speaker), G. Cesaro, B. Di Camillo *“scSeqComm: a statistical and network-based framework to infer inter- and intra-cellular communication from single-cell RNA sequencing data”*
Conference oral presentation	at **19th ISCB Student Council Symposium (SCS 2023)**, Lyon, France, July 23, 2023 G. Cesaro (speaker), G. Baruzzo, B. Di Camillo, *“CClens: a cellular communication workflow for large-scale single-cell RNA sequencing data”*
Conference oral presentation	at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**, Padova, Italy, September 6, 2023 M. Baldan (speaker), G. Baruzzo, B. Di Camillo, *“N2BPC: an algorithmic approach from Networks to Bacteria's metabolite Production and Consumption”*
Conference oral presentation	at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**, Padova, Italy, September 6, 2023 F. Longhin (speaker), E. Hazizaj, G. Baruzzo, B. Di Camillo, *“Leveraging on somatic sample simulators for realistic data-driven generation of tumoral genomes”*
Conference oral presentation	at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**, Padova, Italy, September 8, 2023 G. Cesaro (speaker), G. Baruzzo, B. Di Camillo, *“Differential cellular communication analysis from large-scale single-cell RNA sequencing data”*
Conference oral presentation	at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2024,** Trento, Italy, June 14, 2024 G. Tussardi (speaker), G. Cesaro, B. Di Camillo, G. Baruzzo, *“Interactive exploration of cell-cell communication results from single-cell RNA sequencing data through a webapp”*
Conference oral presentation	at **Annual Meeting of the Bioinformatics Italian Society (BITS) 2024,** Trento, Italy, June 14, 2024 P. Mariotto (speaker), M. Baldan, B. Di Camillo, G. Baruzzo, *“Limitations of the co-occurrence-based approach in the inference of microbiota interaction networks”*
Conference oral presentation	at **19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)**, Benevento, Italy, September 6, 2024 M. Milia (speaker), G. Baruzzo, B. Di Camillo, *“Network-Based Cross-Entropy Approach for Continuous Genotype-Phenotype Association Analysis”*
Conference oral presentation	at **19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)**, Benevento, Italy, September 4, 2024 P. Maritotto, M. Baldan, B. Di Camillo, G. Baruzzo (speaker), *“Comprehensive benchmarking of network inference methods for 16S rDNA-Seq data”*
Conference oral presentation	at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**, Virtual Event. December 11, 2024 G. Tussardi (speaker), G. Cesaro, B. Di Camillo, G. Baruzzo, *“Addressing the Biological Interpretation of High-Dimensional Cell-Cell Communication Data from Single Cell Transcriptomics Through an Interactive Web Application”*
Conference oral presentation	at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW) 2024**, Virtual Event. December 11, 2024 M. Baldan (speaker), G. Baruzzo, A. Rossato, M. Cappellato, B. Di Camillo, *“Simulation of bacteria interaction networks: from topology to species abundances”*
Conference oral presentation	at **33rd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP) 2025**, Torino, Italy, March 14, 2025 G. Baruzzo (speaker), G. Cesaro, B. Di Camillo, *“quickSparseM: a library for memory- and time-efficient computation on large, sparse matrices with application to omics data”*

Software projects

ABACUS	A memory-efficient and parallel application for phenotype-genotype association based on bivariate statistics and cross-entropy approaches. C++ software available at https://gitlab.com/sysbiobig/abacus . Role: project coordination.
CClens	A dashboard for the interpretation and exploration of multi-dimensional scRNA-seq cell-cell communication data through an interactive and user-friendly interface. R/Shiny package and Docker container available at https://gitlab.com/sysbiobig/cclens . Role: developer, maintainer, project coordination.
bewareToIgnoreTheRare	A simulation and assessment framework for normalization and missing data imputation methods applied on 16S count data. R package and Docker container available at https://gitlab.com/sysbiobig/beware-to-ignore-the-rare-imputation-16s . Role: lead developer, lead maintainer, project coordination.
MAST	A hybrid PDE and Multi-Agents based Spatio-Temporal model of tumor microenvironment informed using omics data. Python/Fortran code and Docker container available at https://gitlab.com/sysbiobig/mast . Role: project coordination.
maxcounts	A computational approach to compute genomic feature abundance based on read coverage. C++ software available at https://gitlab.com/sysbiobig/maxcounts . Role: developer, lead maintainer, project coordination.
metaBenchDA	A simulation and assessment framework for differential abundance methods applied on 16S count data. R package and Docker container available at https://gitlab.com/sysbiobig/metabenchda . Role: project coordination.
metaSPARSim	A flexible simulation framework of compositional 16S count data based on a gamma-multivariate hypergeometric model. R/C++ package available at https://gitlab.com/sysbiobig/metasparsim . Role: developer, maintainer, project coordination.
mopo16S	A multithread application for multi-objective combinatorial optimization of 16s PCR primer sequences based on two-phase iterated best improvement local search approach. C++ software available at https://gitlab.com/sysbiobig/mopo16s . Role: developer, lead maintainer, project coordination.
mopo16Sweb	A webapp for the preprocessing of bacteria genome and 16S PCR primers, the multi-objective combinatorial optimization of PCR primers, and the interactive visualization of output primer scores. Python/C++ software and Docker container available at https://gitlab.com/sysbiobig/mopo16s-web . Role: developer, project coordination.
MOV&RSim	A computational model of cancer-specific mutations and sequencing reads characteristics for realistic tumoral sample simulation. Python/C++ software and Docker container available at https://gitlab.com/sysbiobig/movarsim . Role: project coordination.
N2SIMBA	An algorithmic approach to simulate 16S compositional count data and the underling bacteria interaction network based on Microbial Consumer Resource model. Python software and Docker container available at https://gitlab.com/sysbiobig/microcommunitynetworks . Role: project coordination.
quickSparseM	A library for memory- and time-efficient computation on large, sparse matrices with application to omics data. R/C++ package available at https://gitlab.com/sysbiobig/quicksparsem . Role: lead developer, lead maintainer, project coordination.
scSeqComm	A memory efficient, parallel and scalable data mining tool based on statistical and network science methodologies to infer and quantify intercellular and intracellular signaling from scRNA-seq data. R/C++ package available at https://gitlab.com/sysbiobig/scseqcomm . Role: lead developer, lead maintainer, project coordination.
SPARSim	A flexible simulation framework of compositional scRNA-seq count data based on a gamma-multivariate hypergeometric model. R/C++ package available at https://gitlab.com/sysbiobig/sparsim . Role: lead developer, lead maintainer, project coordination.

Third mission / Public engagement

2023 Scientific divulgation project “DEI^3” – Third mission initiative founded by University of Padova

- Science pill “*Le cellule comunicano: l’informatica le ascolta*”, Giacomo Baruzzo and Giulia Cesaro
- Science pill “*I batteri sono ovunque: che fortuna!*”, Giacomo Baruzzo and Massimo Bellato

2024 Scientific divulgation event with private enterprises “AI@DEI - Biomedics and Health” – Third mission initiative organized by Department of Information Engineering, University of Padova

- Talk “*AI in Bioinformatics & Medical Informatics*” (speaker: Giacomo Baruzzo)

Refereeing and editorial activities

Journal Referee

- IEEE/ACM Transactions on Computational Biology and Bioinformatics
- IEEE Journal of Biomedical and Health Informatics
- Lecture Notes in Bioinformatics
- BMC Bioinformatics
- BMC Genomics
- Bioinformatics
- Briefings in Bioinformatics
- Bioinformatics Advances
- PLOS Computational Biology
- Journal of Biomedical Informatics
- Computational and Structural Biotechnology Journal
- Frontiers in Bioinformatics
- NAR Genomics and Bioinformatics

Conference Referee

- Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB) 2024
- MODIMO Workshop on Multi-Omics Data Integration for Modelling Biological Systems (within ACM International Conference on Information and Knowledge Management (CIKM) 2023)
- Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB) 2023
- Research in Computational Molecular Biology (RECOMB) 2022
- IEEE-EMBS International Conference on Biomedical and Health Informatics (BHI) 2021
- Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB) 2021
- Research in Computational Molecular Biology (RECOMB) 2021
- Research in Computational Molecular Biology (RECOMB) 2020

Editor (proceedings)

Proceedings of the **16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology**, Certosa di Pontignano, Siena, Italy, 9-11 July, 2019

Guest Editor (special issue)

- **BMC Medical Informatics and Decision Making**. Special issue dedicated to the 18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023).
- **Springer Lecture Notes in Bioinformatics (LNBI)**. Proceedings of the 18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023). [ongoing]
- **BMC Bioinformatics**. Special issue dedicated to the 18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023). [ongoing]

Role in organization of international scientific conferences/events

Publicity co-chair Proceedings co-chair Organizing committee Program committee	**16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (IEEE CIBCB 2019)** Certosa di Pontignano, Siena, Italy, from July 9 to July 11, 2019
Local committee	**18th Annual Meeting of the Bioinformatics Italian Society (BITS 2022)** Verona, Italy, from June 27 to June 29, 2022
Co-chair workshop Co-chair organizing committee Co-chair scientific committee	**Workshop** ***“Spatial transcriptomics and cell-cell communication modeling: new opportunities to study the cellular dynamics of biological systems”*** at **New Trends in Bioinformatics by ECCB - 21st European Conference on Computational Biology (ECCB 2022)** Virtual event, September 13, 2022
Co-chair Co-organizer Instructor	**Tutorial** “***Software containerization in bioinformatics: how to make reproducible, portable and reusable bioinformatics software&pipelines***” at **New Trends in Bioinformatics by ECCB - 21st European Conference on Computational Biology (ECCB 2022)** Sitges, Barcellona, Spain, September 18, 2022
Publicity, web and social media committee	**8th National congress of Bioengineering (GNB 2023)** Padova, Italy, from June 21 to June 23, 2023
Co-chair	**YOUNG BITS, RSG-Italy & CINI Young-InfoLife Symposium at 19th Annual Meeting of the Bioinformatics Italian Society (BITS 2023)** Bari, Italy, from June 21 to June 23, 2023
Co-chair Co-organizer Instructor	**Tutorial** “***How to make reproducible, portable and reusable bioinformatics software using software containerization***” at **31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)** Lyon, France, July 23, 2023
Program committee Local committee Session Chair	**18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)** Padova, Italy, from September 6 to September 8, 2023
Co-organizer Co-chair	**Special session** ***“An Italian snapshot on present and future informatics research in bioinformatics - CINI Infolife”*** at **18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)** Padova, Italy, from September 6 to September 8, 2023
Scientific committee	**YOUNG BITS, RSG-Italy & CINI Young-InfoLife Symposium at 20th Annual Meeting of the Bioinformatics Italian Society (BITS 2024)** Trento, Italy, from June 12 to June 15, 2024
Co-organizer	**Special session** ***“Informatics research in bioinformatics: contributions from the CINI-InfoLife network”*** at **19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)** Benevento, Italy, from September 4 to September 6, 2024
Program committee	**19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)** Benevento, Italy, from September 4 to September 6, 2024
Co-organizer Scientific committee Session Chair	**Young Minds at Work: Blending Biochemistry and Bioinformatics – 2nd edition** Virtual Event, from December 10 to December 12, 2024
Co-organizer Speaker/trainer	**1st International Biohackathon of the Bioinformatics Italian Society 2025** Napoli, Italy, June 10, 2025

Teaching activities in Master and Bachelor degrees

2024-2025
Lecturer *(with responsibility of the course)* at *"Scientific Computing and Object Oriented Programming"* (48 hours, 6 CFU – responsible for 5 CFU) [ING-INF/05]
Master Degree course of Mathematical Engineering (A.Y. 2024/2025)
Department of Civil, Environmental and Architectural Engineering, University of Padova, Padova, Italy

2023-2024
Lecturer *(with responsibility of the course)* at *"Scientific Computing and Object Oriented Programming"* (48 hours, 6 CFU – responsible for 4 CFU) [ING-INF/05]
Master Degree course of Mathematical Engineering (A.Y. 2023/2024)
Department of Civil, Environmental and Architectural Engineering, University of Padova, Padova, Italy

2023-2024
Lecturer *(with responsibility of the course)* at *"Computational Genomics"* (48 hours, 6 CFU) [INF/01 and ING-INF/06]
Master Degree course of Computer Engineering (A.Y. 2023/2024)
Master Degree course of Bioengineering (A.Y. 2023/2024)
Department of Information Engineering, University of Padova, Padova, Italy

2022-2023
2021-2022
Lecturer *(with responsibility of the course)* at *"Scientific Computing and Object Oriented Programming"* (48 hours, 6 CFU) [ING-INF/05]
Master Degree course of Mathematical Engineering (A.Y. 2022/2023, A.Y. 2021/2022)
Department of Civil, Environmental and Architectural Engineering, University of Padova, Padova, Italy

2021-2022
2020-2021
2019-2020
2018-2019
Teaching assistant (*Didattica integrativa*) at "*Elementi di Informatica e Programmazione*" (Prof. Marcello Dalpasso, Prof. Barbara Di Camillo) - 30 hours in A.Y. 2021/22 and A.Y. 2020/21, 40 hours in A.Y. 2019/20, 50 hours in A.Y. 2018/19 [INF/01 and ING-INF/05]
Bachelor Degree course of Biomedical Engineering (A.Y. 2021/22, 2020/21, 2019/20, 2018/19)
Department of Information Engineering, University of Padova, Padova, Italy

2015-2016
Teaching assistant at "*Bioingegneria per la Genomica*" (Prof. Barbara Di Camillo) [ING-INF/06]
Master Degree course of Bioengineering (A.Y. 2015/2016)
Department of Information Engineering, University of Padova, Padova, Italy

Teaching activities in PhD programs

2024-2025
Lecturer *(with responsibility of the course)* at "*Advanced scientific and parallel programming with HPC infrastructures*" (20 hours, 5 credits)
PhD Program in Information Engineering (XL series 2024/25)
Department of Information Engineering, University of Padova, Padova, Italy

2023-2024
2022-2023
2021-2022
2020-2021
Lecturer *(with responsibility of the course)* at "*Advanced topics in scientific and parallel programming with practical application to the CAPRI HPC infrastructure*" (20 hours, 5 credits)
PhD Program in Information Engineering (XXXIX series 2023/24, XXXVIII series 2022/23, XXXVII series 2021/22, XXXVI series 2020/21)
Department of Information Engineering, University of Padova, Padova, Italy

2019-2020
Co-lecturer *(with responsibility of the course)* at "*Advanced topics in scientific and parallel programming with practical application to the CAPRI HPC infrastructure*" (Giacomo Baruzzo – 10 hours, 2.5 credits; Michele Schimd – 10 hours, 2.5 credits)
PhD Program in Information Engineering (XXXV series 2019/20)
Department of Information Engineering, University of Padova, Padova, Italy

Teaching activities in 2° level Short Specialisation degrees

2023-2024
Faculty staff at "*Analisi di dati omici*" (60 CFU)
Second-level Short Specialisation Degree (Master 2° livello)
University of Padova, Padova, Italy

Teaching evaluation (ANVUR)

2023-2024 Course "Scientific Computing and Object Oriented Programming" (32 hours, 4 CFU)
Master Degree course of Mathematical Engineering (A.Y. 2023/2024)
Department of Civil, Environmental and Architectural Engineering, University of Padova, Padova, Italy
Role: Lecturer *(with responsibility of the course)*

- Global satisfaction: mean 8.4/10 ; median 9/10
- Organizational aspects: mean 8.15/10 ; median 8.75/10
- Didactic action: mean 7.8/10 ; median 8.5/10

2023-2024 Course "Computational Genomics" (48 hours, 6 CFU)
Master Degree course of Computer Engineering (A.Y. 2023/2024)
Master Degree course of Bioengineering (A.Y. 2023/2024)
Department of Information Engineering, University of Padova, Padova, Italy
Role: Lecturer *(with responsibility of the course)*

- Global satisfaction: mean 7.47/10 ; median 8/10
- Organizational aspects: mean 7.95/10 ; median 8.25/10
- Didactic action: mean 8.09/10 ; median 8.75/10

2022-2023 Course "Scientific Computing and Object Oriented Programming" (48 hours, 6 CFU)
Master Degree course of Mathematical Engineering (A.Y. 2022/2023)
Department of Civil, Environmental and Architectural Engineering, University of Padova, Padova, Italy
Role: Lecturer *(with responsibility of the course)*

- Global satisfaction: mean 9/10 ; median 10/10
- Organizational aspects: mean 9.44/10 ; median 10/10
- Didactic action: mean 9.25/10 ; median 9.75/10

2021-2022 Course "Scientific Computing and Object Oriented Programming" (48 hours, 6 CFU)
Master Degree course of Mathematical Engineering (A.Y. 2021/2022)
Department of Civil, Environmental and Architectural Engineering, University of Padova, Padova, Italy
Role: Lecturer *(with responsibility of the course)*

- Global satisfaction: mean 7.33/10 ; median 8/10
- Organizational aspects: mean 8.67/10 ; median 9.25/10
- Didactic action: mean 8.17/10 ; median 9/10

Training activities

2020 Instructor at "*WebValley 2020 – Artificial Intelligence for Computational Biology*"
FBK Data Science Summer School for Interdisciplinary Research, 20th Edition
Fondazione Bruno Kessler (FBK), Trento, Italy

2020 Instructor of the course "*CAPRI-HPC: Theory and Practice in Sequential and Parallel Job Scheduling*" (Giacomo Baruzzo, Michele Schimd)
Calcolo Avanzato Per la Ricerca e l'Innovazione - Users training course
University of Padova, Padova, Italy

Theses/students advisor or co-advisor

PhD Students Advisor [ongoing]

PhD Course in Information Engineering, Department of Information Engineering, University of Padova, Padova, Italy

- Mariotto Piero, XL series, tentative thesis title: *"Computational methods and network science approaches to infer and analyze bacteria interactions from microbiome sequencing data"*

PhD Students Co-advisor [ongoing]

PhD Course in Information Engineering, Department of Information Engineering, University of Padova, Padova, Italy

- Mikele Milia, XXXVIII series, tentative thesis title: *"Multi-omics data integration to infer driver genes in ALS"*
- Matteo Baldan, XXXIX series, tentative thesis title: *"From spatial transcriptomics to differential cellular communication in multi experimental conditions"*
- Gaia Tussardi, XXXIX series, tentative thesis title: *"Development of computational methods for the identification of regulatory modules and biomarkers from transcriptomic data"*
- Andriolo Matteo, XL series, tentative thesis title: *"Computational efficient solutions for network based analysis of large datasets with applications in genomics and neurosciences"*

PhD Thesis Co-advisor

Department of Information Engineering, University of Padova, Padova, Italy

- Ilaria Patuzzi, "*16S rRNA gene sequencing sparse count matrices: a count data simulator and optimal pre-processing pipelines*", PhD Course in Information Engineering, XXXI series
- Marco Cappellato, *"Evaluation of differential abundance and network inference methods for microbiota sequencing data*", XXXV series
- Giulia Cesaro, *"Development of computational methods to infer cell-cell communication using single-cell RNA sequencing data"* PhD Course in Information Engineering, XXXVII series
- Francesca Longhin, *"Enhancing variant calling and interpretation pipelines using data-driven in-silico simulation and artificial-intelligence",* PhD Course in Information Engineering, XXXVII series

Master Thesis Advisor

Department of Information Engineering, University of Padova, Padova, Italy

- Riccardo Michelotto, *"Spatial analysis of cell-cell communication in colon cancer",* Master Degree in Bioengineering, A.Y. 2024/25
- Alessandro Tiveron, *"Orange Virtual Assistant: Investigating Large Language Models' Ability to Understand and Construct Data Mining Workflows",* Master Degree in Bioengineering, A.Y. 2024/25
- Lucchiari Alessandro *"Computational methods to analyze biological networks from transcriptomics data",* Master Degree in Computer Engineering, A.Y. 2023/24
- Andriolo Matteo *"Archetypal analysis for single-cell RNA sequencing data",* Master Degree in Computer Engineering, A.Y. 2023/24
- Matteo Girotto, *"Transforming Histopathology: A Preprocessing Pipeline for Extracting Features from H&E Whole-Slide Images Using a Transformer-Based Model.",* Master Degree in Bioengineering, A.Y. 2023/24
- Piermarco Giustini, *"Analisi bioinformatica di dati longitudinali di microbiota fecale da allevamento di suini"*, Master Degree in Computer Engineering, A.Y. 2023/24
- Brian De Marchi, *"Analisi comparativa di tre approcci computazionali per investigare la comunicazione cellula-cellula in dati di single cell RNA-seq di tumore polmonare non a piccole cellule",* Master Degree in Bioengineering, A.Y. 2023/24
- Piero Mariotto, *"Benchmarking of network inference methods applied to 16S rDNA-seq data"*, Master Degree in Bioengineering, A.Y. 2023/24
- Federico Ballarini, "*Confronto e analisi di tre strumenti computazionali per l'analisi della comunicazione cellula-cellula in dati sul cancro del colon-retto*", Master Degree in Bioengineering, A.Y. 2022/23

Department of Biology, University of Padova, Padova, Italy

- Gaia Tussardi, *"Bioinformatics tools for cellular communication analysis from single cell RNA sequencing data"*, Master Degree in Molecular Biology, A.Y. 2022/23

Master Thesis Co-advisor

Department of Information Engineering, University of Padova, Padova, Italy

- Mikele Milia, *"Data-driven approach to inform a multi-agent spatio-temporal simulator of tumor micro-enviroment"*, Master Degree in Computer Engineering, A.Y. 2020/21
- Alice Codogno, *"Modeling cell communication from single-cell RNA sequencing data and ligand-receptor molecular complexes signaling"*, Master Degree in Computer Engineering, A.Y. 2020/21
- Marco Marangia, *"Simulazione di geni differenzialmente espressi in esperimenti di sequenziamento di RNA a singola cellula"*, Master Degree in Bioengineering, A.Y. 2020/21
- Alberto Gastaldello, "*Progettazione e sviluppo di un'applicazione web per l'identificazione di primer ottimi per l'amplificazione*", Master Degree in Computer Engineering, A.Y. 2019/20
- Filippo Saretta, *"Quantificazione e caratterizzazione delle popolazioni cellulari nei tumori tramite scRNA-sequencing"*, Master Degree in Bioengineering, A.Y. 2019/20
- Marco Donà, *"A graphical user interface for single-cell data annotation and visualization of cell-cell interactions"*, Master Degree in Computer Engineering, A.Y. 2019/20
- Giulia Cesaro, *"Inference and analysis of cell-cell communication using scRNA-seq data"*, Master Degree in Bioengineering, A.Y. 2019/20
- Marco Cappellato, "*Mappatura nello spazio 2-dimensionale di cellule da dati di sequenziamento a singola cellula*", Master Degree in Bioengineering, A.Y. 2018/19
- Federica Corso, "*Confronto di metodi per la pre-elaborazione e l'identificazione di sottopopolazioni cellulari in dati di sequenziamento a singola cellula*", Master Degree in Bioengineering, A.Y. 2017/18

Bachelor Thesis Advisor

Department of Information Engineering, University of Padova, Padova, Italy

- Arianna Zuanazzi, *“Comparison of single cell RNA sequencing data integration methods with application to breast cancer data”*, Bachelor Degree in Biomedical Engineering, A.Y. 2023/24
- Francesco Vendramin, *“Confronto di metodi bioinformatici per l'inferenza della comunicazione cellulare da dati di trascrittomica a singola cellula”*, Bachelor Degree in Biomedical Engineering, A.Y. 2022/23
- Aurora Pasquetto, *“Archetypal Analysis e sue applicazione nel campo della bioinformatica”*, Bachelor Degree in Biomedical Engineering, A.Y. 2022/23

Bachelor Thesis Co-advisor

Department of Information Engineering, University of Padova, Padova, Italy

- Ludovica Bucciarelli, *“Simulazione dell’interazione tra cellular tumorali e del Sistema immunitario tramite un modello multi-agente”*, Bachelor Degree in Biomedical Engineering, A.Y. 2020/21
- Alessio Lazzarini, *“Simulazione e analisi dell’interazione tra cellule tumorali e del sistema immunitario tramite un modello multi-agente”*, Bachelor Degree in Biomedical Engineering, A.Y. 2019/20
- Giovanni Finco, “*A cellular automata model simulating the effect of the immune system on tumor growth*”, Bachelor Degree in Information Engineering, A.Y. 2017/18
- Francesco Morandin, “*A cellular automata model simulating the effects of intratumoral heterogeneity on immune response*”, Bachelor Degree in Information Engineering, A.Y. 2017/18

Attended workshops, training courses and summer schools

Workshop	**RNA-seq Full Day Hands-on Workshop for the Bioinformatician**, University of Milan, Milan, Italy, June 11, 2014
Workshop	**AxA Workshop – Workshop on Advanced Algorithms on Strings**, Venice, Italy, from June 21 to June 24, 2016
Training course	**Analysis of single cell RNA-seq data**, University of Cambridge, Cambridge, UK, from October 31 to November 1, 2017
Summer School	**CINECA Summer School on Parallel Computing**, CINECA Rome offices, Rome, Italy, from July 9 to July 20, 2018
Workshop	**Workshop on Research and Education in Computer Engineering,** Castelfranco Veneto (TV), Italy, October 19, 2021
Summer School	**8th Mediterranean School of Complex Networks (MSCX 2023)**, Catania, Italy, from June 26 to June 30, 2023

Computer and programming skills

OS	Unix/Linux, Windows
Programming and scripting	Java, C, C++, C#, openMP, MPI, Shell Bash, Python, Perl, Matlab, R
Database	MySQL, PostgreSQL, SQLite
Other	Git, Docker, Singularity, LaTeX

Languages

Italian	Native
English	Proficient user (B/C CEFR level)

Personal skills

Communication skill	Excellent communication and presentation skills, written and verbal communication skills (built up through presentations and scientific writing during my research activity)
Managerial and interpersonal skill	Good managerial and interpersonal skills, several teamwork experiences, ability to work in interdisciplinary projects
Other skills	Ability to work well under pressure, excellent logical thinking and problem-solving skills