europass Curriculum vitae

PERSONAL INFORMATION

Giulia Cesaro

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Date of birth 4 July 1996 | Nationality Italian

RESEARCH EXPERIENCE

October 2024 – Present

Junior postdoctoral researcher (research grant type B)

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

Research project: “Developing computationally-efficient network science methods to model cell-specific dynamics of cell-cell communication using single-cell transcriptomics data”

Research area: Bioinformatics and network science applied to single-cell RNA-sequencing data

January 2024 – July 2024

Visiting Ph.D. student

Institute for Computational Genomics, RWTH Aachen University, Aachen, Germany

Research area: Network science applied to single-cell RNA-sequencing data

Host supervisor: Prof. Ivan G. Costa

February 2021 – September 2021

Research grant (type A)

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

Research project: “Modeling interactions between ligands and receptors in neurodegenerative diseases (ALS)”

Research area: Bioinformatics and computational modeling on single-cell RNA-sequencing data

March 2018 – June 2018

Traineeship at Human Movement Bioengineering Lab (BiomovLab)

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

Research project: “Biomechanical analysis of running”

Research area: Biomechanics of movement

EDUCATION

October 2021 –September 2024

Ph.D. in Information Engineering (curriculum ICT)

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

Thesis: Development of computational models to infer cell-cell communication using single-cell RNA sequencing data

Research area: Bioinformatics, network science and computer science applied to single-cell RNA-sequencing data

Advisor: Barbara Di Camillo

October 2018–November 2020

Master’s degree in Bioingegneria, 110/110 cum laude

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

Thesis: Inference and analysis of cell-cell communication using scRNA-seq data

Research area: Bioinformatics applied to single-cell RNA-sequencing data

Advisor: Barbara Di Camillo

October 2015–July 2018

Bachelor’s degree in Ingegneria Biomedica, 110/110 cum laude

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

Thesis: Sprinters’ Biomechanical analysis: comparison between a male and a female élite team

Research area: Biomechanics of movement

Advisor: Zimi Sawacha

TRAINING

4-5 February 2025

Course "Advanced technologies in single cell omics"

Federazione Italiana Scienze della Vita (FISV)

Topic: Bioinformatics applied to single cell omics data

11 September – 16 October 2024

Webinar series "Advances in spatial omics: Exploring concepts, innovations, and resources"

European Molecular Biology Laboratory-European Bioinformatics Institute (EMBL-EBI)

Topic: Bioinformatics applied to spatial omics data

14-15 September 2023

Workshop "Frontiers of High Performance Computing for Modeling and Simulation"

University of Padova

Topic: High performance computing

18-22 September 2023

Workshop "Epigenomics Data Analysis: from bulk to single cell"

NBIS-National Bioinformatics Infrastructure Sweden

Topic: Bioinformatics applied to epigenomics

25-30 June 2023

VIII Mediterranean School of Complex Networks

Consorzio Cometa, University of Padova, University of Catania, Rovili I Virgili University

Topic: network science for complex systems and dynamical processes, with applications to biology, economic, social sciences

22 September 2022

Workshop “Spatial transcriptomics and cell-cell communication modeling: new opportunities to study the cellular dynamics of biological systems”

21st European Conference on Computational Biology (ECCB 2022)

Topic: Bioinformatics applied to single-cell and spatial transcriptomics data.

7-10 Octorber 2020

XXXIX Annual School of Bioengineering “Artificial intelligence-enabled heath care: from decision support to autonomous robots”

National Bioengineering Group (GNB), online

Topic: Artificial Intelligence for health care and life sciences

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.*
Track: "High Performance Computing in Modelling and Simulation"

Long-mobility grant	**Fondazione Ing. Aldo Gini** based at the University of Padova, 2023
Best Oral Talk	At **Student Council Symposium at 31st Conference on Intelligent Systems for Molecular Biology and 22nd European Conference on Computational Biology** (ISMB/ECCB 2023), 23-27 July 2023, Lyon, France. Abstract: *CClens: a cellular communication workflow for large-scale single-cell RNA sequencing data*
Best Flash Talk and Scholarship	**Young BITS-RSG PhD Symposium at Bioinformatics Italian Society** (BITS 2022), 27-29 June 2022, Verona, Italy. Abstract: *Development of computational models to infer and analyze cell-cell communication using scRNA-seq data*
Award	**“Mille e una lode” merit-based award**, University of Padova, A.Y. 2018/2019
Award	**“Mille e una lode” merit-based award**, University of Padova, A.Y. 2017/2018
Award	**Merit-based incentive for scientific degree programs**, University of Padova, A.Y. 2017/2018
Award	**“Mille e una lode” merit-based award**, University of Padova, A.Y. 2016/2017

MEMBERSHIP

Member	International Society for Computational Biology (ISCB)
Secretary	Italian regional young researcher group of the International Society of Computational Biology (RSG-Italy)
Member	Young-InfoLife group, InfoLife National Laboratory of CINI

TEACHING ACTIVITY

October 2024 - January 2025	**Teaching assistant** at "Computational Genomics" course in Bioengineering degree
October 2023 - January 2024	**Tutor Junior** at "Elementi di Informatica e Programmazione" course in Ingegneria Biomedica degree
October 2022 - January 2023	**Tutor Junior** at "Elementi di Informatica e Programmazione" course in Ingegneria Biomedica degree

THESES/STUDENT CO-ADVISOR

Thesis co-advisor	– Lucchiari Alessandro, *Computational methods to analyze biological networks from transcriptomics data*, Master Degree in Computer Engineering, A.Y. 2023/2024 – Arianna Zuanazzi, *Comparison of single cell RNA sequencinf data integration methods with application to breast cancer data*, Bachelor Degree in Biomedical Engineering, A.Y. 2023/2024 – Brian De Marchi, *Analisis comparativa di tre approacci computationali 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. 2023/2024 – 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. 2023/2024 – Gaia Tussardi, *Bioinformatics tools for cellular communication analysis from single cell RNA sequencing data*, Master Degree in Molecular Biology, A.Y. 2022/2023 – Mikele Milia, *Data-driven approach to inform a multi-agent spatio-temporal simulator of tumor micro-environment*, Master Degree in Computer Engineering, A.Y. 2020/2021 – Alice Codogno, *Modeling cell communication from single-cell RNA sequencing data and ligand-receptor molecular complexes signaling*, Master Degree in Computer Engineering, A.Y. 2020/2021 – Ludovica Bucciarelli, *Simulazione dell’interazione tra cellule tumorali e del sistema immunitario tramite un modello multi-agente*, Bachelor Degree in Biomedical Engineering, A.Y. 2020/2021

ROLE IN ORGANIZATION OF INTERNATIONAL SCIENTIFIC CONFERENCES/EVENTS

Co-organizer, Instructor	**Tutorial “Software containerization in Bioinformatics: how to make reproducible, portable and reusable bioinformatics software & pipelines”** at 21st European Conference on Computational Biology (ECCB 2022), 18 September, 2022, Sitges, Spain

Co-organizer, Instructor	**Tutorial "How to make reproducible, portable and reusable bioinformatics software containerization"** at 31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023), 23 July, 2023, Lyon, France
Program committee, Scientific committee, Co-chair	**RSG-Italy Young Symposium at 18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**, 8 September, 2023, Padova, Italy
Program committee, Local committee	**18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)**, 6-8 September, 2023, Padova, Italy
Co-organizer, Scientific committee, Session Chair	**Young Minds at Work: Blending Biochemistry and Bioinformatics - 2nd edition**, 10-12 December, 2024, Virtual
Co-organizer, Scientific committee, Chair	**YOUNG BITS, RSG-Italy & CINI Young-InfoLife Symposium at 21st Annual Meeting of the Bioinformatics Italian Society (BITS2025)**, June 13, 2025, Napoli, Italy
Co-organizer, Instructor, Speaker	**Tutorial "Computational approaches for deciphering cell-cell communication from single-cell transcriptomics and spatial transcriptomics data"** at 33rd Conference on Intelligent Systems for Molecular Biology & 24th European Conference on Computational Biology (ISMB/ECCB 2025), 15 July, 2025, Virtual
Co-organizer, Speaker/trainer	**1st International Biohackathon of the Bioinformatics Italian Society 2025**, June 10, 2025, Napoli, Italy

JOURNAL ARTICLE

Journal article J1	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**, Volume 7, Issue 2, June 2025, lqaf084 [Scimago Q1] DOI: `https://doi.org/10.1093/nargab/lqaf084` Contributions: conceptualization, literature review, data curation, formal analysis, methodology, software, manuscript writing, visualization
Journal article J2	G. Cesaro, J. S. Nagai, N. Gnoato, A. Chiodi, G. Tussardi, V. Klöker, C. V. Musumarra, E. Mosca, I. G. Costa, B. Di Camillo, E. Calura, G. Baruzzo, *"Advances and challenges in cell–cell communication inference: a comprehensive review of tools, resources, and future directions"*, **Briefings in Bioinformatics**, Volume 26, Issue 3, May 2025, bbaf280 [Scimago Q1] DOI: `https://doi.org/10.1093/bib/bbaf280` Contributions: formal analysis, literature review, methodology, software, data analysis and interpretation, manuscript writing and reviewing
Journal article J3	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**, Volume 2, Issue 1, 2022, vbac092 [Scimago Q1] DOI: `https://doi.org/10.1093/bioadv/vbac092` Contributions: literature review, methodology, manuscript writing, data analysis and interpretation, conceptualization
Journal article J4	G. Baruzzo, G. Cesaro, B. Di Camillo, *"Identify, quantify and characterize cellular communication from single-cell RNA sequencing data with scSeqComm"*, **Bioinformatics**, Volume 38, Issue 7, 1 April 2022, Pages 1920-1929 [Scimago Q1] DOI: `https://doi.org/10.1093/bioinformatics/btac036` Contributions: methodology, literature review, data analysis and interpretation, software
Conference article	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, May 2025 DOI: `https://dx.doi.org/10.1109/pdp66500.2025.00045` Contributions: formal analysis, literature review, methodology, software, data analysis and interpretation, manuscript writing and reviewing

NATIONAL AND INTERNATIONAL CONFERENCE CONTRIBUTIONS

C1	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 **17th Annual Meeting of the Bioinformatics Italian Society (BITS 2021)**

C2 Abstract w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *"Analyze cellular communication from single cell RNA sequencing data with scSeqComm"* at **16th Bioinformatics and Computational Biology Conference (BBCC 2021)**

C3 Abstract/poster: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Differential cellular communication analysis from single cell RNA sequencing data with scSeqComm"* at **18th Annual Meeting of the Bioinformatics Italian Society (BITS 2022)**

C4 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 **18th Annual Meeting of the Bioinformatics Italian Society (BITS 2022)**

C5 Abstract w/ oral presentation: G. Cesaro, *"Development of computational models to infer and analyze cell-cell communication using scRNA-seq data"* at **Young BITS-RSG PhD Symposium at 18th Annual Meeting of the Bioinformatics Italian Society (BITS 2022)**

C6 Abstract w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Differential cell-cell communication analysis with scSeqComm"* at **workshop on "Spatial transcriptomics and cell-cell communication modeling: new opportunities to study the cellular dynamics of biological systems" at 21st European Conference on Computational Biology (ECCB 2022)**

C7 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 on Computational Biology (ECCB 2022)**

C8 Abstract/poster: M. Milia, G. Cesaro, G. Baruzzo, G. Finco, F. Morandini, P. Alotto, NF. 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 on Computational Biology (ECCB 2022)**

C9 Abstract w/ oral presentation: G. Cesaro, G. Baruzzo, B. Di Camillo, *"Differential cellular communication analysis across multi-condition and multipatient scRNA-seq data"* at **17th Bioinformatics and Computational Biology Conference (BBCC 2022)**

C10 Abstract/poster: G. Cesaro, M. Milia, G. Baruzzo, P. Alotto, NF. 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 1**7th Bioinformatics and Computational Biology Conference (BBCC 2022)**

C11 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 conference 2023**

C12 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 **19th Annual Meeting of the Bioinformatics Italian Society (BITS 2023)**

C13 Abstract w/ oral presentation: G. Cesaro, *"A statistical and network-based method to infer cellular communication from single-cell rna sequencing data"* at **8th Mediterranean School of Complex Networks (MSCX 2023)**

C14 Long abstract/poster w/ oral presentation: G. Cesaro, M. Milia, G. Baruzzo, P. Alotto, NF. 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)**

C15 Long 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)**

C16 Long 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)**

C17 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)**

C18 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 **Student Council Symposium - 31st Conference on Intelligent Systems for Molecular Biology & 22nd European Conference on Computational Biology (ISMB/ECCB 2023)**

C19 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)**

C20 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 **20th Annual Meeting of the Bioinformatics Italian Society (BITS 2024)**

C21 Abstract w/ oral presentation: H. F.E. Gleitz, J. S. Nagai, M. Ruiz, S. Fuchs, I. Snoeren, A. Boeree, G. Cesaro, R. Kramann, I. Costa, R. K. Schneider, *"Physically interacting cell sequencing in bone marrow fibrosis reveals distinct cellular niches in fibrosis"* at **53rd Annual Scientific Meeting of International Society for Experimental Hematology (ISEH 2024)**

C22 Abstract w/ oral presentation: G. Tussardi, G. Cesaro, B. Di Camillo, G. Baruzzo, *"Addressing the Biological Interpration of High-Dimensional Cell-Cell Communication Data from Single Cell Transcriptomics Through an Interative Web Application"* at **2nd Young Minds at Work: Blending Biochemistry and Bioinformatics (YMW2024)**

C23 Full article w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *"quickSparseM: a library for memory- and time-efficient computation on large, sparse marices with application to omics data"* at **33rd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP2025)**

C24 Abstract/poster: G. Cesaro, J. Nagai, G. Baruzzo, B. Di Camillo, I. Costa, *"Intracellular signaling pathway reconstruction at single-cell resolution"* at **21st Annual Meeting of the Bioinformatics Italian Society (BITS2025)**

C25 Abstract w/ oral presentation: G. Baruzzo, G. Cesaro, B. Di Camillo, *"Sustainable computation on large, sparse omics matrices with quickSparseM"* at **21st Annual Meeting of the Bioinformatics Italian Society (BITS2025)**

C26 Full article w/ oral presentation: M. Baldan, G. Cesaro, G. Baruzzo, B. Di Camillo, *"Biologically Informed procedure for Feature Summarization in Spatial Transcriptomics"* at **International Joint Conference on Neural Networks (IJCNN2025)**

C27 Abstract/poster: G. Tussardi, G. Cesaro, G. Baruzzo, B. Di Camillo, *"Multilevel Network Visualization for Deciphering Dysregulated Cellular Signalling"* at **33rd Conference on Intelligent Systems for Molecular Biology and the 24th European Conference on Computational Biology (ISMB/ECCB 2025)**

C28 Abstract/poster: M. Baldan, G. Cesaro, G. Baruzzo, B. Di Camillo, *"Integrating Biological Knowledge for Feature Summarization in Spatial Transcriptomics"* at **33rd Conference on Intelligent Systems for Molecular Biology and the 24th European Conference on Computational Biology (ISMB/ECCB 2025)**

C29 Abstract w/ oral presentation: H. Gleitz, M. L. Ruiz, J. Nagai, G. Cesaro, I. Costa and R. Schneider, *"Nichesphere: A method to identify disease specific physical cell-cell interactions and underlying cellular communication networks"* at **33rd Conference on Intelligent Systems for Molecular Biology and the 24th European Conference on Computational Biology (ISMB/ECCB 2025)**

C30 Abstract w/ oral presentation: G. Cesaro, J. Nagai, G. Baruzzo, B. Di Camillo, I. Costa, *"Cell-specific Graph Operation Strategy on Signaling Intracellular Pathways"* at **33rd Conference on Intelligent Systems for Molecular Biology and the 24th European Conference on Computational Biology (ISMB/ECCB 2025)**

REFEREE ACTIVITY

Journal Referee

- IEEE Journal of Biomedical and Health Informatics (IEEE JBHI)
- Journal of Biomedical Informatics (JBI)
- Systems Biology and Applications

Conference Referee

- 20th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2025)
- 23rd International Conference of "Artificial Intelligence in Medicine" (AIME 2025)
- 19th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2024)
- 18th Conference on Computational Intelligence Methods for Bioinformatics & Biostatistics (CIBB 2023)
- 21st International Conference of "Artificial Intelligence in Medicine" (AIME 2023)
- 21st International Conference of "Artificial Intelligence in Medicine" (AIME 2023)

SOFTWARE PROJECTS

`scSeqComm`	A R package to infer and quantify intercellular and intracellular communication from single-cell RNA-sequencing data based on statistical and network science methodologies. Available at `https://gitlab.com/sysbiobig/scseqcomm`
`quickSparseM`	A R/C++ library package for memory- and time-efficient computation on large, sparse matrices with application to omics data. Available at `https://gitlab.com/sysbiobig/quicksparsem`
`CClens`	A R/Shiny package for the interpratation and exploration of multi-dimensional scRNA-seq cell-cell communication data. Available at `https://gitlab.com/sysbiobig/cclens`
`MAST`	A hybrid Multi-Agents based Spatio-Temporal model of tumor microenvironment informed using omics data. Available at `https://gitlab.com/sysbiobig/mast`

PERSONAL SKILLS

Mother tongue: Italian

Other languages	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
English	B2	B2	B2	B2	B2

Levels: A1 and A2: Basic user – B1 and B2: Independent user – C1 and C2: Proficient user
Common European Framework of Reference for Languages

Organisational/Communication skills

- Good teaching and supervision skills acquired through my roles as co-supervisor, instructor, teaching assistant and tutor.
- Good attitude to work autonomously, as demonstrated in my research experiences
- Effective communication skills honed through various research presentations to diverse audiences (conferences, workshops and other events).
- Problem-solving attitude acquired through research experiences
- Good organizational skills developed through my involvement in organizing conferences, workshops and tutorials
- Collaborative and team-oriented approach in multidisciplinary environment gained collaborating with individuals from diverse backgrounds

Computer skills

- Advanced skill: R (e.g. Seurat, Bioconductor libraries, igraph), Matlab, Linux environment, Singulary container engines
- Intermediate skill: Python, Docker container engines, Cytoscape
- Basic skill: SQL, C++