

Curriculum vitae

Postdoctoral Researcher

Department of Computing Sciences, Bocconi University

Tangherloni Andrea

07/02/1990

Via Guglielmo Röntgen 1, 20136, Milan, Italy

(+39) 340 7752531 | (+44) (0) 773 282 6479
andrea.tangherloni@unibocconi.it
andrea.tangherloni@arubapec.it



Work experience

Assistant Professor

SEPTEMBER 2023 - CURRENT

Department of Computing Sciences, Bocconi University, Italy
Bocconi Institute for Data Science and Analytics, Bocconi University, Italy

Postdoctoral Researcher

DECEMBER 2022 - CURRENT

Bocconi Institute for Data Science and Analytics, Bocconi University, Italy
Department of Computing Sciences, Bocconi University, Italy

Postdoctoral Researcher

DECEMBER 2020 - NOVEMBER 2022

Department of Human and Social Sciences, University of Bergamo, Italy

Research Associate (Postdoctoral Researcher)

NOVEMBER 2018 - NOVEMBER 2020

Department of Haematology, University of Cambridge, Cambridge, UK
Wellcome – MRC Stem Cell Institute, Cambridge, UK
Visiting worker at Wellcome Trust Sanger Institute, Hinxton, UK

Education and training

PhD in Computer Science

NOVEMBER 2015 - FEBRUARY 2019

Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy

Dissertation title: *“High-Performance Computing to tackle complex problems in life sciences”*. Supervisors: Prof. Daniela Besozzi and Prof. Paolo Cazzaniga

Master of Science in Computer Science

NOVEMBER 2013 - OCTOBER 2015 (110/110 summa cum laude)

Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy

Dissertation title: *“Design and development of a large-scale biochemical simulator accelerated on GPUs”*. Supervisor: Prof. Giancarlo Mauri

Bachelor of Science in Computer Science

OCTOBER 2010 - OCTOBER 2013 (107/110)

Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy

Dissertation title: *“Development of a food database for feature-based classification and retrieval”*. Supervisor: Prof. Raimondo Schettini

Education/training abroad

Erasmus+ Traineeship Program (A.Y. 2017/18, 05/04/2018 – 05/07/2018) with the highest evaluation (90/90): visiting PhD student at the Department of Computer Science and Technology (The Computer Laboratory), University of Cambridge, Cambridge, UK

ExtraUE Exchange Program (A.A. 2016/17, 06/06/2017 – 06/08/2017) with the highest evaluation (100/100): visiting PhD student at the Department of Cancer Biology, School of Medicine, Vanderbilt University, Nashville, TN, USA

Research interests

Artificial Intelligence and Machine Learning
Computational Intelligence
High-Performance Computing
Computational Biology and Systems Biology
Bioinformatics
Mathematical modelling and simulation of complex biological systems
Biomedical image analysis

Awards and prizes

Second place at the Start Cup Bergamo 2021 (Start Cup School and Competition) with the project “ReHubAI: il rimedio a portata di click!”, Department of Management Information and Production Engineering, and Center for Young and Family Enterprise (CYFE), University of Bergamo, Italy

Teaching activity

First and second level master’s degrees

Lectures (4 hours, A.Y. 2022/23): Neural networks and deep learning, Second Level Master’s Degree in Methods and Data Analysis in Biomedical Research (MEDAL), University of Milano-Bicocca, Italy

Master’s degrees

Lecturer (32 hours, A.Y. 2023/24): Deep Learning and Reinforcement Learning, Master’s Degree in Artificial Intelligence, Bocconi University, Italy

Laboratory lectures (16 hours, A.Y. 2021/22): ICT Systems Management, Master’s Degree in Management Engineering, University of Bergamo, Italy

Laboratory tutor (30 hours, A.Y. 2017/18): Data Technology and Machine Learning, Master’s Degree in Computer Science, University of Milano-Bicocca, Italy

Bachelor’s degrees

Lecturer (30 hours, A.Y. 2023/24): Machine Learning and Artificial Intelligence, Bachelor’s Degree in Mathematical and Computing Sciences for Artificial Intelligence, Bocconi University, Italy

Lecturer (40 hours, A.Y. 2023/24): Computer Science, Bachelor’s Degrees, Bocconi University, Italy

Teaching assistant (30 hours, A.Y. 2022/23): Topics in Computational Modelling: from Information Theory to Evolutionary Models, Bachelor’s Degree in Mathematical and Computing Sciences for Artificial Intelligence, Bocconi University, Italy

Laboratory lectures (6 hours, A.Y. 2022/23): Fundamentals of informatics and statistics, Bachelor’s Degree in Psychological Studies, University of Bergamo

Laboratory tutor (30 hours, A.Y. 2021/22): Computer Science, Bachelor’s Degree

in Biotechnology, University of Milano-Bicocca, Italy

Laboratory lectures (6 hours, A.Y. 2020/21): Fundamentals of informatics and statistics, Bachelor's Degree in Psychological Studies, University of Bergamo

Laboratory lectures (24 hours, A.Y. 2016/17): Computer Architecture, Bachelor's Degree in Computer Science, University of Milano-Bicocca, Italy

E-learning tutor (30 hours, A.Y. 2014/15): Operating Systems and Computer Networks, Bachelor's Degree in Computer Science, University of Milano-Bicocca, Italy

Other

Lessons and laboratory (June 21 - 30, 2023): Transcriptomics Advanced Course, EMBL-EBI, Wellcome Genome Campus, Hinxton, UK

Lessons and laboratory (24 hours May 30 - 31 and June 1, 2017): Python for Beginners, Micron Semiconductor Italia S.R.L., Milan, Italy

Students' supervision

First level master's degrees

2021: co-supervision of a first-level Master's thesis (with Dr Marabini Leonardo) in Marketing Management, Scuola di Alta Formazione, Bergamo, Italy

Master's degrees

2019: co-supervision of two Master's theses (with Prof. Daniela Besozzi and Dr. Ana Cvejic) in Computer Science, Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy

Bachelor's degrees

2023: co-supervision of a Bachelor's thesis (with Prof. Francesca Buffa Besozzi) in Computer Science, Bachelor's Degree in Mathematical and Computing Sciences for Artificial Intelligence, Bocconi University, Italy

2018: co-supervision of a Bachelor's thesis (with Prof. Daniela Besozzi) in Computer Science, Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy

2017: co-supervision of two Bachelor's theses (with Prof. Daniela Besozzi) in Computer Science, Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy

Conferences and talks

Conferences

Speaker at the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology, The Netherlands, 2023. Title of the talk: *"Consensus clustering strategy for cell type assignments of scRNA-seq data"*

Speaker at the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology, Canada, 2022. Title of the talk: *"Multi-objective Optimization for Marker Panel Identification in Single-cell Data"*

Speaker at the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology, Canada, 2022. Title of the talk: *"A Deep Learning Pipeline for the Automatic cell type Assignment of scRNA-seq Data"*

Speaker at the IEEE International Conference on Bioinformatics and Biomedicine, Virtual, 2021. Title of the talk: *"Integration of Multiple scRNA-Seq Datasets on the Autoencoder Latent Space"*

Speaker at the 17th International Conference on Computational Intelligence Methods For Bioinformatics And Biostatistics, Virtual, 2021. Title of the talk:

“Genetic Algorithms for the identification of marker panels in single-cell RNA Data”

Speaker at the IEEE Congress on Evolutionary Computation, Virtual, 2021. Title of the talk: *“The Impact of Representation on the Optimization of Marker Panels for Single-cell RNA Data”*

Speaker at the 24th International European Conference on Parallel and Distributed Computing, Turin, Italy, 2018. Title of the talk: *“High Performance Computing for Haplotyping: Models and Platforms”*

Speaker at the 17th International Workshop on Network Tools and Applications in Biology, Palermo, Italy, 2017. Title of the talk: *“GenHap: A Novel Computational Method Based on Genetic Algorithms for Haplotype Assembly”*

Speaker at the 12th International Meeting on Computational Intelligence Methods For Bioinformatics And Biostatistics, Naples, Italy, 2015. Title of the talk: *“Deterministic Simulations of Large-Scale Models of Cellular Processes Accelerated on Graphics Processing Units”*

Seminars

Speaker at the Milan meeting on “Next Generation Sequencing”, University of Milano-Bicocca, Italy, 2022. Title of the talk: *“Automatic cell-type annotation of scRNA-seq data: an overview”*

Speaker at the Internal Seminar Series, Wellcome - MRC Stem Cell Institute, Cambridge, UK, 2019. Title of the talk: *“Advanced Machine Learning approaches for the downstream analysis of scRNA-Seq data”*

Speaker at the Department of Computer Science and Technology, University of Cambridge, Cambridge, UK, 2018. Title of the talk: *“High-Performance Computing Applied to Computational Intelligence in Systems Biology and Genome Analysis”*

Speaker at the 1st Computational Intelligence and Biomathematics, Rio de Janeiro, Brasile, 2017. Title of the webinar: *“Biomedical Image Segmentation and Analysis Using Machine Learning and Computational Intelligence Techniques”* (co-author Dr. Leonardo Rundo)

Speaker at the Department of Cancer Biology, Vanderbilt University, Nashville, TN, USA, 2017. Title of the talk: *“High Performance Computing to Tackle Complex Problems in Life Sciences”*

Program Committee and Organization Committee

Conferences

Member of the Organizing Committee of the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology, 2023

Member of the Program Committee of the 14th International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies, 2022

Member of the Program Committee of the 8th International Conference on Machine Learning, Optimization, and Data Science, 2022

Member of the Program Committee of the 7th International Conference on Machine Learning, Optimization, and Data Science, 2021

Member of the Program Committee of the 6th International Conference on Machine Learning, Optimization, and Data Science, 2020

Special Sessions and workshops

Co-chair of the Special Session *“Candidate Solution Representation and Fitness Landscape Manipulation”*, IEEE Congress on Evolutionary Computation, 2023

Co-chair of the Special Session *“Candidate solution representation and fitness landscape manipulation”*, IEEE International Conference on Computational

Intelligence in Bioinformatics and Computational Biology, 2022

Member of the Program Committee of the Special Session “*Candidate solutions representation and fitness landscape manipulation*”, IEEE Congress on Evolutionary Computation, 2021

Co-chair of the Workshop “*Machine Learning and Computational Intelligence in multi-omics and medical image analysis*”, 16th International Conference on Artificial Intelligence Applications and Innovations, 2020,

Local Organizer of the International Workshop on Bio-Design Automation, 2019

Co-chair of the Special Session “*Machine Learning and Computational Intelligence in multi-omics and medical image analysis*”, 16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, 2019

Member of the Program Committee of the post-proceedings of the 16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, 2019, LNCS

Member of the Program Committee of the Special Session “*Fast and Efficient Solutions for Computational Intelligence Methods in Bioinformatics, Systems and Computational Biology*”, 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, 2018

Member of the Program Committee of the Special Session “*Modeling and Simulation Methods for System Biology and System Medicine*”, 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, 2018

Member of the Program Committee of the Special Session “*Advances in High-Performance Bioinformatics and Biomedicine*”, 26th Euromicro International Conference on Parallel, Distributed, and Network-Based Processing, 2018

Member of the Program Committee of the Special Session “*Advances in High-Performance Bioinformatics, Systems and Synthetic Biology*”, 25th Euromicro International Conference on Parallel, Distributed, and Network-Based Processing, 2017

Special Session “*Parallel and distributed high performance computing solutions for computational intelligence methods*”, IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology, 2016

Referee activity

Peer-Reviewed journals

Mathematical Biosciences and Engineering (AIMS Press); Applied Soft Computing (Elsevier); Artificial Intelligence in Medicine (Elsevier); Biosafety and Health (Elsevier); Computational and Structural Biotechnology Journal (Elsevier); Computer Methods and Programs in Biomedicine (Elsevier); Computers in Biology and Medicine (Elsevier); Expert Systems With Applications (Elsevier); Journal of Industrial Information Integration (Elsevier); Knowledge-based Systems (Elsevier); Neurocomputing (Elsevier); Parallel Computing Systems & Applications (Elsevier); Frontiers in Bioengineering and Biotechnology (Frontiers); Frontiers in Cell and Developmental Biology (Frontiers); Frontiers in Genetics (Frontiers); Frontiers in Immunology (Frontiers); Frontiers in Neurology (Frontiers); Frontiers in Oncology (Frontiers); Frontiers in Plant Science (Frontiers); Computational and Mathematical Methods in Medicine (Hindawi); IEEE Access (IEEE); IEEE Computational Intelligence Magazine (IEEE); IEEE Transactions on Artificial Intelligence (IEEE); Fundamenta Informaticae (IOS Press); Concurrency and Computation: Practice and Experience (John Wiley & Sons); Algorithms (MDPI); Applied Sciences (MDPI); BioChem (MDPI); Biomolecules (MDPI); Cancers (MDPI); Diagnostics (MDPI); Electronics (MDPI); Genes (MDPI); Journal of Imaging (MDPI); Mathematics (MDPI); Sensors

(MDPI); Signals (MDPI); Sustainability (MDPI); Symmetry (MDPI); Bioinformatics (Oxford Academic); Nucleic Acids Research (Oxford Academic); PLoS Computational Biology (PLOS); BMC Bioinformatics (Springer Nature); BMC Medical Informatics and Decision Making (Springer Nature); Communications Biology (Springer Nature); International Journal of Machine Learning and Cybernetics (Springer Nature); Nature Methods (Springer Nature); The Journal of Supercomputing (Springer Nature); Engineering Optimization (Taylor & Francis); Smart Science (Taylor & Francis)

International conferences

Euromicro International Conference on Parallel, Distributed, and Network-Based Processing; IEEE Congress on Evolutionary Computation; IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology; International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies; International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics; International Conference on Machine Learning, Optimization, and Data Science

PhD students

Reviewer for a PhD thesis at the University of Eastern Finland and Sapienza University of Rome

Transfer of Status Assessor for a PhD student at the University of Oxford

Editorial activities

Associate Editor

PLoS ONE, Public Library of Science

Heliyon (Computer Science Section), Cell Press

BMC Bioinformatics, Springer-Nature

Review Editor

"*Computational Genomics*", Frontiers in Genetics, Frontiers in Bioengineering and Biotechnology, and Frontiers in Plant Science

Topic Editor

"*Biomedical Engineering*", Applied Sciences (MDPI)

Guest Editor

"*Artificial Intelligence Techniques for Medical Imaging and Computational Biology*", Special Issue, Applied Sciences (MDPI)

"*Artificial Intelligence Approaches for the Analysis and Integration of Omics Data*", Research Topic in Integrative Bioinformatics, Frontiers in Bioinformatics

"*Machine Learning Applied to Medical Imaging and Computational Biology*", Special Issue, Applied Sciences (MDPI)

Ancillary activities

2022-Current: Member of the IEEE CIS Task Force on advanced representation in biological and medical search and optimization

2020: Member of the Stem Cell Institute Public Engagement network, Wellcome – MRC Stem Cell Institute, Cambridge, UK

2015-2018: PhD Representative, Department of Informatics, Systems and Communication, University of Milano-Bicocca

Other information

Author/co-author of more than 40 publications in international peer-reviewed journals, international conference proceedings, and book chapters.
Google Scholar: 1249 citations; h-index = 17
Scopus: 831 citations; h-index = 14

Languages

Italian: mother tongue
English: excellent

Date

05/09/2023

SignatureA handwritten signature in black ink, written over a horizontal line. The signature is stylized and appears to be 'Antonio M. J.'.

Publications

Journals

1. **Tangherloni A†**, Riva SG, Myers B, Buffa FM, Cazzaniga P (2023). *MAGNETO: Marker pAnels GeNEraTor with multi-Objective optimization*. **Journal of Biomedical Informatics**, accepted
2. Papetti DM, **Tangherloni A**, Farinati D, Cazzaniga P, Vanneschi L (2023). *Simplifying Fitness Landscapes using Dilation Functions evolved with Genetic Programming*. **IEEE Computational Intelligence Magazine**, 18(1): 22-31. DOI: 10.1109/MCI.2022.3222096
3. Riva SG, Cazzaniga P, Nobile MS, Spolaor S, Rundo L, Besozzi D, **Tangherloni A†** (2022). *SMGen: A generator of synthetic models of biochemical reaction networks*. **Symmetry**, 14(1): 119. DOI: 10.3390/sym14010119
4. Castelli M, Manzoni L, Mariot L, Nobile MS, **Tangherloni A** (2022). *Salp Swarm Optimization: a Critical Review*. **Expert Systems with Applications**, 189: 116029. DOI: 10.1016/j.eswa.2021.116029
5. **Tangherloni A†**, Nobile MS, Cazzaniga P, Capitoli G, Spolaor S, Rundo L, Mauri G, Besozzi D (2021). *FiCoS: a fine- and coarse-grained GPU-powered deterministic simulator for biochemical networks*. **PLoS Computational Biology**, 17(9): e1009410. DOI: 10.1371/journal.pcbi.1009410
6. **Tangherloni A†**, Ricciuti F, Besozzi D, Liò P, Cvejic A (2021). *Analysis of single-cell RNA sequencing data based on autoencoders*. **BMC Bioinformatics**, 22(1): 309. DOI: 10.1186/s12859-021-04150-3
7. Ranzoni AM*, **Tangherloni A***, Berest I*, Riva SG, Myers B, Strzelecka PM, Xu J, Panada E, Mohorianu I, Zaugg JB, Cvejic A (2021). *Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis*. **Cell Stem Cell**, 28(3): 472-487. DOI: 10.1016/j.stem.2020.11.015
8. Rundo L*, **Tangherloni A***, Cazzaniga P, Mistri M, Galimberti S, Woitek R, Sala E, Mauri G, Nobile MS (2021). *A CUDA-powered method for the feature extraction and unsupervised analysis of medical images*. **The Journal of Supercomputing**. DOI: 10.1007/s11227-020-03565-8
9. Rundo L*, **Tangherloni A***, Tyson DR*, Betta R, Militello C, Spolaor S, Nobile MS, Besozzi D, Lubbock ALR, Quaranta V, Mauri G, Lopez CF, Cazzaniga P (2020). *ACDC: Automated cell detection and counting for time-lapse fluorescence microscopy*. **Applied Sciences**, 10(18), 6187. DOI: 10.3390/app10186187
10. Besozzi D, Manzoni L, Nobile MS, Spolaor S, Castelli M, Vanneschi L, Cazzaniga P, Ruberto S, Rundo L, **Tangherloni A** (2020). *Computational Intelligence for Life Sciences*. **Fundamenta Informaticae**, 171(1-4), 57-80. DOI: 10.3233/FI-2020-1872
11. **Tangherloni A**, Spolaor S, Cazzaniga P, Besozzi D, Rundo L, Mauri G, Nobile MS (2019). *Biochemical parameter estimation vs. benchmark functions: A comparative study of optimization performance and representation design*. **Applied Soft Computing**, 81: 105494. DOI: 10.1016/j.asoc.2019.105494
12. Rundo L*, **Tangherloni A***, Cazzaniga P, Nobile MS, Russo G, Gilardi MC, Vitabile S, Mauri G, Besozzi D, Militello C (2019). *A novel framework for MR image segmentation and quantification by using MedGA*. **Computer Methods and Programs in Biomedicine**, 176(1): 59-172. DOI: 10.1016/j.cmpb.2019.04.016
13. Rundo L*, **Tangherloni A***, Nobile MS, Militello C, Besozzi D, Mauri G, Cazzaniga P (2019). *MedGA: A Novel Evolutionary Method for Medical Image Enhancement in Medical Imaging Systems*. **Expert Systems with Applications**, 119: 387-399. DOI: 10.1016/j.eswa.2018.11.013
14. **Tangherloni A†**, Spolaor S, Rundo L, Nobile MS, Cazzaniga P, Mauri G, Liò P, Merelli I, Besozzi D (2019). *GenHap: A Novel Computational Method Based on Genetic Algorithms for Haplotype Assembly*. **BMC Bioinformatics**, 20(4): 172. DOI: 10.1186/s12859-019-2691-y
15. Rundo L, Han C, Nagano Y, Zhang J, Hataya R, Militello C, **Tangherloni A**, Nobile MS, Ferretti C, Besozzi D, Gilardi MC, Vitabile S, Mauri G, Nakayama H, Cazzaniga P (2019). *USE-Net: Incorporating Squeeze-and-Excitation blocks into U-Net for prostate zonal segmentation of multi-institutional MRI datasets*. **Neurocomputing**, 365: 31-43. DOI: 10.1016/j.neucom.2019.07.006
16. Rundo L, Militello C, **Tangherloni A**, Russo G, Vitabile S, Gilardi MC, Mauri G (2018). *NeXt for*

neuro-radiosurgery: A fully automatic approach for necrosis extraction in brain tumor MRI using an unsupervised machine learning technique. **International Journal of Imaging Systems and Technology**, 28(1): 21-37. DOI: 10.1002/ima.22253

17. **Tangherloni A**, Nobile MS, Besozzi D, Mauri G, Cazzaniga P (2017). LASSIE: simulating large-scale models of biochemical systems on GPUs. **BMC Bioinformatics**, 18(1): 246. DOI: 10.1186/s12859-017-1666-0
18. **Tangherloni A†**, Nobile MS, Cazzaniga P, Besozzi D, Mauri G (2017). Gillespie's Stochastic Simulation Algorithm on MIC Coprocessor. **The Journal of Supercomputing**, 73(2): 676-686. DOI: 10.1007/s11227-016-1778-8
19. Nobile MS, Cazzaniga P, **Tangherloni A**, Besozzi D (2017). Graphics Processing Units in Bioinformatics, Computational Biology and Systems Biology. **Briefings in Bioinformatics**, 18(5): 870-885. DOI: 10.1093/bib/bbw058

Book chapters and contributed volumes

1. Ivan Berest, **Tangherloni A†** (2023). Integration of scATAC-Seq with scRNA-Seq Data. In **Methods in Molecular Biology**, 2584, Springer. DOI: 10.1007/978-1-0716-2756-3_15
2. Rundo L, Han C, Zhang J, Hataya R, Nagano Y, Militello C, Ferretti C, Nobile MS, **Tangherloni A**, Gilardi MC, Vitabile S, Nakayama H, Mauri G (2020). CNN-Based Prostate Zonal Segmentation on T2-Weighted MR Images: A Cross-Dataset Study. In **Neural Approaches to Dynamics of Signal Exchanges**, 151: 269-280, Springer. DOI: 10.1007/978-981-13-8950-4_25
3. Cazzaniga P, Nobile MS, **Tangherloni A**, Besozzi D (2018). Accelerating stochastic simulations of mechanistic models of biological systems: Advantages and issues in the parallelization on Graphics Processing Units. In **Quantitative Biology: Theory, Computational Methods, and Models**, 423-440, MIT Press.
4. Rundo L, Militello C, **Tangherloni A**, Russo G, Lagalla R, Mauri G, Gilardi MC, Vitabile S (2018). Computer-assisted Approaches for Uterine Fibroid Segmentation in MRgFUS Treatments: Quantitative Evaluation and Clinical Feasibility Analysis. In **Quantifying and Processing Biomedical and Behavioral Signals, Smart Innovation, Systems and Technologies**, 103: 229-241, Springer. DOI: 10.1007/978-3-319-95095-2_22

Conference Proceedings

1. Riva SG, Myers B, Cazzaniga P, Buffa FM, **Tangherloni A†** (2023). Consensus clustering strategy for cell type assignments of scRNA-seq data. Proceeding of **International Conference on Computational Intelligence in Bioinformatics and Computational Biology**, pp. 1-8, IEEE
2. Coelho V, Papetti D, **Tangherloni A**, Cazzaniga P, Besozzi D, Nobile MS (2023). The Domination Game: Dilating Bubbles to Fill Up Pareto Fronts. Proceeding of **Congress on Evolutionary Computation**, pp. 1-8, IEEE
3. **Tangherloni A†**, Riva SG, Myers B, Cazzaniga P (2022). Multi-objective Optimization for Marker Panel Identification in Single-cell Data. Proceeding of **International Conference on Computational Intelligence in Bioinformatics and Computational Biology**, pp. 1-8, IEEE. DOI: 10.1109/CIBCB55180.2022.9863042
4. Riva SG, Myers B, Cazzaniga P, **Tangherloni A†** (2022). A Deep Learning Pipeline for the Automatic cell type Assignment of scRNA-seq Data. Proceeding of **International Conference on Computational Intelligence in Bioinformatics and Computational Biology**, pp. 1-8, IEEE. DOI: 10.1109/CIBCB55180.2022.9863034
5. Riva SG, Cazzaniga P, **Tangherloni A†** (2021). Integration of Multiple scRNA-Seq Datasets on the Autoencoder Latent Space. Proceeding of **International Conference on Bioinformatics and Biomedicine**, pp. 2155-2162, IEEE. DOI: 10.1109/BIBM52615.2021.9669807
6. **Tangherloni A†**, Riva SG, Spolaor S, Besozzi D, Nobile MS, Cazzaniga P (2021). The impact of representations in the optimization of marker panels for single-cell RNA data. Proceeding of **Congress on Evolutionary Computation**, pp. 1-8, IEEE. DOI: 10.1109/CEC45853.2021.9504808
7. Totis N*, **Tangherloni A***, Beccuti M, Cazzaniga P, Nobile MS, Besozzi D, Pennisi M, Pappalardo F (2020). Efficient and Settings-Free Calibration of Detailed Kinetic Metabolic Models with Enzyme Isoforms Characterization. In **Computational Intelligence Methods for Bioinformatics and Biostatistics, Lecture**

8. Rundo L*, **Tangherloni A***, Galimberti S, Cazzaniga P, Woitek R, Sala E, Nobile MS, Mauri G (2019). *HaraliCU: GPU-powered Haralick Feature Extraction on Medical Images Exploiting the Full Dynamics of Gray-Scale Levels*. In **International Conference on Parallel Computing Technologies, Lecture Notes in Computer Science**, 11657: 304-318, Springer. DOI: 10.1007/978-3-030-25636-4_24
9. **Tangherloni A†**, Rundo L, Spolaor S, Nobile MS, Merelli I, Besozzi D, Mauri G, Cazzaniga P, Liò P (2019). *High Performance Computing for Haplotyping: Models and Platforms*. In **Euro-Par 2018: Parallel Processing Workshops, Lecture Notes in Computer Science**, 11339: 650-661, Springer. DOI: 10.1007/978-3-030-10549-5_51
10. Beccuti M, Cazzaniga P, Pennisi M, Besozzi D, Nobile MS, Pernice S, Russo G, **Tangherloni A**, Pappalardo F (2019). *GPU accelerated analysis of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis*. In **Euro-Par 2018: Parallel Processing Workshops, Lecture Notes in Computer Science**, 11339: 626-637, Springer. DOI: 10.1007/978-3-030-10549-5_49
11. Spolaor S, **Tangherloni A**, Rundo L, Cazzaniga P, Nobile MS (2019). *Estimation of Kinetic Reaction Constants: Exploiting Reboot Strategies to Improve PSO's Performance*. In **Computational Intelligence Methods for Bioinformatics and Biostatistics, Lecture Notes in Computer Science**, 10834: 92-102, Springer. DOI: 10.1007/978-3-030-14160-8_10
12. Nobile MS, **Tangherloni A**, Rundo L, Spolaor S, Besozzi D, Mauri G, Cazzaniga P (2018). *Computational Intelligence for Parameter Estimation of Biochemical Systems*. Proceeding of **Congress on Evolutionary Computation**, pp. 1-8, IEEE. DOI: 10.1109/CEC.2018.8477873
13. **Tangherloni A†**, Rundo L, Spolaor S, Cazzaniga P, Nobile MS (2018). *GPU-Powered Multi-Swarm Parameter Estimation of Biological Systems: A Master-Slave Approach*. Proceeding of **26th Euromicro International Conference on Parallel, Distributed and Network-based Processing**, pp. 698-705, IEEE. DOI: 10.1109/PDP2018.2018.00115
14. Spolaor S, **Tangherloni A**, Rundo L, Nobile MS, Cazzaniga P (2017). *Reboot Strategies in Particle Swarm Optimization and their Impact on Parameter Estimation of Biochemical Systems*. Proceeding of **International Conference on Computational Intelligence in Bioinformatics and Computational Biology**, pp. 1-8, IEEE. DOI: 10.1109/CIBCB.2017.8058550
15. **Tangherloni A**, Rundo L, Nobile MS (2017). *Proactive Particles in Swarm Optimization: a Settings-Free Algorithm for Real-Parameter Single Objective Optimization Problems*. Proceeding of **Congress on Evolutionary Computation**, pp. 1940-1947, IEEE. DOI: 10.1109/CEC.2017.7969538
16. Rundo L, **Tangherloni A**, Militello C, Gilardi MC, Mauri G (2016). *Multimodal medical image registration using Particle Swarm Optimization: A review*. Proceeding of **Symposium Series on Computational Intelligence**, pp. 1-8, IEEE. DOI: 10.1109/SSCI.2016.7850261
17. **Tangherloni A†**, Nobile MS, Cazzaniga P (2016). *GPU-powered Bat Algorithm for the parameter estimation of biochemical kinetic values*. Proceeding of **International Conference on Computational Intelligence in Bioinformatics and Computational Biology**, 1-6, IEEE. DOI: 10.1109/CIBCB.2016.7758103
18. Nobile MS, **Tangherloni A**, Besozzi D, Cazzaniga P (2016). *GPU-powered and settings-free parameter estimation of biochemical systems*. Proceeding of **Congress on Evolutionary Computation**, pp. 32-39, IEEE. DOI: 10.1109/CEC.2016.7743775

* Equal contribution

† Corresponding author/contact author

Others

- Chen Z, **Tangherloni A**, Liò P (2021). *What architectures could lead next generation single cell analysis pipelines?* Proceeding of **17th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics**, IEEE
- **Tangherloni A**, Riva SG, Spolaor S, Nobile MS, Cazzaniga P (2021). *Genetic Algorithms for the identification of marker panels insingle-cell RNA Data*. Proceeding of **17th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics**, IEEE
- Totis N, **Tangherloni A**, Beccuti M, Cazzaniga P, Nobile MS, Besozzi D, Pennisi M, Pappalardo F (2018). *GPU powered Parameter Estimation of a Large-Scale Kinetic Metabolic Model*. Proceeding of **15th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics**
- **Tangherloni A**, Spolaor S, Rundo L, Nobile MS, Cazzaniga P, Mauri G, Liò P, Besozzi D, Merelli I (2018). *GenHap: Evolutionary Computation for Haplotype Assembly*. Proceeding of **15th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics**
- **Tangherloni A**, Cazzaniga P, Nobile MS, Besozzi D, Mauri G (2015). *Deterministic simulations of large-scale models of cellular processes accelerated on Graphics Processing Units*. Proceeding of **12th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics**