curriculum vitae

PERSONAL INFORMATION

Surname	**Cascianelli**
Name	**Silvia**
E-mail	silvia.cascianelli@polimi.it
Date of birth	07/02/1992
Place of birth	Assisi (Perugia), Italy
Nationality	ITALIANA

Education and training

• Date (from – to)	2020-2024
• Name and type of organisation providing education and training	Politecnico di Milano – Dipartimento di Elettronica, Informazione e Bioingegneria
Duration of the program of study	3 years
• Principal subjects/occupational skills covered	**PhD Programme in Information Technology -. Departmental Scholarship for** research on a topic of **Computer Science and Engineering**: *'Machine Learning in Oncogenomics: a key to dissecting cancer inner heterogeneity'* Characterizing courses: Analysis of complex networks: theory and applications | Data and results visualization Data and Information Quality | Research Skills | Professional Communication
• Title of qualification awarded	**PhD cum laude in Information Technology**

• Date (from – to)	2015-2018
• Name and type of organisation providing education and training	Politecnico di Milano – Dipartimento di Elettronica, Informazione e Bioingegneria
Duration of the program of study	2 years
• Principal subjects/occupational skills covered	**Computer Science and Engineering.** Characterizing courses: Software Engineering | Foundations of Operations Research | Advanced Computer Architectures Computing Infrastructures | Artificial Intelligence | Soft Computing | Data Bases Model Identification and Data Analysis | Machine Learning E-health Methods and Applications | Biologia e Fisiologia Bioinformatics and Computational Biology | Genomic Computing
• Title of qualification awarded	**M.Sc. degree in Computer Science and Engineering**

• Date (from – to)	2010-2014
• Name and type of organisation providing education and training	Università degli Studi di Perugia – Dipartimento di Ingegneria
Duration of the program of study	3 years
• Principal subjects/occupational skills covered	**Ingegneria Elettronica-Informatica con percorso Informatica** Characterizing courses: Fondamenti di Informatica | Algoritmi e strutture di dati | Architetture dei calcolatori Sistemi Operativi | Teoria dei circuiti | Elettronica applicata | Reti logiche Elettronica dei sistemi digitali | Teoria dei segnali | Fondamenti di telecomunicazioni Teoria dei sistemi | Ingegneria del controllo | Additional course: Introduction to System Biology
• Title of qualification awarded	**Laurea Triennale in Ingegneria Elettronica-Informatica**

• Date (from – to)	2005-2010
• Name and type of organisation providing education and training	Liceo Jacopone da Todi
Duration of the program of study	5 years
• Principal subjects/occupational skills covered	**Liceo scientifico** Piano bilinguistico - Piano Nazionale Informatica
• Title of qualification awarded	**Diploma di Liceo Scientifico**

Graduation theses

Title	Machine Learning in Oncogenomics: a key to dissecting cancer inner heterogeneity
Language	English
Supervisor	M. Masseroli
PhD Thesis Summary	Computational oncogenomics has a pivotal role to solve biological and clinical issues and support translational medicine in cancer research through computer science and bioinformatics methods. Leveraging advanced computational methods for comprehensive omics analysis is increasingly essential to deepen the understanding of tumor molecular complexity. To this aim, my PhD research emphasised the synergistic use of Data Science techniques and omics data processing to tackle clinical challenges of cancer diseases and face their inherent intricacy and heterogeneity. These often pose an insurmountable barrier to traditional research approaches; therefore, in my PhD work, I designed and developed computational workflows that follow every step of a typical Data Science process while being enhanced and tailored for omics data, considering all their peculiarities and issues. To this aim, a fusion of skills and knowledge spanning Computer Science, Data Science, Machine Learning, Bioinformatics, and Oncogenomics was essential. Rigorous data processing, model development, and performance evaluation were merged with clinical validation and interpretability efforts to strengthen computational findings with clear biological evidence. Indeed, to obtain robust, noteworthy results, it was decisive to explore, implement, and optimize proper, fully legit machine learning solutions, whose results were carefully tested and validated from both computational and clinical/biological perspectives. Collaborations with experts in Medicine and Biology steered the research towards hot topics in Oncogenomics, aligning with real translational needs, and provided valuable guidance for the medical-bioinformatics perspective, perfectly complementary to the computational-bioinformatics perspective given by my computer science and engineering background. The endeavour of my PhD research was first directed to the enhancement of a R/Bioconductor package designed for efficient investigation and integration of omics data. Then, it delved into robust Machine Learning-based cancer subtyping for reliable patient predictions, also transitioning towards multi-label transcriptional classification of patients to better reflect the underlying molecular heterogeneity. Lastly, it focused on mutation-based stratifications to identify variants with therapeutic or prognostic roles in patient groups of critical clinical handling. My work achieved remarkable methodological advances in cancer subtyping, proved by successful applications to breast and colorectal cancer. These include defining a new feature selection method to tackle unbalanced classification scenarios; investigating multi-omics, deep and semi-supervised solutions in light of the increasing omics data availability; introducing multi-label subtyping strategies to account for cancer inner heterogeneity, enhancing patient molecular characterization and improving the clinical value of the predictions considering both primary and secondary assignments. Innovative mutation-based feature engineering and supervised frameworks were combined with variant prioritisation approaches and search for actionable genes to find new potential therapeutic targets for cancer patient groups of critical handling. Lastly, the integration of class discovery, transfer learning, and multi-label predictions led to a relevant and robust methodology, currently under a patent application process, and also demonstrated its efficacy in finding a more exhaustive colorectal cancer stratification. Overall, my PhD research placed its priority on meticulously designing, implementing and assessing Omics Data Science workflows, where Machine Learning-based solutions emerged as a key to dissecting cancer inner heterogeneity, unlocking robust and clinically relevant omics-based patient predictions and shaping new trajectories towards precision medicine.

Title		RNA sequencing-based computational subtyping of breast cancer for clinical outcome prediction
Language		English
Supervisor		M. Masseroli
M.Sc Thesis Summary		Breast cancer is a complex disease whose molecular traits are strictly implicated in progression, response to treatment and clinical outcome. Therefore, investigating the gene profile offers significant advantages. Suffice it to say that it is estimated that in 25% of cases an in-depth risk assessment could avoid administering post-surgical adjuvant chemotherapy to patients. To date, molecular stratification techniques are performed on different platforms and gene signatures and show poor concordance. However, categorization into intrinsic subtypes (Luminal A, Luminal B, Her2-enriched and Basal) is a well-known standard, summarizing molecular features and providing clinical outcome indicators, which can also be exploited in risk of recurrence prognostic models. RNA-Seq Profiling is a method of genomic investigation that could both improve and spread further in clinical practice the analysis of the individual patient's molecular traits, by replicating different known stratification strategies and integrating innovative classification approaches on a single RNA-seq profile. All this in order to consolidate the robustness of the subtyping and the accuracy of the clinical outcome prediction, with significantly lower costs. In this context, the thesis work is part of a wider project, in collaboration between the Istituto di Ricerca di Candiolo-IRCCS and the Politecnico di Milano, aimed at encouraging the introduction of RNA-seq technology in the clinical practice of the breast cancer. Two were the computational paths followed. On the one hand, the emulation of a classification method already validated on other platforms and focused on the PAM50 panel, a well-known signature from the state of the art, showed the value of its replicability on RNA-Seq. On the other hand, a typical machine learning survey led us to compare different supervised techniques to perform the subtyping task starting from the complete RNA-Seq profiles, up to delineate as the most promising approach a Multiclass Logistic Regression combined with a suitably designed strategy of feature selection.

Title		Analisi di Sensitività del modello di trasduzione del segnale nelle cellule di NSCLC
Language		Italiano
Supervisor		P. Valigi
. B. Sc Thesis Summary		La Sistems Biology è una disciplina emergente che coniuga la prospettiva ingegneristica, propria della Teoria dei Sistemi e del Controllo, alla ricerca medico-farmacologica, interpretando i fenomeni biologici come complessi sistemi caratterizzati da interazioni non lineari modellabili matematicamente, al fine di investigarne l'evoluzione dinamica, le mutue connessioni, la stabilità e la robustezza. In tale contesto, è stato analizzato il modello proposto da Bianconi et al, 2012, relativo alle vie di segnalazione intracellulare che si dipartono dai recettori del fattore di crescita dell'epidermide e dell'insulina, e realizzato ricorrendo all'utilizzo di equazioni differenziali ordinarie (ODEs). Evidenze cliniche e sperimentazione wet su linee cellulari hanno evidenziato nel carcinoma polmonare non a piccole cellule un legame tra la co-espressione dei suddetti recettori e meccanismi anomali di trasduzione del segnale e di proliferazione cellulare; la sperimentazione in silico ha consentito di sviluppare delle reti, atte a connettere le specie e le reazioni biochimiche coinvolte nei pathways di interesse, e modelli matematici, in grado di fornire predizioni circa il comportamento temporale delle specie al variare delle condizioni d'indagine. In particolare, il lavoro qui proposto ha focalizzato l'attenzione sulle analisi di sensitività, locale e globale, delle specie coinvolte nelle reti, in relazione a tutti i parametri presenti nella modellazione matematica, ovvero, costanti cinetiche pertinenti alle reazioni biochimiche modellate, nonché concentrazioni totali delle specie, legate all'applicazione della legge di conservazione di massa. Tutte le simulazioni pertinenti ai sistemi di ODEs e gli studi di sensitività, sono stati svolti in ambiente Matlab, integrando nel codice implementato functions sviluppate in questo lavoro e preesistenti.

Publications and submitted articles

Journal articles

Author(s) and title		**Silvia Cascianelli,** Iva Milojkovic, Marco Masseroli. *A novel Machine Learning-based workflow to capture intra-patient heterogeneity through transcriptional multi-label characterization and clinically relevant classification*
Language		English
Publication place		Journal of Biomedical Informatics
Pages and Date of publication		pp. 1-28; **Accepted for publication - March 2025**

Author(s) and title		Sofia Mongardi, **Silvia Cascianelli,** Marco Masseroli. *Biologically weighted LASSO: enhancing functional interpretability in gene expression data analysis*
Language		English
Publication place		Bioinformatics
Pages and Date of publication		pp. 1-8; **October 2024**

Author(s) and title		**Silvia Cascianelli,** Gaia Ceddia, Alberto Marchesi, Marco Masseroli. *Identification of transcription factor high accumulation DNA zones.*
Language		English
Publication place		BMC Bioinformatics
Pages and Date of publication		pp. 1-20; **November 2023**

Author(s) and title		**Silvia Cascianelli**, Arianna Galzerano, Marco Masseroli. *Supervised Relevance-Redundancy assessments for feature selection in omics-based classification scenarios.*
Language		English
Publication place		Journal of Biomedical Informatics
Pages and Date of publication		pp. 1-32; **August 2023**

Author(s) and title		**Silvia Cascianelli,** Chiara Barbera, Alexandra Ulla, Elena Grassi, Barbara Lupo, Diego Pasini, Andrea Bertotti, Livio Trusolino, Enzo Medico, Claudio Isella, Marco Masseroli. *Multi-label transcriptional classification of colorectal cancer reflects tumour cell population heterogeneity.*
Language		English
Publication place		Genome Medicine
Pages and Date of publication		pp. 1-35; **May 2023**

Author(s) and title		Simone Pallotta, **Silvia Cascianelli**, Marco Masseroli. *RGMQL: Scalable and interoperable computing of heterogeneous omics big data and metadata in R/Bioconductor.*
Language		English
Publication place		BMC Bioinformatics
Pages and Date of publication		pp. 1-28; **April 2022**

Author(s) and title		Francisco Cristovao, **Silvia Cascianelli**, Arif Canakoglu, Mark Carman, Luca Nanni, Pietro Pinoli, Marco Masseroli. *Investigating Deep Learning based Breast Cancer Subtyping using Pan-cancer and Multi-omic Data.*
Language		English
Publication place		IEEE/ACM Transactions on Computational Biology and Bioinformatics
Pages and Date of publication		pp. 1-12; **January 2021**

Author(s) and title		**Silvia Cascianelli,** Ivan Molineris, Claudio Isella, Marco Masseroli, Enzo Medico. *Machine learning for RNA sequencing-based intrinsic subtyping of breast cancer*
Language		English
Publication place		Nature Scientific Reports
Pages and Date of publication		pp. 1-14; **August 2020**

Under submission:

Author(s) and title		**Cascianelli Silvia,** Mainetti Amos, Cassisa Anna, Medico Enzo, Isella Claudio, Masseroli Marco. *Integrative approach for tumor class discovery and prediction applied to colorectal cancer.*

Conference Proceedings

Author(s) and title		**Silvia Cascianelli**, Cristina Iudica, Marco Masseroli. *A Data Science approach to investigate the mutational landscape of a critical patient subgroup.*
Language		English
Publication place		19th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2024).
Pages and Date of publication		pp. 1-6, **September 2024**

Author(s) and title		Sofia Mongardi, **Silvia Cascianelli**, Marco Masseroli. *Enhancing feature selection with biological insights: a novel forward approach for gene selection.*
Language		English
Publication place		19th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2024).
Pages and Date of publication		pp. 1-6, **September 2024**

Author(s) and title		Simone Tomè, **Silvia Cascianelli**, Erika Salvi, Marco Masseroli. *Supervised Relevance-Redundancy assessment for feature selection in high-dimensional genotype data.*
Language		English
Publication place		19th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2024).
Pages and Date of publication		pp. 1-6, **September 2024**

Author(s) and title		Camila Riccio-Rengifo **& Silvia Cascianelli**, Gaia Ceddia, Marco Masseroli. *Non-negative Matrix Tri-Factorization for data integration and knowledge inference on breast cancer subtyping*
Language		English
Publication place		18th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2023).
Pages and Date of publication		pp. 1-7, **September 2023**

Author(s) and title		Sofia Mongardi, **Silvia Cascianelli**, Marco Masseroli. *Biologically-driven feature selection for improved functional interpretability of gene expression data analysis*
Language		English
Publication place		18th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2023).
Pages and Date of publication		pp. 1-6, **September 2023**

Author(s) and title		Lorenzo Perino, **Silvia Cascianelli**, Marco Masseroli. *Hybrid Evolutionary Framework for Selection of Genes Predicting Breast Cancer Relapse.*
Language		English
Publication place		IEEE International Joint Conference on Neural Networks (IJCNN) 2020
Pages and Date of publication		pp. 1-8; **July 2020**

Author(s) and title		Francisco Cristovao, Arif Canakoglu, Mark Carman, **Silvia Cascianelli,** Luca Nanni, Pietro Pinoli, Marco Masseroli. *Comparing classic, deep and semi-supervised learning for whole-transcriptome breast cancer subtyping*
Language		English
Publication place		16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2019).
Pages and Date of publication		pp. 1-6; **September 2019**

Contributions to volumes

Author(s) and title		• Mongardi Sofia, Masseroli Marco, **Cascianelli Silvia**. *Semi-Supervised Learning.* • Mongardi Sofia, Masseroli Marco, **Cascianelli Silvia**. *Supervised Learning: Multi-label Classification.* • Mongardi Sofia, Masseroli Marco, **Cascianelli Silvia**. *Performance Measures for Multi-Class Classification*. • **Cascianelli Silvia**, Masseroli Marco. *Biological and Medical Ontologies: Introduction* • **Cascianelli Silvia**, Masseroli Marco. *Biological and Medical Ontologies: GO and GOA* • **Cascianelli Silvia**, Masseroli Marco. *Integrative Bioinformatics*
Language		English
Publication place		Encyclopedia of Bioinformatics and Computational Biology, 2nd Edition, Elsevier, edited by Shoba Ranganathan, Mario Cannataro and Mohammad Asif Khan (**Under publication**)

Author(s) and title		**Silvia Cascianelli,** Cristina Iudica, Marco Masseroli. *Three-stage Data Science methodology to explore genetic heterogeneity of diseases.*
Language		English
Publication place		Springer LNBI volume
Pages and Date of publication		pp. 1-15; (**Under publication**)

Author(s) and title		Sofia Mongardi, **Silvia Cascianelli,** Marco Masseroli. *Forward and backward feature selection guided by prior biological knowledge for enhanced interpretability.*
Language		English
Publication place		Springer LNBI volume
Pages and Date of publication		pp. 1-15; (**Under publication**)

Author(s) and title		Simone Tomè, **Silvia Cascianelli**, Erika Salvi, Marco Masseroli. *Benchmark study on supervised Relevance-Redundancy assessment for feature selection in genomic data.*
Language		English
Publication place		Springer LNBI volume
Pages and Date of publication		pp. 1-15; (**Under publication**)

Author(s) and title		Camila Riccio Rengifo **& Silvia Cascianelli,** Gaia Ceddia, Marco Masseroli. *Inferring breast cancer subtype associations using an original omics integration based on Non-negative Matrix Tri-Factorization.*
Language		English
Publication place		Springer LNBI volume
Pages and Date of publication		pp. 1-22; **May 2025**

Author(s) and title		Sofia Mongardi, **Silvia Cascianelli,** Marco Masseroli. *Enhancing functional interpretability in gene expression analysis through biologically-guided feature selection.*
Language		English
Publication place		Springer LNBI volume
Pages and Date of publication		pp. 1-15; **May 2025**

Author(s) and title		Anna Bernasconi & **Silvia Cascianelli**. *Scenarios for the integration of microarray gene expression profiles in COVID-19-related studies.* Chapter of *Microarray Data Analysis.*
Language		English
Publication place		Springer Nature Book.
Pages and Date of publication		pp. 1-28; **January 2022**

Author(s) and title		**Silvia Cascianelli**, Francisco Cristovao, Arif Canakoglu, Mark Carman, Luca Nanni, Pietro Pinoli, Marco Masseroli. *Evaluating deep semi-supervised learning for whole-transcriptome breast cancer subtyping.*
Language		English
Publication place		Springer LNBI volume
Pages and Date of publication		pp. 1-12; **January 2021**

Under submission:

Author(s) and title		• Mongardi Sofia &Tomè Simone, Masseroli Marco, **Cascianelli Silvia**. *Machine learning and deep learning.*
Publication place		The evolution of Artificial Intelligence in Healthcare and Medicine: from basic methods to clinical practice, Elsevier.

Work experience

• Date (from – to)		**Feb 2025 – Present**
• Name and address of firm/university		**Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria** Milano, via Giuseppe Ponzio

• Type of business or sector		Teaching activity
• Type of employment		**Member of the Interuniversity Teaching Board for the Master "Bioinformatics for Computational Genomics" (Politecnico di Milano & University of Milan) as Professor**
• Main activities and responsibilities		• Scientific Programming course

• Date (from – to)		**Feb 2024 – Present**
• Name and address of firm/university		**Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria** Milano, via Giuseppe Ponzio
• Type of business or sector		Academic Research activity and supervision
• Type of employment		**Post-doctoral Researcher at the Data Science and Bioinformatics Lab**
• Main activities and responsibilities		Data Science investigations and computational analysis of NGS omics data to study cancer and other complex diseases. Patient predictions and stratification through Machine Learning, System Biology and Network-based methods. Computational analysis and functional validation of intra-cellular interactions supporting tumour onset and progression

• Date (from – to)		**Jan 2024 – Mar 2024**
• Name and address of firm/university		**Department of Computational Biology of the University of Lausanne** Computational Systems Oncology lab led by Professor Ciriello
• Type of business or sector		Academic Research activity
• Type of employment		Visiting Researcher
• Main activities and responsibilities		Shared project on cancer cell plasticity. Introduction to approaches exploring combinations of genetic, epigenetic, and/or transcriptional changes occurring in cancer and related to different phenotypes, prognosis, and response to treatments.

• Date (from – to)		**Sep 2020 – Present**
• Name and address of firm/university		**Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria** Milano, via Giuseppe Ponzio
• Type of business or sector		Teaching activity
• Type of employment		**Teaching assistant**
• Main activities and responsibilities		• Bioinformatics practice classes and biological networks theory within the Bioinformatics and computational biology course of Prof. Masseroli. • XML theory and practices within the ICT for health care course of Prof. Masseroli. • Co-supervisor of 12 Master Students

• Date (from – to)		**Nov 2020 – Present**
• Name and address of firm/university		**Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria** Milano, via Giuseppe Ponzio
• Type of business or sector		Academic Research activity and co-supervision of master student theses
• Type of employment		**PhD candidate in Information Technology**
• Main activities and responsibilities		Computational analysis of oncogenomic NGS data (mainly at gene-level) to study cancer development and differentiation and to improve molecular stratification and clinical outcome predictions through Data Science, System Biology and Network-based methods.

• Date (from – to)		**June 2019 – Nov 2020**
• Name and address of firm/university		**Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria** Milano, via Giuseppe Ponzio
• Type of business or sector		Academic Research activity
• Type of employment		Research assistant;
• Main activities and responsibilities		NGS data analysis for molecular stratification and clinical outcome prediction Computational analysis of oncogenomic data collected through high-throughput profiling technologies to improve prognostic stratification and predictive models

• Date (from – to)		**Mar. 2019 – June 2019**
• Name and address of firm/university		**Istituto Europeo di Oncologia (IEO Campus)** Milano, via Adamello

• Type of business or sector	Research activity
• Type of employment	Research fellowship
• Main activities and responsibilities	“Individuazione di signature prognostiche da RNA-Sequencing su campioni tumorali chirurgici o bioptici nell’ambito dei progetti della rete di Alleanza Contro il Cancro” Computational analysis of genomic data for tumor stratification and clinical outcome predictions

• Date (from – to)	**Sep. 2018 – Mar. 2019**
• Name and address of firm/university	**Consorzio Interuniversitario “Istituto Nazionale Biostrutture e Biosistemi – I.N.B.B.”** Roma, viale delle Medaglie d’oro
• Type of business or sector	Research activity
• Type of employment	Research collaborator
• Main activities and responsibilities	“Systematic screening of novel diagnostic markers and therapeutic targets in oncology” Computational analysis of genomic data to define of tumor prognostic markers and classifiers.

Conferences, presentations

• Date (from – to)	**7-8 Novermber 2024**
• Conference	**Mathematics for our Health (M4H) Workshop, 2024** Poster presentation: Silvia Cascianelli, Marco Masseroli. Omics Data Science for Capturing Intra-Tumor Heterogeneity via Transcriptional Multi-Label Subtyping.

• Date (from – to)	**4-6 September 2024**
• Conference	**CIBB 2024: 19th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics** Oral presentation: Silvia Cascianelli, Cristina Iudica, Marco Masseroli. A Data Science approach to investigate the mutational landscape of a critical patient subgroup.

• Date (from – to)	**12-14 June 2024**
• Conference	**BITS 2024: 20th Annual Meeting of the Bioinformatics Italian Society** Oral presentation: Silvia Cascianelli, Marco Masseroli. Machine learning for expression-based multi-label patient subtyping and advanced recognition of primary and secondary assignments.

• Date (from – to)	**29-31 May 2024**
• Conference	**EMBO Workshop "The many faces of cancer evolution"** Poster presentation: Silvia Cascianelli, Marco Masseroli. Machine learning for multi-label subtyping and advanced recognition of primary and secondary assignments.

• Date (from – to)	**17 Apr 2024**
• Conference	**MMNGS24 - Milan meeting on "Next Generation Sequencing",** University of Milan-Bicocca. Oral presentation: Silvia Cascianelli, Sofia Mongardi. Is (expertise in) feature selection crucial for improving omics-based patient stratifications?

• Date (from – to)	**17 Apr 2024**
• Conference	**MMNGS24 - Milan meeting on "Next Generation Sequencing",** University of Milan-Bicocca. Oral presentations: Silvia Cascianelli, Sofia Mongardi. Is (expertise in) feature selection crucial for improving omics-based patient stratifications?

• Date (from – to)	**06-08 Sept. 2023**
• Conference	**CIBB 2023: 18th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics** Oral presentations: Camila Riccio Rengifo & Silvia Cascianelli, Gaia Ceddia, Marco Masseroli. Non-negative Matrix Tri-Factorization for data integration and knowledge inference on breast cancer subtyping; Sofia Mongardi, Silvia Cascianelli, Marco Masseroli. Biologically-driven feature selection for improved functional interpretability of gene expression data analysis

• Date (from – to)	**28 June - 1 July 2022**
• Conference	**ESMO 2023 World Congress on Gastrointestinal Cancers**

		Oral presentation: Cascianelli S, Barbera C, Ulla AA, Grassi E, Lupo B, Pasini D, Bertotti A, Trusolino L, Medico E, Isella C, Masseroli M ‘Multi-label transcriptional classification of colorectal cancer reflects tumour cell population heterogeneity’

• Date (from – to)		**21-23 June 2023**
• Conference		**BITS 2023: 19th Annual Meeting of the Bioinformatics Italian Society** Poster presentations: Silvia Cascianelli, Marco Masseroli – ‘Machine learning for multi-label subtyping: a key to dissecting intra-tumor heterogeneity at the bulk sample level’; Mongardi Sofia, Cascianelli Silvia, Masseroli Marco – ‘Adapting feature selection in gene expression-based classification for higher biological interpretability’; Tomè Simone, Cascianelli Silvia, Medico Enzo, Isella Claudio, Masseroli Marco - ‘Gene co-expression network analysis for identifying cell populations in RNA-seq patient-derived xenografts’

• Date (from – to)	**27-29 June 2022**
• Conference	**BITS 2022: 18th Annual Meeting of the Bioinformatics Italian Society** Oral presentation: 'Machine learning to discover genes predictive of RAS-mutated cases in mutational profiles of colorectal cancer patients'

• Date (from – to)	**1-2 July 2021**
• Conference	**BITS 2021: 17th Annual Meeting of the Bioinformatics Italian Society** Oral presentation: 'Investigating transcript isoform RNA-seq data and machine learning techniques for breast cancer subtyping'

• Date (from – to)	**28-30 Oct. 2020**
• Conference	**5th Annual meeting of Alliance Against Cancer. New technologies and strategies to fight cancer. European Institute of Research (IEO).** Oral presentation: 'Boosting perspectives for breast cancer intrinsic subtyping on RNA-sequencing data' in 'Cancer Prevention and early-detection' session

• Date (from – to)	**19-24 July 2020**
• Conference	**IEEE World Congress on Computational Intelligence 2020.** Oral presentation: Lorenzo Perino, Silvia Cascianelli, Marco Masseroli. 'Hybrid Evolutionary Framework for Selection of Genes Predicting Breast Cancer Relapse'

• Date (from – to)	**20-22 Nov. 2019**
• Conference	**4th Annual meeting of Alliance Against Cancer. New technologies and strategies to fight cancer. University of Rome "Sapienza".** Poster presentation: 'RNA sequencing-based intrinsic subtyping of breast cancer'

• Date (from – to)	**4-6 Sep. 2019**
• Conference	**16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics** (CIBB2019). University of Bergamo. Oral presentation: Francisco Cristovao, Arif Canakoglu, Mark Carman, Silvia Cascianelli, Luca Nanni, Pietro Pinoli, Marco Masseroli.

Summer schools

• Date (from – to)	**26-30 July 2021**
• Conference	**4th International School on Deep Learning, Deep Learn 2021 Summer School,** organized by Università Politecnica delle Marche, Universitat Roviri I Virgili, IRDTA Brussels-London

Awards and honors

Departmental Scholarship for PhD in Information Technology at the Politecnico di Milano with research on a topic of Computer Science and Engineering - funded by the Italian Ministry of University and Scientific Research, 2020

Organization of events

Among the organizers of the **3rd International Workshop on Web Applications for Life Sciences** - In conjunction with the 24th International Conference on Web Engineering (ICWE 2024) 17-20 June 2024 (Tampere, Finland)

Among the organizers and General Chairs of the **20th Conference on Computational Intelligence methods for Bioinformatics and Biostatistics** (CIBB2025) 10-12 September 2024 (Politecnico di Milano, Milano, Italy)

Projects

Research collaborator for 'STRA-RNA: Machine Learning Techniques for Engineering Prognostic Classifiers' – funded by the Foundation of Piemonte for Oncology (2019-2020)

Research collaborator for 'Machine Learning for GerSom project' – funded by Alliance Against Cancer and supported by Ministry of Health (2021-2024)

Research collaborator for 'PRIN ARTUSI: Computational analysis and functional validation of epithelial-mesenchymal interactions supporting tumour onset and progression using patient-derived models of colorectal cancer' – funded by the Ministry of University and Scientific Research as a Project of Relevant National Interest (PRIN) (2023-present)

Ongoing collaborations

Ongoing collaboration with the Oncogenomics group led by Enzo Medico at the Candiolo Cancer Institute, IRCCS, Torino

Ongoing collaboration with the AI-ON-Lab (Artificial Intelligence for Oncology Lab) led by Arsela Prelaj at the Istituto Nazionale dei Tumori, Fondazione IRCCS, Milano

Ongoing collaboration with the Istituto Neurologico Carlo Besta, Fondazione IRCCS, Milano – affiliation to the joint MIND lab (Laboratory of coMputational multI-omics of Neurological Disorders) led by Marco Masseroli and Erika Salvi