# RAFFAELLA RIZZI – Curriculum Vitae

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#### **RESEARCH INTERESTS**

Algorithms and data structures in Bioinformatics; analysis and assembly of genomic and transcriptomic sequences; indexing structures for texts and text collections.

#### POSITIONS

**March 2021–present**: Associate Professor at the Department of Computer Science, Systems and Communication at the University of Milan-Bicocca. Primarily collaborates with the BIAS laboratory (Bioinformatics and Experimental Algorithmics), focusing on the design and implementation of efficient algorithms to solve computational problems in Bioinformatics. Member of the PhD board in Computer Science at the Department of Computer Science, Systems and Communication.

**December 2008–February 2021**: Tenured Researcher at the Department of Computer Science, Systems and Communication at the University of Milan-Bicocca.

**February 2007–December 2008**: Contract Researcher on the topic 'Design, development, and implementation of software for the computational analysis of alternative splicing in eukaryotic genes' (Supervisor: Prof. Giulio Pavesi) at the Department of Biosciences, University of Milan.

**April 2006–January 2007**: Collaboration position at the Department of Computer Science, Systems and Communication at the University of Milan-Bicocca.

**April 2005–March 2006**: Research Fellow at the Department of Biotechnology and Biosciences at the University of Milan-Bicocca (Supervisor: Prof. Piercarlo Fantucci).

**April 2001–March 2005**: Research Fellow on the topic 'Methods for the analysis and comparison of biological sequences' (Supervisor: Prof. Paola Bonizzoni) at the Department of Computer Science, Systems and Communication at the University of Milan-Bicocca.

#### EDUCATION

<u>PhD in Geodetic and Topographic Sciences</u> (13th cycle) at the Politecnico di Milano (October 2000). Thesis title: 'Development of methodologies for the analysis of microarray images.' Supervisors: Prof. Luigi Mussio (Politecnico di Milano) and Dr. Luciano Milanesi (CNR-ITB, Segrate, MI).

<u>Degree in Civil Engineering</u> (Transportation section) at the Politecnico di Milano (July 1997). Thesis title: 'Experiments on 3D reconstruction of objects by coupling contours extracted from digital images.' Supervisor: Prof. Gianfranco Forlani.

## **RESEARCH ACTIVITY**

The research activities primarily focus on the field of algorithms in Bioinformatics, with a particular emphasis on designing and experimenting with methods for the analysis and comparison of primary sequences of DNA and RNA. Currently, RR is engaged in algorithmic problem-solving arising from the study of gene structure prediction and the various alternative transcripts that a gene can express. This includes indexing structures for genome and transcript assembly, phylogenetics, and efficiently determining overlaps within a set of sequencing reads through Lyndon word-based fingerprints.

## Journal articles

[J23] S. Ciccolella, L. Denti, J. Avila Cartes, G. Della Vedova, Y. Pirola, R. Rizzi, P. Bonizzoni. Differential analysis of alternative splicing events in gene regions using residual neural networks. *Neural Computing & Applications* (2025). https://doi.org/10.1007/s00521-025-10992-2.

[J22] J. Baaijens, P. Bonizzoni, C. Boucher, G. Della Vedova, Y. Pirola, R. Rizzi, J. Sirén. Computational graph pangenomics: a tutorial on data structures and their applications. *Natural Computing* (2022), 21:81–108.

[J21] P. Bonizzoni, M. Costantini, C. De Felice, A. Petescia, Y. Pirola, M. Previtali, R. Rizzi, J. Stoye, R. Zaccagnino, R. Zizza. Numeric Lyndon-based feature embedding of sequencing reads for machine learning approaches. *Information Sciences* (2022), 607:458–476.

[J20] L. Denti, Y. Pirola, M. Previtali, T. Ceccato, G. Della Vedova, R. Rizzi, P. Bonizzoni. Shark: fishing relevant reads in an RNA-Seq sample. *Bioinformatics* (2021), 37(4):464-472.

[J19] P. Bonizzoni., G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. Computing the multistring BWT and LCP array in External Memory. *Theoretical Computer Science* (2021).

[J18] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. Multithread Multistring Burrows-Wheeler Transform and Longest Common Prefix Array. *Journal of Computational Biology* (2019), 26(9):948-961.

[J17] R. Rizzi, S. Beretta, M. Patterson, Y. Pirola, M. Previtali, G. Della Vedova, P. Bonizzoni. Overlap graphs and de Bruijn graphs: data structures for de novo genome assembly in the big data era. *Quantitative Biology* (2019), 7(4):278-292.

[J16] L. Denti, R. Rizzi, S. Beretta, G. Della Vedova, M. Previtali, P. Bonizzoni. ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. *BMC Bioinformatics* (2018), 19(1):444.

[J15] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. FSG: Fast String Graph Construction for de Novo Assembly. *Journal of Computational Biology* (2017), vol. 24, p. 953-968.

[J14] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. An External-Memory Algorithm for String Graph Construction. *Algorithmica* (2017), 78:394-424.

[J13] P. Bonizzoni, A.P. Carrieri, G. Della Vedova, R. Rizzi, G. Trucco. A colored graph approach to perfect phylogeny with persistent characters. *Theoretical Computer Science* (2017), 658:60-73.

[J12] P. Bonizzoni, A.P. Carrieri, G. Della Vedova, R. Rizzi, G. Trucco. Species-driven persistent phylogeny. *Fundamenta Informaticae* (2017), 154:47-63.

[J11] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. LSG: An External-Memory Tool to Compute String Graphs for Next-Generation Sequencing Data Assembly. *Journal of Computational Biology* (2016), vol. 23, p. 137-149.

[J10] Palorini, R., Votta, G., Pirola, Y., De Vitto, H., De Palma, S., Airoldi, C., et al. Protein Kinase A Activation Promotes Cancer Cell Resistance to Glucose Starvation and Anoikis. *PLoS Genetics* (2016), 12(3): e1005931.

[J9] S. Beretta, P. Bonizzoni, G. Della Vedova, Y. Pirola, R. Rizzi. (2014). Modeling Alternative Splicing Variants from RNA-Seq Data with Isoform Graphs. *Journal of Computational Biology* (2014), 21:16-40.

[J8] Y. Pirola, R. Rizzi, E. Picardi, G. Pesole, G. Della Vedova, P. Bonizzoni. PIntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. *BMC Bioinformatics* (2012), 13(Suppl 5):S2.

[J7] P. L. Martelli, M. DAntonio, P. Bonizzoni, T. Castrignanò, A. M. D'Erchia, P. D'Onorio De Meo, P. Fariselli, M. Finelli, F. L., M. Mangiulli, F. Mignone, G. Pavesi, E. Picardi, R. Rizzi,
I. Rossi, A. Valletti, A. Zauli, F. Zambelli, R. Casadio, G. Pesole. ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. *Nucleic Acids Research* (2011), 39:D80-5.

[J6] P. Bonizzoni, G. Mauri, G. Pesole, E. Picardi, Y. Pirola, R. Rizzi. Detecting alternative gene structures from spliced ESTs: a computational approach. *Journal of Computational Biology* (2009), 16(1):43-66.

[J5] T. Castrignanò, M. D'Antonio, et al. ASPicDB: a database resource for alternative splicing analysis. *Bioinformatics* (2008), 24(10):1300-1304.

[J4] P. Bonizzoni, G. Della Vedova, R. Dondi, G. Fertin, R. Rizzi, S. Vialette. Exemplar Longest Common Subsequence. IEEE/ACM *Transactions on Computational Biology and Bioinformatics* (2007), 4(4):535-543.

[J3] T. Castrignanò, R. Rizzi, I. G. Talamo, P. D'Onorio De Meo, A. Anselmo, P. Bonizzoni, G. Pesole. ASPIC: a web resource for alternative splicing prediction and transcript isoforms characterization. *Nucleic Acids Research* (2006), 34:W440-3.

[J2] P. Bonizzoni, R. Rizzi, G. Pesole. Computational methods for alternative splicing prediction. *Briefings in Functional Genomics and Proteomics* (2006), 5:46-51.

[J1] P. Bonizzoni, R. Rizzi, G. Pesole. ASPIC: a novel method to predict the exon-intron structure of a gene that is optimally compatible to a set of transcript sequences. *BMC Bioinformatics* (2005), 6(1):244.

## Book chapters

[B1] P. Bonizzoni, G. Della Vedova, G. Pesole, E. Picardi, Y. Pirola, R. Rizzi. (2015) Transcriptome assembly and alternative splicing analysis. *Methods in Molecular Biology* (2015), 1269:173-188.

#### International conference papers

[C15] P. Bonizzoni, C. De Felice, Y. Pirola, R. Rizzi, R. Zaccagnino, R. Zizza. Identification of Chimeric RNAs: a novel machine learning perspective. In: Computational Advances in Bio and Medical Sciences (ICCABS). Vol. 14548. LNCS. Springer Cham., 2023. doi.org/10.1007/978-3-031-82768-6\_2.

[C14] P. Bonizzoni, G. Della Vedova, Y. Pirola, R. Rizzi, M. Sgrò. Multiallelic Maximal Perfect Haplotype Blocks with Wildcards via PBWT. In: Bioinformatics and Biomedical Engineering (IWBBIO). Vol. 13919. LNCS. Springer, 2023, 3–12. doi: 10.1007/978-3-031-34953-9\_5.

[C13] P. Bonizzoni, A. Petescia, Y. Pirola, R. Rizzi, R. Zaccagnino, R. Zizza. KFinger: Capturing Overlaps Between Long Reads by Using Lyndon Fingerprints. In: Bioinformatics and Biomedical Engineering (IWBBIO). Vol. 13347. LNCS. Springer, 2022, 3–12. doi: 10.1007/978-3-031-07802-6\_37.

[C12] P. Bonizzoni, C. De Felice, Y. Pirola, R. Rizzi, R. Zaccagnino, R. Zizza. Can Formal Languages Help Pangenomics to Represent and Analyze Multiple Genomes?. In: Developments in Language Theory (DLT). Vol. 13257. LNCS. Springer, 2022, 3–12. doi:

10.1007/978-3-031-05578-2\_1.

[C11] P. Bonizzoni, C. De Felice, A. Petescia, Y. Pirola, R. Rizzi, J. Stoye, R. Zaccagnino, R. Zizza. Can We Replace Reads by Numeric Signatures? Lyndon Fingerprints as Representations of Sequencing Reads for Machine Learning. In: Algorithms for Computational Biology (AlCoB). Vol. 12715. LNCS. Springer, 2021, 16–28. doi: 10.1007/978-3-030-74432-8\_2.

[C10] P. Bonizzoni, G. Della Vedova, S. Nicosia, Y. Pirola, M. Previtali, R. Rizzi. Divide and Conquer computation of the multi-string BWT and LCP array. *Lecture Notes in Computer Science* (CiE 2018), 10936:107-117.

[C9] G. Della Vedova, M. Patterson, R. Rizzi, M. Soto. Character-based phylogeny construction and its application to evolution. *Lecture Notes in Computer Science* (CiE 2017), 10307:3-13.

[C8] S. Beretta, P. Bonizzoni, L. Denti, M. Previtali, R. Rizzi. Mapping RNA-seq data to a transcript graph via approximate pattern matching to a hypertext. *Lecture Notes in Computer Science* (ALCoB 2017), 10252:49-61.

[C7] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. FSG: Fast string graph construction for de novo assembly of reads data. *Lecture Notes in Computer Science* (ISBRA 2016), 9683:27-39.

[C6] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, R. Rizzi. Constructing String Graphs in External Memory. *Lecture Notes in Computer Science* (WABI 2014), 8701:311-325.

[C5] S. Beretta, P. Bonizzoni, G. Della Vedova, R. Rizzi. Reconstructing isoform graphs from RNA-Seq data. Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine, BIBM 2012, 6392734:499-502.

[C4] P. Bonizzoni, G. Della Vedova, Y. Pirola, R. Rizzi. PIntron: a fast method for gene structure prediction. Proceedings of the 1st IEEE International Conference on Computational Advances in Bio and Medical Sciences ICCABS 2011, 5729935:33-39.

[C3] P. Bonizzoni, G. Della Vedova, R. Dondi, Y. Pirola, R. Rizzi. Minimum factorization agreement of spliced ESTs. *Lecture Notes in Computer Science* (WABI 2009), 5724:1-12.

[C2] P. Bonizzoni, G. Pesole e R. Rizzi. A Method to detect gene structure and alternative splice sites by agreeing ESTs to a genomic sequence. *Lecture Notes in Computer Science* (WABI 2003), 2812:63-77.

[C1] L. Milanesi, R. Rizzi. Microarray Imaging Data Reader SPOTVIEW. Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure BGRS 2002, Novosibirsk 14-20 Luglio 2002, Vol. 2, p. 196-198.

# TEACHING ACTIVITY

- **Statistics** (Bachelor's degree in Territorial, Urban, and Environmental Planning Old Curriculum, Faculty of Architecture, Politecnico di Milano) (responsible teacher: Prof. Federica Migliaccio). Exercises in the academic year 1999/2000.
- Algorithms and Data Structures (Basics) (Bachelor's degree in Computer Science -Old Curriculum, University of Milano-Bicocca). Exercises in the academic years 2002/2003 and 2003/2004.
- Informatics (Bachelor's degree in Biotechnology, University of Milano-Bicocca). Laboratory lessons in the academic year 2005/2006; 8 CFU of lectures in the academic years 2006/2007, 2007/2008, 2011/2012, and 2012/2013.
- Bioinformatics: Basic Techniques I MOD (Master's degree in Bioinformatics, University of Milano-Bicocca). 2 CFU of laboratory lessons in the academic years 2007/2008 and 2008/2009.
- **Bioinformatics: Basic Techniques** (Master's degree in Bioinformatics, University of Milano-Bicocca). 4 CFU of laboratory lessons in the academic years 2009/2010 and 2010/2011.
- Foundations of Computer Science, Complexity Module 1 CFU (Master's degree in Computer Science, University of Milano-Bicocca). 1 CFU of exercises in the academic year 2008/2009.
- Informatics, Programming, and Database Modules (Bachelor's degree in Biotechnology, University of Milano-Bicocca). 6 CFU of lectures in the academic year 2009/2010.
- Informatics, Programming Module (Bachelor's degree in Biotechnology, University of Milano-Bicocca). 4 CFU of lectures in the academic years 2013/2014 and 2014/2015.
- **Programming** (Master's degree in Bioinformatics, University of Milano-Bicocca). 4 CFU of lectures in the academic years 2009/2010 and 2010/2011.
- Models and Systems, Algorithm Design and Analysis Module (Master's degree in Computer Science, University of Milano-Bicocca). 1 CFU of exercises in the academic year 2010/2011.
- **Bioinformatics Methodologies** (Master's degree in Industrial Biotechnology, University of Milano-Bicocca). 1 CFU of exercises from the academic year 2011/2012 to the academic year 2015/2016.
- Bioinformatics (Master's degree in Computer Science, University of Milano-Bicocca).
   2 CFU of exercises in the academic year 2012/2013; 1 CFU of exercises from the academic year 2013/2014 to the academic year 2021/2022; 1 CFU of lectures + 2 CFU of laboratory in the academic year 2022/2023; 2 CFU of laboratory in the

academic year 2023/2024; 2 CFU of lectures + 1 CFU of laboratory in the academic year 2024/2025.

- Elements of Bioinformatics (Bachelor's degree in Computer Science, University of Milano-Bicocca). 2 CFU of laboratory from the academic year 2013/2014 to the academic year 2020/2021; 4 CFU of laboratory in the academic years 2021/2022 and 2022/2023; 2 CFU of laboratory in the academic year 2023/2024; 4 CFU of laboratory in the academic year 2023/2024; 4 CFU of laboratory in the academic year 2024/2025.
- Models and Computation, Computation Theory Module (Master's degree in Computer Science, University of Milano-Bicocca). 2 CFU of exercises from the academic year 2016/2017 to the academic year 2022/2023; 2 CFU of lectures + 1 CFU of exercises in the academic year 2023/2024; 1 CFU of exercises in the academic year 2024/2025.
- Algorithm Analysis and Design (Bachelor's degree in Computer Science, University of Milano-Bicocca). 2 CFU of exercises in the academic years 2020/2021, 2021/2022, and 2022/2023; 4 CFU of lectures in the academic year 2023/2024; 2 CFU of exercises in the academic year 2024/2025.
- Mobile Device Programming (Bachelor's degree in Computer Science, University of Milano-Bicocca). 2 CFU of laboratory in the academic year 2020/2021.
- Security and Reliability (Bachelor's degree in Computer Science, University of Milano-Bicocca). 2 CFU of exercises in the academic year 2020/2021.

## TEACHING IN DOCTORAL COURSES

- Doctoral course 'String Algorithms" (2024) within the Computer Science doctoral program at the University of Milano-Bicocca.
- Doctoral course **"Advanced Techniques for Combinatorial Algorithms"** (2018, 2020) within the Computer Science doctoral program at the University of Milano-Bicocca.
- Doctoral course "Hands on Translational Genomics and Bioinformatics" (2017) within the Molecular Medicine, Immunology and Basic and Applied Oncology doctoral program at Vita-Salute San Raffaele University.

## TEACHING IN A MASTER'S PROGRAM AND SUMMER SCHOOLS

- Genome Assembly (Second-level Master's "qOmics: quantitative methods for Omics Data", University of Milan-Bicocca and University of Pavia). Year: 2021
- **Beyond Genome Assembly** (Second-level Master's "qOmics: quantitative methods for Omics Data", University of Milan-Bicocca and University of Pavia). Year: 2021
- **Bioinformatics Algorithms** (First-level Master's in Bioinformatics University of Milan-Bicocca). Year: 2004/2005
- ISCD Summer School 2017 "Scientific Trends at the Interfaces Bioinformatics Visual Data Analysis", July 17 to August 11, 2017, (Roscoff Marine Station, France)

organized by Alessandra Carbone (CNRS - Université Pierre et Marie Curie, Paris), Pascal Frey, and Elodie Laine (Sorbonne Université, Paris).

#### SUPERVISION ACTIVITY

- **Co-supervision** of the PhD thesis of Luca Denti, cycle XXXII, PhD program in Computer Science at the Department of Computer Science, Systems and Communication, University of Milano-Bicocca. This thesis work led to the development of software (ASGAL) for detecting novel splicing events compared to an annotation (provided by a splicing graph), through graph-based alignment of NGS (Next-Generation Sequencing) reads.
- **Supervisor** of Davide Cesare Monti, cycle XL, PhD program in Computer Science at the Department of Computer Science, Systems and Communication, University of Milano-Bicocca.
- Tutor/Advisor for 30 bachelor's internships and 13 master's theses.

## PARTICIPATION AND EVENT ORGANIZATION

- Speaker at the Bioinformatics Cooperation Group Meeting, Certosa di Pontignano, February 17-18, 2001. Presentation title: "Microarray Imaging Data Pre-processing."
- Speaker at the Third International Workshop, WABI 2003, Budapest, Hungary, September 15-20, 2003. Presentation title: "A Method to Detect Gene Structure and Alternative Splice Sites by Aligning ESTs to a Genomic Sequence."
- Member of the organizing committee for the Workshop "Alternative Splicing in Animals and Plants," Department of Computer Science, Systems, and Communication, University of Milan-Bicocca, October 3, 2008.
- Speaker at the Workshop "Alternative Splicing in Animals and Plants,"October 3, 2008, Department of Computer Science, Systems, and Communication, University of Milan-Bicocca. Presentation title: "A Suffix-Tree Based Method to Predict the Exon-Intron Structure of a Gene from a Set of EST Sequences."
- Member of the organizing committee for the Workshop "Colloquium on Unconventional Models of Computation," a 1-day workshop within ICTCS'09 (Italian Conference on Theoretical Computer Science), Cremona, September 28, 2009.
- Speaker at the Workshop "Sysbiohealth Symposium, Milan, November 25-27, 2009." Presentation title: "EST Clustering for Gene Identification."
- Speaker at the "1st Post-EURASNET Symposium Regulation of Gene Expression through RNA Splicing," International Centre for Theoretical Physics, March 24-27, 2012, Trieste. Presentation title: "PIntronNext: a Fast Method for Detecting

the Gene Structure Due to Alternative Splicing via ESTs, mRNAs, and RNA-Seq Data."

- Member of the organizing committee for the conference "Computability in Europe (CiE) 2013: The Nature of Computation," Milan, July 1-5, 2013.
- Speaker at the "1st Bioinformatics, Computational Biology and System Biology Lombardy Day," MILANO, November 27, 2013. Presentation title: "ASPicDBnext: an NGS Development of a Database of Alternative Splicing Events."
- Member of the organizing and scientific committee for the Workshop "Graph Assembly Algorithms for Omics Data," Department of Computer Science, Systems, and Communication, University of Milan-Bicocca, November 18, 2016.
- Member of the organizing and scientific committee for the Workshop "Workshop on Combinatorial Algorithms in Bioinformatics," Department of Computer Science, Systems, and Communication, University of Milan-Bicocca, January 26, 2018.
- Member of the organizing and scientific committee for the "First Workshop On Pangenomics Algorithms for Omics Data," June 21st, 2019, Univ. Milano-Bicocca.
- Program committee member for the "46th International Conference on Current Trends in Theory and Practice of Computer Science" (SOFSEM 2020).
- Member of the organizing committee for the 7th workshop "Data Structure in Bioinformatics" (DSB21), February 11-12, 2021, online event.

## **RESPONSIBILITIES IN PROJECTS**

- Responsible for the following University Funds: "Design and experimentation of algorithmic approaches for computational problems in Bioinformatics" (2017), "Innovative algorithmic approaches for Bioinformatics" (2018), "Efficient algorithms and data structures for combinatorial problems" (2019), "Advanced approaches for the analysis of complex systems and biological data through formal models and graph-based algorithms" (2024).
- Beneficiary of FFABR 2017 Researchers (Funding for basic research activities).
- Responsible for a fund associated with the SPAC3 project (Smart Services for the New Public Administration for Citizen-Centricity in Cloud) Lombardy Region.
- Participation in the PANGAIA project (Pan-genome Graph Algorithms and Data Integration) - Horizon 2020 Marie Skłodowska-Curie Research and Innovation Staff Exchange (RISE). Participation as an Experienced Researcher, supervising ESR (Early Stage Researchers), organizing events and workshops, and teaching at schools planned within the project.

# ACTIVITY OF REVIEWING

- Reviewing activities for the following journals: Bioinformatics, Genomics, Genome Research, BMC Bioinformatics e Theoretical Computer Science.
- Reviewing activities for the following international conferences: CIE (Computability in Europe), WABI (Workshop on Algorithms in Bioinformatics), ICCABS (IEEE International Conference on Computational Advances in Bio and Medical Sciences) ISBRA (International Symposium on Bioinformatics Research and Applications) BIBM (IEEE International Conference on Bioinformatics and Biomedicine) ACM-BCB (ACM Conference on Bioinformatics, Computational Biology, and Health Informatics IWOCA (International Workshop on Combinatorial Algorithms), ICCS (International Conference on Computational Science), SPIRE (International Symposium on String Processing and Information Retrieval), CPM (Combinatorial Pattern Matching).
- Reviewer for the international project "Modeling Alternative Splicing and its Structural Impact during Evolution" (MASSIV) funded by Agence Nationale de la Recherche (ANR).

## PROFESSIONAL ACTIVITY

- November 2024–present: Quality assurance officer for the Computer Science Degree Program at the Department of Computer Science, Systems and Communication, University of Milan-Bicocca.
- **2022–present**: Responsible for the Double Master's Degree in Computer Science with Université Côte-d'Azur.
- 2022–2024: Member of the AQR commission at the Department of Computer Science, Systems and Communication, University of Milan-Bicocca.
- **2020–present**: Member of the Orientation Commission for the Computer Science Degree Program at the Department of Computer Science, Systems and Communication, University of Milan-Bicocca.
- **2020**: Participation in the examination committee for the state exam for Senior and Junior Information Engineer certification.
- **2013–2020**: Member of the Schedule Commission at the Department of Computer Science, Systems and Communication, University of Milan-Bicocca.
- **2015–present**: Representative for the University of Milan-Bicocca in the "NERD? Not for girls" initiative, created by IBM, aimed at female students in the final years of high school.
- October, December 2021: Additional member of the Computer Science commission for the public competition at the Customs and Monopolies Agency.

## **ORIENTATION ACTIVITY IN HIGH SCHOOLS**

• 2022/2023: Discipline-based laboratory titled "DNA Lab with Python" as part of the PNRR initiatives, aimed at introducing high school students to Python programming and its application in biological data analysis. The activities conducted during the

laboratory were recognized as PCTO (Pathways for Transversal Skills and Orientation) activities. Two 15-hour courses held at the Ernesto Breda Salesian Don Bosco Institute in Sesto San Giovanni (Milan) and at IIS Machiavelli in Pioltello (Milan).

• 2020/2021, 2021/2022: Discipline-based laboratory "Informatics and DNA Analysis" as part of the Scientific Degrees Plan (PLS) of the University of Milan-Bicocca, aimed at introducing high school students to Python programming and its application in biological data analysis. The activities conducted during the laboratory were recognized as PCTO activities.