Yuri Pirola / Curriculum Vitae

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Research Interests

Algorithms and data structures in Bioinformatics / Computational and parameterized complexity / Genomic and transcriptomic sequence analysis and assembly / Haplotype inference and reconstruction / Evolutionary metaheuristics and genetic programming

Positions

- Associate Professor / Oct. 2022–current
  Dept. of Informatics, Systems and Communications, Univ. degli Studi di Milano-Bicocca

  Member of the Bioinformatics and Experimental Algorithmic lab and of the Interdisciplinary Research Centre "Bicocca Bioinformatics Biostatistics and Bioimaging centre" (B4) at Univ. degli Studi di Milano-Bicocca
- Assistant Professor / Oct. 2019–Sept. 2022
  Dept. of Informatics, Systems and Communications, Univ. degli Studi di Milano-Bicocca
- Post-Doctoral Fellow / May 2012–Dec. 2015 / *"Algorithmic methods for Next-Generation Sequencing data analysis"*
  Funding: Univ. degli Studi di Milano-Bicocca
- Post-Doctoral Fellow / Jan. 2011–Apr. 2012 / *"Efficient haplotype inference in livestock from high-density SNP chips"*
  Funding: Univ. degli Studi di Milano-Bicocca / Lombardy Region / Parco Tecnologico Padano (Lodi)
- Post-Doctoral Researcher / Mar. 2010–Dec. 2010 / *"PROZOO Project"*
  Funding: Parco Tecnologico Padano (Lodi)

Education

- Ph.D. in Computer Science / Univ. degli Studi di Milano-Bicocca / February 3, 2010
  "Combinatorial Problems in Studies of Genetic Variations: Haplotyping and Transcript Analysis"
  Supervisor: Prof. Paola Bonizzoni
- M.Sc. in Computer Science, magna cum laude / Univ. degli Studi di Milano-Bicocca / February 23, 2006
  "Analisi della Neutralità degli Spazi di Ricerca Booleani in Programmazione Genetica"
  Supervisors: Dr. Leonardo Vanneschi & Prof. Giancarlo Mauri

Research projects

- *"PANGAIA: Pan-genome Graph Algorithms and Data Integration"*
  Funding: EU Horizon 2020, RISE Marie Skłodowska-Curie Action / Role: participant
- *"CORSAI: Raman analysis of saliva from COPD patients as new biomarker"*
  Funding: ERA PerMed / Role: participant
- *"Modulation of anti-cancer immune response by regulatory non-coding RNAs"*
  Funding: Cariplo Foundation / Role: participant

- *"Automata and formal languages: mathematical and applicative aspects"*
  Funding: MIUR (Italian Ministry of Education), PRIN 2010/11 Action / Role: participant
- *"Next Generation methods to preserve farm animal biodiversity by optimizing present and future breeding options"*
  Funding: European Commission, 7th Framework Programme / Role: participant
- *"PROZOO: Applications of genomics to fertility, disease resistance, and product quality assurance in cattle and pigs"*
  Funding: Cariplo Foundation & Lombardy Region / Role: participant

Fellowships

- Ph.D. fellowship / MIUR (Italian Ministry of Education) / Nov. 2006–Oct. 2009.
- Scholarship for graduate students / Univ. degli Studi di Milano / May–Oct. 2006

Publications

International peer-reviewed journal articles

[J30] Bonizzoni, P., Costantini, M., De Felice, C., Petescia, A., **Pirola, Y.**, Previtali, M., Rizzi, R., Stoye, J., Zaccagnino, R., and Zizza, R. "Numeric Lyndon-based feature embedding of sequencing reads for machine learning approaches." *Inf. Sci.* 607 (2022), 458–476. DOI: 10.1016/j.ins.2022.06.005.
arXiv: 2202.13884v2 [q-bio.GN].

[J29] Ciccolella, S., Denti, L., Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, and Previtali, M. "MALVIRUS: an integrated application for viral variant analysis." *BMC Bioinformatics* 22.15 (2022), 625.
DOI: 10.1186/s12859-022-04668-0.

[J28] Baaijens, J. A., Bonizzoni, P., Boucher, C., Della Vedova, G., **Pirola, Y.**, Rizzi, R., and Sirén, J. "Computational graph pangenomics: a tutorial on data structures and their applications." *Nat. Comput.* 21 (2022), 81–108. DOI: 10.1007/s11047-022-09882-6.

[J27] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "Computing the multi-string BWT and LCP array in external memory." *Theor. Comput. Sci.* 862 (2021), 42–58. DOI: 10.1016/j.tcs.2020.11.041.

[J26] Denti, L., **Pirola, Y.**, Previtali, M., Ceccato, T., Della Vedova, G., Rizzi, R., and Bonizzoni, P. "Shark: fishing relevant reads in an RNA-Seq sample." *Bioinformatics* 37.4 (2021), 464–472.
DOI: 10.1093/bioinformatics/btaa779.

[J25] Rizzi, R., Beretta, S., Patterson, M., **Pirola, Y.**, Previtali, M., Della Vedova, G., and Bonizzoni, P. "Overlap graphs and de Bruijn graphs: data structures for de novo genome assembly in the big data era." *Quant. Biol.* 7.4 (2019), 278–292. DOI: 10.1007/s40484-019-0181-x.

[J24] Calabria, A., Beretta, S., Merelli, I., Spinozzi, G., Brasca, S., **Pirola, Y.**, Benedicenti, F., Tenderini, E., Bonizzoni, P., Milanesi, L., and Montini, E. "γ-TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites." *Bioinformatics* 36.5 (2020), 1622–1624. DOI: 10.1093/bioinformatics/btz747.

[J23] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "Multithread Multistring Burrows–Wheeler Transform and Longest Common Prefix Array." *J. Comput. Biol.* 26.9 (2019), 948–961.
DOI: 10.1089/cmb.2018.0230.

[J22] Grüning, B., Dale, R., Sjödin, A., Chapman, B. A., Rowe, J., Tomkins-Tinch, C. H., Valieris, R., Köster, J., and The Bioconda Team (including **Pirola, Y.**) "Bioconda: sustainable and comprehensive software distribution for the life sciences." *Nature Methods* 15.7 (2018), 475–476. DOI: 10.1038/s41592-018-0046-7.

[J21] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "FSG: Fast String Graph Construction for De Novo Assembly." *J. Comput. Biol.* 24.10 (2017), 953–968. DOI: 10.1089/cmb.2017.0089.

[J20] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "An External-Memory Algorithm for String Graph Construction." *Algorithmica* 78.2 (2017), 394–424. DOI: 10.1007/s00453-016-0165-4.

[J19] Biscarini, F., Schwarzenbacher, H., Pausch, H., Nicolazzi, E. L., **Pirola, Y.**, and Biffani, S. "Use of SNP genotypes to identify carriers of harmful recessive mutations in cattle populations." *BMC Genomics* 17 (2016), 857. DOI: 10.1186/s12864-016-3218-9.

[J18] Chiaradonna, F., **Pirola, Y.**, Ricciardiello, F., and Palorini, R. "Transcriptional profiling of immortalized and K-ras-transformed mouse fibroblasts upon PKA stimulation by forskolin in low glucose availability." *Genomics Data* 9 (2016), 100–104. DOI: 10.1016/j.gdata.2016.07.004.

[J17] Bonizzoni, P., Dondi, R., Klau, G. W., **Pirola, Y.**, Pisanti, N., and Zaccaria, S. "On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes." *J. Comput. Biol.* 23.9 (2016), 718–736. DOI: 10.1089/cmb.2015.0220.

[J16] Palorini, R., Votta, G., **Pirola, Y.**, De Vitto, H., De Palma, S., Airoldi, C., Vasso, M., Ricciardiello, F., Lombardi, P. P., Cirulli, C., Rizzi, R., Nicotra, F., Hiller, K., Gelfi, C., Alberghina, L., and Chiaradonna, F. "Protein Kinase A Activation Promotes Cancer Cell Resistance to Glucose Starvation and *Anoikis*." *PLoS Genet.* 12.3 (2016), 1–41. DOI: 10.1371/journal.pgen.1005931.

[J15] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "LSG: An External-Memory Tool to Compute String Graphs for NGS Data Assembly." *J. Comput. Biol.* 23.3 (2016), 137–149. DOI: 10.1089/cmb.2015.0172.

[J14] **Pirola, Y.**, Zaccaria, S., Dondi, R., Klau, G. W., Pisanti, N., and Bonizzoni, P. "HapCol: Accurate and Memory-Efficient Haplotype Assembly from Long Reads." *Bioinformatics* 32.11 (2016), 1610–1617. DOI: 10.1093/bioinformatics/btv495.

[J13] Beerenwinkel, N., Beretta, S., Bonizzoni, P., Dondi, R., and **Pirola, Y.** "Covering Pairs in Directed Acyclic Graphs." *Comput. J.* 58.7 (2015), 1673–1686. DOI: 10.1093/comjnl/bxu116.

[J12] Batini, C., Bonizzoni, P., Comerio, M., Dondi, R., **Pirola, Y.**, and Salandra, F. "A Clustering Algorithm for Planning the Integration Process of a Large Number of Conceptual Schemas." *J. Comput. Sci. Technol.* 30.1 (2015), 214–224. DOI: 10.1007/s11390-015-1514-5.

[J11] Beretta, S., Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, and Rizzi, R. "Modeling Alternative Splicing Variants from RNA-Seq Data with Isoform Graphs." *J. Comput. Biol.* 21.1 (2014), 16–40. DOI: 10.1089/cmb.2013.0112.

[J10] Bonizzoni, P., Della Vedova, G., Dondi, R., and **Pirola, Y.** "Parameterized Complexity of k-Anonymity: Hardness and Tractability." *J. Comb. Optim.* 26.1 (2013), 19–43. DOI: 10.1007/s10878-011-9428-9.

[J9] Bonizzoni, P., Dondi, R., and **Pirola, Y.** "Maximum Disjoint Paths on Edge-Colored Graphs: Approximability and Tractability." *Algorithms* 6.1 (2013), 1–11. DOI: 10.3390/a6010001.

[J8] **Pirola, Y.**, Della Vedova, G., Biffani, S., Stella, A., and Bonizzoni, P. "A Fast and Practical Approach to Genotype Phasing and Imputation on a Pedigree with Erroneous and Incomplete Information." *IEEE/ACM Trans. Comput. Biol. Bioinform.* 9.6 (2012), 1582–1594. DOI: 10.1109/TCBB.2012.100.

[J7] **Pirola, Y.**, Rizzi, R., Picardi, E., Pesole, G., Della Vedova, G., and Bonizzoni, P. "PIntron: A Fast Method for Detecting the Gene Structure Due to Alternative Splicing Via Maximal Pairings of a Pattern and a Text." *BMC Bioinformatics* 13.S5 (2012), S2. DOI: 10.1186/1471-2105-13-S5-S2.

[J6] Vanneschi, L., **Pirola, Y.**, Mauri, G., Tomassini, M., Collard, P., and Verel, S. "A Study of Neutrality of Boolean Function Landscapes in Genetic Programming." *Theor. Comput. Sci.* 425 (2012), 34–57. DOI: 10.1016/j.tcs.2011.03.011.

[J5] **Pirola, Y.**, Bonizzoni, P., and Jiang, T. "An Efficient Algorithm for Haplotype Inference on Pedigrees with Recombinations and Mutations." *IEEE/ACM Trans. Comput. Biol. Bioinform.* 9.1 (2012), 12–25. DOI: 10.1109/TCBB.2011.51.

[J4] Bonizzoni, P., Della Vedova, G., Dondi, R., and **Pirola, Y.** "Variants of Constrained Longest Common Subsequence." *Inf. Process. Lett.* 110.20 (2010), 877–881. DOI: 10.1016/j.ipl.2010.07.015.

[J3] Bonizzoni, P., Della Vedova, G., Dondi, R., **Pirola, Y.**, and Rizzi, R. "Pure Parsimony Xor Haplotyping." *IEEE/ACM Trans. Comput. Biol. Bioinform.* 7.4 (2010), 598–610. DOI: 10.1109/TCBB.2010.52.

[J2] Della Vedova, G., Dondi, R., Jiang, T., Pavesi, G., **Pirola, Y.**, and Wang, L. "Beyond Evolutionary Trees." *Nat. Comput.* 9.2 (2010), 421–435. DOI: 10.1007/s11047-009-9156-6.

[J1] Bonizzoni, P., Mauri, G., Pesole, G., Picardi, E., **Pirola, Y.**, and Rizzi, R. "Detecting Alternative Gene Structures from Spliced ESTs: A Computational Approach." *J. Comput. Biol.* 16.1 (2009), 43–66. DOI: 10.1089/cmb.2008.0028.

International peer-reviewed conference papers

[C17] Bonizzoni, P., Petescia, A., **Pirola, Y.**, Rizzi, R., Zaccagnino, R., and Zizza, R. "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.

[C16] Bonizzoni, P., De Felice, C., **Pirola, Y.**, Rizzi, R., Zaccagnino, R., and Zizza, R. "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.

[C15] Bonizzoni, P., De Felice, C., Petescia, A., **Pirola, Y.**, Rizzi, R., Stoye, J., Zaccagnino, R., and Zizza, R. "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.

[C14] Bonizzoni, P., Della Vedova, G., Nicosia, S., **Pirola, Y.**, Previtali, M., and Rizzi, R. "Divide and Conquer Computation of the Multi-string BWT and LCP Array." In: *Computability in Europe (CiE)*. Vol. 10936. LNCS. Springer, 2018, 107–117. DOI: 10.1007/978-3-319-94418-0_11.

[C13] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "FSG: Fast String Graph Construction for De Novo Assembly of reads data." In: *Bioinformatics Research and Applications (ISBRA)*. Vol. 9683. LNCS. Springer, 2016, 27–39. DOI: 10.1007/978-3-319-38782-6_3.

[C12] Bonizzoni, P., Dondi, R., Klau, G. W., **Pirola, Y.**, Pisanti, N., and Zaccaria, S. "On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction problem." In: *Combinatorial Pattern Matching (CPM)*. Vol. 9133. LNCS. Springer, 2015, 100–113. DOI: 10.1007/978-3-319-19929-0_9.

[C11] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, Previtali, M., and Rizzi, R. "Constructing String Graphs in External Memory." In: *Algorithms in Bioinformatics (WABI)*. Vol. 8701. LNCS. Springer, 2014, 311–325. DOI: 10.1007/978-3-662-44753-6_23.

[C10] Beerenwinkel, N., Beretta, S., Bonizzoni, P., Dondi, R., and **Pirola, Y.** "Covering Pairs in Directed Acyclic Graphs." In: *Language and Automata Theory and Applications (LATA)*. Vol. 8370. LNCS. Springer, 2014, 126–137. DOI: 10.1007/978-3-319-04921-2_10.

[C9] **Pirola, Y.**, Della Vedova, G., Bonizzoni, P., Stella, A., and Biscarini, F. "Haplotype-based prediction of gene alleles using pedigrees and SNP genotypes." In: *Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB)*. ACM, 2013, 33–41. DOI: 10.1145/2506583.2506592.

[C8] **Pirola, Y.**, Della Vedova, G., Biffani, S., Stella, A., and Bonizzoni, P. "A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information." In: *Computational Advances in Bio and medical Sciences (ICCABS)*. IEEE, 2012. DOI: 10.1109/ICCABS.2012.6182643.

[C7] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, and Rizzi, R. "PIntron: a fast method for gene structure prediction via maximal pairings of a pattern and a text." In: *Computational Advances in Bio and medical Sciences (ICCABS)*. IEEE, 2011, 33–39. DOI: 10.1109/ICCABS.2011.5729935.

[C6] **Pirola, Y.**, Bonizzoni, P., and Jiang, T. "Haplotype Inference on Pedigrees with Recombinations and Mutations." In: *Algorithms in Bioinformatics (WABI)*. Vol. 6293. LNCS. Springer, 2010, 148–161. DOI: 10.1007/978-3-642-15294-8_13.

[C5] Bonizzoni, P., Della Vedova, G., Dondi, R., and **Pirola, Y.** "Parameterized Complexity of k-Anonymity: Hardness and Tractability." In: *Combinatorial Algorithms (IWOCA)*. Vol. 6460. LNCS. Springer, 2011, 242–255. DOI: 10.1007/978-3-642-19222-7_25.

[C4] Bonizzoni, P., Della Vedova, G., Dondi, R., **Pirola, Y.**, and Rizzi, R. "Minimum Factorization Agreement of Spliced ESTs." In: *Algorithms in Bioinformatics (WABI)*. Vol. 5724. LNCS. Springer, 2009, 1–12. DOI: 10.1007/978-3-642-04241-6_1.

[C3] Bonizzoni, P., Della Vedova, G., Dondi, R., **Pirola, Y.**, and Rizzi, R. "Pure Parsimony Xor Haplotyping." In: *Bioinformatics Research and Applications (ISBRA)*. Vol. 5542. LNCS. Springer, 2009, 186–197. DOI: 10.1007/978-3-642-01551-9_19.

[C2] Vanneschi, L., Tomassini, M., Collard, P., Verel, S., **Pirola, Y.**, and Mauri, G. "A Comprehensive View of Fitness Landscapes with Neutrality and Fitness Clouds." In: *Genetic Programming (EuroGP)*. Vol. 4445. LNCS. Springer, 2007, 241–250. DOI: 10.1007/978-3-540-71605-1_22.

[C1] Vanneschi, L., **Pirola, Y.**, and Collard, P. "A quantitative study of neutrality in GP boolean landscapes." In: *Genetic and Evolutionary Computation (GECCO)*. ACM, 2006, 895–902. DOI: 10.1145/1143997.1144152.

Book chapters

[B2] Dondi, R. and **Pirola, Y.** "Beyond Evolutionary Trees." In: *Encyclopedia of Algorithms*. Ed. by M.-Y. Kao. Springer, 2016, 183–189. ISBN: 978-3-642-27848-8. DOI: 10.1007/978-3-642-27848-8_599-1.

[B1] Bonizzoni, P., Della Vedova, G., Pesole, G., Picardi, E., **Pirola, Y.**, and Rizzi, R. "Transcriptome Assembly and Alternative Splicing Analysis." In: *RNA Bioinformatics*. Ed. by E. Picardi. Vol. 1269. Methods in Molecular Biology. Springer, 2015, 173–188. ISBN: 978-1-4939-2290-1. DOI: 10.1007/978-1-4939-2291-8_11.

In: ISI WoS,Scopus.

Talks, schools, and visits

Invited talks

› Università degli Studi di Milano / invited by Prof. Giovanni Righini / Feb. 8, 2010

› Parco Tecnologico Padano (Lodi) / invited by Dr. Alessandra Stella / Mar. 25, 2010

Talks

› *Bioinformatics and Biomedical Engineering (IWBBIO)* / Gran Canaria, Spain / Jun. 2022

› *Bioinformatics and Computational Biology Conference (BBCC)* / Naples, Italy / Nov. 2020

› *Bioinformatics Open Source Conference (BOSC)* / Toronto, Canada / Jul. 2020

› *Int. Workshop on Data Structures in Bioinformatics (DSB)* / Rennes, France / Feb. 2020

› *Int. Conf. on Language and Automata Theory and Applications (LATA)* / Madrid, Spain / Mar. 2014

› *Workshop "Combinatorial structures for sequence analysis in bioinformatics"* / Milan, Italy / Nov. 2013

- *ACM Int. Conf. on Bioinf., Computational Biol., and Biomedical Inform. (ACM BCB)* / Washington DC, USA / Sep. 2013
- *Italian Conf. on Theoretical Computer Science (ICTCS)* / Palermo, Italy / Sep. 2013
- *IEEE Int. Conf. on Computational Advances in Bio and medical Sciences (ICCABS)* / Las Vegas NV, USA / Feb. 2012
- *IEEE Int. Conf. on Computational Advances in Bio and medical Sciences (ICCABS)* / Orlando FL, USA / Feb. 2011
- *Int. Workshop on Algorithms in Bioinformatics (WABI)* / Liverpool, UK / Sep. 2010
- *Int. Workshop on Algorithms in Bioinformatics (WABI)* / Philadelphia PA, USA / Sep. 2009
- *Int. Symp. on Bioinformatics Research and Applications (ISBRA)* / Ft. Lauderdale FL, USA / May 2009

Schools

- *Lipari Int. Summer School on Bioinformatics and Computational Biology* / Univ. degli Studi di Catania / 2008
- Summer school on *Parallel and Scientific Computing* / CINECA / 2006

Research visits

- *Centrum Wiskunde & Informatica* / Amsterdam, The Netherlands / Dr. Gunnar W. Klau / Jul. 14–17, 2015
- *Université Paris-Est Marne-la-Vallée* / Paris, France / Dr. Gregory Kucherov / Jan. 12–18, 2014
- *University of California, Riverside* / Riverside CA, USA / Prof. Tao Jiang / Feb.–Jun. 2009

Professional activities

- Local Technical Coordinator (LTeC) for Univ. of Milano-Bicocca of the Italian node of ELIXIR
- *Co-organizer* (with S. Pissis, CWI) of a satellite workshop of ECCB 2020
- *Program commitee* member of: ICTCS 2022 / BICOB 2020–2022 / HPC4COVID-19 2020 (part of IEEE BIBM) / IWBBIO 2020,2022 / BBC 2015–2022 (part of ICCS) / PDP 2015–2017
- *Organizing commitee* member of: PhD School "Introduction to Pangenomics" 2022 / DSB 2021 / CiE 2013 / "Unconventional Models of Computation" 2009 / ASWorkshop 2008
- Member of the reviewer board of Algorithms
- Review editor in the *editorial board* of Frontiers in Bioinformatics
- *Reviewer* for the following journals: Discrete Applied Mathematics / Bioinformatics / Briefings in Bioinformatics / IEEE-ACM Trans. Computational Biology and Bioinformatics / IEEE Access / J. Computational Science / J. Biomedical Informatics / Computers & Operations Research / Int. Trans. in Operational Research / GigaScience / Applied Sciences / Mathematics / Genes / Processes / Systems / Technologies / Concurrency and Computation: Practice and Experience / BMC Genomics / Int. J. Bioinformatics Research and Applications / Int. J. Molecular Sciences / BioMed Research Int.
- *Reviewer* for the following international conferences: IEEE BIBM 2022, 2021, 2020, 2013, 2012, 2009 / WABI 2022, 2021, 2014, 2012 / ISBRA 2021, 2015, 2014 / RECOMB-CG 2021 / APBC 2020 / CIBB 2019, 2014 / SODA 2018 / IWOCA 2016, 2015 / AAIM 2016 / WALCOM 2016 / BSB 2013 / CiE 2013 / CATS 2013 / ECCB 2012 / ICCABS 2011

Supervision activities

- Co-supervisor for 1 Ph.D. thesis in CS at Univ. degli Studi di Milano-Bicocca
- Supervisor for 5 M.Sc. theses in CS at Univ. degli Studi di Milano-Bicocca
- Supervisor for 9 B.Sc. theses in CS at Univ. degli Studi di Milano-Bicocca

Teaching

- Member of the board of the Ph.D. program in Computer Science at Univ. degli Studi di Milano-Bicocca
- *Teacher/Teaching assistant*, at Univ. degli Studi di Milano-Bicocca, of:

Theory of computing	16h, class	M.Sc.	School of Computer Science	2022/23
Algorithms and DS	52h, class	B.Sc.	School of Computer Science	2022/23
Algorithms and DS	40h, lab.	B.Sc.	School of Computer Science	2022/23
Software design	12h, lab.	M.Sc.	School of Computer Science	2019/20–22/23
Computer science	16h, class	MD	School of Medicine	2018/19–21/22
Genome assembly	20h, class	2nd level master (EQF/RQF level 8)		2020/21
Algorithms and DS	20h, class	B.Sc.	School of Computer Science	2019/20–21/22
Algorithms and DS	20h, lab.	B.Sc.	School of Computer Science	2019/20–21/22
Elements of Bioinformatics	16h, lab.	B.Sc.	School of Computer Science	2013/14
Algorithms and DS 2	12h, class	B.Sc.	School of Computer Science	2010/11
Bioinformatics	4h, lectures	M.Sc.	School of Computer Science	2009/10
Bioinformatics	8h, class	M.Sc.	School of Computer Science	2008/09
Analysis of algorithms	12h, class	M.Sc.	School of Computer Science	2007/08
Bioinformatics	4h, lectures	B.Sc.	School of Computer Science	2007/08
Programming languages	24h, lab.	B.Sc.	School of Computer Science	2006/07
Algorithms and DS	12h, lab.	B.Sc.	School of Computer Science	2005/06
Operating systems	24h, lab.	B.Sc.	School of Computer Science	2005/06
Operating systems	48h, lab.	B.Sc.	School of Computer Science	2004/05

- *Teaching assistant*, at Univ. degli Studi di Bergamo, of:

Introduction to Informatics	30h, class	B.A.	School of Foreign Languages	2007/08–08/09

- *Lecturer* for the course "Population-based Optimisation Methods" (4h, June 2022) of the Ph.D. program in Computer Science at Univ. degli Studi di Milano-Bicocca
- *Lecturer* for the course "Do we need data structures?" (4h, Oct. 2020) of the Ph.D. program in Computer Science at Univ. degli Studi di Milano-Bicocca
- *Lecturer* on the topic "Introduction to programming in C" (16h) for post-graduate LS researchers at PTP, Lodi