

Yuri Pirola / Curriculum Vitae

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🏠 <https://algotlab.eu/pirola>

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

- Assistant Professor / Oct. 2019–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
- 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
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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
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Publications

- 30 articles on international peer-reviewed scientific journals (indexed on Scopus and/or WoS)
- 17 papers on proceedings of international peer-reviewed conferences (indexed on Scopus and/or WoS)
- 2 invited book chapters (indexed on Scopus and/or WoS)
- Several posters presented at national and international conferences

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](https://doi.org/10.1016/j.ins.2022.06.005).
arXiv: [2202.13884v2](https://arxiv.org/abs/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1089/cmb.2015.0220).
- [J16] Palorini, R., Votta, G., **Pirola, Y.**, De Vito, H., De Palma, S., Airolidi, 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1109/ICCABS.2012.6182643).
- [C7] Bonizzoni, P., Della Vedova, G., **Pirola, Y.**, and Rizzi, R. “PItron: 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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 committee* 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 committee* 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 / 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: ISBRA 2021, 2015, 2014 / WABI 2022, 2021, 2014, 2012 / RECOMB-CG 2021 / IEEE BIBM 2021, 2020, 2013, 2012, 2009 / 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:

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
Software design	12h, lab.	M.Sc. School of Computer Science	2019/20–21/22
Computer science	16h, class	MD School of Medicine	2018/19–20/21
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
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- *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