

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

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

Experience

- › 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)

Research projects

- › “*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

International peer-reviewed journal articles

- [J16] P. Bonizzoni, R. Dondi, G. W. Klau, Y. Pirola, N. Pisanti, and S. Zaccaria. “On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes”. *J. Comput. Biol.* (accepted, in press). IF (JCR 2014): 1.737 In: ISI WoS,Scopus.
- [J15] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, and R. Rizzi. “LSG: An External-Memory Tool to Compute String Graphs for NGS Data Assembly”. *J. Comput. Biol.* (accepted, in press). IF (JCR 2014): 1.737 In: ISI WoS,Scopus.
- [J14] Y. Pirola, S. Zaccaria, R. Dondi, G. W. Klau, N. Pisanti, and P. Bonizzoni. “HapCol: Accurate and Memory-Efficient Haplotype Assembly from Long Reads”. *Bioinformatics* (in press, available online). DOI: [10.1093/bioinformatics/btv495](https://doi.org/10.1093/bioinformatics/btv495). IF (JCR 2014): 4.981 In: ISI WoS,Scopus.
- [J13] N. Beerenwinkel, S. Beretta, P. Bonizzoni, R. Dondi, and Y. Pirola. “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). IF (JCR 2014): 0.787 In: ISI WoS,Scopus.
- [J12] C. Batini, P. Bonizzoni, M. Comerio, R. Dondi, Y. Pirola, and F. Salandra. “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). IF (JCR 2014): 0.672 In: ISI WoS,Scopus.
- [J11] S. Beretta, P. Bonizzoni, G. Della Vedova, Y. Pirola, and R. Rizzi. “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). IF (JCR 2014): 1.737 In: ISI WoS,Scopus.
- [J10] P. Bonizzoni, G. Della Vedova, R. Dondi, and Y. Pirola. “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). IF (JCR 2014): 0.939 In: ISI WoS,Scopus.
- [J9] P. Bonizzoni, R. Dondi, and Y. Pirola. “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). In: Inspec,Scopus.
- [J8] Y. Pirola, G. Della Vedova, S. Biffani, A. Stella, and P. Bonizzoni. “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). IF (JCR 2014): 1.438 In: ISI WoS,Scopus.
- [J7] Y. Pirola, R. Rizzi, E. Picardi, G. Pesole, G. Della Vedova, and 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* 13.S5 (2012), S2. DOI: [10.1186/1471-2105-13-S5-S2](https://doi.org/10.1186/1471-2105-13-S5-S2). IF (JCR 2014): 2.576 In: ISI WoS,Scopus.
- [J6] L. Vanneschi, Y. Pirola, G. Mauri, M. Tomassini, P. Collard, and S. Verel. “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). IF (JCR 2014): 0.657 In: ISI WoS,Scopus.
- [J5] Y. Pirola, P. Bonizzoni, and T. Jiang. “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). IF (JCR 2014): 1.438 In: ISI WoS,Scopus.
- [J4] P. Bonizzoni, G. Della Vedova, R. Dondi, and Y. Pirola. “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). IF (JCR 2014): 0.546 In: ISI WoS,Scopus.
- [J3] P. Bonizzoni, G. Della Vedova, R. Dondi, Y. Pirola, and R. Rizzi. “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). IF (JCR 2014): 1.438 In: ISI WoS,Scopus.
- [J2] G. Della Vedova, R. Dondi, T. Jiang, G. Pavesi, Y. Pirola, and L. Wang. “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). IF (JCR 2014): 0.757 In: ISI WoS,Scopus.

- [J1] P. Bonizzoni, G. Mauri, G. Pesole, E. Picardi, Y. Pirola, and R. Rizzi. “Detecting Alternative Gene Structures from Spliced ESTs: A Computational Approach”. *J. Comput. Biol.* 16.1 (2009), 43–66. DOI: 10.1089/cmb.2008.0028. IF (JCR 2014): 1.737 In: ISI WoS,Scopus.

International peer-reviewed conference papers

- [C12] P. Bonizzoni, R. Dondi, G. W. Klau, Y. Pirola, N. Pisanti, and S. Zaccaria. “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. In: ISI WoS,Scopus.
- [C11] P. Bonizzoni, G. Della Vedova, Y. Pirola, M. Previtali, and R. Rizzi. “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. In: ISI WoS,Scopus.
- [C10] N. Beerenwinkel, S. Beretta, P. Bonizzoni, R. Dondi, and Y. Pirola. “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. In: Inspec,Scopus.
- [C9] Y. Pirola, G. Della Vedova, P. Bonizzoni, A. Stella, and F. Biscarini. “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. In: Scopus.
- [C8] Y. Pirola, G. Della Vedova, S. Biffani, A. Stella, and P. Bonizzoni. “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. In: Inspec,Scopus.
- [C7] P. Bonizzoni, G. Della Vedova, Y. Pirola, and R. Rizzi. “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. In: Inspec,Scopus.
- [C6] Y. Pirola, P. Bonizzoni, and T. Jiang. “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. In: ISI WoS,Scopus.
- [C5] P. Bonizzoni, G. Della Vedova, R. Dondi, and Y. Pirola. “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. In: ISI WoS,Scopus.
- [C4] P. Bonizzoni, G. Della Vedova, R. Dondi, Y. Pirola, and R. Rizzi. “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. In: ISI WoS,Scopus.
- [C3] P. Bonizzoni, G. Della Vedova, R. Dondi, Y. Pirola, and R. Rizzi. “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. In: ISI WoS,Scopus.
- [C2] L. Vanneschi, M. Tomassini, P. Collard, S. Verel, Y. Pirola, and G. Mauri. “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. In: ISI WoS,Scopus.
- [C1] L. Vanneschi, Y. Pirola, and P. Collard. “A quantitative study of neutrality in GP boolean landscapes”. In: *Genetic and Evolutionary Computation (GECCO)*. ACM, 2006, 895–902. DOI: 10.1145/1143997.1144152. In: ISI WoS,Scopus.

Book chapters

- [B2] R. Dondi and Y. Pirola. “Beyond Evolutionary Trees”. In: *Encyclopedia of Algorithms*. Ed. by M.-Y. Kao. Springer, in press, available online. ISBN: 978-3-642-27848-8. DOI: 10.1007/978-3-642-27848-8_599-1.

- [B1] P. Bonizzoni, G. Della Vedova, G. Pesole, E. Picardi, Y. Pirola, and R. Rizzi. “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: Medline, Scopus.

PhD thesis

- [T1] Y. Pirola. “Combinatorial Problems in Studies of Genetic Variations: Haplotyping and Transcript Analysis”. PhD thesis. Università degli Studi di Milano-Bicocca, 2010. HDL: [10281/7891](https://hdl.handle.net/10281/7891).
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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

- › *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
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Professional activities

- › *Program committee member of: BBC 2015, 2016 (part of ICCS) / PDP 2015, 2016*
- › *Organizing committee member of: CiE 2013 / “Unconventional Models of Computation” 2009 / ASWorkshop 2008*

- > *Reviewer* for the following journals: Discrete Applied Mathematics / IEEE-ACM Trans. Computational Biology and Bioinformatics / Algorithms / Concurrency and Computation: Practice and Experience / BMC Genomics / Int. J. Bioinformatics Research and Applications
 - > *Reviewer* for the following international conferences: WALCOM 2016 / IWOCA 2015 / ISBRA 2014, 2015 / WABI 2012, 2014 / CIBB 2014 / BIBM 2009, 2012, 2013 / BSB 2013 / CiE 2013 / CATS 2013 / ECCB 2012 / ICCABS 2011
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Teaching

- > *Teaching assistant*, at Univ. degli Studi di Milano-Bicocca, of:

Elements of Bioinformatics	16h, lab.	B.Sc.	School of Computer Science	2013/14
Algorithms and data structures 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 data structures	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	2008/09
Introduction to Informatics	30h, class	B.A.	School of Foreign Languages	2007/08
- > *Lecturer* on the topic "Introduction to programming in C" (16h) for post-graduate life-sciences researchers at PTP, Lodi
- > *Supervisor* for 2 M.Sc. theses in CS at Univ. degli Studi di Milano-Bicocca
- > *Supervisor* for 4 B.Sc. theses in CS at Univ. degli Studi di Milano-Bicocca