

Stefano Beretta

PERSONAL INFORMATION *Date of birth:* 18/04/1984
Nationality: Italian
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AFFILIATION Dipartimento di Informatica, Sistemistica e Comunicazione,
Università degli Studi di Milano-Bicocca,
Viale Sarca 336, I-20126 Milan, Italy.

RESEARCH INTERESTS Bioinformatics, Algorithms, Theoretical Computer Science, Computational Complexity, Approximation Algorithms, Next-Generation Sequencing (NGS) data Analysis, Genomics, Transcriptomics, Metagenomics

EDUCATION 2010-2012. Università degli Studi di Milano - Bicocca, Italy.
 Ph.D. in Computer Science
 Dissertation Topic: *Algorithms for next generation sequencing data analysis*

2006-2009. Università degli Studi di Milano - Bicocca, Italy.
 Master Degree *with honors* in Computer Science

2003-2006. Università degli Studi di Milano - Bicocca, Italy.
 Bachelor Degree in Computer Science

POSITIONS 2015, January - Now. Università degli Studi di Milano - Bicocca, Italy.
 New Computational Methods for Translational Bioinformatics Analysis
 Postdoctoral research fellow, supervisor Paola Bonizzoni

2014, May - 2014, December. Institute for Biomedical Technologies - CNR.
 Hepatocarcinoma Innovative Research MARKers (HIRMA)
 Research collaboration contract, supervisor Luciano Milanese

2013, May - 2014, May. Institute for Biomedical Technologies - CNR.
 MEdical Research in ITaly (MERIT)
 Postdoctoral research fellow, supervisor Luciano Milanese

OTHER TITLES 2016. Qualification a *Maître de conférences* en Informatique (n. 16227292702)
 French qualification as Assistant Professor in Computer Science.

VISITING 2016, February 29 - 2016, March 13. University of Stirling, Stirling, UK.
 ICT COST Action IC1406 - cHiPSet grant
 Invited by Dott. Andrea Bracciali

2012, April - 2012, July. Technical University of Catalonia (UPC), Barcelona, Spain.
 Algorithms, Bioinformatics, Complexity and Formal Methods Research Group

Invited by Prof. Gabriel Valiente

AWARDS

- 2015 - 2017. Italian Ministry of University and Research, Postdoc 2-years grant.
2014. Dip. di Informatica, Sistemistica e Comunicazione, Università degli Studi di Milano - Bicocca.
Special mention for “Best Journal Paper Award” of the year:
Alonso-Aleman D., Barré A., Beretta S., *et al.* Bioinformatics, Vol 30(1):17-23, 2014.
- 2013, May - 2014, May. National Research Council (CNR), Postdoc 1-year grant.
- 2010 - 2012. Italian Ministry of University and Research, Ph.D. 3-years scholarship.
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Teaching Activity

CLASSES

- a.a. 2015/2016. Teaching Assistant (40h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Informatica I”, degree in Physics.
- a.a. 2014/2015. Teaching Assistant (20h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Informatica I”, degree in Physics.
- a.a. 2014/2015. Lecturer (30h). Università degli Studi di Bergamo, Italy.
Course “Informatica di Base 1”, degree in Foreign Languages and Literatures.
- a.a. 2012/2013. Teaching Assistant (32h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Matematica e Informatica II”, degree in Mathematics.
- a.a. 2011/2012. Lecturer (60h). Università degli Studi di Bergamo, Italy.
Course “Informatica di Base 1”, degree in Foreign Languages and Literatures.
- a.a. 2010/2011. Teaching Assistant (24h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Algoritmi e Strutture Dati”, degree in Computer Science.
- a.a. 2010/2011. Teaching Assistant (24h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Informatica I”, degree in Physics.
- a.a. 2010/2011. Lecturer (60h). Università degli Studi di Bergamo, Italy.
Course “Informatica di Base 1”, degree in Foreign Languages and Literatures.
- a.a. 2010/2011. Teaching Assistant (48h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Matematica e Informatica I”, degree in Mathematics.
- a.a. 2009/2010. Teaching Assistant (12h). Università degli Studi di Milano - Bicocca, Italy.
Course “Algoritmi e Ricerca Operativa”, degree in Computer Science.
- 08/02/2010 - 12/02/2010. Tutor. C.I.L.F (Centro per l’innovazione del Lavoro e della Formazione).
Learning Week Project titled: *Informatica ieri, oggi e domani* - edition n. 286.
- a.a. 2009/2010. Teaching Assistant (24h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Algoritmi e Strutture Data”, degree in Computer Science.

2008, May - 2009, May. Help-desk support. Bytech - servizi informatici.
Bio-Rad Laboratories IT Operations for European offices (Italy, Spain, Portugal, and Greece).

2007, October - 2008, March. Tutor. Università degli Studi di Milano - Bicocca, Italy.
Student help-desk support at IT campus laboratories.

2007, April - 2007, September. Tutor. Università degli Studi di Milano - Bicocca, Italy.
Student help-desk support at IT campus laboratories.

Scientific Activity

PROJECTS *Automi e Linguaggi Formali: Aspetti Matematici e Applicativi*.
MIUR PRIN 2010/2011.

Hepatocarcinoma Innovative Research MARKers (HIRMA).
MIUR FIRB 2011.

MEDical Research in ITaly (MERIT).

ORGANIZATION *9th Workshop on Biomedical and Bioinformatics Challenges for Computer Science (BBC 2016)*
In conjunction with *International Conference on Computational Science (ICCS)*
6-8 June 2016, San Diego (CA), USA.

8th Workshop on Biomedical and Bioinformatics Challenges for Computer Science (BBC 2015)
In conjunction with *International Conference on Computational Science (ICCS)*
1-3 June 2015, Reykjavik, Iceland.

Computability in Europe (CiE) - The Nature of Computation
1-5 July 2013, Università degli Studi di Milano - Bicocca, Italy.

PROGRAM *Workshop on Biomedical and Bioinformatics Challenges for Computer Science*
COMMITTEE

- BBC 2015 (8th ed.).
- BBC 2016 (9th ed.).

Advances in High-Performance Bioinformatics, Systems and Synthetic Biology

- PDP 2015.
- PDP 2016.

REFEREEING CONFERENCES: EPIA 2013, PDP 2015, ICCS-BBC 2015, PDP 2016.

Peer-reviewed Publications

JOURNALS [1] Ivan Kel, Zisong Chang, Nadia Galluccio, Margherita Romeo, **Stefano Beretta**, Luisa Diomede, Alessandra Mezzelani, Luciano Milanese, Christoph Dieterich, and Ivan Merelli. "SPIRE: a modular pipeline for eQTL analysis of RNA-Seq data reveals a regulatory hotspot controlling miRNA expression." *Molecular BioSystems* (2016), (in press). DOI: 10.1039/C6MB00453A.

- [2] **Stefano Beretta**, Mauro Castelli, and Riccardo Dondi. “Parameterized tractability of the maximum-duo preservation string mapping problem”. *Theoretical Computer Science* 646 (2016), 16–25. DOI: 10.1016/j.tcs.2016.07.011.
- [3] **Stefano Beretta** and Riccardo Dondi. “Correcting Gene Trees by Leaf Insertions: Complexity and Approximation”. *Electronic Notes in Theoretical Computer Science* 322 (2016). Proceedings of ICTCS 2015, the 16th Italian Conference on Theoretical Computer Science, 35–50. DOI: 10.1016/j.entcs.2016.03.004.
- [4] **Stefano Beretta**, Mauro Castelli, and Riccardo Dondi. “Correcting gene tree by removal and modification: Tractability and approximability”. *Journal of Discrete Algorithms* 33 (2015), 115–129. DOI: 10.1016/j.jda.2015.03.005.
- [5] Niko Beerenwinkel, **Stefano Beretta**, Paola Bonizzoni, Riccardo Dondi, and Yuri Pirola. “Covering Pairs in Directed Acyclic Graphs”. *The Computer Journal* 58.7 (2015), 1673–1686. DOI: 10.1093/comjnl/bxu116.
- [6] Daniel Alonso-Aleman, Aurlien Barré, **Stefano Beretta**, Paola Bonizzoni, Macha Nikolski, and Gabriel Valiente. “Further Steps in TANGO: Improved Taxonomic Assignment in Metagenomics”. *Bioinformatics* 30.1 (2014), 17–23. DOI: 10.1093/bioinformatics/btt256.
- [7] **Stefano Beretta**, Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, and Raffaella Rizzi. “Modeling Alternative Splicing Variants from RNA-Seq Data with Isoform Graphs”. *Journal of Computational Biology* 21.1 (2014), 16–40. DOI: 10.1089/cmb.2013.0112.
- [8] Mauro Castelli, **Stefano Beretta**, and Leonardo Vanneschi. “A hybrid genetic algorithm for the repetition free longest common subsequence problem”. *Operations Research Letters* 41.6 (2013), 644–649. DOI: 10.1016/j.orl.2013.09.002.

PROCEEDINGS

- [9] **Stefano Beretta**, Mauro Castelli, Ivo Gonçalves, Ivan Kel, and Ivan Merelli. “A Logistic Model Tree Based Approach For eQTL Data Prediction Integration”. In: *Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB): 13th International Meeting, Stirling, UK, September 1-3, 2016*. 2016, in press.
- [10] **Stefano Beretta**, Mauro Castelli, Yuliana Martínez, Luis Muñoz, Silva Silva, Leonardo Trujillo, Luciano Milanesi, and Ivan Merelli. “A Machine Learning Approach for the Integration of miRNA-Target Predictions”. In: *2016, 24th Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP)*. Feb. 2016, 528–534. DOI: 10.1109/PDP.2016.125.
- [11] Niko Beerenwinkel, **Stefano Beretta**, Paola Bonizzoni, Riccardo Dondi, and Yuri Pirola. “Covering Pairs in Directed Acyclic Graphs”. In: *LATA*. Ed. by Adrian Horia Dediu, Carlos Martín-Vide, José Luis Sierra-Rodríguez, and Bianca Truthe. Vol. 8370. Lecture Notes in Computer Science. Springer, Mar. 2014, 126–137. DOI: 10.1007/978-3-319-04921-2_10.
- [12] **Stefano Beretta** and Riccardo Dondi. “Gene Tree Correction by Leaf Removal and Modification: Tractability and Approximability”. English. In: *Language, Life, Limits*. Ed. by Arnold Beckmann, Erzsébet Csuhaj-Varj, and Klaus Meer. Vol. 8493. Lecture Notes in Computer Science. Springer International Publishing, 2014, 42–52. DOI: 10.1007/978-3-319-08019-2_5.
- [13] **Stefano Beretta**, Paola Bonizzoni, Raffaella Rizzi, and Gianluca Della Vedova. “Reconstructing isoform graphs from RNA-Seq data”. In: *Bioinformatics and Biomedicine (BIBM), 2012 IEEE International Conference on*. Oct. 2012, 1–4. DOI: 10.1109/BIBM.2012.6392734.

EDITORIALS

- [14] **Stefano Beretta**, Mario Cannataro, and Mauro Castelli. “9th Workshop on Biomedical and Bioinformatics Challenges for Computer Science (BBC2016)”. *Procedia Computer Science* 80 (2016). International Conference on Computational Science (ICCS) 2016, June 6-8, 2016, San Diego, California, {USA}, 962–964. DOI: 10.1016/j.procs.2016.05.390.
- [15] **Stefano Beretta**, Mario Cannataro, and Riccardo Dondi. “8th Workshop on Biomedical and Bioinformatics Challenges for Computer Science (BBC2015)”. *Procedia Computer Science* 51 (2015). International Conference On Computational Science (ICCS) 2015 - Computational Science at the Gates of Nature, 680–682. DOI: 10.1016/j.procs.2015.05.184.
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ABSTRACTS

- [16] **Stefano Beretta**, Yuri Pirola, Valeria Ranzani, Grazisa Rossetti, Raoul Bonnal, Raffaella Rizzi, Gianluca Della Vedova, Massimiliano Pagani, and Paola Bonizzoni. “A tool for the comparison of transcript differential expression analysis pipelines”. *PeerJ Preprints* 4 (July 2016), e2212v1. DOI: 10.7287/peerj.preprints.2212v1.
- [17] Andrea Calabria, Giulio Spinozzi, Stefano Brasca, **Stefano Beretta**, Ivan Merelli, Fabrizio Benedicenti, Erika Tenderini, Luciano Milanese, and Eugenio Montini. “A New Bioinformatics Pipeline for Retroviral Integration Site Analysis in Hematopoietic Stem Cell Gene Therapy Applications.” In: *12th annual meeting of the Bioinformatics Italian Society (BITS), Milan, Italy*. 2015.
- [18] Yuri Pirola, Raffaella Rizzi, **Stefano Beretta**, Ernesto Picardi, Graziano Pesole, Gianluca Della Vedova, and Paola Bonizzoni. “PintronNext: a fast method for detecting the gene structure due to alternative splicing via ESTs, mRNAs, and RNA-Seq data”. In: *EURASNET Symposium on Regulation of Gene Expression through RNA Splicing*. Mar. 2012.
- [19] **Stefano Beretta**, Paola Bonizzoni, Raffaella Rizzi, and Gianluca Della Vedova. “Identification of Alternative Splicing variants from RNA-seq Data”. In: *Next Generation Sequencing Workshop*. Oct. 2011.
- [20] **Stefano Beretta**, Paola Bonizzoni, Raffaella Rizzi, and Gianluca Della Vedova. “Alternative Splicing from RNA-seq Data without the Genome”. In: *ISMB/ECCB - 8th Special Interest Group meeting on Alternative Splicing (AS-SIG)*. July 2011.
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POSTERS

- [21] **Stefano Beretta**, Ivan Merelli, Alessandra Mezzelani, Maria Giulia Pini, Martina Landini, Nandia Galluccio, Maria Elisabetta Raggi, Anna Marabotti, and Luciano Milanese. “An integrative approach to discover changes in the association of miRNA and target genes.” In: *12th annual meeting of the Bioinformatics Italian Society (BITS), Milan, Italy*. 2015.
- [22] Anna Paola Carrieri, **Stefano Beretta**, Gianluca Della Vedova, Ernesto Picardi, Yuri Pirola, Raffaella Rizzi, Graziano Pesole, and Paola Bonizzoni. “An in-silico framework for comparing and validating transcripts predicted from single and paired-end reads”. In: *Next Generation Sequencing Workshop*. Oct. 2012.
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THESIS

- [23] **Stefano Beretta**. “Algorithms for next generation sequencing data analysis”. PhD thesis. Università degli Studi di Milano-Bicocca, Feb. 2013.
- [24] **Stefano Beretta**. “Algoritmi per la Predizione della Struttura Secondaria dell’RNA”. Master Degree Thesis. Università degli Studi di Milano-Bicocca, 2009.
- [25] **Stefano Beretta**. “Un framework per la simulazione di sistemi complessi: metodologie di visualizzazione scientifica”. Degree Thesis. Università degli Studi di Milano-Bicocca, 2006.
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DEVELOPER

RNA-seq Graph Builder: method to reconstruct the Isoform Graph from RNA-seq data.

References

REFERENCES

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