

Stefano Beretta

PERSONAL INFORMATION *Date of birth:* 18/04/1984
Nationality: Italian
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AFFILIATION San Raffaele Telethon Institute for Gene Therapy,
Ospedale San Raffaele S.r.l.,
Via Olgettina n. 60, 20132 Milan, Italy.

RESEARCH INTERESTS Bioinformatics, Next-Generation Sequencing (NGS), Genomics, Transcriptomics, Metagenomics, Single-Cell RNA-seq, Chip-seq, Algorithms, Graph Theory, Theoretical Computer Science, Computational Complexity, Approximation Algorithms, Machine Learning

POSITIONS 2019, January - Now. San Raffaele Telethon Institute for Gene Therapy, Italy.
Bioinformatic Analyses
Research collaboration contract

2015, January - 2018, December. 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

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

OTHER TITLES 2017. ELIXIR-IIB HPC - CINECA
Grant for HPC computations at CINECA.

2016. Qualification a *Maitre 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

2018. International Conference on Research in Computational Molecular Biology (RECOMB).
“Best Poster Award” of the conference:
Luca Denti, Raffaella Rizzi, Stefano Beretta, Gianluca Della Vedova, Marco Previtali and Paola Bonizzoni. *ASGAL: Aligning RNA-Seq Data to a Splicing Graph to Detect Novel Alternative Splicing Events*.

2017 - 2018. Italian Ministry of University and Research, Postdoc 2-years grant.

2015 - 2016. 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.

Peer-reviewed Publications

JOURNALS

- [1] Riccardo Biavasco, Emanuele Lettera, Kety Giannetti, Diego Gilioli, **Stefano Beretta**, Anastasia Conti, Serena Scala, Daniela Cesana, Pierangela Gallina, Margherita Norelli, Luca Basso-Ricci, Attilio Bondanza, Giulio Cavalli, Maurilio Ponzoni, Lorenzo Dagna, Claudio Doglioni, Alessandro Aiuti, Ivan Merelli, Raffaella Di Micco, and Eugenio Montini. “Oncogene-induced senescence in hematopoietic progenitors features myeloid restricted hematopoiesis, chronic inflammation and histiocytosis”. *Nature Communications* 12 (2021). DOI: 10.1038/s41467-021-24876-1.
- [2] Samuele Ferrari, **Stefano Beretta**, Aurelien Jacob, Davide Cittaro, Luisa Albano, Ivan Merelli, Luigi Naldini, and Pietro Genovese. “BAR-Seq clonal tracking of gene edited cells”. *Nature Protocols* 16 (2021), 2991–3025. DOI: 10.1038/s41596-021-00529-x.
- [3] Valentina Vavassori, Elisabetta Mercuri, Genni E. Marcovecchio, Maria C. Castiello, Giulia Schiroli, Luisa Albano, Carrie Margulies, Frank Buquicchio, Elena Fontana, **Stefano Beretta**, Ivan Merelli, Andrea Cappelleri, Paola MV Rancoita, Vassilios Lougaris, Alessandro Plebani, Maria Kanariou, Arjan Lankester, Francesca Ferrua, Eugenio Scanziani, Cecilia Cotta-Ramusino, Anna Villa, Luigi Naldini, and Pietro Genovese. “Modeling, optimization, and comparable efficacy of T cell and hematopoietic stem cell gene editing for treating hyper-IgM syndrome”. *EMBO Molecular Medicine* 13 (2021). DOI: 10.15252/emmm.202013545.

- [4] Samuele Ferrari, Aurelien Jacob, **Stefano Beretta**, Giulia Unali, Luisa Albano, Valentina Vavassori, Davide Cittaro, Dejan Lazarevic, Chiara Brombin, Federica Cugnata, Anna Kajaste-Rudnitski, Ivan Merelli, Pietro Genovese, and Luigi Naldini. “Efficient gene editing of human long-term hematopoietic stem cells validated by clonal tracking”. *Nature Biotechnology* 38 (2020), 1298–1308. DOI: 10.1038/s41587-020-0551-y.
- [5] Annamaria Aprile, Alessandro Gulino, Mariangela Storto, Isabella Villa, **Stefano Beretta**, Ivan Merelli, Alessandro Rubinacci, Maurilio Ponzoni, Sarah Markt, Claudio Tripodo, Maria Rosa Lidonnici, and Giuliana Ferrari. “Hematopoietic stem cell function in β -thalassemia is impaired and is rescued by targeting the bone marrow niche”. *Blood* 136 (2020), 610–622. DOI: 10.1182/blood.2019002721.
- [6] Raffaella Rizzi, **Stefano Beretta**, Murray Patterson, Yuri Pirola, Marco Previtali, Gianluca Della Vedova, and Paola Bonizzoni. “Overlap graphs and de Bruijn graphs: data structures for de novo genome assembly in the big data era”. *Quantitative Biology* (2019), 1–15. DOI: 10.1007/s40484-019-0181-x.
- [7] Andrea Calabria, **Stefano Beretta**, Ivan Merelli, Giulio Spinozzi, Stefano Brasca, Yuri Pirola, Fabrizio Benedicenti, Erika Tenderini, Paola Bonizzoni, Luciano Milanese, and Eugenio Montini. “ γ -TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites”. *Bioinformatics* 36.5 (Oct. 2019). btz747, 1622–1624. ISSN: 1367-4803. DOI: 10.1093/bioinformatics/btz747.
- [8] Giulia Schirotti, Anastasia Conti, Samuele Ferrari, Lucrezia della Volpe, Aurelien Jacob, Luisa Albano, **Stefano Beretta**, Andrea Calabria, Valentina Vavassori, Patrizia Gasparini, Eralda Salataj, Delphine Ndiaye-Lobry, Chiara Brombin, Julie Chaumeil, Eugenio Montini, Ivan Merelli, Pietro Genovese, Luigi Naldini, and Raffaella Di Micco. “Precise Gene Editing Preserves Hematopoietic Stem Cell Function following Transient p53-Mediated DNA Damage Response”. *Cell Stem Cell* 24.4 (2019), 551–565.e8. ISSN: 1934-5909. DOI: <https://doi.org/10.1016/j.stem.2019.02.019>.
- [9] Luca Denti, Raffaella Rizzi, **Stefano Beretta**, Gianluca Della Vedova, Marco Previtali, and Paola Bonizzoni. “ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events”. *BMC Bioinformatics* 19.1 (Nov. 2018), 444. DOI: 10.1186/s12859-018-2436-3.
- [10] **Stefano Beretta**, Murray D. Patterson, Simone Zaccaria, Gianluca Della Vedova, and Paola Bonizzoni. “HapCHAT: adaptive haplotype assembly for efficiently leveraging high coverage in long reads”. *BMC Bioinformatics* 19.1 (July 2018), 252. DOI: 10.1186/s12859-018-2253-8.
- [11] **Stefano Beretta**, Mauro Castelli, Ivo Gonçalves, Roberto Henriques, and Daniele Ramazzotti. “Learning the Structure of Bayesian Networks: A Quantitative Assessment of the Effect of Different Algorithmic Schemes”. *Complexity* 2018 (2018), 1591878:1–1591878:12. DOI: 10.1155/2018/1591878.
- [12] **Stefano Beretta**, Mauro Castelli, Ivo Gonçalves, Ivan Kel, Valentina Giansanti, and Ivan Merelli. “Improving eQTL Analysis using a Machine Learning Approach for Data Integration: a Logistic Model Tree Solution”. *Journal of Computational Biology* 25.10 (2018), 1091–1105. DOI: 10.1089/cmb.2017.0167.
- [13] **Stefano Beretta**, Mauro Castelli, Luis Muñoz, Leonardo Trujillo, Yuliana Martínez, Ales Popovic, Luciano Milanese, and Ivan Merelli. “A Scalable Genetic Programming Approach to Integrate miRNA-Target Predictions: Comparing Different Parallel Implementations of M3GP”. *Complexity* 2018 (2018), 4963139:1–4963139:13. DOI: 10.1155/2018/4963139.
- [14] Giulio Spinozzi, Andrea Calabria, Stefano Brasca, **Stefano Beretta**, Ivan Merelli, Luciano Milanese, and Eugenio Montini. “VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites”. *BMC Bioinformatics* 18.1 (Nov. 2017), 520. DOI: 10.1186/s12859-017-1937-9.

- [15] Daniela Cesana, Francesca R. Santoni de Sio, Laura Rudilosso, Pierangela Gallina, Andrea Calabria, **Stefano Beretta**, Ivan Merelli, Elena Bruzzesi, Laura Passerini, Silvia Nozza, Elisa Vicenzi, Guido Poli, Silvia Gregori, Giuseppe Tambussi, and Montini Eugenio. “HIV-1-mediated insertional activation of STAT5B and BACH2 trigger viral reservoir in T regulatory cells”. *Nature Communications* 8 (2017). DOI: 10.1038/s41467-017-00609-1.
- [16] 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.” *Mol. BioSyst.* 12 (11 2016), 3447–3458. DOI: 10.1039/C6MB00453A.
- [17] **Stefano Beretta**, Mauro Castelli, and Riccardo Dondi. “Corrigendum to “Parameterized tractability of the maximum-*duo* preservation string mapping problem”.” *Theoretical Computer Science* 653 (2016), 108–110. ISSN: 0304-3975. DOI: <http://dx.doi.org/10.1016/j.tcs.2016.09.015>.
- [18] **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.
- [19] **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.
- [20] **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.
- [21] 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.
- [22] Daniel Alonso-Alemany, Aurélien 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.
- [23] **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.
- [24] 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

- [25] Valentina Giansanti, Mauro Castelli, **Stefano Beretta**, and Ivan Merelli. “Comparing Deep and Machine Learning Approaches in Bioinformatics: A miRNA-Target Prediction Case Study”. In: *Computational Science – ICCS 2019*. Ed. by João M. F. Rodrigues, Pedro J. S. Cardoso, Jânio Monteiro, Roberto Lam, Valeria V. Krzhizhanovskaya, Michael H. Lees, Jack J. Dongarra, and Peter M.A. Sloot. Cham: Springer International Publishing, 2019, 31–44. ISBN: 978-3-030-22744-9.
- [26] Valentina Giansanti, **Stefano Beretta**, Daniele Cesini, Daniele D’Agostino, and Ivan Merelli. “Parallel Computing in Deep Learning: Bioinformatics Case Studies”. In: *2019 27th Euromicro International Conference on Parallel, Distributed and Network-Based Processing (PDP)*. IEEE. 2019, 329–333.

- [27] Valentina Giansanti, Daniele D’Agostino, Carlo Maj, **Stefano Beretta**, and Ivan Merelli. “Computing Empirical P-Values for Estimating Gene-Gene Interactions in Genome-Wide Association Studies: A Parallel Computing Approach”. In: *2018 26th Euromicro International Conference on Parallel, Distributed and Network-based Processing (PDP)*. 2018, 406–409. DOI: 10.1109/PDP2018.2018.00071.
- [28] **Stefano Beretta**, Paola Bonizzoni, Luca Denti, Marco Previtali, and Raffaella Rizzi. “Mapping RNA-seq Data to a Transcript Graph via Approximate Pattern Matching to a Hypertext”. In: *Algorithms for Computational Biology - 4th International Conference, AlCoB 2017, Aveiro, Portugal, June 5-6, 2017, Proceedings*. Ed. by Daniel Figueiredo, Carlos Martín-Vide, Diogo Pratas, and Miguel A. Vega-Rodríguez. Vol. 10252. Lecture Notes in Computer Science. Springer, 2017, 49–61. DOI: 10.1007/978-3-319-58163-7_3.
- [29] **Stefano Beretta**, Carlo Maj, and Ivan Merelli. “Rank miRNA: a web tool for identifying polymorphisms altering miRNA target sites”. *Procedia Computer Science* 108:Supplement C (2017). International Conference on Computational Science, ICCS 2017, 12-14 June 2017, Zurich, Switzerland, 1125–1134. ISSN: 1877-0509. DOI: <https://doi.org/10.1016/j.procs.2017.05.189>.
- [30] **Stefano Beretta**, Lucia Morganti, Elena Corni, Andrea Ferraro, Daniele Cesini, Daniele D’Agostino, Luciano Milanese, and Ivan Merelli. “Low-Power Architectures for miRNA-Target Genome Wide Analysis”. In: *25th Euromicro International Conference on Parallel, Distributed and Network-based Processing, PDP 2017, St. Petersburg, Russia, March 6-8, 2017*. Ed. by Igor V. Kotenko, Yiannis Cotronis, and Masoud Daneshmand. IEEE, 2017, 309–312. DOI: 10.1109/PDP.2017.88.
- [31] **Stefano Beretta**, Mauro Castelli, Ivo Gonçalves, Ivan Merelli, and Daniele Ramazzotti. “Combining Bayesian Approaches and Evolutionary Techniques for the Inference of Breast Cancer Networks”. In: *Proceedings of the 8th International Joint Conference on Computational Intelligence, IJCCI 2016, Volume 1: ECTA, Porto, Portugal, November 9-11, 2016*. Ed. by Juan Julián Merelo Guervós, Fernando Melício, José Manuel Cadenas, António Dourado, Kurosh Madani, António E. Ruano, and Joaquim Filipe. SciTePress, 2016, 217–224. DOI: 10.5220/0006064102170224.
- [32] **Stefano Beretta**, Mauro Castelli, Yuliana Martínez, Luis Muñoz, Silva Silva, Leonardo Trujillo, Luciano Milanese, 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.
- [33] 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.
- [34] **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-Varjú, 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.
- [35] **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.

- [36] **Stefano Beretta**, Denti Luca, and Previtali Marco. “Graph theory and definitions”. In: *Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics*. Vol. 1. Elsevier, 2019, 922–927. DOI: 10.1016/B978-0-12-809633-8.20421-4.
- [37] **Stefano Beretta**, Denti Luca, and Previtali Marco. “Network properties”. In: *Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics*. Vol. 1. Elsevier, 2019, 928–932. DOI: 10.1016/B978-0-12-809633-8.20422-6.
- [38] **Stefano Beretta**. “Algorithms for strings and sequences: Pairwise alignment”. In: *Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics*. Vol. 1. Elsevier, 2019, 22–29. DOI: 10.1016/B978-0-12-809633-8.20317-8.

EDITORIALS

- [39] **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.
- [40] **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.

ABSTRACTS

- [41] Samuele Ferrari, Aurelien Jacob, **Stefano Beretta**, Davide Cittaro, Luisa Albano, Giulia Unali, Valentina Vavassori, Dejan Lazarevic, Chiara Brombin, Federica Cugnata, Anna Kajaste-Rudnitski, Ivan Merelli, Pietro Genovese, and Luigi Naldini. “BAR-seq: a Novel Barcode Strategy to Track Clones in Human Edited Hematopoietic Stem Cells”. In: *Research in Computational Molecular Biology (RECOMB)*. May 2020.
- [42] Annamaria Aprile, Alessandro Gulino, Isabella Villa, **Stefano Beretta**, Ivan Merelli, Alessandro Rubinacci, Maurilio Ponzoni, Sarah Markt, Claudio Tripodo, Maria Rosa Lidonnici, and Giuliana Ferrari. “Hematopoietic Stem Cell Function in β -Thalassemia Is Impaired and Is Rescued By Targeting the Bone Marrow Niche”. *Blood* 134.Supplement1 (Nov. 2019), 967–967. DOI: 10.1182/blood-2019-126829.
- [43] Valentina Gambacorta, Daniela Gnani, Laura Zito, **Stefano Beretta**, Lucia Zanotti, Oliveira Giacomo, Davide Cittaro, Ivan Merelli, Fabio Ciceri, Raffaella Di Micco, and Luca Vago. “Integrated Epigenetic Profiling Identifies EZH2 As a Therapeutic Target to Re-Establish Immune Recognition of Leukemia Relapses with Loss of HLA Class II Expression”. *Blood* 134.Supplement1 (Nov. 2019), 514–514. DOI: 10.1182/blood-2019-127395.
- [44] Matteo Maria Naldini, Gabriele Casirati, Matteo Barcella, **Stefano Beretta**, Ivan Merelli, Carolina Caserta, Giacomo Desantis, Francesca Pavesi, Fabio Ciceri, and Bernhard Gentner. “Longitudinal Tracking of Acute Myeloid Leukemia Stem Cells in Xenografts and Patients By microRNA Reporters and Single Cell RNA Sequencing”. *Blood* 134.Supplement1 (Nov. 2019), 916–916. DOI: 10.1182/blood-2019-131167.
- [45] Aurelien Jacob, Samuele Ferrari, Luisa Albano, Martina Fiumara, Valentina Vavassori, Davide Cittaro, **Stefano Beretta**, Dejan Lanzarevic, Ivan Merelli, Luigi Naldini, et al. “Cell cycle” push-up” to boost targeted genome editing in hematopoietic stem cells”. In: *HUMAN GENE THERAPY*. Vol. 30. 11. MARY ANN LIEBERT, NEW ROCHELLE, NY 10801 USA. 2019, A183–A183.
- [46] Anastasia Conti, Lucrezia della Volpe, Giulia Schirotti, **Stefano Beretta**, Ivan Merelli, Pietro Genovese, Luigi Naldini, and Raffaella Di Micco. “Impact of DNA damage response activation in haematopoietic stem and progenitor cells upon gene-targeting”. In: *HUMAN GENE THERAPY*. Vol. 29. 12. MARY ANN LIEBERT, NEW ROCHELLE, NY 10801 USA. 2018, A57–A57.

- [47] Giulia Schirotti, Samuele Ferrari, Aurelien Jacob, Anastasia Conti, Luisa Albano, **Stefano Beretta**, Ivan Merelli, Raffaella di Micco, Luigi Naldini, and Pietro Genovese. “Single cell transcriptomic analysis of gene edited HSPC uncovers molecular targets to improve long-term cell repopulation ability”. In: *HUMAN GENE THERAPY*. Vol. 29. 12. MARY ANN LIEBERT, NEW ROCHELLE, NY 10801 USA. 2018, A104–A104.
- [48] **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.
- [49] **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.
- [50] 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.
- [51] Yuri Pirola, Raffaella Rizzi, **Stefano Beretta**, Ernesto Picardi, Graziano Pesole, Gianluca Della Vedova, and Paola Bonizzoni. “PItronNext: 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.
- [52] **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.
- [53] **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.

POSTERS

- [54] **Stefano Beretta**, Paola Bonizzoni, Andrea Calabria, Daniela Cesana, and Ivan Merelli. “HaploVir: Inferring Viral Haplotypes from Deep Sequencing of a Mixture of Strains using a Path Decomposition Algorithm”. In: *Intelligent Systems for Molecular Biology (ISBM)*. 2018.
- [55] **Stefano Beretta**, Valentina Giansanti, Carlo Maj, Mauro Castelli, Ivo Goncalves, and Ivan Merelli. “HappyMirna: a Library to Integrate miRNA-Target Predictions using Machine Learning Techniques”. In: *Intelligent Systems for Molecular Biology (ISBM)*. 2018.
- [56] Luca Denti, Raffaella Rizzi, **Stefano Beretta**, Gianluca Della Vedova, Marco Previtali, and Paola Bonizzoni. “ASGAL: Aligning RNA-Seq Data to a Splicing Graph to Detect Novel Alternative Splicing Events”. In: *Research in Computational Molecular Biology (RECOMB)*. 2018. DOI: 10.1101/260372.
- [57] **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.
- [58] 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
- [59] **Stefano Beretta**. “Algorithms for next generation sequencing data analysis”. PhD thesis. Università degli Studi di Milano-Bicocca, Feb. 2013.
 - [60] **Stefano Beretta**. “Algoritmi per la Predizione della Struttura Secondaria dell’RNA”. Master Degree Thesis. Università degli Studi di Milano-Bicocca, 2009.
 - [61] **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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Scientific Activity

- PROJECTS
- Modulation of anti-cancer immune response by regulatory non-coding RNAs.*
CARIPLO 2013-0955, 2014-2016.
 - Automati 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
- Local organizer of 16th *International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB)*
4-6 September 2019, Università degli Studi di Bergamo, Italy.
 - Special Session: *Fast and Efficient Solutions for Computational Intelligence Methods in Bioinformatics, Systems and Computational Biology*
In conjunction with *International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB)*
6-8 September 2018, Caprica, PT.
 - Publicity chair of 26th *Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP)*
21-23 March 2018, University of Cambridge, UK.
 - 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
COMMITTEE

Workshop on Biomedical and Bioinformatics Challenges for Computer Science

- BBC 2015 (8th ed.).
- BBC 2016 (9th ed.).
- BBC 2017 (10th ed.).
- BBC 2018 (11th ed.).
- BBC 2019 (12th ed.).
- BBC 2020 (13th ed.).
- BBC 2021 (14th ed.).

Advances in High-Performance Bioinformatics, Systems and Synthetic Biology

- PDP 2015.
- PDP 2016.
- PDP 2018.
- PDP 2019.

REFEREEING

CONFERENCES: EPIA 2013, PDP 2015, ICCS-BBC 2015, ICCS-BBC 2016, PDP 2016, ICCS-BBC 2017, PDP 2017, MFCS 2017, PDP 2018, CIBB 2018, ICCS-BBC 2018, CIBB 2019, ICCS-BBC 2019, PDP 2019, ICCS-BBC 2020, ICCS-BBC 2021.

Teaching Activity

CLASSES

- a.a. 2018/2019. Lecturer (30h). Università Vita-Salute San Raffaele, Italy.
Course “Informatica”, master degree in Psychology.
- a.a. 2017/2018. Lecturer (16h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Informatica I”, degree in Physics.
- a.a. 2016/2017. Teaching Assistant (60h). Università degli Studi di Milano - Bicocca, Italy.
Course “Laboratorio di Informatica I”, degree in Physics.
- 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.

SUPERVISOR

I supervised or co-supervised the following final projects (BSc) and thesis (MSc).

Università degli Studi di Milano - Bicocca, BSc in Computer Science.

- Alessandro Longhi (2017), *Confronto di tecniche innovative per l’assemblaggio di aptotipi*
- Massimiliano Gilardi (2012), *Sviluppo di software per l’identificazione di variazioni strutturali da dati NGS*

Software

PROJECTS

BAR-Seq

Software for the analysis of Homology-Directed Repair barcoded cells for clonal tracking of gene edited cells.

γ -tris

Graph-Algorithm Making Multi-labeling Annotations for Tracking Retroviral Integration Sites: a graph-based method capable of handling vector insertions in gene therapy analysis even if embedded in repeated sequences allowing the generation of a comprehensive repertoire of insertion sites.

SPIRE

Software for Polymorphism Identification Regulating Expression: pipeline for quantitative trait locus analysis using expression data as phenotypes (eQTL).

RNA-seq Graph Builder

Method to reconstruct the Isoform Graph from RNA-seq data.

HapCHAT

Adaptive haplotype assembly for efficiently leveraging high coverage in long reads.

Autorizzo il trattamento dei dati personali contenuti nel mio curriculum vitae in base all'art. 13 del D. Lgs. 196/2003 e all'art. 13 del Regolamento UE 2016/679 relativo alla protezione delle persone fisiche con riguardo al trattamento dei dati personali.

Le dichiarazioni rese nel presente curriculum sono da ritenersi rilasciate ai sensi degli artt. 46 e 47 del D.P.R. 445/2000

Milan, 2/8/2021

A handwritten signature in black ink, appearing to read "Stephan Barth". The signature is written in a cursive style with a large initial 'S' and 'B'.