

Alberto Riva, PhD

National Facility for Data Handling and Analysis
Fondazione Human Technopole
Milano, Italy

E-mail: alberto.riva@fht.org
GitHub: <https://github.com/albertoriva/>

CURRICULUM VITAE

General Information

Current Position: Head, National Facility for Data Handling and Analysis
Fondazione Human Technopole, Milano, Italy

Other affiliations: Interdisciplinary Center for Biotechnology Research, University of Florida
(courtesy appointment)

Office address: Fondazione Human Technopole
V.le Rita Levi Montalcini 1
20157 Milano, Italy

Telephone: +393666259535

E-mail address: alberto.riva@fht.org

Citizenship: Italy, USA.

Education

1995 Ph.D., Bioengineering,
University of Pavia, Italy.

1992 Laurea, Electrical Engineering (*Cum laude*),
University of Pavia, Italy.

Previous Appointments

2019 - 2024 Scientific Director, Bioinformatics Core, Interdisciplinary Center for Biotechnology Research (ICBR), University of Florida.

2018 - 2024 Scientist, ICBR Bioinformatics, University of Florida.

2014 - 2018 Associate Scientist, ICBR Bioinformatics, University of Florida.

2006 - 2014 Assistant Professor, Department of Molecular Genetics and Microbiology.

- 2005** Member of the Affiliated Faculty of the Harvard-MIT Division of Health Sciences and Technology, Massachusetts Institute of Technology.
- 2000 - 2005** Instructor in Pediatrics, Harvard Medical School.

Professional Societies

- 2007 -** Italian Bioinformatics Society (BITS), Member
- 2006 -** International Society for Computational Biology (ISCB), Member.
- 2002 - 2013** Association of Lisp Users (ALU), Member.

Original Articles

1. Ramoni M, Riva A, Stefanelli M, Patel V. An ignorant belief network to forecast glucose concentration from clinical databases. *Artif Intell Med.* 1995; 7(6):541-59.
2. Riva A, Ramoni M. LispWeb: a specialized HTTP server for distributed AI applications. *Computer Networks and ISDN Systems.* 1996; 28(711):953-961.
3. Riva A, Bellazzi R. Learning temporal probabilistic causal models from longitudinal data. *Artif Intell Med.* 1996; 8(3):217-34.
4. Ramoni M, Riva A. Basic Science in Medical Reasoning: An Artificial Intelligence Approach. *Adv Health Sci Educ Theory Pract.* 1997; 2(2):131-140.
5. Riva A, Bellazzi R, Stefanelli M. A Web-based system for the intelligent management of diabetic patients. *MD Comput.* 1997; 14(5):360-4.
6. Bellazzi R, Riva A. Learning Bayesian Networks Conditional Probabilities from Longitudinal Data. *IEEE Transactions on Systems, Man and Cybernetics.* 1998; (28):629-636.
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8. Riva A, Bellazzi R, Lanzola G, Stefanelli M. A development environment for knowledge-based medical applications on the World-Wide Web. *Artif Intell Med.* 1998; 14(3):279-93.
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10. Bellazzi R, Riva A, Montani S, Larizza C, Bestazza M, Fiocchi S, d'Annunzio G, Lorini R, Stefanelli M. Application report: preliminary evaluation of the T-IDDM project in Pavia. *Stud Health Technol Inform.* 1999; 68:99-101.
11. Bellazzi R, Montani S, Riva A, Stefanelli M. Web-based telemedicine systems for home-care: technical issues and experiences. *Comput Methods Programs Biomed.* 2001; 64(3):175-87.
12. Riva A, Mandl KD, Oh DH, Nigrin DJ, Butte A, Szolovits P, Kohane IS. The personal internetworked notary and guardian. *Int J Med Inf.* 2001; 62(1):27-40.

13. Bellazzi R, Larizza C, Montani S, [Riva A](#), Stefanelli M, d'Annunzio G, Lorini R, Gomez EJ, Hernando E, Bragues E, Cermeno J, Corcoy R, de Leiva A, Cobelli C, Nucci G, Del Prato S, Maran A, Kilkki E, Tuominen J. A telemedicine support for diabetes management: the T-IDDM project. *Comput Methods Programs Biomed.* 2002; 69(2):147-61.
14. Lazarus R, Vercelli D, Palmer LJ, Klimecki WJ, Silverman EK, Richter B, [Riva A](#), Ramoni M, Martinez FD, Weiss ST, Kwiatkowski DJ. Single nucleotide polymorphisms in innate immunity genes: abundant variation and potential role in complex human disease. *Immunol Rev.* 2002; 190:9-25.
15. [Riva A](#), Kohane IS. SNPper: retrieval and analysis of human SNPs. *Bioinformatics.* 2002; 18(12):1681-5.
16. [Riva A](#), Kohane IS. A SNP-Centric Database for the Investigation of the Human Genome. *BMC Bioinformatics.* 2004; 5(33).
17. Cai Z, Tsung EF, Marinescu VD, Ramoni MF, [Riva A](#), Kohane IS. Bayesian approach to discovering pathogenic SNPs in conserved protein domains. *Human Mutation.* 2004; 24(2):178-184.
18. Santagata S, Demichelis F, [Riva A](#), Varambally S, Hofer MD, Kutok JL, Kim R, Tang J, Montie JE, Chinnaiyan AM, Rubin MA, Aster JC. JAGGED1 expression is associated with prostate cancer metastasis and recurrence. *Cancer Research.* 2004; 64(19):6854-7.
19. Marinescu VD, Kohane IS, [Riva A](#). The MAPPER database: a multi-genome catalog of putative transcription factor binding sites. *Nucleic Acids Res.* 2005; 33 (Database issue):D91-7.
20. Marinescu VD, Kohane IS, [Riva A](#). MAPPER: a search engine for the computational identification of putative transcription factor binding sites in multiple genomes. *BMC Bioinformatics.* 2005; 6(79).
21. Agresti A, Scaffidi P, [Riva A](#), Caiolfa VR, Bianchi ME. GR and HMGB1 interact only within chromatin and influence each other's residence time on functioning promoters. *Molecular Cell.* 2005;18:109-121.
22. Kim R, Demichelis F, Tang J, [Riva A](#), Shen R, Gibbs DF, Mahavishno V, Chinnaiyan AM and Rubin MA. Internet-based Profiler system as integrative framework to support translational research. *BMC Bioinformatics.* 2005; 6 (304).
23. Marinescu VD, Kohane IS and [Riva A](#). START: an automated tool for serial analysis of chromatin occupancy data. *Bioinformatics*, 2006; 22(8):999-1001.
24. Samols MA, Skalsky RL, Maldonado AM, [Riva A](#), Lopez MC, Baker HV, Renne R. Modulation of cellular gene expression by KSHV microRNAs. *PLoS Pathogens.* 2007; 3(5):e65.
25. Skalsky RL, Samols MA, Plaisance KB, Boss IW, [Riva A](#), Lopez MC, Baker HV, Renne R. Kaposi's Sarcoma-associated Herpesvirus Encodes an Ortholog of miR-155. *J Virol.* 2007 Sept 19.
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the discovery of robust associations in genome-wide association studies from pooled DNA samples. BMC Genetics. 2008; 9:6.

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33. [Riva A](#), Nuzzo A, Stefanelli M, and Bellazzi R. An automated reasoning framework for translational research. Journal of Biomedical Informatics. doi:10.1016/j.jbi.2009.11.005.
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54. El Roubi N, Alrwisan A, Langae T, Lipori G, Angiolillo DJ, Franchi F, [Riva A](#), Elsey A, Johnson JA, Cavallari LH, Winterstein AG. Clinical utility of pharmacogene panel-based testing in patients undergoing percutaneous coronary intervention (PCI). *Clin Transl Sci* 13: 473-481. 2020. doi: [10.1111/cts.12729](#) PMID: [31758664](#).
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Spread of Severe Acute Respiratory Syndrome Coronavirus 2 Gamma (P.1) Variant in Haiti. *Clin Infect Dis* 2022. doi: [10.1093/cid/ciab736](https://doi.org/10.1093/cid/ciab736) PMID: [34471930](https://pubmed.ncbi.nlm.nih.gov/34471930/).

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