

Anna Bernasconi

POST-DOCTORAL RESEARCHER · INFORMATION TECHNOLOGY

Department of Electronics, Information and Bioengineering

Politecnico di Milano, Italy

Personal Information

Name Anna Bernasconi
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Summary

Anna Bernasconi is a postdoctoral researcher with the Dipartimento di Elettronica, Informazione e Bioingegneria at the Politecnico di Milano and a visiting researcher at Universitat Politècnica de València. She received her Ph.D. in Information Technology from the Politecnico di Milano in February 2021.

Her research areas are Bioinformatics, Databases, and Data Science Methods, where she applies conceptual modeling, data integration, semantic web technologies to biological and genomic data. Starting from a PhD thesis on the modeling and integration of data and metadata of human genomic datasets, she has then extended her expertise on the fastly growing field of viral genomics, particularly relevant since the COVID-19 pandemic outbreak.

She is active in the conceptual modeling and database communities, with several paper presentations and the organization of two tutorials (ER and EDBT conferences) and two workshops on conceptual models and web applications for life sciences (ER and ICWE conferences).

Education

Politecnico di Milano *Milan, Italy*
PHD IN INFORMATION TECHNOLOGY (CUM LAUDE) *Nov 2016 - Oct 2020*

- Advisor: Prof. Stefano Ceri, Co-advisor: Prof. Alessandro Campi
- Thesis title: Model, Integrate, Search... Repeat: a Sound Approach to Building Integrated Repositories of Genomic Data
- Award: Dimitris N. Chorafas Foundation

University of Illinois at Chicago *Chicago, Illinois, USA*
MS IN COMPUTER SCIENCE *Mar 2013 - Dec 2015*

- Advisor: Prof. Lenore D. Zuck
- Mark: 3.85/4.00

Politecnico di Milano *Milan, Italy*
MS IN COMPUTER ENGINEERING *Sep 2012 - July 2015*

- Advisor: Prof. Carlo Ghezzi, Co-advisors: Prof. Paola Spoletini, Dr. Claudio Menghi
- Thesis title: Building Deductive Proofs of LTL Properties for Iteratively Refined Systems
- Mark: 110/110

Politecnico di Milano *Milan, Italy*
BS IN MATHEMATICAL ENGINEERING *Sept 2009 - Sept 2012*

- Advisor: Prof. Alessandro Campi
- Mark: 100/110

Honors & Awards

- 2021 **Winner of Dimitris N. Chorafas Foundation 2021 Prize (for the PhD thesis)**, Weizman Institute of Science and Feinberg Graduate School
- 2021 **Recipient of the Springer award (for the PhD thesis)**, Politecnico di Milano IT PhD Board of professors

Research Activities

PRESENT POSITIONS

- Jan 2022 - **Post Doctoral Visiting Researcher**, Universitat Politècnica de València, Topic: Conceptual modeling and data management for genomics
- Nov 2020 - **Post Doctoral Researcher (Assegnista di Ricerca)**, Politecnico di Milano, Topic: Evolution of genomic data and metadata repositories for supporting novel research applications

PAST POSITIONS

- Apr 2021 - **Post Doctoral Visiting Researcher (Remote Status)**, Universitat Politècnica de València, Topic: Conceptual modeling and ontologies for representing the genome
- Dec 2021
- Mar 2016 - **Graduate Research Assistant**, Politecnico di Milano, Topic: Input and output data standardization for the
- Oct 2016 **GenoMetric Query Language**
- Nov 2014 - **Junior Business Intelligence Consultant and Data Warehouse Architect**, Quantyca S.R.L., Monza, Italy, Topic:
- Feb 2016 **ETL/integration processes and web application development**
- Nov 2013 - **Undergraduate Research Assistant**, University of Illinois at Chicago, Topic: Self-certifying compilers design
- Dec 2013

EXTERNAL RESEARCH COLLABORATIONS

- Mar 2022 - **Dr. Luigi Bellomarini (Banca d'Italia)**, Topic: Design of Vadalog extensions for resolving domain-specific
- present **viral genomics problems**
- Feb 2022 - **Group of Prof. Manuela Sironi (Istituto IRCCS "Eugenio Medea" - Associazione La Nostra Famiglia)**,
- present **Topic: Development of tools for viral genomics applications**
- Feb 2022 - **Prof. Valeria Micheli (Azienda Ospedaliera Polo Universitario L. Sacco) and Shay Fleishon (Israel**
- present **Central Virology Laboratory)**, Topic: Development of SARS-CoV-2 sub-types identification strategies
- June 2021 - **Prof. Matteo Chiara (Università degli Studi di Milano) and Erica Ferrandi (Consiglio Nazionale delle**
- present **Ricerche, Bari)**, Topic: Identification of diverging SARS-CoV-2 spatio-temporal mutational patterns
- Mar 2021 - **Group of Professor Oscar Pastor (with Prof. Giancarlo Guizzardi and Prof. Veda Storey), Universitat**
- present **Politécnica de València - Research Center on Software Production Methods**, Topic: Conceptual modeling for biological and genomic systems
- Apr 2020 - **The COVID-19 Host Genetics Initiative (<https://www.covid19hg.org/>)**, Topic: Design of
- Jul 2021 **clinical/phenotype COVID-19 dictionary for structuring data collection**
- Apr 2020 - **Prof. Silvia Grandi, University of Bologna - Dipartimento di Scienze Statistiche "Paolo Fortunati"**,
- Dec 2020 **Topic: Geographies of clinical and genomic data for COVID-19**
- Jan 2019 - **Dr. Claudio Menghi (with Prof. Paola Spoletini and Dr. Alessandro Maria Rizzi), University of**
- Nov 2020 **Luxembourg – Centre for Security Reliability and Trust**, Topic: Formal verification techniques for partial models
- Sep 2017 - **Group of Prof. Emanuel Weitschek, Italian National Research Council – Institute of Systems Analysis**
- Mar 2020 **and Computer Science**, Topic: metadata integration on cancer data from Genomic Data Commons
- Jun 2019 - **Group of Prof. Mario Cannataro, Università Magna Graecia**, Topic: integrative applications of
- Sep 2019 **GenoMetric Query Language using private and public datasets**

PARTICIPATION IN INTERNATIONAL RESEARCH PROJECTS

Nov 2016 -	Data-Driven Genomic Computing, ERC Advanced Investigator Grant N. 693174, Role: Task leader – Data repository and search systems	<i>Politecnico di Milano</i>
Aug 2021		
Jul 2021 -	EIT Digital “DATA against COVID-19” program, Innovation Activity ‘Virusurf’ N. 20663,	<i>Politecnico di Milano</i>
Dec 2021	Role: Task leader – User experience and interfaces	<i>Milano</i>

Outreach Scientific Activities

BIBLIOMETRICS

Verified reviews (on Publons, query date 21/06/2022)	26
Verified editor records (on Publons, query date 21/06/2022)	4

ORGANIZATION OF EVENTS

to happen:	Third International Workshop on Conceptual Modeling for Life Sciences (CMLS 2022),	<i>(online)</i>
Oct 2022	co-located with ER 2022 conference, Chair and co-organizer	
to happen:	First International Workshop on Web Applications for Life Sciences (WALS 2022),	<i>Bari, Italy</i>
July 2022	co-located with ICWE 2022 conference, Chair and co-organizer	
Oct 2021	Second International Workshop on Conceptual Modeling for Life Sciences (CMLS 2021),	<i>(online)</i>
	co-located with ER 2021 conference, Chair and co-organizer	
Nov 2020	First International Workshop on Conceptual Modeling for Life Sciences (CMLS 2020),	<i>(online)</i>
	co-located with ER 2020 conference, Chair and co-organizer	
Feb 2020	Politecnico di Milano Genomic Computing Group “gong-like presentations”, Co-organizer	<i>Milano, Italy</i>
Mar 2019	“Challenges in Data-Driven Genomic Computing” Workshop, Member of organization team (for the Advanced ERC Project 693174 “GeCo”)	<i>Como, Italy</i>

CONFERENCE CHAIR AND PROGRAM COMMITTEE SERVICE

Program Committee Member of the Foundation of Network Analysis Workshop at IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2022)

Program Committee Member of the 1st International Workshop on Data Analysis for Life Science (DALIS 2022)

Track Chair and **Publication Chair** for the 8th IEEE International Conference on Big Data Computing Service and Machine Learning Applications (IEEE BigDataService 2022) Special Track on Big Data and Analytics for Healthcare

Program Committee Member of the 9th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2022)

Program Committee Member of the 17th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2021)

EDITORIAL SERVICE

Ongoing: **Topic Editor** for Research Topic “Approaches for the integration of annotation resources for variant filtering and prioritization” on Frontiers in Bioinformatics (EISSN: 2673-7647, Publisher: Frontiers Media S.A.). Topic editors: Heron, E., Bernasconi, A., Valle, G. (<https://www.frontiersin.org/research-topics/39186/>)

Ongoing: **Editor** for CIBB 2021 conference Proceedings Book in Springer Lecture Notes in Bioinformatics (LNBI). Volume editors: Chicco, D., Bernasconi, A. et al.

Ongoing: **Supplement Editor** for the BMC Bioinformatics/BMC Medical Informatics and Decision Making Journals (ISSN: 1471-2105, 1472-6947, Publisher: Springer Nature), for the joint supplements “Selected articles from the CIBB 2021 conference”. Guest editors: Chicco, D., Bernasconi, A. et al.

Ongoing: **Supplement Editor** for the BMC Bioinformatics Journal (ISSN: 1471-2105, Publisher: Springer Nature), for the supplement “Selected articles on Conceptual Modeling for Life Sciences (CMLS/ER 2021)”. Guest editors: Bernasconi, A., Canakoglu, A., Chicco, D., Pinoli, P., and Reyes Román, J.F.

Ongoing: **Guest Editor** for the BioTech Journal (EISSN 2673-6284, Publisher: MDPI), Special Issue “Bioinformatics: Present and Future challenges”. Guest editors: Pinoli, P. and Bernasconi, A. (https://www.mdpi.com/journal/biotech/special_issues/Bioinformatics_Present_Future_Biotechnology)

Supplement Editor for the BMC Bioinformatics Journal (ISSN: 1471-2105, Publisher: Springer Nature), for the supplement “Selected articles from the 1st International Workshop on Conceptual Modeling for Life Sciences (CMLS 2020)”. Guest editors: Bernasconi, A., Chicco, D., and Reyes Román, J.F. (<https://bmcbioinformatics.biomedcentral.com/articles/supplements/volume-22-supplement-13>)

Editorial Board Member of BMC Bioinformatics (ISSN 1471-2105, Publisher: Springer Nature) – since May 2022

Review Editor of Frontiers in Microbiology (EISSN: 1664-302X, Publisher: Frontiers Media S.A.) – Virology – since June 2022 (<https://www.frontiersin.org/journals/microbiology#editorial-board>)

Reviewer Board Member of Big Data and Cognitive Computing Journal (ISSN 2504-2289, Publisher: MDPI) – since April 2022 (https://www.mdpi.com/journal/BDCC/submission_reviewers)

Review Editor of Frontiers in Systems Biology (EISSN: 2674-0702, Publisher: Frontiers Media S.A.) – Multiscale Mechanistic Modeling – since June 2021 (<https://www.frontiersin.org/journals/systems-biology#editorial-board>)

REVIEWER SERVICE FOR INTERNATIONAL JOURNALS

Advances and Applications in Bioinformatics and Chemistry – Dove Press (ISSN: 1178-6949); Applied Clinical Informatics Journal – Thieme Medical Publishers (ISSN: 1869-0327); Applied System Innovation – MDPI (ISSN: 2571-5577); Briefings in Bioinformatics – Oxford University Press (ISSN: 1477-4054); Frontiers in Medicine – Frontiers Media S.A. (E-ISSN: 2296-858X); Frontiers in Microbiology – Frontiers Media S.A. (E-ISSN: 1664-302X); Frontiers in Systems Biology – Frontiers Media S.A. (E-ISSN: 2674-0702); Information – MDPI (ISSN 2078-2489); International Journal of Electrical and Computer Engineering – Institute of Adv. Engineering and Science (ISSN: 2088-8708); International Journal of Human-Computer Interaction – Taylor & Francis (ISSN: 10447318); International Journal of Medical Informatics – Elsevier (ISSN: 1386-5056); JMIR Formative Research – JMIR Publications Inc. (ISSN: 2561-326X); mSystems – American Society for Microbiology (ISSN: 2379-5077); npj Digital Medicine – Springer Nature (ISSN: 2398-6352); The Innovation – Cell Press (ISSN: 2666-6758); Transactions in Urban Data, Science, and Technology – Sage publishing (ISSN: 2754-1231)

MEMBERSHIPS

IEEE Student Member 2020, 2021 ; IEEE Women Society 2021 ; IEEE Computer Society 2020 .

ACM Professional Membership 2022

Presentations

INVITED TALKS

to happen: Jul 2022	Seminar, Data-bases-driven research on viral genomes and SARS-CoV-2. At Universidade Eduardo Mondlane, Maputo, Mozambique (https://ict4dev.uem.mz)	(online)
Jan 2022	Seminar, Data-driven SARS-CoV-2 understanding and hunting (searching for the new Omicron). At Politecnico di Milano and Universitat Politècnica de València (https://youtu.be/VHgb1Dz00ho)	(online)
Nov 2021	Invited talk, Modeling, integrating, and searching processed genomic datasets. At “Integrating Diverse Datasets Webinar Series” by Front Line Genomics	(online)
Mar 2019	Invited talk, Metadata Integration Framework for Genomic Datasets. At “Challenges in Data-Driven Genomic Computing” Workshop	Como, Villa del Grumello
Feb 2019	Seminar, Data-Driven Genomic Computing: Making Sense of the Signals from the Genome through systematic application design and open data repository. At EPFL	Lausanne, Switzerland
Jan 2019	Seminar, Meta-awareness: towards agreement on experimental metadata. At “Genomic Computing & Data Science Meetings”, Politecnico di Milano.	Milan, Italy
Jul 2017	Seminar, Metadata Management for Genomics. At ETH (with Stefano Ceri and Pietro Pinoli)	Zurich, Switzerland
Jul 2017	Seminar, Metadata Management for Genomics. At IBM Research Lab (with Stefano Ceri and Pietro Pinoli)	Zurich, Switzerland
Jan 2017	Seminar, Metadata Modeling for Genomics. Seminar at IEO-IIT research institute	Milan, Italy

CONFERENCE AND WORKSHOP TALKS

ER 2022	41st Int. Conference on Conceptual Modeling, October 17-20, 2022 , Talk: <i>A comprehensive approach for the conceptual modeling of genomic data</i>	online
SWAT4HCLS 2022	13th Int. Conference on Semantic Web Applications and Tools for Health Care and Life Sciences, to happen January 11-12, 2022 , Poster presentation: <i>A unique approach to SARS-CoV-2 data and knowledge ingestion, integration and querying</i>	online
ICC 2021	30th Int. Cartographic e on, December 14-18, 2021 , Talk: <i>Geo-Online Explanatory Data Visualization Tools as Crisis Management and Communication Instruments</i>	online
ER 2021	40th Int. Conference on Conceptual Modeling, October 18-21, 2021 , Talk: <i>Ontological Unpacking as Explanation: The Case of the Viral Conceptual Model</i>	online
REFSQ 2021	27th Int. Working Conference on Requirement Engineering: Foundation for Software Quality, April 12-15, 2021 , Poster presentation: <i>Extreme Requirements Elicitation: Lessons Learnt from the COVID-19 Case Study</i>	online
ER 2020	39th Int. Conference on Conceptual Modeling, November 3-6, 2020 , Talk: <i>Empowering Virus Sequence Research Through Conceptual Modeling</i>	online
EmpER 2019	2nd Int. Workshop on Empirical Methods in Conceptual Modeling, November 4-7, 2019 , Talk: <i>Exploiting conceptual modeling for searching genomic meta-data: A quantitative and qualitative empirical study</i>	Salvador (BR)
ER 2019	38th Int. Conference on Conceptual Modeling, November 4-7, 2019 , Talk: <i>From a conceptual model to a knowledge graph for genomic datasets</i>	Salvador (BR)
SWAT4HCLS 2018	11th Int. Conference Semantic Web Applications and Tools for Healthcare and Life Sciences, December 3-6, 2018 , Talk: <i>Ontology-driven metadata enrichment for genomic datasets</i>	Antwerp (BE)
DTMbio 2018	12th Int. Workshop on Data and Text Mining in Biomedical Informatics, October 22-26, 2018 , Talk: <i>Using metadata for locating genomic datasets on a global scale</i>	Torino (IT)
ER 2017	36th Int. Conference on Conceptual Modeling, November 6-9, 2017 , Talk: <i>Conceptual modeling for genomics: building an integrated repository of open data</i>	Valencia (ES)

TUTORIALS

EDBT 2022	25th International Conference on Extending Database Technology, March 29-April 1, 2022 , Tutorial topic: <i>Conceptual models and databases for searching the genome</i> (with Pietro Pinoli)	online
ER 2021	40th International Conference on Conceptual Modeling, October 18-21, 2021 , Tutorial topic: <i>Conceptual models for searching the genome</i> (with Pietro Pinoli)	online

ONLINE DEMONSTRATIONS

During the year May 2020 - Apr 2021, I gave several introductions to the Viral Conceptual Model and demonstrations of ViruSurf, VirusViz, Virus-Lab, and EpiSurf tools, used for data-driven knowledge discovery based on viral sequences data. The presentations were conducted online, due to the COVID-19 pandemic traveling restrictions. List of recipients: Ilaria Capua (One Health Center of Excellence, University of Florida, US); Luca Ferretti (Oxford Big Data Institute, UK); Shay Fleishon (Central Virology Laboratory – Israel Ministry of Health, IL); Alice Fusaro and Stefania Leopardi (Istituto Zooprofilattico Sperimentale delle Venezie, IT); Alba Grifoni (La Jolla Institute, US); Susanna Lamers (BioInfoExperts, US); Alessio Lorusso (Istituto Zooprofilattico Sperimentale dell’Abruzzo e del Molise); Wolfgang Nejdil (Leibniz Universität Hannover); Graziano Pesole, Matteo Chiara, and Federico Zambelli (Università di Bari and Università degli Studi di Milano, IT); Francesca Mari and Alessandra Renieri (Università di Siena); Brittany Rife Magalis, Carla Mavian, and Marco Salemi (University of Florida, US); Anna Sandionigi (Università degli Studi di Milano-Bicocca); Stephen Tsui (The Chinese University of Hong Kong, HK); Limsoon Wong (National University of Singapore, SGP).

Service to Students

TEACHING

To happen: 2022-2023	Data Management and Analysis for Computational Biology , Professor – PhD School of Information Technology (2 CFUs)	<i>Politecnico di Milano</i>
Jun 2022	Ontological Unpacking: a Conceptual Model of the Human Genome , Guest Lecturer for a intensive course of the Master ‘Systèmes d’Information et de Connaissance’ – The University Paris 1 Pantheon-Sorbonne (5 hours)	<i>Universitat Politècnica de València</i>
Apr 2022	UML and OntoUML modeling languages and ontological unpacking applications to the genomics domain , Guest Lecturer in Bachelor/Master courses of Engineering of Computing Systems (10 hours)	<i>Universitat Politècnica de València</i>
2021-2022	Data Bases 1 for Engineering of Computing Systems (Bachelor Degree) , Teaching Assistant (10 hours)	<i>Politecnico di Milano</i>
2021-2022	Data Bases (Master Degree in Bioinformatics for Computational Genomics) , Teaching Assistant (10 hours)	<i>Politecnico di Milano</i>
2021-2022	Computer Science Fundamentals for Mathematical Engineering (Bachelor Degree) , Teaching Assistant (20 hours)	<i>Politecnico di Milano</i>
2016-2017	Computer Science Fundamentals for Mathematical Engineering (Bachelor Degree) , Teaching Assistant (40 hours)	<i>Politecnico di Milano</i>
2017-2018	Computer Science Fundamentals for Mathematical Engineering (Bachelor Degree) , Teaching Assistant (40 hours)	<i>Politecnico di Milano</i>

PHD CO-SUPERVISION

Nov 2020 - present	Tommaso Alfonsi , “Methods and tools for data and knowledge management and integration for viral genomics”	<i>Politecnico di Milano</i>
Nov 2020 - present	Ruba Al Khalaf , “Developing knowledge structures for biological data modeling and analysis”	<i>Politecnico di Milano</i>

MASTER THESIS CO-SUPERVISION

2022-present	Elena Righini , Master thesis “Analysis of clinical outcomes of COVID-19 patients with given SARS-CoV-2 variants infections”	<i>Politecnico di Milano</i>
2021-present	Francesco Invernici , Master thesis “SARS-CoV-2 knowledge graph construction by automatic literature mining”	<i>Politecnico di Milano</i>
2020-2021	Federico Comolli , Master thesis “Integration of genome-wide association studies into the GeCo repository”	<i>Politecnico di Milano</i>
2019-2020	Tommaso Alfonsi , Master thesis “Integration of DNA variation data into a GDM repository and API development for identification of genomic populations”	<i>Politecnico di Milano</i>
2019-2020	Giuseppe Cannizzaro , Master thesis “Automatic data integration for genomic metadata through sequence-to-sequence models”	<i>Politecnico di Milano</i>
2018-2019	Andrea Colombo , Master thesis “Ontology-driven metadata enrichment for genomic datasets”	<i>Politecnico di Milano</i>
2017-2018	Federico Gatti , Master thesis “Progettazione e realizzazione di una procedura di integrazione per dati genomici”	<i>Politecnico di Milano</i>

BACHELOR-LEVEL PROJECTS AND POST-GRADUATE SUPERVISION

2021-present	Giuseppe Garcia Serna , Post-Master degree project “CoEffect: SARS-CoV-2 mutations’ effects extraction from literature”	<i>Politecnico di Milano</i>
2022-present	Lorenzo Battiston , Bachelor degree project “Visualization of SARS-CoV-2 of sequencing statistics over a world map”	<i>Politecnico di Milano</i>
2020-2020	Elisabetta Fedele , Bachelor degree project “Visualization techniques for SARS-CoV-2 data”	<i>Politecnico di Milano</i>
2019-2019	Silvia Ferraris , Bachelor degree project “Integration of ENCODE gene/transcript quantification data with GENCODE annotations”	<i>Politecnico di Milano</i>

Publications

BIBLIOMETRICS

Refereed international journals	20
Refereed international conferences	14
Refereed international workshops, posters, or national conferences	8
Refereed international books and book chapters	5
Publons/Web of Science (query date: 21/06/2022)	8 H-index, 30 Publications, 277 Citations
Scopus (query date: 21/06/2022)	8 H-index, 38 Publications, 294 Citations
Google Scholar (query date: 21/06/2022)	12 H-index, 54 Publications, 649 Citations

INTERNATIONAL JOURNALS

- [J20] Grandi, S., & **Bernasconi, A.** (2022) Risk perception, spatial data, legal response during COVID-19 pandemic: a conceptual model. Accepted on *GeoProgress*, 7(2), vol. 2020 [in print].
- [J19] Serna G., G., Leone, M., **Bernasconi, A.**, & Carman, M.J. (2022). GeMI: Interactive Interface for Transformer-based Genomic Metadata Integration. *Database*, 2022. <http://doi.org/10.1093/database/baac036> IF 2020: 3.451, Q1
- [J18] Alfonsi, T., Al Khalaf, R., Ceri, S., & **Bernasconi, A.** (2022). CoV2K model, a comprehensive representation of SARS-CoV-2 knowledge and data interplay. *Scientific Data*, 9, 260. <https://doi.org/10.1038/s41597-022-01348-9> IF 2020: 6.444, Q1
- [J17] **Bernasconi, A.**, & Ceri, S. (2022). Interoperability of COVID-19 clinical phenotype data with host and viral genetics data. *BioMed*, 2(1), 69-81. <https://doi.org/10.3390/biomed2010007>
- [J16] Cilibrasi, L., Pinoli, P., **Bernasconi, A.**, Canakoglu, A., Chiara, M., & Ceri, S. (2022). ViruClust: direct comparison of SARS-CoV-2 genomes and genetic variants in space and time. *Bioinformatics*, 38(7), 1988-1994. <https://doi.org/10.1093/bioinformatics/btac030>. IF 2020: 6.937, Q1
- [J15] Pinoli, P., **Bernasconi, A.**, Sandionigi, A., & Ceri, S. (2021). VirusLab: a tool for customized SARS-CoV-2 data analysis. *BioTech*, 10(4), 27. <https://doi.org/10.3390/biotech10040027>
- [J14] **Bernasconi, A.**, Mari, L., Casagrandi, R., & Ceri, S. (2021). Data-driven analysis of amino acid change dynamics timely reveals SARS-CoV-2 variant emergence. *Scientific Reports*, 11(1), 21068. <https://doi.org/10.1038/s41598-021-00496-z>. IF 2020: 4.380, Q1
- [J13] **Bernasconi, A.**, Cilibrasi, L., Al Khalaf, R., Alfonsi, T., Ceri, S., Pinoli, P., & Canakoglu, A. (2021). EpiSurf: metadata-driven search server for analyzing amino acid changes on epitopes of SARS-CoV-2 and other viral species. *Database*, 2021. <https://doi.org/10.1093/database/baab059>. IF 2020: 3.451, Q1
- [J12] Menghi, C., Rizzi, A.M., **Bernasconi, A.** & Spoletini, P. (2021). TORPEDO: Witnessing Model Correctness with Topological Proofs. *Formal Aspects of Computing*, 33(6), 1039-1066. <https://doi.org/10.1007/s00165-021-00564-1>. IF 2020: 0.627, Q4
- [J11] Crovari, P., Pidò, S., Pinoli, P., **Bernasconi, A.**, Canakoglu, A., Garzotto, F., & Ceri, S. (2022). GeCoAgent: a Conversational Agent for Empowering Genomic Data Extraction and Analysis. *ACM Transactions on Computing for Healthcare*, 3(1), 1-29. <https://doi.org/10.1145/3464383>
- [J10] **Bernasconi, A.**, Gulino, A., Alfonsi, T., Canakoglu, A., Pinoli, P., Sandionigi, A., & Ceri, S. (2021). VirusViz: Comparative analysis and effective visualization of viral nucleotide and amino acid variants. *Nucleic Acids Research*, 49(15), e90. <https://doi.org/10.1093/nar/gkab478>. IF 2020: 16.971, Q1
- [J9] **Bernasconi, A.** (2021). Data quality-aware genomic data integration. *Computer Methods and Programs in Biomedicine Update*, 1, 100009. <https://doi.org/10.1016/j.cmpbup.2021.100009>
- [J8] **Bernasconi, A.**, & Grandi, S. (2021). A Conceptual Model for Geo-Online Exploratory Data Visualization: The Case of the COVID-19 Pandemic. *Information*, 12(2), 69. <https://doi.org/10.3390/info12020069>. Q3
- [J7] Canakoglu, A., Pinoli, P., **Bernasconi, A.**, Alfonsi, T., Melidis, D. P., & Ceri, S. (2021). ViruSurf: an integrated database to investigate viral sequences. *Nucleic acids research*, 49(D1), D817-D824. <https://doi.org/10.1093/nar/gkaa846>. IF 2020: 16.971, Q1
- [J6] **Bernasconi, A.**, Canakoglu, A., Masseroli, M., Pinoli, P., & Ceri, S. (2021). A review on viral data sources and search systems for perspective mitigation of COVID-19. *Briefings in Bioinformatics*, 22(2), 664-675. <https://doi.org/10.1093/bib/bbaa359>. IF 2020: 11.622, Q1
- [J5] **Bernasconi, A.**, Canakoglu, A., Masseroli, M., & Ceri, S. (2021). The road towards data integration in human genomics: players, steps and interactions. *Briefings in Bioinformatics*, 22(1), 30-44. <https://doi.org/10.1093/bib/bbaa080>. IF 2020: 11.622, Q1
- [J4] Cappelli, E., Cumbo, F., **Bernasconi, A.**, Canakoglu, A., Ceri, S., Masseroli, M., & Weitschek, E. (2020). OpenGDC: Unifying, Modeling, Integrating Cancer Genomic Data and Clinical Metadata. *Applied Sciences*, 10(18), 6367. <https://doi.org/10.3390/app10186367>. IF 2020: 2.679, Q2

- [J3] **Bernasconi, A.**, Canakoglu, A., Masseroli, M., & Ceri, S. (2022). META-BASE: a Novel Architecture for Large-Scale Genomic Metadata Integration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1), 543-557. <https://doi.org/10.1109/TCBB.2020.2998954>. IF 2020: 3.710, Q1
- [J2] Canakoglu, A., **Bernasconi, A.**, Colombo, A., Masseroli, M., & Ceri, S. (2019). GenoSurf: metadata driven semantic search system for integrated genomic datasets. *Database*, 2019. <https://doi.org/10.1093/database/baz132>. IF 2020: 3.451, Q1
- [J1] Masseroli, M., Canakoglu, A., Pinoli, P., Kaitoua, A., Gulino, A., Horlova, O., Nanni, L., **Bernasconi, A.**, Perna, S., Stamoulakatou, E., & Ceri, S. (2019). Processing of big heterogeneous genomic datasets for tertiary analysis of Next Generation Sequencing data. *Bioinformatics*, 35(5), 729-736. <https://doi.org/10.1093/bioinformatics/bty688>. IF 2020: 6.937, Q1

CONSORTIUM PAPERS JOURNALS

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- [Co1] Van Blokland, I.V., Lanting, P., Ori, A.P., Vonk, J.M., Warmerdam, R.C., Herkert, J.C., Boulogne, F., Claringbould, A., Lopera-Maya, E.A., Bartels, M. and Hottenga, J.J., Ganna, A., Karjalainen, J., Lifelines COVID-19 cohort study, The COVID-19 Host Genetics Initiative, et al. (2021) Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. *PloS one*, 16(8), p.e0255402. <https://doi.org/10.1371/journal.pone.0255402> [**Bernasconi, A.** was part of the “COVID-19 Host Genetics Initiative Coordination (Data dictionary)”. IF 2020: 3.240, Q2

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- [C13] **Bernasconi, A.**, & Pinoli, P. (April, 2022). Conceptual models and databases for searching the genome. *Proceedings of the 25th International Conference on Extending Database Technology, EDBT 2022, Edinburgh, UK, March 29 - April 1, 2022* (pp. 1-4). [OpenProceedings.org. https://doi.org/10.48786/edbt.2022.57](https://doi.org/10.48786/edbt.2022.57)
- [C12] Garcia S., A., Guizzardi, G., Pastor, O., Storey, V.C. & **Bernasconi, A.** (2022, June). An Ontological Characterization of a Conceptual Model of the Human Genome. In *International Conference on Advanced Information Systems - CAiSE Forum* (pp. 27-35). Springer, Cham. https://doi.org/10.1007/978-3-031-07481-3_4
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- [C7] Cannizzaro, G., Leone, M., **Bernasconi, A.**, Canakoglu, A., & Carman, M.J. (2020, September). Automated Integration of Genomic Metadata with Sequence-to-Sequence Models. In *Joint European Conference on Machine Learning and Knowledge Discovery in Databases* (pp. 187-203). Springer, Cham. https://doi.org/10.1007/978-3-030-67670-4_12
- [C6] Menghi, C., Rizzi, A. M., & **Bernasconi, A.** (2020, April). Integrating Topological Proofs with Model Checking to Instrument Iterative Design. In *International Conference on Fundamental Approaches to Software Engineering* (pp. 53-74). Springer, Cham. https://doi.org/10.1007/978-3-030-45234-6_3

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- [C3] **Bernasconi, A.**, Ceri, S., Campi, A., & Masseroli, M. (2017, November). Conceptual modeling for genomics: building an integrated repository of open data. In International Conference on Conceptual Modeling (pp. 325-339). Springer, Cham. https://doi.org/10.1007/978-3-319-69904-2_26
- [C2] **Bernasconi, A.**, Menghi, C., Spoletini, P., Zuck, L. D., & Ghezzi, C. (2017, September). From model checking to a temporal proof for partial models. In International Conference on Software Engineering and Formal Methods (pp. 54-69). Springer, Cham. https://doi.org/10.1007/978-3-319-66197-1_4
- [C1] Ceri, S., **Bernasconi, A.**, Canakoglu, A., Gulino, A., Kaitoua, A., Masseroli, M., Nanni, L., & Pinoli, P. (2017, October). Overview of GeCo: A project for exploring and integrating signals from the genome. In International Conference on Data Analytics and Management in Data Intensive Domains (pp. 46-57). Springer, Cham. https://doi.org/10.1007/978-3-319-96553-6_4

WORKSHOP PAPERS, POSTERS, AND ABSTRACTS

- [W8] **Bernasconi, A.**, Al Khalaf, R., Alfonsi, T., Canakoglu, A., Cilibrasi, L., Gulino, A., Pinoli, P., & Ceri, S. (January, 2022). A unique approach to SARS-CoV-2 data and knowledge ingestion, integration and querying. In 13th International Conference Semantic Web Applications and Tools for Life Sciences, SWAT4LS 2022 CEUR-WS. *[in print]*
- [W7] **Bernasconi, A.** (April, 2021). Extreme Requirements Elicitation: Lessons Learnt from the COVID-19 Case Study. In Joint Proceedings of REFSQ 2021 Workshops, OpenRE, Poster and Tools Track, and Doctoral Symposium co-located with the 27th International Conference on Requirements Engineering: Foundation for Software Quality, REFSQ 2021 (Vol. 2857). CEUR-WS.
- [W6] **Bernasconi, A.**, Canakoglu, A., & Ceri, S. (2019, November). Exploiting conceptual modeling for searching genomic metadata: A quantitative and qualitative empirical study. In: Guizzardi G., Gailly F., Suzana Pitangueira Maciel R. (eds) Advances in Conceptual Modeling. ER 2019. Lecture Notes in Computer Science, vol 11787. Springer, Cham. https://doi.org/10.1007/978-3-030-34146-6_8
- [W5] Settino, M., **Bernasconi, A.**, Ceddia, G., Agapito, G., Masseroli, M., & Cannataro, M. (2019, September). Using GMQL-Web for Querying, Downloading and Integrating Public with Private Genomic Datasets. In Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (pp. 688-693). <https://doi.org/10.1145/3307339.3343466>
- [W4] Masseroli, M., Pinoli, P., Canakoglu, C., **Bernasconi, A.**, Gulino, A., Nanni, L., Orlova, O., Pallotta, S., & Ceri, S. Genomic big data management, modeling and computing. In Analysis of Big Omics Data Workshop at BITS 2019.
- [W3] Cannizzaro, G., **Bernasconi, A.**, Canakoglu, A., Leone, M., & Carman, M.J. Sequence Labelling Techniques for Automatically Integrating Unstructured Genomic Metadata. In BITS 2019.
- [W2] **Bernasconi, A.** (2019). Using metadata for locating genomic datasets on a global scale. In 2018 Conference on Information and Knowledge Management Workshops, CIKM 2018 (Vol. 2482). CEUR-WS.
- [W1] Cappelli, E., Cumbo, F., **Bernasconi, A.**, Masseroli, M., & Weitschek, E. (2018). OpenGDC: standardizing, extending, and integrating genomics data of cancer. In ESCS 2018: 8th European Student Council Symposium, International Society for Computational Biology (ISCB).

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- [B5] **Bernasconi, A.** (2022) Model, Integrate, Search... Repeat: a Sound Approach to Building Integrated Repositories of Genomic Data. In: Piroddi L. (eds) Special Topics in Information Technology. SpringerBriefs in Applied Sciences and Technology. Springer, Cham. https://doi.org/10.1007/978-3-030-85918-3_8
- [B4] **Bernasconi A.**, Cascianelli S. (2022) Scenarios for the Integration of Microarray Gene Expression Profiles in COVID-19-Related Studies. In: Agapito G. (eds) Microarray Data Analysis. Methods in Molecular Biology, vol 2401. Humana, New York, NY. https://doi.org/10.1007/978-1-0716-1839-4_13
- [B3] **Bernasconi, A.**, & Masseroli, M. Biological and Medical Ontologies: Disease Ontology (DO). In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology. Volume 1, 2019, Pages 838-847. <https://doi.org/10.1016/B978-0-12-809633-8.20397-X>
- [B2] **Bernasconi, A.**, & Masseroli, M. Biological and Medical Ontologies: Human Phenotype Ontology (HPO). In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology. Volume 1, 2019, Pages 848-857. <https://doi.org/10.1016/B978-0-12-809633-8.20398-1>

- [B1] **Bernasconi, A.**, & Masseroli, M. Biological and Medical Ontologies: Systems Biology Ontology (SBO). In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology. Volume 1, 2019, Pages 858-866. <https://doi.org/10.1016/B978-0-12-809633-8.20399-3>

NON-PEER REVIEWED POSTS

- [P1] **Bernasconi, A.**, Pinoli, P., Al Khalaf, R., Alfonsi, T., Canakoglu, A., Cilibrasi, L., & Ceri, S. Report on Omicron Spike mutations on epitopes and immunological/epidemiological/kinetics effects from literature. Posted Nov. 30th, 2021 on [Virological.org](https://virological.org) – Discussion forum for analysis of virus genomes (15.8k views)
- [P2] Chiara, M., Pinoli, P., Minotti, L., **Bernasconi, A.**, Canakoglu, A., Ferrandi, E., & Ceri, S. Using VariantHunter for detecting emerging SARS-CoV-2 variants Posted May. 11th, 2022 on [Virological.org](https://virological.org) – Discussion forum for analysis of virus genomes

UNDER REVIEW

- [U1] **Bernasconi, A.**, Guizzardi, G., Pastor, O., & Storey, V.C. OntoVCM: Achieving Semantic Interoperability for Viral Sequence Data. Submitted to BMC Bioinformatics. [IF 2020: 3.169, Q1](#)
- [U2] **Bernasconi, A.**, Canakoglu, A., & Comolli, F.. Processing Genome-Wide Association Studies within a repository of heterogeneous genomic datasets. Submitted to BMC Bioinformatics. [IF 2020: 3.169, Q1](#)
- [U3] Pinoli, P., Minotti, L., **Bernasconi, A.**, Canakoglu, Chiara, M., Ceri, S. VariantHunter: a tool for fast detection of emerging SARS-CoV-2 variants. Submitted to Bioinformatics. [IF 2020: 6.937, Q1](#)
- [U4] Al Khalaf, R., **Bernasconi, A.**, Pinoli, P., Ceri, S. Analysis of co-occurring and mutually exclusive amino acid changes and detection of convergent and divergent evolution events in SARS-CoV-2. Submitted to the Computational and Structural Biotechnology Journal. [IF 2020: 7.271, Q1](#)
- [U5] Alfonsi, T., **Bernasconi, A.**, Canakoglu, A., & Masseroli, M. Genomic data integration and user-defined sample-set extraction for population variant analysis. Submitted to BMC Bioinformatics. [IF 2020: 3.169, Q1](#)
- [U6] Garcia S., A., **Bernasconi, A.**, Guizzardi, G., Pastor, O., Storey, V.C., & Mireia Costa. An Initial Empirical Assessment of an Ontological Model of the Human Genome. Submitted to the EmpER Workshop @ER 2022.

Skills & Background Knowledge

LANGUAGE SKILLS

Italian: Native speaker

English: Proficient user (TOEFL 107/120 and C1 Advanced Certificate)

Spanish: Advanced user (C1)

PROGRAMMING SKILLS

Programming languages: C (proficient), C++ (basic), Java (advanced), Scala (intermediate), Javascript (intermediate), Python (proficient)

Data Management Languages/Formats: SQL (PostgreSQL, MySQL, Vertica, Oracle), XML, Xquery, JSON, Cypher (Neo4J), yaml, owl, SPARQL

Numerical computing and statistical software: MATLAB (intermediate), R (basic), SPSS (basic), RapidMiner and WEKA (basic)

Specification languages: UML, OntoUML, Alloy, TRIO, KeyMaera

Operating systems: Windows (proficient), MacOS (proficient), GNU/Linux (intermediate)

Typesetting: Microsoft Word, LaTeX, Lyx, HTML

Others: SoapUI, Amazon WebServices, JIRA for software bugs tracking, SVN, Tortoise, GitHub for software versioning

ADDITIONAL EDUCATION

February 2011. Clarinet conservatory diploma, 7 years curricula. Conservatoire of Music of Bologna, Italy.