

# Anna Bernasconi

INFORMATION TECHNOLOGY

*Department of Electronics, Information, and Bioengineering*  
Politecnico di Milano, Italy



## Personal Information

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**Name** Anna Bernasconi  
**Date and Place of Birth** July 8th, 1990 – Bologna, Italy  
**Address** via Giuseppe Ponzio 34/5, 20133 Milan, Italy  
**Phone** (+39) 02 23993494  
**E-Mail** anna.bernasconi@polimi.it  
**Web Page** <http://annabernasconi.faculty.polimi.it>  
**ORCID** 0000-0001-8016-5750  
**Google Scholar Page** <https://scholar.google.com/citations?user=rCn19L4AAAAJ>  
**Scopus Page** <https://www.scopus.com/authid/detail.uri?authorId=57195587336>  
**Web of Science Page** <https://www.webofscience.com/wos/author/rid/AAF-2594-2019>

## Summary

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I am Tenured-Track Researcher (RTT) with the Dipartimento di Elettronica, Informazione e Bioingegneria at the Politecnico di Milano, holding 09/H1 and 01/B1 national scientific habilitation (2nd category); I was a visiting researcher at Universitat Politècnica de València Jan-Jun 2022. I received my Ph.D. in Information Technology from Politecnico di Milano in February 2021, with a thesis on genomic data integration that won three prizes (including the Dimitris N. Chorafas Foundation Award 2021).

At Politecnico di Milano, I co-taught the Doctoral course on Data Management and Analysis for Computational Biology. I teach the course on Programming (in the Master on Bioinformatics for Computational Genomics), have been a Teaching Assistant in Database courses for the last three years, and co-advised 8 master thesis and 4 PhD students.

My research interests lie at the intersection of Bioinformatics, Databases, and Data Science Methods, where I apply conceptual modeling, data integration, and knowledge engineering in several life sciences and other applied sciences domains, with a focus on building open-source tools and services. I authored more than 30 journal papers (including NatComm, NAR, SciData, GigaScience, Bioinformatics, Brief. in Bioinf.) and 30 conference/workshop papers (including ACM SIGMOD, IEEE ICDE, ECML-PKDD, CAiSE, ER), as well as 10 book chapters and 1 book. I collaborate with several scholars in national and international institutions and recently was awarded primary leadership of two research projects (to build – respectively – viral genomics early-warning systems and topic modeling web explorers).

I actively engage with the research community beyond my academic responsibilities. I participated in the conceptual modeling and database communities with several paper presentations, Programme Committees service, commitment as Program Chair, organization of two tutorials (ER and EDBT conferences), and two workshops on conceptual models and web applications for life sciences (ER and ICWE conferences). I am an academic editor in Plos One and BMC Bioinformatics, for which I also organized several special issues.

## Academic and Industry Positions

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- May 2024 - present **Tenured-Track Researcher (RTT)**, Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria
- Oct 2022 - Apr 2024 **Research Fellow – RTDA with 0.4 PO (university-funded units)**, Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria
- Nov 2020 - Sep 2022 **Post Doctoral Researcher (Assegnista di Ricerca)**, Politecnico di Milano, Topic: Evolution of genomic data and metadata repositories for supporting novel research applications
- Jan 2022 - Jun 2022 **Post Doctoral Visiting Researcher**, Universitat Politècnica de València, Topic: Conceptual modeling and data management for genomics
- Apr 2021 - Dec 2021 **Post Doctoral Visiting Researcher (remote status)**, Universitat Politècnica de València, Topic: Conceptual modeling and ontologies for representing the genome
- Mar 2016 - Oct 2016 **Graduate Research Assistant**, Politecnico di Milano, Topic: Input and output data standardization for the GenoMetric Query Language
- Nov 2014 - Feb 2016 **Junior Business Intelligence Consultant and Data Warehouse Architect**, Quantyca S.R.L., Monza, Italy, Topic: ETL/integration processes and web application development
- Nov 2013 - Dec 2013 **Undergraduate Research Assistant**, University of Illinois at Chicago, Topic: Self-certifying compilers design

## National Scientific Qualification

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- Dec 2023 **Abilitazione Scientifica Nazionale, Settore: 01/B1**, Informatica, Associate Professor (Seconda Fascia)
- Jun 2023 **Abilitazione Scientifica Nazionale, Settore: 09/H1**, Sistemi di elaborazione delle informazioni, Associate Professor (Seconda Fascia)

## Education

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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
- Awards: Dimitris N. Chorafas Foundation, CINI Lab on Big Data, CAISE PhD Award

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

Sep 2009 - Sep 2012

- Advisor: Prof. Alessandro Campi
- Mark: 100/110
- Extra: 9 months Erasmus Program at Universidad Autonoma de Madrid, Spain

## Awards and Recognitions

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- 2023 **CAiSE PhD Award 2023, 35th International Conference on Advanced Information Systems Engineering**, granted to an outstanding Ph.D. thesis in the field of Information Systems Engineering, co-sponsored by the CAiSE Steering Committee and Springer, reviewed by a standing committee of the CAiSE Advisory Committee, the CAiSE Steering Committee, and Program Committee
- 2022 **'Runner Up Paper' Award, 41st International Conference on Conceptual Modeling, ER 2022**, recognizing high-quality research work with future potential impact on conceptual modeling practices, granted by the ER 2022 Program Committee Chairs – the paper was invited for a Journal extension in Data & Knowledge Engineering Journal
- 2022 **Award for the Best Ph.D. Thesis on Big Data & Data Science 2022**, granted by CINI Lab on Big Data to excellent PhD theses based on originality and potential impact on the Big Data e Data Science community ([https://www.itadata.it/2023/award\\_winners](https://www.itadata.it/2023/award_winners))
- 2021 **Chorafas Award 2021**, granted by the Dimitris N. Chorafas Foundation (Weizman Institute of Science and Feinberg Graduate School) in recognition of results obtained during the research activity pursued during my PhD – the foundation awards prizes in engineering/medicine/natural sciences where results can have a significant impact on future research and practical applications (<https://www.weizmann.ac.il/feinberg/about/dimitris-n-chorafas-prize/about-foundation-and-prize>)
- 2021 **Springer award**, for the PhD thesis, granted by PhD Board of professors, Politecnico di Milano

## Leadership and Participation in Funded Research Projects

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- Dec 2023 - Nov 2025 **MUR PRIN PNRR 2022 project “SENSIBLE: Small-data Early warNing System for viral pathogens In puBLic hEalth”, project n. P2022CNN2J**, Research Units: Politecnico di Milano and Università degli Studi di Milano; Funding PoliMi Unit: 186,175 Euros; Role: Principal Investigator *Politecnico di Milano*
- Dec 2023 - May 2027 **Horizon Europe Framework Programme (HORIZON) project “BETTER: Better rEal-world healTh-daTa distributEd analytics Research platform”, grant agreement n. 101136262**, Funding: 638,950 Euros; Role: Proposal co-editor and Leader of Tasks 4.3 ‘Design and develop a unified schema repository for medical centres data and metadata integration’ and 4.4 “FAIRification of medical centres datasets” *Politecnico di Milano*
- Sep 2023 - Aug 2024 **Next Generation Internet (NGI) Search, 2nd open call, project “TETHYS: Topics Evolution That You See”, agreement n. SEARCH OC2\_18**, Funding: 150,000 Euros; Role: Principal Investigator *Politecnico di Milano*
- Jan 2023 - Dec 2025 **NextGenerationEU program project “FAIR: Future Artificial Intelligence Research”, within the PNRR-PE-AI scheme (M4C2, Investment 1.3, Line on Artificial Intelligence)**, Role: Task Leader – “Graph-based ML for Network Medicine” *Politecnico di Milano*
- Jul 2020 - Dec 2020 **EIT Digital “DATA against COVID-19” program, Innovation Activity ‘Virusurf’ n. 20663**, Role: Task Leader – “User experience and interfaces” *Politecnico di Milano*
- Nov 2016 - Aug 2021 **Data-Driven Genomic Computing, ERC Advanced Investigator Grant n. 693174**, Role: Work Package Leader – WP4: Integrated access to large data sources *Politecnico di Milano*

## Research Collaborations

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- Feb 2024 - **Dr. Daniele Focosi (North-Western Tuscany Blood Bank, Pisa University Hospital), Federico Gueli (independent researcher)**, Topic: SARS-CoV-2 convergent evolution knowledge graphs
- Sep 2023 - **Co-Chair of the FAIRification of Genomic Annotations RDA Working Group** (<https://www.rd-alliance.org/groups/fairification-genomic-annotations-wg>), Topic: Standardization of Genomic Annotations and FAIRification of related (meta)data and processing pipelines
- Sep 2023 - **Chiara Leonardi (Independent Systemic Design Researcher)**, Topic: Complex systems dynamics represented with Causal Loop Diagrams
- Mar 2022 - **Dr. Luigi Bellomarini and Davide Magnanini (Banca d'Italia)**, Topic: Graph-based reactive systems
- Jun 2021 - **Prof. Matteo Chiara (Università degli Studi di Milano), Erika Ferrandi (Consiglio Nazionale delle Ricerche, Bari), Iliaria Capua (Johns Hopkins University), Shay Fleishon (Israel Central Virology Laboratory)**, Topic: Bioinformatic Methods for studying the evolution of SARS-CoV-2 and other viruses
- Sep 2022 - **Prof. Giancarlo Guizzardi and Prof. Luiz Olavo Bonino da Silva Santos (University of Twente and Leiden University Medical Center)**, Topic: Ontologies for scientific datasets FAIRification
- Jun 2023
- Feb 2022 - **Dr. Andrea Giacomelli, Dr. Valeria Micheli, and Prof. Giuliano Rizzardini (Azienda Ospedaliera Polo Universitario L. Sacco)**, Topic: SARS-CoV-2 viremia, variants, and COVID-19 mortality
- Dec 2022
- Mar 2021 - **Group of Professor Oscar Pastor (with Prof. Giancarlo Guizzardi and Prof. Veda Storey), Universitat Politècnica de València - Research Center on Software Production Methods**, Topic: Conceptual modeling for biological and genomic information systems
- Nov 2023
- Apr 2020 - **The COVID-19 Host Genetics Initiative** (<https://www.covid19hg.org/>), Topic: Design of clinical/phenotype COVID-19 dictionary for structuring data collection
- Jul 2021
- Apr 2020 - **Prof. Silvia Grandi, University of Bologna - Dipartimento di Scienze Statistiche "Paolo Fortunati"**, Topic: Geospatial data perspective of clinical and genomic information on COVID-19
- Dec 2022
- Jan 2019 - **Dr. Claudio Menghi (with Prof. Paola Spoletini and Dr. Alessandro Maria Rizzi), University of Luxembourg - Centre for Security Reliability and Trust**, Topic: Formal verification for partial models
- Nov 2020
- Sep 2017 - **Group of Prof. Emanuel Weitschek, Italian National Research Council - Institute of Systems Analysis and Computer Science**, Topic: metadata integration on cancer data from Genomic Data Commons
- Mar 2020
- Jun 2019 - **Group of Prof. Mario Cannataro, Università Magna Graecia**, Topic: integrative applications of GenoMetric Query Language using private and public datasets
- Sep 2019

## Open source tools, products and services

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Contribution to several tools (all registered under the ELIXIR Italian node PoliMi, see bio.tools, related to corresponding journal publications). These aim facilitate the work of cancer genomics researchers, clinicians, geneticists, virologists, phylogeneticists, epidemiologists, pathogenists, and immunologists.

**OpenGDC** (<http://www.bioinformatics.deib.polimi.it/opengdc>). Extraction and integration tool for cancer genomics data.

**GenoSurf** (<http://gmql.eu/genosurf>). Multi-ontology semantic search system that provides access to a consolidated collection of human genome datasets for bioinformatic tertiary analysis.

**GeMI** (<http://gmql.eu/gemi>). Interactive interface to annotate genomic samples exploiting a deep-learning-based prediction model, whose impact is to accelerate unstructured genomic metadata extraction into structured formats.

**VarSum** (<http://gmql.eu/popstudy>). API that returns summary statistics on user-defined populations and their variants, using the genomic data repository maintained in the group.

**META-BASE** (<https://github.com/DEIB-GECO/Metadata-Manager>). Tool that integrates and enriches heterogeneous biological and clinical data sources, exploiting several configurations to build a repository.

**VirusSurf** (<http://gmql.eu/virusurf>). Search system for public viral sequences described by their metadata and exhibiting nucleotide and amino acid mutational patterns.

**EpiSurf** (<http://gmql.eu/epivirusurf>). Search system for evaluating the impact of viral mutational patterns on epitopes, i.e., areas of the virus recognized by the human immune system.

**VirusViz** (<http://gmql.eu/virusviz>). Visualization tool for comparing mutation distributions of selected viral populations.

**VirusClust** (<http://gmql.eu/virusclust>). Data analysis tool to perform temporal and spatial comparison of mutational patterns of SARS-CoV-2 sequences.

**VariantHunter** ([http://gmql.eu/variant\\_hunter](http://gmql.eu/variant_hunter)). Tool for fast detection of emerging SARS-CoV-2 (sub)variants.

**CoV2K API** (<http://gmql.eu/cov2k/api>). Knowledge base of SARS-CoV-2 sequence mutations, variants, and effects.

**CoVEffect** (<http://gmql.eu/coveffect>). Interactive web interface for deep learning-assisted curation of data annotation on the effects of SARS-CoV-2 mutations and variants.

**CORToViz** (<http://gmql.eu/cortoviz>). Visualizer for trending topics extracted from the CORD-19 dataset on COVID-19-related research abstracts.

**GRAPH-SEARCH** (<http://gmql.eu/graph-search>). Explorer of COVID-19-related literature using graph-based queries with shortest paths and sophisticated ranking.

## Outreach Scientific Activities

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### ORGANIZATION OF EVENTS

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|                        |  |                             |
|------------------------|--|-----------------------------|
| To happen:<br>Oct 2024 | <b>Fifth International Workshop on Conceptual Modeling for Life Sciences (CMLS 2024),</b><br>co-located with ER 2024 conference, Chair and co-organizer  | <i>Pittsburgh, US</i>       |
| To happen:<br>Jun 2024 | <b>Third International Workshop on Web Applications for Life Sciences (WALS 2024),</b><br>co-located with ICWE 2024 conference, Co-organizer             | <i>Tampere,<br/>Finland</i> |
| Nov 2023               | <b>Fourth International Workshop on Conceptual Modeling for Life Sciences (CMLS 2023),</b><br>co-located with ER 2023 conference, Chair and co-organizer | <i>Lisbon,<br/>Portugal</i> |
| Jun 2023               | <b>Second International Workshop on Web Applications for Life Sciences (WALS 2023),</b><br>co-located with ICWE 2023 conference, Co-organizer            | <i>Alicante,<br/>Spain</i>  |
| Oct 2022               | <b>Third International Workshop on Conceptual Modeling for Life Sciences (CMLS 2022),</b><br>co-located with ER 2022 conference, Chair and Co-organizer  | <i>(online)</i>             |
| Jul 2022               | <b>First International Workshop on Web Applications for Life Sciences (WALS 2022),</b><br>co-located with ICWE 2022 conference, Chair and Co-organizer   | <i>Bari, Italy</i>          |
| Oct 2021               | <b>Second International Workshop on Conceptual Modeling for Life Sciences (CMLS 2021),</b><br>co-located with ER 2021 conference, Co-organizer           | <i>(online)</i>             |
| Nov 2020               | <b>First International Workshop on Conceptual Modeling for Life Sciences (CMLS 2020),</b><br>co-located with ER 2020 conference, Chair and Co-organizer  | <i>(online)</i>             |
| Feb 2020               | <b>Politecnico di Milano Genomic Computing Group “gong-like presentations”,</b> Co-organizer   | <i>Milano, Italy</i>        |
| Mar 2019               | <b>“Challenges in Data-Driven Genomic Computing” Workshop,</b> Member of organization team (for the Advanced ERC Project 693174 “GeCo”)                  | <i>Como, Italy</i>          |

## ORGANIZING COMMITTEE SERVICE

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**Publicity Chair** of the 43rd International Conference on Conceptual Modeling (ER 2024), Pittsburgh, Portugal, 28-31 October 2024

**Publicity Chair** of the 42nd International Conference on Conceptual Modeling (ER 2023), Lisbon, Portugal, 17-20 October 2023

**Program Chair** of the 9th IEEE International Conference on Big Data Computing Service and Machine Learning Applications (IEEE BigDataService 2023), Athens, Greece, 17-20 July 2023

**Special Track Chair** (Big Data and Analytics for Healthcare) and **Publication Chair** for the 8th IEEE International Conference on Big Data Computing Service and Machine Learning Applications (IEEE BigDataService 2022), San Francisco Bay Area, USA, 15-18 August 2022

## SCIENTIFIC PROGRAM COMMITTEE SERVICE

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**Program Committee Member** in the Full Papers Program Committee of the 33rd ACM International Conference on Information and Knowledge Management (CIKM 2024), Boise, Idaho, 21-25 October 2024

**Program Committee Member** in the Main Track of the 43rd International Conference on Conceptual Modeling (ER 2024), Pittsburgh, USA, 28-31 October 2024

**Review Board Member** for PVLDB Volume 18, for the period of April 2024 through March 2025. The accepted papers from this volume will be presented at VLDB 2025, to be held in London, UK.

**Program Committee Member** of the 16th International Conference on Knowledge Discovery and Information Retrieval (KDIR 2024, part of IC3K), Porto, Portugal, 18-20 November 2024

**Program Committee Member** of the 16th International Conference on Knowledge Engineering and Ontology Development (KEOD 2024, part of IC3K), Porto, Portugal, 18-20 November 2024

**Program Committee Member** of the 19th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2024), Benevento, Italy, 4-6 September 2024

**Program Committee Member** for 36th International Conference on Advanced Information Systems Engineering (CAiSE 2024), Limassol, Cyprus, June 3-7, 2024

**Demonstration track reviewer** for ACM SIGMOD/PODS International Conference on Management of Data, Santiago, Chile, 9-15 June, 2024

**Program Committee Member** of the Foundations of Network Analysis Workshop at IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2023), Istanbul, Turkey, 5-8 December 2023

**Program Committee Member** of the 6th International Workshop on Empirical Methods in Conceptual Modeling (EmpER 2023), at the International Conference on Conceptual Modeling, Lisbon, Portugal, 6-9 November 2023

**Program Committee Member** of the 15th International Conference on Knowledge Discovery and Information Retrieval (KDIR 2023, part of IC3K), Rome, Italy, 13-15 November 2023

**Program Committee Member** of the 15th International Conference on Knowledge Engineering and Ontology Development (KEOD 2023, part of IC3K), Rome, Italy, 13-15 November 2023

**Program Committee Member** in the ER Forum of the 42th International Conference on Conceptual Modeling (ER 2023), Lisbon, Portugal, 6-9 November 2023

**Program Committee Member** in the Main Track of the 42th International Conference on Conceptual Modeling (ER 2023), Lisbon, Portugal, 6-9 November 2023

**Program Committee Member** of the 18th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2023), Padua, Italy, 6-8 September 2023

**Program Committee Member** of the 1st High-Throughput Data Processing and Knowledge Mining in Bioinformatics (HiDa) at the 27th European Conference on Advances in Databases and Information Systems (ADBIS 2023), Barcelona, Spain, 4-7 September 2023

**Program Committee Member** of the 10th International Work-Conference on Bioinformatics and Biomedical Engineering (IWWBIO 2023), Gran Canaria, Spain, 12-14 July 2023

**Program Committee Member** of the Network and Pathway Analysis in Health Informatics (NPAHI) at the 11th IEEE International Conference on Healthcare Informatics (IEEE ICHI 2023), Houston, Texas, USA, 26-29 June 2023

**Program Committee Member** of the Research Project Exhibition (RPE) at the 35th International Conference on Advanced Information Systems Engineering (CAiSE 2023), Zaragoza, Spain, 12-16 June 2023

**Program Committee Member** of the Foundation of Network Analysis Workshop at IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2022), Las Vegas, NV, USA, 6-8 December 2022

**Program Committee Member** of the 1st International Workshop on Data Analysis for Life Science (DALIS 2022) at the European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML-PKDD 2022), Grenoble, France, 19-23 September 2022

**Program Committee Member** of the 9th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2022), Gran Canaria, Spain, 27-30 June 2022

**Program Committee Member** of the 17th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2021), online, 15-17 November 2021

## BIBLIOMETRICS

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Verified editor records (on Web of Science, query date 08/05/2024) ..... 38  
Verified reviews (on Web of Science, query date 08/05/2024) ..... 78

## BOARD MEMBERSHIPS

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**Editorial Board Member** of BMC Bioinformatics (ISSN 1471-2105, Publisher: Springer Nature) – since May 2022 (<https://bmcbioinformatics.biomedcentral.com/about/editorial-board>)

**Academic Editor** of Plos ONE (ISSN 1932-6203, Publisher: Public Library of Science) – since Feb 2023 (<https://journals.plos.org/plosone/static/editorial-board>)

## GUEST EDITORIAL SERVICE

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**Editorial Review Board Member** for the Journal of Data and Information Quality (ISSN: 1936-1955, Publisher: ACM). (<https://dl.acm.org/journal/jdiq/reviewers-board>)

(ongoing): **Guest Editor** for the Journal of Data and Information Quality (ISSN: 1936-1955, Publisher: ACM), Special Issue on “Data quality dimensions in Data FAIRification design and processes”. Guest editors: Bernasconi, A., Cirillo, S., García S., A., Harmouch, H. (<https://dl.acm.org/journal/jdiq/special-issues>)

(ongoing): **Guest Editor** for BMC Bioinformatics (ISSN: 1471-2105, Publisher: Springer Nature), Collection “Big data management in biological domains”. Guest editors: Bernasconi, A., Ferraro Petrillo, U., Rombo, S.E. (<https://www.biomedcentral.com/collections/bdmbd>)

(ongoing): **Guest Editor** for the Journal Future Generation Computer Systems (ISSN: 0167-739X, Publisher: Elsevier), for the Special Issue “Special Issue on Big Data Computing Service and Machine Learning Applications”. Guest editors: Potika, K., Eirinaki, M., Vitali, M., Bernasconi, A., Fujioka, H.

(ongoing): **Supplement Editor** for the Journals BMC Bioinformatics Journal (ISSN: 1471-2105, Publisher: Springer Nature) and BMC Medical Informatics and Decision Making (ISSN: 1472-6947, Publisher: Springer Nature), for the Supplement “Selected articles from the 3rd International Workshop on Conceptual Modeling for Life Sciences (CMLS 2022) and the 1st International Workshop on Web Applications for Life Sciences (WALS 2022)”. Guest editors: Bernasconi, A. et al.

**Guest Associate Editor** for Research Topic “Identification of phenotypically important genomic variants” on Frontiers in Bioinformatics (ISSN: 2673-7647, Publisher: Frontiers Media S.A.). Topic editors: Heron, E., Bernasconi, A., Valle, G. (<https://www.frontiersin.org/research-topics/39186/>)

**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](https://www.mdpi.com/journal/biotech/special_issues/Bioinformatics_Present_Future_Biotechnology))

**Volume Editor** for “Current Trends in Web Engineering - ICWE 2022 International Workshops, BECS, SWEET and WALS, Bari, Italy, July 5–8, 2022, Revised Selected Papers”. Conference Proceedings Book in Springer Communications in Computer and Information Science (CCIS, volume 1668). Volume editors: Agapito, G., Bernasconi, A. et al. <https://link.springer.com/book/10.1007/978-3-031-25380-5>

**Volume Editor** for “Computational Intelligence Methods for Bioinformatics and Biostatistics”, 17th International Meeting, CIBB 2021, Virtual Event, November 15–17, 2021, Revised Selected Papers. Conference Proceedings Book in Springer Lecture Notes in Bioinformatics (LNBI, LNCS volume 13483). Volume editors: Chicco, D., Bernasconi, A. et al.

**Supplement Editor** for the Journals: BMC Bioinformatics (ISSN: 1471-2105, Publisher: Springer Nature) and BMC Medical Informatics and Decision Making (ISSN: 1472-6947, Publisher: Springer Nature), for the joint Supplement “Selected articles on Conceptual Modeling for Life Sciences (CMLS 2021 workshop and ER 2021 conference)”. Guest editors: Bernasconi, A., Canakoglu, A., Chicco, D., Pinoli, P., and Reyes Román, J.F. (<https://bmcbioinformatics>)

biomedcentral.com/articles/supplements/volume-23-supplement-11, <https://bmcmidinformedecismak.biomedcentral.com/articles/supplements/volume-22-supplement-4>)

**Supplement Editor** for the Journals BMC Bioinformatics Journal (ISSN: 1471-2105, Publisher: Springer Nature) and BMC Medical Informatics and Decision Making (ISSN: 1472-6947, Publisher: Springer Nature), for the Supplement “Selected articles from the 17th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2021)”. Guest editors: Chicco, D., Bernasconi, A. et al. (<https://bmcbioinformatics.biomedcentral.com/articles/supplements/volume-23-supplement-6>, <https://bmcmidinformedecismak.biomedcentral.com/articles/supplements/volume-22-supplement-6>)

**Supplement Editor** for the Journal BMC Bioinformatics (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., Canakoglu, A., Chicco, D., Leon Palacio, A., and Reyes Román, J.F. (<https://bmcbioinformatics.biomedcentral.com/articles/supplements/volume-22-supplement-13>)

**Review Editor** of Frontiers in Artificial Intelligence (ISSN 2624-8212, Publisher: Frontiers Media S.A.) – Medicine and Public Health – since February 2023 (<https://www.frontiersin.org/journals/artificial-intelligence/editors>)

**Review Editor** of Frontiers in Bioinformatics (ISSN 2673-7647, Publisher: Frontiers Media S.A.) – Integrative Bioinformatics – since June 2022 (<https://www.frontiersin.org/journals/bioinformatics/editors>)

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

**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](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/editors>)

## REVIEWER SERVICE FOR INTERNATIONAL JOURNALS

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**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); **F1000Research** – Taylor & Francis (ISSN: 2046-1402); **Frontiers in Bioinformatics** – Frontiers Media S.A. (E-ISSN: 2673-7647); **Frontiers in Medicine** – Frontiers Media S.A. (E-ISSN: 2296-858X); **Frontiers in Microbiology** – Frontiers Media S.A. (E-ISSN: 1664-302X); **Frontiers in Plant Science** – Frontiers Media S.A. (E-ISSN: 1664-462X); **Frontiers in Public Health** – Frontiers Media S.A. (E-ISSN: 2296-2565); **Frontiers in Systems Biology** – Frontiers Media S.A. (E-ISSN: 2674-0702); **Genomics, Proteomics & Bioinformatics** – Elsevier (ISSN: 2210-3244); **GigaScience** – Oxford University Press (ISSN: 2047-217X); **Health Informatics Journal** – SAGE (ISSN: 17412811); **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); **Journal of data and information quality** – ACM (ISSN: 1936-1955); **Machine Learning** – Springer Nature (E-ISSN 1573-0565); **mSystems** – American Society for Microbiology (ISSN: 2379-5077); **npj Digital Medicine** – Springer Nature (ISSN: 2398-6352); **Scientific Data** – Springer Nature (EISSN: 20524463); **Soft Computing** – Springer Nature (ISSN: 14327643); **The Innovation** – Cell Press (ISSN: 2666-6758); **Transactions in Urban Data, Science, and Technology** – Sage publishing (ISSN: 2754-1231)

## MEMBERSHIPS

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IEEE Membership , 2020–2023

IEEE Women in Engineering Membership , 2020–2023

ACM Professional Membership 2022–2024

ELIXIR-IIB (Italian Bioinformatics Infrastructure) Joint Research Unit Participant , since 2023

## INVITED TALKS

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|          |  |                          |
|----------|--|--------------------------|
| May 2024 | <b>Lightning Talk</b> , <i>Building Integrated and FAIR Repositories for Genomic Data</i> . For the Research Data Alliance 22nd Plenary meeting (VP22), Working Group: FAIRification of Genomic Annotations – metadata harmonisation at scale  | (online)                 |
| Oct 2023 | <b>Lightning Talk</b> , <i>Building an Integrated Repository for Genomic Data</i> . For the Research Data Alliance collaborative meeting on FAIRification of Genomic Tracks ( <a href="https://tinyurl.com/FAIRificationGenomicTracks">https://tinyurl.com/FAIRificationGenomicTracks</a> )  | (online)                 |
| Sep 2023 | <b>Interview</b> , <i>Building a metadata model for COVID-19</i> . For CSC – IT Center for Science Ltd, administered by the Finnish Ministry of Education and Culture. ( <a href="https://youtu.be/wkLebyoQz54?si=IzN1UYQ-X9L69BRe">https://youtu.be/wkLebyoQz54?si=IzN1UYQ-X9L69BRe</a> )   | (online)                 |
| Sep 2022 | <b>Seminar</b> , <i>Data-driven SARS-CoV-2 understanding and hunting</i> . At Information Sciences Institute - University of Southern California ( <a href="https://www.isi.edu/events/2966/data-driven-sars-cov-2-understanding-and-hunting/">https://www.isi.edu/events/2966/data-driven-sars-cov-2-understanding-and-hunting/</a> ) | (online)                 |
| Sep 2022 | <b>Seminar</b> , <i>Data analysis for unveiling the SARS-CoV-2 evolution</i> . At the First International Workshop on Data Analysis for Life Science (DALSA@ECML-PKDD2022)   | (online)                 |
| Jul 2022 | <b>Seminar</b> , <i>Data-bases-driven research on viral genomes and SARS-CoV-2</i> . At Universidade Eduardo Mondlane, Maputo, Mozambique ( <a href="https://ict4dev.uem.mz/index.php/ict4dev-talks/">https://ict4dev.uem.mz/index.php/ict4dev-talks/</a> )  | (online)                 |
| Jan 2022 | <b>Seminar</b> , <i>Data-driven SARS-CoV-2 understanding and hunting (searching for the new Omicron)</i> . At Politecnico di Milano and Universitat Politècnica de València ( <a href="https://youtu.be/VHgb1Dz00ho">https://youtu.be/VHgb1Dz00ho</a> )  | (online)                 |
| Nov 2021 | <b>Invited talk</b> , <i>Modeling, integrating, and searching processed genomic datasets</i> . At “Integrating Diverse Datasets Webinar Series” by Front Line Genomics   | (online)                 |
| Mar 2019 | <b>Invited talk</b> , <i>Metadata Integration Framework for Genomic Datasets</i> . At “Challenges in Data-Driven Genomic Computing” Workshop   | Como, Villa del Grumello |
| Feb 2019 | <b>Seminar</b> , <i>Data-Driven Genomic Computing: Making Sense of the Signals from the Genome through systematic application design and open data repository</i> . At EPFL  | Lausanne, Switzerland    |
| Jan 2019 | <b>Seminar</b> , <i>Meta-awareness: towards an agreement on experimental metadata</i> . At “Genomic Computing & Data Science Meetings”, Politecnico di Milano.   | Milan, Italy             |
| Jul 2017 | <b>Seminar</b> , <i>Metadata Management for Genomics</i> . At ETH (with Stefano Ceri and Pietro Pinoli)  | Zurich, Switzerland      |
| Jul 2017 | <b>Seminar</b> , <i>Metadata Management for Genomics</i> . At IBM Research Lab (with Stefano Ceri and Pietro Pinoli)   | Zurich, Switzerland      |
| Jan 2017 | <b>Seminar</b> , <i>Metadata Modeling for Genomics</i> . Seminar at IEO-IIT research institute   | Milan, Italy             |

## CONFERENCE AND WORKSHOP TALKS

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|                              |  |                      |
|------------------------------|--|----------------------|
| to happen:<br>SIGMOD<br>2024 | <b>ACM SIGMOD/PODS Int. Conference on Management of Data, June 9-14, 2024</b> , Poster presentation: <i>Achieving data FAIRification in a distributed analytics research platform for rare diseases</i>                  | Santiago, Chile      |
| to happen:<br>CAiSE 2024     | <b>36th Int. Conference on Advanced Information Systems Engineering, June 3-7, 2024</b> , Talk (Research Project Exhibition): <i>SENSIBLE: implementing data-driven early warning systems for future viral epidemics</i> | Limassol, Cyprus     |
| to happen:<br>CAiSE 2024     | <b>36th Int. Conference on Advanced Information Systems Engineering, June 3-7, 2024</b> , Talk (Research Project Exhibition): <i>TETYS: towards the next-generation open-source Web topic explorer</i>                   | Limassol, Cyprus     |
| to happen:<br>ICDE 2024      | <b>40th IEEE Int. Conference on Data Engineering, May 13-17, 2024</b> , Talk (Future Technology Track): <i>Reactive Knowledge Management</i>   | Utrecht, Netherlands |

|                   |  |                        |
|-------------------|--|------------------------|
| SWAT4HCLS<br>2024 | <b>15th Int. Conference on Semantic Web Applications and Tools for Health Care and Life Sciences, February 26-29, 2024</b> , Poster presentation: <i>Achieving data FAIRification in a distributed analytics research platform for rare diseases</i> | Leiden,<br>Netherlands |
| ER 2023           | <b>42nd Int. Conference on Conceptual Modeling, November 6-9, 2023</b> , Talk (Journal-first track): <i>CoV2K model, a comprehensive representation of SARS-CoV-2 knowledge and data interplay</i>   | Lisbon,<br>Portugal    |
| IEEE SOSE<br>2023 | <b>Int. Congress on Intelligent and Service-Oriented Systems Engineering, July 17-20, 2023</b> , Talk: <i>The opportunity of data-driven services for viral genomic surveillance</i> (invited paper)   | Athens,<br>Greece      |
| CAiSE 2023        | <b>35th Int. Conference on Advanced Information Systems Engineering, June 12-16, 2023</b> , Talk: <i>Ontological representation of FAIR principles: A blueprint for FAIRer data sources</i>  | Zaragoza,<br>Spain     |
| ER 2022           | <b>41st Int. Conference on Conceptual Modeling, October 17-20, 2022</b> , Talk: <i>A comprehensive approach for the conceptual modeling of genomic data</i>  | online                 |
| SWAT4HCLS<br>2022 | <b>13th Int. Conference on Semantic Web Applications and Tools for Health Care and Life Sciences, January 11-12, 2022</b> , Poster presentation: <i>A unique approach to SARS-CoV-2 data and knowledge ingestion, integration and querying</i>       | online                 |
| ICC 2021          | <b>30th Int. Cartographic e on, December 14-18, 2021</b> , Talk: <i>Geo-Online Explanatory Data Visualization Tools as Crisis Management and Communication Instruments</i>   | online                 |
| ER 2021           | <b>40th Int. Conference on Conceptual Modeling, October 18-21, 2021</b> , Talk: <i>Ontological Unpacking as Explanation: The Case of the Viral Conceptual Model</i>  | online                 |
| REFSQ 2021        | <b>27th Int. Working Conference on Requirement Engineering: Foundation for Software Quality, April 12-15, 2021</b> , Poster presentation: <i>Extreme Requirements Elicitation: Lessons Learnt from the COVID-19 Case Study</i>                       | online                 |
| ER 2020           | <b>39th Int. Conference on Conceptual Modeling, November 3-6, 2020</b> , Talk: <i>Empowering Virus Sequence Research Through Conceptual Modeling</i>   | online                 |
| EmpER<br>2019     | <b>2nd Int. Workshop on Empirical Methods in Conceptual Modeling, November 4-7, 2019</b> , Talk: <i>Exploiting conceptual modeling for searching genomic meta-data: A quantitative and qualitative empirical study</i>                               | Salvador (BR)          |
| ER 2019           | <b>38th Int. Conference on Conceptual Modeling, November 4-7, 2019</b> , Talk: <i>From a conceptual model to a knowledge graph for genomic datasets</i>  | Salvador (BR)          |
| SWAT4HCLS<br>2018 | <b>11th Int. Conference on Semantic Web Applications and Tools for Healthcare and Life Sciences, December 3-6, 2018</b> , Talk: <i>Ontology-driven metadata enrichment for genomic datasets</i>  | Antwerp (BE)           |
| DTMbio<br>2018    | <b>12th Int. Workshop on Data and Text Mining in Biomedical Informatics, October 22-26, 2018</b> , Talk: <i>Using metadata for locating genomic datasets on a global scale</i>   | Torino (IT)            |
| ER 2017           | <b>36th Int. Conference on Conceptual Modeling, November 6-9, 2017</b> , Talk: <i>Conceptual modeling for genomics: building an integrated repository of open data</i>   | Valencia (ES)          |

## TUTORIALS

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

## ONLINE DEMONSTRATIONS

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During the COVID-19 pandemic period **May 2020 - Apr 2021**, I gave several introductions to the Viral Conceptual Model and demonstrations of ViruSurf, VirusViz, VirusLab, and EpiSurf tools, used for data-driven knowledge discovery based on viral sequences data. The presentations were conducted online, due to the pandemic traveling restrictions.

**Auditors:** 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 Nejdl (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).

## INSTITUTIONAL RESPONSIBILITIES

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|              |   |  |
|--------------|---|--|
| 2023-present | <b>Member of the Scientific Committee of the Honours Programme, Computer Science and Engineering Track (Data, web, and society)</b> | <i>Politecnico di Milano</i>                         |
| 2022-present | <b>Member of the Interuniversity Teaching Board for the Master “Bioinformatics for Computational Genomics”, Professor</b>           | <i>Politecnico di Milano and University of Milan</i> |

## RECURRING TEACHING ACTIVITIES

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|                            |  |                              |
|----------------------------|--|------------------------------|
| 2022/23 – 2023/24          | <b>Programming, 6 CFU (Master Degree, Bioinformatics for Computational Genomics)</b> , Lecturer          | <i>Politecnico di Milano</i> |
| 2021/22 – 2023/24          | <b>Basi di Dati, 5 CFU (Bachelor Degree, Engineering of Computing Systems)</b> , Teaching Assistant      | <i>Politecnico di Milano</i> |
| 2021/22 – 2023/24          | <b>Data Bases, 6 CFU (Master Degree, Bioinformatics for Computational Genomics)</b> , Teaching Assistant | <i>Politecnico di Milano</i> |
| 2016/17 – 2017/18, 2021/22 | <b>Informatica A, 10 CFU (Bachelor Degree, Mathematical Engineering)</b> , Teaching Assistant            | <i>Politecnico di Milano</i> |

## NON-RECURRING TEACHING ACTIVITIES

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|          |  |  |
|----------|--|--|
| Jan 2023 | <b>Data Management and Analysis for Computational Biology</b> , Professor – Ph.D. School of Information Technology (2 CFUs)  | <i>Politecnico di Milano</i>               |
| Jun 2022 | <b>Ontological Unpacking: a Conceptual Model of the Human Genome</b> , Guest Lecturer for an 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 | <b>UML and OntoUML modeling languages and ontological unpacking applications to the genomics domain</b> , Guest Lecturer in Bachelor/Master courses of Engineering of Computing Systems (10 hours)                           | <i>Universitat Politècnica de València</i> |

## PHD CO-SUPERVISION

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|                     |   |                              |
|---------------------|---|------------------------------|
| Nov 2023 - Oct 2026 | <b>Francesco Cambria</b> , “Reactive Knowledge Management”  | <i>Politecnico di Milano</i> |
| Feb 2023 - Jan 2026 | <b>Francesco Invernici</b> , “Knowledge management techniques for exploring data corpora on biomedical research”  | <i>Politecnico di Milano</i> |
| Nov 2020 - Jan 2024 | <b>Tommaso Alfonsi</b> , “Methods and tools for data and knowledge management and integration for viral genomics” – Graduated <i>cum Laude</i> , April 19th, 2024 | <i>Politecnico di Milano</i> |
| Nov 2020 - Jan 2024 | <b>Ruba Al Khalaf</b> , “Developing knowledge structures for biological data modeling and analysis”   | <i>Politecnico di Milano</i> |

## MASTER THESIS CO-SUPERVISION

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|              |  |                              |
|--------------|--|------------------------------|
| 2024-present | <b>Emma Fanfoni</b> , Master thesis “Analysis of convergent evolution in SARS-CoV-2 impacting anti-viral therapies”  | <i>Politecnico di Milano</i> |
| 2024-present | <b>Amirhossein Samavi</b> , Master thesis “An interactive statistical testing dashboard for research topic modeling”   | <i>Politecnico di Milano</i> |
| 2024-present | <b>Francesca Curati</b> , Master thesis “Evaluating a visual framework for the exploration of scientific research topics and their trends”                     | <i>Politecnico di Milano</i> |
| 2024-present | <b>Laura Maftei</b> , Master thesis “A data-driven approach for storing and analyzing Causal Loop Diagrams”  | <i>Politecnico di Milano</i> |
| 2024-present | <b>Jelena Jakimov</b> , Master thesis “An architecture for extracting topics evolution in Sustainable Development Goals”                                       | <i>Politecnico di Milano</i> |
| 2024-present | <b>Ana Drmic</b> , Master thesis “FAIR (Findable Accessible Interoperable Reusable) assessment of biological and virological data sources”                     | <i>Politecnico di Milano</i> |
| 2024-present | <b>Luca Cassenti</b> , Master thesis “Warning system for viral genomic surveillance in public health contexts”   | <i>Politecnico di Milano</i> |
| 2022-2023    | <b>Alessia Gagliardi</b> , Master thesis “Simulation of COVID-19-related graph-based reactive knowledge bases”   | <i>Politecnico di Milano</i> |
| 2021-2022    | <b>Francesco Invernici</b> , Master thesis “Exploring and searching the COVID-19 big data corpus for supporting COVID-19 research”                             | <i>Politecnico di Milano</i> |
| 2021-2022    | <b>Luca Minotti</b> , Master thesis “Variant Hunter: a tool for fast detection emerging SARS-CoV-2 variants”   | <i>Politecnico di Milano</i> |
| 2020-2021    | <b>Federico Comolli</b> , Master thesis “Integration of genome-wide association studies into the GeCo repository”  | <i>Politecnico di Milano</i> |
| 2019-2020    | <b>Tommaso Alfonsi</b> , 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    | <b>Giuseppe Cannizzaro</b> , Master thesis “Automatic data integration for genomic metadata through sequence-to-sequence models”                               | <i>Politecnico di Milano</i> |
| 2018-2019    | <b>Andrea Colombo</b> , Master thesis “Ontology-driven metadata enrichment for genomic datasets”   | <i>Politecnico di Milano</i> |
| 2017-2018    | <b>Federico Gatti</b> , 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

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Giuseppe Serna (Post-Master proj. “CoVEffect: SARS-CoV-2 mutations’ effects extraction from literature”), Lorenzo Battiston (Bachelor proj. “Visualization of SARS-CoV-2 sequencing statistics over a world map”), Elisabetta Fedele (Bachelor proj. “Visualization techniques for SARS-CoV-2 data”), Silvia Ferraris (Bachelor proj. “Integration of ENCODE gene quantification data with GENCODE annotations”).

# Publications

## BIBLIOMETRICS

|  |    |
|--|----|
| Refereed international journals .....                                      | 32 |
| Editorial articles, Consortium papers, and National journal articles ..... | 4  |
| Refereed international conferences .....                                   | 23 |
| Refereed international workshops, posters, or national conferences .....   | 14 |
| Refereed international books and book chapters .....                       | 11 |

|                             | H-index | Publications | Citations | Co-authors |
|-----------------------------|---------|--------------|-----------|------------|
| Web of Science <sup>1</sup> | 11      | 43           | 759       | > 100      |
| Scopus <sup>2</sup>         | 14      | 75           | 934       | 3,730      |
| Google Scholar <sup>3</sup> | 16      | 76           | 1,491     | -          |

<sup>1</sup> <https://www.webofscience.com/wos/author/rid/AAF-2594-2019>, queried on 08/05/2024,

<sup>2</sup> <https://www.scopus.com/authid/detail.uri?authorId=57195587336>, queried on 08/05/2024,

<sup>3</sup> <https://scholar.google.com/citations?user=rCn19L4AAAAJ>, queried on 08/05/2024,

## INTERNATIONAL JOURNALS

Publications, where A.B. is the corresponding author, are marked with \* after her name.

- [J32] Invernici, F., **Bernasconi, A.\***, Ceri, S. Exploring the evolution of research topics during the COVID-19 pandemic. Accepted for publication in *Expert Systems with Applications [in press]*. <https://doi.org/10.48550/arXiv.2310.03928>.  
WoS JIF 2022: 8.5, WoS Rank: Q1, Scopus Citescore: 12.6, Scimago Rank: Q1
- [J31] Invernici, F., **Bernasconi, A.\***, Ceri, S. Searching COVID-19 clinical research using graphical abstracts. Accepted for publication in the *Journal of Medical Internet Research [in press]*. <http://dx.doi.org/10.2196/52655>.  
WoS JIF 2022: 7.4, WoS Rank: Q1, Scopus Citescore: 12.1, Scimago Rank: Q1
- [J30] Alfonsi, T., **Bernasconi, A.\***, Chiara, M., & Ceri, S. Data-driven recombination detection in viral genomes. (2024) *Nature Communications* 15, 3313. <https://doi.org/10.1038/s41467-024-47464-5>.  
WoS JIF 2022: 16.6, WoS Rank: Q1, Scopus Citescore: 24.9, Scimago Rank: Q1
- [J29] **Bernasconi, A.\***, Garcia S., A., Ceri, S., & Pastor, O. PoliViews: A comprehensive and modular approach to the conceptual modeling of genomic data. (2023) *Data & Knowledge Engineering*, 102201. <https://doi.org/10.1016/j.datak.2023.102201>. WoS JIF 2022: 2.5, WoS Rank: Q3, Scopus Citescore: 4.0, Scimago Rank: Q2
- [J28] Pinoli, P., Canakoglu, Ceri, S., Chiara, M., Ferrandi, E., Minotti, L., & **Bernasconi, A.\*** (2023) VariantHunter: a method and tool for fast detection of emerging SARS-CoV-2 variants. *Database*, 2023, baad044. <https://doi.org/10.1093/database/baad044>. WoS JIF 2022: 5.8, WoS Rank: Q1, Scopus Citescore: 8.1, Scimago Rank: Q1
- [J27] Garcia S., A., **Bernasconi, A.**, Guizzardi, G., Pastor, O., Storey, V.C. & Panach, I. (2023) Assessing the value of ontologically unpacking a conceptual model for human genomics. *Information Systems*, 118, 102242. <https://doi.org/10.1016/j.is.2023.102242>. WoS JIF 2022: 3.7, WoS Rank: Q2, Scopus Citescore: 7.9, Scimago Rank: Q1
- [J26] Serna Garcia, G., Al Khalaf, R., Invernici, F., Ceri, S., & **Bernasconi, A.\*** (2023). CoVEffect: Interactive Deep Learning-based SARS-CoV-2 Mutations and Variants Effect Extraction. *GigaScience*, 12, giad036. <https://doi.org/10.1093/gigascience/giad036>. WoS JIF 2022: 9.2, WoS Rank: Q1, Scopus Citescore: 13.7, Scimago Rank: Q1
- [J25] Giacomelli, A., Righini, E., Micheli, V., Pinoli, P., **Bernasconi, A.**, Rizzo, A., Oreni, L., Ridolfo, A.L., Antinori, S., Ceri, S., & Rizzardini, G. (2023). SARS-CoV-2 viremia and COVID-19 mortality: an observational study. *PLOS ONE*, 18(4), e0281052. <https://doi.org/10.1371/journal.pone.0281052>. WoS JIF 2022: 3.7, WoS Rank: Q2, Scopus Citescore: 6.0  
Scimago Rank: Q1
- [J24] **Bernasconi, A.\***, Canakoglu, A., & Comolli, F. (2023). Processing Genome-Wide Association Studies within a repository of heterogeneous genomic datasets. *BMC Genomic Data*, 24, 13. <https://doi.org/10.1186/s12863-023-01111-y>.  
WoS JIF 2022: 1.9, WoS Rank: Q4, Scopus Citescore: 5.3, Scimago Rank: Q3
- [J23] **Bernasconi, A.\***, Guizzardi, G., Pastor, O., & Storey, V.C. (2022). Semantic interoperability: ontological unpacking of a viral conceptual model. *BMC Bioinformatics*, 23(Suppl 11), 491. <https://doi.org/10.1186/s12859-022-05022-0>.  
WoS JIF 2022: 3.0, WoS Rank: Q2, Scopus Citescore: 6.2, Scimago Rank: Q1
- [J22] Alfonsi, T., **Bernasconi, A.**, Canakoglu, A., & Masseroli, M. (2022). Genomic data integration and user-defined sample-set extraction for population variant analysis. *BMC Bioinformatics*, 23, 401. <https://doi.org/10.1186/s12859-022-04927-0>. WoS JIF 2022: 3.0, WoS Rank: Q2, Scopus Citescore: 6.2, Scimago Rank: Q1
- [J21] Al Khalaf, R., **Bernasconi, A.\***, Pinoli, P., Ceri, S. (2022). Analysis of co-occurring and mutually exclusive amino acid changes and detection of convergent and divergent evolution events in SARS-CoV-2. *Computa-*

tional and Structural Biotechnology Journal, 20, 4238-4250. <https://doi.org/10.1016/j.csbj.2022.07.051>.  
WoS JIF 2022: 6.0, WoS Rank: Q1, Scopus Citescore: 7.8, Scimago Rank: Q1

- [J20] Grandi, S., & **Bernasconi, A.** (2020) Risk perception, spatial data, legal response during COVID-19 pandemic: a conceptual model. *GeoProgress Journal*, 7(2), 2020, Geoprogess Editions ISSN 2384-9398. <https://www.geoprogess-edition.eu/geoprogess-journal-vol-7-issue-2-2020-2/>.
- [J19] Serna Garcia, 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>.  
WoS JIF 2022: 5.8, WoS Rank: Q1, Scopus Citescore: 8.1, Scimago Rank: 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>.  
WoS JIF 2022: 9.8, WoS Rank: Q1, Scopus Citescore: 11.2, Scimago Rank: 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>.  
WoS JIF 2022: 5.8, WoS Rank: Q1, Scopus Citescore: 12.2, Scimago Rank: Q1
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WoS JIF 2022: 5.8, WoS Rank: Q1, Scopus Citescore: 8.1, Scimago Rank: 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>.  
WoS JIF 2022: 1.0, WoS Rank: Q4, Scopus Citescore: 3.0, Scimago Rank: Q2
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- [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>.  
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WoS JIF 2022: 2.7, WoS Rank: Q2, Scopus Citescore: 4.5, Scimago Rank: 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*

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- [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>.  
WoS JIF 2022: 5.8, WoS Rank: Q1, Scopus Citeseore: 8.1, Scimago Rank: Q1
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WoS JIF 2022: 5.8, WoS Rank: Q1, Scopus Citeseore: 12.2, Scimago Rank: Q1

## EDITORIAL ARTICLES, CONSORTIUM PUBLICATIONS, AND NATIONAL JOURNAL ARTICLES

- [Ed1] Heron, E. A., Valle, G., & **Bernasconi, A.** (2023). Identification of phenotypically important genomic variants. Frontiers in Bioinformatics, 3. <https://doi.org/10.3389/fbinf.2023.1328945>
- [Co2] COVID-19 Host Genetics Initiative (2021). Mapping the human genetic architecture of COVID-19. Nature 600, 472–477 (2021). <https://doi.org/10.1038/s41586-021-03767-x> [**Bernasconi, A.** was part of the “Project management group (Data dictionary)”). IF 2022: 64.8, WoS Rank: Q1, Scopus Citeseore: 83.4, Scimago Rank: Q1
- [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)”). WoS JIF 2022: 3.7, WoS Rank: Q2, Scopus Citeseore: 6.0, Scimago Rank: Q1
- [N1] Grandi, S., & **Bernasconi, A.** (2020). Convergenza di Web Design e Informazione Spaziale, Statistica, Genomica ed Epidemiologica: il Caso delle Geo-Gashboard nella Crisi COVID-19. Documenti geografici, (1), 463-476. [https://doi.org/10.19246/D0CUGED02281-7549/202001\\_29](https://doi.org/10.19246/D0CUGED02281-7549/202001_29) WoS JIF 2022: 0.2, Scopus Citeseore: 0.6, Scimago Rank: Q2/Q4

## CONFERENCE PROCEEDINGS

- [C23] Bellomarini, L., **Bernasconi, A.**, Ceri, S., Gagliardi, A., Magnanimi, D., Martinenghi, D. Towards a Standard for Triggers in Property Graphs. Accepted for publication in the SEBD 2024 conference.
- [C22] Bertetto, L., Bettinelli, F., Buda, A., Da Mommio, M., Di Bari, S., Savelli, C., Baralis, E., **Bernasconi, A.**, Cagliero, L., Ceri, S., Pierri, F. Towards an explorable conceptual map of Large Language Models. Accepted for publication in the Forum of the CAiSE 2024 conference. *[in press]*
- [C21] Ceri, S., **Bernasconi, A.**, Gagliardi, A. Reactive Knowledge Management. Accepted for publication in ICDE 2024, Future Technologies Special Session. *[in press]*
- [C20] Ceri, S., **Bernasconi, A.**, Gagliardi, A., Martinenghi, D., Bellomarini, L., & Magnanimi, D. PG-Triggers: Triggers for Property Graphs. Accepted for publication in SIGMOD 2024, industrial track. *[in press]* <https://doi.org/10.48550/arXiv.2307.07354>
- [C19] Al Khalaf, R., **Bernasconi, A.**, & García S., A. (2023, November). OntoEffect: an OntoUML-based ontology to explain SARS-CoV-2 variants' effects. In Proceedings of the 15th International Joint Conference on Knowledge Discovery, Knowledge Engineering and Knowledge Management (IC3K 2023) – Vol 2, KEOD (pp. 62-72). SciTePress. <https://doi.org/10.5220/0012183900003598>
- [C18] Costa, M., García S., A., León, A., **Bernasconi, A.**, & Pastor, O. (2023, November). A Reference Meta-Model to Understand DNA Variant Interpretation Guidelines. In International Conference on Conceptual Modeling (pp.375-393). Springer, Cham. [https://doi.org/10.1007/978-3-031-47262-6\\_20](https://doi.org/10.1007/978-3-031-47262-6_20)
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- [C15] Alfonsi, T., Bellomarini, L., **Bernasconi, A.**, & Ceri, S. Expressing Biological Problems with Logical Reasoning Languages. Proceedings of the 6th International Joint Conference on Rules and Reasoning (RuleML+RR 2022) – 16th International Rule Challenge. (Vol. 3229). CEUR-WS
- [C14] **Bernasconi, A.**, García S., A., Ceri, S., & Pastor, O. (2022, October). A comprehensive approach for the conceptual modeling of genomic data. In International Conference on Conceptual Modeling (pp. 194-208). Springer, Cham. [https://doi.org/10.1007/978-3-031-17995-2\\_14](https://doi.org/10.1007/978-3-031-17995-2_14). **Runner Up Paper Award, ER 2022**

- [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>
- [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](https://doi.org/10.1007/978-3-031-07481-3_4)
- [C11] Grandi, S., & **Bernasconi, A.** (2021, December). Geo-online explanatory data visualization tools as crisis management and communication instruments. In Proceedings of the International Cartographic Association, 4, 41, 2021. <https://doi.org/10.5194/ica-proc-4-41-2021>
- [C10] Guizzardi, G., **Bernasconi, A.**, Pastor, O., & Storey, V. C. (2021, October). Ontological Unpacking as Explanation: The Case of the Viral Conceptual Model. In International Conference on Conceptual Modeling (pp. 356-366). Springer, Cham. [https://doi.org/10.1007/978-3-030-89022-3\\_28](https://doi.org/10.1007/978-3-030-89022-3_28)
- [C9] Al Khalaf R., Alfonsi T., Ceri S., & **Bernasconi A.** (2021, May). CoV2K: a Knowledge Base of SARS-CoV-2 Variant Impacts. In International Conference on Research Challenges in Information Science (pp. 274-282). Springer, Cham. [https://doi.org/10.1007/978-3-030-75018-3\\_18](https://doi.org/10.1007/978-3-030-75018-3_18)
- [C8] **Bernasconi, A.**, Canakoglu, A., Pinoli, P., & Ceri, S. (2020, November). Empowering Virus Sequence Research Through Conceptual Modeling. In International Conference on Conceptual Modeling (pp. 388-402). Springer, Cham. [https://doi.org/10.1007/978-3-030-62522-1\\_29](https://doi.org/10.1007/978-3-030-62522-1_29)
- [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](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](https://doi.org/10.1007/978-3-030-45234-6_3)
- [C5] **Bernasconi, A.**, Canakoglu, A., & Ceri, S. (2019, November). From a conceptual model to a knowledge graph for genomic datasets. In International Conference on Conceptual Modeling (pp. 352-360). Springer, Cham. [https://doi.org/10.1007/978-3-030-33223-5\\_29](https://doi.org/10.1007/978-3-030-33223-5_29)
- [C4] **Bernasconi, A.**, Canakoglu, A., Colombo, A., & Ceri, S. (2018, December). Ontology-driven metadata enrichment for genomic datasets. In 11th International Conference Semantic Web Applications and Tools for Life Sciences, SWAT4LS 2018 (Vol. 2275). CEUR-WS.
- [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](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](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](https://doi.org/10.1007/978-3-319-96553-6_4)

## WORKSHOP PAPERS, POSTERS, AND ABSTRACTS

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- [W14] Invernici, F., **Bernasconi, A.**, Ceri, S. TETYS: towards the next-generation open-source Web topic explorer. Accepted for publication in CAiSE 2024, Research Projects Exhibition. *[in press]*
- [W13] **Bernasconi, A.**, Chiara, M., Alfonsi, T., Ceri, S. SENSIBLE: implementing data-driven early warning systems for future viral epidemics. Accepted for publication in CAiSE 2024, Research Projects Exhibition. *[in press]*
- [W12] **Bernasconi, A.**, Cappiello, C., Ceri, S., & Pinoli, P. Achieving data FAIRification in a distributed analytics research platform for rare diseases. In 15th International Conference Semantic Web Applications and Tools for Life Sciences, SWAT4HCLS 2024. <https://doi.org/10.4126/FRL01-006473178>
- [W11] **Bernasconi, A.** (Sept, 2022). A Sound and Repeatable Approach to Building Integrated Repositories of Genomic Data. In Proceedings of the 1st Italian Conference on Big Data and Data Science (ITADATA 2022). Milan, Italy, September 20-21, 2022. Vol. 3340, pp. 212-213. CEUR-WS.
- [W10] Giacomelli, A., Righini, E., Micheli, V., Pinoli, P., **Bernasconi, A.**, Rizzo, A., Oreni, L., Ridolfo, A.L., Antinori, S., Ceri, S., & Rizzardini, G. SARS-CoV-2 viremia e mortalità in pazienti ospedalizzati per COVID-19: studio osservazionale prospettico. XXI National Congress SIMIT (Società Italiana Malattie Infettive e Tropicali)



- [W9] Garcia S., A., **Bernasconi, A.**, Guizzardi, G., Pastor, O., Storey, V.C., & Mireia Costa. (2022, October). An Initial Empirical Assessment of an Ontological Model of the Human Genome. In: Guizzardi, R., Neumayr, B. (eds) *Advances in Conceptual Modeling*. ER 2022. Lecture Notes in Computer Science, vol 13650. Springer, Cham.
- [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.
- [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](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).

## BOOKS AND CHAPTERS

- [B11] **Bernasconi, A.** Model, Integrate, Search... Repeat: A Sound Approach to Building Integrated Repositories of Genomic Data. LNBIP Vol. 496. Springer Nature, 2022. <https://doi.org/10.1007/978-3-031-44907-9>
- [B10] **Bernasconi, A.**, & García S. Conceptual Modeling for Bioinformatics. In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology, 2nd Edition. <https://doi.org/10.1016/B978-0-323-95502-7.00003-8>
- [B9] **Bernasconi, A.** Data-driven methods for viral variants' identification. In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology, 2nd Edition. *[To be published in 2024]*
- [B8] Al Khalaf, R. & **Bernasconi, A.** Transformer-based biomedical text extraction. In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology, 2nd Edition. *[To be published in 2024]*
- [B7] Al Khalaf, R., **Bernasconi, A.**, & Masseroli, M. Biological and Medical Ontologies: Disease Ontology (DO). In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology, 2nd Edition. <https://doi.org/10.1016/B978-0-323-95502-7.00038-5>
- [B6] Al Khalaf, R., **Bernasconi, A.**, & Masseroli, M. Biological and Medical Ontologies: Human Phenotype Ontology (PO). In Reference Module in Life Sciences, Encyclopedia of Bioinformatics and Computational Biology, 2nd Edition. *[To be published in 2024]*
- [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](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](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

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[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 – Discussion forum for analysis of virus genomes (2.2k views)

[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 – Discussion forum for analysis of virus genomes (19.1k views, 8 citations on Google Scholar)

**UNDER REVIEW** \_\_\_\_\_ Manuscripts submitted to Conferences with -C, to Journals are indicated with -J (for these, when A.B. is the corresponding author, \* is used after her name).

[U1-J] Al Khalaf, R., **Bernasconi, A.\***, Pinoli, P. Impact of Omicron subvariants' mutations on B cell and T cell epitopes: A systematic data analysis. Submitted to Plos ONE.

[U2-C] Magnanimi, D., Bellomarini, L., **Bernasconi, A.**, Ceri, S., Martinenghi, D. Enabling light-weight reasoning using Neo4j triggers. Submitted to the Industrial Track of the VLDB 2024 conference.

[U3-J] Costa, M., García S., A., Leon, A., **Bernasconi, A.**, Pastor, O. Metamodel for Variant Guidelines Explanation Submitted to Data & Knowledge Engineering.

## Skills & Background Knowledge

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### LANGUAGE SKILLS

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**Italian:** Native speaker

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

**Spanish:** Advanced user (C1)

### PROGRAMMING SKILLS

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

**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

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February 2011. Clarinet conservatory diploma. Conservatorio di Musica “Giovanni Battista Martini”, Bologna, Italy. This is equivalent to a second-level degree in LM 45 (Musicologia e beni musicali).

## Autorizzazioni

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Autorizzo al trattamento dati ai sensi del GDPR 2016/679 del 27 aprile 2016 (Regolamento Europeo relativo alla protezione delle persone fisiche per quanto riguarda il trattamento dei dati personali).

Autorizzo la pubblicazione del Curriculum Vitae sul sito istituzionale del Politecnico di Milano (sez. Amministrazione Trasparente) in ottemperanza al D. Lgs n. 33 del 14 marzo 2013 (e s.m.i.).