Gherard Batisti Biffignandi

Professional experience

2025 (April)	**Independent Researcher, Department of Biology and Biotechnology "L. Spallanzani", University of Pavia** Application of machine learning methods to bacterial and fungal genomics
2024-March 2025	**Postdoctoral Research Associate, Department of Genetics, University of Cambridge, UK / Pathogen informatics and modelling Group, European Bioinformatic Institute (EMBL-EBI), Hinxton** Development of evolutionary model to track the transmissible antimicrobial resistance in bacterial populations
2023	**Postdoctoral Research Associate, Department of Biology and Biotechnology "L. Spallanzani", University of Pavia** Omic and bioinformatic approaches to study arthropod vectors: characterization of ticks and associated microorganisms
2021-2022	**Visiting Fellow,-Bacterial Evolutionary Epidemiology Group, Imperial College, London -Pathogen informatics and modelling Group, European Bioinformatic Institute (EMBL-EBI), Hinxton** GWAS simulations and optimization of machine learning methods to predict Minimum Inhibitory Concentration in *Klebsiella pneumoniae*
2019-2023	**Ph.D in Genetics, Molecular and Cellular Biology, University of Pavia** My research activity was focused on the genomic epidemiology and evolution of nosocomial pathogens, specifically MDR bacteria. In parallel, I worked on software development for the epidemiological investigation and machine learning models to predict antibiotic resistance starting from genomic markers
2018-2019	**Granted Research Fellow, Department of Biology and Biotechnology "L. Spallanzani", University of Pavia** Antigen discovery through bioinformatic analyses applied to the development of novel techniques for Cystic Echinococcosis diagnosis

Education

2019-2023	**PhD in Genetics, Molecular and Cellular Biology, University of Pavia**
2016-2018	**M.Sc. in Medical and Pharmaceutical Biotechnology, University of Pavia** Thesis - “Oxford VS Pasteur: bioinformatic comparative analyses aimed at the evaluation of MLST schemes in the bacterium *Acinetobacter baumannii*”
2008-2016	**B.Sc. in Biological Sciences, University of Pavia** Thesis: “Inactivation of an operon coding for an efflux pump RND16 in *Burkholderia cenocepacia”*

Software skills and expertise

Programming languages: Python, R, Bash, Stan (basics), Latex (Basics) | **Operating System**: Linux, Windows

Bioinformatics:

- Pan-genome investigation, phylodynamics, outbreak reconstruction, GWAS, RNA-seq analysis, molecular clock, deep sequencing analysis, selective pressures, gene calling, local alignment, short and long read genome assembly, reads mapping, localization of secretion systems in eukaryotes and prokaryotes, antigen discovery,
- Statistical and Machine Learning models, including supervised (e.g. Random Forest, Regularized Regressions, XDG-Boosting) and unsupervised (e.g. UMAP, DBSCAN)
- Development of bioinformatic pipelines

Principal softwares: PopPUNK, FastBAPS, BLAST, Bowtie, GBlocks, HyPhy, BEAST, Kleborate, Mash, MMseqs, Muscle, Orthofinder, Pangolin, Prodigal, Samtools, Spades, RAxML, Tempest, Unicycler

Github: https://github.com/gbatbiff

Computing: HPC, git, server management and configuration**,** Nextflow (basics)

Languages

Italian: native speaker ; **English**: fluent

Selected publications

- **Batisti Biffignandi G**, Chindelevitch L, Corbella M, [...], Lees JA. (2024) Optimising machine learning prediction of minimum inhibitory concentrations in *Klebsiella pneumoniae*. Microb Genom. Mar;10(3):001222

- **Batisti Biffignandi, G.**, Bellinzona, G., Petazzoni, G., [...], Comandatore, F. & Gaiarsa, S. (2023). P-DOR, an easy-to-use pipeline to reconstruct bacterial outbreaks using genomics. *Bioinformatics* , *39*(9).

- **Batisti Biffignandi, G**, Vola A., Sassera D., [...], Linda Petrone L. and Tamarozzi F. (2023). “Antigen Discovery by Bioinformatics Analysis and Peptide Microarray for the Diagnosis of Cystic Echinococcosis.” *PLoS Neglected Tropical Diseases* 17 (4): e0011210.

- Postiglione, U.*, **Batisti Biffignandi, G.***, Corbella, M., [...], Brilli M. & Sassera, D. (2023). Combining Genome Surveillance and Metadata To Characterize the Diversity of Staphylococcus aureus Circulating in an Italian Hospital over a 9-Year Period. *Microbiology Spectrum*, *11*(4), e0101023.

- Gaiarsa, S.*, Giardina, F.*, **Batisti Biffignandi, G.***, [...], Baldanti, F. (2022). Comparative analysis of SARS-CoV-2 quasispecies in the upper and lower respiratory tract shows an ongoing evolution in the spike cleavage site. *Virus Research*, *315*, 198786.

- Perini, M., **Batisti Biffignandi G**, Di Carlo D, [...], Comandatore F. (2021). MeltingPlot, a user-friendly online tool for epidemiological investigation using High Resolution Melting data. BMC Bioinformatics 22, 76

- Gaiarsa, S., **Batisti Biffignandi, G.**, Esposito, E. P., [...], Sassera, D., & Zarrilli, R. (2019). Comparative Analysis of the Two *Acinetobacter baumannii* Multilocus Sequence Typing (MLST) Schemes. *Frontiers in microbiology*, *10*, 930.

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Google scholar: https://scholar.google.com/citations?user=ssTueUcAAAAJ&hl=it

Tutoring and co-supervising

2020/2021	Tutor in Bioinformatic course, MSc in Molecular Biology and Genetics, University of Pavia
2021/2022	Tutor in Bioinformatic course, MSc in Molecular Biology and Genetics, University of Pavia
2023/2024	Tutor in Genomics and Evolution in Emerging Infectious Diseases, University of Pavia
2019-2023	Co-supervisor of 2 BSc and 2 MSc students

Peer review

Reviewer: Microbial genomics and Bioinformatics Journal

Additional information

- Co-author of 11 Conference Abstracts and Poster Presentations

- Member of ESGEM-AMR Consortium Escherichia coli/Shigella spp., and KlebNET-GSP Geno-Pheno group