Matteo Bolner

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EDUCATION AND WORK EXPERIENCE

- **Post-Doc - Animal and food genomics group, University of Bologna**
  Projects on animal genomics and metabolomics *Nov 2024 - Present*
- **PhD student - Applied genomics for sustainable animal production systems**
  Projects ranging from genomics to metabolomics in various livestock species *Nov. 2021 – Nov 2024*
- **Visiting student - INIA-CSIC Madrid, Department of Animal Breeding**
  RNA-seq and metabolomics analyses for nutrigenomics *Feb. 2024 – June 2024*
- **Internship - Software containerization for HPC systems**
  CINECA - SuperComputing Applications and Innovation department (SCAI), Bologna *May 2021 – Nov. 2021*
- **Master's degree in Bioinformatics - 110/110 cum Laude**
  International Bologna master in Bioinformatics - University of Bologna, Italy *Oct. 2018 – Mar. 2021*
- **Bachelor's degree in Biological Sciences - 107/110**
  University of Bologna, Italy *Sep. 2015 – Jul. 2018*

PUBLICATIONS

- Bovo S.; Ribani A.; Fanelli F.; Galimberti G.; Martelli P.L.; Trevisi P.; Bertolini F.; Bolner M.; Casadio R.; Dall'Olio S.; Gallo M.; Luise D.; Mazzoni G.; Schiavo G.; Taurisano V.; Zambonelli P.; Bosi P.; Pagotto U.; Fontanesi L. *Merging metabolomics and genomics provides a catalog of genetic factors that influence molecular phenotypes in pigs linking relevant metabolic pathways*, ≪Genetics Selection Evolution≫, 57, 11, (2025)
- Bovo S.; Bolner M.; Schiavo G.; Bertolini F.; Dall'Olio S.; Ribani A.; Zambonelli P.; Gallo M.; Fontanesi L. *High-throughput untargeted metabolomics reveals metabolites and metabolic pathways that differentiate two divergent pig breeds*, ≪Animal≫, 19, 1 (2025)
- Bolner M.; Bovo S.; Ballan M.; Schiavo G.; Taurisano V.; Ribani A.; Bertolini F.; Fontanesi L. *A comprehensive atlas of nuclear sequences of mitochondrial origin (NUMT) inserted into the pig genome*, ≪Genetics Selection Evolution≫, 56, 64 (2024)
- Bolner M.; Bertolini F.; Bovo S.; Schiavo G.; Fontanesi L.*Investigation of ABO Gene Variants across More Than 60 Pig Breeds and Populations and Other Suidae Species Using Whole-Genome Sequencing Datasets*, ≪ANIMALS≫, 2024, 14, Article number: 5, pp. 1 - 19
- Bovo S.; Schiavo G.; Bolner M.; Ballan M.; Fontanesi L. *Mining livestock genome datasets for an unconventional characterization of animal DNA viromes*, ≪Genomics≫, 2022, Vol. 114, Issue 2
- Bovo S.; Ribani A.; Utzeri V.J.; Taurisano V.; Schiavo G.; Bolner M.; Fontanesi L., *Application of next generation semiconductor-based sequencing for the identification of apis mellifera complementary sex determiner (Csd) alleles from honey dna*, ≪INSECTS≫, 2021, 12, pp. 1 - 15

CONGRESS PROCEEDINGS AND AWARDS

- Scholarship winner for the 75th EEAP congress with *"Molecular phenotyping through metabolomic analyses in pig breeds"* (Florence; Italy; 2024)
- Scholarship winner for the WCGALP congress with *"A comprehensive overview of mitochondrial DNA insertions in the nuclear genome of the pig."* (Rotterdam; Netherlands; 2022)

- Bolner M.; Bovo S.; Schiavo G.; Bertolini F.; Ballan M.; Fontanesi L. *Dissecting the genetic variability of major genes for pig production traits using whole genome sequencing data.* 25th ASPA Congress (Bari; Italy; 2023)
- Schiavo G.; Bovo S.; Bertolini F.; Bolner M.; Ribani A.; Taurisano V.; Dall'Olio S.; Bonacini M.; Fontanesi L. *Reconstructing pedigree information in the Reggiana cattle breed based on high density SNP data.* 25th ASPA Congress (Bari; Italy; 2023)
- Ballan M.; Bovo S.; Schiavo G.; Bolner M.; Bertolini F.; Cappelloni M.; Tinarelli S.; Gallo M.; Fontanesi L. *Mining high density SNP chip data and whole genome sequencing information to identify putative unfavorable alleles in pig breeds.* 25th ASPA Congress (Bari; Italy; 2023)
- Ballan M.; Bovo S.; Schiavo G.; Bertolini F.; Bolner M.; Cappelloni M.; Tinarelli S.; Gallo M.; Fontanesi L. *A comparative genome analysis across pig breeds can help to identify putative deleterious alleles.* European Federation of Animal Science Congress (Lyon, France, 2023)
- Taurisano V.; Ribani A.; Bolner M.; Ballan M.; Bovo S.; Schiavo G.; Fontanesi L. *Variability of NUMT regions in the genome of autochthonous and cosmopolitan pig breeds.* International Symposium on the Mediterranean Pig (Vodice, Croatia, 2022)
- Bolner M.; Ballan M; Bovo, S; Schiavo G; Fontanesi L. *A comprehensive overview of mitochondrial DNA insertions in the nuclear genome of the pig.* World Congress on Genetics Applied to Livestock Production (Rotterdam, Netherlands, 2022)
- Bovo S.; Schiavo G.; Ballan M.; Bolner M.; Fontanesi L. *Mining livestock genomes for a One Health perspective in the management of animal genetic resources.* 24th ASPA Congress (Padova, Italy, 2021)

Skills - Bioinformatics

- **Genomics**: Mining of genomics data, genome alignment, variant calling, and annotation. Practical and theoretical knowledge of the most widely used algorithms
- **Databases**: Programmatic mining and interpretation of metadata and data deposited on bioinformatics databases (ENA, SRA, UNIPROT, PDB, GWAS Catalog)
- **Metabolomics**: Analysis of metabolomic data, from missing data imputation methods to ML algorithms for the identification of discriminating metabolites
- **Machine learning**: Training, usage, feature selection and interpretation of results for widely used ML algorithms applied to bioinformatics such as Support Vector Machines, Random Forests, Boruta, etc)
- **Structural bioinformatics**: Analysis, prediction, modeling and functional annotation of protein structures - Building by homology, Hidden Markov Models, Support Vector Machines
- **Wet lab work**: Bacterial cultures, PCR, primer building, electrophoresis

Skills - Programming

- **Programming languages**: Python, R, Bash, currently learning Rust
- **Programming practices**: Version control, working knowledge of unit/integration testing and python package development
- **Working environments**: AWS, Docker, Singularity, HPC systems
- **Workflow management**: Proficient use of Snakemake for building reproducible and scalable pipelines

Languages

- **Italian**: Mothertongue
- **English**: C1 level (Cambridge ESOL certificate)
- **German**: B1 level (Goethe institut certificate)

GitHub portfolio

- **metabotk**: Metabolomics ToolKit - A Python package for reading, preprocessing and analysis of metabolomics data, with CLI and importable libraries
- **ENA-Tools**: Functions for querying the ENA API to obtain metadata, integrate the information with different databases such as Biosamples and ENA XREF, and download sample data.
- **genomers**: Rust package for downloading genome assembly sequences and metadata from NCBI
- **pySERRF**: Python conversion of the R code for the Systematic Error Removal with Random Forests package used for high dimensional metabolomics data normalization
- **NCBI-Assembly**: Snakemake pipeline for automatic download of assembled genomes from NCBI and all-to-all alignment with different algorithms for comparative genomics analyses
- **comprehensive-atlas-of-numts-pig**: Snakemake pipeline for the discovery and analisis of NUMTs in Suinae species, described in the paper ”A comprehensive atlas of nuclear sequences of mitochondrial origin (NUMTs) inserted into the pig genome”

Courses

- **20th Bologna Winter School - Data Science for Bioinformatics**
- **Exact string matching in bioinformatics and NGS analysis** One week course from Prof. Anders Krogh - Bioinformatics Center - University of Copenhagen
- **RNA Analysis** One week course from Prof. Cedric Notredame - Centro de Regulacio Genomica (CRG) - Barcelona
- **Protein-protein interaction and docking** One week course from Prof. Allegra Via
- **Protein-Protein Interactions** Course from the groups ”Proteins” and ”Computational and Systems Biology” of the Italian Biochemistry and Molecular Biology Society

University projects

- **Curation and mining of public datasets of Whole Genome Sequencing for applications in livestock genomics** Master’s thesis
- **Identification of a DNA methylation signature in blood cells from patients with Down Syndrome** Project developed for the ”Practical application of data mining in R environment” module of the ”DNA / RNA dynamics” course.
- **Predicting secondary structure of proteins: a comparison between GOR method and Support Vector Machines** Project developed for the ”Laboratory of Bioinformatics 2” course.
- **MNIST Handwriting classifier** Project developed for the ”Applied Machine Learning” course.
- **A hidden Markov model for the functional annotation of kunitz-type domains** Project developed for the ”Laboratory of Bioinformatics 1” course.
- **3D modelling and functional annotation of proteins** Project developed for the ”Laboratory of Bioinformatics 1” course.