Nelson Nazzicari (PhD)
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Scientific career

- Scientist, then senior scientist, CREA (Italy), 2014 - present
- Research scholar, bioinformatician, PTP Science Park (Italy), 2013-2015
- Adjunct Professor, University of Mantua (Italy), 2012
- Research Scholar, George Mason University (USA), Center for Secure Information Systems, 2009-2011
- Ph.D. (Informatics and Electrics Engineering), University of Pavia (Italy), 2008
- M. Sc (Informatics Engineering), cum Laude. University of Pavia (Italy), 2005
- B. Sc. (Informatics Engineering), cum Laude. University of Pavia (Italy), 2003

Teaching Experience

- “Deep Learning for biologists”, Physalia-courses, Berlin, since 2020 (six editions as of May 2026)
- “Introduction to the analysis of longitudinal data in biology using R”, Physalia-courses, Berlin, year 2024
- “Data Visualization in Python”, Physalia-courses, Berlin, year 2021 and 2022
- “Introduction to C programming”, Adjunct professor, University of Mantua, Spring 2012
- “Introduction to Informatics ”, University of Pavia, set of seminars, Fall 2007
- “Introduction to object oriented programming”, University of Pavia, Laboratory teacher, Fall 2006
- “Introduction to computer programming”, Laboratory teacher, University of Pavia, Fall 2005

Fellowships and academic merits

- Member of the Scientific committee of the International Legume Society (www.legumesociety.org)
- Organizer and host of the ILS webinar series (31 episodes as of May 2026)
- Affiliated to Centre of Excellence for Biodiversity and Molecular Plant Breeding, Zagabria, Croatia
- Affiliated to the Netherlands Plant Eco-phenotyping Centre (NPEC), University of Wageningen, the Netherlands
- Rotary International ambassadorial scholarship, year 2009-2010
- Innovate Italy – Altera Design Contest, 2009, third place
- Innovate Italy – Altera Design Contest, 2008, second place

Other Education

- 2013: Gene2Farm Winter School
- 2013: 7.00x: Introduction to Biology - The Secret of Life [EDX platform]
- 2013: Innovagen Winter School II
- 2008: CILEA, specialization course on Parallel and Distributed Computation
- 2005, 2006: ACACES International Summer School on Advanced Computer Architecture and Compilation for Embedded Systems

Scientific publications

- 50+ papers in peer reviewed journals, mainly first quartile for the appropriate category (list at https://scholar.google.it/citations?hl=en&user=i2dlVhgAAAAJ)
- h-index: 23 (Google Scholar, checked on May 2026)
- co-author of the book: "*Deep Learning for Life Sciences: with Python Notebooks for Examples and Exercises", Filippo Biscarini and Nelson Nazzicari*. Springer Nature, 2026.
- 11 contributed chapters in Scientific Volumes
- 30+ international conference abstracts, papers, posters

Research Projects and Tasks

- AGER project "LEGACY – LEgume Genetic Adaptation for Community-based Yields" (2026-2029): head of CREA team, bioinformatics analysis (genomic selection, selection signatures, association studies)
- Horizon project "Breeding European Legumes for Increased Sustainability – BELIS" (https://www.belisproject.eu/): role as head of CREA team, bioinformatics analysis, coordination of soybean genotyping. Project approved on March 2024, ongoing.
- European Regional Development Fund (ERDF)2021-2027: "Studio e sviluppo di una piattaforma tecnologica agrorobotica evoluta per l'automazione delle coltivazioni agricole per una elevata efficienza e sostenibilità ambientale – ROBOVEG" (2026-2030): role as head of computer vision development
- PRIN "Expanding the toolbox for cereal breeding: high-throughput genomics, 2D-3D phenomics and artificial intelligence for breeding with increasing genome complexity, from barley to durum and bread wheat - POLYPLOIDBREEDING (2024-2026)" (https://polyploidbreeding.ibba.cnr.it): head of CREA-ZA team, analysis of drone imagery
- Horizon project "Innovations in plant variety testing in Europe to foster the introduction of new varieties better adapted to varying biotic and abiotic conditions and to more sustainable crop management practices – INVITE" (2019-2024): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS)
- Horizon project "Redesigning European cropping systems based on species mixtures – REMIX" (2017-2021): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS)
- Horizon project "Improving the performance of organic agriculture by boosting organic seed and plant breeding efforts across Europe – LIVESEED" (2017-2021): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS)
- FP7 project "Legumes for the agriculture of tomorrow – LEGATO" (2013-2017): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS)
- FP7-EraNet project "Resilient, water- and energy-efficient forage and feed crops for Mediterranean agricultural systems – REFORMA" (2012-2016): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS)
- FP7-Core Organic project "Coordinating organic plant breeding activities for diversity – COBRA" (2013-2016): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS)
- Bilateral Italy - USA ("di grande rilevanza" MAE) "Genomic selection in alfalfa – GENALFA" (2014-2015): bioinformatics analysis of molecular data aimed to Genomic Selection and Genome Wide Association Studies (GWAS) in alfalfa
- RGV – Trattato FAO (D.M. 3825 18/02/2014): assessment of Cultivar Distinctness in alfalfa

Other Research Projects – focus on data science and engineering

- **DRONE2REPORT**: a CLI tool to analyze orthomosaics and extract summary statistics, vegetation indexes, subimages. Python based, https://github.com/ne1s0n/drone2report
- **GROAN:** Workbench for testing genomic regression accuracy on (optionally noisy) phenotypes – R package https://cran.r-project.org/package=GROAN
- **Foetal heartbeat isolation**: realization of a wearable device able to sense and separate maternal ECG from foetal ECG under real time constraints (part of Telefetalcare project).
- **Plasmonic resonance on-field analysis**: realization of a portable tool capable to perform angle resolved reflectance and transmittance measurements under low-power constraints. In collaboration with the physics department, the devices employs a patented solution.
- **MINESTRONE** (role: GMU team leader): in collaboration with Columbia University, Stanford University and Symantec, project funded by United States Air Force Research Laboratory (AFRL). MINESTRONE is a novel architecture integrating static analysis, dynamic confinement, and code diversification techniques to enable the identification, mitigation and containment of a large class of software vulnerabilities.
- **CyNomiX** (role: Virtualization team leader): in collaboration with Invincea, project funded under the DARPA Cyber Genome Program. CyNomiX is a scalable, scientifically rigorous methodology for analyzing, understanding, and ultimately detecting new malware.
- **GO**: data store and management software for structural analysis data, as part of the “Risk Mitigation for Earthquakes and Landslides – LESSLOSS” project, funded by the European Commission, Directorate General of Research under the Contract No. GOCE-CT-2003-505448.
- **Switchwall**: non-SNMP autonomous tool able to leverage a single vantage point to monitor the network topology and activate alarms in case of unexpected changes.
- **Embedded fingerprint recognition chip**: FPGA based multicore architecture that efficiently implements the high computationally demanding core of a fingerprint matching algorithm based on Band-Limited Phase Only spatial Correlation (BLPOC)
- **SPRINTS**: data exchange protocol among systems and machines of the footwear production field. Realized in collaboration with Assomac, SPRINTS describes both "vertical" transfers (i.e., between different steps of the design/production chain), and "horizontal" transfers (e.g., to allow data exchange between CADs from different vendors).
- **F1 race car video system:** in collaboration with Magneti Marelli Motorsport division, we realized a video acquisition system to be installed on F1 race cars for tire or wing monitoring, together with a low-cost field-programmable gate array (FPGA)-based video deinterlacer.
- **Montecarlo on FPGA**: an accelerator based on field-programmable gate array technology accelerates double-precision floating-point operations present in the energy calculation of Monte Carlo-Metropolis simulations. The accelerator uses COTS components and is scalable in terms of clock frequency, memory capability, and number of computing units. It could also be part of a cluster of accelerated workstations.

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- Zanotto, Stefano, Nelson Nazzicari, Gesine Schmidt, Ulrike Böcker, Francesca Vurro, Antonella Pasqualone, Anne Kjersti Uhlen, and Paolo Annicchiarico. “Characterization of Genetic Diversity and Genomic Prediction of Secondary Metabolites in Pea Genetic Resources.” Plants 15, no. 3 (2026): 357. https://doi.org/10.3390/plants15030357.
- Nazzicari, Nelson, Giulia Moscatelli, Agostino Fricano, Elisabetta Frascaroli, Roshan Paudel, Eder Groli, Paolo De Franceschi, Giorgia Carletti, Nicolò Franguelli, and Filippo Biscarini. “Drone2report: A Configuration-Driven Multi-Sensor Batch-Processing Engine for UAV-Based Plot Analysis in Precision Agriculture.” Drones 10, no. 4 (2026): 301. https://doi.org/10.3390/drones10040301.
- Annicchiarico, Paolo, Nelson Nazzicari, Luciano Pecetti, Tommaso Notario, Barbara Ferrari, Nicolò Franguelli, and Daniele Cavalli. “White Lupin Genomic Selection for Adaptation to Drought or Moderately Calcareous Soil: A Proof-of-Concept Study.” International Journal of Molecular Sciences 27, no. 9 (2026): 4057. https://doi.org/10.3390/ijms27094057.
- Annicchiarico, Paolo, Nicolò Franguelli, Luciano Pecetti, Barbara Ferrari, and Nelson Nazzicari. “Implications of Morphological and Molecular Distinctness on the Registration of Alfalfa Candidate Varieties Issued by a Breeding Program: A Case Study.” Frontiers in Plant Science 17 (2026): 1809996. https://doi.org/10.3389/fpls.2026.1809996.
- Annicchiarico, Paolo, Meriem Laouar, Imane Thami-Alami, Margherita Crosta, Nelson Nazzicari, Luciano Pecetti, and Luigi Russi. “Comparison of Phenotypic Selection of Inbred Lines, Genomic Selection of Inbred Lines, and Evolutionary Populations for Field Pea Breeding in Three Mediterranean Regions.” Frontiers in Plant Science 16 (2025). https://doi.org/10.3389/fpls.2025.1565087.
- Annicchiarico, Paolo, Claudia Osorio, Nelson Nazzicari, Barbara Ferrari, Stefania Barzaghi, Elisa Biazzi, Aldo Tava, et al. “Genetic Variation and Genome-Enabled Selection of White Lupin for Key Seed Quality Traits.” BMC Genomics 26, no. 1 (2025): 922. https://doi.org/10.1186/s12864-025-12048-0.
- Crosta, Margherita, Nelson Nazzicari, Luciano Pecetti, Tommaso Notario, Massimo Romani, Barbara Ferrari, Giovanni Cabassi, and Paolo Annicchiarico. “Genomic Selection for Pea Grain Yield and Protein Content in Italian Environments for Target and Non-Target Genetic Bases.” International Journal of Molecular Sciences 26, no. 7 (2025): 2991. https://doi.org/10.3390/ijms26072991.
- Franguelli, Nicolò, Daniele Cavalli, Nelson Nazzicari, Luciano Pecetti, Tommaso Notario, and Paolo Annicchiarico. “Genetic Variation and Genome-Enabled Prediction of White Lupin Frost Resistance in Different Reference Populations.” International Journal of Molecular Sciences 26, no. 20 (2025): 10224. https://doi.org/10.3390/ijms262010224.
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"Biologically Meaningful Genome Interpretation Models to Address Data Underdetermination for the Leaf and Seed Ionome Prediction in Arabidopsis Thaliana." Scientific Reports 14, no. 1 (2024): 13188. https://doi.org/10.1038/s41598-024-63855-6.

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prone Growing Regions." The Plant Genome 15, no. 4 (2022): e20264. https://doi.org/10.1002/tpg2.20264.
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