

Personal details and date of CV

- Surname: Giudice
- First names: Luca
- Researcher identifier: <https://orcid.org/0000-0003-0593-4067>
(<https://www.researchgate.net/profile/Luca-Giudice>)
- Date of CV: 27/02/2025

Degrees

- 06/05/2022, PhD in Computer Science, Artificial Intelligence Techniques Integrate Biological Omics into Graphs for the Prediction and Pathway Analysis of Patient's Disease, University of Verona, Verona, Italy. Contact Details: (Via San Francesco, 22 - 37129 Verona, +39 045802 8078 | 8134, dottorati.ricerca@ateneo.univr.it)
- August 2018, Master's degree in Medical Bioinformatics, University of Verona, Verona, Italy
- June 2016, Bachelor's degree in Bioinformatics, University of Verona, Verona, Italy

Language Skills

- Italian C2
- English C1

Current employment

- 01/06/2022- 31/12/2027, Postdoctoral Researcher, Tarja Malm, University of Eastern Finland, Stage II

Previous work experience

- 01/02/2020 - 01/06/2022, Early Stage Researcher, Prof. Tarja Malm, University of Eastern Finland
- 01/09/2018 – 31/18/2021, PhD student, Prof. Rosalba Giugno, University of Verona

Career breaks

No

Research funding and grants

- I was awarded the grant "Neuroendocrine Carcinomas: Towards a Molecular Classification of the Disease Subtypes for Precision Medicine" (grant reference AdR3826/21) in October 2021. This research was conducted at the University of Verona, with Prof. Rosalba Giugno as the Principal Investigator (PI).

Research output

Publications:

- **Total Number of Publications:** 17
- **Choice of research career:** My research career is focused on becoming an expert medical bioinformatician specialized in the patient similarity network paradigm (computational choice) and in neurological disorders (biological choice), and a data scientist skilled in analyzing next-generation sequencing data. I am particularly interested in developing novel computational methods to improve our understanding of neurological diseases.

Publications: ¹⁻³ **Focus on Software Development and Machine Learning**

- **Role:** Bioinformatician, software developer, and project manager.

- **Goals:** Develop interpretable machine learning software for:
 - Patient classification, Enhancer prediction, lncRNA function prediction.
- **Software Engineering Contributions:**
 - Designed and implemented supervised classifiers (using network science) with prioritized interpretability, usability, and biological applications.
 - Developed a reverse-engineering strategy for biological information.
 - Developed novel software for de novo transcriptome assembly.
 - Developed software that is deployable using Docker and Singularity.

Publications: ⁴⁻⁶ **Focus on Non-Coding RNA and Stroke Research**

- **Role:** Bioinformatician, data scientist, and stroke expert.
- **Goals:** Investigate the role of specific non-coding RNAs in brain ischemia and stroke:
 - The ciRS-7, miR-7, and Cyrano network in the context of brain ischemia.
 - miR-21a-5p in the context of ischemic stroke.
 - miR-669c-3p in modulating microglial polarization and its impact on outcomes in ischemic stroke.
- **Data Analysis Skills:**
 - RNA-seq data analysis, deconvolution of bulk RNA-seq data, Global Run-On sequencing (GRO-seq) data analysis, HITS-CLIP data analysis, differential gene expression analysis.

Publications: ⁷⁻⁹ **Focus on Neurodegenerative Diseases**

- **Role:** Bioinformatician, data scientist, and expert in neurological disorders, including Multiple Sclerosis (MS), Alzheimer's disease (AD), and Parkinson's disease (PD).
- **Goals:**
 - Investigate the transcriptional signatures of phagocytic microglia in Alzheimer's disease (AD) to identify key non-coding RNA regulators of phagocytosis.
 - Investigate the role of the mechanotransduction ion channel PIEZO1 in microglia and its impact on Alzheimer's disease (AD), specifically, relating to A β clearance.
 - Investigate the effects of the LRRK2-G2019S on the transcription of human iPSC-derived microglia-like cells (iMGLs) in Parkinson's disease (PD).
- **Data Analysis Skills:** Multi-omics data analysis of spatial, imaging, single-cell, long, and small RNA sequencing data. Electrophysiological analysis of recordings.

Other Publications:

10-17

Research supervision and leadership experience

- **2024-Current:** Supervisor of two Molecular Medicine PhD students and one Master student at the University of Eastern Finland. I am going to be the last author in their publications. **Topics:** Development of software to analyse Microelectrode Array recordings **Names:** Mohammad Rezaie, Mohammadamin Beheshti Dehkordi and Faezeh Saeeyekta.
- **2023-Current:** I am the Supervisor of two Molecular Medicine PhD students at the University of Eastern Finland. **Topics:** Data analysis of sequencing data **Names:** Ahmed Mohamed and Olga Neustroeva.
- **2019-2020:** I have been the supervisor of two Master students who achieved the degree in Medical Bioinformatics at the University of Verona. **Topic:** Development of software for the analysis of molecular networks such as protein-protein interaction networks. **Names:** Laura Fedrizzi (Data Engineer at Würth). Luca Parmigiani (PhD student at Bielefeld University).

Teaching Merits

- **October 2024:** I provided a four-day bioinformatics course organized by Dr. Shen Li at Beijing Shijitan Hospital, Capital Medical University, in China

Awards and honours

I received the Best Paper Award at the IARIA 2022 conference for our paper, "Simpati: Patient Classifier Identifies Signature Pathways Based on Similarity Networks for Disease Prediction."

- <https://doi.org/10.1101/2021.09.23.461100>
- https://www.iaria.org/conferences2022/awardsBIOTECHNO22/biotechno2022_a1.pdf

Other key academic merits, such as

- **November 2023:** Organized and presented the Finnish Symposium on Computational Biology 2023. Secured €3,500 in sponsorship from the NeIC, ISCB, Olink, and Orion Pharma (<https://www.uef.fi/en/event/finnish-symposium-on-computational-biology-2023>).
- **2023-Current:** President of the Bioinformatics Regional Student Group of Finland, under the International Society for Computational Biology (ISCB).
- **2023-2024:** Member of the committee of the Finnish Bioinformatics Society.

Scientific and societal impact

- **Telegram, LinkedIn and Twitter with RSG Finland (ISCB):** I authored a monthly column on new bioinformatics R packages for the RSG Finland ISCB community. I interviewed bioinformatics professors, such as Sampsa Hautaniemi from Helsinki University.
- **Resource Contribution:** I have contributed personal resources to the Malm research group including a server with the following specifications: Intel i9-7900X 3.30GHz 20-core CPU, 120 GB of RAM, and a NVIDIA GeForce GTX 1080 Ti GPU with 10 GB of vRAM.

Other merits

- **December 2024:** NLC Health Ventures offered me 150,000 euros to develop and expand the StellarPath software, aiming to make it accessible to hospitals and clinicians.
- **Apr 2018 - Jul 2021** · Daniel Rico's Lab, University of Newcastle, Research + Visiting PhD student (3 months): I developed a network-based classifier to predict activity of non-coding regulatory regions.
- **Sep 2017 - Apr 2019** · Gary Bader's Lab, University of Toronto, Research + Visiting student (6 months): I implemented the first patient classifier called netDx, based on patient similarity networks. My contribution was the integration of somatic mutation data with other genetic data types using graph theory.

1 Giudice, L et al. (2024). *PLOS Comput. Biol.* 20, e1012022 // **2** Giudice, L et al. (2023). *Nucleic Acids Res.* 51, e55 // **3** Pai, S et al. (2021). *F1000Research* 9, 1239 // **4** Scoyni, F et al. (2024). *Cell Rep.* 43, // **5** Korvenlaita, N et al. (2023). *J. Extracell. Vesicles* 12, 12297 // **6** Kolosowska, N et al. (2020). *J. Neuroinflammation* 17, 194 // **7** Scoyni, F et al. (2024). *Alzheimers Dement.* 20, 954–974 // **8** Jäntti, H et al. (2022). *J. Neuroinflammation* 19, 147 // **9** Ohtonen, S et al. (2023). *Sci. Rep.* 13, 22118 // **10** Bonnici, V et al. (2019) LERNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis. in *2019 IEEE (CIBCB)* 1–8 doi:10.1109/CIBCB.2019.8791487 // **11** Giudice, L et al. *BIOTECHNO 2022 Fourteenth Int. Conf. Bioinforma. Biocomput. Syst. Biotechnol.* // **12** Giudice, L et al. (2019). *Non-Coding RNA* 5, 47 // **13** Bosutti, A et al. (2021). *Acta Physiol.* 233, e13702 // **14** Niskanen, J et al. (2025). *Glia* 73, 159–174 // **15** Hyvärinen, T et al. (2024). 2024.12.10.627477 doi:10.1101/2024.12.10.627477 // **16** Giannuzzi, D et al. (2020). *Vet. Comp. Oncol.* 18, 645–655 // **17** Simbolo, M et al. (2022). *Cancers* 14, 4653 //