

+4915755964003
Heidelberg, Germany
anamariaelek@gmail.com

Anamaria Elek

Computational Biologist

[linkedin.com/in/anamaria-elek](https://www.linkedin.com/in/anamaria-elek)
github.com/anamariaelek
scholar.google.com/citations

SUMMARY

I study gene regulation and cell type-specific expression changes across evolution, development, and disease. I have extensive experience in biological data analysis and machine learning, with a track record of developing data-driven analysis approaches and visualizations that drive meaningful biological discoveries.

SKILLS

Coding	Python, R, Bash, Docker, HPC, Git, Markdown, Shiny
Analysis	Statistical analysis, Machine Learning, Deep Learning
Languages	Croatian (native), English (proficient), Spanish (intermediate), German (basic)

EXPERIENCE

Postdoctoral Researcher in Kaessmann and Sasse labs Center for Molecular Biology of Heidelberg University (ZMBH); Heidelberg, Germany	July 2025 — Present
<ul style="list-style-type: none">Using <u>deep learning</u> to study tissue- and cell-type-specific regulatory logic of alternative splicingModeling alternative splicing in vertebrates, across organs and development.	
Bioinformatician at Biodiversity Cell Atlas Centre for Genomic Regulation (CRG); Barcelona, Spain	April 2024 — July 2025
<ul style="list-style-type: none">Processing, analysis, integration and comparisons of <u>single cell RNA-seq</u> atlases, including data generated using different technologies, as well as curation of public datasets.	
Visiting PhD Student in Computational biology lab (Stein Aerts lab) Center for AI & Computational Biology, VIB-KU Leuven; Leuven, Belgium	January 2024 — March 2024
<ul style="list-style-type: none">Regulatory sequence analysis using <u>convolutional neural network</u> models.	
PhD Student in Comparative regulatory genomics group (Arnaud Sebé-Pedrós lab) Centre for Genomic Regulation (CRG); Barcelona, Spain	November 2019 — April 2024
<ul style="list-style-type: none">Analysis and integration of <u>multiomics data</u> (<u>single cell RNA-seq</u> and <u>single cell ATAC-seq</u>, <u>ChIP-seq</u>, <u>DAP-seq</u>).Training <u>machine learning models</u> for analysis of gene expression and regulation (e.g. gene regulatory networks modeling, sequence based cell type classifiers).Developing <u>interactive web applications</u> for visualization, exploration and summary of single cell datasets.	
Bioinformatician in Genomics Facility (former Tumor Profiling Unit) The Institute of Cancer Research (ICR); London, UK	March 2019 — November 2019
<ul style="list-style-type: none">Developing computational pipelines for processing and analysis of next-generation sequencing data (<u>RNA-seq</u>, <u>WGS</u> and <u>WES</u>).	

EDUCATION

PhD in Biomedicine , Universitat Pompeu Fabra; Barcelona, Spain	2019 — 2024
Master's degree in Molecular Biology , University of Zagreb; Zagreb, Croatia	2017 — 2018
Bachelor's degree in Molecular Biology , University of Zagreb; Zagreb, Croatia	2013 — 2017

PUBLICATIONS

	ORCID: 0000-0002-3938-2494
Elek, A.* Iglesias, M.* Mahieu, L., Zolotarov, G., Grau-Bové, X., Aerts, et al. (2025). "Decoding cnidarian cell type gene regulations". <i>Nature Ecology Evolution</i> . DOI: 10.1038/s41559-025-02906-1 .	
Levy, S.* Elek, A.* Grau-Bové, X., Menéndez-Bravo, S., Iglesias, M., Tanay, A., et al. (2021). "A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity". <i>Cell</i> 184.11, 2973–2987.e18. DOI: 10.1016/j.cell.2021.04.005 .	
Kim, I. V., Navarrete, C., Grau-Bové, X., Iglesias, M., Elek, A., Zolotarov, G., et al. (2025). "Chromatin loops are an ancestral hallmark of the animal regulatory genome". <i>Nature</i> 642.8069, pp. 1097–1105. ISSN: 1476-4687. DOI: 10.1038/s41586-025-08960-w .	
Grau-Bové, X.* Subirana, L.* Meister, L.* Soubigou, A., Neto, A., Elek, A., et al. (2024). "An amphioxus neurula stage cell atlas supports a complex scenario for the emergence of vertebrate head mesoderm". <i>Nature Communications</i> 15.1, p. 4550. DOI: 10.1038/s41467-024-48774-4 .	
Najle, S. R.* Grau-Bové, X.* Elek, A., Navarrete, C., Cianferoni, D., Chiva, C., et al. (2023). "Stepwise emergence of the neuronal gene expression program in early animal evolution". <i>Cell</i> 186.21, 4676–4693.e29. ISSN: 0092-8674. DOI: 10.1016/j.cell.2023.08.027 .	

- Li, Y., Slavik, K. M., Toyoda, H. C., Morehouse, B. R., Oliveira Mann, C. C. de, Elek, A., et al. (2023). “cGLRs are a diverse family of pattern recognition receptors in innate immunity”. *Cell* 186.15, 3261–3276.e20. ISSN: 0092-8674. doi: [10.1016/j.cell.2023.05.038](https://doi.org/10.1016/j.cell.2023.05.038).
- Miguel-Escalada, I., Maestro, M. Á., Balboa, D., Elek, A., Bernal, A., Bernardo, E., et al. (2022). “Pancreas agenesis mutations disrupt a lead enhancer controlling a developmental enhancer cluster”. *Developmental Cell* 57.16, 1922–1936.e9. ISSN: 1534-5807. doi: [10.1016/j.devcel.2022.07.014](https://doi.org/10.1016/j.devcel.2022.07.014).
- García-Castro, H., Kenny, N. J., Iglesias, M., Álvarez-Campos, P., Mason, V., Elek, A., et al. (2021). “ACME dissociation: a versatile cell fixation-dissociation method for single-cell transcriptomics”. *Genome Biology* 22.1. ISSN: 1474-760X. doi: [10.1186/s13059-021-02302-5](https://doi.org/10.1186/s13059-021-02302-5).
- Roje, B.*, Elek, A.*[†], Palada, V., Bom, J., Iljazovic, A., Simic, A., et al. (2020). “Microbiota alters urinary bladder weight and gene expression”. *Microorganisms* 8.3. doi: [10.3390/microorganisms8030421](https://doi.org/10.3390/microorganisms8030421).
- Elek, A., Kuzman, M., and Vlahovicek, K. (2018). *coRdon: codon usage analysis and prediction of gene expressivity*. doi: [10.18129/B9.bioc.CORDON](https://doi.org/10.18129/B9.bioc.CORDON).

* These authors contributed equally.

PRESENTATIONS

EMBO Meeting: The evolution of animal genomes Sevilla, Spain	September 2023
Regulatory characterization of cell types in <i>Nematostella vectensis</i> . (poster)	
Single Cell Biology Wellcome Trust Campus, Hinxton, UK	June 2022
Integration of whole-organism single cell atlases for comparative studies of animal cell types. (poster)	
Single Cell Genomics Symposium Barcelona, Spain	March 2022
Single cell approaches for comparative and regulatory characterization of animal cell types. (presentation)	
BCN Single Cell Club online	July 2021
Coral cell atlas and a quest to understand cell type evolution. (presentation)	
EMBO Meeting: The Identity and Evolution of Cell Types online	May 2021
A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. (poster)	

AWARDS

EMBO Postdoctoral Fellowship	2026 – 2027
SSC Fellows Program Scientific Software Center, Heidelberg University	2025
FPI Severo Ochoa PhD Scholarship Spanish Ministry of Science	2019 – 2024
Best Poster Award EMBO meeting: The Identity and Evolution of Cell Types	May 2021
Vienna Biocenter Summer School Fellowship	July – August 2017

TEACHING AND OUTREACH

Deep Learning for Regulatory Genomics: Modeling Sequence-to-Function course at the Heidelberg University	January 2026
This was a project course for the Molecular Biosciences Master’s degree programme. I contributed to preparing course content and teaching materials, and held a lecture with practical workshop on TF-MoDISCo. I also mentored a group of students working on 10-weeks-long project.	
UBDS3 , data science summer school; Uzhhorod, Ukraine	August 2024
I prepared and conducted workshops on clustering and supervised machine learning.	
NGSchool , bioinformatics summer school; Warsaw, Poland and online	2021 – 2022
I was a member of the organizing committee and developed NGSchool website .	
I was teaching machine learning and programming in R, and mentored a hackathon team working on a week long RNA-seq analysis project.	
Introduction to Machine Learning , CRG internal training course; Barcelona, Spain	May 2021
I gave a lecture on feature selection and dimensionality reduction, with a hands-on session using scikit-learn.	