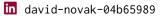
David Novak









Employment History

Assistant lecturer (machine learning). Department of Applied Mathematics, Computer Science and Statistics, Ghent University. Ghent, Belgium.

Guiding practical sessions and student projects. Consulting role for experimental design and HPC use.

Bioinformatics researcher. FWO Strategic Basic research fellow at Center for Inflammation Research, VIB-UGent. Ghent, Belgium.

Research into applied ML and deep learning in cytometry and single-cell transcriptomics analysis pipelines. Algorithm development.

Programmer and bioinformatics researcher. Childhood Leukaemia Investigation Prague, 2nd Faculty of Medicine and Faculty Hospital Motol. Prague, Czech Republic.

Development of automated pipelines for processing of flow and mass cytometry clinical and research data. R and C++ development of a novel semi-automated trajectory inference solution.

Translator and assistant. MIDA Consulting. Prague, Czech Republic.

Czech-English & English-Czech translations and research into European Union subsidy programmes and maintenance of projects supported by them.

Lecturer (ESL). Channel Crossings. Prague, Czech Republic.

Teaching individual English prep course for CAE qualification. English conversation course.

2017–2018 Lecturer (algorithmisation). Logiscool. Prague, Czech Republic.

Teaching principles of programming and algorithmisation to elementary-school students.

Research intern. Cellular neurophysiology, Institute of Physiology, Czech Academy of Sciences. Prague, Czech Republic.

Primer design, bacterial transformation, plasmid preparation, IHC staining and fluorescent microscopy.

Education

2020 – (2024) Ph.D. Bioinformatics (ongoing) at Ghent University, Ghent, Belgium.

Topic: Novel applications of structure learning and deep learning for single-cell data.

2018 – 2020 M.Sc. Bioinformatics at Charles University, Prague, Czech Republic. Thesis title: Studying lymphocyte development using mass cytometry.

B.Sc. Biological Sciences at Charles University, Prague, Czech Republic. Thesis title: *Human lymphopoiesis and its examination via single-cell analysis*.

Research Publications

Journal Articles

T. Liechti, S. Van Gassen, M. Beddall, *et al.*, "A robust pipeline for high-content, high-throughput immunophenotyping reveals age- and genetics-dependent changes in blood leukocytes," *Cell Reports Methods*, vol. 3, no. 10, p. 100 619, 2023, ISSN: 2667-2375. ODOI: https://doi.org/10.1016/j.crmeth.2023.100619.

- A. Couckuyt, R. Seurinck, A. Emmaneel, *et al.*, "Challenges in translational machine learning," *Human Genetics*, vol. 141, pp. 1–16, Sep. 2022. ODOI: 10.1007/s00439-022-02439-8.
- T. A. Liechti, M. Beddall, S. Van Gassen, *et al.*, "Leveraging high-dimensional flow cytometry to reveal the human immune system at a population-wide scale," *The Journal of Immunology*, vol. 206, no. 1_Supplement, pp. 26.11–26.11, May 2021, ISSN: 0022-1767. ODOI: 10.4049/jimmunol.206.Supp. 26.11.

Conference Papers

Pre-prints

- M. Bakardjieva, J. Stuchly, O. Pelak, *et al.*, "Tviblindi algorithm identifies branching developmental trajectories of human b cell development," 2024. ODI: 10.1101/2024.01.11.575178. eprint: https://www.biorxiv.org/content/early/2024/01/15/2024.01.11.575178.full.pdf.
- D. Novak, C. de Bodt, P. Lambert, J. A. Lee, S. V. Gassen, and Y. Saeys, "A framework for quantifiable local and global structure preservation in single-cell dimensionality reduction," 2023. ODOI: 10.1101/2023.11.23.568428.eprint: https://www.biorxiv.org/content/early/2023/11/24/2023.11.23.568428.full.pdf.
- J. Stuchly, D. Novak, N. Brdickova, *et al.*, "Deconstructing complexity: A computational topology approach to trajectory inference in the human thymus with tviblindi," 2023. ODI: 10.1101/2023.07.13.547329. eprint: https://www.biorxiv.org/content/early/2023/09/14/2023.07.13.547329.full.pdf.

Skills and competencies

Languages Strong reading, writing and speaking competencies for English, Czech, Slovak. Conversational German.

Coding Python, TensorFlow, PyTorch, sklearn, numba, matplotlib, R, ggplot2, Shiny, C++, OpenMP, .NET, xUnit, Java, JavaScript, React, HTML, CSS, SQL, Git, GitLab CI/CD, Slurm, Unix, Docker.

Misc. Statistical data analysis, machine learning, NGS data analysis, single-cell 'omics analyses, molecular biology theory, scientific writing, teaching.

In 2014-2015 I volunteered at the Thomayer hospital in Prague as part of the Lékořice foundation, holding weekly visits with elderly hospitalised patients.

References

Available on request.