

David Novak

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in david-novak-04b65989

🔗 davnovak.github.io

Employment History

- 2020–(Q4 2024) **Bioinformatics researcher.** FWO Strategic Basic research fellow at Saeys Lab, Center for Inflammation Research, VIB-UGent. Ghent, Belgium.
Research into applied ML and deep learning in cytometry and single-cell transcriptomics analysis pipelines: batch effect correction, large differential expression analyses. Algorithm development: interpretable dimensionality reduction.
- 2021–(Q4 2024) **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.
- 2018–2020 **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.
- 2012–2020 **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.
- 2018 **Lecturer (ESL).** Channel Crossings. Prague, Czech Republic.
Teaching individual English prep course for CAE qualification. English conversation course.
- 2017–2018 **Lecturer (algorithmisation).** Logischool. Prague, Czech Republic.
Teaching principles of programming and algorithmisation to elementary-school students.
- 2015 **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 – (Q4 2024) **Ph.D. Bioinformatics** (ongoing) at Ghent University, Ghent, Belgium. Supervisor: Prof Yvan Saeys.
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.
- 2015 – 2018 **B.Sc. Biological Sciences** at Charles University, Prague, Czech Republic.
Thesis title: Human lymphopoiesis and its examination via single-cell analysis.


Published Research

Journal Articles




- 1 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. 🔗 DOI: <https://doi.org/10.1016/j.crmeth.2023.100619>.
- 2 A. Couckuyt, R. Seurinck, A. Emmaneel, *et al.*, “Challenges in translational machine learning,” *Human Genetics*, vol. 141, pp. 1–16, Sep. 2022. 🔗 DOI: [10.1007/s00439-022-02439-8](https://doi.org/10.1007/s00439-022-02439-8).

- 3 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.  DOI: 10.4049/jimmunol.206.Supp.26.11.




Conference Papers

- 1 D. Novak, S. Van Gassen, and Y. Saeys, “GroupEnc: Encoder with group loss for global structure preservation,” in *BNAIC/BeNeLearn 2023*, Delft, Netherlands, 2023.  URL: https://bnaic2023.tudelft.nl/static/media/BNAICBENELEARN_2023_paper_46.9317ce00beb72bf31803.pdf.

Pre-prints

- 1 M. Bakardjieva, J. Stuchly, O. Pelak, *et al.*, “Tviblindi algorithm identifies branching developmental trajectories of human b cell development,” 2024.  DOI: 10.1101/2024.01.11.575178. eprint: <https://www.biorxiv.org/content/early/2024/01/15/2024.01.11.575178.full.pdf>.
- 2 J. Stuchly, D. Novak, N. Brdickova, *et al.*, “Deconstructing Complexity: A Computational Topology Approach to Trajectory Inference in the Human Thymus with tviblindi,” May 2024.  DOI: <https://doi.org/10.7554/eLife.95861.1>.
- 3 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.  DOI: 10.1101/2023.11.23.568428. eprint: <https://www.biorxiv.org/content/early/2023/11/24/2023.11.23.568428.full.pdf>.

Skills and competencies

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| Languages |  Strong reading, writing and speaking competencies for English, Czech, Slovak. Conversational German. |
| IT |  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, AWS, NextFlow. |
| Misc. |  Statistical data analysis, machine learning, NGS data analysis, computational cytometry and single-cell ‘omics analyses, molecular biology theory, scientific writing, teaching. |

In May 2024 I co-organised the Computational Cytometry Summer School at VIB-UGent, teaching a tutorial on statistical analyses and interpretation of experimental cytometry data.

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.