

# Zuzana Ševčovičová

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## Summary

Bioinformatics researcher with a keen interest in machine learning and deep learning architectures to analyze bulk, single-cell, and spatial transcriptomics through high-performance computing.

## Education

### MS in Bioinformatics

Charles University  
Sept 2024 – present

- **Diploma Thesis:** Investigating the transcriptomic landscape of non-melanoma skin cancers using a multi-scale approach. Integrating data across platforms, from global bulk transcriptomics to high-resolution Xenium spatial transcriptomics in human skin samples.
- **Model of  $NF-\kappa B$  Dynamics:** Simulated immune regulation via ODEs; performed sensitivity analysis and bifurcation mapping to identify pathological states, see [Repository](#)
- **Spotify Data Analysis:** Think outside the box case where we applied scRNA-seq analogy to music data. Developed TF-IDF embeddings and an [interactive visualization](#) of user sound-feature spaces.

### BS in Molecular Biology and Biochemistry of Organisms

Charles University  
Sept 2021 – June 2024

- **Bachelor thesis:** [Algorithms for integration of single-cell transcriptomic data](#)

Benchmarked 7 algorithms (scVI, Seurat, Harmony, FastMNN, Scanorama, STACAS, CanSig) for scRNA-seq integration on HPC clusters. Implemented end-to-end pipelines including QC, normalization, and dimensionality reduction (PCA, tSNE, UMAP).

## Experience

### Institute of Molecular Genetics of the CAS

Prague, Czechia  
2023 – present

- **Bulk RNA-seq:** Analyzed datasets in R using ComBat, limma, and clusterProfiler.
- **scRNA-seq:** Conducted heterogeneity and DEG analysis using Seurat and Scampy.
- **Spatial Transcriptomics:** Utilizing Xenium in situ data for Diploma thesis.
- **Infrastructure:** Working on high-performance computing clusters of Czech Academy of science and MetaCentrum Virtual Organization.

## Skills

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**Languages:** Slovak - Native, Czech - C2, English - C1, Russian - C1

**Languages & Tools:** R (Seurat, Harmony, FastMNN, ComBat), Python (Numpy, Pandas, Pyplot, PyTorch, Scanpy, scVI, scikit-learn, CanSig), LaTeX, Git, Bash/Shell Scripting

**Analysis:** Single-Cell RNA-seq, Bulk RNA-seq, Spatial Transcriptomics, ODE Modeling, Germline and Somatic variant calling

**Computing:** High-Performance Computing (HPC/Slurm), Bash Scripting

## Courses

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**Single Cell Transcriptomics** — [Certificate ↗](#)

*IMG & ELIXIR Czech Republic*

*Dec 2025*

- Built R workflows for droplet-based scRNA-seq: from raw counts to cell annotation and functional enrichment. Applied QC, normalization, dataset integration, and Differential Expression (DE) analysis.

**Deep Learning & Neural Networks** — [Certificate ↗](#)

*Charles University*

*Oct 2024 - Jan 2025*

- Implemented FFN, RNN, CNN, and Transformer architectures in PyTorch for CV and NLP tasks. Optimized training pipelines using SGD/Adam, Dropout, Batch Norm, and hardware acceleration.

**Genomics – Approaches and Algorithms**

*Charles University*

*Oct 2024 - Feb 2025*

- Developed a reproducible Bash pipeline for NGS germline variant calling (BWA, Samtools, BCFtools).

**Machine Learning in Biology**

*Charles University*

*Feb 2025 - May 2025*

- Applied ML models to complex biological datasets with an emphasis on method selection and interpretation.

**Elements of AI** — [Certificate ↗](#)

*University of Helsinki*

*Oct 2024 - Jan 2025*

- Completed foundational training in AI theory, search algorithms, and practical machine learning.