Erik Fasterius, PhD

Bioinformatician, scientist, developer

Skills

- Computational biology
- Transcriptomics
- Spatial transcriptomics
- NGS
- Genomics
- Pipeline development
- Statistics
- Data visualisation
- Reproducibility
- Problem solving
- Teaching
- Public speaking
- Scientific writing

Contact

(+46) 070 714 36 96

erik.fasterius@outlook.com

fasterius.github.io

fasterius

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Summary

I am a bioinformatician and scientist specializing in computational biology, pipeline development, and advanced training. I have led projects involving bulk and single-cell **RNA-seq**, **spatial transcriptomics**, RNA-seq/WES-based **variant analysis**, **transcriptional pharmacodynamics** and high-throughput **drug screening**. I frequently collaborate with clinicians and other non-bioinformaticians, guiding **experimental design** and generating hypotheses that drive publications.

I am passionate about reproducibility and data visualization, excelling at designing scalable and reliable bioinformatic **pipelines** that empower scientific discovery. Known for being analytical, thorough, and a natural problem-solver, I thrive in **collaborative environments** and enjoy sharing knowledge, whether through formal teaching, mentoring, or casual discussions with colleagues. My curiosity, adaptability, and creativity drive me to continuously learn and contribute to scientific research.

Experience

Bioinformatician — **2019 - Present**

National Bioinformatics Infrastructure Sweden

SciLifeLab, Stockholm, Sweden

At NBIS I provided advanced bioinformatic support and guidance to life science researchers in Sweden within the SciLifeLab community. Collaborating within interdisciplinary teams, I delivered **tailored bioinformatics solutions for diverse research projects**, involving both bulk and single-cell RNA-seq, transcriptional pharmacodynamics as well as novel technologies for spatial transcriptomics and high-throughput drug screenings. I designed and implemented several reproducible **bioinformatic pipelines**, facilitating scalability and reliability for life science research. Additionally, I **led training initiatives** locally in Sweden and at the European level, equipping researchers with state-of-the-art computational biology techniques.

PhD Student — **2014 - 2018**

KTH Royal Institute of Technology

Stockholm, Sweden

During my PhD I investigated genetic heterogeneity in **human cancer models** using (sc)RNA-seq technologies. I developed innovative approaches by leveraging both traditional **gene expression** and non-traditional **single nucleotide variant analysis** of publicly available datasets, available as R and Python packages.

Open Source

nf-core/spatialvi *(creator & maintainer)*
A Nextflow pipeline for analysing 10x Visium **spatial transcriptomics data**.

nf-core/rifseq *(creator & maintainer)*
A Nextflow pipeline for analysing the RIF-seq sequencing method for **large-scale drug screening** (currently not publicly available pending publication).

seqCAT *(creator & maintainer)*
An R/Bioconductor package for **variant analysis** of NGS data.

VarClust *(creator & maintainer)*
A Python package for **variant analysis** of single-cell NGS data.

RNA-VC *(creator & maintainer)*
A Snakemake pipeline for **variant analysis** of publicly available RNA-seq data.

Tools

- R
- Python
- Unix / Bash
- High-performance computing
- Git / GitHub
- Nextflow / nf-core
- Snakemake
- Conda
- Docker
- Pixi
- Quarto
- R Markdown
- LaTeX

nf-core/spaceranger *(contributor)*
A nf-core module for processing 10x Visium **spatial transriptomics** data.

nf-core/quartonotebook *(creator & maintainer)*
A nf-core module for rendering Quarto notebooks.

Quarto nf-core template *(creator & maintainer)*
A Quarto template for the nf-core community.

simple-zoom.nvim *(creator & maintainer)*
A simple plugin to add a Tmux-like zoom functionality to Neovim.

slime-peek.nvim *(creator & maintainer)*
A Neovim plugin for working with data exploration within R and Python.

Teaching

I have designed and led advanced bioinformatics courses, teaching over 250 PhD students, postdocs and group leaders through the NBIS and ELIXIR networks. I have delivered training sessions across Sweden, Europe and online, mainly through **Tools for Reproducible Research**, for which I am a course leader, but also **Single cell RNA-seq data analysis** and **Introduction to bioinformatics using NGS data**. A comprehensive teaching portfolio is available at **my website**.

Publications

Amoedo-Leite et al. (2024). "Macrophages upregulate mural cell-like markers and support healing of ischemic injury by adopting functions important for vascular support". In: *Nature Cardiovascular Research* 3.6, pp. 685–700. DOI: 10.1038/s44161-024-00478-0.

Söderhäll, Irene et al. (2022). "Characterization of hemocytes and hematopoietic cells of a freshwater crayfish based on single-cell transcriptome analysis". In: *iScience* 25.8, p. 104850. DOI: 10.1016/j.isci.2022.104850.

Selvin, Tove et al. (2022). "Single-cell transcriptional pharmacodynamics of trifluridine in a tumor-immune model". In: *Scientific Reports* 12.1, p. 11960. DOI: 10.1038/s41598-022-16077-7.

Kennedy, Susan A. et al. (2020). "Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D". In: *Nature Communications* 11.1, pp. 1–14. DOI: 10.1038/s41467-019-14224-9.

Strandberg, Kristin et al. (2020). "Blood-derived biomarkers correlate with clinical progression in Duchenne muscular dystrophy". In: *Journal of Neuromuscular Diseases* 7.3, pp. 231–246. DOI: 10.3233/JND-190454.

Fasterius, Erik, Mathias Uhlén, and Cristina Al-Khalili Szigyarto (2019). "Single-cell RNA-seq variant analysis for exploration of genetic heterogeneity in cancer". In: *Scientific Reports* 9.1, pp. 1–11. DOI: 10.1038/s41598-019-45934-1.

Fasterius, Erik and Cristina Al-Khalili Szigyarto (2019). "SeqCAT: A bioconductor R-package for variant analysis of high throughput sequencing data". In: *F1000Research* 7.1466. DOI: 10.12688/F1000RESEARCH.16083.2.

Charitou, Theodosia et al. (2019). "Transcriptional and metabolic rewiring of colorectal cancer cells expressing the oncogenic KRASG13D mutation". In: *British Journal of Cancer* 121.1, pp. 37–50. DOI: 10.1038/s41416-019-0477-7.

Fasterius, Erik and Cristina Al-Khalili Szigyarto (2018). "Analysis of public RNA- sequencing data reveals biological consequences of genetic heterogeneity in cell line populations". In: *Scientific reports* 8(1).1, pp. 1–11. DOI: http://dx.doi.org/10.1038/s41598-018-29506-3.

Danielsson, Frida et al. (2018). "Transcriptome profiling of the interconnection of pathways involved in malignant transformation and response to hypoxia". In: *Oncotarget* 9.28, pp. 19730–19744. DOI: 10.18632/oncotarget.24808.

Fasterius, Erik, Cinzia Raso, et al. (2017). "A novel RNA sequencing data analysis method for cell line authentication." In: *PloS one* 12.2, e0171435. DOI: 10.1371/journal.pone.0171435.