
# Erik Fasterius

Senior Bioinformatician

- Lives in Stockholm, Sweden
- Married to wife Linda
- Twin daughters Saga and Tilda


## Tools

**Git / GitHub** 8 years

**Docker** 4 years

**Conda** 5 years

**R** 10 yrs.

**Python** 4 years

**Unix / Bash** 10 yrs.

**Nextflow / nf-core** 4 years

**Snakemake** 7 years

**Quarto** 1 years

**R Markdown** 8 years

**LaTeX** 6 years

**HPC** 10 yrs.

**Vim** 7 years

## Summary


I am a bioinformatician and a scientist working mainly with computational biology, pipeline development and advanced training. I come from a background in biotechnology and thus have an understanding of both bioinformatics and the underlying biology. I have experience working with software development, machine learning, cancer biology, drug screening and cell line authentication. I am also very interested in reproducibility and data visualization.

I am analytically minded, thorough and enjoy problem-solving at all levels. I have always liked sharing my knowledge with others, be that through more traditional teaching avenues or through corridor-conversations with colleagues. Learning new things is something I have always appreciated. I'm creative, adaptable and social.


## Experience

**Senior Bioinformatician** **2019 - Present**
National Bioinformatics Infrastructure Sweden
SciLifeLab, Stockholm, Sweden

At NBIS I offer advanced bioinformatic support and guidance to life science researchers in Sweden through the SciLifeLab community. My current focus involves transcriptomics and its applications in bulk and single cell RNA sequencing, as well as several pipeline development projects with Nextflow and nf-core. I am also engaged in advanced computational biology and data analysis training at the European level through ELIXIR. My work at NBIS allows me to help life science researchers in Sweden bring their projects to completion with tailor-made bioinformatics solutions.

**PhD Student** **2014 - 2018**
KTH Royal Institute of Technology
Stockholm, Sweden

During my PhD studies I worked on genetic heterogeneity in human cancer models using both bulk and single cell RNA-seq technologies. My project involved leveraging both traditional gene expression-based analyses with non-traditional single nucleotide variant analysis of publicly available (sc)RNA-seq datasets.

## Open Source projects

**nf-core/spatialtranscriptomics**
Creator & Maintainer
A nf-core pipeline for analysing Visium spatial transcriptomics data.

**nf-core/rifseq**
Creator & Maintainer
A nf-core pipeline for analysing the new RIF-seq sequencing method for large-scale, in-plate drug screening by the Mats Nilsson laboratory at SciLifeLab (currently not publicly available).

**nf-core/modules/quartonotebook**
Creator & Maintainer
A nf-core module for rendering Quarto notebooks.

**nf-core/modules/spaceranger**
Contributor
A nf-core module for processing Visium data using the Space Ranger software.

**Quarto nf-core template**
Creator & Maintainer
A Quarto template for the nf-core community.

## Skills

- Computational biology
- Transcriptomics
- Genomics
- Pipeline development
- Reproducibility
- Data visualisation
- Statistics
- Creative problem solving
- Teaching
- Public speaking
- Scientific writing

## Contact

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Erik Fasterius

**seqCAT**
Creator & Maintainer
An R/Bioconductor package for variant analysis and cell authentication using HTS data.

**VarClust**
Creator & Maintainer
A Python package for variant analyses of single-cell HTS data.

**RNA-VC**
Creator & Maintainer
A Snakemake pipeline for variant analyses of publicly available RNA-seq data.

## Teaching

I have been involved in several advanced bioinformatics courses, all of which are offered to PhD students, post-docs and other researchers in Sweden (NBIS), Switzerland (SIB) and countries in the ELIXIR network. I am a Course Leader for the NBIS Tools for Reproducible Research NBIS course. For a full list of the courses I have taught, please visit 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.