Erik Fasterius

Bioinformatician

About me

I am a bioinformatician and scientist working mainly with computational biology, pipeline development and advanced training. I come from a background in biotechnology and thus have a deep understanding of both bioinformatics and the underlying biology. I have experience working with machine learning, software development, cancer biology, drug screening and cell line authentication. Additional special interests include 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.

At my current workplace, the National Bioinformatics Infrastructure Sweden (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. 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, which is something I greatly enjoy.

Employment

2019 - present **Senior Bioinformatician**, *National Bioinformatics Infrastructure Sweden*, Stockholm.

2013 - 2014 **Research engineer**, *Royal Institute of Technology*, Stockholm.

Education

2014 - 2018 **PhD (Biotechnology & Bioinformatics)**, *Royal Institute of Technology*, Stockholm.

2006 - 2013 **Master of Science in Engineering (Biotechnology)**, *Royal Institute of Technology*, Stockholm.

Selected courses

2021 **Research Supervision - Theory and Practice**, *Stockholm University*, Stockholm.

2019 **Carpentry Instructor Certification**, *The Carpentries & ELIXIR*, Stockholm.

2018 **Visualize Your Science**, *Visualize Your Science AB*, Stockholm.

Teaching

I have been involved in a number of advanced courses related to bioinformatics in the last few years. All of the courses are offered to PhD students, post-docs and other high-level researchers in Sweden (NBIS), Switzerland (SIB) and other countries in the ELIXIR network. I am a Course Leader for the Tools for Reproducible Research NBIS course. I am also a certified Carpentry Instructor. I have taught in both classroom and online settings.

2021 **Tools for Reproducible Research (autumn)**, *NBIS*, Online.

2021 **Snakemake Bring-Your-Own-Code Workshop**, *NBIS*, Online.

2021 **Tools for Reproducible Research (spring)**, *NBIS*, Online.

2020 **Tools for Reproducible Research (autumn)**, *NBIS*, Online.

2020 **Snakemake Bring-Your-Own-Code Workshop**, *NBIS*, Online.

2020 **RNA Summer School (single cell)**, *NBIS/SIB*, Schwarzenberg, Switzerland.

2019 **Omics Integration and Systems Biology**, *NBIS*, Stockholm, Sweden.

2019 **Software Carpentry**, *Royal Institute of Technology*, Stockholm, Sweden.

2019 **Introduction to Bioinformatics using NGS data**, *NBIS*, Uppsala, Sweden.

2019 **Tools for Reproducible Research (spring)**, *NBIS*, Stockholm, Sweden.

Resources

seqCAT, *a R/Bioconductor package for variant analysis and cell authentication using HTS data, https://www.bioconductor.org/packages/release/bioc/html/seqCAT.html.*

VarClust, *a Python package for variant analyses of single-cell HTS data, https://github.com/fasterius/VarClust.*

RNA-VC, *a Snakemake pipeline for variant analyses of publicly available RNA-seq data, https://github.com/fasterius/RNA-VC.*

Publications

1. Kennedy, S. A., Jarboui, M. A., Srihari, S., Raso, C., Bryan, K., Dernayka, L., Charitou, T., Bernal-Llinares, M., Herrera-Montavez, C., Krstic, A., Matallanas, D., Kotlyar, M., Jurisica, I., Curak, J., Wong, V., Stagljar, I., LeBihan, T., Imrie, L., Pillai, P., ... Kolch, W. (2020). Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. *Nature Communications*, *11*(1), 1–14.
2. Strandberg, K., Ayoglu, B., Roos, A., Reza, M., Niks, E., Signorelli, M., Fasterius, E., Ponten, F., Lochmüller, H., Domingos, J., Ala, P., Muntoni, F., Aartsma-Rus, A., Spitali, P., Nilsson, P., & Szigyarto, C. A. K. (2020). Blood-derived biomarkers correlate with clinical progression in Duchenne muscular dystrophy. *Journal of Neuromuscular Diseases*, *7*(3), 231–246.

3. Fasterius, E., Uhlén, M., & Al-Khalili Szigyarto, C. (2019). Single-cell RNA-seq variant analysis for exploration of genetic heterogeneity in cancer. *Scientific Reports*, *9*(1), 1–11.
4. Fasterius, E., & Al-Khalili Szigyarto, C. (2019). SeqCAT: A bioconductor R-package for variant analysis of high throughput sequencing data. *F1000Research*, *7*(1466).
5. Charitou, T., Srihari, S., Lynn, M. A., Jarboui, M. A., Fasterius, E., Moldovan, M., Shirasawa, S., Tsunoda, T., Ueffing, M., Xie, J., Xin, J., Wang, X., Proud, C. G., Boldt, K., Al-Khalili Szigyarto, C., Kolch, W., & Lynn, D. J. (2019). Transcriptional and metabolic rewiring of colorectal cancer cells expressing the oncogenic KRASG13D mutation. *British Journal of Cancer*, *121*(1), 37–50.
6. Fasterius, E., & Szigyarto, C. A.-K. (2018). Analysis of public RNA- sequencing data reveals biological consequences of genetic heterogeneity in cell line populations. *Scientific Reports*, *8(1)*(1), 1–11.
7. Danielsson, F., Fasterius, E., Sullivan, D., Hases, L., Sanli, K., Zhang, C., Mardinoglu, A., Al-Khalili, C., Huss, M., Uhlén, M., Williams, C., & Lundberg, E. (2018). Transcriptome profiling of the interconnection of pathways involved in malignant transformation and response to hypoxia. *Oncotarget*, *9*(28), 19730–19744.
8. Fasterius, E., Raso, C., Kennedy, S., Rauch, N., Lundin, P., Kolch, W., Uhlén, M., & Al-Khalili Szigyarto, C. (2017). A novel RNA sequencing data analysis method for cell line authentication. *PloS One*, *12*(2), e0171435.