Filip **Horvat**

Max Perutz Labs, Vienna, Austria

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| 🎓 scholar.google.com/citations?user=aA_cIdYAAAAJ

Bioinformatics postdoc at the DNA Damage Response and Transcription Regulation Lab

Profile

Highly skilled computational biologist with strong expertise in developing and implementing computational methods for analyzing complex biological data. Proficient in R programming framework and comfortable with working in Linux environments utilizing high-performance clusters. Possesses extensive experience working in multidisciplinary scientific teams on elucidating mechanisms of biological processes.

Professional Competence

Computational biology and bioinformatics

- Extensive experience in analyzing single-cell RNA-seq data, including preprocessing, quality control, normalization, batch effect correction, integration, clustering, differential expression analysis, and trajectory inference
- Strong background in transcriptomics data analysis: RNA-seq, small RNA-seq and TT-seq
- Significant expertise with genomics and epigenomics data analysis: ChIP-seq, CUT&RUN, ATAC-seq, WGBS-seq
- Familiarity with processing datasets produced with 3rd and 4th generation sequencing methods: PacBio, Nanopore
- Solid understanding of essential machine-learing algorithms

Programming languages	**R framework**
R (advanced) | Bash (advanced) | Python (beginner)	Bioconductor | Seurat | Shiny RMarkdown | tidyverse | ggplot2

Reproducibility and Automation	**General computational tools**
Nextflow | Git | Docker | Singularity Conda	Unix/Linux system administration High-performance clusters (HPC)

Personal skills

- Highly motivated and dedicated scientist with a passion for learning and implementing new technologies
- Team player with excellent interpersonal and communication skills
- Proficient in presenting intricate data, as evidenced by peer-reviewed publications
- Strong ability to discuss data, modeling, and analytics with non-computational team members

Languages

English (fluent) | German (basic)
Croatian (native)

Education

Charles University, Faculty of Science *Prague*
PHD IN DEVELOPMENTAL AND CELL BIOLOGY *2017 - 2023*

University of Zagreb, Faculty of Science *Zagreb*
MASTER IN MOLECULAR BIOLOGY *2013 - 2016*

University of Zagreb, Faculty of Science *Zagreb*
BACHELOR IN MOLECULAR BIOLOGY *2009 - 2013*

Professional Experience

Max Perutz Labs, DNA Damage Response and Transcription Regulation *Vienna*
POSTDOC - COMPUTATIONAL RESEARCH *2024 - current*
- Roles of proteins with SPOC domain in transcription regulation
- Regulation of neuronal gene expression and differentiation
- Molecular mechanisms of radiation-induced anti-tumor immunogenicity

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations *Prague*
PHD STUDENT - COMPUTATIONAL RESEARCH *2017 - 2023*
- Bioinformatic analysis of RNA dynamics in mammalian oocytes and early embryos
- Developing pipelines for automatic processing of next generation sequencing datasets generated in the lab
- Bioinformatic contribution to 12 high-level publications

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations *Prague*
SPECIALIST OF SCIENCE AND RESEARCH - COMPUTATIONAL RESEARCH *2016 - 2017*
- Statistical and differential expression analysis of RNA-seq datasets

Teaching Experience

University of Zagreb, Faculty of Science, Bioinformatics Group *Zagreb*
COMPUTATIONAL GENOMICS MODULE *2017 - 2023*
- Annual participation as a lecturer in 'Algorithms and programming' course for 2nd year master students - teaching R programming, designing and grading practical homework assignments, designing hackathon sessions and providing consultations to approx. 10 students per year

Mediterranean Institute for Life Sciences *Split*
SUMMER SCHOOL IN BIOINFORMATICS *2022*
- Presenting a practical, hands-on lecture on basics of RNA-seq data analysis for 30 participants
- Designing and teaching a 3 day interactive workshop - tutoring 6 participants how to find and download RNA-seq data from published papers, do the quality check, trim adapters and map reads to the genome using Galaxy framework, with subsequent exploratory and differential expression analysis done in R

Selected Peer-reviewed Publications

Kataruka, S., Kinterova, V., **Horvat, F.**, Kulmann, M. I. R., Kanka, J., & Svoboda, P. (2022). Physiologically relevant miRNAs in mammalian oocytes are rare and highly abundant. *EMBO Reports*, *23*(2), e53514.

Petrzilek, J., Pasulka, J., Malik, R., **Horvat, F.**, Kataruka, S., Fulka, H., & Svoboda, P. (2022). De novo emergence, existence, and demise of a protein-coding gene in murids. *BMC Biology*, *20*(1), 1–14.

Zapletal, D., Taborska, E., Pasulka, J., Malik, R., Kubicek, K., Zanova, M., Much, C., Sebesta, M., Buccheri, V., **Horvat, F.**, et al. (2022). Structural and functional basis of mammalian microRNA biogenesis by dicer. *Molecular Cell*, *82*(21), 4064–4079.

Loubalova, Z., Fulka, H., **Horvat, F.**, Pasulka, J., Malik, R., Hirose, M., Ogura, A., & Svoboda, P. (2021). Formation of spermatogonia and fertile oocytes in golden hamsters requires piRNAs. *Nature Cell Biology*, *23*(9), 992–1001.

Ganesh, S., **Horvat, F.**, Drutovic, D., Efenberkova, M., Pinkas, D., Jindrova, A., Pasulka, J., Iyyappan, R., Malik, R., Susor, A., et al. (2020). The most abundant maternal lncRNA Sirena1 acts post-transcriptionally and impacts mitochondrial distribution. *Nucleic Acids Research*, *48*(6), 3211–3227.

Kataruka, S., Modrak, M., Kinterova, V., Malik, R., Zeitler, D. M., **Horvat, F.**, Kanka, J., Meister, G., & Svoboda, P. (2020). MicroRNA dilution during oocyte growth disables the microRNA pathway in mammalian oocytes. *Nucleic Acids Research*, *48*(14), 8050–8062.

Demeter, T., Vaskovicova, M., Malik, R., **Horvat, F.**, Pasulka, J., Svobodova, E., Flemr, M., & Svoboda, P. (2019). Main constraints for RNAi induced by expressed long dsRNA in mouse cells. *Life Science Alliance*, *2*(1).

Taborska, E., Pasulka, J., Malik, R., **Horvat, F.**, Jenickova, I., Jelić Matošević, Z., & Svoboda, P. (2019). Restricted and non-essential redundancy of RNAi and piRNA pathways in mouse oocytes. *PLoS Genetics*, *15*(12), e1008261.

Horvat, F., Fulka, H., Jankele, R., Malik, R., Jun, M., Solcova, K., Sedlacek, R., Vlahovicek, K., Schultz, R. M., & Svoboda, P. (2018). Role of Cnot6l in maternal mRNA turnover. *Life Science Alliance*, *1*(4).

Franke, V., Ganesh, S., Karlic, R., Malik, R., Pasulka, J., **Horvat, F.**, Kuzman, M., Fulka, H., Cernohorska, M., Urbanova, J., et al. (2017). Long terminal repeats power evolution of genes and gene expression programs in mammalian oocytes and zygotes. *Genome Research*, *27*(8), 1384–1394.