



Filip Horvat

BIOINFORMATICIAN

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Professional Profile

Highly skilled and experienced computational biologist finishing a PhD in the field. Strong expertise in developing and implementing computational methods for analyzing complex biological data, including genomic and transcriptomic data. Proficient in programming languages such as R and Bash, with experience working in Linux environments. Extensive experience collaborating with multidisciplinary and international teams of scientists on elucidating mechanisms of various biological processes. Seeking a challenging role in industry where my skills and experience can be leveraged to advance scientific discovery and bridge the gap between the computational and experimental research.

Professional Experience

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations

Prague

PHD STUDENT - COMPUTATIONAL RESEARCH

2017 - current

- Computational analysis and integration of high-throughput datasets
- Conducting highly customized analyses and visualizations of complex biological data in R
- Developing pipelines that automate processing of next generation sequencing datasets generated in the lab
- Bioinformatic contribution to 10 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

University of Zagreb, Faculty of Science, Bioinformatics Group

Zagreb

INTERN - COMPUTATIONAL RESEARCH

2015 - 2016

- Management, interpretation, visualization, and statistical analysis of high-throughput sequencing data

Max F Perutz Laboratories, DNA Damage Response and Transcription Regulation

Vienna

INTERN - LABORATORY RESEARCH

Apr 2015 - Sep 2015

- Hands-on experience with various techniques such as PCR, gel electrophoresis, cell culture and DNA extraction

Education

Charles University, Faculty of Science

Prague

PHD IN DEVELOPMENTAL AND CELL BIOLOGY

2017 - current

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

Skills and Qualifications

Programming languages

R (ADVANCED), BASH (INTERMEDIATE), PYTHON (BEGINNER)

R framework

SHINY, RMARKDOWN, BIOCONDUCTOR, TIDYVERSE, GGLOT2, PLOTLY

Other computational tools

UNIX/LINUX, COMMAND LINE INTERFACE, NEXTFLOW, GIT

Languages

ENGLISH (FLUENT), GERMAN (BASIC), CROATIAN (NATIVE)

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

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., Vlahovick, 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.

Book Chapters

Horvat, F., & Svoboda, P. (2019). Microarray-based transcriptomics of early mammalian development. In *Advances in disease models*. OPTIO CZ.