



# Filip Horvat

BIOINFORMATICIAN

*Institute of Molecular Genetics, Prague, Czech Republic*

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## Professional Profile

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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 Competence

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### NGS data analysis

DIFFERENTIAL EXPRESSION ANALYSIS, CHIP-SEQ, RIP-SEQ, CNV, SNP, ASSEMBLY, BIOINFORMATICS  
SEQUENCE ANALYSIS METHODS

### applied NGS data analysis

TRANSCRIPTOMICS (RNA-SEQ, SCRNA-SEQ)

## Personal Skills

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## Professional Experience

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### Institute of Molecular Genetics, Laboratory of Epigenetic Regulations

PHD STUDENT - COMPUTATIONAL RESEARCH

*Prague*  
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

SPECIALIST OF SCIENCE AND RESEARCH - COMPUTATIONAL RESEARCH

*Prague*  
2016 - 2017

- Statistical and differential expression analysis of RNA-seq datasets

### University of Zagreb, Faculty of Science, Bioinformatics Group

INTERN - COMPUTATIONAL RESEARCH

*Zagreb*  
2015 - 2016

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

### Max F Perutz Laboratories, DNA Damage Response and Transcription Regulation

INTERN - LABORATORY RESEARCH

*Vienna*  
Apr 2015 - Sep 2015

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

## Education

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### Charles University, Faculty of Science

PHD IN DEVELOPMENTAL AND CELL BIOLOGY

*Prague*  
2017 - current

### University of Zagreb, Faculty of Science

MASTER IN MOLECULAR BIOLOGY

*Zagreb*  
2013 - 2016



## Skills and Qualifications

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### 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

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### 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

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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

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