Filip **Horvat**

PhD student, Bioinformatician

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Research Interests

Bioinformatics; computational biology; transcriptomics; developmental biology; small RNAs; retrotransposons

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*

Research Experience

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations — *Prague*
PhD student - computational research — *2017 - current*
- Bioinformatic analysis of RNA dynamics in mammalian oocytes and early embryos
- Maternal mRNA degradation
- Roles and distribution of small RNAs and long non-coding RNAs
- Profiling and analysis of retrotransposon expression and silencing

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations — *Prague*
Specialist of science and research - computational research — *2016 - 2017*
- Control of gene expression during mammalian oocyte-to-embryo transition

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*
- Activity of PARG protein in relation to loss of post-translational modifications in human cells

Teaching Experience

University of Zagreb, Faculty of Science, Bioinformatics Group — *Zagreb*
Computational Genomics module — *2017 - 2023*
- I annually participated as one of the lecturers in the Algorithms and programming course for 2nd year master students where I gave lectures in R programming, created and graded practical homework assignments, designed and chaired hackaton sessions and provided consultations to approx. 10 students per year

Mediterranean Institute for Life Sciences — *Split*
Summer School in Bioinformatics — *2022*
- I presented a practical, hands on lecture about basics of RNA-seq data analysis for 30 participants
- I designed and taught a 3 days interactive workshop where I tutored 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 differential expression and exploratory 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., 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.

Book Chapters

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

Skills

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

R framework
SHINY, RMARKDOWN, BIOCONDUCTOR, TIDYVERSE, GGPLOT2, PLOTLY

Other computational tools
UNIX/LINUX, COMMAND LINE INTERFACE, NEXTFLOW, GIT

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