



Filip Horvat

PHD STUDENT, BIOINFORMATICIAN

Institute of Molecular Genetics, Prague, Czech Republic

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Research Interests

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

Education

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

University of Zagreb, Faculty of Science

BACHELOR IN MOLECULAR BIOLOGY

Zagreb

2009 - 2013

Research Experience

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations

PHD STUDENT - COMPUTATIONAL RESEARCH

Prague

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

SPECIALIST OF SCIENCE AND RESEARCH - COMPUTATIONAL RESEARCH

Prague

2016 - 2017

- Control of gene expression during mammalian oocyte-to-embryo transition

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

- 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

COMPUTATIONAL GENOMICS MODULE

Zagreb

2017 - current

- I annually participated 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

SUMMER SCHOOL IN BIOINFORMATICS

Split

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

- I gave private lectures with goal to introduce several of my colleagues working in laboratory research to the basics of computational biology and R programming

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.** others. (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. others. (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. others. (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, GGLOT2, PLOTLY

Other computational tools

UNIX/LINUX, COMMAND LINE INTERFACE, NEXTFLOW, GIT

Languages

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