Filip **Horvat**

BIOINFORMATICIAN

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Profile

Highly skilled and experienced computational biologist finishing a PhD in the field with strong expertise in developing and implementing computational methods for analyzing complex biological data. Proficient in programming languages such as R and Bash and comfortable with working in Linux environments utilizing high-performance clusters. Possessing 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

Computational biology and bioinformatics

- Computational integration of high-throughput datasets, from experimental design to data analysis
- Extensive experience in analysing RNA-seq, small RNA-seq, ChIP-seq, ATAC-seq and WGBS-seq data
- Familiarity with single-cell genomics and transcriptomics datasets
- Skilled in curation and managment of both in-house produced as well as publicly availible datasets
- Experienced in processing datasets produced with 3rd and 4th generation sequencing methods (PacBio, Nanopore)
- Solid understanding of essential machine-learing algorithms
- Demonstrated knowledge of various bioinformatic algorithms and procedures, such as sequence alignment, differential expression and gene ontology analysis, genome and transcriptome assembly methods, phylogenetic analysis and variant calling

Personal skills

- Highly motivated and dedicated scientist with a passion for learning and implementing new technologies
- Team player that thrives in diverse teams, 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

Software and languages

Programming languages	R framework	Other computational tools
R (advanced) – Bash (intermediate) – Python (beginner)	Shiny – RMarkdown – Bioconductor – tidyverse – ggplot2 – plotly	Unix/Linux – Command line interface – High-performance clusters – Nextflow – Git – Docker – Conda

Languages

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

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*

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
- Developing pipelines for automatic 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

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., 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.