

Michel Moser

BIOINFORMATICIAN | SCIENTIFIC COLLABORATOR

Stationsstrasse 37, 3645 Gwatt

☎ +41 76 831 7226 | ✉ michel.moser@babs.admin.ch | 🏠 michelmoser.github.io | 📷 [michelmoser](#) | 🌐 [in](#)

[michel-moser001](#) | 🐦 [michel_moser](#)



Currently a research associate employed by SUPSI at Spiez Laboratory with a focus on computational proteomics, protein toxin detection pipelines and information management. Experienced Data Scientist with a demonstrated history of working in research industry. Skilled in Bioinformatics, Python and R programming, Statistical Modelling, Machine Learning, High Performance Computing, Containerization, Genomics and Transcriptomics with PacBio, NanoPore and Illumina sequencing data. Strong engineering professional with hands-on experience in proteomics, molecular biology, PCR, nanopore sequencing and LC-MSMS.

Employment

Scientific collaborator / Bioinformatician

Spiez, Switzerland

SUPSI/LABOR SPIEZ

August 2022 → Present

- Establishment and validation of wetlab protein toxin detection pipelines using immunoenrichment and nanoLC-IMS-MSMS
- Setup of computational proteomics and LC-MS data analysis workflows
- Administration and setup of High Performance Computing cluster
- Participation at international proficiency tests for the detection of toxins and viruses
- Training and teaching of military B-specialists in toxin detection
- Assistance in genomic sequencing projects and data analysis
- Collaboration on metagenomics project of waste water and bacterial genome assemblies
- In-house application development to optimize and digitalize lab measurements
- Evaluation and setup of information management software with integration of in-house applications

Data Scientist

Bern, Switzerland

W-HOCH2

August 2017 → Present

- External advisor for data analytics and graphical illustration
- Dashboard application development
- LANGUAGES: R, Python, PACKAGES: shiny, leaflet, sf

Medical Data Scientist

Bern, Switzerland

INTENSIVE CARE UNIT, UNIVERSITY HOSPITAL BERN INSELSPIITAL

Juli 2020 → August 2022

- Planning and analysing medical trial studies
- Applied machine learning to find factors for critical-illness induced neuromuscular changes
- Biomarker development
- LANGUAGES: R, Python

Postdoctoral Researcher in Salmonid genomics

Ås, Norway

CENTER FOR INTEGRATIVE GENETICS (CIGENE, NMBU)

November 2018 → August 2020

- Nanopore long read sequencing and de novo genome assembly of Salmonid species
- Study of Salmonid evolution and rediploidization in Salmonid species
- Main tasks: Generation of chromosome-scaled assemblies with Hi-C scaffolding and haplotype phasing, gene and repeat annotation
- LANGUAGES: R, Python, C++, TOOLS: flye, juicer, 3D-DNA, whatshap

Postdoctoral Researcher in plant genomics

Bern, Switzerland

UNIVERSITY OF BERN

Februar 2018 → October 2018

- Computational research in plant speciation
- Long read genome assembly,
- Population genomics in hybrid zones of Petunia
- Floral gene expression analysis and statistical inference of allele-specific expression using RNAseq data
- Main tasks: De novo genome sequencing and assembly (PacBio, Illumina, Hi-C), genome annotation, genetic map construction (GBS)
- LANGUAGES: R, Python, C++, Perl, Bash, APPLIED METHODS: Hi-C, PCR, RT-PCR, RNAseq, DNAseq

Research assistant 50%

INSTITUTE OF PLANT SCIENCES, UNIVERSITY OF BERN

- Completion of the first genome assembly of Petunia
- Contributions to the identification of genes responsible for UV absorbance and floral scent in Petunia

Bern, Switzerland

June 2013 → January 2018

Landscape Gardener

PARADIESGAERTEN.CH

- Construction of terraces, pools, walls and maintenance of garden and tree cutting

Bern, Switzerland

July 2006 → September 2010

Education

University of Bern

PHD OF SCIENCE IN CELL BIOLOGY

- Thesis title: Speciation genomics in Petunia
- COURSES: Applied Biostatistics I + II, Machine Learning, High-Performance Computing, Programming with Python

Bern, Switzerland

June 2013 → January 2018

University of Bern

MSC IN MOLECULAR LIFE SCIENCES

- Thesis title: RNA-seq analysis of floral tissue from Petunia
- Main tasks: De novo transcriptome assembly, differential gene/exon expression
- COURSES: Biochemie I + II, Java Programming I + II, Phylogeny with Beast

Bern, Switzerland

June 2011 → May 2013

University of Bern

BSC IN MOLECULAR LIFE SCIENCES

- Thesis title: Test of interaction and localisation of AtPTR2 and AtWLM2b
- Main tasks: investigation of protein-interactions using yeast2hybrid screening

Bern, Switzerland

September 2008 → May 2011

Berufsfachschule Bern

FEDERAL DIPLOMA OF HIGHER EDUCATION IN LANDSCAPE GARDENING AND VOCATIONAL BACCALAUREATE

- Apprenticeship at paradiesgaerten.ch in landscape gardening
- Special educations: dry stone walling, wild plant pastures

Bern, Switzerland

August 2003 → June 2006

software

- PROGRAMMING LANGUAGES: Python, R, bash, C++, SQL, VBA
- DATA INTERCHANGE FORMATS: CSV, JSON, XML, Parquet, bed, bam, vcf, fastq
- VERSION CONTROL: Git
- DATABASES: Postgres, MySQL
- CONTAINERIZATION: docker, docker-compose, singularity
- HPC: SLURM, SGE
- DATA VISUALIZATION: ggplot2, plotly, dash
- MICROSOFT OFFICE: Excel, Outlook, PowerPoint, Word, OneNote, Teams
- TEXT EDITORS: Vim, RStudio, Visual Studio Code

wetlab

- Automated protein purification with unspecific protein enrichment using carboxylated magnetic beads (SP3)
- Automated specific protein enrichment using antibody-coated magnetic beads
- ELISA
- Q-Bit concentration measurement of DNA/RNA/proteins, gel-electrophoresis, PCR
- DNA sample preparation, library preparation and sequencing with nanopore PromethION

mass spectrometry

- method and sample setup using nanoUPLC - IMS-MSMS system
- DIA: data-analysis with DIA-NN, result interpretation with custom R code
- DDA: data-analysis with Peaks
- PRM: data-analysis with Skyline, PRM optimization
- MALDI-TOF sample prep and data analysis

statistics

- MACHINE LEARNING: linear regression, linear mixed models, support vector machines, random forests, PCA, K-means, feature selection and feature engineering
- DEEP LEARNING: tensorflow, torch

genomics

- GENOME ASSEMBLY: flye, soap denovo
- READ ALIGNMENT: minimap2, bwa
- VARIANT CALLING: freebayes, GATK, sniffles
- PHASING: whatshap
- GENOME ANNOTATION: maker, PGAP

transcriptomics

- ASSEMBLY: trinity
- DIFFERENTIAL GENE EXPRESSION: DESeq2
- ALLELE SPECIFIC EXPRESSION: MBASED

languages

- Proficient in multiple languages - German, English (fluent), French (intermediate), Norwegian (basic)

1. Bombarely, A., Moser, M., Amrad, A., Bao, M., Bapaume, L., Barry, C. S., Bliet, M., Boersma, M. R., Borghi, L., Bruggmann, R., et al. (2016). Insight into the evolution of the solanaceae from the parental genomes of *petunia hybrida*. *Nature Plants*, 2(6), 16074.
2. Hermann, K., Klahre, U., Moser, M., Sheehan, H., Mandel, T., & Kuhlemeier, C. (2013). Tight genetic linkage of prezygotic barrier loci creates a multifunctional speciation island in *petunia*. *Current Biology*, 23(10), 873–877.
3. Esfeld, K., Berardi, A. E., Moser, M., Bossolini, E., Freitas, L., & Kuhlemeier, C. (2018). Pseudogenization and resurrection of a speciation gene. *Current Biology*, 28(23), 3776–3786.
4. Amrad, A., Moser, M., Mandel, T., Vries, M. de, Schuurink, R. C., Freitas, L., & Kuhlemeier, C. (2016). Gain and loss of floral scent production through changes in structural genes during pollinator-mediated speciation. *Current Biology*, 26(24), 3303–3312.
5. Sheehan, H., Moser, M., Klahre, U., Esfeld, K., Dell’Olive, A., Mandel, T., Metzger, S., Vandenbussche, M., Freitas, L., & Kuhlemeier, C. (2016). MYB-FL controls gain and loss of floral UV absorbance, a key trait affecting pollinator preference and reproductive isolation. *Nature Genetics*, 48(2), 159.
6. Kent, M., Kirubakaran, G. T., Andersen, Ø., Moser, M., Árnýasi, M., McGinnity, P., & Lien, S. (2019). A nanopore based chromosome-level assembly representing atlantic cod from the celtic sea. *bioRxiv*, 852145.
7. Pearse, D. E., Barson, N. J., Nome, T., Gao, G., Campbell, M. A., Abadía-Cardoso, A., Anderson, E. C., Rundio, D. E., Williams, T. H., Naish, K. A., et al. (2019). Sex-dependent dominance maintains migration supergene in rainbow trout. *Nature Ecology & Evolution*, 1–12.
8. Messmer, A. S., Moser, M., Zuercher, P., Schefold, J. C., Müller, M., & Pfortmueller, C. A. (2022). Fluid overload phenotypes in critical illness—a machine learning approach. *Journal of Clinical Medicine*, 11(2), 336.
9. Kent, M., Moser, M., Boman, I. A., Lindtveit, K., Árnýasi, M., Sundsaasen, K. K., & Våge, D. I. (2021). Insertion of an endogenous jaagsiekte sheep retrovirus element into the BCO2-gene abolishes its function and leads to yellow discoloration of adipose tissue in norwegian spælsau (*ovis aries*). *BMC Genomics*, 22(1), 1–8.
10. Mérot, C., Stenløkk, K. S., Venney, C., Laporte, M., Moser, M., Normandeau, E., Árnýasi, M., Kent, M., Rougeux, C., Flynn, J. M., et al. (2022). Genome assembly, structural variants, and genetic differentiation between lake whitefish young species pairs (*coregonus* sp.) with long and short reads. *bioRxiv*.
11. Martínez, P., Robledo, D., Taboada, X., Blanco, A., Moser, M., Maroso, F., Hermida, M., Gómez-Tato, A., Álvarez-Blázquez, B., Cabaleiro, S., et al. (2021). A genome-wide association study, supported by a new chromosome-level genome assembly, suggests *sox2* as a main driver of the undifferentiated ZZ/ZW sex determination of turbot (*scophthalmus maximus*). *Genomics*, 113(4), 1705–1718.
12. Zuercher, P., Moser, M., Waskowski, J., Pfortmueller, C. A., & Schefold, J. C. (2022). Dysphagia post-extubation affects long-term mortality in mixed adult ICU patients—data from a large prospective observational study with systematic dysphagia screening. *Critical Care Explorations*, 4(6), e0714.
13. Martínez Portela, P., Robledo Sánchez, D., Taboada Penoucos, X., Blanco Hortas, A., Moser, M., Maroso, F., Hermida Prieto, M., Gómez Tato, A., Blázquez, B., Álvarez, Cabaleiro, S., et al. (n.d.). *A genome-wide association study, supported by a new chromosome-level genome assembly, suggests sox2 as a main driver of the undifferentiated ZZ/ZW sex determination of turbot (scophthalmus maximus)*.
14. Pearse, D., Barson, N., Nome, T., Gao, G., Campbell, M., Abadía-Cardoso, A., Anderson, E., Rundio, D., Williams, T., Naish, K., et al. (2019). Sex-dependent dominance maintains migration supergene in rainbow trout. *Nat. Ecol. Evol.* 3: 1731–1742.
15. Stenløkk, K., Saitou, M., Rud-Johansen, L., Nome, T., Moser, M., Árnýasi, M., Kent, M., Barson, N. J., & Lien, S. (2022). The emergence of supergenes from inversions in atlantic salmon. *Philosophical Transactions of the Royal Society B*, 377(1856), 20210195.
16. Pearse, D. E., Barson, N. J., Nome, T., Gao, G., Campbell, M. A., Abadia-Cardoso, A., Anderson, E. C., Rundio, D. E., Williams, T. H., Naish, K. A., et al. (2020). Sex-dependent dominance maintains migration supergene in rainbow trout (vol 3, pg 1731, 2019). *NATURE ECOLOGY & EVOLUTION*, 4(1), 170–170.
17. Zürcher, P., Lang, B., Moser, M., Messmer, A. S., Waskowski, J., & Schefold, J. C. (2022). Dysphagia incidence in ICU patients with COVID-19-a retrospective analysis following systematic dysphagia screening. *The Journal of Laryngology and Otology*, 1–17.
18. Tang, H., Kong, W., Nabukalu, P., Lomas, J. S., Moser, M., Zhang, J., Jiang, M., Zhang, X., Paterson, A. H., & Yim, W. C. (2024). GRABSEEDS: Extraction of plant organ traits through image analysis. *Plant Methods*, 20(1), 140.

19. Camilla, P., Roger, K., Maurizio, C., Elisa, P., Maye, S., Di Maggio, L., Moser, M., Fabian, F., & Pamela, P. (2025). *Shewanella oneidensis* and *methanosarcina barkerii* augmentation and conductive material effects on long-term anaerobic digestion performance. *Biotechnology for Biofuels and Bioproducts*, 18(1), 1–12.