CONTACT

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LinkedIn · GitHub · Google Scholar

IVI & Vetsuisse Faculty, University of Bern, Länggassstrasse 120, 3012 Bern

SKILLS

Programming
Python, R / Shiny, Bash, Git

Single-Cell & Omics
Scanpy, Seurat, Scverse, ESM, CellBender, STAR(solo),Salmon, edgeR, GATK

Repertoire
MiXCR, IPD-MHC

Statistics & ML
Exploring data through statistical modelling and machine learning in Python (scikit-learn) and R (caret)

Compute
Linux, SLURM, Apptainer, Docker, GPU

Visualisation
ggplot2, circos, Cytoscape, Shiny, Streamlit

LANGUAGES

Spanish	native
Romanian	native
English	fluent
German	intermediate
French	survival

INTERESTS

Paragliding, skiing, climbing and outdoor sports. Nutrition, machine learning and protein language models, and more.

Marius Alexandru Botos Rogozsan

· Computational Biologist and Immunologist · Single-Cell & Systems Immunology · Non-Model Species Bioinformatics

Profile

Computational immunologist and molecular biologist focused on transcriptomics and genomics across model and domestic species, including zebrafish heart regeneration and obesity genomics. Skilled in developing and deploying HPC workflows and statistical models to extract biological insight from bulk and single-cell data.

Research experience

PhD candidate — Immunology of non-model species
Jan 2024 – Jun 2027
Institute of Virology and Immunology (IVI) & Vetsuisse Faculty, University of Bern

- Systems vaccinology: BTM / GSEA profiling of sheep whole blood across adjuvant regimens.
- Single-cell atlas: 10x scRNA-seq of sheep whole blood with a STARsolo SLURM pipeline, CellBender and scVI-based annotation.
- Bulk deconvolution: own Python pipeline estimating cell-type fractions in 170 blood samples, benchmarked against CIBERSORTx, MuSiC and Bisque.
- MHC, immune repertoire & TFs: allele expression (Salmon, custom IPD-MHC reference), TCR/BCR repertoires (MiXCR, custom sheep IMGT library) and inferred TF activities (decoupleR).
- Responder prediction: modelling high vs low antibody responders from early RNA-seq, gene signature (BTMs), TF activity, repertoire, and MHC variants.
- Comparative DC: transitional DC and MPS in pig and horse blood, with protein language model and gene expression cross-species integration.
- Digital pathology: comparison of manual vs computational quantification of SARS-CoV-2 in infected mice.

Bioinformatician research assistant
Nov 2022 – Dec 2023
Laboratory of Systems Biology and Genetics, EPFL & Swiss Institute of Bioinformatics, Lausanne

- Joints, BMI and bone marrow: analysed knee and hip associations with BMI and how bone-marrow cells shift towards a more inflammatory profile in obesity.
- Drosophila genomics: NUMT (nuclear mitochondrial insertion) analysis across inbred Drosophila genomes with Unix/Python/R pipelines and circos.
- Obesity genomics: single-cell RNA/ATAC-seq (scVI, Scanpy, Signac, PeakVI on GPU/HPC) of adipose precursor cells in subcutaneous and visceral fat from mice and humans, linked to genetic associations with obesity.

Bioinformatician research assistant
Nov 2018 – Oct 2022
Developmental Biology and Regeneration, Institute of Anatomy, University of Bern

- Heart regeneration meta-analysis: first-author meta-analysis of 36 RNA-seq samples across three cardiac injury models, published with an interactive Shiny / Cytoscape app.
- Reporting: results shared through Shiny and Streamlit web apps.
- Genomics support: bulk RNA-seq, SNP / indel variant calling and early single-cell analyses behind three co-authored zebrafish papers.

Education

PhD candidate
Jan 2024 – present
Graduate School for Cellular and Biomedical Sciences, University of Bern

CAS in Applied Data Science and Machine Learning
2019 – 2020
University of Bern

MSc Bioinformatics & Omics Applied to Personalized Medicine
2017 – 2018
Escuela Nacional de Sanidad (ISCIII) with CNIO, Madrid · Thesis: GATK pipeline for single-nucleotide variant detection in rare diseases (IIS-Fundación Jiménez Díaz).

MSc Biotechnology
2016 – 2017
Universidad Autónoma de Madrid · Thesis: age-related NUMTs in Drosophila melanogaster genomes (InnoHealth group, Parque Científico de Madrid).

BSc Biology
2012 – 2016
Universidad de Alcalá, Madrid · Thesis: antibiotic-resistance genes in environmental waters, University of Hertfordshire (UK).

COURSES

Docker & Singularity
SIB/University of Bern, 2019

Cellular and Molecular Immunology
University of Bern, 2024

Introduction to Bayesian Statistics
SIB, 2024 - 2025

Immunology Book Club
University of Bern, 2024 - 2025

Winter School in Deep Learning
University of Bern, 2026

PRESENTATIONS

Presentation · Early Blood Transcriptomic Signatures Predict Long-Term Antibody Responses and Inform on Adjuvant Selection · VIA meeting, 2026

Poster · Deciphering dendritic-cell heterogeneity across species using protein language model-based tools · IVIS, 2025

Publications

1. Botos-Rogozsan MA, Mitrovic J, Brito F, Mohn U, Neulen ML, Summerfield A. Baseline immune tone and early innate activation predict long-term antibody responses to adjuvanted vaccines in Ovis aries. (In preparation)
2. Kozarac N*, Botos M* , Burgener L*, de Brot S, Brito F, Berenguer Veiga I, Taddeo A, Devisme C, Bagatella S, Ebert N, Barut GT, Moreira ÉA, Leborgne NGF, Brügger M, Thiel V, Benarafa C, Graña-Roma L. Computational analysis of immunohistochemistry enables quantitative assessment of SARS-CoV-2 nucleocapsid immunolabeling in experimentally infected mice. Viruses 2026;18(10):1142. doi:10.3390/v18101142
3. Baillou A, Botos M, Oberhaensli S, Cvitas I, Jonsdottir S, Ziegler A, Brito F, Summerfield A, Marti E, Talker SC. Dendritic-cell diversity in equine blood revealed by single-cell transcriptomics. Discovery Immunology 2026;5(1):kyag012. doi:10.1093/discim/kyag012
4. Baillou A, Auray G, Brito F, Botos M, Huber A, Summerfield A, Talker SC. Unraveling porcine dendritic-cell diversity: welcome tDC and DC3. Frontiers in Immunology 2025;16:1639553. doi:10.3389/fimmu.2025.1639553
5. Botos MA, Arora P, Chouvardas P, Mercader N. Transcriptomic data meta-analysis reveals common and injury model specific gene expression changes in the regenerating zebrafish heart. Scientific Reports 2023;13:5418. doi:10.1038/s41598-023-32272-6
6. García-Poyatos C, Cogliati S, Calvo E, Hernansanz-Agustín P, Lagarrigue S, Magni R, Botos M, Langa X, Amati F, Vázquez J, Mercader N, Enríquez JA. Scaf1 promotes respiratory supercomplexes and metabolic efficiency in zebrafish. EMBO Reports 2020;21(7):e50287. doi:10.15252/embr.202050287
7. Sande-Melón M, Marques IJ, Galardi-Castilla M, Langa X, Pérez-López M, Botos MA, Sánchez-Iranzo H, Guzmán-Martínez G, Ferreira Francisco DM, Pavlinic D, Benes V, Bruggmann R, Mercader N. Adult sox10⁺ cardiomyocytes contribute to myocardial regeneration in the zebrafish. Cell Reports 2019;29(4):1041–1054.e5. doi:10.1016/j.celrep.2019.09.041
8. Sanz-Morejón A, García-Redondo AB, Reuter H, Marques IJ, Bates T, Galardi-Castilla M, Große A, Manig S, Langa X, Ernst A, Piragyte I, Botos MA, González-Rosa JM, Ruiz-Ortega M, Briones AM, Salaices M, Englert C, Mercader N. Wilms tumor 1b expression defines a pro-regenerative macrophage subtype and is required for organ regeneration in the zebrafish. Cell Reports 2019;28(5):1296–1306.e6. doi:10.1016/j.celrep.2019.06.091

* Equal contribution.