



I am a qualified Biologist with research experience in single-cell transcriptomics and data image analysis from mIF. I worked for two years at ETH in the System Physiology Group. Currently, I am a Shiny DevOp designing qPCR pipelines for hospitals in Shiny production mode.

WORK EXPERIENCE

Shiny DeVop, HSLU (70%)

Space Biology Group, Institute of Medical Devices (Pr. Dr Fabian Ille)
Data Cockpit for qPCR, FACS, spacial proteomics, bulk and sc RNA-seq, etc
Writing grants, student support (html, CSS, HTC, python, R, shiny)

June 2024 - Current

Luzern, Switzerland

Data Analyst, ETH Zurich, BSSE (100%)

System physiology group (Pr. Dr Med. Andreas Moor)
Spatial transcriptomics (Merscope, Xenium, Visium data), Molecular cartography (ReSolve Bioscience), IF (COMET antibody staining, manual), flow cytometry (FlowJo, QuPath, ImageJ2, R, ssh, JupyterLab, Julia, Python)

June 2022 - Mar 2024

Basel, Switzerland

EDUCATION

Yuriy Fedkovych Chernivtsi National University

MSc, Biology

Sep 2021 – Dec 2022

Chernivtsi, Ukraine

University of the People

BSc, [Health](#) Science

Jan 2021 – current

Passadena, USA
online

Yuriy Fedkovych Chernivtsi National University

MSc, Biotechnology and Bioengineering

Sep 2019 – Dec 2020

Chernivtsi, Ukraine

Institute of Energy Saving and Energy Management

BSc, MSc, Chemical Engineering

Sep 2000 – May 2005

TEACHING EXPERIENCE

R and RNA sequencing, spatial biology

Collaboration DAAD and LifeSciencesCourse, UniTubingen
IMC, image analysis, practical workshops (200 students) [GitHub](#)
Course project leading

Feb - Apr 2025

GenomicsUA
online

RESEARCH EXPERIENCE

Spatial transcriptomics data analysis

Merscope spatial autocorrelation analysis [GitHub](#)
Resolve segmentation quality assessment [GitHub](#)
Segmentation Baysor, data post-analysis (Docker, Julia, Python) [GitHub](#)

Spatial proteomics data analysis

Probability-based algorithm for deep phenotyping COMET images [GitHub](#)

20-plex images (CRC) via **MCMICRO** pipeline (NextFlow, Docker, Singularity)

Whole-cell segmentation **MESMER**

Manual and unbiased classification (FlowSom, MEM, Phenograph)

Coordinated Cellular **neighborhoods** (Python)

Quality assessment via FlowJo and dynamic range (QuPath, Python)

Stemness model for assessing oncogenic states to single-cell and spatial omic cancer datasets (Visium, R, ML model) [GitHub](#)

June 2022 - Mar

2024

D-BSSE ETH,
Moor's lab
Basel, Switzerland

Steinbock pipeline for IF images. Visualization and spatial analysis. (Docker, R, Napari) [GitHub](#)

Tissue cellular neighborhoods **CytoCommunity** (R, Python) [GitHub](#)

Project: computational bioimaging OME-TIFF analysis, COMET, manual IF

R Shiny data visualization - **COSMOS** [shinyapps.io](#) (HTML, CSS, testthat):

qPCR: example [RDML](#) file: amplification, melting curves, stats, gene expression (R6, data.table, md, purrr, checkmate);

FACS: example: [dir & wsp](#): sample vol analysis, gating, etc.

bulkRNA-seq: GO, power analysis, stats, volcano, heatmap, etc. (DeSeq2, etc.)

spatial proteomics: preprocessing, segmentation (normalization, OTSU, cellpose), spatial analysis (EBImage, cytomapper, etc.)

June 2024 - current

Luzern, Switzerland

MSc student, Yuriy Fedkovych Chernivtsi National University (ChNU)

Supervisor – Prof. Roman Volkov

MSc thesis: Histology of bee intestines

Techniques involved: histological techniques (microscopy, microtomy, paraffin section, tissue processing, R)

Sep 2021 – Dec

2022

Chernivtsi, Ukraine

MSc student, Yuriy Fedkovych Chernivtsi National University (ChNU)

Supervisor – Prof. Roman Volkov

MSc thesis: [Analysis of the COI gene region in local bees *Apis mellifera* L.](#)

Techniques involved: DNA extraction, PCR, DNA Seq analysis, population genetics analysis, phylogenetic analysis, DNA sequences into GenBank

Sep 2019 – Dec

2020

Chernivtsi, Ukraine

NGS data analysis, Bioinformatics Institute - intensive course

Project: [NGS data analysis: introduction to medical and statistic genetics](#)

Techniques involved: reads filtration, quality control (fastQC, trimmomatic); SNP calling, Read alignment (IGV, bwa, samtools, VarScan, .vgf, bedtools); variant annotation (wANNOVAR, Ensembl VEP); GWAS (plink, .qassoc, R)

Nov 2021

online

Biological and medical statistics, Bioinformatics Institute - intensive course

Techniques involved: R data preprocessing; statistical analysis of multivariate data, correct processing of the results, data visualization; testing hypotheses, planning a clinical trial

Apr 2021

online

RESEARCH SKILLS

Histology	Microscopy, microtomy, paraffin section, tissue processing, ImageG, QPath, microscopy, mIHC, microfluidic IF, COMET
Molecular Biology	DNA and RNA extraction from animal tissues and cells, from insects, viruses, bacteria, plasmid, and genomic DNA isolation, gene cloning from bacteria, PCR, DNA sequence analysis, protein isolation
Bioinformatics	Chromatogram analysis, DEG, single cell analysis (scRNA Seq, Seurat, statistics: PCA, QC), Python, Linux, R, Shiny, SQL, stats, spatial analysis, NextFlow, Docker, FlowJo

PUBLICATIONS

Chernivtsi National University, Ukraine

Cherevatov O, **Melnik E**, Volkov R. (2020) Polymorphism of *COI* gene in honey bees from different regions of Ukraine. *The Bulletin of Vavilov Society of Geneticists and Breeders of Ukraine*. Vol 18(1-2). <https://doi.org/10.7124/visnyk.utgis.18.1-2.1351>

ETH, Basel

Leśniewska, A., Dziągiewski, S., **Melnik, E.**, Okoniewski, M.J., Wrembel, R. (2025). Integrating the Biological Knowledge from Protein Databases Into Spatial RNA Sequencing Analyses. In: Delir Haghighi, P., Greguš, M., Kotsis, G., Khalil, I. (eds) Information Integration and Web Intelligence. iiWAS 2024. Lecture Notes in Computer Science, vol 15343. Springer, Cham. https://doi.org/10.1007/978-3-031-78093-6_23

LANGUAGES

English (conversational, C1), **Russian, Ukrainian** (native), **Dutch, German, Romanian** (elementary)

References

Prof. Fabian Ille HSLU (Luzern)

Team leader

fabian.ille@hslu.ch

Dr. Xenia Ficht ETH D-BSSE

PostDoc in Moorlab

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Kirstie Meldrum Roche, Switzerland *Senior Clinical Operations Lead - Oncology* kirstie.meldrum@roche.com