Scientific Public Review Session • 2025

Aleksandra G. Bilska

Doctoral School
of Molecular Medicine
Medical University of Lodz

MEDICAL
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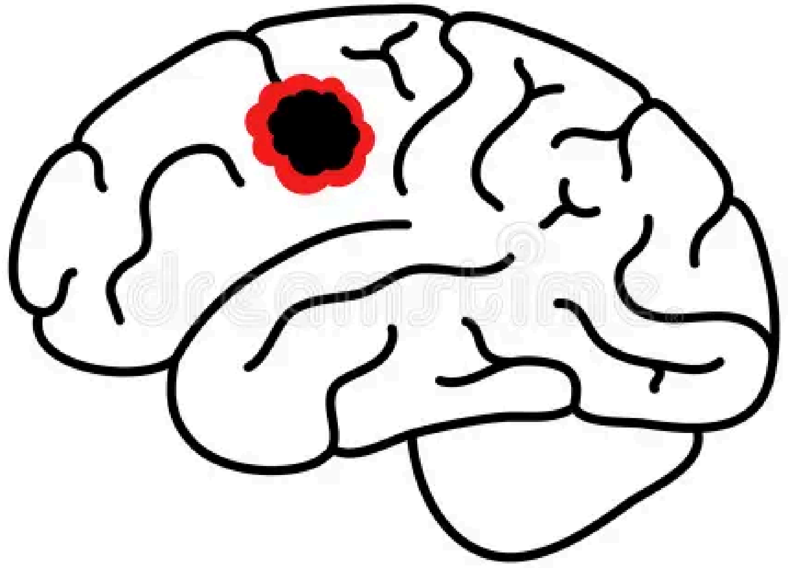
New Direction – Glioma Epigenetics ••••

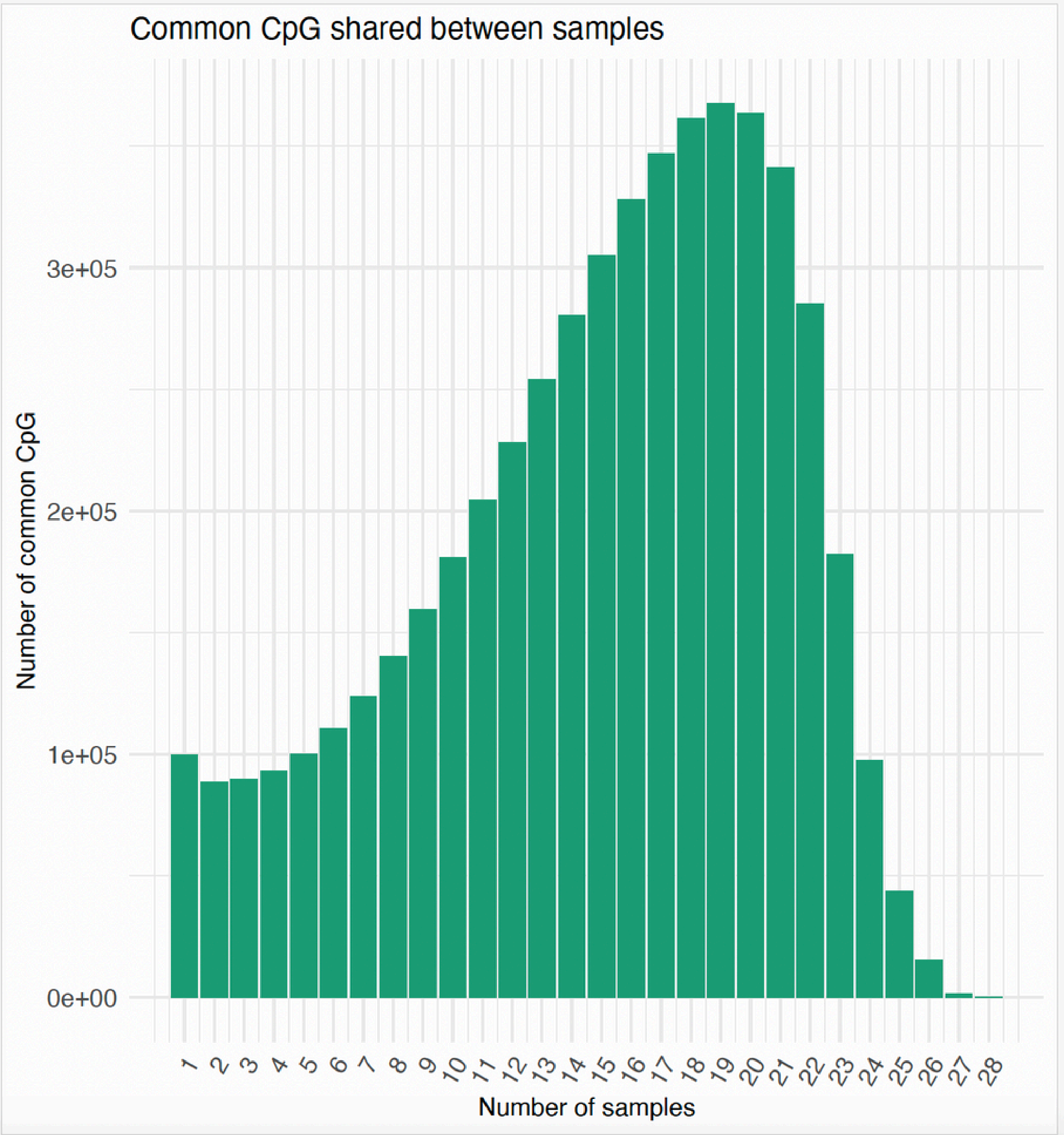
- Initial step: DNA methylation variance of regulatory regions across glioma grade samples from Symfonia project with a special attention on TF motifs
- Special attention on:
    - TAD boundaries in relation to the areas inside and outside the loops
    - early relative to later replicated DNA regions on subsequent chromosomes

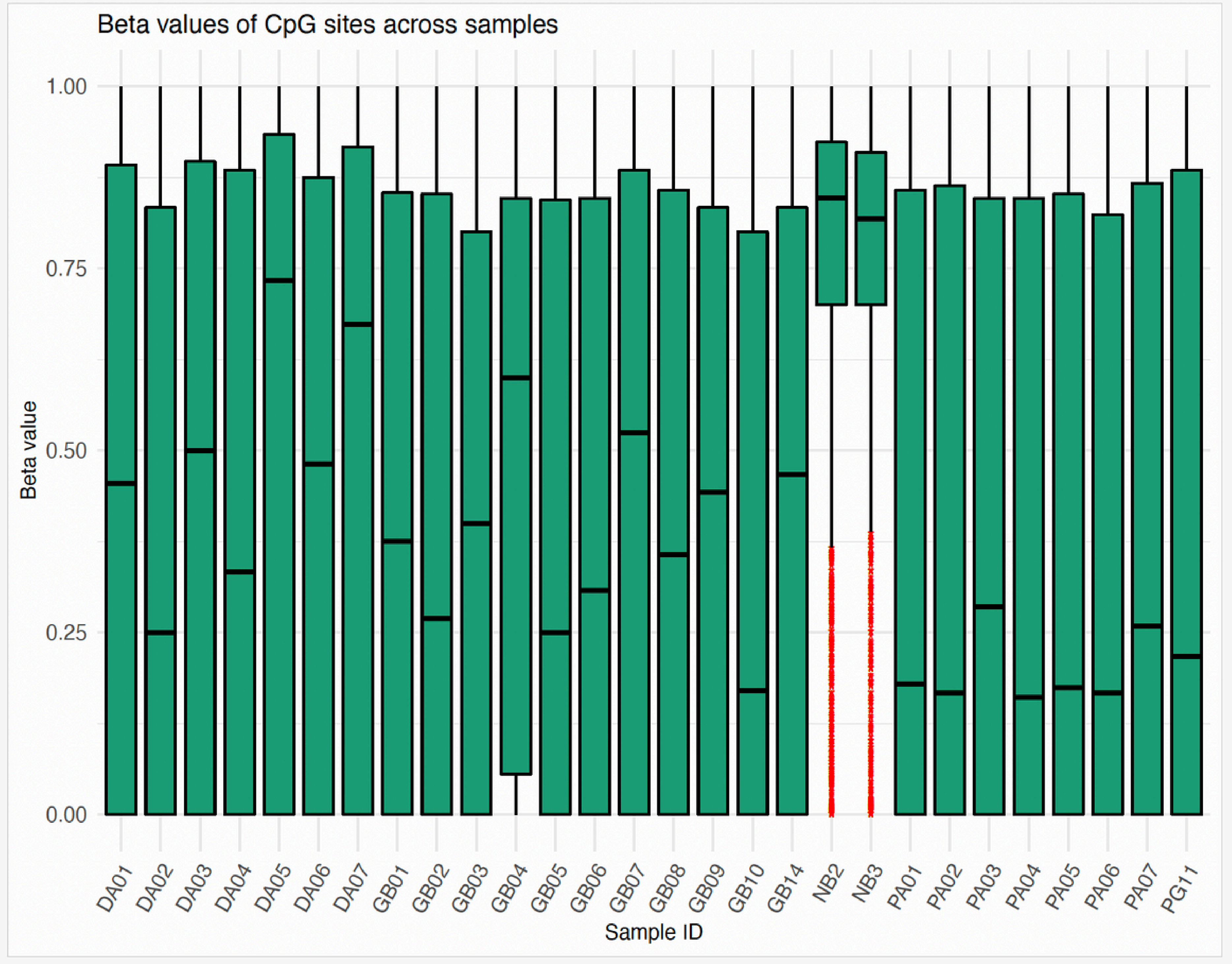
- **The new topic maintains conceptual continuity by building on prior bioinformatic methods and applying them to a new biological context**
- Given the substantial development of bioinformatic expertise and tools, the transition to a new research focus is feasible and scientifically justified

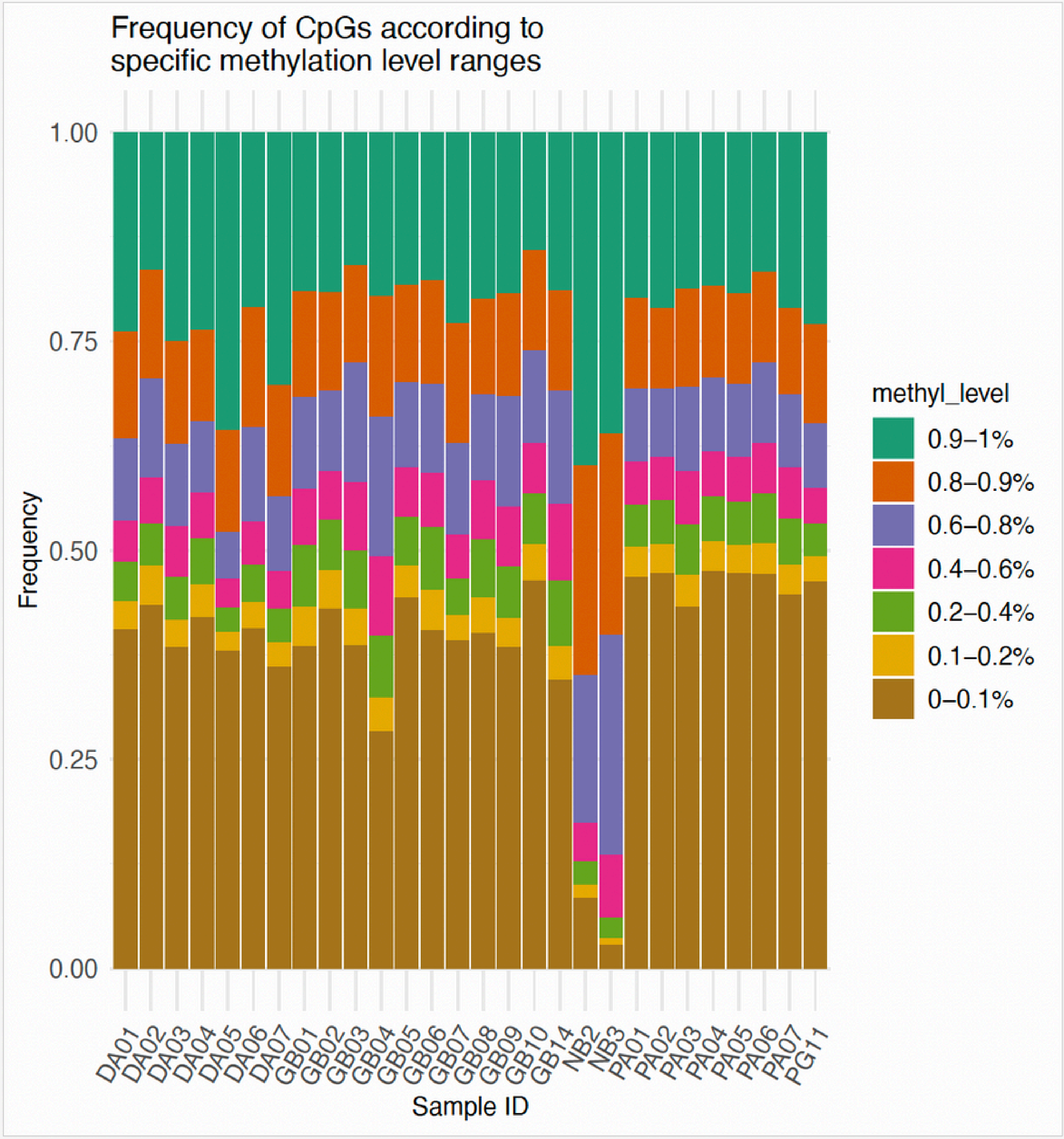


Sample	WHO grade	n	adult	pediatric	IDH-mut
pilocytic astrocytoma (PA)	G1	7	0	7	NA
diffuse astrocytoma (DA)	G2/G3	8	8	0	4
glioblastoma (GBM)	G4	11	10	1	0
non-tumour	-	2	2	0	NA

- High Bisulfite Conversion Efficiency
- Robust CpG Coverage
- Substantial On-Target Read Proportion
- Effective Filtering and Duplication Removal
- Good Mean Coverage Across Samples (~40%)




Beta values of CpG sites across samples
Beta value
1.00
0.75
0.50
0.25
0.00
DA01
DA02
DA03
DA04
DA05
DA06
DA07
GB01
GB02
GB03
GB04
GB05
GB06
GB07
GB08
GB09
GB10
GB14
NB2
NB3
PA01
PA02
PA03
PA04
PA05
PA06
PA07
PG11
Sample ID


Frequency of CpGs according to
specific methylation level ranges
Frequency
1.00
0.75
0.50
0.25
0.00
DA01
DA02
DA03
DA04
DA05
DA06
DA07
GB01
GB02
GB03
GB04
GB05
GB06
GB07
GB08
GB09
GB10
GB14
NB2
NB3
PA01
PA02
PA03
PA04
PA05
PA06
PA07
PG11
Sample ID
methyl_level
0.9–1%
0.8–0.9%
0.6–0.8%
0.4–0.6%
0.2–0.4%
0.1–0.2%
0–0.1%

PHD RESEARCH PROJECT

- A full project and an INDIVIDUAL RESEARCH PLAN will be submitted by the end of July 2025
- Raw and processed data are owned by collaborators:

  SYMFONIA NCN: 2015/16/W/NZ2/00314

UNIVERSITY OF WARSAW

Bartosz Wojtaś, PhD

Laboratory of Sequencing

Michał J. Dąbrowski, PhD

Computational Biology Lab

CytoMeth

github.com/mdraminski/CytoMeth

PAN

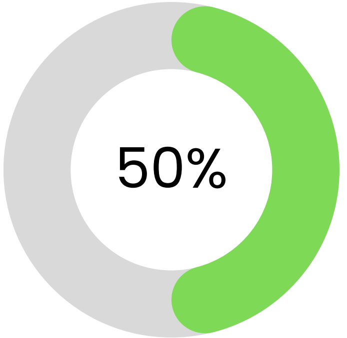
nencki institute of experimental biology

CytoMeth is a user-friendly bioinformatic tool designed for comprehensive DNA methylation analysis from raw sequencing data to interpretable results, including differential methylation and variant calling.

- Full methylation analysis pipeline from FASTQ to beta values.
- Variant (SNP) calling using BS-Snper.
- Generation of descriptive plots across samples and genomic regions.
- Differential methylation analysis via DiffMeth module.
- Grouping of neighboring cytosines into biologically relevant c-rich regions.
- Correlation analysis between methylation and gene expression (optional).
- Available as a Docker container or GitHub scripts (Linux).

Genetic basis of vocal communication and its importance in dog domestication

NCN OPUS no. 2021/43/B/NZ8/03316



- Comparative transcriptomics
- RNA-seq data
- Biostatistics: hypothesis testing, variance, correlations
- Signaling pathway analysis (FoxP networks)

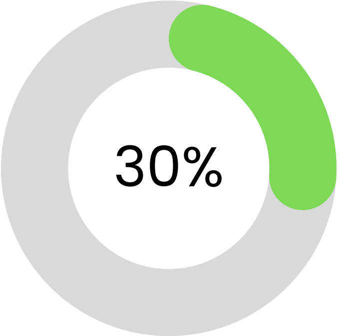
Wiesław Bogdanowicz, Professor

PROJECTS

A machine learning usage to predict venetoclax efficacy and toxicity in chronic lymphocytic leukemia.

PRELUDIUM NCN - 2024

MEDICAL UNIVERSITY OF WARSAW



- Machine learning (MCFS-ID, feature selection, clustering)
- Predictive modeling (expression ↔ phenotype)

Dorota Kruk-Kwapisz, MSc, BEng

Medical University of Warsaw

Krzysztof Jamroziak, Professor

Institute of Hematology and Blood Transfusion

Warsaw
CLL Workshop

21-22 marca 2025 r.

Machine learning usage to predict venetoclax efficacy and toxicity in chronic lymphocytic leukemia.

Dorota Kruk-Kwapisz
Aleksandra G. Bilska

WYDARZENIE
INFARMA
9131
CERTYFIKOWANE

MED_SPACE

VPS10P domain receptors in phenotypic polarization of astrocytes and microglia in the diseased brain.

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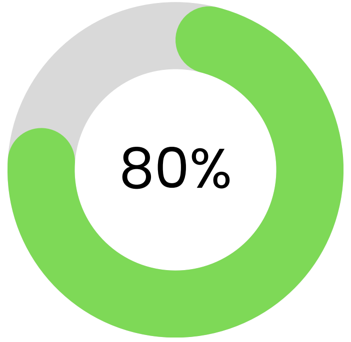
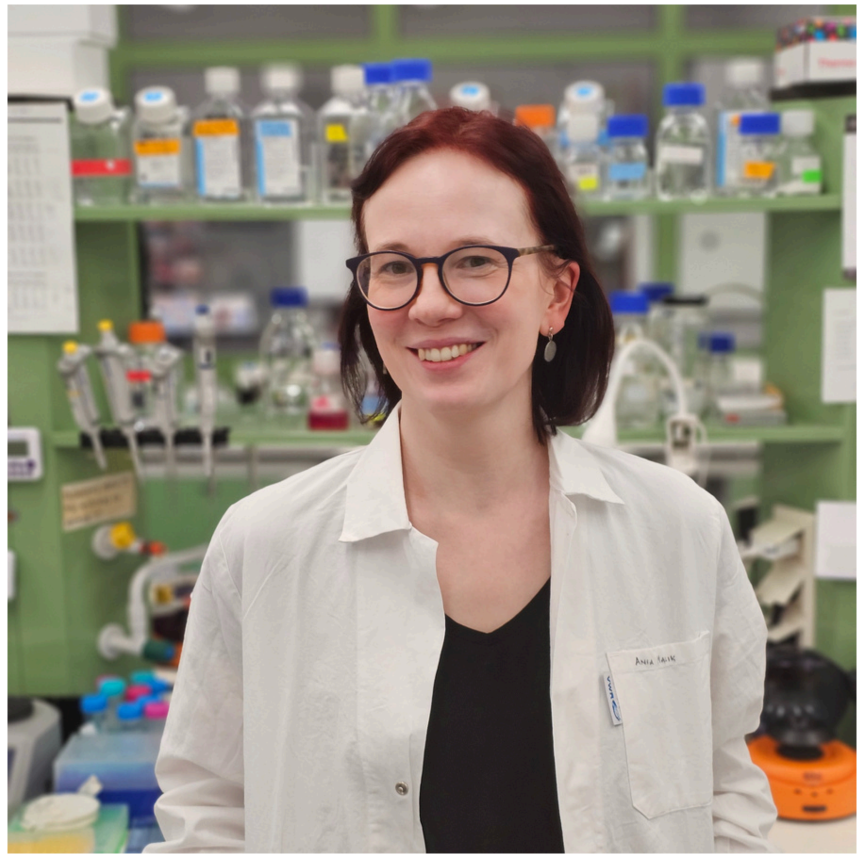


OPUS NCN 2020/37/B/NZ3/00761

- Machine learning (feature selection, clustering, dimension reduction)
- Public data reuse and benchmarking
- Functional clustering with NLP
- Signaling pathway analysis
- Single-cell RNA-seq analysis (clustering, UMAP, cell-type DEGs)



Anna R. Malik, PhD
Cellular Neurobiology Research Group

PROJECTS

Bioinformatic Tool for Identifying and Characterizing Glioma-Associated Macrophages and Microglia (GAMs) in Single-Cell RNA Sequencing Data

Parylation as a factor regulating the expression of genes involved in immune processes

MEiN „Nauka dla Społeczeństwa II” NdS-II/SP/0461/2024/01

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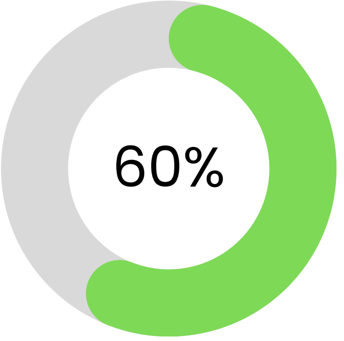


- Gene expression analysis (public RNA-seq, scRNA-seq)
- Machine learning (feature selection, clustering)
- Functional clustering with NLP
- Multi-omics integration (expression + phenotype)
- Public data benchmarking
- Bioinformatics-to-bench validation (e.g., EMSA, ChIP-PCR)

Marta Maleszewska, PhD
Department of Animal Physiology

Paweł Majewski, PhD
Department of Animal Physiology

PROJECTS

Identification of genes with a promoter DNA sequence similar to the promoter structure of the *Phex* gene

Aleksandra Bilska,
Ludmiła Szewczak,
Michał J. Dąbrowski,
Marta Maleszewska-Bobińska,
Paweł Majewski

XII MIĘDZYNARODOWA KONFERENCJA
MŁODYCH ADEPTÓW FIZJOLOGII
- WSPÓLNIE TWORZYMY PRZYSZŁOŚĆ
15–16 maja 2025, Kraków

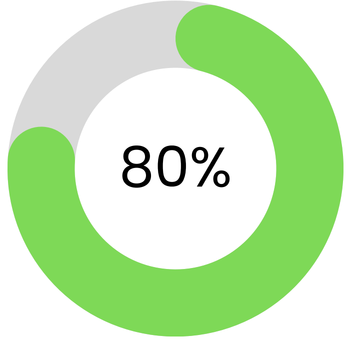
UNIWERSYTET
JAGIELLOŃSKI

ODDZIAŁ KRAKOWSKI
POLSKIEGO TOWARZYSTWA
FIZJOLOGICZNEGO

THE UNIVERSITY OF ARIZONA STEELE
CHILDREN'S RESEARCH CENTER PANDA
Core for Genomics & Microbiome Research

Unsupervised learning for detecting relative importance of pathway activity in individual cells based on scRNA- seq data

Silesian University of Technology



- Biostatistics: hypothesis testing, variance, correlations
- Single-cell RNA-seq analysis (clustering, UMAP, cell-type DEGs)
- Gene expression (bulk & single-cell RNA-seq)
- Machine learning (MCFS-ID, interactions, clustering)
- Functional clustering with NLP
- Signaling pathway analysis
- Public data benchmarking

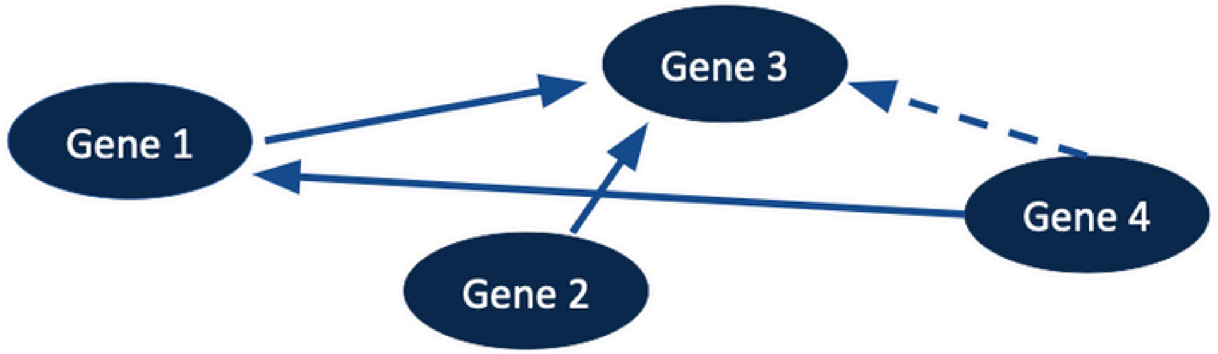
Joanna Żyła, BEng, PhD
Department of Data Science and Engineering
Faculty of Automatic Control, Electronics and Computer Science

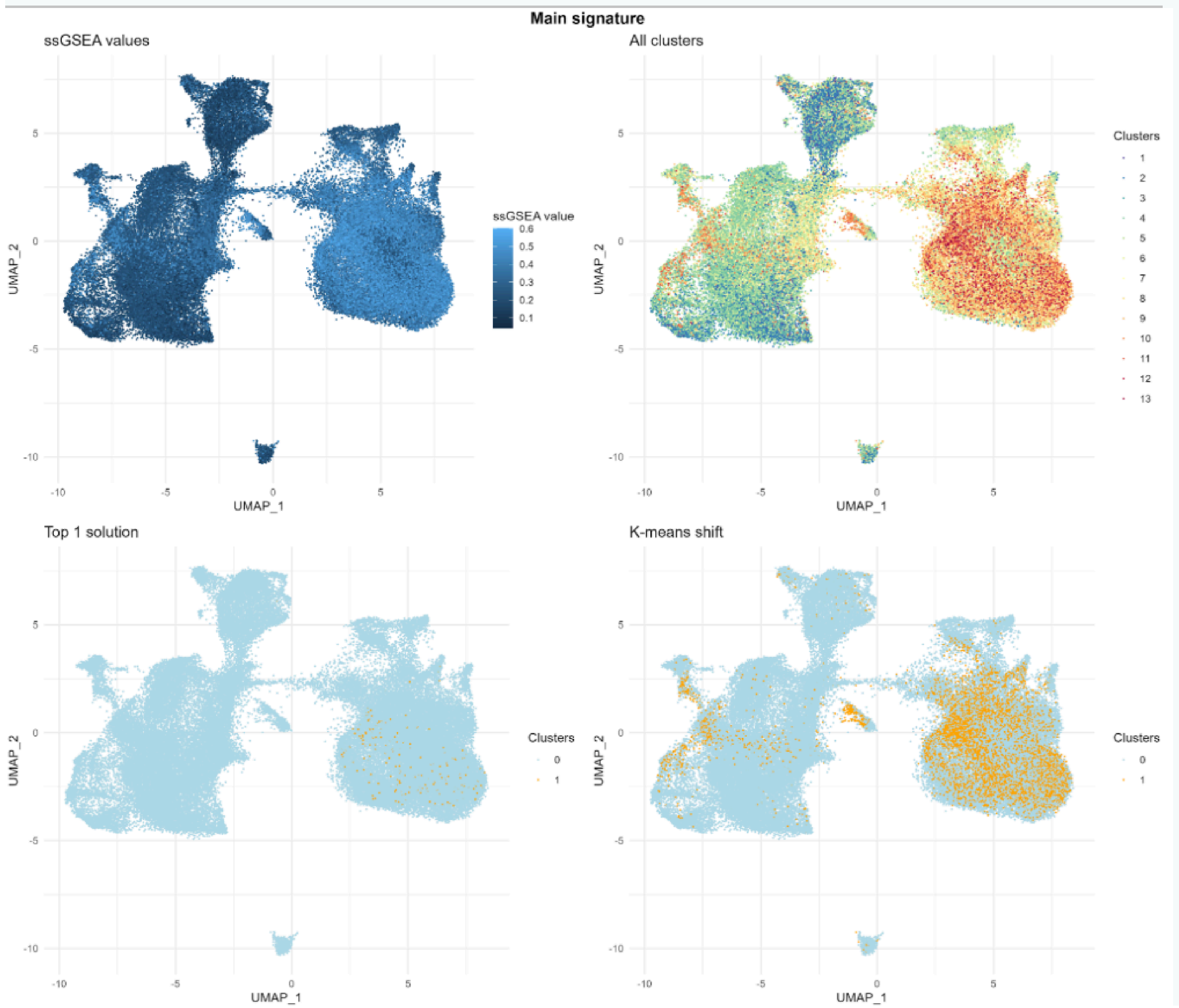
datacamp

PROJECTS

GitHub SinglePathGMM

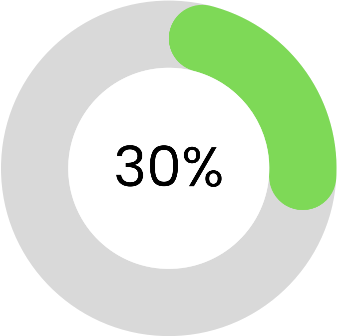
Here is created a package for single-sample pathway enrichment with GMM cell clustering





The impact of nanoplastics on human PBMCs: single-cell analysis of immune functions with a focus on mitochondrial and glycolytic metabolism

WROCLAW MEDICAL UNIVERSITY



- Single-cell RNA-seq analysis (clustering, UMAP, cell-type DEGs)
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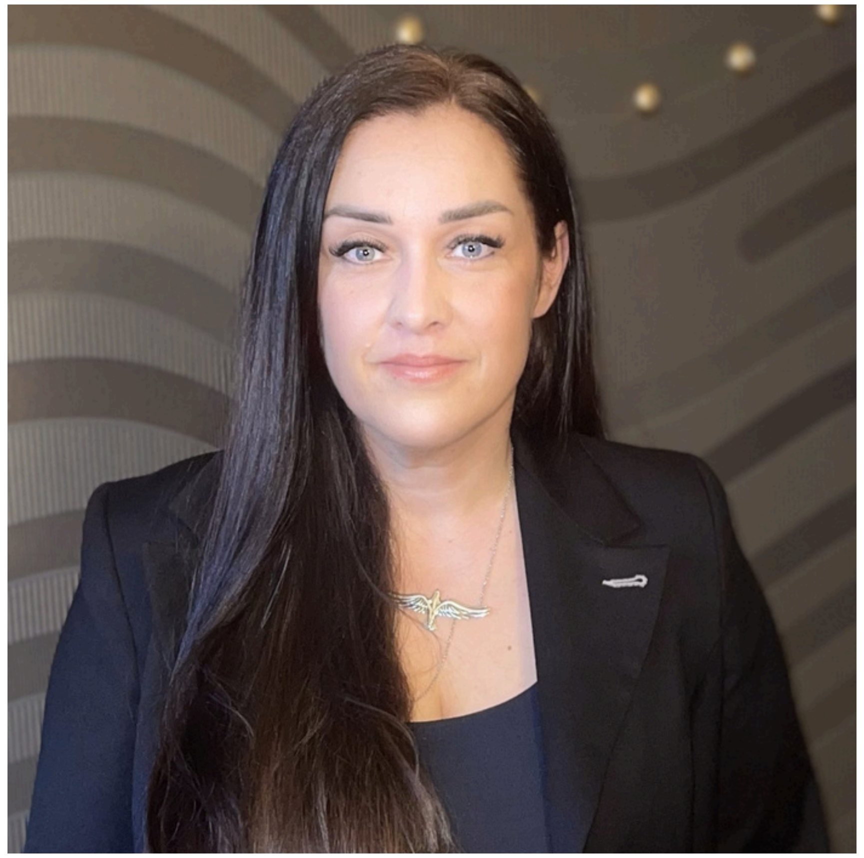

Magdalena Zemelka-Wiącek, PhD
Department of Clinical Immunology
Faculty of Medicine

FNP Foundation for Polish Science

START

April-June 2025

L'Oréal-UNESCO For Women in Science

For Women in Science
unesco FONDATION L'ORÉAL

June 2025

PLANS

ptbi

Polish Bioinformatics Society

XVIII Symposium of the Polish Bioinformatics Society

Białystok 15-17 September 2025

Campus of the University of Białystok.

PLANS

main scope:

- Topological and Epigenetic Interactions in Glioma Chromatin Architecture
- DNA Methylation Dynamics at Chromatin Domains and Replication Origins in Gliomas

NARODOWE CENTRUM NAUKI

PRELUDIUM

PLANS

MEDICAL UNIVERSITY OF LODZ

Katarzyna Płoszka, MSc & PhD Student

Department of
Biostatistics and
Translational Medicine

Wojciech Fendler, Professor

Department of
Biostatistics and
Translational Medicine

Thank You

nencki institute of experimental biology

ZBS IPI PAN

Doctoral School of Molecular Medicine
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