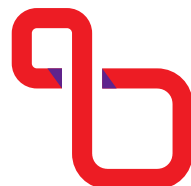




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Computational Oncology and Personalized Medicine From Genome to Treatment: AI & Precision Medicine

Konferencja Onkologia Obliczeniowa i Spersonalizowana Medycyna
Od Genomu do Terapii: SI oraz Medycyna Precyzyjna

COPM2026 Conference
Book of Abstracts

Gliwice, April 29th, 2026

Preface

We are pleased to introduce the sixth event in the series of Computational Oncology and Personalized Medicine (COPM) conferences, titled COPM2026 From Genome to Treatment: AI & Precision Medicine. The online event, organized by the First Priority Research Area (POB1) of the Silesian University of Technology within the Excellence Initiative – Research University program, will be held on April 29th, 2026. The conference is organized under the honorary patronage of His Magnificence, the Rector of the Silesian University of Technology, Prof. Marek Pawełczyk, under the auspices of the Academy of Young Scientists, and several patronages and partners. COPM2026 offers early-stage researchers, particularly young doctors and PhD students, as well as experienced scientists, the opportunity to show their work within an international and interdisciplinary forum of experts. This booklet collects the abstracts of 76 presentations, and one invited keynote lecture by our notable guest prof. Paweł Łabaj from the Małopolska Centre of Biotechnology, Jagiellonian University. The best presenters will be invited to publish in the European Journal of Pharmacology or Bio-Algorithms and Med-Systems. Moreover, we encourage all participants to publish their work in Acta Biochimica Polonica, a journal belonging to the Polish Biochemical Society and published by Frontiers, which covers fields of enzymology and metabolism, membranes and bioenergetics, gene structure and expression, structure and metabolism of proteins, nucleic acids, and carbohydrates. Also, the Best Presentation Award, funded by Elsevier, is expected. We warmly invite all interested participants to join us and make the most of this remarkable opportunity to broaden their knowledge and establish connections with fellow researchers. We extend our sincere gratitude to all participants for contributing their valuable research, to Prof. Łabaj for kindly agreeing to deliver the keynote lecture, and to the members of the Scientific Committee for their dedicated and professional work in reviewing the submitted abstracts. We would also like to convey our warmest wishes to everyone attending the conference, and we trust that your time here will be both fruitful and inspiring, filled with stimulating discussions and productive exchanges of ideas.

Gliwice, April 2026

Michał Marczyk

Department of Data Science and Engineering
Silesian University of Technology
Head of an Organizing Committee

Joanna Polańska

Department of Data Science and Engineering
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Coordinator of POB1: Computational Oncology and Personalized Medicine
Head of Scientific Committee

COPM 2026 conference program - April 29th, 2026

Plenary session (1A)		
	Chairman: prof. dr hab. Marek Łos	
13:00 – 13:15	Opening session: prof. dr hab. inż. Joanna Polańska	
13:15 – 14:00	Prof. Paweł Łabaj (Małopolska Centre of Biotechnology, Jagiellonian University) Genomic reproducibility in the bioinformatics era	
Parallel session (2A)		Parallel session (2B)
	Chairman: dr hab. inż. Michał Marczyk	Chairman: dr inż. Marek Socha
14:00	Liu J, Beule D, Blanc E: Relevance based supervised detection of clinically actionable variants	14:00 Machaj A: Imaging-based assessment of porous anatomical models of the L5 vertebra using micro-CT for applications in personalized medicine
14:10	Fochtman D, Marczak Ł, Pietrowska M, Polańska J, Wojakowska A: Label-free prmpASEF proteomics data analysis workflow selection - benchmarking AI-based and data-driven approaches	14:10 Kempski A, Borys D, Hebda A, Wawrzyniak P, Kijonka M, Mazgaj P, Bobek-Billewicz B: Prediction of 2-Hydroxyglutarate (2HG) based on nuclear magnetic resonance spectroscopy, using a GLX3/4 ratio between tumorous and healthy regions
14:20	Kaźmierczak M, Skalska M, Kalafova A, Jaszczka K, Wojtysiak D, Capcarova M: Impact of optimized ToF-SIMS data preprocessing and normalization strategies on the metabolic profiling of diabetic rat liver	14:20 Klocek M, Śmigiel S: MRI image analysis for Alzheimer's disease diagnosis using machine learning methods
14:30	Limanówka P, Sędek Ł: Integrated CITE-seq analysis links leukemic differentiation to lymphoid microenvironmental signalling network	14:30 Koruba S, Stańczak A, Psiuk-Maksymowicz K, Student S: Comparison of deep learning methods for coronary vessel segmentation from angiographic images
14:40	Moio N, Fantini S, Bisceglia G, Żyła J, Markiel M, Vattemi G, D'Antona G, Polańska J, Tupler R: Longitudinal multi-omics analysis of FRG1-mice identifies Cdkn1a as a therapeutic target for FSHD	14:40 Szerwiński M, Śmigiel S: Application of artificial intelligence in musculoskeletal X-ray analysis for fracture detection
14:50	Natraj Gayathri S, Lillback V, Udd B, Hackman P, Savarese M, Oghabian A: RNA-Seq library preparation bias affects long transcript detection	14:50 Siekanowicz A: Augmentation influence on classification of selected tumor types in MRI Images
15:00	Kuliś K, Wolfsberger W, Shchubelka K, Oleksyk T, Polańska J: Performance evaluation of different machine learning algorithms for classifying type 1 diabetes on genomic data	15:00 Markiel M, Marczyk M, Nuredini A, Schoser B, Mendelsohn D, Santorelli FM, Tupler R, Polańska J: Machine learning-based classification of neuromuscular disorder patients using H&E-stained muscle biopsies
15:10	Urban A, Kocikowska O, Adamiec-Organisciok M, Gendosz de Carrillo D: Evaluation of the cutoff significance for genetic targets of selected miRNAs in pathway enrichment analysis	15:10 Żur M, Piórecki Ł, Socha M, Verdu-Diaz J, Diaz-Manera J, Straub V, Tupler R, Polańska J: MRI-based deep radiomic phenotyping of neuromuscular disorders: A topology-driven classification
15:20	Skutnik K, Żyła J: Semantic similarity of LLMs and overrepresentation results in pathway enrichment analysis	15:20 Piórecki Ł, Socha M, Verdu-Diaz J, Topf A, Diaz-Manera J, Straub V, Tupler R, Polańska J: CoMPaSS-NMD: Directional radiomics as a segmentation-free approach for muscular dystrophy characterisation on T1-weighted MRI
15:30	Zamojski D, Pudełko A, Marczyk M: Towards intelligent risk assessment in infertility diagnosis: Preliminary results of a machine learning-based approach	15:30 Seweryńska Z, Borys D, Klaja B, Ochocka L, Michalik T: State Space Models for precise 3D glioma segmentation

15:40	Szyszk M , Zamojski D, Pudelko A, Marczyk M: Building a Polish medical language corpus for LLMs training	15:40	Żydowicz M , Gaik K, Węgrzyn M, Borys D, Lupa D, Lipiec E, Ruciński A: Dual-stage segmentation of DNA plasmids from atomic force microscopy images
15:50	Merta J , Jarosz L, Ochocki M, Marczyk M: Improvement of the C-Mixup method for effective reduction of batch effects in prediction models based on whole-exome sequencing data	15:50	Al Drabee DA : Chest X-Ray–predicted age as a biomarker for short- and long-term mortality: Development and validation of a deep learning model
16:00	Płonka W , Kostka D, Lalik A, Kurpas M, Kimmel M, Jaksik R: Enhancing variant detection accuracy in FFPE samples: Comparative evaluation of computational and enzymatic correction approaches	16:00	Rudnicka M , Bidzińska J, Dziadziuszko K, Szurowska E, Ułasiński J, Górec J, Dziedzic R, Rzyman W, Polańska J: Emphysema as a significant risk factor for lung cancer: preliminary results from the Pilot National Lung Cancer Screening in Poland
16:10	Meng K , Bartlett T: Early excess methylation at disease-associated CpGs in endometrial cancer inferred from bulk tissue	16:05	Gorczevska I , Borys D, Kijonka M, Jurkiewicz E, Sokół M: Age-related differences in paediatric brain morphology: a comparative analysis of global tissue volumes and subcortical structures
16:15	Sharma P : Multi-modal deep learning predicts cell-type-specific chromatin accessibility	16:10	Kijonka M , Woźnica A, Kapek Ł, Matkowski M, Woźniak B, Bekman A, Niewiadomska B, Prażmowska B, Orlef A, Wendykier J, Ciszek W: Evaluation of image quality and mean glandular dose in grid and non-grid mammography techniques
16:20	Zielińska K , Rudnicki W, Łabaj PP: From single markers to bacterial synergies: MultiDimensional Feature Selection reveals conserved microbiome signatures for personalized medicine	16:15	Mrukwa A , Socha M, Rzyman W, Szurowska E, Dziadziuszko R, Polańska J: Patient-specific lung CT quantification
16:25	Bhandari A , Rana M, Subedi D, Sapkota AS, Poudel P, Aryal P: What omics modalities reveal about lung cancer: A machine learning study of subtype classification and immune stratification in LUSC	16:20	Michalik T , Seweryńska Z, Gaik K, Ochocka L, Klaja B, Borys D: Segment Anything Model evaluated on medical segmentation dataset
16:30	Dorczak J , Drygała B, Seget S, Jarosz-Chobot P, Polańska J: Exploring clinical heterogeneity among patients diagnosed with type 1 diabetes	16:25	Drygała B , Stańczak A, Student S, Psiuk-Maksymowicz K: Automatic detection of stenosis in coronary vessels from angiographic images
16:35	Radwan E , Pini S, Nuredini A, Tupler R, Polańska J: Analysis of genetic variants in trio WES sequencing in support of the diagnosis of neuromuscular diseases – preliminary analysis	16:30	Golik-Paryż J , Gorczevska I, Borys D, Handkiewicz-Junak D: Influence of time-point selection on organ dose assessment in patients treated with ¹⁷⁷Lu-DOTATATE
16:40	Kostka D , Sztromwasser P, Jaksik R: Integrative classification of loss of function variants in ovarian cancer genomes	16:35	Klaja B , Borys D: Implant landmark detection and implant-aware bone segmentation in postoperative hip AP radiographs
		16:40	Gaik K , Żydowicz M, Węgrzyn M, Borys D, Nurzyńska K, Lupa D, Lipiec E, Ruciński A: Coupled application of GANs and YOLO models for data augmentation and automated detection of DNA plasmids in AFM imagery
		16:45	Mołdawa A , Koc A, Nowak N, Skórzewska O, Turczyn A, Wójcik A, Wróblewska K, Sage A, Cholewka A, Hebda A, Kijonka M, Borys D: Validation of automatic segmentation of subcortical structures using multiple filtering methods compared to manual delineation in multi-parametric MRI analysis

Parallel session (2B)
time 14:00 – 16:50

Chairperson:
Marek Socha

Chest X-Ray–predicted age as a biomarker for short- and long-term mortality: Development and validation of a deep learning model

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Keywords: biological age, chest radiograph, deep learning, CXR-age gap, mortality prediction, convolutional neural network, DenseNet-121, medical imaging biomarker, risk stratification, cardiopulmonary aging, radiological age estimation, all-cause mortality, prognostic imaging, biological age estimation, chest X-ray

Abstract

Background: Chronological age is an imperfect proxy for physiological health. Biological age estimated from medical imaging may more accurately reflect an individual's true health status and mortality risk. This study developed a deep learning model to estimate age from chest radiographs (CXR) and evaluated whether the discrepancy between predicted “CXR-age” and chronological age predicts all-cause mortality.

Methods: We collected 404,812 frontal CXRs from five databases (MIMIC-CXR, CheXpert Plus, PadChest, RexGradient, CASIA CXR). A DenseNet-121 CNN was trained on 80% of images, with a dual-input architecture incorporating sex and race/ethnicity. The CXR-age gap (predicted minus chronological age) was assessed as a predictor of 30-day, 90-day, and 1-year all-cause mortality using multivariable logistic regression and Cox proportional hazards models. *Results:* The model predicted age with MAE 3.6 years and $r=0.85$. Mean CXR-age gap was -0.2 years (SD 4.6). Each 5-year increase in CXR-age gap was independently associated with higher mortality at 30 days (aOR 1.22, 95% CI 1.19–1.25), 90 days (aOR 1.25, 95% CI 1.22–1.28), and 1 year (aHR 1.18, 95% CI 1.16–1.20). Adding the gap to a baseline clinical model improved 1-year mortality discrimination (AUC 0.79→0.83). Saliency maps highlighted the heart, mediastinum, and pulmonary vasculature. *Conclusions:* The CXR-age gap is an independent, incremental predictor of short- and long-term mortality. This accessible imaging biomarker could meaningfully support clinical risk stratification and decision-making.

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