Silesian University of Technology

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Computational Oncology and Personalized Medicine
New technologies - new challenges!

Konferencja Onkologia obliczeniowa i spersonalizowana medycyna
Nowe technologie, nowe wyzwania!

COPM2025 Conference
Book of Abstracts

Gliwice, May 21st, 2025

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Book of abstracts
Conference programme

COPM2025

Computational Oncology and Personalized Medicine —
— New technologies - new challenges!

Onkologia obliczeniowa i spersonalizowana medycyna —
— Nowe technologie, nowe wyzwania!

Gliwice, May 21st, 2025

Silesian University of Technology

Computational Oncology and Personalized Medicine COPM2025 — New technologies - new challenges!
Onkologia obliczeniowa i spersonalizowana medycyna COPM2025 — Nowe technologie, nowe wyzwania!
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Preface

We are pleased to introduce the fifth event in the series of Computational Oncology and Personalized Medicine (COPM) conferences, titled COPM2025 NEW TECHNOLOGIES - NEW CHALLENGES! The event is organized by the First Priority Research Area (POB1) of the Silesian University of Technology, within the Excellence Initiative – Research University program, on May 21st, 2025, as an online event. The conference is organized under the honorary patronage of His Magnificence, the Rector of the Silesian University of Technology, Prof. Marek Pawełczyk. As in previous years, the conference is organized under the auspices of the Committees of the Polish Academy of Sciences: Biomechanics Section Committee of Mechanics, Committee of Medical Physics, Radiobiology and Image Diagnostics, Committee of Biocybernetics and Biomedical Engineering, Committee of Mathematics, and Academy of Young Scientists.

COPM2025 is a chance for early-stage researchers, particularly young doctors and Ph.D. students, as well as experienced scientists, to present their research in an international and interdisciplinary forum of specialists. This booklet collects the abstracts of 43 presentations and two invited keynote lectures that our notable guests will deliver: Dr. Theresa Whiteside (University of Pittsburgh Medical Center, USA) and Dr. Serghei Mangul (University of Southern California, USA). The best presenters will be invited to publish in the European Journal of Pharmacology (Elsevier) or Bio-Algorithms and Med-Systems. Also, the Best Presentation Award, funded by Elsevier, is expected. We encourage all interested participants to attend and take advantage of this exciting opportunity to expand their knowledge and network with their peers.

We thank all participants for submitting their valuable research results to us, Dr. Whiteside and Dr. Mangul for agreeing to deliver keynote lectures, and the members of the Scientific Committee for their professional service when reviewing the submitted abstracts. Moreover, we wish to send our best wishes to everyone attending the conference. We hope you will have a productive time, filled with lots of insightful discussions and brainstorming sessions.

Gliwice, May 2025

Michał Marczyk
Department of Data Science and Engineering
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Head of an Organizing Committee

Joanna Polańska
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Silesian University of Technology
Coordinator of POB1: Computational Oncology and Personalized Medicine
Head of Scientific Committee

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Parallel session (2A)

Chairman: dr hab. inż. Michał Marczyk

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Chairwoman: dr inż. Joanna Tobiasz

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Chairwoman: prof. dr hab. inż. Joanna Polańska

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Chairman: dr hab. inż. Michał Marczyk

18:50 – 19:00 **Conference summary and closing**

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Plenary session (1A)
time 14:15 – 15:00

Chairperson:
Joanna Polańska

Transcriptional activation of cellular stress response genes by melanoma-derived exosomes leads to intrinsic apoptosis of activated T cells

Dr. Theresa Whiteside[1], Professor of Pathology, Immunology and Otolaryngology

[1]University of Pittsburgh Medical Center, USA

Keywords: tumor-derived exosomes (TEX), T cell apoptosis, RNAseq of T cells, stress response genes

Abstract

Melanoma-derived extracellular vesicles (MTEX) represent a variable fraction of circulating small EVs in melanoma patients. MTEX interacting with effector T cells induce mitochondrial dysfunction resulting in intrinsic T cell apoptosis. We studied the sequence of genetic/molecular changes occurring in T cells interacting with MTEX . Functionally, these interactions result in dose-dependent T cell apoptosis, suppressed T cell proliferation, and inhibited cytokine production. The functional changes associate with time-dependent alterations in proteins involved in response to stress, metabolic signaling, apoptosis, autophagy, or survival. Immunoblots show rapid (1-3h) upregulation of IRE1α, PERK, CHOP, and ATF6 proteins and activation of MAPK signaling. RNAseq of mRNA in Jurkat cells after 2h to 4h co-incubation with MTEX identified 11,871 involved genes, and in silico profiling of activated genes was correlated with functional alterations. Among 909 differentially expressed genes (FDR<0.05), upregulation of transcripts for genes regulating stress responses at vesicle entry was followed by activation of genes regulating major metabolic pathways, mitochondrial dysfunction, apoptosis, and/or autophagy. A map of the sequential genetic and protein changes confirmed that upon entry, MTEX induce activation of genes associated with cellular stress in activated T cells which is followed by intrinsic apoptosis in most or survival in some T cells, depending on the strength of the MTEX signal.

Parallel session (2A)
time 15:00 – 16:45

Chairperson:
Michał Marczyk

Text pre-processing methods to enhance the performance of natural language processing models for supporting infertility treatment planning in Poland

Dawid Zamojski[1,2*], Adam Pudełko[2,3], Michal Marczyk[1,4*]

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Keywords: text pre-processing, Polish electronic health records, infertility treatment, natural language processing models, artificial intelligence

Abstract

Infertility treatment begins with an interview, during which all medical information related to the patient's history and diagnostic test results are collected. As natural language processing (NLP) models allow the classification of relevant clinical information from electronic health records (EHRs), interest in their use in the medical field has increased significantly in recent years. However, the complexity of the Polish language has become a key problem, so efficient text pre-processing is needed for further model training and evaluation.

In this work, we tested several algorithms of text pre-processing techniques, including: (i) tokenization; (ii) handling negations; (iii) multiword grouping; (iv) the conversion of all letters to lowercase; (v) the removal of numbers, punctuations, whitespaces, elongated words, stop words; (vi) application of stemming and lemmatization. The dataset included EHRs from 80 patients on their first visit to an infertility clinic.

As a result, the data pre-processing successfully removed the undesirable text elements, reducing the number of characters and unifying text length. Considering the values of assessment measures, like accuracy, precision, recall, and F1-score, improved performance of NLP models was observed after text pre-processing. The results of the project should increase the efficiency of the models used in infertility treatment process in Poland.

Acknowledgments: The project was conducted in cooperation with the Genetic Laboratory of the Gyncentrum Sp. z o.o. in Sosnowiec. This work was supported by the Ministry of Science and Higher Education 'Implementation Doctorate' grant number DWD/7/0396/2023.

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Workplace mental health: a predictive modelling approach to help-seeking behaviour

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[2]Department of Data Science and Engineering, Silesian University of Technology, Poland

Keywords: mental health, help-seeking behaviour, machine learning, feature selection, predictive modelling

Abstract

Mental health concerns, including depression, anxiety, and stress-related conditions, are increasingly prevalent and often go untreated due to stigma, lack of awareness, and personal barriers. Understanding and predicting help-seeking behaviour can enable timely interventions, especially in workplaces prone to high stress. This study aims to predict such behaviour using machine learning on a dataset of 1259 observations with 25 features, which, after outlier and missing value filtration, yielded 1190 observations. Next, statistical inference was conducted which results were corrected by Bonferroni method. For obtained 11 features (p-value<0.05), two logistic regression models were trained with F1 tuning. First, which used all features, second using stepwise selection with AIC minimization. Comparing overall performance metrics on the test data, the stepwise model showed to be slightly stronger, despite less number of features, with higher sensitivity (0.7500), specificity (0.6107), and balanced accuracy (0.6804). Model selection identified five key features: age, family history, coworkers, anonymity, and prior mental health interviews. These findings support the models in predicting mental health help-seeking behaviour and the creation of workplace wellness strategies.

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Clustering of data from mass cytometry with the use of deep learning techniques

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[2]Department of Data Science and Engineering, Silesian University of Technology, Poland

Keywords: mass cytometry, neural network, variational autoencoder, deep learning

Abstract

Mass cytometry allows for high-dimensional single-cell analysis, offering insights into complex biological systems, including disease diagnostics. Identifying cellular populations is key, done through manual gating, which is time-consuming and prone to bias and variability. To overcome these limitations, automated clustering techniques have emerged. This study compares traditional clustering methods with deep learning approaches, focusing on variational (VAE) and classical autoencoders, for mass cytometry data analysis.

A publicly available bone marrow dataset, comprising 514,386 cells and 38 surface marker proteins, was used. Clustering analyses were performed using both traditional and deep learning-based methods. The optimal number of clusters was determined using Gap Statistics. The analysis included traditional methods such as PhenoGraph, Deep Embedded Clustering, and BIRCH, alongside unsupervised deep learning approaches leveraging latent space representations learned by autoencoders.

Performance varied notably between the evaluated methods. Among traditional algorithms, BIRCH achieved the best performance with an Adjusted Rand Index of 0.4101. In contrast, VAE with k-means clustering achieved superior cluster separation as indicated by a Calinski-Harabasz score of 532,824.67 and highest cluster homogeneity. The results show the superiority of VAEs in capturing complex structures in mass cytometry data, providing a strong alternative to traditional clustering methods.

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Deciphering clinical variability in FSHD: a post-Mendelian comprehensive genotype-phenotype correlation framework

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Keywords: Facioscapulohumeral Muscular Dystrophy (FSHD), personalized medicine, genotype-phenotype correlation, genetics, gene ranking, telomere-to-telomere

Abstract

Facioscapulohumeral muscular dystrophy (FSHD) is a hereditary myopathy with wide clinical variability presenting two genetic forms linked to loss of epigenetic silencing at 4q35: FSHD1, due to heterozygous contraction of D4Z4 repeats (DRA); FSHD2, caused by DNA hypomethylation associated with damaging variants in chromatin remodeling genes. These Mendelian models fail in explaining non penetrance and phenotypic variability, creating a gap between molecular findings and clinical presentation. This advocates for a revised diagnostic and counseling approach for individuals carrying a DRA or showing FSHD phenotype. We propose an integrated, personalized framework combining standardized neurological evaluation, clinical family history, D4Z4 sizing and molecular investigations, including meth-seq, WGS, WES, long-read sequencing, and optical genome mapping considering telomere-to-telomere (T2T) assembly. We developed a gene-ranking system designed to prioritize the most impaired pathways rather than focusing on individual variants. This approach supports understanding of inter- and intra-familial variability and elicits more accurate diagnosis, prognosis, and counseling. Though developed for FSHD, our framework holds the potential to be applied to other complex genetic disorders, offering a model for interpreting phenotypic heterogeneity beyond classical inheritance models.

Acknowledgments: The work was partially supported by the Silesian University of Technology grant for the launch of a research activity in a new research topic under the Excellence Initiative - Research University programme [to JT].

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Deep learning-based analysis of EEG signals for schizophrenia detection

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Keywords: Schizophrenia detection, deep learning, EEG signal analysis, clinical decision support

Abstract

Schizophrenia is a complex psychiatric disorder that remains difficult to diagnose in clinical practice. Modern systems and technologies can support specialists in the diagnostic process, with deep learning models capable of identifying patterns characteristic of the disease.

This work presents the development and evaluation of a system for supporting schizophrenia detection based on electroencephalographic (EEG) data using deep learning techniques. Open-source EEG data were analyzed, collected from a study showing that individuals with schizophrenia have disrupted mechanisms for predicting and suppressing stimuli caused by their own actions.

Various deep learning techniques and preprocessing strategies were tested. Particular focus was placed on the analysis of event-related potentials (ERP), which enabled the achievement of the best classification results. The highest performance was obtained by using spectrograms combined with convolutional neural networks, reaching an F-score of 87%.

The final model was integrated into a user-friendly web application designed for clinical specialists, enabling automatic EEG data analysis and patient data management. The system was also equipped with an explainable AI module to help clinicians better understand the model's decisions.

The results confirmed the potential of the developed system to assist in clinical decision-making.

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Application of a logistic model for the analysis of T cell receptor diversity profiles using simulation data

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Keywords: T cell receptors, TCR, Rényi entropy, diversity profile

Abstract

T cell receptors (TCR) form the primary element of the adaptive immune response, enabling the body to maintain its homeostasis. It relies on continuous evolution to expand the diversity of the repertoire. TCR diversity can be characterized by richness (number of unique TCR clones) and evenness (the distribution of copy numbers of TCR clones).

This study aimed to verify the use of a logistic model for describing TCR diversity as a new and universal indicator of TCR diversity. We analyzed the diversity profiles of the TCR repertoire using power-law based simulation data, which were generated in 100 repeats for combinations of different values of richness (from 10 to 1,000,000 unique TCR clones) and evenness (from very skewed to even). Diversity profiles were calculated with Rényi entropy for a wide range of scales. A five-parameter logistic model (LL5) was fitted to these profiles, and its parameters were analyzed to assess how richness and evenness impact the diversity.

The obtained results indicate a good fit of the model to the data, which is confirmed by high values of the log-likelihood function and narrow confidence intervals of the parameters, showing their high precision. The analysis of the parameter values allowed for assessing the impact of richness and evenness on the structure of TCR repertoires. The results suggest the potential of the LL5 model as a tool that integrates different aspects of diversity in a more comprehensive manner than traditional indices.

Genome-wide association studies (GWAS) as a tool for revealing risk genes in Type 1 Diabetes

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[2]Department of Biological Sciences, Oakland University, United States
[3]Department of Biological Sciences, Uzhhorod National University, Ukraine

Keywords: GWAS, type 1 diabetes (T1D), Whole Exome Sequencing (WES), bioinformatics, immunology

Abstract

Many diseases, including subtypes of Type 1 Diabetes (T1D), are hard to predict due to their complex and under-studied aetiology. Computational tools are therefore vital to provide insights into the relevant molecular mechanisms. The findings consulted with medical professionals, may help to understand the underlying causes of various diseases, develop treatments and thus, help patients. Genome-wide association studies (GWAS) is a valuable tool that identifies genes linked to specific diseases. There are three main types of inheritance in GWAS analysis: additive (linear increase with risk variants); dominant (one copy of a risk variant is enough for the effect to appear); and recessive (two copies of a risk variant are needed). In this study, the three GWAS models were calculated for data consisting of 2598 T1D Ukrainian patients and 4240 controls. The data had different types of inheritance, but effects of variants on the phenotype were mostly stepwise (dominant or recessive) rather than linear (additive). The lead variants were identified within genes that are well documented in the literature as risk genes in T1D. These included HLA-DRB1 (lead variant $p<1e-9$, $OR>4$) and BACH2 (lead variant $p<1e-9$, $OR>1.2$). Functional analysis of genes linked to all such variants showed not only a strong connection to pathways from the Immune system (Regulation of T cell activation; Interferon gamma signaling), but also from the Generic Transcription (Transcriptional regulation by RUNX1).

Acknowledgments: The Genomics of T1D in Ukraine project was funded by The Leona M. and Harry B. Helmsley Charitable Trust Grant "A comprehensive study of T1D exomes" (Phase I and Phase 2).

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Sequencing data characteristics following ionizing radiation: a comparative ONT study

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Keywords: sequencing, long reads, oxford nanopore technology

Abstract

Introduction: Long-read RNA sequencing enables comprehensive transcriptome profiling following environmental stressors such as ionizing radiation. This study compares two datasets generated using Oxford Nanopore Technologies (ONT) sequencing platforms to assess how sequencing strategy, chemistry, and sample type affect data quality and utility.

Material and methods: Two datasets were analysed. The first used a cDNA-PCR library kit, PromethION R10 flow cells, and RNA from irradiated human white blood cells (0.1–5Gy, 24h post-exposure). The second applied direct RNA sequencing on a GridION platform, using RNA from the HT1080 cell line exposed to 10Gy X-rays, also collected 24h post-exposure. Key metrics included read count, Q-score distribution, read length, and mapping rates.

Results: The PromethION dataset produced more reads with higher base quality (mean Q-score 11.8 vs. 9.0) and shorter read lengths (mean: 849nt, median: 748nt). Direct RNA reads from GridION generated longer reads (mean: 1228nt, median: 1010nt) but with lower accuracy. Both datasets were suitable for transcript-level analysis, but differed in terms of overall sequence accuracy and data distribution, which may influence transcript isoform reconstruction, and consistency.

Conclusion: Library preparation method and sequencing platform exert a substantial impact on RNA-seq data quality and structure. These findings underscore the importance of workflow selection in radiation transcriptomics studies.

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Comprehensive RNA-Seq analysis for biomarker identification in non-small cell lung cancer using bioinformatics approaches

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Keywords: RNA-seq, non-small cell lung cancer, signaling pathways, gene expression, linear modeling

Abstract

Non-small cell lung cancer (NSCLC), the most prevalent and biologically heterogeneous lung cancer subtype, poses challenges for effective treatment. We aimed to identify potential NSCLC biomarkers by analyzing RNA-seq data from two GEO datasets (GSE81089, GSE120795; 179 NSCLC, 151 controls). Using generalized linear models, we identified differentially expressed genes (DEGs) by correcting for batch effects and tissue-type variability (FDR<0.05, |log2FC|>0.6). Pathway enrichment analysis was performed using CERNO and PLAGE across KEGG, Reactome, and MSigDB databases. CERNO revealed enrichment in cancer-related, immune, and inflammatory pathways, with the inclusion of tissue-type effects uncovering more DEGs and pathways compared to batch correction alone (e.g., KEGG: 51 vs. 67). PLAGE analysis confirmed tissue heterogeneity and showed distinct clustering between NSCLC and control samples, validated by Silhouette and WSS metrics. GAP statistic supported the inclusion of tissue-type effects. Adjusting for tissue type revealed DEGs strongly linked to NSCLC, including several biologically relevant genes with currently uncharacterized functions. Our findings emphasized the importance of tumor context in transcriptomic analyses. These results advance our understanding of NSCLC biology and highlight promising diagnostic and prognostic biomarkers. Future work should focus on validating these findings in independent datasets and investigating the functional roles of identified genes.

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Exome capture kit-driven stratification in multi-cohort germline WXS data

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Keywords: batch effects, exome sequencing, capture kits

Abstract

Batch effects—technical differences from sample handling, library preparation, sequencing chemistry, or bioinformatic tools—are common in large-scale sequencing studies, including germline whole-exome sequencing (WXS). We analyzed WXS data from 1,194 breast cancer patients across three cohorts: TCGA, BEAUTY, and EOC. UMAP visualization of gene-level features revealed distinct sample groupings both between and within studies, indicating batch effects. While race was a strong stratifier in TCGA, restricting to white individuals (n=806) still showed five clusters reflecting cohort origin. Capture kits emerged as a major source of variation: six kits were used, with target sizes ranging from 36 to 70 Mb and mean pairwise differences of 31 ± 18 Mb. Despite high gene-level overlap (18,305/19,292 genes), base-level differences were substantial. Standardizing the variant caller (Varscan2) mitigated intra-cohort differences in TCGA but did not eliminate inter-cohort effects; capture kits continued to drive clustering. Gene-level analysis revealed that 28% of genes showed significantly different weighted allele frequencies across groups, frequently with nearly binary detection patterns. These findings highlight exome capture kits as a dominant source of systematic, non-biological variation in germline WXS data. Their impact must be carefully addressed to ensure robust and unbiased analysis in integrated multi-cohort studies.

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Antimicrobial resistance in diverse urban microbiomes: uncovering patterns and predictive markers

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Keywords: antimicrobial resistance, metagenomics, AMR, machine learning, microbiome

Abstract

Antimicrobial resistance (AMR) is a critical global health threat, exacerbated by urbanization and anthropogenic pressures. This study investigates AMR distribution across 143 metagenomic samples from six U.S. cities and 145 clinical isolates, using a multi-layered approach that includes resistome, virome, and mobilome profiling. We benchmarked four tools—AMR++, Bowtie, AMRFinderPlus, and RGI—for resistome analysis. AMR++ outperformed others by detecting the highest number of diverse resistance markers and achieving the best classification accuracy. Binary normalization significantly enhanced model performance, and machine learning models, particularly random forests, revealed predictive AMR signatures tied to geographic origin. Mobile genetic elements (MGEs), especially those involved in replication and transfer, were found to be strongly associated with AMR genes, shaping resistome diversity and inter-city variation. Filtering out MGE-associated AMRs disrupted clustering and decreased predictive power, highlighting their central role in resistance dissemination. Virome analysis identified over 70,000 viral contigs, but only a small fraction passed quality thresholds, with minimal viral-AMR associations. K-mer profiling confirmed high complexity in New York City samples, aligning with their high ARG diversity. Our findings underscore the importance of MGEs in AMR dynamics, the potential of machine learning for resistome modeling, and the value of integrated multi-omics approaches for understanding urban microbiome resistance landscapes.

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Parallel session (2B)
time 15:00 – 16:40

Chairperson:
Joanna Tobiasz

Multimodal mobile applications in the treatment of visual and spatial perceptual impairments

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Keywords: rehabilitation, assistive technologies, mobile applications, sonification

Abstract

Multimedia programs are used in the rehabilitation process of various neurological disorders. Desirable effects of such interventions have been demonstrated among patients with hemiplegia syndrome or disorders of executive and visuospatial functions. The use of such tools is aimed at an improvement (or lack of change) in the test results of individual cognitive functions.

The aim of the study is to prepare a mobile application that builds upon existing therapy methods by leveraging a multimodal approach of real-time sonification of drawn shapes, letters, and graphs through software synthesizers. The parameters of the synthesized sound are directly controlled by the patient's interaction with the mobile device's touchscreen, with the amplitude of the sound waves being indicative of the patient's finger's position in relation to the explored figure and the frequency being indicative of the absolute position of the figure on the screen. Patients with perceptual impairments can thus be aided in their rehabilitation through numerous hints provided by the application's sound cues, while streamlining the therapists' work.

The preliminary character of this research intends to delve deeper into the field of computerized rehabilitation methods, which could possibly open a way for a more personalized approach to every patient's unique needs by providing an engaging combination of sensory experiences through widely available mobile solutions.

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Optimizing ATRA-induced muscle differentiation in Zebrafish: implications for ARMS therapy

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Keywords: alveolar rhabdomyosarcoma (ARMS), all-trans retinoic acid (ATRA), juvenile zebrafish model, preclinical model

Abstract

Alveolar rhabdomyosarcoma (ARMS) is an aggressive pediatric cancer characterized by impaired differentiation and therapeutic resistance. Promoting differentiation is a promising strategy to overcome ARMS aggressiveness. All-trans retinoic acid (ATRA) is a potent inducer of differentiation in cancer therapies; however, its in vivo efficacy during early development and impact on ARMS require further investigation. This study aimed to establish the efficacy and safety of ATRA in promoting skeletal muscle differentiation in juvenile zebrafish, providing a novel preclinical model for ARMS. Juvenile zebrafish (2.5 months old) were treated with ATRA (5, 10, or 20 µM) over 14 days, dosed every 72 hours. Behavioral analyses (locomotion, eye size) assessed systemic toxicity, while differentiation was evaluated via MyoD immunohistochemistry, nuclei density quantification, and skeletal muscle morphology. Zebrafish treated with 20 µM ATRA showed significantly enhanced muscle differentiation, with increased MyoD localization and higher skeletal muscle nuclei density, indicating successful induction. Importantly, locomotion and developmental indicators remained unchanged, demonstrating absence of systemic toxicity. These results demonstrate that ATRA (20 µM) promotes skeletal muscle differentiation in juvenile zebrafish without adverse effects, establishing a robust preclinical model to investigate differentiation therapies for ARMS and advancing the potential for clinical translation.

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Loss of BCL2L13 and ceramide dysregulation may define lymphatic spread and survival in lung cancer

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Keywords: lung cancer, metastasis, ceramide metabolism, BCL2L13, lipidomics

Abstract

Lung cancer remains the leading cause of cancer-related mortality worldwide, responsible for over 1.8 million deaths annually, with lymph node metastasis being a major determinant of poor prognosis. In our recent study using human lung cancer tissue microarrays, we observed a significant reduction in BCL2L13 expression—a mitochondrial protein and inhibitor of Ceramide Synthase 2 (CerS2) and Ceramide Synthase 6 (CerS6)—in metastatic lymph nodes compared to primary tumors from the same patients. To further investigate ceramide metabolism during metastasis, we collected paired primary tumor (PT) and lymph node (NODE) samples from five lung cancer patients under an approved University of Manitoba protocol and performed comprehensive lipidomic analysis. Long- and very-long-chain ceramides (Cer 24:0, Cer 24:1, MHC 24:0, THC 24:0) were enriched in NODEs, suggesting enhanced CerS2 activity and metastatic adaptation, while short-chain ceramides (Cer 16:0, Cer 18:0, DHC 16:0), linked to CerS6, were elevated in PTs and associated with pro-apoptotic signaling. Principal component analysis (PCA) and partial least squares discriminant analysis (PLS-DA) separated PT and NODE profiles. KEGG pathway enrichment identified links to anoikis resistance, epithelial-mesenchymal transition (EMT), mitophagy, and inflammatory remodeling. Future studies will explore targeting ceramide pathways to inhibit lymphatic spread and improve lung cancer outcomes.

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From lipid remodeling to therapeutic failure: the role of Cholesterol and autophagy in glioblastoma resistance

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Keywords: glioblastoma, chemoresistance, cholesterol metabolism, autophagy, metabolic adaptation

Abstract

Aim:Glioblastoma (GB) is the most aggressive and therapeutically resistant brain tumor. Temozolomide (TMZ), the current standard-of-care chemotherapeutic, often fails due to the rapid development of cellular resistance. This study aimed to delineate the molecular mechanisms underlying TMZ resistance in GB cells.

*Approach:*Using TMZ-resistant (R) and non-resistant (NR) GB U251 cells, autophagic flux was assessed via immunoblotting and transmission electron microscopy. Lipidomic profiling was performed to define cholesterol species, and findings were validated through real-time PCR and measurements of de novo cholesterol synthesis and esterification. Metabolic conditions were characterized using Seahorse extracellular flux analysis.

*Results:*TMZ-resistant cells exhibited impaired autophagic flux due to lysosomal dysfunction, along with accumulation of some cholesterol esters and reduced de novo cholesterol synthesis and estrification. These changes were accompanied by mitotic quiescence and a metabolic shift toward oxidative phosphorylation (OXPHOS).

*Conclusion:*TMZ resistance in GB involves a complex interplay of impaired autophagy, lipid remodeling, and mitochondrial metabolic adaptations. Effective therapeutic strategies may require targeting cholesterol esterification, restoring autophagic flux, or inhibiting OXPHOS.

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Juvenile zebrafish as a model to study the impact of autophagy on enhancing cell proliferation

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Keywords: autophagy flux, cell differentiation, cell proliferation, Bafilomycin-A1

Abstract

This study is investigating the alveolar rhabdomyosarcoma (ARMS) as an aggressive pediatric cancer. ARMS is a cancer characterized by poor cell differentiation and resistance to current treatments, leading to side effects on the patient. This study focuses on the role of autophagy in regulating tumour cell differentiation and the potential side effects of the Bafilomycin-A1 on the juvenile zebrafish. Juvenile zebrafish were treated with two concentrations of baf-A1 (2.5 nM and 10 nM) for 14 days (dosed every 72 hours). At each time point, the velocity, distance travelled, and eye diameter were measured to analyze the zebrafish's health status during interaction with the drug. Additionally, the Edu was administered twenty-four hours before dissection to label proliferating cells. After dissection, the fish tissue was analyzed by immunohistochemistry for LC3 and SQSTM1 as the autophagosome markers. The results indicate that the juvenile zebrafish exposed to 10nM baf-A1 show the focalization of LC3 and SQSTM1 punctuation in their skeletal muscle tissue, confirming the inhibition of autophagy flux. The presence of Edu-positive cells in the area where autophagy inhibition occurs indicates cell proliferation. The zebrafish model showed no behavioural and physical changes, indicating that baf-A1 has no side effects. In the conclusion, this study achieves a reliable and non-toxic method to inhibit the autophagy blockade via baf-A1 and promote skeletal muscle proliferation.

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ATG5 loss drives a contractile phenotype and enhances TGF-β1-induced migration in mouse embryonic fibroblasts

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Keywords: autophagy, phenotypic conversion, EMT, Smad signaling, TGFβ, MEFs

Abstract

Mouse embryonic fibroblasts (MEFs) are a widely used model to study cytoskeletal remodeling, differentiation, migration, and autophagy. Here, we explored how deletion of autophagy-related genes ATG5 and ATG3, essential for LC3 lipidation and ATG5–ATG12 conjugation, affects epithelial-mesenchymal transition (EMT) marker expression and migration behavior. Wild-type (WT), ATG5 knockout (KO), and ATG3 KO MEFs were cultured in low-serum ITS (1%) medium and analyzed by Western blotting over 24, 48, and 72 hours. Notably, α-smooth muscle actin (α-SMA) was absent in WT cells but robustly expressed in both KO groups, indicating a marked phenotypic switch toward a contractile profile. In contrast, vimentin and E-cadherin remained detectable in all groups but showed significant modulation: vimentin decreased and E-cadherin increased in KO cells compared to WT. Interestingly, only ATG5 KO MEFs demonstrated enhanced migration following TGF-β1 (5 ng/ml) stimulation at 48 hours, whereas ATG3 KO cells behaved similarly to WT. These findings reveal that ATG5 loss selectively promotes a contractile, migration-competent phenotype with suppressed mesenchymal plasticity. Future research will dissect how ATG5 regulates cytoskeletal tension and mechanical adaptation during EMT, opening new avenues to control fibrosis, metastasis, and regenerative responses.

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Advances in aptamer-based transferrin receptor targeting – review

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Keywords: aptamers, blood-brain barrier, transferrin receptor

Abstract

There are numerous brain diseases, and one of the main challenges in their treatment is the effective drug delivery across the blood-brain barrier (BBB). The BBB is a tight, selective barrier that is permeable to lipophilic substances. It restricts the passive diffusion of most molecules while precisely regulating active transport mechanisms. One of the main components of the BBB is endothelial cells, which are connected by tight junctions. The transferrin receptor is highly expressed by both endothelial cells and gliomas, and has attracted interest as a target in drug delivery via receptor-mediated endocytosis. Transferrin receptor-specific aptamers are being actively investigated for facilitating receptor-mediated transport across the BBB and into tumor cells. Aptamers are short, single-stranded DNA or RNA oligonucleotides that are able to bind to target molecules with high affinity in a manner similar to antibodies. Compared to antibodies, aptamers offer several advantages, including high chemical stability, low immunogenicity, and ease of modification and conjugation with various therapeutic agents. Consequently, aptamers are gaining increasing attention for diverse applications, particularly in precision medicine for both diagnostic and therapeutic purposes. This review summarizes recent advances in the design and application of transferrin receptor-specific aptamers for diagnostic and therapeutic use.

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Modeling of protective shield for intraocular brachytherapy

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Keywords: intraocular melanoma, brachytherapy, protective shield, dose reduction

Abstract

Introduction: Intraocular tumors, such as choroidal melanoma, pose a significant threat to patients, primarily due to their tendency to metastasize to other parts of the body. These metastases, if left untreated, can lead to death. The tumor spreads hematogenously, commonly affecting organs such as the liver, lungs, skin, bones, and brain. Without effective treatment, patient survival time is approximately one year, with chemotherapy being the main option for life extension. Brachytherapy is one of the principle treatment methods for the most common primary intraocular tumor, choroidal melanoma. This technique includes radioactive sources such as ruthenium-106 (a beta emitter) and iodine-125 (a gamma emitter). Iodine-125 based brachytherapy is a highly effective treatment. However, it is associated with serious side effects, which in some cases may lead to enucleation, despite successful tumor control.

Materials and methods: The study was based on Monte Carlo computer simulations using the GEANT-4 code (CERN). The conducted analysis included various radioisotopes, in addition to those used in clinical practice.

Results and conclusions: The protective shield has been designed to effectively reduce radiation dose in surrounding healthy tissues. This innovation may significantly improve the quality of life for oncology patients following treatment. Benefits include lower risk of radiation side effects and better chances of preserving vision.

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The effect of non-classical factors on the incidence of acute myocardial infarction

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Keywords: acute myocardial infarction, seasonal variation, air pollution, meteorological factors

Abstract

Acute Myocardial Infarction (AMI) occurs when a coronary artery is narrowed or closed by an intravascular thrombus, thus impairing or cutting off blood flow to the heart muscle. It can present as a silent, undetected event, but mostly, it is a life-threatening condition that may lead to hemodynamic and electrical instability and sudden cardiac death. Given AMI's multifactorial nature, studying both clinical and environmental data is crucial to better understand its risk factors. This study aimed to evaluate the effect of meteorological factors, including temperature and atmospheric pressure changes, and the COVID-19 pandemic on AMI incidence. We utilized data from 3 778 consecutive patients with AMI, sourced from the hospital in Gliwice between 2007-2025. AMI cases were classified according to the ICD system. The data were analyzed through an in-house pipeline. AMI incidence was higher in men and appeared at younger ages compared to women. A significant increase in AMI and ST-segment elevation myocardial infarction incidence occurred during the COVID-19 pandemic. The analysis confirmed the typical presentation of the patients with AMI. At this stage, there were weak or no data suggesting that elevated air pollution and rapid meteorological changes notably increased the incidence of AMI in Gliwice. The observation that COVID-19 pandemic increased AMI incidence requires further analysis

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Can an AI controlled pump outrun diabetes?

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Keywords: diabetes, insulin pump, AI in medicine

Abstract

Type 1 diabetes is an incurable condition that significantly affects quality of life. To support patients, technologies such as AI-assisted insulin pumps have been developed to automate blood glucose regulation, reducing the need for constant monitoring. This study evaluated the impact of such devices on glycemic control, BMI, and the frequency of hypo- and hyperglycemic episodes. The study followed 50 children using insulin pumps over three years. Data were collected every six months, including standardized BMI, insulin dosage, glucose levels, and sensor usage. Statistical analysis included the Shapiro–Wilk test for normality. Parametric tests (e.g., t-test) were used for normally distributed data. Nonparametric alternatives (e.g., Wilcoxon Signed-Rank) were used otherwise. Changes across multiple time points were examined using Friedman's ANOVA test, with Benjamini-Hochberg correction applied, where the results with FDR <= 0.05 were treated as significant. Results showed a significant increase in average glucose levels (p=0.00005) and BMI (p=0.0437) with Kendall W coefficient in order W= 0.12600 and W = 0.0490, showing little to no agreement. Hypoglycemia decreased (p=0.0129), while hyperglycemia increased (p=0.01165). Hemoglobin A1c levels showed no significant change (p=0.1212). These findings suggest that AI-driven insulin pumps function effectively, though further optimization is needed, such as better management to reduce amount of hyperglycemic episodes.

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Verification of the planned dose in trigeminal neuralgia radiotherapy using the CyberKnife

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Keywords: dose verification, dosimetry, dose calculation

Abstract

Introduction: According to the recommendations of the Polish Minister of Health, the conditions for the safe use of ionizing radiation in medical exposures require independent verification of planned doses in radiotherapy. However, small dimensions of the target volume in trigeminal neuralgia often lead to unreliable measurement results. We present here our original method called BeamAutomat for fast and independent calculation of the absolute dose.

Materials and Methods: Eleven CyberKnife VSI plans for trigeminal neuralgia, with target volumes of 8.7-20.7mm^3, were analyzed. The doses from MULTIPLAN were compared with the values from the self-made BeamAutomat and the RadCalc ones.

Our algorithm uses the transformed AAPM TG 114 formalism of the monitor unit calculation for the point dose evaluation. Most parameters were obtained via a linear interpolation of the measured values. The Tissue Maximum Ratio (TMR) for the fields <5 mm was modeled using a 6th-order polynomial fit on the 12 fixed collimator data sets.

Results: The comparison of the 1177 beams showed the differences to be within ±1% for 93.5% and 87.3% of the BeamAutomat and RadCalc values, respectively. The average plan dose differences were 0.07% and 0.27%, respectively.

Conclusions: The BeamAutomat method showed a better agreement with the planning system than RadCalc. This approach allows for dose verification, potentially meeting regulatory requirements for trigeminal nerve irradiation.

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The effect of miRNA-146A silencing on melanoma Me45 cells

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Keywords: miRNA, ionizing radiation, miR-146a, Me45

Abstract

MicroRNAs (miRNAs) are short, non-coding RNA molecules involved in post-transcriptional gene regulation. Their dysregulation may affect key processes such as proliferation, apoptosis, and the cell cycle, contributing to cancer. This study aimed to identify miRNAs with altered expression in Me45 melanoma cells after ionizing radiation (4 Gy) and to investigate the role of miR-146a. Eight hours post-irradiation, G2/M cell cycle arrest was observed; at 24 hours, apoptosis increased compared to control. Small RNA sequencing identified one upregulated miRNA (miR-1260) and two downregulated miRNAs (miR-933 and novel miRNA chrM:11954-11969). MiR-146a was found to be the most highly expressed. Lentiviral inhibition of miR-146a was performed using miR-Zip-146a vectors co-expressing GFP. Flow cytometric GFP competition assay showed that silencing miR-146a significantly reduced the number of Me45 cells compared to wild-type cells in co-culture. These findings suggest a role for miR-146a in promoting melanoma cell survival. Further studies are underway to explore the function of these miRNAs in melanoma.

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Baseline characterization of Hs27 and Hs68 fibroblasts reveals endogenous TGF-β1 activity and autophagy status

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Keywords: fibroblast characterization, TGF-β1 signaling, autophagy, Smad pathway, ECM remodeling, wound healing, fibrosis

Abstract

Establishing baseline biological profiles of fibroblast cell lines is critical for accurately interpreting their responses in mechanobiology, wound healing, and fibrosis models. Intrinsic differences in proliferation, autophagy, extracellular matrix (ECM) production, epithelial-to-mesenchymal transition (EMT), and Smad signaling can significantly influence experimental outcomes. We characterized two human foreskin fibroblast lines, Hs27 and Hs68, to define their biological baseline. Doubling times, measured by trypan blue exclusion every 12 hours over 72 hours, were approximately 21.5 hours (Hs27) and 18.5 hours (Hs68). After 72 hours in DMEM with 1% ITS, Western blotting revealed low LC3B-II/LC3B-I ratios and high p62 levels, indicating reduced basal autophagic flux. Collagen 1α2 and fibronectin levels were comparable between the two lines. Elevated phospho-Smad3 suggested active endogenous TGF-β1 secretion, meaning the cells autonomously activate Smad signaling without exogenous TGF-β1. Both cell lines exhibited a mesenchymal phenotype, characterized by low E-cadherin and high Vimentin expression. This intrinsic signaling profile suggests that even ”unstimulated” fibroblasts are primed for matrix remodeling and contraction. These findings provide a crucial foundation for future investigations into how stiffness-mediated autophagy shapes fibroblast behavior, enabling the development of tunable 3D biomimetic models for fibrosis and regenerative medicine.

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Influence of ionizing irradiation on burkitt lymphoma cells

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Keywords: onizing irradiation, Burkitt lymphoma, apoptosis, cell cycle arrest

Abstract

Radiotherapy with ionizing radiation (IR) is a common treatment for cancer patients, and its effectiveness largely depends on the radiosensitivity of cancer cells. In this study, we investigated the effects of ionizing irradiation on the expression of protein-coding genes in Burkitt Lymphoma (BL). Three BL cell lines, CA46, DG75, and ST486, were irradiated with a dose of 4 Gy. Apoptosis was induced in all cell lines 24 hours post-irradiation. However, the proportion of apoptotic cells varied between lines. Additionally, irradiation led to cell cycle arrest at the G2 phase in all examined cell lines.

Gene Set Enrichment Analysis (GSEA) of Biocarta pathways revealed upregulation of the FAS, ATM, and death signaling pathways. RNA sequencing identified 30 protein-coding genes consistently affected across all three BL cell lines. IR affected the expression of 95 to 120 protein-coding genes, depending on the cell line. Notably, BIRC2, NFKB1, CD40, and FAS were upregulated by at least 1.5-fold in all cell lines. Overall, ionizing radiation affected the expression of a limited number of protein-coding genes in Burkitt lymphoma cells. Further studies are ongoing.

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Plenary session (3A)
time 17:00 – 17:45

Chairperson:
Joanna Polańska

Computational strategies for T-cell receptor repertoire analysis in cancer RNA sequencing

Dr. Serghei Mangul[1], Assistant Professor of Clinical Pharmacy and Computational Biology

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Keywords: Adaptive Immune Receptor Repertoire (AIRR), AIRR-Seq, T cell receptors, cancer immune profiling, next-generation sequencing (NGS)

Abstract

Recent advances in high-throughput sequencing technologies are revolutionizing our understanding of the immune system, offering unprecedented opportunities for profiling the adaptive immune receptor repertoire (AIRR) at scale. AIRR analysis is proving critical in the field of oncology and personalized medicine, providing key insights into cancer development, progression, immune evasion, and response to therapies like immunotherapy. Detailed profiling of T and B cell receptors via technologies like AIRR-Seq offers granular views, but limitations in sample diversity across studies can hinder the comprehensive detection of novel population-specific V(D)J alleles, particularly relevant in diverse patient cohorts crucial for personalized approaches. Non-targeted next-generation sequencing (NGS) data, readily available from large-scale cancer genomics and transcriptomics projects across various ancestries, presents a promising, yet computationally challenging, avenue to overcome this data diversity gap. This talk will address the challenges posed by analyzing vast, diverse, and often non-targeted NGS datasets for AIRR profiling in the context of computational oncology and personalized medicine. We will focus on the development of scalable bioinformatics algorithms specifically designed to extract adaptive immune receptor information and assemble novel population-specific alleles directly from non-targeted data. These computational approaches are essential for leveraging existing cancer genomics resources to deepen our understanding of immune responses in diverse patient populations and ultimately inform personalized therapeutic strategies. We will highlight how these novel technologies and associated computational solutions are critical steps towards unlocking the full potential of immune repertoire profiling in cancer care.

Parallel session (4A)
time 17:45 – 18:45

Chairperson:
Michał Marczyk

Reducing technical differences between datasets after application of different foundation models in histopathology

Julia Merta[1*], Michal Marczyk[1*], Miłosz Pietrus[2]

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Keywords: histopathology, foundation models, whole slide imaging, batch effect, H&E-stained images, image processing

Abstract

Histopathological whole-slide images (WSIs) are characterized by high complexity and variability due to differences in staining protocols and various artifacts across datasets. Additionally, the manual annotation of tissue slides is time-consuming, so there is growing interest in developing unsupervised foundation models for various tasks. These universal models are trained on large and diverse datasets of tissue images from different organs, which aim to overcome problems with model generalization between different tissue types and datasets.

In this study, we assessed the performance of four models: SSL ResNet18, UNI, CTransPath, and H-Optimus, using WSIs of endometrial cancer in three histological grades, sourced from TCGA UCEC, CPTAC UCEC, and a hospital in Cracow. Images were divided into 256×256-pixel patches at 10x magnification. The extracted features were visualized after UMAP dimensionality reduction.

The results showed that the use of foundation models is insufficient, since major differences between datasets are observed. We proposed a preprocessing pipeline involving patch filtering and stain normalization to reduce these technical differences between samples and remove patches with artifacts such as marker annotations, image blurring, overexposure, and tissue folds. The proposed pipeline reduced the occurrence of the batch effect for all tested models. Furthermore, preprocessing eliminated most patches containing artifacts.

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New computational models for stratification of neuromuscular disorders patients

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Keywords: neuromuscular disorders, genetics, histopathology, MRI, neurology, AI

Abstract

Diagnostic approach to Hereditary Neuromuscular Diseases (HNMDs) remains critical as over 60% of patients remain molecularly unsolved or misdiagnosed. Artificial Intelligence (AI) offers transformative opportunities for data integration and precision diagnostics.

CoMPaSS-NMD integrates clinical, genetic, histopathological, and imaging data by developing AI-based tools for patient stratification. The study analyses 3,900 genetic, 2,000 histopathological, 2,000 MRI existing data from European centres through unsupervised machine learning (ML) to develop stratification algorithms. ML-based algorithms for patient stratification will be validated studying 500 undiagnosed HNMD patients who will undergo standardized clinical, whole genome sequencing, histological, and MRI evaluations and collected in the CoMPaSS-NMD ATLAS, a public repository created to address the fragmentation of information leading to delays in diagnosis and incomplete knowledge of multifaceted diseases.

A new ranking tool for genetic variants has been created. Algorithms for histopathological and MRI analysis have been developed, addressing challenges of variability and identification of cluster-specific signatures.

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CoMPaSS-NMD leverages AI to revolutionize the diagnosis of HNMDs, beyond the one gene-one phenotype paradigm. This multidimensional approach will boost diagnostic rates by 30%, optimize healthcare strategies, and significantly improve the lives of patients and caregivers.

Acknowledgments: We thank all the partners of CoMPaSS-NMD consortium. We are grateful to all our patients and their families. This research was supported by the EU under Grant Agreement n°101080874.

Radiomics based stratification of neuromuscular disorders based on the lower leg MRI

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Keywords: magnetic resonance imaging, neuromuscular disorder, UMAP, leg, radiomics

Abstract

Neuromuscular diseases (NMDs) are conditions that cause skeletal muscles to weaken and break down over time. As the disease progresses, healthy muscle is replaced by non-functional fat and connective tissue. Each NMD has a different pattern of progression, so identifying the correct type is important for treatment and care.

The proposed method aims to recognise an NMD type in the lower body. A radiomic-based method was developed to group and compare patients based on MRI scans. A dataset of 2,012 T1-weighted MRIs from 763 patients with genetically confirmed neuromuscular diseases (NMDs) was utilised. A pipeline was established to automatically segment skin and bone structures from the legs and pelvis. Consistent anatomical subregions in the thigh and shin were defined based on bone positions, and radiomic features were extracted from these areas.

These features are used to create a 2D map that reflects how similar or different patients are from each other in terms of muscle damage. This helps classify new patients, compare disease severity, and track progression.

Unlike traditional methods that rely on precise muscle borders, which become unclear due to fat infiltration, our method focuses on stable structures like bone and surrounding tissue. This makes it more robust and scalable, offering a useful tool for personalised monitoring and treatment planning in NMD care.

Acknowledgments: Financed from CoMPaSS-NMD grant.

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Comparison of the kerma area product displayed and measured in radiographic systems

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Keywords: X-ray radiography, kerma area product (KAP)

Abstract

Introduction:

X-ray radiography remains a cornerstone in medical diagnostics by providing non-invasive, detailed images of internal body structures. The Kerma Area Product(KAP) is the primary metric to quantify ionizing radiation during these procedures. This study evaluates the accuracy of these console-displayed KAP values by comparing them with the independently measured and calculated values.

Material and methods:

Four X-ray systems(Siemens Axiom Luminos dRF Wall and Table, Arcoma Precision I5 Wall, RTG Mobile Solutions !M1) were evaluated at two kVp values to determine the accuracy of the internal exposure index in various clinical applications. The displayed KAP values were compared to those obtained in the independent measurements with a calibrated RTI Piranha Black multimeter. The measurements were made at SDD=110cm with a field of 20cm x 20cm using inherent tube filtration only.

Results:

The discrepancies were observed between the displayed and measured KAP values, with the deviations up to 28%. The largest deviations occurred at the highest kVp in all systems, especially in both Siemens systems. The mobile RTG system showed the differences of ca. 7.5%.

Conclusions:

The displayed KAP values should be interpreted with caution. Accurate dose evaluation requires independent annual verification with a calibrated multimeter. Significant deviations(>35%) in the displayed KAP values require service intervention to ensure compliance with established radiation dose standards.

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Comparative analysis of brain structure segmentation accuracy using two anatomical atlases

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Keywords: magnetic resonance imaging, brain segmentation, brain volumetry, anatomical atlases, pediatric brain data

Abstract

Introduction:
Anatomical brain atlases play a crucial role in the segmentation process of grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF), which is essential for MRI-based volumetric studies. However, pediatric analyses are particularly challenging due to the limited availability of age-specific atlases. This study aimed to compare two segmentation approaches using different anatomical atlases for pediatric brain data.
Material and methods:
The dataset included 147 healthy, ethnically homogeneous children. High-resolution 3D T1-weighted images were obtained using a consistent, rapid gradient-echo protocol. The original MR images, encoded in DICOM, were converted to the NIfTI format. Image segmentation procedures were performed in Matlab Statistical Parametric Mapping (SPM) software using two atlases: ICBM (International Consortium for Brain Mapping) as the default and POL96young (nonparametric). The structures were classified into WM, GM, and CSF. Paired t-tests, Wilcoxon signed-rank tests, and Cohen's d were used for statistical analysis.
Results:
The results revealed significant differences between the segmentation methods: WM and GM volumes were higher using the ICBM template, while CSF volumes were greater with the POL96young atlas.
Conclusions:
These findings emphasize that the choice of brain atlas significantly impacts tissue segmentation results and is critical for reliable volumetric measurements in pediatric neuroimaging studies.

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Impact of clothing color and pattern on the quality of 3D body reconstruction using multi-view photogrammetry for medical applications

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Keywords: multi-view photogrammetry, point cloud, 3D scanning technology, human body scan, reconstruction artifacts, image reconstruction, surface quality

Abstract

Three-dimensional (3D) body scans are increasingly used in the medical field for designing personalized orthopedic and rehabilitation devices, creating digital patient avatars, and assessing posture and asymmetries. One technique for obtaining such scans is multi-view photogrammetry (MVS), a rapidly developing method for capturing objects. A key factor affecting the quality of resulting 3D models is the preparation of the scanned individual, particularly clothing color and pattern.

This study aimed to determine the influence of clothing color and pattern on the quality of 3D models created using MVS and to develop practical guidelines for clothing selection. The experiment was conducted under controlled studio conditions (Big Alice Studio) with one individual photographed in various clothing types, including plain black, plain white, and patterned fabrics with different scales and contrasts. 3D mesh models were generated using RealityCapture software. The analysis focused on surface detail and reconstruction artifacts.

High-contrast patterns created clear feature points, facilitating more accurate reconstruction. Plain clothing lacked distinctive features, making it difficult for photogrammetric algorithms to capture fine details, resulting in lower model quality and distortions. Proper preparation of the subject, particularly careful clothing selection, is crucial for enhancing 3D model quality, essential for medical diagnostics and personalized rehabilitation planning.

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Sexual dimorphism in volumetric analysis of the central nervous system

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Keywords: volumetric analysis, sexual dimorphism, magnetic resonance, cortical and subcortical structures

Abstract

Introduction: Volumetric analysis (VA) allows for precise quantification of cortical and subcortical brain structures. This study explored sexual dimorphism in brain volumes and their age dependence, both before and after normalization for total brain volume (TBV).

Materials and Methods: A total of 101 structural magnetic resonance (MR) scans of the brain were initially included in the study, but only 66 scans were successfully processed in the final dataset (due to poor image quality). The segmentation was performed using SPM and FSL-FIRST. The following structures were analyzed: thalamus, caudate, putamen, pallidum, hippocampus, amygdala, and nucleus accumbens (bilaterally), as well as gray matter, white matter, and cerebrospinal fluid. Statistical analyses were performed using t-test, Mann-Whitney U test as well as Spearman's Rank Correlation Test for age dependance analysis.

Results: Significant age-related volume changes were observed in almost all brain structures. The TBV parameter showed a negative correlation with age and was higher in men. The analysis of non-normalized MR data showed the presence of sexual dimorphism (larger in men), after the TBV normalization differences were no longer statistically significant.

Conclusions: Sexual dimorphism disappears after the TBV normalization, indicating a monomorphic character of brain structures. This highlights the importance of brain size normalization in morphometric studies to avoid overestimating sex-related effects.

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Radiomics-based comparative analysis of breast tumor MRI images using FCM and X-Means clustering

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Keywords: MRI, breast cancer, clustering, radiomics, machine learning

Abstract

Introduction: Radiomics has emerged as a powerful tool in medical imaging, enabling the extraction of quantitative features from imaging data that reflects tumor phenotype and heterogeneity. Magnetic Resonance Imaging offers rich, multiparametric data that can be used for detailed tumor characterization. Unsupervised machine learning clustering algorithms such as Fuzzy C-Means and X-Means are widely used to detect tumor regions.

Materials and Methods: The dataset consisted of 63 breast cancer patients, acquired from the National Oncology Institute of Maria Sklodowska-Curie. High-resolution 3D subtraction images were obtained using a consistent T1-weighted dynamic contrast-enhanced protocol. The original MRI images, encoded in DICOM were converted to the NRRD format. Fuzzy C-Means and X-Means clustering algorithms were applied to the defined ROI. Statistical tools such as the Shapiro-Wilk test, Wilcoxon signed-rank tests, and rank-biserial correlation were used for statistical analysis to compare the two masks.

Results: Results revealed statistically significant differences between FCM and X-Means based masks for certain features.

Conclusions: These findings suggest that the choice of clustering technique can impact the accuracy and reliability of tumor characterization in MRI breast cancer studies.

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Comparative analysis of the accuracy of segmentation of brain structures using different image de-noising methods

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Keywords: magnetic resonance imaging, central nervous system, image denoising, segmentation, brain

Abstract

Introduction: Atlas-based methods are highly effective for segmenting brain regions, particularly for delineating grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF). An essential pre-processing step is image denoising, which can influence segmentation quality.

Materials and Methods: The study involved 38 healthy, ethnically homogeneous adults. High-resolution 3D T1-weighted MRI scans were acquired using a uniform rapid gradient-echo protocol. Five denoising algorithms were applied: SUSAN, non-local means, Noise2void, wavelet-based, and total variation. DICOM images were converted to NIfTI format. Segmentation was performed using the ICBM atlas in MATLAB's SPM software, classifying tissues into WM, GM, and CSF. Volumes of these structures were calculated, and Friedman's rank test was used for statistical analysis.

Results & Conclusions: Volumetric results significantly varied depending on the denoising method used. This indicates that the choice of denoising algorithm significantly impacts tissue segmentation results and is vital for reliable volumetric measurements in neuroimaging studies.

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Parallel session (4B)
time 17:45 – 18:50

Chairperson:
Justyna Mika

Inducted pelvic asymmetry in response to single-leg landing: a case series with 60-minute observation

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Keywords: biomechanics, motion analysis, optoelectronic measurement, pelvic asymmetry

Abstract

Introduction and Aim of the study: Asymmetrical pelvic alignment occurs in healthy, asymptomatic individuals as well as in those with various musculoskeletal disorders. It can also arise in response to repeated movement patterns, for example in athletes, or as a result of a single physical load. The aim of this case series analysis is to assess the impact of single-leg landing after a drop jump on pelvic alignment symmetry, with measurements taken immediately after the intervention and every 10 minutes during a 60-minute observation period.

Results and Conclusion: All participants demonstrated pelvic symmetry in the sagittal plane prior to the jump. Immediately after the jump, asymmetry was observed in 67% of participants, and the number of individuals exhibiting asymmetry gradually decreased, reaching 33% after 60 minutes. In the frontal plane asymmetry was noted in 50% of participants before the jump, and in 100% both immediately after the jump and after 60 minutes. Single-leg landing after a drop jump has the potential to induce pelvic asymmetry in the sagittal plane, which gradually decreases over time. In frontal plane, a tendency for asymmetry was also observed, however no clear trend of change over time was noted.

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Tantalum (V) Oxide ALD layer as an innovative approach to enhance physicochemical properties of NiTi alloy for cardiovascular applications

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Keywords: susceptibility to deformation, NiTi alloy, tantalum oxide, atomic layer deposition (ALD)

Abstract

The rising incidence of cardiovascular diseases has driven the search for innovative solutions, including the application of a NiTi alloy coated with a Ta_2O_5 layer to mitigate the risk of pathological complications. Shape memory alloys are widely utilized in medicine, particularly in the fabrication of stents and biomedical devices that require materials responsive to temperature changes. On the other hand, they can release nickel ions, posing potential risks of side effects. In this study, NiTi samples compliant with ASTM 2063-18 standards were electropolished and subsequently coated with thin Ta_2O_5 films using Atomic Layer Deposition. The deposition was performed with $Ta(OC_2H_5)_5$ and H_2O precursors over 400 cycles at 300°C. Adhesion testing demonstrated excellent coating adherence, with failure occurring only under a load of 22 N, accompanied by continuous plastic deformation. The coating exhibited a nanohardness of 2724 MPa and a Young's modulus of 73.4 MPa. Both coated and uncoated surfaces showed hydrophilic properties, which may contribute to reduced blood clotting, enhancing the material's suitability for cardiovascular implants. Deformation resistance studies revealed coating cracking at a bending angle of approximately 40°, which was corroborated by shifts in the open-circuit potential. In conclusion, the findings indicate a strong potential for the use of Ta_2O_5 coatings in implantology, underscoring the necessity for further biological evaluations.

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Synthesis and characterization of hydroxyapatite-modified biomorphic carbon materials for potential bone implant applications

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Keywords: hydroxyapatite, bone scaffolds, pyrolysis, porosity, biomaterials

Abstract

The field of bone implantology is in constant pursuit of innovative biomaterials that can effectively support bone tissue regeneration and serve as substitutes for damaged or lost bone fragments. The ideal material should not only provide structural support but also promote tissue integration and exhibit suitable biomechanical properties. This study explores the potential of biomorphic carbon materials derived from wood as a promising candidate for bone implant applications.

Wood's natural structure, after controlled pyrolysis and CO_2 activation, yields carbonized scaffolds with enhanced porosity. Further modification with hydroxyapatite (HAp) improves bioactivity, as HAp is a key bone mineral. The synthesized materials were thoroughly characterized. Porosity analysis revealed a well-developed network of meso- and macropores, supporting nutrient transport and tissue ingrowth. Mechanical testing showed elasticity within the range of human bone, offering effective load transfer and bone remodeling. Electrical resistivity was also evaluated, confirming compatibility with biological tissues. SEM confirmed HAp presence and successful modification, while FTIR analysis validated the formation of characteristic functional groups. The results highlight the potential of HAp-modified carbon biomorphic scaffolds for bone tissue engineering, combining porosity, mechanical strength, and biocompatibility. Further research will optimize their properties for clinical applications.

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Patient-specific orthosis for the thumb CMC joint: design and manufacturing workflow

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Keywords: orthoses, CAD modeling, fused filament fabrication

Abstract

Thumb carpometacarpal (CMC) joint orthoses are commonly used in the treatment of conditions such as osteoarthritis, aiming to stabilize the joint, reduce pain, and improve hand function. Personalization of such devices significantly enhances patient comfort and therapeutic outcomes. This project focused on the design and fabrication of a custom-fit orthosis tailored to the anatomical structure of an individual patient's hand. The design process included anatomical data acquisition via 3D scanning, CAD modeling in SolidWorks (using surface and solid modeling techniques), and additive manufacturing using the Fused Filament Fabrication (FFF) method with PETG filament. The resulting prototype demonstrated a high degree of anatomical conformity and functional usability. It featured an adjustable hook-and-loop strap fastening, allowing further adaptability in case of swelling or changes in hand size. The implemented approach proved to be effective in creating a functional, patient-specific medical device. This workflow highlights the potential of 3D printing as a fast, economical, and scalable method for producing customized orthotic equipment, particularly in rehabilitation and low-volume clinical applications.

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3D printing in the work of a medical physicist

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Keywords: 3D printing, quality control, phantom

Abstract

3D printing is currently widely used to create phantoms and devices supporting quality control in radiotherapy and X-ray diagnostics. Here we present several original and simple solutions, developed at NIO PIB in Gliwice, that significantly facilitate the every-day work of a medical physicist.

The first of our projects is a phantom for positioning a stand for measuring the focus of an X-ray tube. The idea for this solution was taken from a commercial device from Gammex. The printout is in a form of a hollow cuboid of 0.4x1x10mm with the mount for two steel wires on one of the bases and a mount for a 1 mm diameter steel ball in the other base.

The other one is a phantom for controlling the mechanical isocenter. In this case, the existing bases of the Varian OBI system were used, which allowed for a stable attachment of the phantom to the treatment table. The construction consists of two connected concentric rings, in the middle of which a positioning indicator. Additionally, a plotting paper was placed at the top of the cylinder to facilitate checking any isocenter shifts.

The third project is a cylinder for positioning the ionization chambers during the verification of their stability using the control sources. Without such tool the exact positioning of the chamber is difficult, which in turn affects the results. 3D printing offers many possibilities for quality control and streamlining the every-day work of a medical physicist. The only limiting factors is creativity.

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3D-printed patient-specific bone model of osteochondral exostoses

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Keywords: patient-specific model, osteochondroma, 3D printing, medical education, preoperative planning, FDM technology

Abstract

Osteochondroma, the most common type of osteochondral exostosis, is a benign bone tumor typically located in the metaphyses of long bones. It consists of a cartilage-capped bony outgrowth that remains continuous with the cortex and medullary cavity of the parent bone. Due to its structure and location, it provides a relevant context for the application of 3D modelling. The printed model enables assessment of lesion topography, size, and spatial relations with surrounding tissues, supporting preoperative planning and the evaluation of potential need for bone grafting. This study aimed to develop a patient-specific, 3D-printed model of the humerus with osteochondral exostoses, based on computed tomography (CT) imaging, to evaluate its utility in medical education and preoperative planning. Segmentation was performed in 3D Slicer using DICOM data obtained from a real patient. Models were fabricated using 3D printer work in fused deposition modeling (FDM) technology. Two variants were created: a uniform PLA model with exostoses in the same color as the bone, and a two-color version consisting of a transparent PET bone with contrasting PLA outgrowths, intended to facilitate visual identification of the pathological changes. The prints enabled the analysis of the lesions' morphology and spatial relationships with surrounding structures. The results confirmed the potential of such models for clinical education and for personalized planning of orthopedic or oncological procedures.

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Smoothing of the PLA 3D-printed microfluidic matrices

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Keywords: 3D printing, microfluidics, surface finishing techniques, chemical smoothing

Abstract

Microfluidics is a rapidly developing field, and the use of 3D printing—particularly Fused Deposition Modeling (FDM)—has become increasingly popular due to its flexibility and low cost. Polylactic acid (PLA), one of the most popular material in FDM, offers an affordable option for producing microfluidic chips, significantly reducing the cost per device. However, the inherent surface roughness of FDM prints can impede precise fluid handling. Several PLA smoothing methods exist, including thermal treatment, chemical smoothing (e.g., with acetone), and mechanical abrasion. This study investigates surface finishing techniques aimed at enhancing the surface quality of FDM 3D-printed components for microfluidic applications. PLA post-processing was performed using abrasive sanding with 180- and 320-grit sandpaper, followed by chemical smoothing via acetone rinsing. Surface roughness was quantitatively evaluated before and after treatment to assess the effectiveness of each method. The combined approach resulted in a significant reduction in surface irregularities, leading to smoother channel walls and improved flow dynamics within microfluidic systems. The findings demonstrate that mechanical and chemical post-processing can substantially enhance the functional performance of FDM-printed devices in precision fluid handling contexts.

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Ensuring proper flow control in a syringe pump system for microfluidic applications

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Keywords: microfluidics, pump, flow meter, drug testing

Abstract

Precise flow control is critical for microfluidic experiments, where slight deviations can significantly impact results. Maintaining a stable and accurate flow rate requires systems capable of real-time monitoring and automatic adjustment of pump parameters.

The system integrates a New Era NE-1000 syringe pump and a CorSolutions ECO nano flow meter for real-time flow monitoring within a closed feedback loop. Both systems are connected to the computer, communicating with the devices over the serial connection. Then, the software sends commands to the pump correcting its parameters to keep up with the selected flow rate.

Flow control software was written in Python which allows for a modular, scalable architecture. This solution ensures stable flow control during experiments without the need for exact measurements of the syringes, reducing user errors and improving reproducibility.

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Effect of PEO treatment on surface morphology and hydrogen evolution of magnesium alloys for biomedical applications

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Keywords: magnesium alloy, hydrogen evolution, plasma electrolytic oxidation, calcium-phosphate coating

Abstract

Magnesium alloys are considered promising materials for orthopedic applications due to their biodegradability and mechanical properties close to natural bone. However, their rapid corrosion and associated hydrogen evolution in physiological environments pose significant challenges. Plasma Electrolytic Oxidation (PEO) was applied to fabricate calcium-phosphate (Ca-P) coatings on WE43 magnesium alloys for biomedical applications. The main objective was to improve the corrosion resistance of the substrate and reduce hydrogen evolution during immersion in simulated physiological conditions. Samples with and without coatings were immersed in phosphate-buffered saline (PBS) for 7 days, and the volume of released hydrogen was measured. The results showed a significant reduction in hydrogen evolution for PEO-coated samples compared to uncoated ones. Surface morphology examined by scanning electron microscopy (SEM) revealed a characteristic porous structure with visible cracks. Elemental analysis by energy-dispersive spectroscopy (EDS) confirmed the presence of calcium and phosphorus within the coatings. These findings indicate that PEO treatment effectively enhances the degradation behavior of WE43 alloy, suggesting its potential for future orthopedic implant applications.

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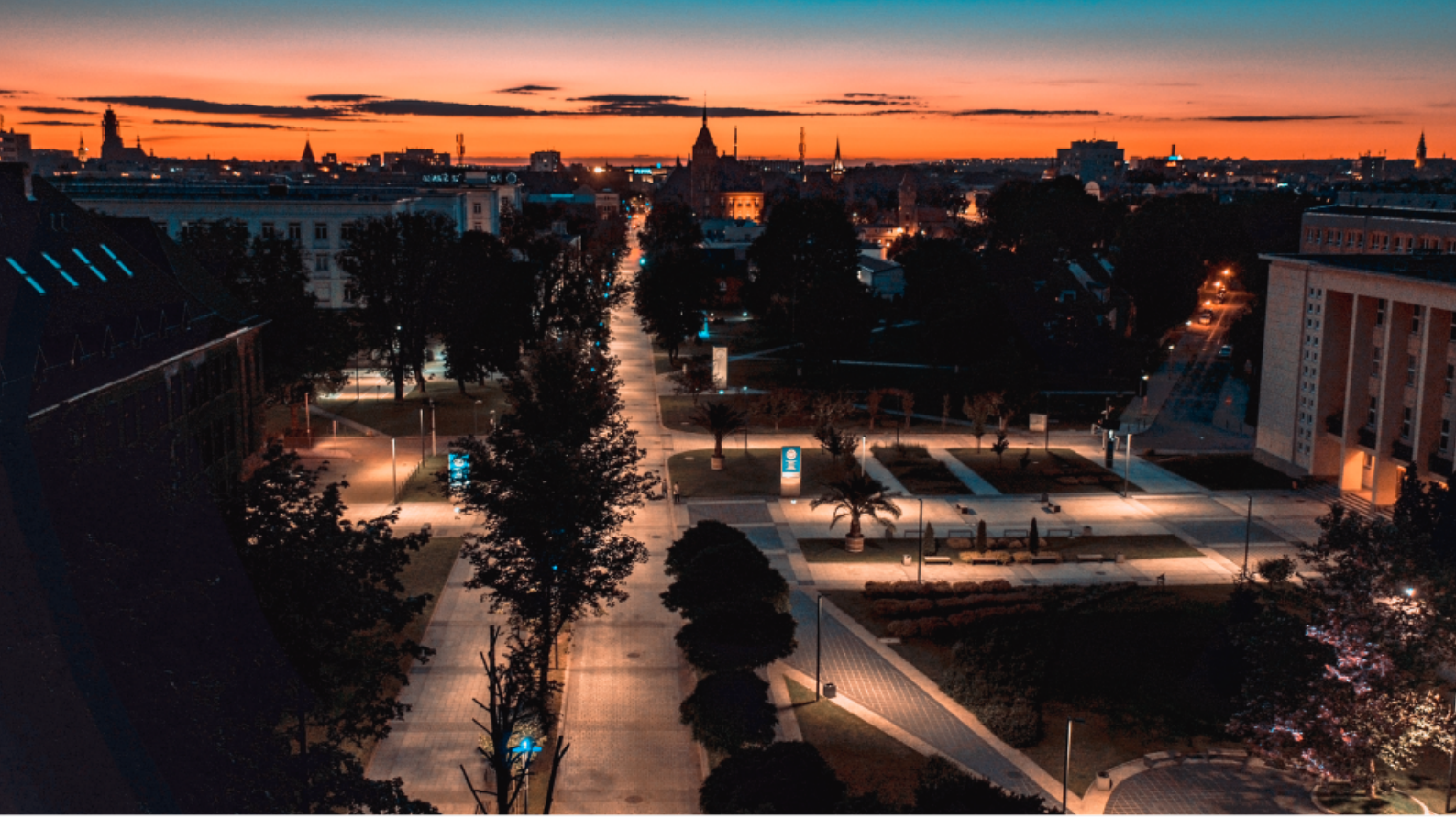

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