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November 27-29, 2024,Kragujevac, Serbia

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BIBE2024

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BioIRC

Biological & Artificial Intelligence FOUNDATION

СДРМ
СРПСКО ДРУШТВО ЗА РАЧУНСКУ МЕХАНИКУ
SERBIAN SOCIETY FOR COMPUTATIONAL MECHANICS

IEEE COMPUTER SOCIETY

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WELCOME NOTE

Dear colleagues,

On behalf of the Organizing Committee, it is our pleasure to invite you to the 24th International Conference on BioInformatics and BioEngineering (IEEE BIBE 2024) which will take place in Kragujevac, Serbia, on November 27th-29th, 2024.

The IEEE International Conference on Bioinformatics and Bioengineering (BIBE) promotes complementary disciplines that hold great promise for the advancement of research and development in complex medical and biological systems, agriculture, environment, public health, drug design, and so on. The BIBE series provides a common platform for the symbiosis of ideas by bridging these two very important and complementary disciplines into an interactive and attractive forum.

The main conference encompasses sixteen technical sections. The topics covered range from Bioinformatics, Bioengineering, Cancer, Tissue Engineering, Cardiovascular Diseases, to Image Processing, Chemical Computing and so on. Also, the conference includes workshop dedicated to Horizon 2020 project DECODE.

We also have the pleasure to host 8 world renowned scientists as IEEE BIBE 2024 keynote speakers:

- **Prof. Valentin Djonov**, University of Bern, Berne, Switzerland
- **Prof. Aleksandar Novaković**, School of Mathematics and Physics, Queen's University Belfast, United Kingdom
- **Prof. Miloš Kojić**, Houston Methodist Research Institute, USA; Serbian Academy of Science and Arts
- **Prof. Branislav Jeremić**, University Clinical Centre, Kragujevac
- **Prof. Milica Radišić**, University of Toronto, Canada
- **Prof. Dimitrios I. Fotiadis**, University of Ioannina, Ioannina, Greece
- **Prof. Đorđe Jakovljević**, Coventry University, United Kingdom and
- **Prof. Wei Zhang**, Dalian University of Technology, Dalian, China.

BIBE 2024 gathers eminent scientists and researchers, as well as students and representatives of companies, aiming to promote interdisciplinary and multidisciplinary approaches needed for solving complex problems, which requires expertise in the field of biomedical sciences and engineering.

This year, IEEE BIBE 2024 has received more than 100 high-quality research papers. Each paper was reviewed and ranked by at least 2 reviewers from the scientific review committee. As a result of the strict review process and evaluation, the committee selected almost 70 papers as full research papers.

Lastly, we must also say that the conference would certainly not have been so successful without the efforts of many people who were actively engaged in organization and support of such a major internationally recognized academic event. We give our special gratitude to the members of the program and scientific review committee as well as to all chairs, organizers and committee members for their dedication and support.

Serbia has already proved as an excellent host of BIBE conferences in the past, so we believe that IEEE BIBE 2024 will again be an excellent opportunity for all authors to present their research achievements in these challenging areas.

On behalf of the Organizing Committee, we wish you all a pleasant stay in Kragujevac and a productive conference.

Prof. Nenad Filipović, Conference General Chair

Technical Program

Wednesday 27th November 2024

10:00 - 10:30	Opening Ceremony - Welcome Speech: **Prof. Nenad Filipović**, *Conference General Chair* **Jelena Begović,** *Minister of Science, Technological Development and Innovation* **Nikola Dašić,** *Mayor of the City of Kragujevac*

10:30 - 11:00	Keynote speaker: Topic: **Technological Innovations in Diagnosis of Heart Failure** **Prof. Đorđe Jakovljević, Research Centre for Health and Life Sciences of Coventry University, United Kingdom** Chair: Nenad Filipović

Session W.1A: 11:00-12:00

Bioinformatics I

Chair: Marko Zivanovic

W.1A.1 **Navigating the explainable Molecular Graph: Best Practices for Representation Learning in Bioinformatics -** Rocco Zaccagnino, Gerardo Benevento, Gianpaolo Laurenzano, Delfina Malandrino, Alessia Petescia and Gianluca Zaccagnino

W.1A.2 **Design of the Amorphous Solid Dispersion (ASD) Drugs by Hot Melt Extrusion (HME), for the Inhibition of Bone Graft Rejection -** Đorđe Milošević, Marija Brankovic, Mihailo Jovanović, Janko Đorđević, Nenad Grujović and Fatima Živić

W.1A.3 **Depression Diagnosis: Bioinformatics Uncover Cellular Abnormalities in Female - Specific Genes with AI-Driven blood biomarker-based prediction -** Neda Firoz, Nivedita Yadav, Olga Grigorievna Berestneva and Sergey Aksyonov Vladimirovich

Session W.2A: 12:00-12:30

Pulmonary disease

Chair: Miljan Milošević

W.2A.1 **CAT Score Prediction in COPD patients using a Chest-wearable Respeck -** Dk Arvind, P Peters, CA Bates, M Prior and L Gray

W.2A.2 **Data-driven analysis of irregular respiratory signals derived from the chest- wearable Respeck monitor -** Dk Arvind and Filip Futera

12:30 - 13:00	Coffee Break

Session W.3A: 13:00-14:30

Cardiovascular I

Chair: Đorđe Jakovljević

W.3A.1 **EI-ViT-Net: A Vision Transformer Approach for Diabetic Retinopathy's Decision Support Pipeline -** Alexandru Farcaş, Alesia Lobonţ, Diogen Babuc, Todor Ivaşcu and Sebastian-Aurelian Ştefănigă

W.3A.2 **Short Overview of Left Ventricular Action Potential Simulations: Integrating Numerical**

Methods with Machine Learning - Bogdan Milićević, Miljan Milošević, Vladimir Milovanović, Mina Vasković Jovanović, Miloš Kojić and Nenad Filipović

W.3A.3 **HyperECG: ECG Signal Inference from Radar with Hyperdimensional Computing -** Matilda Gaddi, Flavio Ponzina, Fatemeh Asgarinejad, Baris Aksanli and Tajana Rosing

W.3A.4 **Heart Failure: Machine Learning Prediction within a 5-Year Framework -** Konstantina-Helen Tsarapatsani, Vassilis D. Tsakanikas, Antonis Sakellarios, Hans J. Trampisch, Efterpi Karapintzou, Henrik Rudolf, George K. Matsopoulos and Dimitrios I. Fotiadis

W.3A.5 **Adventitia Segmentation On Superficial Femoral Artery Optical Coherence Tomography Images –** Miloš Anić, Sotirios Nikopolous, Konstantinos Siaravas, Christos S. Katsouras, Vasiliki Potsika, Nenad Filipović and Dimitris Fotiadis

W.3A.6 **Kolmogorov-Arnold-based Network with Lightweight Feature Fusion Schema for Single-Lead Electrocardiogram Atrial Fibrillation Detection -** Zijian Zhao, Likun Sui, Yang Song, Branka Vučetić and Zihuai Lin

Session W.1B: 13:00-14:00

Bioengineering I

Chair: Aleksandra Vulović

W.1B.1 **Analysis of DNA Sequences from Human Sweat and Comparison with Blood Sample -** Tirthankar Paul, Daniel Fischer, Seppo Vainio and Juha Roning

W.1B.2 **AI-Enhanced Tele-Rehabilitation: Predictive Modeling for Fall Risk and Treatment Efficacy in Balance Disorders -** Efterpi Karapintzou, Vassilios Tsakanikas, Dimitrios Kikidis, Christos Nikitas, Brooke Nairn, Marousa Pavlou, Doris-Eva Bamiou, Themis Exarchos and Dimitrios Fotiadis

W.1B.3 **PulSense: An AI-driven Cardiovascular Monitoring and Arrhythmia Detection System-** Evangelos Katsoupis, Apostolos Karasmanoglou, Michalis Zervakis and Marios Antonakakis

W.1B.4 **An exploration of k-mer ranges for MEGAHIT in the context of microbial community-wide identification of antimicrobial resistance genes and biosynthetic gene clusters -** Alina Cărunta, Alexandru Eugeniu Mizeranschi, Cristina Cărunta, Horia Leonard Banciu, Oana Teodora Moldovan, Daniela Zaharie and Viorel Negru

14:30 - 15:30	Buffet Lunch

Session W.4A: 15:30-16:00

Cardiovascular II

Chair: Bogdan Milićević

W.4A.1 **Predicting Heart Disease: A Comprehensive Approach to Data Analysis and Machine Learning Model Development -** Uroš Bojanić and Milan Bjelica

W.4A.2 **Estimating the Effect of Danicamtiv on Human Cardiac Function -** Momčilo Prodanović, Vanja Cvetković, Anđela Grujić and Srboljub Mijailovich

Session W.5A: 16:00-16:30

Chemical Computing

Chair: Zoran Marković

W.5A.1 **In vitro and in silico binding studies of chromeno-pyrimidine derivatives with biological important protein-Part III -** Danijela Stojković, Sandra Jovičić Milić, Dušica Simijonović, Edina Avdović, Tamara Mladenović and Zoran Marković

W.5A.2 **Design, In Silico Evaluation, and Toxicological Assessment of N-Protocatechoyl Hydrazone Derivatives as Potential EGFR Kinase Inhibitors -** Dejan Milenković, Marko Antonijević, Edina Avdović, Dušica Simijonović and Zoran Marković

16:30 - 17:00	Keynote speaker: Topic: **Assessing the Impact of Public Health Interventions and Simulating COVID-19 Spread in Northern Ireland Using the CP-ABM Approach** **Prof. Aleksandar Novakovic, School of Mathematics and Physics, Queen's University Belfast, United Kingdom** Chair: Lazar Dašić

17:00 - 17:30	Keynote speaker: Topic: **Physics-Based Computational Models Within the Artificial Intelligence Scheme: Important Features** **Prof. Milos Kojic, Houston Methodist Research Institute** Chair: Vladimir Simić

17:30 - 18:00	Coffee Break

Session W.6A: 18:00-19:00

Tissue engineering

Chair: Jelena Pavić

W.6A.1 **Transformer-Based Real Time Musculoskeletal Anatomical Structure Detection in Clinical Use -** Jyun-Ping Kao, Hao-Yu Hung, Ping-Xuan Chen, Chung-Ping Chen and Wen-Shiang Chen

W.6A.2 **The influence of changes in voltage and flow rate on the diameter of electrospun nanofibers -** Jana Baščarević, Katarina Virijević, Marko Živanović and Nenad Filipović

W.6A.3 **Biomimetic natural electrospun gelatin scaffolds for skin regeneration -** Katarina Virijević, Marko Živanović, Jelena Pavić, Tamara Mladenović, Hilal Girgin Oz, Jana Baščarević and Nenad Filipović

W.6A.4 **Smart Clothes Using Vital Signals for Evaluating Health Conditions: A Comparative Evaluation -** A. Shrivastava, K. A. Kumar Shukla, P. R. Simhadri, S. K. Sunkaraboina V. Thammisetty and N. Bourbakis

W.6A.5 **Biogenic silver nanoparticles causes cell death by inducing oxidative stress in MRC-5 cell line -** Safi Ur Rehman Qamar, Jelana Košarić, Marko Živanović and Nenad Filipović

Thursday 28th November 2024

09:00 - 09:30	Keynote speaker: Topic: **What HPV + status brings to the treatment of HNC?** **Prof. Branislav Jeremić, University Hospital in Kragujevac** Chair: Marija Živković Radojević

Session T.1A: 09:30-11:30

Cancer

Chair: Branislav Jeremić

T.1A.1 **Molecular profile in breast cancer treatment -** Neda Milosavljević, Marija Živković Radojević, Branislav Jeremić, Ivane Kiladze, Pavol Dubinsky and Marko Spasić

T.1A.2 **Novel treatment of high-risk prostate cancer: a clinical trial development -** Pavol Dubinsky

T.1A.3 **Importance of HPV typing in predicting response to definitive chemoradiation in patients with locally advanced cervical cancer -** Marija Živković Radojević, Neda Milosavljević, Branislav Jeremić, Ivane Kiladze and Pavol Dubinsky

T.1A.4 **Selecting frontline immunotherapy in advance NSCLC: Picking the wining card -** Ivane Kiladze

T.1A.5 **HER2 and FISH status Prediction in Breast Biopsy H\&E stained Images using Deep Learning -** Ardhendu Sekhar, Vrinda Goel, Garima Jain, Abhijeet Patil, Ravi Kant Gupta, Tripti Bameta, Swapnil Rane and Amit Sethi

T.1A.6 **Using Ultra-Sound Images and a Multi-Task, Explainable Approach for Thyroid Cancer Detection -** Ahana Roy Choudhury, Radu Paul Mihail and Sorin Dan Chiriac

T.1A.7 **A computer model for simulation of the influence of the cell-platelet interaction on the metastasis of the circulating tumor cells (CTC) -** Miljan Milošević, Vladimir Simić, Aleksandar Nikolić and Miloš Kojić

Session T.1B: 09:30-11:30

Decode Workshop I

Chair: Dimitrios I. Fotiadis

T.1B.1 **Digital twins of percutaneous vascular and cardiac procedures -** Prof. Giancarlo Pennati (POLIMI)

T.1B.2 **Optimizing and Designing Drug Delivery Systems for Drug-Coated Balloons in Addressing Atherosclerosis** – Mohammad Akrami

T.1B.3 **In-Silico Modelling of Drug Distribution in Arteries Using AI Surrogate Techniques –** Leo Benolić

T.1B.4 **Hybrid in silico and ex vivo models for quantitative evaluation of acute coating transfer in drug-coated balloon angioplasty -** Efstathios Stratakos

T.1B.5 **Multiscale model for thrombosis/atherosclerotic plaque formation and progression –** Lemana Spahić

11:30 - 12:00	Coffee Break

Session T.2A: 12:00-13:30

Brain I

Chair: Igor Saveljic

T.2A.1 **DAS-Alz: Alzheimer's Disease Classification Using Downscaled MRI Scans and a**

Reinforced Convolutional Neural Network - Diogen Babuc and Gabrijel Babuc

T.2A.2 **Comparative evolution between different source localizations of epileptic MEG oscillations using different connectivity metrics -** Ichrak Elbehy, Abir Hadriche and Nawel Jmail

T.2A.3 **The Effect of Multi-Channel tDCS on the Directed Connectivity Patterns of a Case with Focal Epilepsy using A Multi-Feature Machine Learning Evaluation -** Alexandra Tsipourakis, Marios Antonakakis, Fabian Kaiser, Stefan Rampp, Stjepana Kovac, Christoph Kellinghaus, Gabriel Möddel, Carsten H. Wolters and Michalis Zervakis

T.2A.4 **An Efficient CNN and RNN Hybrid Model for the Detection of Epileptic Seizures in EEG Signals -** Zayneb Sadek, Abir Hadriche and Nawel Jmail

Session T.2B: 12:00-13:30

Decode Workshop II

Chair: Dimitrios I. Fotiadis

T.2B.1 **Application of nano material in biomedical science -** Safi Ur Rehman Qamar

T.2B.2 **The CT based measurements of vessels geometry in PAD -** Hassan Saeed

T.2B.3 **A computational study to assess the impact of vessel preparation on drug-coated balloon treatment -** Elisabetta Stretti

T.2B.4 **3D Segmentation of Peripheral Arteries through Computed Tomography Images -** Manahil Zulfiqar

T.2B.5 **Drug-loss at Arterial Bend Can Dominate Off-Target Drug Delivery by Paclitaxel -Coated Balloons -** Linnea Tscheuschner

T.2B.6 **Design of a milli-fluidic chamber to evaluate the impact of blood flow on drug-coated balloon during tracking -** Dimitrios Zantzas

13:30 - 14:15	Buffet Lunch

Session T.3A: 14:15-15:30

Brain II

Chair: Wei Zhang

T.3A.1 **Early Screening for Multiple Sclerosis Using Gut Microbiome and Machine Learning -** Bhavicka Mohta and Mai Oudah

T.3A.2 **Beyond the Gut Feeling: Machine-Learning Methods for Autism Screening -** Aigerim Zhusubalieva and Mai Oudah

T.3A.3 **An Enhanced Genetic Algorithm with Clustering for Optimizing Mobile Stroke Unit Deployment -** Muhammad Adil Abid, Johan Holmgren, Fabian Lorig and Jesper Petersson

Session T.3B: 14:15-15:30

Decode Workshop III

Chair: Dimitrios I. Fotiadis

T.3B.1 **Late recruitment in the project-pending -** Alexis Theodorou

T.3B.2 **Cloud-Based Solutions for Peripheral Artery Disease: Data Analysis, and Visualization -** Mohammed AboArab

T.3B.3 **Tunica Intima Segmentation From Porcine IVOCT Images –** Miloš Anić

T.3B.4 **Arterial senescence and novel biomarkers regarding PAD -** Argyro Vagena

T.3B.5 **Micro/Nano characterization of the Drug Coated Balloons -** Deepthishre Gunashekar

15:30 - 16:00	Keynote speaker: Topic: **3D Printing of Bioelastomers and Granular Materials for Engineering of Organotypic Structures** **Prof. Milica Radišić, University of Toronto** Chair: Nenad Filipović

16:00 - 16:30	Coffee Break

16:30 - 17:00	Keynote speaker: Topic: **Leveraging Trust in Healthcare Through a Robust AI Trustworthiness Assessment Framework** **Prof. Dimitrios I. Fotiadis, University of Ioannina / IMBB-FORTH** Chair: Smiljana Tomašević

Session T.4A: 17:00-18:00

Image processing I

Chair: Milica Nikolić

T.4A.1 **Predicting Microsatellite Instability from Histology Images with Dilated Neighborhood Attention Transformer in Colorectal Cancer -** Yun-Chi Chen, Tung Chao, Wimaya Nitya Phandita, Tzu-Yu Sun, Huai-Zhi Wang, Yi-Hsien Hsieh, Le-Yin Hsu and Che Lin

T.4A.2 **GPU-Driven Optimization of Web-Based Volume Rendering in Peripheral Artery Disease CT Imaging -** Mohammed A. Aboarab, Vassiliki T. Potsika, Fragiska Sigala, Alexis Theodorou, Sylvia Vagena and Dimitrios I. Fotiadis

T.4A.3 **CCVA-FL: A Solution for Cross-Client Variations in Federated Learning -** Sunny Gupta, Pankhi Kahyap and Kshitij Jadhav

19:30 - 23:00	Gala Dinner

Friday 29th November 2024

09:30 - 10:00	Keynote speaker: Topic: **How microbeam technology could change the radio-oncology treatment** **Prof. Valentin Djonov, University of Bern** Chair: Igor Saveljic

Session F.1A: 10:00-11:30

Image processing II

Chair: Ognjen Pavić

F.1A.1 **Clustered Patch Embeddings for Permutation-Invariant Classification of Whole Slide Images -** Ravi Kant Gupta, Shounak Das and Amit Sethi

F.1A.2 **Comparing Top-K and Manual Feature Selection for PCG Signal Classification using XGBoost -** Poorv Patil

F.1A.3 **Efficient Whole Slide Image Classification through Fisher Vector Representation** - Ravi Kant Gupta, Dharani Dadi, Shambhavi Shanker and Amit Sethi

F.1A.4 **Classification and Morphological Analysis of DLBCL Subtypes in H&E-Stained Slides -** Ravi Kant Gupta, Mohit Jindal, Garima Jain, Epari Sridhar, Subhash Yadav, Hasmukh Jain, Tanuja Shet, Uma Sakhdeo, Manju Sengar, Lingaraj Nayak, Bhausaheb Bagal, Umesh Apkare, and Amit Sethi

F.1A.5 **Comparative Study of Large Language Models for Lung-RADS Classification in Portuguese CT Reports -** Tarcísio Ferreira, Marcelo Oliveira and Thales Vieira

F.1A.6 **Unsupervised Deep Learning Method for Cell Segmentation of Confocal Microscopy Images -** Ognjen Pavić, Jorge Barrasa-Fano, Lazar Dašić, Tijana Geroski, Apeksha Shapeti, Hans Van Oosterwyck, Vesna Ranković and Nenad Filipović

Session F.1B: 10:00-11:30

Bioengineering II

Chair: Lazar Dašić

F.1B.1 **Modeling Approaches for Assessing the Impact of Air Pollution on Human Health in Serbia -** Aleksandra Vulović and Petar Stanojević

F.1B.2 **Semantic image segmentation of cell volumes using 3D U-net convolutional neural network-** Lazar Dašić, Jorge Barrasa-Fano, Ognjen Pavić, Tijana Geroski, Apeksha Shapeti, Hans Van Oosterwyck, Vesna Ranković and Nenad Filipović

F.1B.3 **Application of Machine Learning in the Analysis of Gene Expression in Colorectal Cancer Cells Treated with Chemotherapeutics** - Jelena Pavić, Marko Živanović, Ognjen Pavić, Katarina Virijević, Tamara Mladenović, Irena Tanasković and Nenad Filipović

F.1B.4 **AI-driven Decision Support System for Heart Failure Diagnosis: INTELHEART Approach Towards Personalized Treatment Strategies -** Smiljana Tomašević, Anđela Blagojević, Tijana Geroski, Gordana Jovičić, Bogdan Milićević, Momčilo Prodanović, Ilija Kamenko, Bojana Bajić, Stefan Simović, Goran Davidović, Dragana Ignjatović Ristić, Andrej Preveden, Lazar Velicki, Edin Doličanin, Arsen Ristić, Nenad Filipović and Svetlana Apostolović

F.1B.5 **Combining Lattice Boltzmann and Agent-based Modeling to Model the Behavior of Cancer Cells In-vitro -** Tijana Djukić, Nevena Milivojević Dimitrijević, Marko Živanović and Nenad Filipović

F.1B.6 **Virtual Coach Platform for Rehabilitation: Platform Overview and its Assessment -** Aleksandra Vulović, Đorđe Ilić, Filip Filipović and Nenad Filipović

11:30 - 12:00	Coffee Break

Session F.2A: 12:00-13:00

Bioinformatics II

Chair: Nevena Milivojevic

F.2A.1 **Use of bioinformatics to extract pharmacogenomic information -** Nevena Milivojević Dimitrijević, Ana Mirić, Radun Vulović, Marko Živanović and Nenad Filipović

F.2A.2 **A Computational Method for Saccade Velocity Profiles Generation** – Smilja Stokanović, Vukašin Spasojević, Ilija Tanasković, Jaka Sodnik and Nadica Miljković

F.2A.3 **Hybrid Combinatorial Problems Used For Multimodal Optimisation -** Daniela Cristea

13:00 - 14:00	Buffet Lunch

14:00 - 14:30	Keynote speaker: Topic: **Application of Hydrogel in Cancer Therapy** **Prof. Wei Zhang, Dalian University of Technology, Dalian, China** Chair: Milica Nikolić

14:30 - 15:00	Closing Ceremony

Keynote Speakers

APPLICATION OF HYDROGEL IN CANCER THERAPY

Wei Zhang

State Key Laboratory of Structural Analysis, Optimization and CAE Software for Industrial Equipment,
School of Mechanics and Aerospace Engineering, Dalian University of Technology, Dalian, China

Abstract

Hydrogels are hydrophilic, three-dimensional and cross-linked polymeric networks capable of imbibing water or biological fluids. Owing to high water content, soft consistency and porosity, hydrogels resemble natural living tissues closely and have been employed in potential applications such as cancer therapy, tissue engineering, bio-sensing, etc. Herein, we will introduce our work on the application of hydrogel in magnetic induction hyperthermia, photothermal therapy, drug delivery, traditional Chinese massage, wound healing and etc..

TECHNOLOGICAL INNOVATIONS IN DIAGNOSIS OF HEART FAILURE

Đorđe Jakovljević

Research Centre for Health and Life Sciences of Coventry University, United Kingdom

Abstract

Heart failure (HF) is a global pandemic currently affecting up to 15 million people in Europe. It is a complex clinical syndrome associated with impaired heart function, poor quality of life for patients and high healthcare costs. Accurate early diagnosis of HF allow implementation of evidence-based prevention and treatment strategies which reduce HF morbidity and mortality and its burden on healthcare. Early diagnosis is challenging, often inaccurate as initial signs and symptoms are non-specific. We developed a novel, cardiac output response to stress (CORS) test to facilitate early diagnosis of heart failure which also can be used as a monitoring tool to evaluate disease progression and response to treatment. The CORS, as a novel test for objective evaluation of cardiac function, demonstrates acceptable reproducibility and can potentially be implemented in primary care. In primary care CORS test can be ised to reduce unnecessary referrals to secondary care and has the potential to serve this purpose. Evidence further demonstrated that the CORS is feasible and patients with HF responded differently to non-HF, and HF reduced ejection fraction from HF with preserved ejection fraction. These findings provide further evidence for the potential use of the CORS to improve HF diagnostic and referral accuracy in primary care. As part of an international interdisciplinary STRATIFYHF project, which aims to develop first ever artificial intelligence-based decision support system for risk stratification and early diagnosis of heart failure, the CORS test, along with voice recognition technologies, presents novel technology which will be integrated in the decision support system. The STRATIFYHF will change the ways in which HF is managed today, thereby improving the quality and length of patients' lives. Our solution will lead towards an efficient and sustainable healthcare systems by reducing the number of HF-related hospital admissions and deaths, and unnecessary referrals from primary to secondary care.

3D PRINTING OF BIOELASTOMERS AND GRANULAR MATERIALS FOR ENGINEERING OF ORGANOTYPIC STRUCTURES

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Abstract

The functional integrity of engineered tissues and organ-on-a-chip systems, including attributes like permeability and contractility, hinges on the characteristics of their scaffolds. Scaffolds designed for soft tissue engineering and organ-on-a-chip applications necessitate meticulous control over several parameters: a) microscale structural precision, b) elasticity ranging from 1kPa to 500 kPa, c) mechanical anisotropy, and d) biocompatibility. While complex structures can be 3D printed using hydrogels, their relatively low mechanical strength (1-10kPa) often leads to structural collapse under cellular traction forces during tissue formation. Conventional polymers like PLGA offer higher rigidity (1-200MPa) but are excessively stiff for soft tissues and inherently impede the permeability of proteins and cells.
These challenges are particularly pertinent in vascularization strategies that demand the embedding of branching conduits within a cell-supportive lattice, simultaneously managing mechanical properties, and in the engineering of complete functional organs such as the heart's left ventricle. In my presentation, I will address the use of extrusion 3D printing with thermoplastic elastomer composites, a development that has enhanced the fabrication efficiency of the Biowire heart-on-a-chip device by more than 60,000%.
Furthermore, I will explore a high-throughput 3D printing method employing coaxial extrusion. This technique facilitates the creation of perfusable elastomeric microtubes with unprecedentedly small inner diameters (350 to 550 μm) and thin walls (40-60 μm), enabling the production of various biomimetic shapes, including those resembling the cochlea and kidney glomerulus, and the efficient generation of perfusable structures suitable for endothelial cell seeding.
Additionally, leveraging capillary microfluidics followed by UV crosslinking, we have produced monodisperse elastomeric polymer particles. These particles have significantly bolstered the structural integrity of hydrogel-based scaffolds in 3D printing, leading to the development of a novel class of self-healing and 3D printable granular materials with enhanced permeability. These advancements represent a significant leap in the fields of soft tissue engineering and organ-on-a-chip technology.

LEVERAGING TRUST IN HEALTHCARE THROUGH A ROBUST AI TRUSTWORTHINESS ASSESSMENT FRAMEWORK

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Abstract

Ensuring patient data privacy and security in the healthcare sector is particularly challenging due to the complexities which are introduced in the measurement of AI trustworthiness. This creates significant barriers to building and maintaining trust in AI among patients. While most active academic research on AI trustworthiness has focused on the algorithmic properties of AI-based models, advancements in algorithmic research alone are insufficient for building trustworthy AI systems. In this work, we present the FAITH Project (Fostering Artificial Intelligence Trust for Humans towards the optimization of trustworthiness through large-scale pilots in critical domains) and particularly FAITH's AI Trustworthiness Assessment Framework which envisages to ensure that AI systems in healthcare adhere to stringent data security protocols and ethical standards, promoting fairness and bias mitigation. The framework aims to promote interoperability and foster the integration of AI into existing healthcare applications through the testing, measurement and optimization of risks associated with AI trustworthiness. To do so, the framework builds upon the NIST (National Institute of Standards and Technology) AI risk management framework (RMF) and upon the ENISA (European Union Agency for Cybersecurity) guidelines to achieve trustworthiness by design, considering the healthcare stakeholders intelligence and users' engagement to facilitate broader adoption. Through this strategy, the proposed framework aims to leverage trust in AI-driven solutions, fostering wider acceptance and utilization in healthcare. A preliminary case study is finally presented with a specific focus on prostate segmentation as a practical implementation of AI in medical imaging.

PHYSICS-BASED COMPUTATIONAL MODELS WITHIN THE ARTIFICIAL INTELLIGENCE SCHEME: IMPORTANT FEATURES

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Abstract

We are witnessing that the era of Artificial Intelligence (AI) has arrived. AI is used in everyday life in all conversations, starting from science to decision-making, to social life. It is of particular interest in medicine, where the hope is that AI as a tool will help in the understanding of diseases as well as in the improvement of medical treatment outcomes. AI in medical research and practice may rely on various types of models, such as statistical, empirical, physics-based, or others. In this presentation, we consider physics-based computational models in biomedical engineering and emphasize the main features of these models to be used as suitable tools within AI. Generally, these models should be robust, accurate, and efficient. Our group in Kragujevac, Serbia, has experience of more than five decades of development of our finite element program PAK with applications in engineering and biomedical engineering. We here outline our methodology in biomedical engineering developed to achieve the mentioned model characteristics. The selected examples include the modeling of motion of deformable bodies (as cells) within a fluid which is based on the strong coupling and remeshing procedure; mass transport and electrophysiology within composite media as tissue, according to our general smeared multiscale-multiphysics concept (Kojic Transport Model) with coupling different physical fields; and solid-fluid interaction. Applications of these models are illustrated in drug delivery with tumor growth; the role of platelets in metastasis; heart mechanics and electrophysiology; lung mechanics, airflow, blood flow, and gas exchange. In conclusion regarding the presented methodologies and applications within AI, we emphasize that model efficiency can be considered of secondary importance since today and future technologies provide larger computational speed, parallel computing, generation of huge number and surrogate model solutions, machine learning, and advanced graphical support.

HOW MICROBEAM TECHNOLOGY COULD CHANGE THE RADIOONCOLOGY TREATMENT

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Abstract

Introduction**:** Microbeam-Radiation-Therapy (MRT) is a type of spatially fractionated radiation therapy which modulates the radiation dose on a micrometre scale. This unique dose distribution makes MRT highly efficient even for the treatment of radioresistant tumours.

Results**:** In murine B16-F10 melanoma model, temporally fractionated MRT completely ablated 50% of tumors and prevented organ metastases and local recurrences for 18-months after treatment. In mouse glioblastoma model, MRT in combination with cisplatin reduced tumor volume 6-fold compared with cisplatin alone and 60-fold compared with untreated mice.

The radiation biology underlying the “MRT effect” include novel radiobiological mechanisms: (1) Induction of selective vascular disruption of immature tumor vasculature or transient vascular permeability in a dose-dependent manner (2) Direct cellular damage in the microbeam path that elicits tissue-specific responses. (3) Induction of a unique, tumor-targeted immune response leading to local and systemic anti-tumor immune responses including infiltration of cytotoxic lymphocytes.

Discussion: spatially fractionated MRT demonstrated one best treatment outcome ever achieved in preclinical models. MRT provides a novel mechanism for drug delivery by increasing vascular transpermeability while preserving vessel integrity and in addition is busting the anti-tumor immune response. These unique features support MRT as a novel therapeutic approach for the treatment of inoperable, radioresistant lesions.

Keywords: cancer treatment, spatially fractionated radiotherapy, cell death, micro beams, vascular permeability

ASSESSING THE IMPACT OF PUBLIC HEALTH INTERVENTIONS AND SIMULATING COVID-19 SPREAD IN NORTHERN IRELAND USING THE CP-ABM APPROACH

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Abstract

This talk presents the CP-ABM approach, a novel methodology developed in response to the challenges of modelling COVID-19 infection spread for the Northern Ireland COVID-19 Modelling Group. This methodology uniquely integrates change point detection (CP) and agent-based modelling (ABM) techniques to identify key events that drive shifts in population contact patterns and simulate individual behaviours and interactions within a population, respectively. Calibrated to replicate the entire 1.8 million population of Northern Ireland, the CP-ABM methodology was used to successfully simulate two waves of the COVID-19 pandemic and capture the infection dynamics of the virus. It also enabled successful quantification of the impact of non-pharmaceutical interventions (NPIs) such as mask mandates and lockdowns on reducing virus transmission, as well as accurate estimation of the role that asymptomatic individuals have in its spread. The CP-ABM methodology is programming language agnostic, thus allowing its wider application.

WHAT HPV+ STATUS BRINGS TO THE TREATMENT OF HNC?

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Abstract

The last three decades provided new insights into the discovery of the entity related to several strains of human papillomavirus (HPV). The viral cause of HPV, primarily found in the oropharynx, was officially recognized by the World Health Organization in 2007. While epidemiologic studies around the world showed an increased incidence of HPV-related heads and neck cancers (HNC), they also established a photo robot of a typical person suffering from HPV: younger white man, suffering from a nonkeratinized type of squamous cell carcinoma, rarely being seen as heavy smoker and/or drinker. The patient with specific sexual behavior pattern usually carried low T and high N burden, HPV16 being detected in the vast majority of HPV+ tumors, mostly in the oropharynx. It was also recognized that HPV-related cancers seem to have a better prognosis than their HPV-unrelated counterparts. This observation served as an important starting point for clinical studies aiming first to identify different risk groups and then to design various de-intensification treatment strategies which aimed to maintain high success rate with e.g. lower radiotherapy and/or chemotherapy doses while decreasing side effects such deintensified treatment strategies should bring.

Book of Abstracts

DEPRESSION DIAGNOSIS: BIOINFORMATICS UNCOVERS CELLULAR ABNORMALITIES IN FEMALE-SPECIFIC GENES WITH AI-DRIVEN BLOOD BIOMARKER-BASED PREDICTION

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Abstract

With an estimated 264 million people affected by MDD globally, there is an urgent need for novel approaches to diagnosis and treatment. This study explored the complex gene expression profiles linked to Major depressive disorder (MDD) using state-of-the-art Next-Generation Sequencing (NGS), namely RNA-Seq. There is a need for accurate non-invasive diagnostics, particularly through gender-specific biomarker research in female RNA-Seq data. To address this disparity, RNA-Seq data was analyzed using Machine Learning (ML) techniques to categorize female-specific MDD identifying 10 critical biomarkers and utilizing Artificial Intelligence (AI) and bioinformatics to extract transcriptome data from publicly available datasets, while employing Generative adversarial networks (GANs) for data augmentation due to the limited availability of large RNA-Seq datasets. Gene set enrichment analysis (GSEA) and other bioinformatics analyses further demonstrated that genes differentially expressed in MDD patients were enriched in pathways related to the cell cycle, neutrophil degranulation, resolution of sister chromatid cohesion, and the formation of mitotic spindles by EML4 and NUDC. Ten important biomarkers associated with MDD were identified by an integrative bioinformatics investigation: IGHV3-64D, IGHV5-10-1, IFI27, LILRB5, PBK, SIGLEC1, IFI44L, CDCA5, and SLC4A1. Machine learning models based on these genes achieved 95% accuracy, highlighting RNA-Seq and ML's potential to enhance MDD diagnosis and reveal its molecular mechanisms.

Keywords: MDD, RNA-seq data analysis, NGS, genetic biomarkers, machine learning, generative adversarial networks (GANs), classification, diagnostic model.

DAS-ALZ: ALZHEIMER'S DISEASE CLASSIFICATION USING DOWNSCALED MRI SCANS AND A REINFORCED CONVOLUTIONAL NEURAL NETWORK

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Abstract

Low-resolution (LR) and high-resolution (HR) images are critical in medical imaging, with HR images often preferred for their detailed information. However, HR MRI scans require significant processing power, posing challenges in computational efficiency. Super-resolution techniques have been developed to enhance LR images, but they often depend on high-quality data and advanced processing capabilities. One type of neurodegenerative illness is Alzheimer's disease (AD), where a precise and timely diagnosis is essential for successful intervention. Despite the importance of HR MRI scans in making the prediagnosis, their processing demands are high. To address these challenges, this paper proposes the DAS-Alz model, a reinforced convolutional neural network designed to classify AD cases using downscaled MRI scans. Even at a lower resolution, DAS-Alz demonstrates the ability of deep learning to extract important information from MRI data, highlighting the potential to overcome computational constraints. The model incorporates a multi-head attention mechanism layer to enable parallel processing, thereby improving efficiency. The DAS-Alz model achieved outstanding accuracy in both training (99.34%) and validation (99.84%), effectively classifying AD from downscaled images. These results suggest that DAS-Alz may play a significant role in AD prediagnosis, potentially leading to improved patient outcomes.

Keywords: downscaled MRI scans, reinforced CNN, machine learning, Alzheimer's disease, computational constraints.

TRANSFORMER-BASED REAL TIME MUSCULOSKELETAL ANATOMICAL STRUCTURE DETECTION IN CLINICAL USE

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Abstract

Medical ultrasound imaging is known as a non-invasive and radiation-free real-time imaging method, making it an indispensable technique for clinical use, especially in musculoskeletal medicine. However, due to the complexity of the body's internal anatomical structures, it is challenging for physicians to rapidly and accurately interpret images to identify each structure for further diagnosis and treatment planning. To address these challenges, we developed a real-time labeling system of anatomical structures for musculoskeletal ultrasound using a transformer-based model, RT-DETR. We selected the 15 most crucial anatomical structures in the human forearm and shoulder as our identification targets. We achieved an overall precision of 0.834, recall of 0.822, mAP50 of 0.855, mAP50:95 of 0.526, and an F1-score of 0.82. Moreover, the real-time annotation results also show high precision in annotating each structure's classes and boundaries, indicating that our model is well-suited for the task and has the potential to be applied in clinical settings.

Keywords: ultrasound, musculoskeletal, transformer, deep learning.

COMPARATIVE EVOLUTION BETWEEN DIFFERENT SOURCE LOCALIZATIONS OF EPILEPTIC MEG OSCILLATIONS USING DIFFERENT CONNECTIVITY METRICS

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Abstract

Electromagnetic sources of biomarkers in magnetoencephalography (MEG) enable recognition of excessive discharges generators in epilepsy. Neurologists rely on MEG biomarker source localization for diagnostic purposes (presurgical epilepsy inquiry). Several ways are proposed to overcome the forward and inverse source localization problems. The goal of this study is to evaluate four distributed inverse problems: minimum norm estimation MNE, standardized low-resolution brain electromagnetic tomography sLORETA, wavelet maximum entropy on the mean wMEM, and dynamic statistical parametric maps (dSPM) used to define network connectivity of oscillatory epileptic events. We employed Jmail et al.'s 2016 pre-processing chain to assess epileptic oscillations among MEG sources in pharmaco-resistant patients. Then, we explored granger causality and spatial granger causality metrics among extended active sources for each inverse approach. Granger causality determines causal influence of one time series on another, providing insights into a directional flow of information between brain regions. Spatial Granger causality extends this concept to incorporate spatial information, evaluating how brain activity in one region can predict future activity in another region, taking into account the brain’s spatial structure. As a result, for granger causality, the wMEM method identifies strong connections between active sources, suggesting robust interaction and influence among these regions. In contrast, dSPM method reveals weaker connections, indicating a less pronounced directional influence between active sources. For spatial granger causality, the wMEM again demonstrates strong connections between active sources, highlighting its sensitivity and effectiveness in detecting robust functional interactions. On the other hand, the MNE and sLORETA methods exhibit weaker connections, suggesting that these techniques may be less effective in capturing directional influences between active sources. These findings underscore the importance of using multiple localization techniques to accurately determine interictal MEG oscillation locations and epileptic zones.

Keywords: oscillatory MEG events, networks connectivity, spatial Granger causality, Granger causality.

EI-VIT-NET: A VISION TRANSFORMER APPROACH FOR DIABETIC RETINOPATHY'S DECISION SUPPORT PIPELINE

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Abstract

One of the main causes of blindness is diabetic retinopathy (DR), which requires early identification for efficient treatment. This study presents a decision support pipeline that incorporates a gray-scaling process for enhancement of the retinal image and a Vision Transformer for classification. Using a dataset of retinal images classified as both DR and non-DR, our proposed technique achieves notable gains in performance. By using grayscaling image enhancement, the average loss was decreased from 0.31 to 0.20 and the model's accuracy rose from 85% to 89%. These outcomes demonstrate how well grayscaling with Gaussian smoothing and sharpening filters works to improve feature extraction and classification precision. Considering the obstacles such as computational intricacy and unpredictability in datasets, our methodology offers a resilient resolution for prompt DR identification. This might enhance patient results by means of prompt action.

Keywords: diabetic retinopathy, image quality enhancement, vision transformer.

IMPORTANCE OF HPV TYPING IN PREDICTING RESPONSE TO DEFINITIVE CHEMORADIATION IN PATIENTS WITH LOCALLY ADVANCED CERVICAL CANCER

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Abstract

HPV infection stimulates a local immune response, because HPV positivity in cervical cancer places these tumors in a prognostically better group in terms of response to radiotherapy (RT). However, the response to RT treatment in locally advanced cervical cancer depending on the presence of a certain subtype of the HPV virus has been very little investigated in previous research. Taking into account the high incidence rate of cervical cancer in developing countries, where the disease is most often diagnosed at a locally advanced stage, the aim of this review of the available literature was to analyse predictive potential of HPV typing in terms of the response to the RT with/without chemopotentiation as a standard treatment approach. A review of studies dealing with the analysis of the predictive significance of HPV typing in locally advanced cervical cancer patients treated with definitive RT with or without chemopotentiation, from 2000 to 2024, was conducted. Six clinical studies were identified that met the search criteria. The most frequently analyzed subtypes were HPV 16, 18, 33 and 52. In five studies, the HPV 16 subtype was identified in more radioresistant cervical cancers. There is an exceptional clinical importance of HPV typing in order to create an individual treatment strategy, especially in the era of immunotherapy given concurrently with definitive RT. It is also necessary to conduct clinical studies with a large number of patients and consider what the treatment outcomes are depending on the applied RT technique, dose, and fractionation regime.

Keywords: human papilloma virus subtypes, radiotherapy, cervical cancer, radiosensitivity, radioresistance.

PREDICTING MICROSATELLITE INSTABILITY FROM HISTOLOGY IMAGES WITH DILATED NEIGHBORHOOD ATTENTION TRANSFORMER IN COLORECTAL CANCER

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Abstract

Microsatellite instability (MSI) is a pivotal genetic marker influencing the efficacy of immunotherapy in colorectal cancer. Traditional MSI examination often requires additional genetic or immunohistochemical tests, whereas histology images, widely available in colorectal cancer diagnosis, offer a valuable alternative for MSI prediction. Although Transformer-based models have demonstrated promising outcomes in predicting MSI from histology images, they are hampered by traditional local attention mechanisms that struggle to capture long-range interdependencies and establish a comprehensive global receptive field. In this study, we introduce DiNAT-MSI, a novel framework for histology-based MSI prediction that incorporates the Dilated Neighborhood Attention Transformer (DiNAT). This model enhances global context recognition and substantially expands receptive fields, all without additional computational burden. Our results demonstrate that DiNAT-MSI achieves a superior patient-wise AUROC compared to ResNet18 and Swin Transformer, along with commendable explainability. Our work not only illustrates a more accessible diagnostic tool for leveraging histological data but also underscores the potential of Transformer-based models with sophisticated attention designs in advancing precision medicine for colorectal cancer patients.

Keywords: deep learning, dilated neighborhood attention transformer, colorectal cancer, histology images, microsatellite instability.

A SHORT OVERVIEW OF LEFT VENTRICULAR ACTION POTENTIAL SIMULATIONS: INTEGRATING NUMERICAL METHODS WITH MACHINE LEARNING

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Abstract

The action potential is a pivotal electrical phenomenon that governs the contraction of cardiac muscle cells, known as cardiomyocytes. This rapid shift in membrane potential is orchestrated by the precise movement of ions across the cell membrane through specific ion channels. In the heart, action potentials are indispensable for initiating and coordinating the contractions of cardiac chambers, ensuring effective blood circulation throughout the body. The left ventricle, responsible for propelling oxygenated blood into the aorta and systemic circulation, is particularly critical. Deviations in the left ventricular action potential can result in severe cardiac conditions, including arrhythmias, heart failure, and sudden cardiac death. Consequently, an accurate understanding and modeling of the left ventricular action potential are essential for elucidating the mechanisms underlying these diseases and developing effective treatments. This paper provides a comprehensive overview of methodologies used to simulate the action potential within the left ventricle. It examines the historical evolution of electrophysiological models, foundational theories of cardiac action potentials, and their specific application to the left ventricle. The review encompasses the clinical relevance of these models and an analysis of simulation outcomes. This paper also explores the application of machine learning (ML) to enhance the accuracy and efficiency of action potential calculations within the left ventricle, highlighting various ML techniques and their potential impact on cardiology.

Keywords: left ventricle, action potential, cardiac electrophysiology, numerical analysis, machine learning.

NAVIGATING THE EXPLAINABLE MOLECULAR GRAPH: BEST PRACTICES FOR REPRESENTATION LEARNING IN BIOINFORMATICS

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Abstract

Machine learning (ML) has shown significant success in real-world scenarios where data is represented in the Euclidean domain. However, in the biomedical field, complex relational information between biological entities is often encapsulated in non-Euclidean structures, such as biomedical graphs, which are difficult to learn by traditional ML methods. Graph representation learning aims to embed graphs into a lowdimensional space while preserving topology and properties. This approach, generally organized into graph embedding techniques and graph neural networks (GNNs), bridges the gap between complex biomedical graphs and modern ML methods. Recently, it has garnered widespread interest as it offers a powerful framework for leveraging relational information inherent in biomedical data. In this context, it becomes challenging to navigate the complexities of graph-based biological problems, since the intricate relational data and the challenge of preserving graph structure during embedding pose substantial obstacles. The goal of this paper is to clarify which of these two main approaches—graph embedding techniques or GNNs—is more suitable for one of the most successful applications of graph representation learning: molecular property prediction. Molecules contain many types of substructures that may affect their properties, and recognizing substructures and relations embedded in a molecular structure representation is crucial for structure-activity relationship and structure-property relationship studies. By examining the effectiveness of different graph representation learning techniques in this context, this paper aims to provide valuable insights and guidelines for researchers and practitioners. To this aim, we carried out experiments on 4 well-known benchmarking datasets for molecular property prediction tasks, showing that GNNs are more effective. We also developed a platform for experiments in molecular property prediction with GNNs, which integrates an attention mechanism to highlight the atoms within a molecule that most significantly impact its biological function. The result of this preliminary study is not only the demonstration of the advantages of GNNs in terms of effectiveness for these tasks but also the validation of their suitability for an “explainable” AI approach. This advancement makes GNNs a powerful tool in the realm of molecular machine learning, facilitating both accurate predictions and enhanced understanding of the underlying molecular mechanisms.

Keywords: graph representation learning, molecular property prediction, explainable AI.

HYPERECG: ECG SIGNAL INFERENCE FROM RADAR WITH HYPERDIMENSIONAL COMPUTING

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Abstract

Contactless ECG monitoring with radar technology is used in both long-term and remote healthcare monitoring. While first attempts were able to only estimate heart rate, more recently deep learning (DL) has been used to infer the continuous ECG signal, which is essential for many health monitoring applications. However, the compute-intensive nature of DL models makes it hard to deploy and personalize them in low-power systems that are critical for remote healthcare monitoring. To address this challenge, we introduce HyperECG, a pioneering approach based on Hyperdimensional Computing (HDC), an efficient alternative machine learning method, to infer ECG signals from radar inputs. We combine a novel learnable HDC projection encoding with state-of-the-art HDC regressors to achieve high-quality ECG estimation. Experimental results reveal that HyperECG achieves output quality comparable to the state-of-the-art DL while reducing inference and training runtime up to 23× and 36×, respectively. HyperECG supports on-device model personalization, crucial in medical settings, with accuracy improvements of up to 68% on patient-specific evaluations, compared to before fine-tuning HyperECG.

Keywords: hyperdimensional computing, ECG monitoring, wireless sensing, model personalization.

GPU-DRIVEN OPTIMIZATION OF WEB-BASED VOLUME RENDERING IN PERIPHERAL ARTERY DISEASE CT IMAGING

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Abstract

This paper presents significant advancements in GPU-driven optimization for web-based volume rendering, which is specifically applied to peripheral artery disease (PAD) CT imaging. The proposed method enhances rendering efficiency and image quality, addressing the critical need for real-time, high-quality visualization of complex anatomical structures of PAD. Key improvements in the preprocessing pipeline, such as efficient chunking of large datasets, contribute to better GPU performance. The results demonstrate a substantial improvement over existing tools, with 95.37% reduction in render time, and 96.87% decrease in GPU memory usage compared with BlueLight, and significant memory optimization over Glance. These enhancements facilitate the detailed and interactive 3D visualization of vascular structures, which is crucial for accurate diagnosis and surgical planning. This paper highlights the potential of the proposed method to transform medical imaging practices, improving clinical outcomes for patients with PAD.

Keywords: GPU-driven optimization, web-based volume rendering, peripheral artery disease, CT imaging visualization.

DESIGN OF THE AMORPHOUS SOLID DISPERSION (ASD) DRUGS BY HOT MELT EXTRUSION (HME), FOR THE INHIBITION OF BONE GRAFT REJECTION

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Abstract

This short review paper presents the most important aspects in developing Amorphous Solid Dispersion (ASD) drugs for the inhibition of bone graft rejection, by Hot Melt Extrusion (HME) processing. Different types of bone tissue grafts are reviewed. Amorphous solid dispersions (ASDs) drug products are elaborated, including the FDA approved ones. Hot Melt Extrusion (HME) technology is discussed for the fabrication of different medication forms. ASD drug products for the inhibition of bone graft rejection are analysed, also related to the immune mechanisms that can lead to immunogenic impairments. The design of the ASD drugs can benefit from considering natural polymer carriers that will inherently prevent harmful immune reactions of the host tissues and enable drug incorporation into the grafts. The addition of new growth factors or bioactive molecules can provide bioactive mechanisms to the grafts and increasingly support cellular growth, proliferation and differentiation and more efficiently prevent atrophic nonunion and graft rejections. Further research on optimization of the ratio of APIs crystallinity to the amorphous polymer carriers, as well as potential of incorporating advanced ASDs formulations into the bone grafts, will be studied.

Keywords: amorphous solid dispersion (ASD), hot melt extrusion (HME), collagen, natural polymer carriers, orthobiologics.

THE EFFECT OF MULTI-CHANNEL TDCS ON THE DIRECTED CONNECTIVITY PATTERNS OF A CASE WITH FOCAL EPILEPSY USING A MULTI-FEATURE MACHINE LEARNING EVALUATION

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Abstract

The present study explores the effect of multichannel transcranial Direct Current Stimulation (mc-tDCS) on directed EEG connectivity patterns in a patient with refractory focal epilepsy. A double-blind, sham-controlled N-of-1 trial was conducted, where mc-tDCS was applied over a two-week period, with EEG recordings acquired before and after stimulation and sham procedures accordingly. After artifact reduction on the EEG recordings, Generalized Partial Directed Coherence (gPDC) was utilized, to investigate effective connectivity alterations in the patient's EEG recordings. Machine learning models were also employed to evaluate the connectivity findings and the interictal spike-related class (spike / non-spike) separability. The connectivity analysis demonstrated a significant reduction in gPDC connectivity around the key EEG channels associated with epileptic activity, specifically interictal epileptiform discharges (IEDs), following mc-tDCS, with no significant changes observed in the sham condition. Following feature extraction from the connectivity analysis, machine learning validation supported these findings, revealing a potential decrease in the severity of epileptic activity, as indicated by IEDs. The results suggest that mc-tDCS effectively moderates brain connectivity in refractory focal epilepsy, with implications for reducing the frequency of IEDs. This study highlights the potential of integrating advanced connectivity analysis with machine learning for evaluating mctDCS and similar neuromodulation therapies in epilepsy, particularly in modulating pathological brain network dynamics associated with epileptic discharges.

Keywords: refractory focal epilepsy, EEG, effective connectivity, tDCS, machine learning.

ANALYSIS OF DNA SEQUENCES FROM HUMAN SWEAT AND COMPARISON WITH BLOOD SAMPLE

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Abstract

Genome studies rely heavily on valuable sources of nucleic acids found in biological fluids. Sweat, an easily collectible and cost-effective biofluid, has emerged as a promising material for genomic research. However, the suitability of sweat DNA for genome sequencing compared to venous blood DNA requires further investigation. Sweat samples were collected from four individuals, and a statistical comparison was conducted between sweat DNA and healthy blood DNA reads. The study focused on four key aspects: genome coverage, fragment lengths, mapping quality, telomere sequences, and chaos game representation (CGR) analysis. The length, quality, and genome coverage of all DNA fragments were examined, and tandem repeats in the telomere sequences of the study samples were identified in this article. The statistical analysis revealed significant similarities in genomic study outcomes between sweat and blood samples. The results suggest that sweat has the potential to be an alternative substitute for genomic analysis, offering a cost-effective and easily accessible avenue for future investigations. Our study highlights the potential utility of sweat as a valuable source of nucleic acids for genomic research. While significant similarities were observed between sweat and blood samples regarding genomic outcomes, further studies are warranted to explore the full capabilities of sweat DNA in genome sequencing. Using sweat in genome research could lead to cost-effective and accessible approaches for future genomic investigations.

Keywords: sweat DNA, telomere, DNA fragments, DNA reads, CGR analysis.

CCVA-FL: A SOLUTION FOR CROSS-CLIENT VARIATIONS IN FEDERATED LEARNING

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Abstract

Federated Learning is a decentralized method in machine learning where numerous clients collaborate to train a model on a central server. It is a promising technique for learning from multi-source decentralised data, which can be of significant use in the medical domain, where privacy preservation is crucial. However, for medical image data, cross-client variation problems (since features extracted from different client data are not uniform) would hinder the development of an optimal server model in a federated setting. This problem is magnified by lesser annotated data availability in the medical domain which by itself contributes to high variability. This paper proposes a Cross-Client Variations Adaptive Federated Learning (CCVAFL) framework on medical images to address the variations between clients that are minimised by transforming medical domain images present at all clients into a common feature space. The method randomly selects a subset of images for each client which are first expert annotated. This is followed by the selection of a client (target client) that has the least data complexity which is then utilised to define the target image feature space. A set of synthetic medical images is then generated using annotated images of the target client via Scalable Diffusion Models with Transformers (DiT). These newly generated images that capture the diversity as well are a representative of the original set of annotated images, which are then shared with other clients. Using these shared synthetic images as a target space an image-to-image translation is applied at each client to translate their local images to the target image space. The translated images at each client are then used in a federated learning setting to develop a server model. We demonstrate that CCVA-FL performs better compared to Vanilla Federated Averaging thereby overcoming the data distribution differences across multiple clients without compromising privacy.

Keywords: cross-client variation, federated learning, diffusion models, image-to-image translation, medical image analysis.

HER2 AND FISH STATUS PREDICTION IN BREAST BIOPSY H&E-STAINED IMAGES USING DEEP LEARNING

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Abstract

The current standard for detecting human epidermal growth factor receptor 2 (HER2) status in breast cancer patients relies on HER2 expression identified through immunohistochemistry (IHC) or amplification identified through fluorescence in situ hybridization (FISH). However, hematoxylin and eosin (H&E) tumor stains are more widely available and accurately predicting HER2 status using H&E could reduce costs and expedite treatment selection. Deep Learning algorithms for H&E have shown effectiveness in predicting various cancer features and clinical outcomes, including moderate success in HER2 status prediction. In our work, we employed a customized weak supervision classification technique combined with MoCov2 contrastive learning for self-supervised feature extraction training to predict HER2 status. We trained our pipeline on 182 publicly available H&E whole slide images (WSIs) from The Cancer Genome Atlas (TCGA), for which annotations by the pathology team at Yale School of Medicine are publicly available. Our pipeline achieved an Area Under the Curve (AUC) of 0.85 ± 0.02 across four different test folds. Additionally, we tested our model on 44 H&E slides from the TCGA-BRCA dataset, which had an HER2 score of 2+ and included corresponding HER2 status and FISH test results. These cases are considered equivocal for IHC, requiring an expensive FISH test on their IHC slides for disambiguation. Our pipeline demonstrated an AUC of 0.81 on these challenging H&E slides. Reducing the need for FISH test can have significant implications in cancer treatment equity for underserved populations.

Keywords: immunohistochemistry, hematoxylin and Eosin, HER2 status, histopathology, human epidermal growth factor 2, classification, deep learning.

HEART FAILURE: MACHINE LEARNING PREDICTION WITHIN A 5-YEAR FRAMEWORK

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Abstract

Heart failure (HF) is a complex syndrome that is affected by many factors and causes. It is crucial to early recognize the disease subtypes and the unidentified clinical pathways that give rise to it. Machine learning (ML) is the tool that is utilized to deal with these challenges and improve the prediction of HF. In this paper, the HF risk prediction was implemented by employed ML classifiers, such as Random Forest (RF), Extreme Grading Boosting (XGBoost) and Light Gradient-Boosting Machine (LGBM). We used the data from the German epidemiological trial on ankle brachial index - getABI cohort, which includes 6,454 patients. The performance of classifiers was estimated by Accuracy (ACC), Sensitivity, Specificity, and the area under the receiver operating characteristic curve (AUC) in mean values for each ML classifier. The results were also interpreted using the Explainable artificial intelligence (XAI) approach, the Shapley Additive exPlanations (SHAP) values. Our work reveals that LGBM classifier predict the HF risk within 5 years follow-up in a general population with 68 % accuracy. Moreover, the N-terminal pro–B-type natriuretic peptide (NT-proBNP) was identified as the most important feature for HF risk prediction.

Keywords: heart failure, machine learning, explainable AI.

CLUSTERED PATCH EMBEDDINGS FOR PERMUTATION-INVARIANT CLASSIFICATION OF WHOLE SLIDE IMAGES

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Abstract

Whole Slide Imaging (WSI) is a cornerstone of digital pathology, offering detailed insights critical for diagnosis and research. Yet, the gigapixel size of WSIs imposes significant computational challenges, limiting their practical utility. Our novel approach addresses these challenges by leveraging various encoders for intelligent data reduction and employing a different classification model to ensure robust, permutation invariant representations of WSIs. A key innovation of our method is the ability to distill the complex information of an entire WSI into a single vector, effectively capturing the essential features needed for accurate analysis. This approach significantly enhances the computational efficiency of WSI analysis, enabling more accurate pathological assessments without the need for extensive computational resources. This breakthrough equips us with the capability to effectively address the challenges posed by large image resolutions in whole-slide imaging, paving the way for more scalable and effective utilization of WSIs in medical diagnostics and research, marking a significant advancement in the field.

Keywords: clustered, embedding, data representation, permutation invariant, whole slide image.

AN EFFICIENT CNN AND RNN HYBRID MODEL FOR THE DETECTION OF EPILEPTIC SEIZURES IN EEG SIGNALS

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Abstract

Electroencephalogram (EEG) is a widely used supplementary test in epilepsy diagnosis. While traditional methods and deep learning networks have shown considerable success, they often rely on extensive human effort, particularly in feature extraction. This study proposes a hybrid Convolutional Neural Network and Recurrent Neural Network (CNN-RNN) algorithm that can autonomously learn features from EEG data. The RNN component calculates dependency and continuity features from the CNN's intermediate layer output, which are then connected to the final fully connected network for classification prediction. The algorithm was trained and tested on four datasets from the University of Bonn. For binary classification tasks, the proposed CNN-RNN model achieved accuracies of 98.33% on dataset 1 and 100% on dataset 2. When tested on datasets 3 and 4, the model attained 98.00% and 100% accuracy, respectively. Notably, the algorithm demonstrated superior performance on datasets 2 and 4 compared to state-of-the-art methods. These results suggest that the proposed CNN-RNN model offers a promising approach for automated EEG analysis in epilepsy diagnosis, potentially reducing the need for manual feature extraction and improving classification accuracy.

Keywords: epilepsy, EEG, CNN-RNN.

COMPARING TOP-K AND MANUAL FEATURE SELECTION FOR PCG SIGNAL CLASSIFICATION USING XGBOOST

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Abstract

Cardiovascular diseases (CVDs) are the leading cause of death, taking 18 million lives annually. Heart auscultation, the process in which clinicians record phonocardiogram signals to detect potential CVD abnormalities, plays an instrumental role in early detection and prevention of CVDs. However, traditional auscultation brings challenges such as requiring extensive clinician experience and skill. Therefore, this paper proposes an algorithm for Computer-Aided Auscultation, based on combining an ensemble gradient-boosting machine learning algorithm called XGBoost and various signal processing methods. A total of 104 signals from clinics and in-home visits were acquired from the 2016 PhysioNet Challenge Dataset. After various preprocessing steps such as downsampling, normalization, and bandpass filtering, 25 time-frequency and spectral density features such as Spectral Power Density and S1 peak interval times were identified. Then, strong (highly predictive) features, especially those with greater than 0.7 correlation scores, were selected by utilizing boxplots and a correlation matrix. On the other hand, the ten best features were chosen using gradient-boosting sequential selectors. Finally, both sets of features were fed into multiple models such as Logistic Regression, KNN, and LDA, and the anticipated XGBoost, which yielded a 92% accuracy and a 93% recall with the 10 manually selected features at a 90% to 10% training vs. test split. These promising results are pivotal in developing an accurate method to reduce clinical stress for heart auscultation, potentially saving lives.

Keywords: machine learning, biomedical signals, feature selection, computational biology.

AI-ENHANCED TELE-REHABILITATION: PREDICTIVE MODELING FOR FALL RISK AND TREATMENT EFFICACY IN BALANCE DISORDERS

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Abstract

This study focuses on the development of artificial intelligence models to enhance telerehabilitation practices. We utilized diverse datasets to create clinically relevant models for predicting two critical outcomes: fall risk and treatment effectiveness. By applying various machine learning techniques, including K-Nearest Neighbors, Random Forest, Decision Tree, Support Vector Machine, and XGBoost, our models demonstrated high accuracy, sensitivity, and specificity. Notably, the Random Forest model achieved an accuracy of 0.97 in predicting fall risk and 0.96 in assessing treatment effectiveness. These models equip clinicians with powerful tools for data-driven decision-making, ultimately improving patient outcomes in rehabilitation settings.

Keywords: AI prognostic analytics, fall risk, treatment effectiveness, rehabilitation.

PULSENSE: AN AI-DRIVEN CARDIOVASCULAR MONITORING AND ARRHYTHMIA DETECTION SYSTEM

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Abstract

PulSense is a portable, low-cost and multi-sensor Cardiovascular monitoring and Arrhythmia detection system. The Movesense Medical (MD) multisensory device is used to capture single-lead electrocardiogram (ECG) signals and is integrated into a Raspberry Pi 4 to perform signal processing and arrhythmia detection for the first time. The system features a new user-friendly interface. It employs machine learning by a Convolutional Neural Network (CNN) trained on the MIT-BIH Arrhythmia Database (110,000 multi-labeled heartbeats) to accurately classify arrhythmia types. Feature extraction is enhanced by applying a median filter followed by a notch filter and a Continuous Wavelet Transform (CWT). High overall F1 scores were observed in different classes compared to the literature. Although the PulSense prototype is in a continuous phase of development and testing, the experimental results are encouraging and support its further development into a viable solution for constant heart monitoring and the timely detection of cardiovascular diseases in clinical and non-clinical environments.

Keywords: cardiovascular diseases, arrhythmia detection, convolutional neural networks, embedded systems, monitoring systems.

USING ULTRA-SOUND IMAGES AND A MULTI-TASK, EXPLAINABLE APPROACH FOR THYROID CANCER DETECTION

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Abstract

The current clinical practice in thyroid nodule malignancy detection and diagnosis consists of ultrasound (US or sonogram) imagery, followed by guided fine needle aspiration (FNA) biopsy if deemed necessary. FNA is performed based on the expert knowledge of trained clinicians, who assess the malignancy risk of the thyroid nodule(s). Thyroid malignancy risk assessment based on ultrasound images rely on experience and heuristics, which cannot be directly and reliably converted into rule-based algorithms. Thus, deep learning-based automated methods for nodule segmentation and risk-assessment are designed as aids for radiologists to enable them to provide timely and successful cancer treatment to patients. Existing AI methods for analyzing thyroid ultrasound imagery are designed to perform either nodule segmentation or output an objective belief of malignancy that drives the decision to perform an FNA. AI solutions that simply output a probability of malignancy suffer from lack of reliability and explainability and are usually not trusted by clinicians. Radiologists rely on the American College of Radiology TI-RADS system for malignancy risk assessment. TI-RADS requires visual analysis of features such as nodule margin, composition, echogenicity, shape and echogenic foci. AI models need to incorporate this domain knowledge to achieve explainability and earn the trust of clinicians. We aim to take a step in this direction by designing a multi-task deep-learning model that performs three important tasks: thyroid nodule segmentation, sonogram feature detection, and explain the risk of malignancy. We evaluate our technique quantitatively using the Thyroid Ultrasound Cine-Clip Dataset from Stanford for training and testing. On the Stanford dataset, our framework achieves an mIoU of 71% for segmentation and 65% accuracy for high/low risk classification. Additionally, we use the Thyroid Digital Image Database (TDID) to test on a different dataset than the training set with a segmentation mIoU of 65% and a risk classification accuracy of 64%.

Keywords: thyroid cancer, thyroid nodule segmentation, classification, CNNs, explainable AI.

ADVENTITIA SEGMENTATION ON SUPERFICIAL FEMORAL ARTERY OPTICAL COHERENCE TOMOGRAPHY IMAGES

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Abstract

Atherosclerotic disease on peripheral arteries, commonly known as peripheral artery disease represents accumulation of cholesterol in peripheral arteries. It causes the formation of different types of depositions called plaques which cause thickening of the arterial walls resulting in reduced blood flow to lower extremities, in case of femoral arteries, upper extremities, in case of brachial artery or brain in case of carotid artery. Current research shows that approximately 8.5 million Americans, aged over 40 years, are affected by peripheral artery disease while one fourth of them falls into a severe category. For these reasons, an early detection of the disease is important. In order to detect the disease, arteries need to be imaged properly. In the recent years, an increase of optical coherence imaging has occurred due to the ease of use and the ability to detect tissue morphology which is extremely important for the detection of the disease. From the tissue morphology, it is of most importance to observe the tissue between lumen and intimal layer of the artery, since the majority of the plaques form in that region, but it is also important to observe the region between intima and adventitia (the outer wall of the artery) since the plaque can penetrate the intimal layer as well. In this paper, a deterministic approach to the detection of the adventitia is described based on the previously detected intimal layer of the artery. The proposed method is evaluated on optical coherence tomography images from 8 specimens of porcine femoral arteries. The results show that the detection of adventitia is possible on this image modality with Dice coefficient 0.9805 and Hausdorff distance 0.1 mm.

Keywords: segmentation, peripheral artery, optical coherence tomography.

AN EXPLORATION OF K-MER RANGES FOR MEGAHIT IN THE CONTEXT OF MICROBIAL COMMUNITY-WIDE IDENTIFICATION OF ANTIMICROBIAL RESISTANCE GENES AND BIOSYNTHETIC GENE CLUSTERS

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Abstract

With the advent of genomics and next generation sequencing, metagenomics has become a discipline in its own right enabling for the first time the study of complex microbial ecosystems containing species that cannot be cultured in the lab. Sequencing and characterizing these microbial genomes enable the identification of novel antimicrobial resistance genes (ARGs) and biosynthetic gene clusters (BGCs), with potential applications in industry. De novo sequence assembly, as a crucial step in metagenomics, is currently being implemented with tools such as MEGAHIT, which employ a multiple k-mer approach, where several intermediate assemblies are built from k-mers from a range of sizes and merged at the end. The objective of this study was to investigate the impact that this range of k-mer sizes could have on a range of quality metrics, including the number of identified ARGs and BGCs, using a series of assembly scenarios involving 7 samples collected from the Movile Cave in Romania. We found that larger k-mer sizes and more fine-grained ranges of intermediate steps were associated with increased metrics, including larger numbers of identified BGCs. Future studies are required in order to better understand the role of the range of k-mer sizes in MEGAHIT in the context of microbial community-wide identification of ARGs and BGCs.

Keywords: metagenomics, benchmark, MAG, antimicrobial resistance gene, biosynthetic gene cluster.

EFFICIENT WHOLE SLIDE IMAGE CLASSIFICATION THROUGH FISHER VECTOR REPRESENTATION

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Abstract

The advancement of digital pathology, particularly through computational analysis of whole slide images (WSI), is poised to significantly enhance diagnostic precision and efficiency. However, the large size and complexity of WSIs make it difficult to analyze and classify them using computers. This study introduces a novel method for WSI classification by automating the identification and examination of the most informative patches, thus eliminating the need to process the entire slide. Our method involves two-stages: firstly, it extracts only a few patches from the WSIs based on their pathological significance; and secondly, it employs Fisher vectors (FVs) for representing features extracted from these patches, which is known for its robustness in capturing fine-grained details. This approach not only accentuates key pathological features within the WSI representation but also significantly reduces computational overhead, thus making the process more efficient and scalable. We have rigorously evaluated the proposed method across multiple datasets to benchmark its performance against comprehensive WSI analysis and contemporary weakly-supervised learning methodologies. The empirical results indicate that our focused analysis of select patches, combined with Fisher vector representation, not only aligns with, but at times surpasses, the classification accuracy of standard practices. Moreover, this strategy notably diminishes computational load and resource expenditure, thereby establishing an efficient and precise framework for WSI analysis in the realm of digital pathology.

Keywords: classification, fisher vector, whole slide image.

CLASSIFICATION AND MORPHOLOGICAL ANALYSIS OF DLBCL SUBTYPES IN H&E-STAINED SLIDES

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Abstract

We address the challenge of automated classification of diffuse large B-cell lymphoma (DLBCL) into its two primary subtypes: activated B-cell-like (ABC) and germinal center Bcell-like (GCB). Accurate classification between these subtypes is essential for determining the appropriate therapeutic strategy, given their distinct molecular profiles and treatment responses. Our proposed deep learning model demonstrates robust performance, achieving an average area under the curve (AUC) of (87.4 ± 5.7) % during cross-validation. It shows a high positive predictive value (PPV), highlighting its potential for clinical application, such as triaging for molecular testing. To gain biological insights, we performed an analysis of morphological features of ABC and GCB subtypes. We segmented cell nuclei using a pre-trained deep neural network and compared the statistics of geometric and color features for ABC and GCB. We found that the distributions of these features were not very different for the two subtypes, which suggests that the visual differences between them are more subtle. These results underscore the potential of our method to assist in more precise subtype classification and can contribute to improved treatment management and outcomes for patients of DLBCL.

Keywords: classification, deep learning, lymphoma, morphological, subtype.

EARLY SCREENING FOR MULTIPLE SCLEROSIS USING GUT MICROBIOME AND MACHINE LEARNING

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Abstract

Multiple Sclerosis is a chronic disease of the central nervous system that affects millions worldwide, and early detection is crucial for better treatment outcomes. Current detection methods are expensive and invasive, leading to a need for a cheaper and non-invasive screening tool. We utilized the gut microbiome and machine learning to develop a reliable screening tool for Multiple Sclerosis that can recommend further clinical examination. We identified optimal combinations of feature selection and machine learning algorithms as well as the associated biomarkers for Multiple Sclerosis in the gut microbiome. Our evaluation revealed that among various classifiers, Logistic Regression and Naive Bayes, particularly when trained on features filtered through Correlation-based Feature Selection and Information Gain methods, exhibited exceptional performance in terms of precision, recall, and F-measure consistently higher than 0.95 and high AUC values. Furthermore, our analysis of the biomarkers identified distinct microbial signatures between healthy and Multiple Sclerosis patients, notably the prevalence of certain taxa, such as genera Streptococcus and Dorea in Multiple Sclerosis patients, and phylum Bacteroides and species uniformis in healthy cases.

Keywords: multiple sclerosis, gut microbiome, machine learning, feature engineering, feature selection.

CAT SCORE PREDICTION IN COPD PATIENTS USING A CHEST-WEARABLE RESPECK

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Abstract

The COPD Assessment Test (CAT) consists of 8 questions, each one scored by patients on a scale of 0 to 5 points, and the aggregate score provides a self-assessment of the impact of their symptoms on their well-being. In the nature of any questionnaire, the CAT score, although numeric, is a subjective assessment of the effect of COPD symptoms on their personal condition. This paper investigates the use of respiratory rate and activity data derived from a wearable Respeck sensor during the daily pulmonary rehabilitation exercises at home as an objective measure of the patient's lung health condition and how well the sensor data predicts the CAT score on the same day and the next day. Results are presented for 16 patients in terms of standard error metrics such as Mean Absolute Error (MAE), Root Mean Square Error (RMSE), and clinically relevant minimum clinically important difference (MCID).

Keywords: COPD, CAT, wearable sensors, pulmonary rehabilitation, home-based monitoring.

MOLECULAR PROFILE IN BREAST CANCER TREATMENT

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Abstract

Introduction: In the past decade, breast cancer prognosis has significantly improved due to early diagnosis, an improvement in molecular characterization and availability of innovative treatments. Breast cancer represents a heterogeneous disease, where different biological subtypes show disease-specific outcomes; that is, different response to applied treatment and different prognosis.

Method: Current literature review was performed, providing up-to-date overview of literature and clinical trials in breast cancer molecular profile topics.

Overview: Standard approach to breast cancer treatment depends on the stage of the disease as well as the clinical and pathological characteristics of the tumor. Gene expression profiling and next generation sequencing can provide additional insight into tumor biology and response to treatment. Available literature shows that the molecular profile of breast cancer has a significant impact on tumor development, plays a role in determining therapy type and response to it, as well as overall survival and progression free survival. Unlike systemic therapy, the role of the molecular profile and its influence on the response to the radiation therapy has not yet been precisely defined and widely applied in clinical practice, although individual studies have been published showing that certain types of breast cancer have a significant benefit from the radiation therapy.

Conclusion: The molecular subtype of breast cancer, in combination with the characteristics of the patient and the disease itself, plays a significant role in response to specific oncological treatment. Future knowledge will provide insight into the complex molecular mechanisms of breast cancer and its treatment responses.

Keywords: breast cancer, molecular profile, systemic treatment, radiation therapy.

DATA-DRIVEN ANALYSIS OF IRREGULAR RESPIRATORY SIGNALS DERIVED FROM THE CHEST-WEARABLE RESPECK MONITOR

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Abstract

The respiratory rate and the respiratory flow/effort are important vital signs monitored during patients' care in the hospital and during remote management of subjects with chronic lung diseases, such as asthma, chronic obstructive pulmonary disease (COPD) and congenital airways malformation. The Respeck is a wireless device worn as a plaster on the chest which continuously monitors respiratory signals, such as the respiratory rate (breaths/minute), and the respiratory flow/effort (amplitude over time). The regularity of the respiratory signal, or rather the nature and frequency of occurrence of irregular breathing episodes can be used to characterise the subjects' clinical status. This paper develops computational methods for classifying episodes of rapid-shallow breathing based on approximating the tidal volume using features such as: the area under the respiratory signal curve, peak respiratory flow and the respiratory rate. Results are presented for a data-driven approach to the analysis of a Respeck dataset of respiratory flow signals gathered from 137 asthmatic subjects.

Keywords: respiratory monitoring, tidal volume, wireless wearable sensors, irregular breathing.

ADVANCES AND EVALUATION OF INTELLIGENT TECHNIQUES IN SHORT-TERM LOAD FORECASTING

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Abstract

In order to maintain the stability of the power grid, various loads forecasting methods have emerged in endlessly. However, due to different characteristics such as algorithm generalization capabilities and model complexity, their applicability to load forecasting varies. This article discusses short-term power load forecasting in the past five years. In summary, this paper summarizes various dimensions such as experimental data sets, data preprocessing, prediction algorithms, optimization models and evaluation methods of current research status in power load forecasting. In addition to the advantages, disadvantages and applicability of various prediction algorithms, this paper also sums up and prospects the development trends of the short-term power load forecasting system, so as to provide a reference for the selection of power system load forecasting models in the future.

Keywords: short-term load forecasting, deep learning combination model, long short-term memory network, machine learning.

BIOGENIC SILVER NANOPARTICLES CAUSES CELL DEATH BY INDUCING OXIDATIVE STRESS IN MRC-5 CELL LINE

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Abstract

This study showcases the synthesis of silver nanoparticles (AgNPs) by the utilization of Borovnica extract (Vaccinium myrtillus) and Bosiljak extract (Ocimum basilicum) in a simple and non-toxic one-step procedure. The method is described as eco-friendly, uncomplicated, and economical, utilizing a water-based plant extract that acts as both reducing and stabilizing agent for AgNPs. The VM-AgNPs and OB-AgNPs were characterized by UV–Vis spectroscopy, field emission scanning electron microscopy (FESEM), and transmission electron microscopy (TEM). UV–Vis spectroscopy detected surface plasmon resonance (SPR) at a wavelength of 305 nm and 344 nm in the VM-AgNPs and OB-AgNPs solutions, respectively. The investigation of VM-AgNPs and OB-AgNPs using FESEM revealed the presence of oval-shaped NPs with average sizes of 52 nm and 55 nm, respectively. TEM analysis showed similar observation with average size of 80 nm and 35 nm, respectively. Both VM-AgNPs and OB-AgNPs showed cytotoxic properties against healthy lung pleura fibroblasts (MRC-5), resulting in a reduction of cell viability that was dependent on the dosage. The inhibitory concentration (IC50) in VM-AgNPs and OB-AgNPs treated group was calculated to be 25.89 ± 1.41 µg/ml and 8.41 ± 1.00 µg/ml, respectively. Moreover, the study investigated the involvement of reactive oxygen species (ROS) in the toxicity to cells. It was noted that both NPs induce oxidative stress over time in MRC-5 cell lines in a dose-depended manner.

Keywords: green nanotechnology, bioengineered nanoparticles, cytotoxicity, reactive oxygen species, oxidative stress, cytotoxicity.

IN VITRO AND IN SILICO BINDING STUDIES OF CHROMENO-PYRIMIDINE DERIVATIVES WITH BIOLOGICAL IMPORTANT PROTEIN-PART III

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Abstract

In this study, in vitro and in silico interactions of bovine serum albumin with chromeno-pyrimidine derivatives (CP), 5-(7-bromo-2,4-dioxo-1,3,4,5-tetrahydro-2H-chromeno-[2,3-d]pyrimidin-5-yl)pyrimidine2,4,6(1H,3H,5H)-tri-one (CP-1) and 8,9-dihydroxy-2H-chromeno[2,3-d] pyrimidine 2,4(3H)-dione (CP-2), are investigated. The high value of in vitro obtained binding constants are the result of good binding of the investigated compounds to BSA. Molecular docking results explain the interactions of BSA to the tested compounds and it is consistent with the experimentally obtained results.

Keywords: chromeno-pyrimidine derivatives, bovine serum albumin, fluorescence spectroscopy, molecular docking study.

KOLMOGOROV-ARNOLD-BASED NETWORK WITH LIGHTWEIGHT FEATURE FUSION SCHEMA FOR SINGLE-LEAD ELECTROCARDIOGRAM ATRIAL FIBRILLATION DETECTION

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Abstract

Atrial fibrillation (AF) is a prevalent cardiac arrhythmia that poses a serious threat to patients’ cardiovascular health. Deep learning-based single-lead wearable ECG devices have been widely studied and shown satisfactory performance in early AF detection. However, most existing models increase complexity by employing deep networks and feature fusion techniques to enhance robustness and generalization. Despite that several model compression techniques have also been applied to reduce model parameters by compromising certain aspects of performance. In this study, to strike a balance between model performance and complexity, we proposed a Piecewise Aggregate Approximation (PAA)-based lightweight feature fusion schema in the proposed KAN-based Network, with an improved connected layer from Kolmogorov-Arnold Network (KAN) to replace the fully connected layer. Our innovation leveraged the learnable nonlinear activation functions of the KAN Layer to enhance the complex high-dimensional representations at our network’s output. Additionally, to reduce the number of parameters generated by feature fusion and the KAN Layer, we applied large-scale dimensionality reduction to the ECG signals using PAA as the secondary feature, allowing the low-dimensional features to represent part of the high-dimensional features through sequence-level fusion. Testing on the PhysioNet- 2017 dataset demonstrates that our method outperformed the benchmark, achieving a 2.2% improvement in the F1 score for AF detection while reducing parameters by 13% compared to traditional feature fusion.

Keywords: single-lead electrocardiogram, atrial fibrillation detection, deep learning, feature fusion, Kolmogorov-Arnold network, piecewise aggregate approximation.

DESIGN, IN SILICO EVALUATION, AND TOXICOLOGICAL ASSESSMENT OF N-PROTOCATECHOYL HYDRAZONE DERIVATIVES AS POTENTIAL EGFR KINASE INHIBITORS

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Abstract

In this study, we explored the potential of novel N-protocatechoyl hydrazone derivatives as inhibitors of epidermal growth factor receptor (EGFR) kinase, a key target in cancer therapy. Using the CReM webserver, we generated 100 unique derivatives starting from compound L, all of which displayed favorable synthetic accessibility and drug-like characteristics as proven by ADME screening (with a LogP value of less than 3). Out of these, 34 compounds satisfied the Lipinski Rule of Five and were further examined for their ability to bind to EGFR using molecular docking simulations and a deep learning algorithm. Nine compounds demonstrated binding energies below -41.2 kJ/mol, surpassing the reference inhibitor Mavelertinib (MAV, -38.5 kJ/mol), and indicating their greater potential for inhibiting EGFR. The molecular docking analysis showed that the interactions were facilitated by specific amino acids such as MET793 and THR854, as well as different non-covalent forces including hydrogen bonds and π-π interactions. Analysis using the ProToxIII website revealed that out of the nine most promising compounds, only two, L and L1, exhibited lower anticipated toxicity than MAV. Among these, L had the biggest safety margin, with an LD50 value of 5000 mg/kg. Based on these findings, compounds L and L1 have been identified as the most promising candidates for further in vitro testing as potential anticancer drugs.

Keywords: anticancer, AI assisted drug design, coumarins.

A COMPUTER MODEL FOR SIMULATION OF THE INFLUENCE OF THE CELL-PLATELET INTERACTION ON THE METASTASIS OF THE CIRCULATING TUMOR CELLS (CTC)

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Abstract

Within the multi-stage process of metastasis, there is a separation of cancer cells, so-called circulating tumor cells (CTCs), from the primary tumor, and their journey to the target organ where they remain. On the way to the target organs, CTCs pass through the circulatory system where they interact with host cells. Recent studies have suggested that platelets have a crucial role in enhancing the survival of circulating tumor cells in the bloodstream and aggravating cancer metastasis. The main physiological function of platelets is to create a blood clot by binding to the injured sites on the vessel to stop bleeding. However, in cancer patients, activated platelets adhere to circulating tumor cells and exacerbate metastatic spreading. To examine the biophysical conditions needed for CTC arrest, we used a custom-built viscoelastic solid-fluid 2D computational model that enables the calculation of the limiting cases for which CTC will get stacked into the capillary by the influence of platelets. Two representative examples were developed: a) cell in narrowing with platelets and b) cell in wide capillary with platelets attached to the cell. By exploring the parameter space, a relationship between the capillary blood pressure gradient and the CTC mechanical properties (size and stiffness) and platelet size is determined. Based on the results obtained using the presented software and platform, it can be concluded that the platform can be a useful tool in studying biological conditions for CTC arrest, studying the mechanism of interaction between cells and platelets, as well as predicting disease progression.

Keywords: finite element analysis, fluid-solid interaction, metastasis, cell-platelet interaction.

COMPARATIVE STUDY OF LARGE LANGUAGE MODELS FOR LUNG-RADS CLASSIFICATION IN PORTUGUESE CT REPORTS

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Abstract

Lung cancer has the highest mortality rate among all cancer types for both males and females. It is estimated that lung cancer accounts for 21% of cancer deaths in each gender. This alarming statistics highlights the significant impact of lung cancer on overall cancer mortality, underscoring the urgent need for effective prevention, early detection, and treatment strategies to combat this disease. Lung cancer screening (LCS) is a process that involves careful selection of high-risk individuals, primarily current or former heavy smokers. It includes annual low-dose computed tomography scans and meticulous interpretation of results followed by appropriate follow-up care. Adherence to LCS follow-up is essential for maximizing the life-saving benefits of this preventive measure. Multiple professional associations, such as the American College of Radiology (ACR) and Fleischner Society, have published guidelines for managing patients with pulmonary nodules. Lung CT Screening Reporting & Data System is a quality assurance tool designed to standardize the reporting of lung cancer screening CT scans and provide consistent management recommendations. In this context, this paper aims to evaluate whether large language models (LLM) could accurately identify and extract lung nodules' characteristics from unstructured chest CT reports in Portuguese, based on the Lung-RADS classification system. This paper assesses the effectiveness of three LLMs: Gemini, GPT-4-o, Llama-3 70B, and a BERT model BioBERTpt. Our findings indicate that LLMs, especially GPT-4- o, have significant potential in automating the extraction of lung nodule characteristics for Lung-RADS classification, which could aid radiologists in their work. Notably, GPT-4-o with few-shot learning using Prompt 4 emerged as the best model, achieving an F1-score of 0.89. Our results highlight the potential of LLMs to assist radiologists in accurately classifying lung nodules according to the Lung-RADS criteria, streamlining the diagnostic process.

Keywords: information extraction, named entity recognition, natural language processing, large language model, chest CT report, lung cancer, lung-RADS.

THE INFLUENCE OF CHANGES IN VOLTAGE AND FLOW RATE ON THE DIAMETER OF ELECTROSPUN NANOFIBERS

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Abstract

Electrospinning is a simple and cost-effective method for producing smooth and thin nanofibers. The relationship between experimental parameters and the properties of the obtained fibers is important to investigate due to their potential applications. By varying the parameter values, the desired fiber diameter and morphology can be achieved. This study examines the effect of process parameters, applied voltage and flow rate on the morphology and diameter of fibers obtained through the electrospinning of a PCL and PEG polymer solution. The results show that these parameters affect fiber diameter, with an increase in voltage generally leading to a decrease in diameter, while an increase in flow rate generally results in thicker fibers.

Keywords: electrospinning, nanofibers, diameter, voltage, flow rate.

THE USE OF BIOINFORMATICS TO EXTRACT PHARMACOGENOMIC INFORMATION

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Abstract

Despite advances in heart research, knowledge about the cardiac conduction system and sinoatrial node (SAN) remains limited, with no effective treatments for SAN dysfunction currently available. Artificial pacemakers and defibrillators are commonly used but can lead to complications, emphasizing the need for better strategies and therapies. Human induced pluripotent stem cells (hiPSCs) offer a promising source for generating SAN-like cells, which can help in studying and treating genetic arrhythmias and modeling cardiac diseases. Publicly available transcriptomic datasets were sourced from the Gene Expression Omnibus (GEO) repository using specific keywords based criteria. Differential gene expression analysis was conducted using the R software environment with the DESeq2 package, involving pre-filtering and normalization of raw counts. Our bioinformatic strategy facilitates disease modeling and drug discovery by analyzing expression profiles. Principal component analysis revealed distinct cell populations, suggesting different responses to drugs, while Gene Ontology enrichment highlighted affected biological pathways for targeted therapy. This method, applicable to various transcriptomic databases, aids in identifying potential therapies.

Keywords: bioinformatics, pharmacogenomics, datasets, transcriptomics, GEO.

PREDICTING HEART DISEASE: A COMPREHENSIVE APPROACH TO DATA ANALYSIS AND MACHINE LEARNING MODEL DEVELOPMENT

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Abstract

This paper presents a detailed overview of an end-to-end machine learning (ML) model development process, with the goal of establishing a precise and fast artificial intelligence (AI) system for heart disease prediction on real-world data. The study also showcases how good practices in data analysis and proper data processing can help in providing reliable and accurate results, even when working with a small number of initial data points. Predictive models are trained on publicly available data, and a subset of common medical indicators is used to detect any increased likelihood of persons developing a heart disease. Our findings outline the essential steps required for a thorough ML model training study, which are critical for optimizing the performance of the algorithms. The results underline the capability of ML techniques to predict the risk of heart disease with considerable accuracy, thereby highlighting the transformative potential of AI in the area of bioinformatics and intelligent systems for clinical diagnostics.

Keywords: artificial intelligence, bioinformatics, cardiovascular diseases, heart disease prediction, machine learning, predictive modeling.

A COMPUTATIONAL METHOD FOR SACCADE VELOCITY PROFILES GENERATION

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Abstract

This study presents a computational method for generating eye movement data (specifically horizontal saccade velocity profiles) with the aim of providing benchmark input for the evaluation of data processing workflows and for the employment of machine and deep learning algorithms. The usability of generated saccades is further explored by comparison of two selected algorithms for saccade detection. Precisely, we assess and compare the modified and adaptive I-VT (Identification by Velocity Threshold) algorithm and the MAD (Median Absolute Deviation) algorithm. Both algorithms are tested on the publicly available dataset recorded in one subject while watching a movie trailer and on synthesized saccade velocity profiles. Obtained results suggest that both algorithms have exactly the same performance when generated saccade velocity is not scarcely contaminated with noise (F1 - Score of 94.42%), while for generated velocity with noise contamination, detection performance of both algorithms significantly degrades (F1 - Score of 36.57% for I-VT and slightly better performance of 40% for MAD algorithm). The proposed method for generating saccadic eye movements' profiles could be further utilized to simulate other types of eye movements' profiles, such as glissades. Also, the presented algorithm could be explored for the evaluation and design of novel algorithms for eye tracker data analysis, hopefully offering more reliability and higher precision in the eye tracker-based studies.

Keywords: adaptive threshold, eye movements, saccade detection, synthesized data.

ESTIMATING THE EFFECT OF DANICAMTIV ON HUMAN CARDIAC FUNCTION

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Abstract

Dilated cardiomyopathy (DCM) is a condition characterized by impaired cardiac contractility and enlargement of the heart chambers, leading to systolic dysfunction. Danicamtiv, a novel myosin activator, shows potential in restoring cardiac function by modulating crossbridge cycling affecting positively on increasing force and calcium sensitivity. While promising results have been observed in mouse and porcine models, the translational gap to human cardiac function remains. To address this, we used the MUSICO computational platform, which models sarcomere dynamics and crossbridge behavior, to simulate the effects of Danicamtiv on human trabeculae affected by DCM. MUSICO simulations were performed using experimental data from mouse and porcine cardiac tissues, incorporating physiological differences such as heart rates and myosin isoforms. The simulations demonstrated that Danicamtiv enhances tension at high calcium concentrations (pCa=4), increases calcium sensitivity, and prolongs muscle relaxation during twitch contractions. These effects are achieved by increasing [Ca2+] sensitivity of the transition rate from the crossbridge “OFF” state to “ON” state and by decreasing ADP release rate, leading to prolonged tension development. Our findings suggest that Danicamtiv has the potential to improve cardiac function in human DCM, providing a valuable tool for predicting drug efficacy in silico. Further validation using human cardiac tissue is needed to confirm its therapeutic impact.

Keywords: dilated cardiomyopathy, danicamtiv, MUSICO, sarcomere mutation, drug testing.

HYBRID COMBINATORIAL PROBLEMS USED FOR MULTIMODAL OPTIMISATION

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Abstract

This paper presents an integrating clustering and local search heuristics for multi-domain optimization applications in the Traveling Salesman and Protein Structure Prediction problems, evaluating their efficacy across diverse optimization scenarios, including single-objective, multi-criteria, dynamic, and multimodal tasks. GA framework is designed for solving the Traveling Salesman Problem (TSP), incorporating clustering and 2-opt local search to refine solutions. The methodologies from the TSP are extended to address the Protein Structure Prediction (PSP) problem using the Hydrophobic-Hydrophilic (HP) model. This novel adaptation showcases the adaptability of GAs in addressing structural prediction in computational biology, defining how route optimization strategies can be transformed to minimize conformational energy and improve folding patterns. Experimental results demonstrate the hybrid approach in achieving both route optimization and stable protein conformations, thereby bridging combinatorial optimization techniques with structural biology applications.

Keywords: single objective optimisation, multi-criteria optimisation, evolutionary algorithms, genetic algorithm, protein structure prediction, travelling salesman problem, K-Means clustering.

BEYOND THE GUT FEELING: MACHINE-LEARNING METHODS FOR AUTISM SCREENING

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Abstract

Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder that manifests itself as speech impairment and difficulties in social and cognitive skills. The onset of ASD is typically before the age of three, but many children are not diagnosed until later in life due to the current diagnosis being based on behavioral assessments. However, early intervention is crucial for minimizing the impact of ASD on both the child and their caregivers, and for developing an effective treatment plan for symptoms. We propose a gut microbiome-based screening tool for ASD utilizing feature selection, feature engineering, and machine learning algorithms. Our approach significantly reduces the feature space to 1-2% of its original size, emphasizing computational efficiency and informative attribute focus. Training and testing on two diverse datasets revealed minimal common features, underscoring the impact of regional differences on taxonomic behavior. Biomarker analysis confirmed known associations and unveiled novel connections, contributing valuable insights to the ongoing debate on ASD biomarkers. Notably, the genus Oscillospira has been identified by our Attribute Selection tools as being increased in ASD. Model performance, measured by Area Under the Curve, showcases the Bayes-Net algorithm on the Hierarchical Feature Engineering subset as the most optimal for ASD prediction. Our findings surpass existing literature, demonstrating the effectiveness of our approach in decoding the complex interplay between gut microbiome and ASD.

Keywords: autism, gut microbiome, machine learning, feature engineering, feature selection.

AN ENHANCED GENETIC ALGORITHM WITH CLUSTERING FOR OPTIMIZING MOBILE STROKE UNIT DEPLOYMENT

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Abstract

Mobile stroke units (MSUs), which are specialized ambulances equipped with a brain imaging device and staffed with trained healthcare personnel, have the potential to provide rapid on-site diagnosis and treatment for stroke patients. However, efficient access to prehospital stroke care requires optimizing the placement of MSUs. The MSU allocation problem has been previously solved using a traditional genetic algorithm that utilizes random starting solutions. The use of random starting solutions can, however, cause the algorithm to converge slowly. This can be especially problematic if the initial solutions are significantly far from the global optimum. To address this problem, we propose an enhanced genetic algorithm with clustering (EGAC), which is a time-efficient method to solve the MSU allocation problem by identifying the optimal locations of MSUs in a geographic region. By leveraging clustering, the EGAC provides diverse and comprehensive coverage, avoiding the pitfalls of starting with closely located and potentially less optimal solutions, thereby effectively steering and accelerating its convergence towards the optimal MSU placements. Our experimental results show that the EGAC significantly outperforms the traditional genetic algorithm, without cluster-based starting solutions, by achieving remarkably faster convergence toward the optimal solution for different number of MSUs to allocate. We validate the performance of the EGAC through qualitative and quantitative analyses.

Keywords: optimization, clustering, mobile stroke unit, fast convergence, genetic algorithm, ambulance allocation, emergency medical service, healthcare.

BIOMIMETIC NATURAL ELECTROSPUN GELATIN SCAFFOLDS FOR SKIN REGENERATION

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Abstract

Recent advances in regenerative medicine provide encouraging strategies to produce artificial skin substitutes. Gelatin scaffolds are successfully used as wound dressing materials due to their superior properties, such as biocompatibility and the ability to mimic the extracellular matrix of the surrounding environment.

In this study, five gelatin combination solutions were prepared and successfully electrospun using an electrospinning technique. After careful screening, the optimal concentration of the most promising combination was selected for further investigation. The obtained scaffolds were crosslinked with 25% glutaraldehyde vapor and characterized by Scanning Electron Microscopy (SEM).

The incorporation of antibiotic agents such as ciprofloxacin hydrochloride and gentamicin sulfate into gelatin membranes improved the already existing antibacterial properties of antibiotic-free gelatin scaffolds against bacteria. Also, the outcomes of the in vivo model study revealed that skin regeneration was significantly accelerated with gelatin/ciprofloxacin scaffold treatment. Finally, the combination of gelatin's extracellular matrix and antibacterial agents in the scaffold suggests its potential for effective wound healing treatments, emphasizing the importance of gelatin scaffolds in tissue engineering.

Keywords: electrospinning, nanofibers, tissue engineering.

SMART CLOTHES USING VITAL SIGNALS FOR EVALUATING HEALTH CONDITIONS: A COMPARATIVE EVALUATION

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Abstract

The advent of wearable technology has ushered in a new era of personalized healthcare, with smart clothes emerging as a promising platform for continuous health monitoring. This study delves into the development and evaluation of smart clothes embedded with sensors capable of selecting vital signals and assessing health conditions in real-time. These innovative garments offer a non-invasive and seamless approach to health monitoring, integrating sensors for tracking physiological parameters such as heart rate, respiratory rate, and body temperature. Advanced algorithms process the collected data to evaluate the wearer's health status, providing insights into potential health issues or abnormalities. The device's design emphasizes comfort, usability and scalability, ensuring long-term wearability and adaptability to various healthcare settings. Preliminary tests demonstrate the device's reliability, accuracy and potential for remote patient monitoring. This research contributes to the growing field of wearable healthcare technology, showcasing the transformative potential of smart clothes in enhancing individual well-being and proactive healthcare management. This paper offers a first level comparative study on a set of published work on devices for smart clothes for evaluation of their level of maturity and applicability.

MODELING APPROACHES FOR ASSESSING THE IMPACT OF AIR POLLUTION ON HUMAN HEALTH IN SERBIA

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Abstract

Air pollution has emerged as one of the most significant environmental issues in recent years, both globally and in Serbia. The high levels of pollutants in the air have been strongly linked to various adverse health outcomes, including increased mortality rates. One of the key factors in addressing this issue is the ability to assess and predict pollutant concentrations, especially when they exceed permissible limits for extended periods. These elevated concentrations can cause a range of health problems, particularly related to the respiratory system. This paper presents modeling approaches used to assess air pollution and its impact on human health. By utilizing different models and methods, we can simulate the emission, dispersion, and transport of pollutants. These models also help to evaluate the health risks associated with specific pollutants by estimating pollutant deposition in the human respiratory system. This study provides an overview of the modeling process in understanding air pollution patterns and their correlation with public health. The results highlight the importance of air quality models in identifying areas with elevated pollution levels and forecasting pollutant behavior under varying meteorological conditions. The insights gained from such research can inform policy decisions and contribute to the development of mitigation strategies aimed at reducing the environmental and health impacts of air pollution in Serbia.

Keywords: air pollution, Gaussian model, computer fluid dynamics, modeling.

UNSUPERVISED DEEP LEARNING METHOD FOR CELL SEGMENTATION OF CONFOCAL MICROSCOPY IMAGES

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Abstract

The use of image segmentation is widespread in many different fields of research including medicine, biology, computer vision and others. In most cases, image segmentation is performed through the use of supervised learning approaches, which utilize ground truth segmentation masks. However, in biomedical research, segmentation masks are not often available, which leads to the use of unsupervised segmentation approaches. In these situations, filtering paired with region expansion and reduction and edge detection techniques are used, which, in some cases, require time-consuming manual parameter tuning in order to achieve satisfactory results. This paper implements fully unsupervised image segmentation based on a deep learning convolutional neural network to segment cell geometries from confocal microscopy images of an in vitro model of angiogenesis. The proposed network architecture is a W-Net which contains a single U-Encoder and U-Decoder, both of which contain 3 convolution blocks and 3 deconvolution blocks, with 2 convolution layers and one max-pooling or up-convolution layer respectively. The results were evaluated using available ground truth images and achieved a pixel wise classification accuracy score of 98.73% and 73.71% intersection over union. The achieved high degree of accuracy shows great promise in cell segmentation without a need for ground truth masks over time and increases the accuracy of calculations of exerted forces.

Keywords: deep learning, image segmentation, unsupervised learning, region of interest, feature extraction.

SEMANTIC IMAGE SEGMENTATION OF CELL VOLUMES USING 3D U-NET CONVOLUTIONAL NEURAL NETWORK

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Abstract

Image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain characteristics. Traditionally, image segmentation was used on 2D imaging data, but due to the increased usage of 3D volumetric data there is a need for 3D segmentation techniques that could utilize spatial information contained in these volumes. One of the fields where there is a great amount of 3D data is microscopy. This paper introduces convolutional neural network based on 3D U-net architecture for segmentation of confocal microscopy images of cells in an in vitro sprouting angiogenesis model. Developed model contains 4 layers where each encoder block contains two 3D convolutional layers, Batch Normalization, ReLU activation function and 3D max pooling layer, while each decoder block contains upconvolution, skip connections and two 3D convolutional layers. Preprocessing of this data resulted in the volumes of shape 256×256×256 voxels which were used for training of the developed model. The model achieves great segmentation results as showed by Jaccard index value of 94.52% and Dice coefficient value of 99.31% compared to the preprocessed dataset. Even when segmentation results are compared to the original dataset, model still achieves respectable results of 84.22% Jaccard index and 88.18% Dice coefficient. This introduction of automatic 3D image segmentation could greatly reduce the time required for data preparation, while achieving high degree of segmentation accuracy.

Keywords: 3D image segmentation, 3D U-net, cell volumes, convolutional neural networks, volume segmentation.

APPLICATION OF MACHINE LEARNING IN THE ANALYSIS OF GENE EXPRESSION IN COLORECTAL CANCER CELLS TREATED WITH CHEMOTHERAPEUTICS

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Abstract

Colorectal cancer is a leading cause of cancer-related deaths, and understanding its molecular mechanisms is key to improving treatments. This study applies machine learning algorithms to analyze the expression of genes related to redox balance, apoptosis and cell migration in HCT-116 colorectal cancer cells treated with chemotherapeutics (5-fluorouracil, oxaliplatin, irinotecan, and leucovorin). The analyzed genes include those for redox homeostasis (GPX1, GPX2, GPX3, GPX4, TXNRD1, GSTP1, NFE2L2, NFKB1, HIF1A), apoptosis (CASP3, CASP8, CASP9, FAS, BCL-2, BAX) and genes coding cytoskeleton proteins (CDH1, CTNNB1, CDH2). Machine learning models, such as decision trees and random forests, were used to analyze gene expression changes based on qPCR data. Notably, GPX4 and BAX were linked to chemoresistance, while CDH1 upregulation suggested an effect on cancer cell migration. This study demonstrates the potential of machine learning in identifying gene expression patterns and aiding in the development of personalized CRC treatments.

Keywords: colorectal cancer, machine learning, gene expression, chemotherapeutics, apoptosis.

AI-DRIVEN DECISION SUPPORT SYSTEM FOR HEART FAILURE DIAGNOSIS: INTELHEART APPROACH TOWARDS PERSONALIZED TREATMENT STRATEGIES

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Abstract

Heart failure is recognized as a modern epidemic and despite the advances in therapy and research, heart failure still carries an ominous prognosis and a significant socioeconomic burden. The main aim of this paper is to demonstrate how novel Decision Support System (DSS) and computational platform like INTELHEART can transform the future of healthcare and early diagnosis of heart failure. The main idea is the integration of patient-specific data (i.e. demographic and physical characteristics, medical history, symptoms and signs) and results obtained using existing and novel diagnostic technologies into the cloud environment. Data will be used by different tools for machine learning and computational modelling, developing virtual patient population. Moreover, voice as a biomarker will be collected among participating patients, in order to create a VoiceHeart mobile app. INTELHEART represents a transformative advancement in heart failure care, aiming to make treatment more personalized and proactive. This initiative centers on precision medicine, using AI-driven analysis and a powerful DSS alongside the cloud-based platform and VoiceHeart mobile app to assist both clinicians and patients. Additionally, it incorporates assessments of psychological resilience and emotional well-being, addressing the often-overlooked mental health factors essential to comprehensive heart failure management.

Keywords: heart failure, decision support system, computational platform, personalised medicine.

COMBINING LATTICE BOLTZMANN AND AGENT-BASED MODELING TO MODEL THE BEHAVIOR OF CANCER CELLS IN-VITRO

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Abstract

In this paper, a hybrid numerical model is used to simulate the growth of cancer cells in-vitro. This model combines the agent-based model (ABM) that is used to simulate the progression of individual cancer cells and the lattice Boltzmann method (LBM) that is used to simulate the change of distribution of nutrients within the system, that is used by these cells within the observed domain. Results of a numerical simulation, that include the change of number of viable, necrotic and apoptotic cells over time are presented. The parameters of the numerical model can be estimated using experimental data and this can provide additional quantitative information about the behavior of cancer cells and about the influence of diverse drug treatments considered experimentally on these parameters. Numerical simulations like the one presented in this paper can be very useful in planning future experiments as they can provide means for a more in-depth analysis of a variety of phenomena occurring during the cell life-cycle.

Keywords: computer modeling, cancer cell cycle dynamics, agent-based modeling, lattice Boltzmann model.

VIRTUAL COACH PLATFORM FOR REHABILITATION: PLATFORM OVERVIEW AND ITS ASSESSMENT

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Abstract

Falls of older adults, especially those with complex comorbidities, like cognitive impairment, present a considerable challenge in rehabilitation settings. Conventional treatment approaches often fall short in addressing these multifaceted needs, underscoring the demand for comprehensive, individualized rehabilitation solutions. Augmented Reality (AR) technologies are emerging as promising tools to meet these challenges, offering tailored interventions that respond to each patient’s unique requirements. AR-based systems facilitate immersive and interactive rehabilitation, enabling patients to engage in activities that support both physical and cognitive health. Additionally, AR allows healthcare providers to offer real-time, remote support, expanding access to care for underserved populations. This paper introduces the Virtual Coach Platform, an AR-based rehabilitation system designed to address both physical and cognitive patients’ needs. The platform comprises an AR headset, which projects a 3D virtual coach, and an Android-based software application that integrates physical exercises, cognitive games and exergames. By examining the challenges and advantages of this system, we highlight how the Virtual Coach Platform can foster greater patient adherence and engagement.

Keywords: augmented reality, hologram, cognitive games, exergames, virtual coach platform.

NOVEL TREATMENT OF HIGH-RISK PROSTATE CANCER: A CLINICAL TRIAL DEVELOPMENT

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Abstract

The presentation is focused on protocol design and preliminary safety analysis of investigator-initiated phase II study of combination of a novel antiandrogen apalutamide, androgen deprivation therapy and prostate and pelvic stereotactic radiotherapy (AD ASTRA). Administration of apalutamide and ultra-hypofractionated stereotactic radiotherapy allows systemic and local treatment escalation with potentially improved outcomes in non-metastatic prostate cancer with high-risk of progression after local treatment and has never been tested in this setting before. Medical background, study logistics, interventions including performance of dedicated technology for stereotactic radiotherapy and protocol design will be presented. AD ASTRA study represents a unique experience with industry partnership and an investigator-initiated study conduction. The study is ongoing, and preliminary analysis of first 20 patients shows high adherence with no safety signal for combination of apalutamide with ADT and prostate and pelvic stereotactic radiotherapy.

SELECTING FRONTLINE IMMUNOTHERAPY IN ADVANCED NSCLC: PICKING THE WINING CARD

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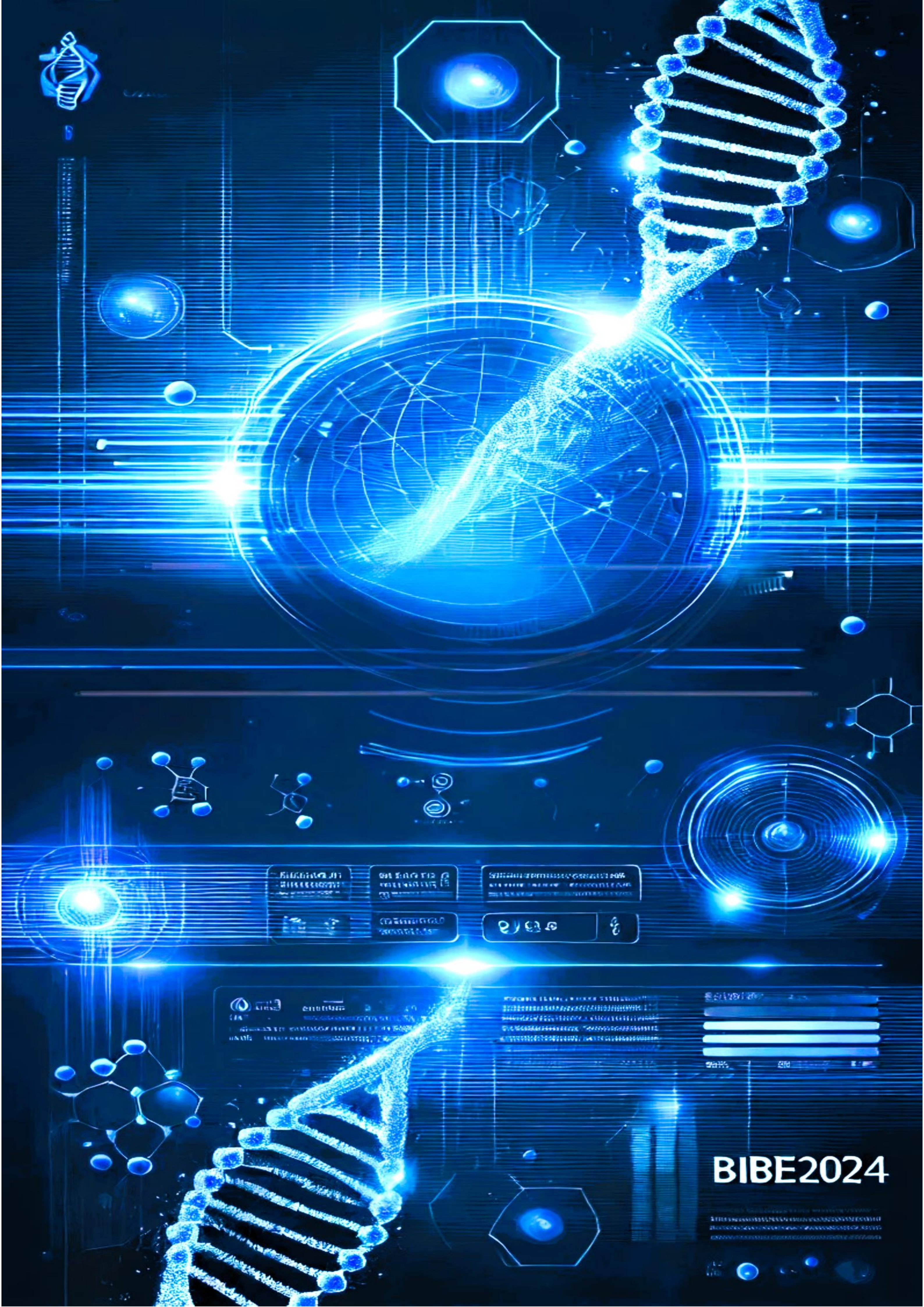
Abstract

Lung cancer is the leading cause of cancer incidence and mortality worldwide. Non-small cell lung cancer (NSCLC) accounts for approximately 85% of all lung cancer cases, and the prognosis for advanced NSCLC (aNSCLC) remains poor. Immune checkpoint inhibitors (ICIs), including anti-programmed cell death-1 (PD-1) and anti-programmed cell death ligand-1 (PD-L1) antibodies, have changed the treatment landscape for patients with aNSCLC. In the era of immunotherapy, these inhibitors are increasingly used, especially for aNSCLC patients without oncogenic driver mutations. The key trials that supported the approval of specific immunotherapy regimens for particular patient populations include the KEYNOTE-024, KEYNOTE-042 and IMpower110 trials (which focused on immunotherapy as monotherapy) as well as the KEYNOTE-189, KEYNOTE-407, IMpower150 and IMpower130 trials (which evaluated chemo-immunotherapy combinations) and the CheckMate-227 trial (which investigated immunotherapy doublets). When choosing a combination of PD-1 inhibition and chemotherapy, several factors must be considered, such as actionable mutations, PD-L1 expression levels, the patient’s performance status and age, smoking history, disease volume, symptoms, and tumor mutational burden (TMB). Additional considerations in the treatment of aNSCLC include comorbidity, histology, contraindications to immunotherapy, availability of treatments and patient preferences. Regional guidelines may vary in how these factors should be prioritized in treatment decision-making. The role of PD-L1 expression and tumor mutational burden as predictive biomarkers for response to single-agent immunotherapy and combination chemo-immunotherapy remains a subject of ongoing debate. PD-L1 is still considered an inadequate biomarker, as some individuals with high PD-L1 expression do not respond to treatment, while those with negative or low expression often show a positive response. When selecting an immunotherapy regimen, it is crucial to consider the accessibility of novel drugs, as many of them are either poorly accessible or unavailable in many low- and middle-income countries, including those in Central and Eastern Europe.

Keywords: non-small cell lung cancer, immunotherapy, immune checkpoint inhibitors.



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