Title: **High-frequency electrical stimulation for noninvasive neuromodulation of the central and peripheral nervous system**

Study program: Biomedical Technology and Bioinformatics

Supervisor: Prof. Eric Daniel Glowacki, PhD

Topic description:

This PhD project focuses on the development and mechanistic understanding of high-frequency (>1 kHz) electrical stimulation waveforms for noninvasive neuromodulation of the central and peripheral nervous system. Building on our recent publications (DOI: 10.1038/s41467-025-64059-w; DOI: 10.1002/mds.30134), the project explores how kilohertz-range stimulation—both amplitude-modulated and unmodulated carriers—modulates neuronal activity in ways fundamentally different from conventional low-frequency sinusoidal or pulsed-current stimulation paradigms.

The PhD topic can span multiple levels of investigation, from biophysical mechanisms in neural tissue to translational studies in humans, and will depend on agreement. Experimental approaches include computational modeling, invertebrate animal models, studies in healthy human volunteers and select clinical populations. The project is highly interdisciplinary and involves close collaboration with clinicians and local hospitals.

Your task:

- Design and implement high-frequency electrical stimulation protocols for noninvasive neuromodulation
- Investigate biophysical mechanisms of amplitude-modulated versus unmodulated kHz stimulation using computational models and experimental systems
- Perform and analyze electrophysiological recordings (e.g., EEG) in animal models, healthy volunteers, and patient populations
- Contribute to human neuromodulation studies, including protocol development, data acquisition, and analysis
- Disseminate results through scientific publications and conference presentations

Requirements:

- Master’s degree in biomedical engineering, physiology, electrical engineering, cognitive sciences, or a related discipline
- Experience with electrophysiology techniques and analysis of time-course electrophysiological data (e.g., EEG)
- ≥Basic programming skills, preferably in Python
- Experience with electrical neuromodulation in animal models and/or humans is a major advantage

We offer:

- Funding support from research grant projects and commercially sponsored research, supplementing the state PhD scholarship
- Support with applications for supplementary stipends and fellowships
- Opportunities to engage in undergraduate teaching and student mentorship
- Collaboration within a multidisciplinary research team and close interaction with clinicians and local hospitals

For more information about this topic please contact Prof. Eric D. Glowacki – glowacki@vutbr.cz

Title: **Deep learning in cardiac MRI applications**
Study program: Biomedical Technology and Bioinformatics
Supervisor: Ing. Vratislav Harabiš, PhD

Topic description:

This thesis focuses on advanced image processing methods in cardiovascular diagnostics using magnetic resonance imaging (MRI). The first step involves determining the radiological planes of the heart using overview images, which is crucial for valid heart imaging for further analysis. Research indicates that applying deep learning methods can accelerate this process.

The second step is to develop new methods for analyzing MRI data and supporting diagnostics, such as segmentation for assessing heart volumes, myocardial thickness, and more.

The research will be conducted in collaboration with national healthcare institutions (FN Brno, ICRC Brno) and international institutions (IRST IRCCS Meldola Italy, Philips Healthcare Netherlands, King's College London, UK).

Your task:

1. **Advanced Image Processing in Cardiovascular Diagnostics**: To introduce yourself into hearth imaging using modern approaches in MRI (magnetic resonance imaging).
2. **Development of New Analysis Methods**: Develop new methods, which include segmentation for assessing heart volumes, myocardial thickness, and more
3. **Testing and Validation of methods**: Test and validate your methods using clinical data. Data is provided by our cooperating institutions.

Requirements:

- Interest in scientific activities, image processing and machine learning
- Knowledge of programming languages (eg. C++, Python, Matlab)
- Relevant degree with appropriate engineering and/or IT knowledge
- English communication skills

We offer:

- Our core objective is to provide the doctoral students with a supportive and highly scientific work environment that fosters collaboration
- The doctoral students complete 3-6 months of internships at partner universities abroad
- The Department provides doctoral students with a scholarship beyond the state scholarship in the form of a supplementary stipend or salary when participating in a grant project

Relevant publications:

https://onlinelibrary.wiley.com/doi/10.1002/jmri.22626
https://aapm.onlinelibrary.wiley.com/doi/10.1002/mp.15327
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6884027/

For more information about this topic please contact Vratislav Harabiš – harabis@gmail.com

Title: Quantitative and Automated Analysis of Medical Images from Modern CT Scanners

Study program: Biomedical Technology and Bioinformatics

Supervisor: Ing. Jiří Chmelík, PhD

Topic description:

Computed tomography (CT) is one of the most extensively used imaging modalities for the diagnosis of a wide range of diseases and pathological conditions. Recent advances in CT technology have led to the clinical deployment of modern scanners capable of multi-energy X-ray imaging through multilayer detector architectures and, in some cases, single-photon–level detection. These systems enable the generation of diverse parametric image types, including virtual monoenergetic images and material decomposition maps. Such capabilities substantially enhance the diagnostic value of CT imaging while enabling significant reductions in radiation dose, which is of major importance.

This PhD research will focus on the development of advanced image processing and image analysis methods for multiparametric CT data acquired using multilayer detector systems, with a particular emphasis on machine learning and deep learning techniques. The student will design, implement, and rigorously validate algorithms for key tasks such as image preprocessing, segmentation, detection, classification, and outcome prediction, while explicitly addressing the specific properties and challenges associated with multiparametric CT images.

The goal of the project is to develop a comprehensive computer-aided diagnosis framework that improves diagnostic accuracy, robustness, and reproducibility, accelerates image interpretation, and reduces inter- and intra-observer variability as well as routine clinical workload.

The research will be carried out at the Department of Biomedical Engineering, in close collaboration with external partners. These include national clinical institutions (FN Brno, VFN Prague, FNUSA/ICRC Brno) and international industrial and research organizations (Philips Healthcare, The Netherlands; DKFZ Heidelberg, Germany). These collaborations will support clinical validation of the developed methods and enable continuous interaction with medical experts.

Your task:

- Get familiar with modern imaging techniques in medicine.
- In cooperation with clinicians acquire the data and propose possible improvements in medical image processing.
- Propose, implement and test novel image processing method to improve clinical outcomes.

Requirements:

- Deep interest in scientific activities in the field of medical imaging, image processing, and machine learning.
- Sound knowledge of programming languages (e.g., Python, MATLAB).
- A relevant degree with appropriate engineering and/or IT knowledge, transferable to the scientific environment.
- English communication skills.

We offer:

- Our core objective is to provide doctoral students with a supportive and highly scientific work environment that fosters collaboration.
- The doctoral students complete 3-6 months of internships at partner universities abroad.
- The Department provides doctoral students with a scholarship beyond the state scholarship in the form of a supplementary stipend or salary when participating in a grant project.

Relevant publications:

https://doi.org/10.1016/j.diii.2024.09.002
https://doi.org/10.1007/s13244-017-0571-4
https://doi.org/10.1002/acm2.13468

For more information about this topic please contact Jiří Chmelík – chmelikj@vut.cz

Title: **New computational approaches in recruiting bacterial genomes from metagenomes**

Study program: Biomedical Technology and Bioinformatics

Supervisor: Ing. Markéta Jakubíčková, Ph.D.

Topic description:

Recent advances in sequencing technologies have enabled routine sequencing of metagenomic samples from various environments, significantly expanding our ability to identify and analyze bacterial species within these systems. In the past, all newly described bacteria had to be isolated and their cultures made publicly available, which posed a significant challenge since many microbial species are uncultivable using current techniques. However, this requirement has been changed by the SeqCode initiative, which introduced a nomenclatural code allowing the description of prokaryotes directly from sequencing data, thereby greatly expanding the possibilities for their classification and study. To confirm their existence, computational methods such as bacterial recruitment are used, enabling the detection of specific bacteria in metagenomic databases. However, there is currently no standardized methodology for this technique, and commonly used approaches, often relying on BLAST, may lead to false-positive results due to shared genetic segments among different species. Therefore, this research aims to find a method for quantification as precise as possible. The methodology will involve processing both short NGS and long TGS sequencing reads to cover all currently used sequencing technologies. The proposed method could contribute to the more efficient detection of novel microorganisms and help to understand better their role in clinical and environmental metagenomes. The project will be primarily carried out at the Department of Biomedical Engineering, with expected collaboration with the Center for Molecular Biology and Genetics, FN Brno, Mendel University in Brno and Faculty of Pharmacy, Masaryk University. PhD students will complete six-month internships at prestigious partner universities abroad as part of their studies. DBME provides doctoral students with a stipend and/or a part-time contract beyond the state stipend when joining a grant project or engaging in teaching.

Your task:

- Develop advanced computational methods for bacterial genome recruitment.
- Present your research at international conferences and publish in scientific journals.
- Write and submit applications for junior research funding (e.g., PhD Talent, IGA, etc.).

Requirements:

- Proficiency in programming (e.g., Python, R); experience with Linux-based environments and Bash scripting is an advantage.
- Basic experience with bioinformatics tools and software applications.
- Strong analytical thinking and ability to work independently as well as in a research team.
- English proficiency allowing effective communication, writing, and presenting.

We offer:

- Participation in GAČR and AZV projects addressing current and relevant scientific challenges.
- Being part of a progressive and growing research team (BioSys_BUT).
- Opportunity to present research findings at prestigious international conferences.
- Flexible working hours, the possibility of home office, and team-building activities.

Relevant publications:

- DOI: 10.3389/fbinf.2021.826701
- DOI: 10.1186/s12967-024-04917-1

For more information about this topic please contact Markéta Jakubíčková – jakubickova@vut.cz.

Title: **Computational Analysis of Retinal Microvasculature and Photoreceptors**
Study program: Biomedical Technology and Bioinformatics
Supervisor: Doc. Ing. Radim Kolář, Ph.D.

Topic description:

Over the past decade, rapid advances in retinal imaging – particularly through adaptive optics (AO) – have brought a significant shift in the ability to achieve resolution down to the level of individual cells. This technological revolution enables in vivo study of previously unexplored microscopic structures of the retina, while at the same time creating the need for entirely new methods for processing such data.

This PhD project focuses on a detailed analysis of retinal vasculature and the photoreceptor layer using modern algorithms, including advanced segmentation and detection of pathological changes, multimodal image registration from various sources, and automated image quality assessment and artefact suppression. The research will involve the use of deep learning for precise segmentation and classification of structures, the development of explainable AI for improved interpretation of results in clinical practice, the design of methodologies for longitudinal tracking of retinal microstructures to predict disease progression, and the application of multimodal imaging data in personalised medicine.

The project offers opportunities to engage in ongoing research conducted in collaboration with the University of Leipzig, specifically in the areas of studying the effects of pregnancy on the ocular vascular system, evaluating the impact of new pharmacological therapies on retinal microstructure, and integrating data from multidimensional.

Your tasks:

- Develop advanced image processing and machine learning methods for high-resolution retinal imaging - segmentation, classification, multimodal image registration of retinal data.
- Conduct longitudinal analysis to track retinal changes and support early disease detection.
- Develop interpretable AI methods in collaboration with clinicians.
- Integrate imaging data with clinical and functional parameters.
- Scientific publishing in peer-reviewed international journals and at conferences.

Requirements:

- Master's degree in a relevant field such as computer science or biomedical engineering.
- Programming skills (preferably in Python, MATLAB, or C++) and experience with machine learning algorithms.
- Good communication skills in English,
- Strong interest or experiences in ophthalmic research is an advantage.

We offer:

- Work in an active team with opportunities for collaboration with a range of experts.
- Friendly and supportive research environment.
- Professional development through participation in international conferences, workshops as well as student's mentorship and teaching.

Relevant publications:

https://doi.org/10.1364/BOE.471881
https://doi.org/10.1016/j.preghy.2023.12.004
https://doi.org/10.1364/BOE.486052

For more information about this topic please contact Radim Kolář - kolarr@vut.cz.

Title: **Objective Assessment of Visual and Neurological Pathways Using Chromatic Pupillometry**

Study program: Biomedical Technology and Bioinformatics

Supervisor: Doc. Ing. Radim Kolář, Ph.D.

Topic description:

Pupillometry has emerged as a powerful, non-invasive tool for assessing visual and neurological function. In particular, chromatic pupillometry, which utilizes different wavelengths of light to stimulate specific retinal and neural pathways, holds significant potential for advancing diagnostics in ophthalmology and neurology.

This PhD project will focus on the development and application of a chromatic pupillometer, enabling precise assessment of pupil responses under controlled chromatic stimuli. The core focus of this PhD project is the development of a chromatic pupillometer, designed for both clinical and research applications. As part of this work, the candidate will actively participate in data acquisition, collecting pupillary response data from both healthy individuals and patient cohorts to investigate dynamic changes in pupil behaviour. Additionally, the project involves developing advanced data processing pipelines to analyse pupillary responses under various chromatic conditions. A key objective is to identify potential biomarkers that could aid in the diagnosis and monitoring of neurological and ophthalmic disorders based on pupillary behaviour.

The project will be conducted at the Department of Biomedical Engineering, with anticipated collaboration with CEITEC MU and St. Anne’s University Hospital Brno.

Your task:

- Development of chromatic pupillometer, protocol design, data acquisition, interaction with ophthalmologists.
- Signal and data analysis, biomarker identification.
- Implementation of chromatic pupillometry to MR acquisition.
- Scientific publishing.

Requirements:

- Master's degree in a relevant field, e.g. computer science, biomedical engineering.
- Programming skills, preferably Python, MATLAB, or C++.
- Familiarity with image processing techniques, experiences with basic electronics or machine vision setups.
- Good communication skills in English and keen interest in ophthalmological research.

We offer:

- Collaboration within an active and highly interdisciplinary team.
- Friendly and supportive research environment.
- Professional development through participation in international conferences, workshops as well as student’s mentorship and teaching.

Relevant publications:

https://doi.org/10.3389/fpsyg.2023.1295129
https://doi.org/10.1007/s00417-016-3351-9

For more information about this topic please contact Radim Kolář - kolarr@vut.cz.

Title: **Spectral Video-Ophthalmoscopy for Retinal Circulation and Oxygenation Assessment**

Study program: Biomedical Technology and Bioinformatics

Supervisor: Doc. Ing. Radim Kolář, Ph.D.

Topic description:

Over the past decade, retinal imaging has advanced significantly, encompassing both anatomical and functional aspects such as flow, perfusion, blood velocity, and tissue oxygenation. These methods are crucial for diagnosing retinal and systemic diseases. This project focuses on developing an ophthalmic device and image processing techniques to evaluate retinal oxygenation and blood circulation. A basic setup of video-ophthalmoscope was designed and validated over three years. It can capture retinal video sequences at specific wavelengths and acquire various biosignals like electrocardiogram, photoplethysmographic, and respiratory signals. This project will contribute to interdisciplinary research covering retinal imaging, functional assessment, advanced image processing, and machine learning. The goal is to establish a methodology for evaluating retinal oxygenation and identifying potential biomarkers for disease diagnosis.

Project will be solved mainly at the Department of Biomedical Engineering. However, cooperation with our foreign partners is expected - Leipzig University in Germany and University of Minnesota, USA.

Your task:

- Analysis of retinal video-sequences with the aim to extract specific parametric feature maps related to blood vessel pulsation, photoplethysmographic blood volume assessment and oxygen saturation estimation.
- Opto-mechanical modification of video-ophthalmoscope for spectral retinal imaging.
- Development of analysis pipeline for multimodal retinal images processing (image segmentation, classification etc.).
- Scientific publishing

Background:

- Master's degree in a relevant field, e.g. computer science, biomedical engineering.
- Strong programming skills, preferably Python, MATLAB, or C++.
- Familiarity with image processing techniques and machine learning algorithms.
- Interest in developing hands-on experimental skills in optics and electronics area.
- Good communication skills in English.
- A keen interest in ophthalmological research.

We offer:

- Collaboration within an active and interdisciplinary team.
- Friendly and supportive research environment.
- Professional development through participation in international conferences, workshops as well as student’s mentorship and teaching.

Relevant publications

https://doi.org/10.1364/BOE.486052
https://doi.org/10.1364/BOE.441451
https://doi.org/10.1002/jbio.202400494

For more information about this topic please contact Radim Kolář - kolarr@vut.cz.

Title: **Advanced image processing in pneumology**
Study program: Biomedical Technology and Bioinformatics
Supervisor: Martin Mézl, PhD

Topic description:
The aim of this dissertation is to perform a comprehensive analysis of image data captured in pneumology. Specifically, it will involve data from an experimental video endoscope that captures lung parenchyma tissue. This is a technique currently under development that will bring new possibilities in the diagnosis and screening of lung diseases. This processing will involve the pre-processing, analysis, and classification of image data with the main focus on the detection of pathological tissue. In addition to this image data, the processing of traditional imaging techniques (classical lung X-rays, CT data, etc.) is also planned.
The work will be carried out as part of a project to develop and test an experimental video endoscope device, which is being carried out in collaboration with the Faculty of Electrical Engineering and Computer Science at the Technical University of Ostrava (FEI VŠB) and Van-Tec Medical company.

Your task:
- Development of a new innovative image analysis for experimental data
- Participation at wet lab with experiments
- Comprehensive testing of algorithms for image analysis
- Scientific publishing

Requirements:
- Master´s in biomedical engineering or similar field
- orientation in biomedical image processing and data acquisition
- practical experience with image processing in Matlab/Python/C
- excellent written and oral presentation skills
- good communication skills in English

We offer:
- Collaboration within an active and interdisciplinary team and with international experts.
- Friendly and supportive research environment.
- Additional financial support beyond the state scholarship through supplementary stipends or
- project-related funding.
- Opportunities for professional development, including participation in international
- conferences, workshops, and specialized training.

Relevant publications:
https://doi.org/10.1038/s41467-025-66620-z
https://doi.org/10.1038/s41598-025-31432-0
https://doi.org/10.1038/s41598-025-12141-0

For more information about this topic please contact Martin Mézl (mezl@vut.cz).

Title: **Computational Methods for Optimizing Treatment of Ventricular Dysfunction**
Study program: Biomedical Technology and Bioinformatics
Supervisor: Filip Plešinger, Ph.D.

Topic description:
This PhD topic focuses on the development of advanced computational methods designed to optimize (mostly invasive) treatment strategies for patients with ventricular dysfunction. The research will address key stages of patient management, including pre-procedural screening, guidance during device implantation, and post-implantation optimization of cardiac pacing systems. Building on methodologies previously developed within the research group, the project aims to significantly accelerate the acquisition and interpretation of clinically relevant parameters, enabling faster and more precise decision-making in clinical practice.

The work will be grounded in a strong interdisciplinary foundation, combining biomedical engineering, computational modelling, software development, and clinical cardiology. Close collaboration with clinical partners (FNUSA Brno, FNKV Prague, Maastricht University, University of Zaragoza, and others) will ensure access to real-world data, continuous feedback from electrophysiologists, and opportunities to validate the proposed methods in practical settings. The expected outcome is a set of computational tools that enhance the effectiveness, personalization, and efficiency of invasive therapies for ventricular dysfunction.

Your task:

- Design new numerical markers associated with the outcome of (pacing-based) treatment of cardiac diseases
- Validate them and compare them to existing approaches
- Implement computation pipeline in Python/C#
- Publish papers based on your research and present results at international conferences

Requirements:

- Skills in data pre-processing, machine learning, and statistics
- Perfect knowledge of Python or C#
- A master's degree focused on engineering/IT
- English at a very good communication level (presenting at international conferences abroad is expected)

We offer:

- Collaboration within an active and interdisciplinary team
- Friendly and (mostly) young environment
- Wide opportunities for professional development

Relevant publications:
https://www.ahajournals.org/doi/10.1161/CIRCEP.117.005719
https://link.springer.com/article/10.1007/s10840-017-0268-0
https://cinc.org/archives/2023/pdf/CinC2023-207.pdf
https://www.cinc.org/archives/2021/pdf/CinC2021-103.pdf

For more information about this topic, please contact Filip Plesinger (fplesinger@isibrno.cz)

Title: **Integrative Methods for Genetic Variant Interpretation Using Multi-Omics Data**
Study program: Biomedical Technology and Bioinformatics
Supervisor: prof. Valentýna Provazník

Topic description:
High-throughput sequencing technologies have fundamentally transformed the diagnosis of genetically driven diseases. While whole-exome sequencing (WES) enables comprehensive variant detection, its routine clinical use is still limited by challenges in data interpretation, particularly for variants of uncertain significance (VUS). At the same time, transcriptomic profiling by RNA sequencing (RNA-Seq) provides functional evidence that can substantially improve variant prioritization and pathogenicity assessment. However, robust computational frameworks for the systematic integration of genomic and transcriptomic data are still lacking.

This PhD project aims to develop advanced bioinformatics and machine-learning-based methods for integrative analysis of genomic and transcriptomic data to improve the interpretation of genetic variants and support personalized medicine. The research will focus on methodological development enabling a smooth transition from targeted gene panel sequencing to WES, while leveraging bulk RNA-Seq data to assess the functional consequences of genetic variants. Emphasis will be placed on algorithm design, *in silico* modeling, variant annotation, and multi-omics data integration in clinically relevant cohorts.

The project will be carried out in close collaboration with CIIRC CTU, the First Faculty of Medicine of Charles University, and University Hospital Ostrava, providing access to real-world sequencing data and clinically relevant research questions.

Your task:

- Development of bioinformatics algorithms for integrated analysis of sequencing data.
- Design of computational methods for interpretation and prioritization of variants of uncertain significance using transcriptomic evidence.
- Integration of genomic and bulk RNA-Seq data, including advanced annotation.
- Application of machine learning approaches for variant classification.
- Scientific publishing in peer-reviewed international journals and at conferences.

Requirements:

- Master’s degree in bioinformatics, biomedical engineering, computer science, computational biology, or a related field.
- Strong programming skills, preferably in Python and/or R.
- Basic knowledge of genomics, transcriptomics, and next-generation sequencing data analysis.
- Ability to work independently as well as within an interdisciplinary research team.
- English communication skills and strong motivation for research in biomedical data analysis.

We offer:

- Participation in an interdisciplinary and clinically oriented research project with access to unique multi-omics datasets.
- Collaboration with leading academic and clinical partners in the Czech Republic and abroad.
- Opportunities for professional development, including international conferences, workshops, and specialized training in bioinformatics and data science.

For more information about this topic please contact Valentýna Provazník, provaznik@vut.cz.

Title: **Structure-Based Design of RAGE/DIAPH1 Interaction Inhibitors: Targeting the N ovel Intracellular Signalling Axis in Neurodegeneration**

Study program: Biomedical Technology and Bioinformatics

Supervisor: doc. Ing. Mgr. Karel Sedlář, PhD (Sudeep Roy, PhD)

Topic description:

The receptor for advanced glycation end products (RAGE) plays a pivotal role in mediating neuroinflammation associated with Alzheimer's disease and neurodegeneration through both extracellular interactions (AGE binding) and intracellular signaling pathways. Recent findings indicate that the cytoplasmic tail of RAGE directly interacts with diaphanous-related formin-1 (DIAPH1), triggering a crucial signaling cascade that results in cytoskeletal rearrangement, NF-κB activation, and the production of reactive oxygen species (ROS). While traditional RAGE antagonists, such as Azeliragon, focus on inhibiting extracellular AGE interactions, their clinical success has been limited. In contrast, the intracellular RAGE-DIAPH1 axis presents an untapped therapeutic opportunity. This project harnesses structure-based computational drug design techniques, including molecular dynamics simulations, MM-PBSA/MM-GBSA binding free energy calculations, and QSAR modeling, to thoughtfully develop novel DIAPH1-RAGE antagonists. Promising lead compounds will undergo validation through cellular assays (measuring ROS and MAPK signaling), followed by in vivo evaluations in STZ-induced Alzheimer's disease models. This innovative approach zeroes in on a well-validated yet underexplored pathway, holding significant therapeutic promise for treating neurodegenerative diseases.

Your task:

- Conduct original research leading to a dissertation or thesis.
- Become an independent researcher with advanced skills in research techniques and project management.
- Engagement with the academic community, presenting at conferences and publishing.
- Enhance knowledge and skills in leadership, mentoring, and teaching.
- Build a professional profile through networking and skill acquisition for career aspirations.

Requirements:

- Strong educational background (Master’s degree) in Bioinformatics/Cheminformatics.
- Proficient in cheminformatics tools like molecular docking, Simulations, QSAR and pharmacophores
- Demonstrates strong written and verbal communication skills for research publication and teamwork.

We offer:

- Molecular Operating Environment (MOE), Schrödinger Suite (Glide, Maestro, Desmond) for drug discovery.
- Collaborating across biology, pharmacology, and computer science.

For more information about this topic please contact Sudeep Roy, **roy@vut.cz**

Relevant publications:

https://doi.org/10.1002/pro.70240

https://doi.org/10.1038/s41598-025-01271-0

https://doi.org/10.1021/acschemneuro.5c00112

Title: **Adaptive control system for microbial cultivations**
Study program: Biomedical Technology and Bioinformatics
Supervisor: doc. Mgr. Ing. Karel Sedlář, Ph.D.

Topic description:

In the last decade, several semi-automated and robotic platforms for cultivation of microorganisms have emerged. Although they are equipped with integrated sensing and control systems to enable reproducible and scalable experiments, the cultivation parameters need to be set up manually.

This PhD project focuses on expanding the sensory capabilities of small-scale bioreactor platforms, such as Chi.Bio or Pioreactor, and integrating these measurements into an automated, adaptive control system. By synthesizing real-time data with precise hardware control, the project provides a framework to optimize bacterial cultivation conditions during data-driven fed-batch or continuous mode. Ultimately, the research aims to orchestrate these cultivations through a fully cybernetic bioinformatics approach, enabling the autonomous triggering of metabolic switches to drive the production of valuable secondary metabolites.

The project will be conducted at the Department of Biomedical Engineering, with anticipated collaboration with national (Faculty of Chemistry, BUT; Masaryk University) and international partners (HES-SO Valais Wallis, Switzerland; Polytechnic University of Valencia, Spain).

Your task:

- To develop a hardware solution for the cultivation of bacteria with a range of sensors to measure various signals.
- To develop a unique software self-adapting intelligent technique to operate the hardware of small modular bioreactors to reveal cultivation conditions for various microbes.
- To publish results in scientific journals and international conferences.

Requirements:

- Master's degree in a relevant field, e.g. microelectronics, biomedical engineering.
- Strong programming skills, preferably Python or C++.
- Familiarity with single-board computers and open hardware platforms.
- Good communication skills in English.
- A keen interest in modern biotechnology and bioinformatics.

We offer:

- Collaboration within an active and interdisciplinary team - Bioinformatics and Systems Biology Lab (BioSys_BUT).
- Project (Czech Science Foundation) co-funded position (financial support beyond the state scholarship).
- Opportunities for professional development, including participation in international conferences, workshops, and specialized training.

Relevant publications:

https://doi.org/10.1021/acs.biochem.4c00149
https://doi.org/10.1016/j.crmeth.2025.101009

For more information about this topic please contact Karel Sedlar – sedlar@vut.cz.

Title: **Modelling microbial pathways using multi-omics data**
Study program: Biomedical Technology and Bioinformatics
Supervisor: doc. Mgr. Ing. Karel Sedlář, Ph.D.

Topic description:

Modelling of various signalling pathways became an integral part of holistic approach used in understanding of diverse microogranisms, especially after the emergence of frameworks allowing integration of multi-omics data.

This PhD project focuses on expanding our knowledge how particular omics technologies, e.g. genome sequencing, transcriptome sequencing, HPLC, mass spectrometry, etc., can be integrated into static and dynamic models describing behaviour of diverse organisms and their interactions with the environment. It particularly offers opportunities to explore interactions of antimicrobial agents, e.g., fungal pigments, with microbes causing food spoilage, e.g., bacteria from the genus *Clostridium*.

The project will be conducted at the Department of Biomedical Engineering, with anticipated collaboration with national (Department of Biotechnology, UCT Prague) and international partners from academia (LMU Munich, Germany; HZAU, China) and private sector (VTT, Finland).

Your task:

- To develop a software solution for the inference of static and dynamic models of microbial interactions.
- To set rules for integrating data from diverse omics technologies.
- To publish results in scientific journals and international conferences.

Requirements:

- Master's degree in a relevant field, e.g., systems biology, bioinformatics, microbiology.
- Strong programming skills, preferably Python or R.
- Familiarity with different omics technologies.
- Good communication skills in English.
- A keen interest in modern biotechnology and bioinformatics.

We offer:

- Collaboration within an active and interdisciplinary team - Bioinformatics and Systems Biology Lab (BioSys_BUT).
- Project (Czech Science Foundation) co-funded position (financial support beyond the state scholarship).
- Opportunities for professional development, including participation in international conferences, workshops, and specialized training.

For more information about this topic please contact Karel Sedlar – sedlar@vut.cz

Relevant publications:

https://doi.org/10.1021/acs.jafc.5c08401
https://doi.org/10.1016/j.csbj.2024.01.013

Title: **Computational analysis of bioremediation capacity in microbial communities**
Study program: Biomedical Technology and Bioinformatics
Supervisor: doc. Mgr. Ing. Karel Sedlář, Ph.D.

Topic description:

Thanks to their diversity, non-model bacteria represent an inexhaustible resource for microbial biotechnology. While tools, including the computational ones, to study pure bacterial cultures are developed to at least a certain point, their counterparts for mixed cultures are underdeveloped or completely missing.

This PhD project is focused on computational methods for a comprehensive analysis of microbial consortia in order to reveal their functional capacity for industrial biotechnology, bioremediation, and production of value added chemicals, primarily bioplastics. It also offers opportunities to set up comprehensive computational pipeline to analyse diversity of a selected mixed bacterial culture, to set up a metagenome of this community, and to match its observed behaviour through analyses of other omics data revealing running biological and metabolic processes.

The project will be conducted at the Department of Biomedical Engineering, with anticipated collaboration with national (Faculty of Chemistry, BUT; Masaryk University) and international partners (HES-SO Valais Wallis, Switzerland; LMU Munich, Germany).

Your task:

- To develop a computational tool to mine and integrade information from diverse omicst techniques.
- To develop a unique software solution for short NGS as well as long TGS reads to cover all currently used sequencing technologies.
- To publish results in scientific journals and international conferences.

Requirements:

- Master's degree in a relevant field, e.g. microbiology, bioinformatics.
- Strong programming skills, preferably Python or R.
- Familiarity with sequencing techniques.
- Good communication skills in English.
- A keen interest in modern biotechnology and bioinformatics.

We offer:

- Collaboration within an active and interdisciplinary team - Bioinformatics and Systems Biology Lab (BioSys_BUT).
- Project (Czech Science Foundation) co-funded position (financial support beyond the state scholarship).
- Opportunities for professional development, including participation in international conferences, workshops, and specialized training.

Relevant publications: (optional)

https://doi.org/10.4137/EBO.S38546
https://doi.org/10.71150/jm.2411006

For more information about this topic please contact Karel Sedlar – sedlar@vut.cz

Title: **Personalized Sudden Cardiac Death Prediction**
Study program: Biomedical Technologies and Bioinformatics
Supervisor: Ing. Radovan Smíšek, Ph.D.

Topic description:
Currently, the implantable cardioverter defibrillator (ICD) represents the most widely adopted therapeutic approach for preventing sudden cardiac death (SCD). However, its implantation criteria lack specificity, it is not cost-effective, and its use can be cumbersome for patients.

This PhD project aims to enhance the accuracy of SCD risk prediction, thereby improving the clinical effectiveness of ICD therapy.

The research will focus on identifying novel predictive markers of SCD using Ultra-High-Frequency ECG (UHF-ECG) and Broad-Band ECG (BBECG), two innovative technologies capable of analyzing cardiac electrical activity at frequencies up to 1000 Hz. These advanced methods enable the detection of microstructural conduction abnormalities and sodium channel dysfunctions that remain undetectable with conventional ECG, providing new insights into the pathological substrates underlying SCD.

This PhD thesis will be conducted within the framework of the European Union’s Doctoral Networks – Marie Skłodowska-Curie Actions (MSCA), under the SEE-YOUR-HEART project. The research will involve close collaboration with partner institutions across nine countries, including universities, companies, and hospitals. The program includes a three-month research stay at the University of Zaragoza and several shorter visits to other partner sites. Funding for the PhD candidate will be provided by the project.

Your task:

- Identification of innovative parameters predictive of sudden cardiac death.
- Development of machine learning models to identify patients at risk of sudden cardiac death.
- Active participation in seminars within the MSCA grant framework.
- Scientific publishing.

Requirements:

- Master's degree in a relevant field, e.g. computer science, biomedical engineering.
- Strong programming skills, preferably Python, or MATLAB.
- Familiarity with signal processing techniques and machine learning algorithms.
- Good communication skills in English.
- Fulfillment of MSCA grant eligibility requirements. Student must not have resided or carried out their main activity (work, studies, etc.) in the country of the recruiting organisation for more than 12 months in the 36 months immediately before their recruitment date.

We offer:

- Collaboration within an active and interdisciplinary team and with international experts.
- Friendly and supportive research environment.
- Participation in an international research project.
- Opportunities for professional development, including participation in international conferences, workshops, and specialized training.

For more information about this topic please contact Radovan Smíšek – smisek@vut.cz

Title: **Real-time identification of pathogenic bacteria during nanopore sequencing**

Study program: Biomedical Technology and Bioinformatics

Supervisor: Ing. Helena Vítková, Ph.D.

Topic description:

Recent advances in third-generation sequencing technologies have enabled routine DNA sequencing of microbial samples in clinical practice. This greatly increases our ability to identify and analyze dangerous bacterial species and allows a more effective approach preventing their spread in the human population. Although the whole-genome sequencing is becoming a leading technique in clinical microbiology, its full-scale deployment is still limited by the high time and computational demands of sequencing data processing. Analysis of sequencing data still takes from tens of hours, for individual samples, to days and weeks for massive deployment of parallelized sequencing of large numbers of samples. The most time-consuming phase of this process is basecalling, i.e. decoding DNA from the "raw" signals. For nanopore sequencing, this phase starts during the sequencing run and for the high-precision models required for clinical diagnostics, it continues for days after the sequencing run is complete. The topic of this dissertation is focused on designing a new method based on machine learning techniques to identify features of bacterial resistance and virulence directly from raw signals without the need to decode the DNA sequence. The advantage of this approach is that complete genetic information of the bacteria is not needed to identify these features, only the partial information available during the first hours of the sequencing run is sufficient. Thus, identification of potential epidemiological risks can be achieved before the sequencing run is finished. The project will be primarily carried out at the Department of Biomedical Engineering, with expected collaboration with the Center for Molecular Biology and Genetics, FN Brno, and Mendel University in Brno.

Your task:

- Develop advanced computational methods for the identification of bacterial pathogens.
- Present your research at international conferences and publish in scientific journals.
- Write and submit applications for junior research funding (e.g., PhD Talent, IGA, etc.).

Requirements:

- Proficiency in programming (e.g., Python, R); experience with Linux-based environments and Bash scripting is an advantage.
- Basic experience with bioinformatics tools and software applications.
- Strong analytical thinking and ability to work independently as well as in a research team.
- English proficiency allowing effective communication, writing, and presenting.

We offer:

- Participation in GAČR and AZV projects addressing current and relevant scientific challenges.
- Being part of a progressive and growing research team (BioSys_BUT).
- Opportunity to present research findings at prestigious international conferences.
- Flexible working hours, the possibility of home office, and team-building activities.

Relevant publications:

https://doi.org/10.1093/bioinformatics/btad272
https://doi.org/10.3389/fmicb.2022.942179
https://doi.org/10.1038/s41579-020-00458-8

For more information about this topic please contact Helena Vítková – vitkovah@vut.cz.