**Title:** **Electrochemical biosensors based on graphene derivates**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Zdenka Fohlerová, PhD

**Topic description:**

Development of electrochemical biosensors based on 2D nanomaterials derived from graphene, specifically graphene acid and nitrogen-doped graphene acid. The potential applications of these graphene derivatives will be investigated for affinity and enzymatic biosensors targeting medically relevant analytes, such as cortisol and bacterial detection. The research aims to advance the development of point-of-care biosensors. This work is carried out in collaboration with the CATRIN Institute at Palacky University in Olomouc.

**Your task:**

- Construction of enzymatic/affinity biosensor
- Testing of various electrochemical methods such as CV, SWV, EIS for biosensor responses
- Optimization of measurement conditions
- Data processing and interpretation
- Result publication

**Requirements:**

- Interest in the development of biosensors for POCT application
- Motivation and creativity
- Work independently
- Good communication and English skills

**We offer:**

- A supportive and friendly work environment
- Extensive experience in the development of biosensors
- Publication in high - quality journals
- Opportunity to apply for student projects to secure independent financial support

For more information about this topic please contact **Zdenka Fohlerova – fohlerova@vut.cz**

**Relevant publications:**

Flauzino JMR, Nguyen EP, Yang Q, et al. Label-free and reagentless electrochemical genosensor based on graphene acid for meat adulteration detection. *Biosens Bioelectron*. 2022;195:113628. doi:10.1016/j.bios.2021.113628

**Title:** **Organs-on-a-chip for drug screening, environmental pollution assessment, and nanoplastics toxicity evaluation.**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Zdenka Fohlerova, PhD

**Topic description:**

The absence of predictive platforms that accurately mimic human physiology highlights the need for more physiologically relevant models. Such models enable a comprehensive and systematic assessment of the toxic properties of micro- and nanoparticles from environmental pollutants (e.g. metal nanoparticles, plastics) or facilitate the screening of newly developed drugs. Advances in microfabrication techniques have enhanced the ability of organ-on-a-chip (OOC) models to replicate vivo-like microenvironments and physiological responses, offering a promising avenue for nanotoxicological research.

**Your task:**

- Design of OOC leading to the improvement its accuracy by eliminating unspecific nanomaterial/drug adsorption while maintaining cellular function (utilization of alternative material or surface modification)
- Developing body-on-a-chip model that consists of multiple engineered tissues to analyse potential indirect effects of nanoparticles/drugs.
- The quantify the overall tissue in real-time fashion will enhance the utility of organ-on-a-chip system (integration of electronic components enabling the analysis of biological molecules and detection of cellular functional changes).

**Requirements:**

- A theoretical background in material science and organ/body on a chip technology desired
- Experience in chip design, microfluidics, and lithography is advantageous
- Motivation and creativity
- Good communication skills

**We offer:**

- A supportive and friendly work environment
- Cell lab with personal support in cell culturing and microscopy
- Publication in high - quality journals
- Opportunity to apply for student projects to secure independent financial support

For more information about this topic please contact **Zdenka Fohlerova – fohlerova@vut.cz**

**Relevant publications:**

Leung, C.M., de Haan, P., Ronaldson-Bouchard, K. *et al.* A guide to the organ-on-a-chip. *Nat Rev Methods Primers* **2**, 33 (2022). https://doi.org/10.1038/s43586-022-00118-6

**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

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

**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/

**Title:**          **Advanced methods of medical image analysis in modern CT scanners**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:**      Ing. Jiří Chmelík, PhD

**Topic description:**

Computed tomography (CT) scanners are among the most widely used modalities for diagnosing various diseases and pathologies. The development and clinical implementation of modern CT scanners now enable multi-energy X-ray imaging using multilayer detectors or even single-photon level imaging. Additionally, these advanced devices provide a range of parametric images, such as monoenergetic images and material decomposition images. This expanded imaging capability enhances the diagnostic yield of CT while significantly reducing radiation dose, a benefit of great interest to the broader medical community.

This research will focus on developing advanced image processing and analysis methods utilizing machine learning and deep learning approaches for multiparametric images acquired through multilayer CT detectors. The student will be responsible for developing, implementing, and validating preprocessing, segmentation, detection, classification, and prediction tasks, considering the unique characteristics of multiparametric images. The proposed comprehensive computer-aided diagnostic tool aims to improve diagnostic accuracy, reproducibility, and examination speed while reducing inter- and intra-expert variability and routine workload.

The research will be conducted at the Department of Biomedical Engineering, with expected collaboration from external partners, including national clinical institutions (FN Brno, VFN Prague, FNUSA/ICRC Brno) and international organizations (Philips Healthcare, Netherlands; DKFZ Heidelberg, Germany). These partnerships will facilitate the clinical evaluation of results and discussions 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 the 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.

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

**Relevant publications:**

Greffier, J., Viry, A., Robert, A., Khorsi, M., & Si-Mohamed, S. (2024). Photon-counting CT systems: A technical review of current clinical possibilities. *Diagnostic and Interventional Imaging*. https://doi.org/10.1016/j.diii.2024.09.002

**Title:** **Advanced methods for MRI image analysis to increase diagnostic yield**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Ing. Roman Jakubíček, Ph.D.

**Topic description:**

AI-assisted analysis of 3D MR data for accurate diagnosis is increasingly replacing traditional diagnostic methods, leading to an increase in imaging data and higher demands on expert analysis. This research focuses on the development and validation of deep learning-based complex tools for automated MR data processing and analysis. Key areas include registration, automatic segmentation of pathologies, and characteristic analysis for diagnosis and prognosis. Current applications focus on MR breast, perfusion brain scans and cardiac examination with an emphasis on data preprocessing, parametric map and characteristics extraction and their clinical interpretation. The student will be a valid member of a *BioImage_BUT* research team that collaborates with leading national (FNUSA Brno, FNB Brno, VFN Prague) and international medical institutions (UMC Amsterdam, KCL London, DKFZ Germany, REUH Riga).

**Your task:**

- developing complex AI-based tools for supported diagnosis
- design and programming implementation of method of image processing
- verification achieved results with clinical outcomes including statistical analysis
- publishing your results on international conferences and in impacted journals
- writing and submitting applications for junior research funding (PhD talent, …)

**Requirements:**

- programming skills (recommended Python, Matlab, …)
- knowledge and experience with 3D data processing and analysis
- enthusiasm for science and pushing the boundaries of science
- English for scientific field (writing, presenting, …)
- creative and independent thinking

**We offer:**

- membership of a growing and stable research team with a tradition at UBMI
- work on real research projects in cooperation with clinical institutions
- deepening knowledge in image processing and machine learning field while improving communication and presentation skills
- professional and active supervision during doctoral study
- flexible office hours, home-office, teambuildings

For more information about this topic please contact Roman Jakubíček – jakubicek@vut.cz

**Relevant publications:**

10.21037/qims-23-1488
10.4103/ijri.IJRI_130_20
10.1007/s00330-022-08626-5
10.1016/j.media.2018.07.008

**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, and Mendel University in Brno. 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.

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

**Relevant publications:**

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

**Title:**  **Advancing the applications of imaging methods in ophthalmology with adaptive optics imaging**

**Study program:** Biomedical Technology and Bioinformatics

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

**Topic description:**

Over the past decade, advancements in retinal imaging—particularly through adaptive optics (AO)—have transformed our ability to achieve cellular-level resolution. This breakthrough enables in-vivo analysis of previously uncharted retinal structures, driving the need for an innovative and robust image analysis pipeline.

This PhD project focuses on the detailed analysis of retinal vascularity and photoreceptors, incorporating techniques such as segmentation, pathology detection, multimodal image registration, and image quality assessment. It also offers opportunities to explore novel research areas, such as the effects of pregnancy on vascularity, potential pathological changes, and the impact of emerging drug treatments on retinal health.

The project will be conducted at the Department of Biomedical Engineering, with anticipated collaboration with international partners, including Leipzig University and the University of Halle.

**Your task:**
- Development of an innovative image analysis pipeline for adaptive optics retinal images.
- Multidimensional statistical analysis of various features measured under different conditions.
- Multimodal image analysis of correlation across the retinal imaging datasets.
- Scientific publishing.

**Requirements:**
- 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.
- Good communication skills in English.
- A keen interest in ophthalmological research.

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

**Title:** **Applications of chromatic pupillometry in vision research and neurology**

**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.
- A keen interest in ophthalmological research.

**We offer:**

- Collaboration within an active and highly interdisciplinary team.
- 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/10.3389/fpsyg.2023.1295129
https://doi.org/10.1007/s00417-016-3351-9

**Title:** Methods for analysis of low-dose CT images

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Martin Mézl, PhD

**Topic description:**

The topic focuses on the processing of imaging data from low-dose CT scans, which are used in screening programs, for example, for the early detection of lung cancer. During the course of this project, methods will be designed and implemented to enhance the utility of data obtained from these examinations. The primary aim is the detection of lung nodules and their subsequent classification based on size, shape, and other characteristics. The topic will be addressed using available datasets from international institutions, and also implementation for data from the Masaryk Memorial Cancer Institute in Brno and the General University Hospital (VFN) in Prague — where screening studies have been conducted for several years—will also be processed. The project will further expand to include clinical data from other areas, as the number of low-dose CT scans is expected to rise not only in screening but also in other medical fields.

**Your task:**
- Conduct comprehensive review of existing methods for automated analysis of low-dose CT scans (specifically in lung cancer screening)
- Design and implement of proper methods for data processing
- Validate and optimize model performance
- Work with medical professionals to validate your methods and results

**Requirements:**
- Deep interest in scientific activities in the field of medical imaging, image and signal processing, machine learning
- A sound knowledge of programming languages (eg. Matlab, Python)
- A relevant degree with appropriate engineering and/or IT knowledge, transferable to the scientific environment
- English communication skills

**We offer:**
- Our primary goal is to offer doctoral students a conducive and research-driven environment that encourages collaboration and intellectual growth
- The doctoral students complete 3-6 months of internships at partner universities abroad
- In addition to the state scholarship, the department offers doctoral students extra financial support through a supplementary stipend or salary when they participate in grant-funded projects.

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

**Relevant publications:**
- Schreuder, et al. Translational Lung Cancer Research, 2021. doi: 10.21037/tlcr-2020-lcs-06
- Jacobs, et al. Radiology: Artificial Intelligence, 2021. doi: 10.1148/ryai.2021210027
- Cellina, et al. Diagnostics, 2022. doi: 10.3390/diagnostics12112644
- Lin, et al. Radiologica Medica, 2024. doi: 10.1007/s11547-023-01730-6

**Title:** **Study of piezoelectric biomaterial-based scaffolds for bone tissue engineering**

**Study program:** Biomedical Technology and Bioinformatics
**Supervisor:** Rima Paul, PhD

**Topic description:**

Signal conduction stiffness in scaffold-based tissue engineering therapies interferes with normal signaling pathways notwithstanding their therapeutic advantages. Consequently, physiological applications necessitate smart biomaterials that produce and convey bioelectric signals akin to biological tissues. Piezoelectric biomaterials respond to moderate mechanical stress by generating electrical impulses that activate signaling pathways and facilitate tissue repair. Illness or injury can cause bone abnormalities. The conventional site-specific critical degeneration treatment is detrimental. Notwithstanding the existing advantages of tissue engineering, its application is constrained by cellular and growth factor therapies. Consequently, the repair and regeneration of hard tissue are necessary. Engineered piezoelectric tissue analogs can reinstate cellular functioning. The project focuses on developing, characterizing, and conducting the required multidimensional analyses for bone tissue engineering using scaffolds made of piezoelectric biomaterials. The project will primarily be carried out in the Department of Biomedical Engineering, however, collaboration with our partner universities and organizations is anticipated.

**Your task:**
- Preparation of piezoelectric biomaterial by chemical synthesis route
- Fabrication of the scaffolds using 3D bioprinter
- Characterization of the material using different microscopic and spectroscopic analyses
- Explore piezoelectric properties of the synthesized material
- Investigate its biocompatibility and make in-vitro and in-vivo studies for bone regeneration

**Requirements:**
- Candidates having a deep interest in the development of materials for biomedical applications
- A relevant degree with appropriate science/engineering knowledge
- 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

For more information about this topic please contact, Rima Paul – paul@vut.cz

**Relevant publications:**

1. Jacob et. al., Inflammation and Regeneration (2018) 38:2;

https://doi.org/10.1186/s41232-018-0059-8

2. Nain et. al., Biomaterials (2024)307: 122528; https://doi.org/10.1016/j.biomaterials.2024.122528

3. Polak et. al., Applied Surface Science **(2023)** 621: 156835;

https://doi.org/10.1016/j.apsusc.2023.156835

**Title:** **New approaches in computational analyses of bacterial communities for biotechnology**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Assoc. Prof. Karel Sedlář, PhD

**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 analysis of mixed cultures are underdeveloped or completely missing. This prevent us to further study biotechnological capacity of bacterial consortia to produce value added chemicals or their bioremediation potential.

The topic 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. While particular tools for taxonomic profiling based on amplicon sequencing and metagenome analysis based on shotgun sequencing exist, they are oriented to perform descriptive rather than functional analysis. This provides only limited use for biotechnology research where the emphasis is put on function. This is partly caused also by the lack of tools oriented on processing of bacterial metatranscriptomes. Finally, there is an absolute lack of tools to connect potential functional capacity inferred from a metagenome with running biological processes measured with metatranscriptomics and metabonomics approaches. The aim of the research is 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 pipeline will include specific steps to process short NGS as well as long TGS reads to cover all currently used sequencing technologies.

The project will be solved mainly at the Department of Biomedical Engineering. However, cooperation with our national (University Hospital Brno, the Faculty of Chemistry BUT, and Czech Collection of Microorganisms) and foreign partners (Ludwig-Maximilians-Universität München in Germany and HES-SO Valais-Wallis in Switzerland) is expected. PhD students will complete a six-month internship at attractive partner universities abroad. UBMI 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:**
- Analysis of various microbial consortia with bioremediation and biosynthetic potential.
- Deploy your own computation pipelines.

**Requirements:**
- Previous education in bioinformatics.
- Good communications skills and desire to work on yourself.

**We offer:**
- To join young investigator's team solving cutting-edge project.
- Possibility to travel to foreign conferences and cooperating institutions.

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

**Title:** **Bioreactor optimization for cultivation of extremophiles**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Assoc. Prof. Karel Sedlář, PhD

**Topic description:**

White biotechnology, i.e. a technology that uses living cells to produce value added chemicals, usually loses the competition with standard petrochemical production due to higher financial costs. The reason can be found in the need to protect these processes against contamination. This inefficiency could be reduced by using naturally robust organisms, so called extremophiles. However, these organisms are not so well studied, partly also because of the lack of instrumentation for extremophilic cultivation on a small scale in laboratory bioreactors.

The topic is focused on developing a small laboratory bioreactor especially suited for thermophilic cultivations. Large industrial processes usually generate waste heat that is unfavourable for mesophiles and needs to be reduced for them to proliferate. On the other hand, this environment is naturally suitable for extremophiles, particularly thermophiles. Unlike large scale processes, small scale lab cultivation does not produce waste heat, therefore, the heat has to be added for successful cultivation and research of thermophiles. Such experiments are needed to develop novel concepts as the Next-Generation Industrial Biotechnology concept that relies on the use of naturally robust organisms. Unfortunately, small bioreactors designed for thermophilic cultivations are currently missing. The aim of the research is to develop novel hardware for cultivations of bacterial thermophiles and its software control for various cultivation modes. A wide range of currently available parts will be used rather than building the reactor up from scratch. Platforms like Chi.Bio can be used as a base for it presents an open system orchestrated through Arduino and programmable in Python. Thus, it offers almost unlimited possibilities for bioreactor augmentation.

The project will be solved mainly at the Department of Biomedical Engineering. However, cooperation with our national (University Hospital Brno, the Faculty of Chemistry BUT, and Czech Collection of Microorganisms) and foreign partners (Ludwig-Maximilians-Universität München in Germany and HES-SO Valais-Wallis in Switzerland) is expected. PhD students will complete a six-month internship at attractive partner universities abroad. UBMI 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:**

- Desing your own bioreactor.
- Deploy your own computation pipelines to control the cultivation.

**Requirements:**

- Previous education in bioinformatics, microelectronics, or informatics.
- Good communications skills and desire to work on yourself.

**We offer:**

- To join young investigator's team solving cutting-edge projects.
- Possibility to travel to foreign conferences and cooperating institutions.

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

**Title:**          **Computational Characterization of Enzymes for Sustainable Design of Bioplastics**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:**      Assoc. Prof. Karel Sedlář, PhD

**Topic description:**

White biotechnology, i.e. a technology that uses living cells to produce value added chemicals, usually loses the competition with standard petrochemical production due to higher financial costs. The biological production of plastics is not an exception, mainly because of insufficient characterization of enzymes responsible for synthesis of various polymers. Although these enzymes are quite abundant in bacteria, systematic computational research based on analysis of their sequences has not been performed so far.

The topic is focused on developing a computational pipeline for analysis of sequences of polyhydroxyalkanoate (PHA) synthases with the ultimate goal of creating their comprehensive database. PHA are microbial polyesters synthesized by various prokaryotic microorganisms with great potential for plastics industry. However, their wider use is still limited by a lack of fundamental knowledge on key genes/enzymes in various prokaryotes responsible for their synthesis, preventing the use of the most suitable organisms and their potential genetic engineering necessary to establish economically feasible processes. The aim of the research is to analyse all currently available genome sequences in order to classify them into four known classes or to propose their novel classification. Additionally, particular classes will be characterized by matching sequences with physicochemical properties of polymers they synthesize. Proposed computational pipelines for analysis of close and distant orthologues will be deployed together with a database of PHA synthases.

The project will be solved mainly at the Department of Biomedical Engineering. However, cooperation with our national (University Hospital Brno, the Faculty of Chemistry BUT, and Czech Collection of Microorganisms) and foreign partners (Ludwig-Maximilians-Universität München in Germany and HES-SO Valais-Wallis in Switzerland) is expected. PhD students will complete a six-month internship at attractive partner universities abroad. UBMI 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:**
- Analysis of all currently available bacterial genomes.
- Deploy your own computation pipelines.

**Requirements:**
- Previous education in bioinformatics or biotechnology.
- Good communications skills and desire to work on yourself.

**We offer:**
- To join young investigator's team solving cutting-edge projects.
- Possibility to travel to foreign conferences and cooperating institutions.

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

**Title: RAGE for Multiple Diseases: A Repurposing Drug Approach Using Artificial Intelligence and Systems Biology**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:** Sudeep Roy, PhD

**Topic description:**

The Receptor for Advanced Glycation End Products (RAGE) is a crucial target in the treatment of several diseases, as it is associated with numerous inflammatory and degenerative conditions. This project will utilize advanced artificial intelligence (AI) and systems biology approaches to explore the potential for drug repurposing targeting RAGE. The impetus for my current research arises from various factors. RAGE is associated with various clinical conditions, including inflammatory illnesses, diabetes, Alzheimer's disease, cardiovascular diseases, and cancer. Repurposing existing pharmaceuticals can significantly reduce the duration and cost of drug research, hence accelerating the introduction of innovative therapies for patients. Recent breakthroughs in AI and systems biology facilitate the prediction of drug-target interactions and the examination of complex biological systems. Innovative therapeutic approaches are urgently required, as numerous RAGE-associated illnesses lack viable treatments.

The applicant possesses an extensive background of collaboration with various national medical institutions, such as Mendel University, FNUSA, and ICRC Brno. Furthermore, he is collaborating with international partners located in Germany, the United Kingdom, and India, each of whom possesses specialized expertise and will contribute to different phases of the project's execution.

**Your task:**

- To undertake original research by planning and carrying out a research project that adds to existing knowledge in one's subject, with the end result being a dissertation or thesis.
- To become an expert independent researcher by developing advanced research abilities in specialised techniques, data analysis, and project management.
- To communicate discoveries through engaging with the academic community, presenting at conferences, and publishing research articles in peer-reviewed publications.
- Learn more about the field and get better at what you do while also getting experience in areas like leadership, mentoring, and teaching.
- Through networking and the acquisition of appropriate skills, establish a professional profile that is in line with aspirations for a career in academia, industry, or another field.

**Requirements:**

- Strong educational background in chemistry, bioinformatics, computer science, mathematics, physics, or biochemistry is required.
- A Master's degree in a relevant field is frequently necessary, along with training or experience in cheminformatics, computational chemistry, or molecular modelling.
- Expertise in programming languages like Python.

- Proficiency in cheminformatics tools and methodologies, including molecular docking, pharmacophore modelling, machine learning, and data analysis. Expertise in computational drug design, database management, and statistical analysis for pharmaceutical applications.

- Demonstrates effective written and verbal communication abilities for publishing research findings and working in multidisciplinary teams.

**We offer:**
- **HPC Clusters:** Essential for large-scale chemical simulations, virtual screening, and machine learning applications (GPU-accelerated servers with NVIDIA GPUs).
- **Modelling and Docking Software:**
- **Molecular Operating Environment (MOE):** Provides tools for docking, pharmacophore modelling, QSAR research, and structural optimisation.
- **AutoDock** is an open-source docking software employed for virtual screening of small compounds against protein targets.
- **Glide** (docking), Maestro (visualisation), and Desmond (molecular dynamics) comprise the Schrödinger Suite, a proprietary drug discovery platform.
- **PyMOL:** Protein-ligand interaction visualisation.
- Engaged in interdisciplinary collaborations across biology, pharmacology, and computer science.

**Contact**: Sudeep Roy; roy@vut.cz; roysudeep28@gmail.com

**Relevant publications:**

- Bhogal I, Pankaj V, Provaznik V and **Roy S**. *In-Silico* investigation of cholesterol-lowering drugs to find potential inhibitors of dehydrosqualene in *staphylococcus aureus*. 3Biotech. **Corresponding author**. 2024 Jan.

- Roy S, **Roy S**, Mahata B, Pramanik J, Hennrich ML, Gavin Claude A, Teichmann AS. CLICK-chemoproteomics and molecular dynamics simulation reveals pregnenolone targets and their binding conformations in Th2 cells. **Frontiers in Immunology**. 2023 Oct.

- Chaturvedi A, Verma A, Thakur J, **Roy S**, Tripathi S, Kumar B, Khwaja S, Sachan N, Sharma A, Chanda D, Shanker K, Saikia D, Negi A. A novel synthesis of 2-arylbenzimidazoles in molecular sieves-MeOH system and their antitubercular activity. **Bioorganic & Medicinal Chemistry**. 2018 Aug.

**Title: Methodological and Empirical Strategies for LAG3-Targeted Immunotherapy in Oncology**

**Study program:** Biomedical Technology and Bioinformatics

**Supervisor:**    Sudeep Roy, PhD

**Topic description:**

Lymphocyte Activation Gene-3 (LAG3; CD223) represents a promising target for cancer immunotherapy, given its function as a negative regulator of T cells and its ability, when paired with PD1, to induce a state of exhaustion. The impetus for investigating LAG-3 as a protein target in cancer immunotherapy arises from its significant function in immune regulation, its synergistic interactions with other immune checkpoints, and its binding affinity to various ligands, including MHC Class II, FGL1, Galectin-3, and LSECtin. The advancement of LAG-3 targeted immunotherapies in oncology depends on both computational and experimental methodologies to discern, refine, and authenticate potential therapeutic candidates. Investigations into the structural dynamics of LAG-3 interactions with its ligands, including MHC class II and FGL1, have elucidated the mechanisms underlying binding processes. These investigations inform the systematic development of small molecules or antibodies that interfere with these interactions. The processes of pre-clinical validation, structural validation, and approaches centered on combination therapies facilitate the development of more effective treatments customized to the unique profiles of individual patients.

The applicant possesses an extensive background of collaboration with various national medical institutions, such as Mendel University, FNUSA, and ICRC Brno. Furthermore, he is collaborating with international partners located in Germany, the United Kingdom, and India, each of whom possesses specialized expertise and will contribute to different phases of the project's execution.

**Your task:**

- To undertake original research by planning and carrying out a research project that adds to existing knowledge in one's subject, with the end result being a dissertation or thesis.
- To become an expert independent researcher by developing advanced research abilities in specialised techniques, data analysis, and project management.
- To communicate discoveries through engaging with the academic community, presenting at conferences, and publishing research articles in peer-reviewed publications.
- Learn more about the field and get better at what you do while also getting experience in areas like leadership, mentoring, and teaching.
- Through networking and the acquisition of appropriate skills, establish a professional profile that is in line with aspirations for a career in academia, industry, or another field.

**Requirements:**

- Strong educational background in chemistry, bioinformatics, computer science, mathematics, physics, or biochemistry is required.
- A Master's degree in a relevant field is frequently necessary, along with training or experience in cheminformatics, computational chemistry, or molecular modelling.
- Expertise in programming languages like Python.
- Proficiency in cheminformatics tools and methodologies, including molecular docking, pharmacophore modelling, machine learning, and data analysis. Expertise in computational drug design, database management, and statistical analysis for pharmaceutical applications.
- Demonstrates effective written and verbal communication abilities for publishing research findings and working in multidisciplinary teams.

**We offer:**

- **HPC Clusters:** Essential for large-scale chemical simulations, virtual screening, and machine learning applications (GPU-accelerated servers with NVIDIA GPUs).
- **Modelling and Docking Software**
- **Molecular Operating Environment (MOE):** Provides tools for docking, pharmacophore modelling, QSAR research, and structural optimisation.
- **AutoDock** is an open-source docking software employed for virtual screening of small compounds against protein targets.
- **Glide** (docking), Maestro (visualisation), and Desmond (molecular dynamics) comprise the Schrödinger Suite, a proprietary drug discovery platform.
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**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. 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 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.

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

**Relevant publications:**
Can Firtina, Nika Mansouri Ghiasi, Joel Lindegger, Gagandeep Singh, Meryem Banu Cavlak, Haiyu Mao, Onur Mutlu. RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes, *Bioinformatics*, Volume 39, Issue Supplement_1, June 2023, Pages i297–i307, https://doi.org/10.1093/bioinformatics/btad272