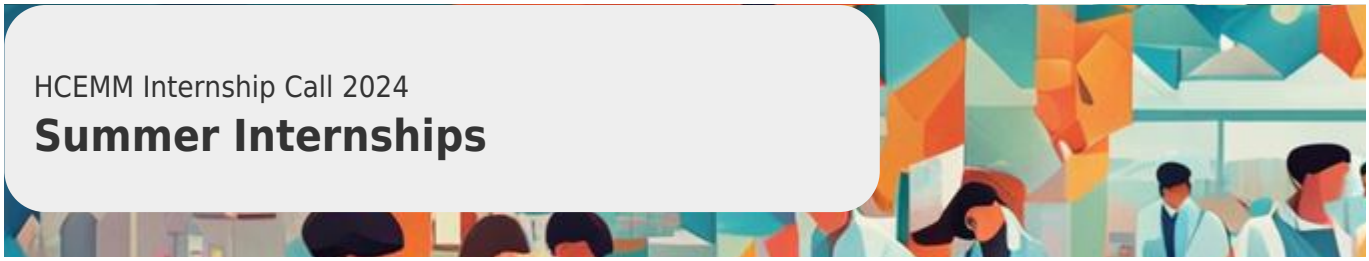

HCEMM Internship Call 2024

Summer Internships

Open Period:
1 June - 31 August 2024

Duration of internship:
4-6 weeks

Location: HCEMM Szeged

Time: 20 hours/week

Venue: Szeged, Hungary Budapesti út. 9

Deadline:
Application until: 1 May 2024

Contacts: Mónika Domoki, Rita Reinhoffer

Application is closed

Share this event

Summer Internship projects - Call 2024

The following projects are available for the HCEMM summer internship:

Project 1: Patch-seq analysis of human cortical fast-spiking interneurons

Hosting group: HCEMM Human Neuron Physiology and Therapy Core Group

Short project description

We are researching the electrical properties of cortical interneurons in human brain tissue, with a focus on the fast-spiking cells. Our study examines their role in the layer 2-3 microcircuitry through the use of whole-cell patch-clamp, immunostaining methods, and full transcriptomics analysis. As part of this research, students will learn how to conduct successful patch-clamp recordings, visualize filled cells, and harvest the nucleus of the recorded cells. This will provide them with valuable insights into the analysis of transcriptomic and electrophysiological data.

Project mentors: Dr. Karri Lamsa, Dr. Abdennour Douida and Dr. Viktor Szegedi

Project 2: OMICS-Based Approach to Unravel DNA Repair Abnormalities in Cancer

Hosting Group:HCEMM Genome Integrity and DNA Repair Core Group

Short project description

We are currently seeking a potential candidate to join our project, which focuses on understanding how DNA repair is dysregulated in cancer patients. The student will utilize transcriptomics and genomics datasets to investigate pathogenic mutations in DNA repair genes, as well as epigenetic alterations driving transcriptomic changes in these genes. The role will involve working with large next-generation sequencing (NGS) datasets and utilizing alignment tools for data analysis. Experience with R programming is considered advantageous. This opportunity offers a unique chance for the student to gain expertise in handling complex NGS data and to contribute to cutting-edge research in cancer biology and genomics. If you are passionate about

unraveling the mysteries of DNA repair dysregulation in cancer and are eager to develop your skills in bioinformatics and computational biology, we encourage you to apply.

Project mentor: Dr. Tibor Pankotai, Dr. Zoltán Páhi

Project 3: Modelling the emergence of tumour drug resistance by cancer cell plasticity

Hosting group: HCEMM Scientific Computing Advanced Core facility

Short project description

This project investigates how changes in gene expression contribute to the adaptation of tumors to drug treatments. By employing mathematical models, the study aims to elucidate the role of cancer cell plasticity leading to the emergence of drug resistance. This research holds promise for deepening our understanding of tumor evolution and informing the development of more effective therapeutic strategies against cancer. A basic knowledge of differential equations and familiarity with their numerical simulations is required.

Project mentor: Dr. Gergely Röst

Project 4: Integrating multi-omics data to identify cancer subtypes.

Hosting group: HCEMM Cancer Genomics and Epigenetics Core Group

Short project description

The goal of the project is to integrate available multi-omics datasets (gene expression, DNA mutations, protein expression) to identify signatures used to stratify cancer patient subgroups and to find cell lines with differential drug response.

Project mentor: Dr. Lőrinc Pongor

Project 5: Microbiome and Cancer Biology: Investigating Interactions and Impacts on Disease Progression.

Hosting group: HCEMM Cancer Microbiome Core Group

Short project description

Our research focuses on exploring the interaction between the human microbiome and cancer biology, investigating the ways in which microbial communities impact cancer development, progression, and response to treatment. Through the use of diverse methodologies, we endeavor to elucidate the role of microbiome in influencing physiological processes and its contribution to complex disease conditions. Our approach integrates various strategies, including DNA damage response profiling and high-resolution whole-genome sequencing (WGS) of cancer cells. Presently, we are in search of a candidate to join our project, with a specific emphasis on understanding the malfunctions of human cells coupled with the microbiome.

Project mentor: Dr. Szilvia Juhász

Project 6: Methodology Mastery: Unlocking the Science of Research

Hosting group: HCEMM Cancer Microbiome Core Group

Short project description

This project aims to provide participants with a comprehensive understanding of research methodologies employed in various academic and professional settings. The project will explore essential research methodologies, encompassing both qualitative and quantitative methods, experimental design, data collection, analysis, and interpretation. Through a combination of theoretical learning and practical exercises, interns will gain hands-on experience in conducting research, critically evaluating existing literature, and developing research proposals. In addition, the project will explore ethical considerations in research, including principles of integrity, confidentiality, and informed consent. By the end of the internship, the participants will acquire the basic skills and knowledge required for research activities in various fields.

Project mentor: Dr. Szilvia Juhász

Project 7: Computer simulated data for validation of high-throughput sequencing data

Hosting group: Circulating Nucleic Acid Biomarker Core Group

Short project description

The availability of huge amount of sequencing data at lower cost and higher speed has helped to explore new avenue of research. Highly accurate measurements are a fundamental requirement, especially for biomedical applications that affect people's life. However, the use of multiple bioinformatics tools to generate and process the raw data can inadvertently introduces biases, noise, errors that can skew the final result. Those undesired effects depend on the technique implemented to perform a specific task and are unavoidable. However, they can be known and, hence, controlled if it is known the relation between the input and the output data. As consequence, it is paramount to develop a standard method to extract a control that can measure how the digital data (suitable for computer elaboration) differ from the real biological data.

Project mentor: Alessandra Vittorini Orgeas, PhD