



2027 IRIC NEXT GENERATION COMPETITION

INTERNSHIP PROJECTS



INSTITUTE FOR RESEARCH
IN IMMUNOLOGY
AND CANCER



Université 
de Montréal

2027 IRIC NEXT GENERATION COMPETITION

INTERNSHIP PROJECTS

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Internship project #1

Characterization of biosensors based on nanoelectronic circuits

Under the supervision of Delphine Bouilly

Design and Application of Electronic Nanobiosensors Research Unit

PROJECT DESCRIPTION

In our laboratory, we work on the development of electronic biosensors for the detection of proteins and nucleic acids. These sensors are made of field-effect transistor (FET) devices based on functionalized conductive nanocarbon materials, such as atomically-thin graphene or carbon nanotubes. Nanocarbon-FETs are a promising technology for the quantitative detection of biomarkers, offering unique advantages such as simplicity, low-cost fabrication and label-free real-time electrical readout. The goal of this internship will be to optimize surface interactions between biological molecules and graphene devices, using a combination of electrical measurements of the nanosensors, high-resolution surface microscopy and/or computational approaches. These experiments will be used to optimize sensitivity metrics of these sensors for the detection of cancer biomarkers.

LAB TECHNIQUES

Microfabrication & micro/nanoelectronics
Surface chemistry
Bioconjugation chemistry
High-resolution microscopy
Computational methods

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/delphine-bouilly



Internship project #2

Role of protein glycosylation in breast cancer metastasis

Under the supervision of Marie-Anne Goyette
Tumor Heterogeneity and Metastasis Research Unit

PROJECT DESCRIPTION

Glycosylation, a posttranslational modification involving glycan attachment, is essential for the regulation of many proteins contributing to cancer progression. Furthermore, altered expression of enzymes regulating glycosylation is common in cancer. The exploration of cancer-associated glycans and related enzymes as therapeutic targets holds great potential in cancer therapy, and the field is emerging with new evolving technologies. Therefore, we study how glycosylation might affect breast cancer metastasis and therapy response.

LAB TECHNIQUES

Cell culture
Flow cytometry
Western blot
Immunofluorescence and microscopy

POUR PLUS D'INFORMATIONS

iric.ca/en/research/principal-investigators/marie-anne-goyette

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Internship project #3

Genomic Evolution of Sarcomas Under Therapeutic Pressure

Under the supervision of Carino Gurjao
Genomic and Integrative Medicine Research Unit

PROJECT DESCRIPTION

Soft-tissue sarcomas are rare and heterogeneous cancers, with several subtypes characterized by high levels of genomic instability, including extensive copy-number variations (CNVs). Treatment, which typically involves a combination of chemotherapy, radiotherapy, and surgery, imposes strong selective pressure on tumor cells and may promote the emergence of resistant clones. However, the genomic evolution of these tumors between the pre- and post-treatment stages remains poorly characterized. The objective of this internship is to characterize genomic changes associated with the treatment of soft-tissue sarcomas. The project will leverage a cohort of seven patients, each with a blood sample serving as a germline reference and paired pre- and post-treatment tumor samples analyzed by whole-exome sequencing (WES) and whole-genome sequencing (WGS). The intern will develop and apply bioinformatics approaches to identify somatic mutations and CNVs in each tumor. Pre- and post-treatment genomic profiles will then be compared to identify alterations that are acquired, lost, or enriched during treatment, with particular attention to key sarcoma driver genes such as TP53, RB1, CDKN2A/B, MDM2, and CDK4. Integration of these data will enable the investigation of tumor clonal evolution and the identification of potential genomic mechanisms underlying therapeutic resistance.

LAB TECHNIQUES

This internship will provide hands-on training in cancer genomics and bioinformatics, including WES/ WGS data analysis, somatic variant and CNV detection, high-performance computing, and genomic data analysis and visualization in R.

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/carino-gurjao

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Internship project #4

Cellular models for cancer and regenerative medicine

Under the supervision of David Knapp
Cellular Engineering Research Unit

PROJECT DESCRIPTION

Several projects are available depending on candidate interests. These include modeling concussion and therapies to treat it using human cerebral organoids, modeling leukemia development with the genome engineering of primary human hematopoietic stem cells, and computational modeling of cell differentiation and treatment response in pancreatic tumours. Students (on wet lab projects) will perform live-cell imaging, immunofluorescence, flow cytometry, CRISPR/Cas9 mediated precise genome editing, molecular cloning, stem cell culture. Students interested in computational projects will work with single-cell RNA and ATAC-seq data, classical and AI based gene regulatory network models and agent-based modeling. They will work under the day-to-day direction of a senior PhD student who is directing the project. There will also be opportunities to learn other techniques and contribute to other projects.

LAB TECHNIQUES

Cell culture
Magnetic cell separation
Nucleofection
Precise genome editing by CRISPR
Live-cell imaging
Flow cytometry
PCR
Gel electrophoresis

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/david-knapp

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Internship project #5

Computational mixology: building complex cellular responses from a minimal vocabulary of small molecules

Under the supervision of Lemieux
Functional and Structural Bioinformatics Research Unit

PROJECT DESCRIPTION

Could a small, carefully selected panel of compounds capture the functional diversity of drug-induced transcriptional responses? In this project, you will explore the hypothesis that combinations, in precise proportions, of 32 to 64 carefully selected compounds can approximate the gene expression responses of thousands of others in a cancer cell line, using a single well-characterized model such as MCF7 or PC3. Using the LINCS L1000 dataset, and a fixed nonlinear model of drug dose-response based on the Loewe additivity principle, you will evaluate how well combinations of selected compounds can mimic the effects of all others and determine how many are needed to span the biologically reachable response space.

You'll work with compact representations of gene expression data, learned using neural networks, that remove redundancy and make the analysis more tractable. Using these representations, you'll simulate how drug mixtures behave under a well-established model of additive effects (Loewe), and test how well small subsets of compounds can recreate the effects of many others. The ultimate goal of the internship is to design an experiment-ready validation panel: a set of complex mixtures predicted to induce a wide range of distinct responses, ready to be tested in a future lab experiment. Along the way, you'll generate and analyze a library of thousands of candidate molecules and learn how to evaluate which ones are likely to be the most biologically informative.

This project is ideal for students with prior programming skills, in any language, and an interest in large-scale data analysis, AI, and computational biology. Prior experience with the Julia programming language or neural networks is not needed, our lab has good expertise in both and we love to get interns started with these tools. All the codes you'll need to work with the LINCS dataset are already available in the lab, and the project involves no wet-lab work. If you're excited by the challenge of learning how cells respond to combinations of molecules, and figuring out how to reduce that complexity, this project will offer a clear, well-scoped research experience with lots of room for creativity.

LAB TECHNIQUES

Julia programming language; Large-scale data analysis

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/sebastien-lemieux
<https://www.lemieux.iric.ca/>



Internship project #6

Mechanisms of action of chemotherapeutic agents used for cancer treatment

Under the supervision of Sylvie Mader
Molecular Targeting for Breast Cancer Treatment Research Unit

PROJECT DESCRIPTION

Drugs used to treat cancer often have complex mechanisms of action and undesirable side effects. In addition, resistance mechanisms specific to cancer cells can limit their effectiveness at suppressing the proliferation and survival of these cells. CRISPR-Cas9 chemogenomic screens performed in cancer cell models can identify drug sensitivity and resistance genes by suppressing the expression of each gene in the genome in cell populations treated or untreated with these molecules and identifying guide RNAs enriched or lost in surviving cells. This approach can thus identify drug mechanisms of action and possible resistance pathways.

The intern will be responsible for validating targets identified during such screening campaigns using CRISPR-Cas9 or shRNA technologies to suppress/decrease the expression of candidate genes and experimental approaches to test the expression and function of these targets as well as the impact of their suppression on cancer cell proliferation and survival.

LAB TECHNIQUES

Recombinant DNA techniques
CRISPR-Cas9 knock-out
Cell culture
Flow cytometry
Proliferation and survival assays

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/sylvie-mader



Internship project #7

Decoding Post-Transcriptional Regulation from RNA Structural Ensembles

Under the supervision of François Major
RNA Engineering Research Unit

PROJECT DESCRIPTION

RNAs exist as ensembles of interconverting structures rather than as single conformations. This project aims to understand how these structural ensembles influence RNA recognition by RNA-binding proteins (RBPs) and microRNAs (miRNAs). The student will use bioinformatics tools developed in the laboratory to analyze RNA structural ensembles and relate their properties to experimental measurements of post-transcriptional regulation.

LAB TECHNIQUES

Bioinformatics and data analysis
RNA structure and post-transcriptional regulation
Programming (Python or Java, depending on the student's background)
Statistical analysis

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/francois-major



Internship project #8

Designing Synthetic RNAs for Multi-Target Gene Regulation

Under the supervision of François Major
RNA Engineering Research Unit

PROJECT DESCRIPTION

MicroRNAs naturally regulate multiple genes simultaneously. Inspired by this principle, this project aims to develop and evaluate synthetic RNA molecules capable of targeting multiple messenger RNAs involved in the same biological pathway. The student will participate in the computational design of these molecules, analyze their targeting specificity, and evaluate their structural properties.

LAB TECHNIQUES

RNA biology and microRNA-mediated regulation
Bioinformatics and sequence design
Gene network analysis
Programming and data science

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/francois-major

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Internship project #9

Optimization of compounds as potential therapeutic agents

Under the supervision of Anne Marinier
Drug Discovery Research Unit

PROJECT DESCRIPTION

The internship position will be with the Medicinal Chemistry Platform of the Institute for Research in Immunology and Cancer (IRIC) at the Université de Montréal (UdeM). During his/her term, the intern will be working with a team of experienced chemists, under the direct supervision of a Ph.D. and/or M.Sc.-level scientist.

The Medicinal Chemistry Platform has a long-standing research partnership with a major pharmaceutical company and is currently engaged in the hit and lead optimization phases of full drug discovery programs. As part of this effort, the student will have full access to program-related data and proprietary structures. The expectation is that the student will be doing hands-on synthesis at the bench, in order to generate designated target molecules to be submitted for biological evaluation. This will involve all aspects of synthetic organic chemistry, including preparation, isolation, purification and spectral analysis of small molecules in various lead series. The work will also necessitate conscientious record-keeping, in the form of a research notebook, and the effective oral and written communication of research results. In order to further develop an understanding of medicinal chemistry, the student will be encouraged to participate in the critical analysis of structure-activity relationships generated by themselves and others and in devising potential strategies for addressing relevant program issues.

The student will be expected to work effectively within a diverse and multi-site team of collaborators, including chemists, molecular biologists, pharmacologists, toxicologists, CADD specialists, etc. As such, the intern will be exposed to all aspects of the drug discovery process and will have a genuine opportunity to make significant contributions to a promising drug discovery program, all in the context of a unique university-industry alliance.

LAB TECHNIQUES

Synthetic organic chemistry:
Preparation, isolation, purification and spectral analysis.

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/anne-marinier

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Internship project #10

Rewiring of cancer-initiating signals to cell death and senescence pathways as a therapeutic strategy

Under the supervision of Matthew J. Smith
Cancer Signaling and Structural Biology Research Unit

PROJECT DESCRIPTION

The RAS GTPases are fundamental regulators of normal development, causative agents in an extraordinary number of human cancers, and key determinants in several developmental disorders termed RASopathies. RAS proteins are encoded by three proto-oncogenes: HRAS, KRAS and NRAS. Of these, KRAS mutations are most frequent in human cancers, present in 22% of all tumours and 61% of pancreatic, 33% of colon and 17% of lung cancers. These are amongst the most clinically refractory cancers we have today, representing the first, third and fourth leading causes of cancer death worldwide. Despite extensive effort over three decades, there remain no clinically successful drugs that target RAS itself. We thus require new approaches to target these cancer-causing proteins, and current approaches are focus on downstream 'effector' pathways through which RAS transmits its activating signals. Several current therapies target activating pathways via inhibition, but the antithesis of such an approach, rewiring or stimulating pathways that control cell death (apoptosis), should also have efficacy. This internship project will contribute to our work in understanding how RAS interacts with proteins involved in apoptosis and control of cellular senescence. The final objective will be creation of RAS mutants that 'rewire' signaling to effective self-termination, with eventual look to small molecule screens for identification of compounds targeting the characterized mutation sites. To accomplish these aims we need to first characterize how individual RAS and RAS-binding proteins interact in a biochemical and structural sense. The trainee will be involved in cloning, expression and production of these proteins. Upon successful isolation of purified components, we will undergo screens to identify crystallography conditions for eventual structure determination of the RAS-effector complexes. This project will improve our knowledge of RAS biochemistry and biology, with an end goal to better the treatment, diagnosis, and prevention of RAS-driven cancers.

LAB TECHNIQUES

Cloning
Protein Biochemistry
X-Ray Crystallography
Tissue Culture

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/matthew-smith

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Internship project #11

Integration of computational pathology and spatial transcriptomics into large-scale clinical databases

Under the supervision of Vincent Quoc-Huy Trinh
Digital Histology and Advanced Pathology Research Unit

PROJECT DESCRIPTION

Whole slide imaging is now routine in high-volume centres, and self-supervised foundation models produce tile embeddings that transfer across organs, stains and scanners. A general-purpose method for converting an archived slide into a variable that joins to a clinical table is still lacking. Targeted models remain interpretable but costly: each is engineered for a single question, depends on pathologist annotation, and rarely survives transfer to a new cohort. We propose C3Pro (cell-centred clustering and processing) is an unsupervised tokenizer that deconvolves tissue at the cell level and semanticizes a whole slide image into successive layers of quantifiable data. Cells are segmented on 40X images, a 224 by 224 pixel patch is extracted at each centroid, patches are embedded with UNiv2 and Google Path Foundation, and embeddings are reduced and clustered with KNN and Leiden at the optimal cLISI score. Neighbourhood analysis and latent Dirichlet allocation recover the cellular networks and regional topics recurring across the tissue. Cell cluster, neighbourhood class and spatial topic are converted into percentage-based tokens that attach directly to clinical records. The approach is evaluated on a fully annotated 600-patient cohort comprising 1178 whole slide images and on an unpublished 210-patient Xenium 5,000-gene dataset, with the same tokenizer extended to the molecular data so that morphology and transcription share a single vocabulary. Gradient-boosted survival models are fitted alongside penalised Cox models with stability selection, folds are split at the patient level, multiplicity is controlled by Westfall-Young permutation, and vocabulary size is set against the observed event count. Accuracy and concordance index are compared across clinical, morphological, transcriptomic and multimodal models, and robustness to stain and scanner variation is tested. The project will convert a passive image into a queryable modality reusable across subsequent studies.

LAB TECHNIQUES

Python, R, Multiplex imaging, Spatial Transcriptomics, Pathology, Vision Transformers, Pathology Foundation Models.

FOR MORE INFORMATION

iric.ca/en/research/principal-investigators/vincent-q-trinh