

1er

symposium

sur les applications de

l' **intelligence artificielle**

en médecine (IAM) de la Faculté
de médecine

4 et 5 mai / May 4 & 5, 2018

PROGRAMME/PROGRAM

Les conférences aborderont quatre grands thèmes :

- Applications en génomique médicale
- Neurosciences et santé mentale
- Aide à la décision clinique
- Imagerie médicale

The scientific program will be structured by four main themes:

- Medical Genomics applications
- Neurosciences and mental health
- Clinical decision support
- Medical imaging

Faculté de médecine

Université 
de Montréal et du monde.



HORAIRE / SCHEDULE

Vendredi 4 mai / Friday May 4, 2018

08:00	Inscriptions / Registration		
08:30	Mots de bienvenue / Welcome	Hébert, Marie-Josée Vice-rectrice / Vice-rector	
		Boisjoly, Hélène Doyenne / Dean	
		Baron, Christian Vice-doyen / Vice-dean	
09:00 09:40	Imagerie médicale – Session plénière / Medical imaging - Plenary session	Liang, JianMing Arizona State University	Computer-aided diagnosis and therapy
09:40 10:00	Imagerie médicale / Medical imaging	Besega, Carolina Stradigi AI (Montréal)	Advancements In Interpretability Is Improving the Medical Decision-Making Process
10:00 10:20	Imagerie médicale / Medical imaging	Tang, An UdeM Radiology & CRCHUM	Predictive model of colorectal cancer liver metastases response to chemotherapy
10:20 10:40	Imagerie médicale / Medical imaging	Cheriet, Farida Polytechnique Montréal & CRCHUSJ	Multimodal medical image analysis: applications and challenges
10:40 11:10	Pause-café / Coffee break		
11:10 11:30	Imagerie médicale / Medical imaging	Leblond, Frédéric Polytechnique Montréal & CRCHUM	Challenges in spectroscopic data acquisition and preparation when designing tissue identification models in pathology and surgical oncology applications
11:30 12:10	Imagerie médicale / Medical imaging	Siegel, Eliot University of Maryland, Radiology	Machine Learning and Artificial Intelligence: Hype, Myth, Reality and How It Will Revolutionize the Practice of Diagnostic Imaging
12:00 13:30	Dîner / Lunch break		
13:30 13:50	Aide à la décision clinique / Clinical decision support	Beauchesne, Louise IBM Watson Health	Application de l'intelligence artificielle en santé
13:50 14:10	Applications en génomique médicale / Medical Genomics applications	Jenna, Sarah My Intelligent Machines (MIM) & UQAM	MIMsOmic: When AI supports the industrialization of Genomics
14:10 14:30	Applications en génomique médicale / Medical Genomics applications	Broët, Philippe UdeM ESPUM & CRCHUSJ	Méthode ensembliste d'arbres de segmentation pour la prédiction en immunologie clinique
14:30 14:50	Applications en génomique médicale / Medical Genomics applications	Jacquemont, Sébastien UdeM Pediatrics & CRCHUSJ	Estimating the effect of genetic mutations on cognition. A tool for the interpretation of genetic tests in the neurodevelopmental clinic.
14:50 15:10	Applications en génomique médicale / Medical Genomics applications	Cossette, Patrick UdeM Neurosciences & CRCHUM	Towards personalized medicine in the management of epilepsy: a machine learning approach in the interpretation of large-scale genomic data
15:10 15:40	Pause-café / Coffee break		
15:40 16:00	Applications en génomique médicale / Medical Genomics applications	Hussin, Julie UdeM Medecine & MHI	Towards Deep Learning Methods in Biomedical Research
16:00 16:40	Applications en génomique médicale – Session plénière / Medical Genomics applications - Plenary session	Lavolette, François Université Laval	The potential and challenges of Artificial Intelligence in multi-omic sciences
16:40	Cocktail et session d'affiches / Cocktail and Posters session		
19:00	Souper VIP (sur invitation) / VIP Dinner (only by invitation)		

HORAIRE/SCHEDULE

Samedi 5 mai / Saturday May 5, 2018

08:30	Inscriptions / Registration		
09:00 09:40	Neurosciences et santé mentale – Session plénière Neurosciences and mental health – Plenary session	Rutledge, Robb Max Planck UCL Centre, London, UK	A neural and computational model for mood dynamics
09:40 10:00	Neurosciences et santé mentale / Neurosciences and mental health	Conrod, Patricia UdeM Psychiatry & CRCHUSJ	Computational Approaches to Early Intervention in Psychiatry
10:00 10:20	Neurosciences et santé mentale / Neurosciences and mental health	Bou Assi, Elie from Dang Nguyen lab UdeM Neurosciences & CRCHUM	Seizure Anticipation to Improve Epilepsy Management
10:20 10:40	Neurosciences et santé mentale / Neurosciences and mental health	Jerbi, Karim UdeM Psychology	Decoding brain dysfunction using MEG and EEG: The promise of data-driven approaches
10:40 11:10	Pause-café / Coffee break		
11:10 11:50	Session plénière / Plenary session	Bengio, Yoshua UdeM Informatics & MILA	AI and Deep Learning
12:00 13:30	Diner / Lunch break		
13:30 14:10	Aide à la décision clinique – Session plénière / Clinical decision support – Plenary session	Celi, Léo A Harvard University	The Challenge of Medical Artificial Intelligence
14:10 14:30	Aide à la décision clinique / Clinical decision support	Larichi, Nadia École Polytechnique	Optimisation en temps réel des rendez-vous de patients en radiothérapie
14:30 14:50	Aide à la décision clinique / Clinical decision support	De Beaumont, Louis UdeM Surgery & CRHSCM	Les contrecoups des commotions cérébrales déchiffrés UdeM Surgery and CRHSCM
14:50 15:10	Applications en génomique médicale / Medical Genomics applications	Chandelier, Florent IMAGIA	Evidens: a purpose-built ecosystem to power discovery of deep radiomics at scale
15:10 15:40	Pause-café / Coffee break		
15:40 16:00	Aide à la décision clinique / Clinical decision support	Jouvet, Philippe UdeM Pediatrics & CRCHUSJ	Challenges for the automated real time diagnosis of an acute disease: acute respiratory distress syndrome
16:00 16:20	Aide à la décision clinique / Clinical decision support	Cardinal, Heloise UdeM Medicine & CRCHUSJ	Can mathematical optimization and machine learning inform shared decision-making between transplant candidates and health providers when deciding to accept an offer for a deceased donor kidney?
16:40	Fermeture / Closing		
17:00	Cocktail		

Plusieurs sommités du domaine des applications de l'intelligence artificielle (IA) se donnent rendez-vous à l'Université de Montréal afin de présenter les applications de l'IA en médecine et discuter de l'avancement des connaissances dans ce domaine d'avenir.

Plus d'une vingtaine de conférenciers sont présents, dont les leaders des applications de l'intelligence artificielle en médecine du réseau de l'UdeM et des experts de renommée internationale, tels le Dr Yoshua Bengio, pionnier mondial, Dr Eliot Siegel qui aborde les applications dans le domaine du diagnostic radiologique, Dr Robb Rutledge qui parle de l'analyse du comportement humain, Dr Léo Celi qui nous entretient sur l'amélioration des soins cliniques et Dr François Lavolette qui entame le sujet sous l'angle de l'apprentissage par renforcement.

Thèmes abordés :

- Génomique médicale (approches de génomique, protéomique, métabolomique pour le diagnostic de maladies et le développement de nouvelles approches thérapeutiques)
- Neurosciences et santé mentale (analyse de données massives pour comprendre le comportement humain et la santé mentale)
- Aide à la décision clinique (analyse de données massives pour suivre le traitement des patients et pour optimiser les décisions cliniques)
- Imagerie médicale (analyse automatisée de larges banques d'images, p. ex. de la radiologie pour le diagnostic de cancers et de maladies rétinienne)



« Nous célébrons cette année le 175^e anniversaire des origines de notre faculté et par ce symposium, nous souhaitons mettre de l'avant toute l'expertise de l'Université de Montréal et poser un regard définitivement tourné vers l'avenir de la médecine ».

Dre Hélène Boisjoly, doyenne de la Faculté de médecine

Many experts in the field of the applications of artificial intelligence (AI) are meeting at the Université de Montréal to present the applications of AI in medicine and to discuss the advancement of knowledge in this field of the future.

More than twenty speakers, including leaders in the applications of artificial intelligence in medicine of the UdeM network and internationally renowned experts, such as Dr. Yoshua Bengio, a world-famous pioneer, Dr. Eliot Siegel, whose work focuses on applications in the field of radiological diagnosis, Dr. Robb Rutledge, who specializes in the analysis of human behaviour, Dr. Leo Celi, who talks about improving clinical care, and Dr. François Laviolette, who will present the topic of reinforcement learning.

Discussed topics:

- Medical genomics (genomics, proteomics, metabolomics approaches for the diagnosis of diseases and the development of new therapeutic approaches)
- Neuroscience and mental health (big data analysis to understand human behaviour and mental health)
- Clinical decision support (massive data analysis to monitor patient treatment and optimize clinical decisions)
- Medical imaging (automated analysis of large image databases, e.g. in radiology for the diagnosis of cancers and retinal diseases)



"This year, we are celebrating the 175th anniversary of our faculty. In this symposium, we wish to put forward all the expertise of the Université de Montréal and take a look at the future of medicine".

Dr. Hélène Boisjoly, Dean of the Faculty of Medicine

CONFÉRENCES
CONFERENCES

Intelligence artificielle

Artificial intelligence

Bengio, Yoshua

Université de Montréal

AI and Deep Learning

Deep learning has arisen around 2006 as a renewal of neural networks research allowing such models to have more layers. It is leading the charge of a renewal of AI both inside and outside academia, with billions of dollars being invested and expected fallouts in the trillions by 2030. Empirical work in a variety of applications has demonstrated that, when well trained, such deep architectures can be highly successful, remarkably breaking through previous state-of-the-art in many areas, including speech recognition, computer vision, playing games, language models, machine translation and transfer learning. In terms of social impact, the most interesting applications probably are in the medical domain, starting with medical image analysis but expanding to many other areas. The number of medical applications of deep learning is rapidly growing and the impact and success of these systems will greatly increase as we manage to bring together larger datasets, enabling precision medicine and transforming the approach to medical research. We conclude by a brief discussion of social impact and ethical concerns which are being raised by the progress in AI.

Applications en génomique médicale

Medical genomics applications

Broët, Philippe

Université de Montréal & CRCHUSJ

Méthode ensembliste d'arbres de segmentation pour la prédiction en immunologie clinique

For clinical studies with high-dimensional data, tree-based ensemble methods offer a powerful solution for variable selection and prediction taking into account the complex interrelationships between explanatory variables. However, in real situation, the presence of a fraction of non-susceptible patients in the studied population is advocating for considering new procedures tailored to this peculiar situation. This was the case for the Abirisk clinical immunology study whose main aim was to develop an immunogenicity predictive tool for predicting the likelihood of occurrence of antibodies against immune-biotherapies in the first year of treatment across various diseases (multiple sclerosis, rheumatoid arthritis, Inflammatory bowel disease) and drugs. For this study, we developed a bagging improper survival tree procedure for variable selection and prediction where the survival tree-building process relies on a splitting criterion that explicitly take into account immune tolerant and immune susceptible patients.

Applications en génomique médicale

Medical genomics applications

Chandelier, Florent

Imagia Cybernetics Inc., Montréal

Evidens: a purpose-built ecosystem to power discovery of deep radiomics at scale

Herein, we provide an overview of Evidens, our purpose-built ecosystem that provides clinician researchers with the necessary tools & infrastructure for collaborative deep radiomics discovery at scale. In radiomics, digitally encrypted medical images that hold information related to pathophysiology are transformed into mineable high-dimensional data that can be extracted and applied within clinical-decision support systems to improve diagnostic, prognostic, and predictive accuracy. Radiomics demonstrates a huge potential to deepen knowledge and broaden the horizons of imaging, in order to achieve greater precision and extraction of in vivo biological information. Using an unsupervised machine learning approach we are enabling clinician researchers to independently mine their data for preliminary evidence of clinically relevant radiomics biomarkers. However, this approach requires access to vast amount of minable data which often transcends institutional and national boundaries. To fully harness the potential of radiomics, research and clinical communities must be given the tools that allow them to embark on a shared discovery process while conforming to regulatory constraints at multiple levels. To this end, we developed ai models that structure hospital data allowing them to participate in a fully traceable federated data network for distributed collaborative research

Applications en génomique médicale

Medical genomics applications

Cossette, Patrick

Université de Montréal & CRCHUM

Towards personalized medicine in the management of epilepsy: a machine learning approach in the interpretation of large-scale genomic data

Epilepsy affects ~3% of individuals, with half of the cases starting during childhood. Although >20 antiepileptic drugs (AEDs) are available, >30% of patients with epilepsy continue to have seizures. The management of pharmaco-resistant epilepsies (PRE) in children is critical since uncontrolled seizures in the developing brain may lead to intellectual disability (ID). There is currently no way to predict which individual will or will not respond to AEDs. Idiopathic epilepsies (not caused by environmental factors) are characterized by great genetic heterogeneity. Our group has assembled the Canadian Epilepsy Network (CENet) to harness the power of genomic sequencing in the investigation of patients with epilepsy. In total, we have performed WES or WGS in >2,500 patients with epilepsy and have identified more than 20 epilepsy-associated genes. However, despite the recent progress of genomic sequencing in epilepsy, at least 65% of patients remain undiagnosed. Novel approaches are therefore needed to diagnose a greater number of patients with PRE. Clearly, the limiting factor resides in the analyses pipelines. However, we hypothesize that pathogenic genetic variants are indeed detectable in our current dataset, but have been currently overlooked because of limitation in conventional analyses paradigms. More specifically, 'missed' genetic variations could be in structural variations or in interactions between single nucleotide variation of unclear significance. In this project, we propose to develop complementary strategies in order to identify a greater number of disease-causing mutations in patients with PRE. Our main strategy will be to use and further develop the latest machine learning algorithms in combination with more conventional bioinformatic tools in order to better analyze the current dataset. More specifically, the major aims of the project will be: 1) To identify genetic variants associated with PRE; 2) To develop innovative machine learning algorithms; 3) To perform genetic and biological validation of genetic variants of unknown significance.

Applications en génomique médicale

Medical genomics applications

Hussin, Julie

Université de Montréal & ICM/MHI

Towards Deep Learning Methods in Biomedical Research

The huge drop in genomic technologies' costs over the last decade has raised hope that individualized disease risk predictions will become common practice. However, building predictive models of complex human phenotypes - useful in a medical setting - has proven extremely difficult. Here, we assess the ability of deep learning techniques to extract useful information in the context of precision medicine, where patient-specific high-dimensional data is used to make predictions on health outcomes. Machine learning problems in biomedical research pose an important challenge, "the fat data problem", when the number of input features can be orders of magnitude larger than the number of training examples. Specifically, the newly available large-scale biobank cohorts worldwide contain deep phenotyping and genotype information from participants, and biological samples to generate high quality genomics data. In this talk, we discuss novel neural network architectures developed to harness such biobank data, and propose a new parametrization, Diet Networks, which considerably reduces the number of free parameters in the fat layers of the model. On a population stratification task, we show experimentally that the proposed approach achieved very high accuracy and significantly reduces the error rate of the classifier. In the next steps, we will use multiple genomics datasets to investigate the performance of new deep learning approaches to predict phenotypes across a spectrum of health-related traits. Improving the applicability of deep learning techniques in handling such datasets and in giving interpretable results will have an important impact in medical research, more specifically in precision medicine.

Applications en génomique médicale

Medical genomics applications

Jacquemont, Sébastien

Université de Montréal & CRCHUSJ

Estimating the effect of genetic mutations on cognition. A tool for the interpretation of genetic tests in the neurodevelopmental clinic.

With the routine implementation of whole genome chromosomal microarrays and exomes in the clinic, "pathogenic" genomic variants are currently identified in 15 to 20 % of children with Neurodevelopmental disorders (NDs) such as intellectual disabilities and autism spectrum disorder. However, for most "pathogenic" mutations reported back to patients, we have little or no data to estimate their quantitative impact on neurodevelopment. It is therefore difficult for clinicians to estimate the extent to which a genetic variant may contribute to the neurodevelopmental symptoms in a patient. This is due to 2 major issues: 1) Over 75% of "pathogenic" mutations are very rare and observed only once or a few times in patients and 2) Most studies have focused on associating mutations with complex categorical diagnoses such as ASD or intellectual disabilities. The cognitive mechanisms underlying these associations remain unknown. To address this issue of undocumented CNVs and SNVs, we propose a novel strategy. Instead of conducting individual association studies for each mutation, we model their effect size on cognitive and behavioral traits relying on genetic and functional annotations. This provides an opportunity to align a landscape of extremely rare events. The deliverables are algorithms estimating the effect size of any CNV or SNV on cognitive and behavioral traits assessed along a continuum. This will allow clinicians to estimate the level of contribution of one or several rare mutations to the neurodevelopmental symptoms of their patient. It also provides insight into mechanisms by which mutations may lead to NDs.

Applications en génomique médicale

Medical genomics applications

Jenna, Sarah

My Intelligent Machines (MIM) & UQAM

MIMsOmic : When AI supports the industrialization of Genomics

Genomics has been used for the past 20 years primarily in research institutes, to understand the origin of life and diseases. The reduction of sequencing costs is currently pushing genomics to its industrial era, which consists in having OMIC data widely used in research institutes and also by BioPharma and Agritech industries to maximize their R&D and production activities. To jump into this new era, scientists need to analyze and interpret, in real time, an increasing flow of OMIC data and to transform them into actionable knowledge. Presently, handling this flow of information constitutes a multidisciplinary challenge, involving life scientists, bioinformaticians and data scientists. Together, they have to manage these data, to process them and to put them in context with a huge amount of knowledge. The present system is manually intensive and complicated and needs to be repeated whenever new data are introduced. The industrial era of genomics requires a TECHNOLOGY that will support an easy, efficient, cost-effective and robust integration of OMIC data into the R&D and production pipelines of companies and research institutes. We created this technology and called it MIMsOmic. To allow Life-scientists to transform data into actionable knowledge on their own, MIMsOmic platform is built around an information technology system that is an Artificial Intelligence, and more particularly a goal-oriented massive multiagent system. With MIMsOmic, life scientists can work with OMIC data without relying on bioinformaticians or data scientists, for a fraction of the actual cost of existing operations and 4 to 5 times faster.

Applications en génomique médicale

Medical genomics applications

Lavolette, François
Université Laval

The potential and challenges of Artificial Intelligence in multi-omic sciences

In recent years, the rise of “omic” sciences has been greatly facilitated by the decreasing cost of high-throughput measurement devices, such as DNA sequencers and mass spectrometers. Each of these disciplines, aims to study a particular aspect of cells. For instance, genomics is the study of the entire genetic material of a cell, while metabolomics is the study of all its metabolites. Much attention has been turned towards using omic data to predict phenotypes of interests, such as diseases. Artificial intelligence, specifically machine learning, has shown great performance in this context, by quickly inferring predictive patterns from volumes of data beyond the processing capabilities of a human expert. For instance, the Set Covering Machine algorithm was recently used to browse hundreds of millions of genomic variations to uncover models that accurately predict antibiotic resistance. Moving forward, the next step consists of breaking the isolation between omic disciplines and combining their respective data to perform large-scale studies that include multiple points-of-view on cells. That is, we need to shift towards a multi-omics approach that has the potential to uncover associations between cellular elements of diverse natures and phenotypes. However, some challenges must be overcome. This includes using machine learning in fat data settings, where each sample is associated with a very large number of measurements compared to the total number of samples, a setting that challenging for statistical methods. Moreover, in order to increase the current understanding of the biological mechanisms that underlie phenotypes, learning algorithms that produce interpretable models must be developed. Also, strategies to combine multi-omic measurements intelligently must be developed. Hence, while the use of artificial intelligence in multi-omic sciences is bound to increase our understanding of diseases and our ability to perform accurate diagnostics and prognostics, fundamental research must be conducted to use this technology at its full potential.

Neurosciences et santé mentale

Neurosciences and mental health

Bou Assi, Elie from Dr. Dang Nguyen lab
Polytechnique Montréal & CRCHUM

Seizure Anticipation to Improve Epilepsy Management

Epilepsy is a chronic condition characterized by recurrent seizures. Long-term drug therapy is the major form of treatment, to which ~30% of patients are refractory. Recent research has investigated the possibility of predicting epileptic seizures. Intervention before the onset of seizure manifestations could be envisioned with accurate seizure forecasting. In this presentation, we will review the general framework of reliable algorithmic seizure prediction studies, discussing each component of the whole block diagram. We will explore steps along the pathway, from signal acquisition to adequate performance evaluation that should be taken into account in the design of an efficient seizure advisory/intervention system. Performance results of our recent seizure prediction algorithm, based on long-term ambulatory canine intracranial electroencephalography recordings will be presented. The presentation ends by a perspective view of how epilepsy can benefit from recent advances in artificial intelligence at both diagnosis and therapy levels.

Neurosciences et santé mentale

Neurosciences and mental health

Conrod, Patricia

Université de Montréal & CRCHUSJ

Computational Approaches to Early Intervention in Psychiatry

Psychiatric conditions are recognized as existing along continua that range from mild psychological traits, to problematic behaviours and psychiatric symptoms, which often have their onset during adolescence and which follow a predictable trajectory. The challenge for clinicians now is how to incorporate this dimensional perspective into practice, particularly around decisions on when to intervene. Using big-data approaches to modelling risk trajectories and predicting psychopathological outcomes, Dr. Conrod and her team have developed predictive instruments and tools that are brief and that are highly sensitive to who will and who will not develop psychological/psychiatric problems, and what type of problems they will develop during adolescence. A series of studies involving machine learning and path modelling using multi-modal longitudinal data (including demographic, historical, psychological, genetic and neuroimaging data) have informed the development of brief, targeted psychological interventions that can be delivered at various points in the course of development, to reduce an individual's risk for mental health and substance use problems. Computational approaches to early intervention delivery allow for population-level improvements in mental health, and can be useful across various domains of medicine.

Neurosciences et santé mentale

Neurosciences and mental health

Jerbi, Karim

Université de Montréal

Decoding brain dysfunction using MEG and EEG: The promise of data-driven approaches

In this talk, I will briefly overview research in my lab that focuses on using machine learning as a data-mining tool in clinical neuroscience. In particular, I will discuss recent results obtained with magnetoencephalography (MEG) and electroencephalography (EEG) data recorded in individuals with Schizophrenia, Parkinsons or Autism. Current challenges and emerging trends will be discussed.

Neurosciences et santé mentale

Neurosciences and mental health

Rutledge, Robb

University College London, UK

A neural and computational model for mood dynamics

The happiness of individuals is an important metric for societies, but we know little about how the cumulative influence of daily life events are aggregated into subjective feelings. Understanding the determinants of subjective feelings is particularly important because these feelings relate closely to many symptoms of psychiatric disorders. I find that momentary happiness in a decision-making task can be explained in a computational model by the recent history of rewards and expectations. Happiness depends not on how well participants are doing but whether they are doing better than expected. The robustness of this account was evident in a large-scale smartphone-based replication (n=18,420). Changes in happiness related both to activity in the striatum measured with neuroimaging and to the neurotransmitter dopamine in pharmacology experiments. Computational psychiatry is an emerging field that seeks to understand the symptoms of psychiatric disorders in terms of aberrant computations in the underlying neural circuits. Large-scale smartphone-based data collection allows the rich behavioral and emotional data necessary to understand heterogeneity in psychiatric illness and to improve treatment assignment. I will show how computational models can be combined with smartphones to better understand psychiatric disorders including major depression and bipolar disorder.

Aide à la décision clinique

Clinical decision support

Beauchesne, Louise

IBM Watson Health

Application de l'intelligence artificielle en santé

IBM Watson Health est un joueur majeur dans le développement et la création de solutions assistées par des algorithmes en intelligence artificielle au service des cliniciens et des patients. Plusieurs applications dans les domaines de l'oncologie, de l'imagerie et de la gestion populationnelle seront présentées lors de cette allocution.

Aide à la décision clinique

Clinical decision support

Cardinal, Heloise

Université de Montréal & CRCHUM

Can mathematical optimization and machine learning inform shared decision-making between transplant candidates and health providers when deciding to accept an offer for a deceased donor kidney?

Renal transplantation improves longevity, quality of life and reduces the financial burden of care for end-stage kidney disease when compared to dialysis. There is a pressing need to increase the number of organ donors as over 3000 patients are currently registered on the deceased donor waiting list for kidney transplantation in Canada. Because of the organ shortage, 15-20% of transplanted kidneys originate from donors with risk features, such as older age or hypertension. Although these transplantations have lower long-term survival, refusing an organ offered prolongs waiting time on dialysis and increases the risk of mortality. The decision to accept or refuse a kidney offered by an organ donation organization must be shared by the transplant physician and the transplant candidate in order to achieve the most appropriate outcome for each individual patient, a process called shared decision-making. This decision can be difficult, as organs acceptable for some patients could be judged unacceptable for others. There are currently no reliable tools that provide personalized information to help patients and transplant physicians decide on whether it is in the best interest of each patient to accept an offered organ or keep on waiting for a better donor. We are currently developing a decision aide to enable transplant physicians and candidates to weigh the consequences of accepting or refusing a kidney. More specifically, we are building a tool that can address the following questions:

- 1- How long is an organ with these characteristics expected to function in someone like me?
- 2- How is that different from the duration of function provided by an average donor, or from the 'best' offer I could get?
- 3- How much longer am I expected to wait for a better offer if I refuse this one?

In addition to improving the quality of the information provided to patients for shared decision-making to occur, our tool could lead to higher acceptance rates of donors with risk features for decreased long-term survival if the disadvantage in terms of expected graft survival is small compared to the expected prolongation in waiting time required to have a better offer.

Aide à la décision clinique

Clinical decision support

Celi, Léo A.
Harvard University

The Challenge of Medical Artificial Intelligence

Medicine presents a particular problem for creating artificial intelligence (AI), because the issues and tasks involved are surprisingly subjective. Valid and useful AI requires not only reliable, unbiased, and extensive data, but also objective definitions and intentions. Assistance is most needed in day-to-day complex decision-making that requires data synthesis and integration, tasks we now approach with clinical intuition. This process is generally accepted as representing the 'art' of medicine despite being riddled with cognitive biases and often based on large information gaps. Resolving the subjectivity of medicine with the objectivity required for digitization—and the secondary creation of AI—first involves resolution of a number of questions: What do we want to do? What do we need to do? What can we do?

Aide à la décision clinique

Clinical decision support

De Beaumont, Louis

Université de Montréal & CRHSCM

Les contrecoups des commotions cérébrales déchiffrés

L'intelligence artificielle, communément surnommée 4^e révolution industrielle, bouleverse profondément les pratiques dans tous les secteurs d'activité de notre société. Pour plusieurs, son application au système de santé public s'avère la seule solution afin d'en assurer la pérennité, dans un contexte où les besoins et les coûts sont en constante croissance, en dépit d'une pénurie aiguë des ressources. L'assistance dans la prise de décision médicale et l'innovation liée au diagnostic, à la pronostication, au traitement et à la gestion des ressources hospitalières sont autant de cibles à la portée de l'intelligence artificielle. C'est ainsi que des forces vives et émergentes de notre centre de recherche de l'hôpital du Sacré-Cœur de Montréal, qui se regroupent autour du thème du neurotraumatisme, se sont alliées afin de formuler une planification stratégique de la recherche faisant appel à l'intelligence artificielle, laquelle promet non seulement d'assurer l'optimisation des ressources consenties, mais aussi et surtout, de nous positionner en tant que chef de file de la recherche innovante en trauma. Des questions à ce jour laissées sans réponse pourront désormais être répondues dans un modèle de prise en charge apprenant, c'est-à-dire qui se raffine constamment par l'ajout de données, un patient à la fois. Sa capacité à mettre en commun en une seule pensée, d'une sophistication inédite, l'ensemble des facteurs de risque et de protection des sphères bio-psycho-sociales qui lui sont fournis concordera avec l'aboutissement d'un idéal médical, celui de la médecine individualisée, lequel se positionne à l'antipode des algorithmes de traitement actuellement en vigueur et de leur uniformité. À titre d'exemple concret de l'utilité de la modélisation diagnostique par intelligence artificielle, l'équipe du Dr De Beaumont a découvert qu'il suffisait d'un seul test de neuroimagerie d'une durée de 6 minutes afin de savoir avec 90 % de précision, ce qui outrepassait largement la précision de quelconque examen clinique effectué par le meilleur des cliniciens du domaine de la neurotraumatologie, si n'importe quel cerveau lui étant soumis a subi une commotion cérébrale plusieurs décennies auparavant. En effet, des algorithmes de classification émanant de l'apprentissage automatique ont su relever que parmi les centaines de faisceaux de matière blanche du cerveau, principales voies de communication de l'organe maître, 6 d'entre eux étaient presque toujours altérés au sein des cerveaux commotionnés, alors qu'ils étaient intacts chez presque tous les cerveaux d'anciens athlètes n'ayant toutefois jamais subi de commotion cérébrale. Lorsque répliquée par des études en cours, cette importante découverte limitera à 6 minutes le temps requis pour accumuler les preuves d'une commotion cérébrale dans le cerveau, au coût de 200 \$, comparativement à un examen conventionnel multidisciplinaire requérant plus de 12 heures d'évaluation et les coûts faramineux qui s'y rattachent. Enfin, le Dr De Beaumont vous exposera sa vision des importantes ramifications qui découleront de l'application de l'intelligence artificielle à la neurotraumatologie et de leurs impacts sur l'amélioration de l'accessibilité, de la qualité et de la pérennité des soins offerts à nos patients traumatisés, la vocation primaire de l'hôpital du Sacré-Cœur de Montréal.

Aide à la décision clinique

Clinical decision support

Jouvet, Philippe

Université de Montréal & CRCHUSJ

Challenges for the automated real time diagnosis of an acute disease: acute respiratory distress syndrome

Intensive care units (ICU) are generating huge amounts of data by the numerous devices required to closely monitor the patients. This amount of data is far above the human analysis abilities. For the last 10 years, several artificial intelligence technologies have made possible the development of real-time computerized clinical decision support systems (CCDSS). Moreover, with high temporal resolution databases that record patients' monitoring data close to 1 Hz, we are now able to recreate the complete evolution of a patient's stay in ICU, which is ideal to train a CCDSS. Despite that Acute Respiratory Distress Syndrome (ARDS) is frequent (up to 10% of ICU admissions) with high mortality rate (up to 45%), ARDS diagnosis is often delayed or missed mainly because of the lack of systematic hypoxemia screening. Moreover, ARDS management guidelines are only followed in a minority of the time probably because ARDS is underdiagnosed and guidelines not perfectly known by physicians. One solution is to develop a real-time CCDSS that will support the caregivers to promptly identify ARDS and once the diagnosis is confirmed to guide them to personalize the treatments according to the most recent guidelines that take into account ARDS severity and organs dysfunction. We expect that such an approach will result in survival and quality of life improvement. In our presentation, we will discuss the challenges to develop and validate a CCDSS able to identify and classify ARDS.

Aide à la décision clinique

Clinical decision support

Larichi, Nadia

Polytechnique Montréal

Optimisation en temps réel des rendez-vous de patients en radiothérapie

La gestion efficace des centres de traitement du cancer par radiothérapie dépend principalement de l'optimisation de l'utilisation des accélérateurs linéaires. Dans ce projet, nous faisons la planification des rendez-vous patients en tenant compte de leur priorité, du temps d'attente maximal et de la durée de traitement en collaboration avec le Centre Intégré de Cancérologie de Laval. De plus, nous intégrons l'incertitude reliée à l'arrivée des patients au centre. Nous développons une méthode hybride alliant optimisation stochastique et optimisation en temps réel pour mieux répondre aux besoins de planification du centre. Nous utilisons donc l'information des arrivées futures des patients pour dresser le portrait le plus fidèle possible de l'utilisation attendue des ressources. De plus, nous utilisons des modèles prédictifs afin de mieux évaluer le temps de rendez-vous des patients (préparation, entrée en salle, traitement, etc.). Nous avons montré qu'il est possible d'offrir des plages de rendez-vous de différentes longueurs selon un ensemble de critères. Le site de la tumeur et le type de traitement en font partie.

Imagerie médicale

Medical imaging

Besega, Carolina
Stradigi AI, Montréal

Advancements In Interpretability Is Improving the Medical Decision-Making Process

The use of deep learning models have been implemented to improve different healthcare prediction tasks, in some cases achieving results similar to a human expert. In order to increase the adoption of this method in clinical decision making, it's necessary to provide clear and comprehensible explanations that detail the reasons the machine came to its conclusion. In this presentation, we will begin by reviewing different types of machine learning model interpretability. Subsequently, we will introduce a framework that can enhance the interpretability of automatically extracted machine learning features from medical images. By taking a closer look at ConvNets feature maps, we'll be able to analyze how taking different sets of feature maps into account can affect output accuracy.

Imagerie médicale

Medical imaging

Cheriet, Farida

Polytechnique Montréal

Multimodal medical image analysis: applications and challenges

This presentation will provide an overview of work done in recent years by our research group to provide reliable tools for diagnosis, treatment planning and assistance in orthopedics, cardiology and ophthalmology. Multimodal image analysis of the trunk of patients with Adolescent idiopathic scoliosis (AIS) treated at Sainte-Justine University Hospital Center, Montreal, Canada will first be presented. We will describe our method for 3D reconstruction of bone structures from radiographs then we will introduce our surface acquisition system and our methods for the representation and the geometric modeling of the trunk's external shape, to quantify its degree of asymmetry. We will show how this technology allowed us to initiate new research programs such as: a) investigating the complex relationship between the external deformities of the trunk surface and the underlying bone structures obtained from X-rays; and b) modeling and simulating the effect of orthopedic treatment on the external appearance of the patient. These research activities opened a paradigm-shift in the treatment strategy as the surgeon presently takes into account the satisfaction of the patient instead of focusing only on the correction of the spine. We will also present our contributions in the development of innovative tools for 3D visualization and reliable clinical assessment of abnormalities in a paediatric population of children with Kawasaki disease treated at Sainte-Justine University Hospital Center. Finally, we will present our ongoing work on automatic assessment and grading of ocular diseases such as diabetic retinopathy (DR), glaucoma and Age-related Macular Degeneration (AMD) from fundus images.

Imagerie médicale

Medical imaging

Leblond, Frédéric

Polytechnique Montréal & CRCHUM

Challenges in spectroscopic data acquisition and preparation when designing tissue identification models in pathology and surgical oncology applications

I will describe recent advances that led to the development and clinical translation of optical spectroscopy (diffuse reflectance, fluorescence and vibrational spectroscopy) techniques to guide surgical procedures including the resection of brain tumors and molecularly-targeted brain needle biopsies. Other work will be presented using optical spectroscopy for: i) prostate tissue characterization and prostate cancer detection during radical prostatectomy procedures, ii) diagnostic and prognostication approaches for improved prostate cancer patients stratification using Raman microspectroscopy. Emphasis will be on challenges associated with data acquisition, calibration and post-processing in relation with the design of classification models using machine learning techniques.

Imagerie médicale

Medical imaging

Liang, JianMing

Arizona State University

Computer-aided diagnosis and therapy

Behind the great success of biomedical imaging, a crisis is looming: the number of imaging examinations is growing exponentially; the workload of image interpretation is increasing dramatically; the health-care cost related to imaging is rising rapidly—we are facing a grant new challenge: image data explosion, a manifestation of big data in biomedical imaging. However, what is paramount are not the images themselves, rather the clinically relevant information contained within the images. Therefore, associated with image data explosion is a fundamental limitation in interpretation, integration, and translation of image data into actionable information and knowledge for diagnosis, therapy and surgery, a large-scale unmet clinical need across multiple specialties including radiology, cardiology, gastroenterology, etc. To address this need, we are developing comprehensive, high-performance systems that automatically and quantitatively extract clinically important imaging biomarkers from multiple image modalities to support clinical decision making in diagnosis, therapy and surgery and facilitate precision medicine. In this talk, I shall first review three of our projects in this area including (1) computer-aided diagnosis of pulmonary embolism, (2) personalized cardiovascular disease risk stratification, and (3) ensuring high-quality colonoscopy, and then outline some of the future research directions: (1) deep learning with limited labeled data, (2) simultaneous detection, segmentation and classification of lesions, and (4) weakly annotate images by understanding readily available radiological reports; and (5) directly synthesize radio-logical reports from medical images.

Imagerie médicale

Medical imaging

Siegel, Eliot

University of Maryland

Machine Learning and Artificial Intelligence:Hype, Myth, Reality and How It Will Revolutionize the Practice of Diagnostic Imaging

Major successes in the application of “Deep Learning/AI” in speech recognition, self-driving cars, translation and strategic games such as Chess, Go, and Poker have resulted in major financial investments and bold and controversial predictions by “experts” about the rapidity of general adoption in Radiology and other medical imaging specialties such as pathology, dermatology, and ophthalmology. However, tremendous challenges exist in the implementation of machine learning. The current state of the art would require thousands of algorithms and many millions of imaging studies to replace more than a tiny fraction of the tasks of a diagnostic radiology and would require hundreds of thousands or millions of hours of “expert” time to tag these. Although algorithm development times have been drastically reduced, the time and effort required for testing, verification, and validation of these algorithms in clinical practice has not decreased. Regulatory bottlenecks and medico-legal issues and constraints will need change substantially for widespread adoption within the next several years or decades. Finally, Deep Learning may actually have its greatest initial success in solving non-image related challenges such as image quality, workflow efficiency, improved communication and patient safety.

Imagerie médicale

Medical imaging

Tang, An

Université de Montréal & CRCHUM

Predictive model of colorectal cancer liver metastases response to chemotherapy

Our team was recently awarded an operating grant by the Institute for Data Valorization (IVADO). The aim of this project is to develop a model based on artificial intelligence techniques to predict response to chemotherapy in patients with colorectal cancer liver metastases. Colorectal cancer is the third most commonly diagnosed cancer in Canada and liver metastases develop in almost half of these patients. The response to chemotherapy influences survival and there is a need to predict which patients will be good responders to chemotherapy, preferably even before initiation of treatment. Monitoring of colorectal cancer liver metastases tumor currently relies on pattern recognition and interpretation of computed tomography (CT) examinations by radiologists, with poor integration of other data. In this presentation, we will discuss the rationale of our project and our approach to problem solving. We will present members of our multi-disciplinary team. We will describe how we built and curated a database of resected liver metastases from colorectal cancer stored in a 'biobank' for research purpose. This database has recently been enriched with imaging and additional types of genetic, molecular and pathological data indicative of tumor biology that may be used for training of a deep learning model. We will illustrate the study schema, the different phases of the project and the study timeline. Ultimately, we believe that deep learning applied to liver imaging may help tailor patient treatment scheme by upfront identification of metastatic colorectal cancer patients most likely to respond or resist to standard chemotherapy.

AFFICHES
POSTERS

Alamian, Golnoush

Université de Montréal

**Unlocking the power of AI in understanding psychiatric illnesses:
a resting-state magnetoencephalography study in Schizophrenia**

Biological systems tend to display complex behaviour with a power-law ($1/f$ - like) distribution. In the brain, this translates into neural activity that exhibits scale-free, temporal or spatial, properties (He, 2014). Beyond common features of rhythmic brain activity, electrophysiology studies have shown the presence of long-range temporal correlations (LRTCs) in the amplitude dynamics of alpha and beta oscillations (Nikulin et al. 2012). This is thought to speak of the integrity of the transferred information in the brain. Disease, such as psychosis, can alter the temporal properties of neuronal activity and, consequently, potentially affect information integration (Fernandez et al. 2013). In this study, sensor and source-level analyses of resting-state magnetoencephalography (MEG) of SZ patients and healthy controls were conducted to compare LRTCs across the cortex. These were found to be overall attenuated in patients. Next, machine-learning was used to objectively classify groups and evaluate the discriminative power of LRTCs. Support vector machine and a 10-fold cross-validation scheme was able to statistically significantly differentiate the two groups with up to 78% decoding accuracy. The results of this novel study, which combines classical statistical measures and machine-learning tools, illustrates the interest of using features of scale-free dynamics to enhance our understanding of schizophrenia and potentially find a new path for early clinical diagnosis.

Bonizzato, Marco

Département de Neurosciences, Université de Montréal; Groupe de Recherche sur le Système Nerveux Central; Centre de Recherche de l'Hôpital du Sacré-Cœur de Montréal

Sous la direction de Marina Martinez

Intelligent neuroprosthetics to guide brain control of locomotion after spinal cord injury

Spinal cord injuries interrupt the pathways between the cortex, which controls voluntary movements, and the spinal networks that generate locomotion. Over time the nervous system modifies its networks to restore voluntary control of movement. A long-standing and fundamental question in spinal cord injury research is how can we harness these mechanisms to foster recovery? We developed a novel neuroprosthetic system based on cortical stimulation. By monitoring muscular patterns we can precisely detect walking phases. Trains of electrical pulses are delivered in closed-loop with muscular activity to increase cortical activity and increase flexion during the leg swing. Rats with spinal cord injury who receive neuroprosthetic therapy showed an immediate alleviation of motor deficits, including reduced leg dragging. We then developed a further layer of video-based real-time control of leg stimulation which succeeded in controlling paw trajectory during treadmill walking in intact and injured rats. Moreover, when closed-loop neuroprosthetic therapy was delivered for 3 weeks, rats displayed an increase in motor recovery, which was retained 4 weeks after the therapy was terminated. In the next months we will proceed to integrate our brain stimulation strategy with state of the art spinal stimulation protocols to obtain the first combined brain-spinal stimulation neuroprosthesis. A learning agent will drive closed-loop control of locomotion to optimize neurostimulation despite the higher number of parameters for maximal improvement of locomotion after spinal cord injury.

Bouazizi, Hala

Université de Montréal

Is there a correlation between some basic clinical parameters and corneal shape?

This study proposes a K-Nearest Neighbor (KNN) regression approach, which uses as input the combination of some basic clinical parameters such as age, horizontal corneal width, emmetropia and astigmatism, to predict corneal shape in a healthy population. Therefore, the prediction is based on the distance to the combination of these simple clinical parameters. There are many models to describe corneal shape but the most common one is the Zernike polynomial approximation due to the simplicity and properties of these radial functions. Consequently, in this work, we estimated a model of the anterior corneal surface by capturing the dependency of Zernike coefficients with simple clinical data. Our approach was validated with two criteria on a large dataset of 8000 corneas captured with a corneal topographer. The first criterion compares the residual errors of the predicted shape by our algorithm with a random choice of corneas (worst case) and corneas of the same person (best case). The second measure compares elevation maps generated with our algorithm with average model obtained with the same clinical data. The results of this approach showed a correlation between clinical parameters and corneal shape, and are suggesting a novel way of exploring clinical data to improve prediction of corneal.

Ghesquiere, Pierre

Polytechnique Montréal

Classification automatique de quatre pathologies oculaires à partir de l'analyse des cartes d'épaisseur de différentes couches de la rétine et de la choroïde

L'imagerie OCT permet d'imager en profondeur les couches de la paroi du globe oculaire. L'objectif de notre étude est de classer 4 pathologies (Dégénérescence maculaire liée à l'âge (DMLA), glaucome, uvéite birdshot, hypertension oculaire) à partir de l'étude des cartes d'épaisseur de la choroïde et de la rétine. Ces cartes sont obtenues grâce à un algorithme de segmentation basé à la fois sur la théorie des graphes et sur une approche d'apprentissage machine. Pour classer les 4 pathologies, nous extrayons plusieurs caractéristiques des cartes d'épaisseur (moyenne et écart type locaux, gradients, descripteurs de Fourier). Deux classifieurs (Random Forrest et classifieur bayésien) sont entraînés puis testés sur une base de données de 294 patients. Notre algorithme est très performant pour diagnostiquer la DMLA (précision du diagnostic : 92 %) et est très prometteur pour classer les patients atteints d'uvéite birshot. Cependant, les résultats sont plus modestes pour classer les autres pathologies. Les caractéristiques les plus pertinentes sont essentiellement extraites de l'épaisseur entre l'épithélium pigmentaire et la zone ellipsoïde. En revanche, les caractéristiques extraites de l'épaisseur de la choroïde ne sont pas pertinentes pour classer ces pathologies.

Kumar, Kuldeep

École de technologie supérieure

Sous la direction de Christian Desrosiers

Analysis of genetically related subjects using multi-modal brain fingerprints

Magnetic resonance imaging (MRI) is a powerful non-invasive tool for inferring the structure and function of the human brain, as well as understanding various neurological diseases like Alzheimer's and Parkinson's. While most studies make group level inferences, researchers have established that structure and function show variability across individuals. Motivated by these, recent studies have focused on defining compact characterizations of individual brains, called brain fingerprints. So far, these studies have mostly focused on single modalities, with functional connectivity based fingerprints gaining considerable research interest. However, due to the challenges of combining multiple modalities in a single framework, defining a multi-modal brain fingerprinting remains to this day an elusive task. Yet, since each modality captures unique properties of the brain, combining multiple modalities could provide a richer, more discriminative information. We proposed a data-driven framework to generate brain fingerprints from multi-modal data (BioRxiv, Kumar et al., Multi-modal brain fingerprinting). The key idea is to represent each image as a bag of local features, and use these multi-modal features to map subjects in a low-dimension subspace called manifold. Experiments using the T1/T2-weighted MRI, diffusion MRI, and resting-state fMRI data of 945 Human Connectome Project (HCP) subjects demonstrate the benefit of combining multiple modalities, with multi-modal fingerprints more discriminative than those generated from individual modalities. The analysis also highlights the link between fingerprint similarity and genetic proximity, with monozygotic twins having more similar fingerprints than dizygotic or non-twin siblings.

Mazzaferri, Javier

Université de Montréal & Hôpital Maisonneuve-Rosemont
Sous la direction de Santiago Costantino

A machine learning approach for automated assessment of retinal vasculature in the oxygen induced retinopathy model

Preclinical studies of vascular retinal diseases rely on the assessment of developmental dystrophies in the oxygen induced retinopathy rodent model. The quantification of vessel tufts and avascular regions is typically done manually from flat mounted retinas images. Manual segmentation is time-consuming and it is hampered by user variability and bias, thus a rapid and objective method is needed. We propose a machine learning technique to segment and characterize vascular tufts, delineate the whole vasculature network, and identify and analyze avascular regions. The quantitative retinal vascular assessment (QuRVA) technique uses a simple machine learning method and morphological analysis to provide reliable computations of vascular density and pathological vascular tuft regions, devoid of user intervention within seconds. We show that manual segmentations yield to high degree of error and variability, and we designed, coded, and implemented a set of algorithms to perform this task automatically. We test and validate the results of our analysis method using the consensus of several manually curated segmentations.

Mekki Berrada, Loubna

Université de Montréal

Application of machine-learning methods for identification of markers of dementia in parkinson's disease

Objective: The prevalence of dementia in Parkinson's disease (PD) ranges from 24% to 50% and more than 75% of PD patients will develop dementia in the course of the disease. Current research aims to identify and characterise early stages of dementia in PD to better identify patients at risk. We aimed to apply machine-learning methods in PD to examine its predictive value on later dementia conversion, and evaluate their ability to discriminate PD patients who developed dementia (PDD) from healthy controls (HC). Participants: Eighty PD patients were followed for a mean of four years. At follow-up, 23 patients developed dementia and 57 were still dementia-free (DF). We pair-matched for age, sex, and education each of the PDD patients with two HC (2:1). Methods: All participants underwent at baseline polysomnographic, clinical, neurological, and neuropsychological assessments. A supervised learning approach was implemented using an alternating decision tree (ADTree) classifier. Different classifications were carried out and for each one, a data cleaning, and permutation tests were conducted to assess the significance of the decoding accuracy (DA). Results: The classifier differentiated PDD vs. DF patients (DA = 0.69 +/- 0.06; p=0.0178). Significant differences were also found for the other comparisons (PDD patients vs. HC, DA = 0.82 +/- 0.04, p=0.0001; DF patients vs. HC, DA = 0.75 +/- 0.03, p=0.0001). Conclusions: Our results suggest that machine-learning methods allow identifying PD patients at risk of dementia in a mean of 4 years before clinical dementia diagnosis. Further studies with larger sample size are needed to better assess the capacities of these methods to differentiate conversion subtypes in PD population.

Prinsen, Vanessa

École de technologie supérieure

Video analysis to automatically extract clinical information from eye features on facial images

Goal: The purpose of this study will be to determine what clinical information can be extracted from facial images of hospitalized paediatric patients, focusing particularly on features in the eye region (for example: eye contour, eye movements, gaze direction). Method: Video and image data will be acquired with patients in a paediatric intensive care unit, using RGB-D cameras capturing the upper body and head. Clinician input and biomedical monitor data will be used to label the acquired data with clinical information, such as diagnoses and the patient's state of consciousness at a given time. Facial features will be extracted from the acquired images using existing open source tools. These features will be used to train learning algorithms to detect clinically-relevant information about the patient. Conclusions: This study will propose a novel method for automatically detecting patient consciousness and other health markers using video analysis and evaluate it in a live intensive care unit. Such a system could help reduce the workload of clinicians and researchers and improve monitoring and care in paediatric ICUs.

Régnier, Philippe

Université de Montréal

Sous la direction du Dr An Tang

Deep Learning for Liver Computed Tomography: Automated Segmentation of Liver Metastases

Purpose: To evaluate the detection and segmentation performance, agreement, and efficiency of a deep learning-based fully automated method on contrast-enhanced computed tomography (CT) examinations in patients with colorectal cancer liver metastases (CLM), using manual segmentation as the reference standard. Materials and Methods: This retrospective study evaluated automated and manual segmentation of CLM. The fully automated method composed of two fully convolutional networks (FCNs) was trained and validated with 120 contrast-enhanced CT from the Liver Tumor Segmentation challenge public dataset. Detection and segmentation performance of the FCN segmentation was tested on 26 contrast-enhanced CT examinations using manual segmentation by a radiologist as reference standard. Performance of fully automated FCN segmentations was compared to FCN segmentations corrected by users. The inter-user agreement and interaction time of manual and user-corrected FCN segmentation were assessed. Analyses included performance detection, overlap and distance metrics, Cohen's kappa, intra-class correlation coefficient (ICC), Bland-Altman analyses on volume, and paired T tests. Results: For lesion size < 10 mm, 10-20 mm, and > 20 mm, the detection sensitivity of the fully automated method was 10%, 71%, and 85%; positive predictive value was 25%, 83%, and 94%; Dice similarity coefficient was 0.15, 0.53, and 0.68; maximum symmetric surface distance of 5.2, 6.3, and 10.0 mm; and an average symmetric surface distance of 2.7, 1.7, and 2.8 mm. For manual and user-corrected segmentation, the kappas were 0.42 and 0.52; ICCs were 0.97 and 0.98; inter-user agreement of -0.10 ± 0.07 mL (bias \pm 95% limits of agreement) and 0.04 ± 0.08 mL; and mean interaction time per CT of 7.7 ± 2.4 min and 4.8 ± 2.1 min ($P < 0.001$). Conclusion: A FCN-based fully automated detection and segmentation method provides higher performance for larger lesions. Agreement is similar for manual and user-corrected segmentation. However, user-corrected FCN segmentation is more time efficient.

Rehouma, Haythem

École de technologie supérieure

Détection de la détresse respiratoire chez les nouveau-nés en unité des soins intensifs pédiatriques à partir de séquences d'images de vidéo

La naissance prématurée engendre souvent des problèmes d'insuffisance respiratoire chez le nouveau-né dû à l'immaturité de ses poumons. L'analyse de l'insuffisance respiratoire par le clinicien comporte des données quantitatives (mesure de la fréquence respiratoire) et qualitatives (évaluation du volume inspiré et des signes de tirage). Afin de transformer l'analyse qualitative en donnée quantitative afin d'améliorer la reproductibilité de l'analyse entre soignants, nous développons l'analyse de la détresse respiratoire chez les naissances prématurées à l'aide de l'imagerie 3D.

Sauthier, Michaël

Université de Montréal & CRCHUSJ

How to Build a Real-Time Clinical Decision Support System on a budget

INTRODUCTION: Intensive care units (ICU) are generating huge amounts of data that are far above the human analysis abilities. High temporal resolution databases (HTRD) that record patients' monitoring data up to 500 Hz are ideal to train computerized clinical decision support systems (CCDSS) but are expensive. Our goal was to build a reliable and low-cost structure to develop multiple real-time CCDSS. **METHOD:** This study was designed as a proof of concept using a CCDSS on acute respiratory distress syndrome (ARDS) with the financial support of IVADO. We reviewed literature and web-based information on software and computers effectiveness. Inclusion criteria were: open-source SQL software able to interface with existing hospital electronic medical records (HIMSS \geq 5, <https://www.himssanalytics.org/>), multi-core CPU with a system on chip (SoC), modern networking technologies and the possibility of stacking the different units to increase redundancy and performance. Exclusion criteria: recurrent licence fee or closed technology. **RESULTS:** The resulting design includes: (1) nanocomputer Raspberry Pi 3 (50\$CAD) (Raspberry Pi Foundation); (2) open-source operating system Raspbian (based on GNU/Linux) (0\$); (3) main programming languages Python3, HTML5 and SQLite3 (0\$). We successfully run our multithreaded CCDSS in real time on ARDS using this infrastructure in a 32 beds pediatric ICU. It uses around 100Mb of RAM and less than 10% of the CPU (average use) to manage a 3-year HTRD representing around 40Gb and more than 250 million lines. **CONCLUSION:** Using open-source software and nanocomputers allowed us to run a real-time CCDSS at a very low cost. We now aim to develop more modular CCDSS that will be easily integrated to our structure.

Schramm, Catherine

Université de Montréal & CRCHUSJ

Sous la direction de Jacquemont S., Greenwood C., Labbe A.

KSPM: an R package for Kernel Semi-Parametric Model

For complex traits, polygenic in nature, most genetic variants have null or small individual effects, and although interactions are thought to exist, there is little power to identify them. Contrary to models assuming additive and linear effects of variants, kernel semi-parametric models (kspm) can capture and test nonlinear effects and interactions between many variables simultaneously and hence may help to analyse these data. Since only few programs are available and none includes a complete set of features, we propose an R package, KSPM, to fit kspm and its extensions in a unified framework. KSPM allows multiple kernels and unlimited interactions in the same model. Coefficients are estimated by maximizing a penalized log-likelihood; penalization terms and hyperparameters are estimated by minimizing leave-one-out error. KSPM includes predictions with confidence/prediction intervals, tests for the significance of each kernel, a procedure for variable selection and graphical tools for diagnostics and interpretation of covariate effects. Currently KSPM is implemented for continuous dependent variables but can be extended to binary outcomes.

Shape Radmacher, Maxime

Ecole polytechnique/Cogmaster, Paris

Sous la direction de Baudouin Forgeot d'Arc

Décoder les stratégies d'interaction sociale dans l'autisme

L'autisme est défini par l'altération des interactions sociales réciproques et des comportements répétitifs et stéréotypés. L'origine neurodéveloppementale est bien attestée, mais la nature des mécanismes neurocognitifs impliqués reste mal comprise. L'hypothèse influente d'un « déficit en théorie de l'esprit » (ToM) est que les personnes avec un trouble du spectre autistique (TSA) auraient plus de difficultés à mettre en oeuvre des raisonnements impliquant des états mentaux (Untel pense que...). Ces raisonnements sont essentiellement récursifs (Untel pense que je crois qu'il ne sait pas...). Les tâches habituellement utilisées pour tester la ToM n'intègrent pas la dimension réciproque et dynamique des interactions sociales, ce qui pourrait négliger une composante essentielle du TSA. Nous avons voulu tester la récursivité et la flexibilité des stratégies cognitives au cours de l'interaction sociale chez les TSA, à l'aide d'une tâche reposant sur un jeu virtuel consistant en blocs de 60 essais à deux options (carte de gauche/droite) et deux issues (gagné/perdu). Le jeu est présenté dans 2 mises en scène différentes : comme un jeu de hasard, comme une compétition contre un autre participant en ligne. En réalité, la carte gagnante est déterminée par : une séquence répétée (contrôle). une intelligence artificielle identifiant de façon récursive les paramètres de réponse, comme le ferait une théorie de l'esprit. Notre étude comportementale (n=48) a montré que les TSA mettaient en oeuvre : des stratégies moins récursives que les contrôles. des stratégies plus rigides d'un bloc à l'autre.

Wang, Diya

Université de Montréal & CRCHUM

Sous la direction de Diya Wang; Mingxi Wan; Guy Cloutier

Automatic Out-of-plane Respiratory Gating for Dynamic Contrast-enhanced-ultrasound-based Parametric Functional Imaging using Principal Component Analysis: in vitro and in vivo validations

Multi-parametric functional imaging (PFI) based on dynamic contrast-enhanced-ultrasound (DCEUS) is increasingly used to characterize the hemodynamic features of abdominal tumors. However, its accuracy is limited by out-of-plane severe 3D distortion induced by respiratory motion. This study developed a fully automatic respiratory gating scheme by using principal component analysis to remove distortions and disturbances in free-breathing DCEUS-based PFI, which was validated through in vitro and in vivo perfusion experiments. Taking the known and controllable in vitro perfusions in a 3D rotary distortion flow model as ground truths, the proposed scheme's accuracy was evaluated and compared with results obtained from non-negative matrix factorization and independent component analysis. Compared with those without respiratory gating, the signal-to-clutter ratio and correlation coefficients of PFI with respiratory gating improved by 3.99 ± 1.71 dB ($p < 0.01$) and 0.39 ± 0.17 ($p < 0.01$), respectively; the corresponding mean square error decreased by 1893.9 ± 763.16 ($p < 0.001$); which were significantly consistent with the ground truths without respiratory motion disturbances. The continuity and visualization of in vivo arterioles in liver and spleen were clearly enhanced, and their perfusion details were also accurately characterized by PFIs with respiratory gating. Quantitative results demonstrated that the out-of-plane serious distortion and other negative disturbances induced by the respiratory kinetics were effectively removed, and the accuracy and robustness of DCEUS-based PFI were significantly improved by the proposed scheme. The proposed automatic scheme benefits clinicians in providing accurate diagnoses and in developing appropriate therapeutic strategies for abdominal diseases.

You, Raymond

McGill University

Sous la direction de Dr Gustavo Turecki

Deep Learning Powered Clinical Decision Tool for Personalized Treatment of Depression

By using deep-learning powered clinical decision aid, personalization of treatment for depression may help improve efficacy, reduce time to remission, and save on healthcare costs. machine learning methods to achieve precision medicine. The tool can be used by healthcare professionals in mental health care to select the most effective treatment plans (pharmacological, psychotherapeutic, etc.) based on individual patient characteristics and mitigate adverse side effects. The clinical decision aid tool was trained on large datasets which include information about socio-demographic factors, symptom profiles, patient preferences, treatment response profiles, as well as genetic, metabolic, endocrine, immunological, and imaging data. This data comes primarily from high-quality clinical trials, such as those sponsored by the NIMH, and large epidemiological studies. Based on the patient profiles, the tool will return a list of possible treatments ranked in order of confidence. The deep-learning powered clinical decision aid was designed with both modularity and ease of use in mind. Our network architecture uses a feed-forward Deep Belief Network (DBN) with self-normalizing Scaled Exponential Linear Units (SELUs). So far, our machine learning model has been able to use over one hundred participant features from the Canadian Community Mental Health Survey to predict lifetime suicidal thoughts with 98% accuracy (sensitivity 98.9% and specificity 98.9%). With this promising proof of concept, we hope to use our system on therapeutics data to build a clinical decision aid."

1er

symposium
sur les applications de
l'**intelligence artificielle
en médecine** (IAM) de la Faculté
de médecine

Nous remercions chaleureusement
nos précieux partenaires financiers
pour leur contribution à la réalisation
de cet évènement.

Or

Commanditaires



Argent



Bronze

