

2023 call for proposal approved projects



ABS-Health

Agent-based simulation modeling for elderly people health care decision support

BIO-CIVIP

Biological control of insect vectors and insect pests

CGFLRVE

Context-guided future liver remnant volume estimation using artificial intelligence models

COMPOUND

Computational ultrasound imaging: from theory to applications

DD-AnDet

Data-driven anomaly detectors for time series data and big data

DL(R)

Dynamic logics (reloaded)

EPAA

Entropy and probabilistic analysis of algorithms

EUVETUS

To support patient-health care system relationship of the elderly and impaired at home

GIMMD

Graph-based analysis and understanding of image, video and multimedia data

MMLARP

Multimodal/multiview learning applied to real problems (mmlarp)

OPCOMPLEX

Optimization and learning based control for complex real systems

PiProBioM - AI

Pipeline for producing programmable biomaterials with artificial intelligence

Agent-based simulation modeling for elderly people health care decision support

Public hospitals tend to collapse due to the large number of patients who arrive in emergencies. In some cases, emergencies happen because many patients, especially older adults, do not undergo medical check-ups on time. This context is even more problematic given the growing population of older adults. Primary care systems aim to help to reduce this problem by making health services accessible. They can be used to reduce the number of emergencies at hospitals and monitor patients. However, monitoring patients and task planning in primary healthcare systems is a non-trivial problem due to the inherent complexity of the individuals involved, the unforeseen future events, and the scarcity of data.

In this project, we intend to collaborate in the development of parallel simulations combined with machine learning techniques to analyze and evaluate the effectiveness of different care management protocols for older patients in primary health centers, with the aim of monitoring and continuously assisting those patients, to prevent them from reaching emergency hospitalizations. The solution we propose to investigate will combine several techniques, such as agent-based simulation, parallel and distributed simulation protocols, optimization-based reinforcement learning techniques, and healthcare informatics.

As an outcome of the collaboration between the researchers in this proposal, we expect to publish the results in high-ranking conferences and journals in the related research fields. Furthermore, we expect to collaborate in thesis supervision of MSc and Ph.D. students and produce proof-of-concept software encapsulating the solutions developed in this project.

The proposed research team is composed of people with complementary expertise. For example, the Chilean team has experience in agent-based simulations and using protocols to characterize the agents (such as BeliefDesire-Intention (BDI), bioinspired optimization techniques, and machine learning techniques. The Argentinian team also has deep experience in parallel and distributed computing and synchronization protocols for parallel and distributed simulation. On the other hand, the French team has a long experience in modeling and clustering of medical data, in particular those resulting from sensors installed in the patient's home or on the patient himself, and also expertise on the subject of the optimal allocation of medical resources in terms of personnel and equipment (at the origin of the Equitime® company of the Horizontal Software group).

Project coordinators

Alonso Inostroza Psijas, Universidad de Valparaíso (UV), Chile
 Veronica Gil Costa, Universidad Nacional de San Luis (UNSL), Argentina
 Mauricio Marin, Universidad de Santiago de Chile (USACH), Argentina
 Mauricio Oyarzún, Universidad Arturo Prat (UNAP), Chile
 Jacques Demongeot, University Grenoble Alpes (UGA), Francia

The present project is concerned with the mathematical study of new strategies to control the spread of some insects. Two types of applications are especially addressed: on the one hand, the control of mosquitoes that may transmit established or potentially (re)emerging diseases, such as *Aedes aegypti* and *Aedes albopictus*, vectors of dengue, chikungunya and Zika; and on the other hand, the control of pests that pose significant threat to agriculture, such as *Cydia pomonella*, which feeds on fruits, *Ceratitis capitata* and *Bactrocera dorsalis*, which oviposit under the skin surface of their host fruits, or *Scaphoideus titanus*, which acts as vector in the transmission of *Flavescence dorée*, one of the most important and damaging phytoplasma diseases of the grapevine. The spread of all these plagues is likely to become a still more important issue in the future, including in the temperate zones of the world, due to global climate changes. Due to the widespread resistance to the insecticides traditionally used to control these species, and also to their impact on the biodiversity, the use of alternative control techniques is now considered. Biological control methods use beneficial insects (predators, parasitoids, competitors...) or pathogens that they transport (bacteria, fungi or viruses) to control unwanted insects, weeds, or diseases, and usually target specific species of interest, without harming other organisms. These biological control techniques aim either at reducing or eliminating insect population in a locality, or at replacing it by a harmless population. How to achieve practically successful release campaign on a large scale and for a limited cost is still a source of some central questions, which are the subject of this study. We will focus more specifically on issues related to the modelling of some sampled applications, on the spatial spreading of the treatment, on the definition of successful and cost-effective release schedule by optimal and non-optimal control approaches, and on the evaluation of the qualitative and quantitative effects of the performance hindrances (depending on the situation: unintentional release of sterile females, shortcomings of the sterilization process, disappearance of the trait rendering the population harmless, etc.).

Project coordinators

Pierre-alexandre Bliman, Inria, Francia

Claudia Pio Ferreira, Instituto de Biociências – Unesp, Brazil

Sergio Muniz Oliva Filho, Universidade de São Paulo, Instituto de Matemática e Estatística, Departamento de Matemática Aplicada, Brazil

Max Oliveira de Souza, Instituto de Matemática e Estatística, Universidade Federal Fluminense, Brazil

Lilian Sofia Sepulveda Salcedo, Department of Mathematics, Faculty of Basic Sciences, Universidad Autónoma de Occidente, Colombia

Pablo Aguirre, Universidad Técnica Federico Santa María, Chile

Héctor Ramírez, CMM Universidad de Chile, Chile

Olga Vasilieva, Universidad del Valle, Colombia

Christian Schaerer, National University of Asuncion, Paraguay

Yves Dumont, CIRAD, Francia

Alain Rapaport, MOCAS team UMR MISTEA, Francia

Nicolas Vauchelet, Université Paris 13, CNRS, Francia



Context-guided future liver remnant volume estimation using artificial intelligence models

Automatic Liver-Segmentation is an essential task in the medical context. Current AI-based models are focused on liver and tumor segmentation, that is not enough for surgical planning, especially for liver metastases. An automatic liver and tumor segmentation method can greatly relieve physicians of the heavy workload of examining CT images. However, for surgery, a more challenging task is required. In this context, it is critical to estimate accurately the remnant liver volume after resection; for instance, in patients with liver metastases.

Estimating the future liver remnant is a challenging task because the type of surgery to be performed depends on each patient's clinical setting, the center's experience, number and location of liver lesions, among others. This means that future liver remnant segmentation depends on the patient's clinical context. Therefore, the goal of this project is to design, implement and evaluate fine-grained liver segmentation guided by the context that allows us to precisely estimate remnant liver volume.

Our work is guided by five objectives: (1) evaluate SOTA liver segmentation models, including the recent published architecture HybridGNet; (2) design and evaluate models for fine-grained liver segmentation models taking into account models like SAM and HybridGNet; (3) estimate remnant liver volume using the fine-grained liver segmentation model; (4) Integrate contextual information by prompts for liver segmentation. Finally, we present results on public and private datasets. For the private case, we collaborate with a local health center, which provides us access to data.

To accomplish the proposed objectives, we have formed a multidisciplinary team, including physicians with specialization in radiology and experts on computer vision applied to medical images.

Project coordinators

Jose M. Saavedra, Universidad de los Andes (UANDES), Chile

Violeta Chang, Universidad de Santiago (USACH), Chile

Héctor Henríquez, Clínica Santa María, Chile

Enzo Ferrante, CONICET, Argentina

Caroline Petitjean, Labo LITIS, University of Rouen, Francia

Maria Vakalopoulou, CentraleSupélec, Francia

COMPOUND (Computational ultrasound imaging: from theory to applications) is a collaboration project whose main objective is to conduct research in a multidisciplinary environment, at the border between signal and image processing, applied mathematics, ultrasound instrumentation, medical applications. Ultrasound (US) imaging is the gold standard technique in numerous medical applications, such as pregnancy monitoring or cancer diseases. However, it still suffers from several limitations including low spatial resolution and signal-to-noise ratio, and huge quantity of data in 3D acquisitions. As device-related solutions based on current technologies approach their physical limitations, performance improvements can be achieved using novel post-processing techniques. Researchers with multidisciplinary skills in the fields addressed by COMPOUND are the solution to tackle these very challenging issues in US imaging. The junior involved in COMPOUND will take advantage of this unique combination of physics, mathematics, engineering and medical imaging.

Project coordinators

Paul Rodriguez, Pontificia Universidad Catolica del Peru, Perú

Henry Arguello, Universidad Industrial de Santander, Colombia

Adrian Basarab, Centre de Recherche en Acquisition et Traitement de l'Image pour la Santé (CREATIS), Francia

Jean-Yves Tournet, Institut de Recherche en Informatique de Toulouse (IRIT), Francia

An anomaly is defined as a state that deviates from a pre-established reference normal state. In data-driven approaches, supported by learning algorithms, the common practice is to create a model that learns the normal state and identifies from the model the data deviations as anomalies. As an anomaly can resemble an "outlier" or data that exit from her normal reference state, creating algorithms with high performance has been a challenge. There are several knowledge domains that address this problem by utilizing data ranging from simple statistical approaches (they mostly compare data distributions) to clustering-based methods and even employing advanced models based on deep learning.

The goal of this project is to propose models capable of identifying anomalies using diverse strategies, leveraging the expertise of each participating laboratory. Specifically, the project is focused on utilizing recent deep learning techniques such as contrastive learning, multimodal learning, domain adaptation, and label shift. The project also aims to address concept drift based on dynamical clustering. Different applications will be studied by using these approaches, including but not limited to fault detection of industrial devices, and recognition of dynamic body gestures, among others. The overarching objective of this project is to foster progress in the field and facilitate the development of innovative, multidisciplinary anomaly detection techniques. By sharing our advancements, we aim to contribute to creating new and effective anomaly detectors.

Project coordinators

Mariela Cerrada Lozada, Universidad Politécnica Salesiana (UPS), Ecuador

Waldo Hasperué, Universidad Nacional de La Plata, Argentina

Carmelo José Albanez Bastos Filho, Universidade de Pernambuco (UPE) - Escola Politécnica de Pernambuco (POLI), Brazil

Fannia Pacheco, Université de Rouen Normandie, Francia

During the project we will advance our understanding of a novel family of logics called dynamic logics. Dynamic logics are characterized by the inclusion of operators that can modify the model in which they are being evaluated. This characteristic made them especially well suited for the description of evolving scenarios like, for example, the temporal evolution of a communication network, where connections are dynamically created and eliminated, constantly changing the actual topology. A number of different dynamic logics have been investigated by members of the project, but a general perspective is still missing, and a number of important open questions remains, ranging from adequate model theoretic characterizations, to a proper understanding of how to define proof calculi for these logics. In recent years, the potential applications of dynamic logics have grown, with the recent rise of AI techniques based on knowledge represented as large graphs. The project aims to pull together the strengths of the five international research teams, to unify existing results and attempt to answer these open problems.

Project coordinators

Carlos Eduardo Areces, Facultad de Matemática, Astronomía, Física y Computación, Universidad Nacional de Córdoba, Argentina

Mario Roberto Folhadela Benevides, Instituto de Computação, Universidade Federal Fluminense, Brazil

Pablo Barceló, Institute for Mathematical and Computational Engineering, Universidad Católica de Chile y Millennium Institute for Foundational Research on Data [CH-PUC], Chile

Lutz Strassburger, Inria Saclay, Francia

Stéphane Demri, Laboratoire Méthodes Formelles (LMF), Francia

The project lies at the interface between Computer Science and Mathematics, in various fields, linked together by the notion of entropy, as a measure of complexity, as well as the presence of randomness. Our objects of study are algorithms, data structures, such as trees and graphs, words, numbers and polynomials. We are interested in their probabilistic analysis, in their random generation as well as in the study of their representation. Our fundamental motivation can be encapsulated in the following questions: What is the behaviour of low-complexity objects ? What does a random object look like ? How to build such objects ? We adopt several perspectives on these questions, from Information Theory and Analytic Combinatorics, to Symbolic Dynamical Systems. The mixing of Analysis of Algorithms and Symbolic Dynamics, complementary subjects, is a distinctive feature of this project. This interaction started during the preceding STIC-AmSud projects and yielded fruitful research directions. This interaction is strengthened in this project through the introduction of new partners in Chile. In this sense, we are interested in various problems, such as the complexity of producing digits in one digit base from those in another, sources of zero entropy and data structures on them, and by random sampling..

Project coordinators

Eda Cesaratto, Universidad Nacional de General Sarmiento, Argentina

Paulina Cecchi, Universidad de Chile, Chile

Pablo Rotondo, Université Gustave Eiffel, Francia

Eduardo Canale, Universidad de la República, Uruguay

Present epidemiology of the world population includes the increase of large shares of aged persons living in decreasing conditions of autonomy. A major challenge of our modern societies is to take care of persons with a wide variety of disabilities in a growing number of institutions or at home. Persons are also concerned by the way their lives will come to an end, which is a very important aspect of our changing global approach to life. Health systems are not prepared neither staff wise nor economically nor from the public policies point of view, to cope with large populations of aged persons with the present personnel and budgets. Our group has reflected on this global problem and has looked into possible ways technology can help to ease isolated lives, to reduce hazards and to better human relationships, among them the physician-patient relationship. Highly interdisciplinary, our group is active in cutting edge technology research and is prepared to develop adapted techniques to be implemented in coming decades to address the living conditions of populations in old age.

Project coordinators

Franco Simini, Universidad de la República, Uruguay

Carla Taramasco, Universidad Andres Bello, Chile

Celso Alberto Saibel Santos, UFES, Brazil

Néstor Darío Duque Méndez, Universidad Nacional de Colombia, Colombia

Anthony Fleury, Institut Mines Télécom, Francia

Dan Istrate, Université de Technologie de Compiègne (UTC), Francia



Graph-based analysis and understanding of image, video and multimedia data

Graphs can be seen as a way of representing relationships between elements, which can be pixels in image analysis, voxels in video analysis, people in contact networks, or even weather stations for data capture. Understanding the relationships between elements, called vertices, as well as identifying groups of elements that have similar characteristics make the use of graphs a powerful tool to solve real problems through their representation (or modeling) in graphs. Still, methods of analyzing images and videos, and even social networks, which use hierarchical representations, aim to explore the visual representation as a space-scale oriented by regions, that is, a set of representations based, for example, on graphs, with different levels of detail, in which representation at finer levels are nested to obtain coarser levels, thus producing a hierarchy of partitions. This type of data structure has been successfully applied in medical imaging, object detection and video captioning, as well as community identification in social networks. Despite the various approaches to computing partition hierarchies, developing efficient and effective methods is not an easy task, due to the semantic information needed to perform the segmentation. In fact, the state-of-the-art in graph partitioning methods are highly dependent on using good gradients, when there is differentiability between elements, to produce good results. Models based on optimal paths in trees represent an excellent direction to consider any problems produced by hierarchies, since any errors in the delineation of the borders of the regions can be corrected. These methods can eventually be transformed, without loss of quality, into hierarchical methods, incorporating new properties thanks to the use of hierarchy. In addition, with the advances of deep learning, it becomes essential to explore semantic relationships through graphs for the annotation of pseudo labels in order to train deep neural networks in addition to estimating saliences through networks to assist in the graphbased segmentation. The main objective of this study is both to advance the state of the art in partition hierarchy, considering aspects of efficiency, quality, hierarchical transformations and interactivity, as well as to explore the relationships of graphs and neural networks in image/video applications like inpainting, video captioning, for instances. Finally, we will explore methods of semi-supervised segmentation through the (semi) automatic location of markers. The results of these studies will be used to resolve various applications such as identification of cancer-susceptible cells in medical images, labeling regions in images and videos, identifying superpixels and supervoxels, inpainting, predicting solar irradiation in regions of interest, among others. We will build upon existing research and skills at LIGM, IRISA, UNICAMP, PUC Minas and UDELAR to develop collaborative work exploiting complementarity of these institutions.

Project coordinators

Silvio Jamil F. Guimarães, Pontifícia Universidade Católica de Minas Gerais - PUC Minas, Brazil

Gregory Randall, Universidad de la República, Uruguay

Simon Malinowski, CNRS, Institut de Recherche en Informatique et Systèmes Aléatoires – IRISA, Francia

Jean Cousty, Université Gustave-Eiffel, Francia

We perceive the world around us in a multimodal way. Consequently, multimodal systems have received much attention in Artificial Intelligence (AI). The challenges in such an approach go far beyond the simple fusion of modalities. In practice, it is relevant to consider: a) the modalities to be used, b) the representation of each modality, c) the way modalities interact, and d) how learning accounts for different modalities (individually or simultaneously). This proposal aims to enhance our understanding of the strategies above and develop novel multimodal and multiview predictive models, investigating alternatives for representing and combining different modalities in Pattern Recognition and Machine Learning. The project specifically focuses on researching and developing solutions using multimodal prediction models, emphasizing the architecture of these models, new strategies for generating representations for each modal (views), and new strategies for the selection/fusion of views and modalities considering possible intermodal relationships. Additionally, the project comprises the investigation of strategies to improve the training process of multiple modalities. Each stage of the working plan has the potential to result in publications in qualified international scientific journals and conferences. The project's social contribution relates to human resource formation and the potential for generating technological innovations that can positively impact society in terms of emotion analysis to help in the diagnosis of depression, medical image analysis, document image retrieval in digital libraries, and car safety (driver assistance systems). Ultimately, this proposal consolidates scientific exchange and collaboration of research teams from France, Brazil, and Chile, started in SticAmsud 2014.

Project coordinators

Alceu de Souza Britto Jr, Pontifícia Universidade Católica do Paraná (PUCPR), Brazil

Luiz Eduardo S. Oliveira, Universidade Federal do Paraná (UFPR), Brazil

Jose M. Saavedra Rondo, Universidad de los Andes (UA), Chile

George D. C. Cavalcanti, Universidade Federal de Pernambuco (UFPE), Brazil

Laurent Heutte, Laboratoire LITIS, Université de Rouen Normandie (UR), Francia

This project aims at developing theoretical and applied results in the fields of Modeling, Identification and Control for complex dynamical systems (such as infinite dimensional, nonlinear, linear parameter varying, and stochastic systems), considering classical approaches and techniques based on machine learning. In particular, we are interested in designing data-driven methodologies that require minimal modeling information. It is well known that model-based controllers heavily rely on knowledge of the controlled phenomena and, thus, their adequate performance is inherently tied to values of physical parameters, which may be valid only on specific conditions. These problems can significantly degrade the performance of the controlled system, leading to serious economic and physical consequences. Taking this context into account, the activities of researchers from Applied Mathematics and from Systems and Control Theory will be combined, seeking to contribute to the organization of the French, Brazilian and Argentinian mathematical and control theory community and to its integration within the international community.

Project coordinators

Gustavo Artur de Andrade, Department of Automation and Systems, Universidade Federal de Santa
Alejandro Hernan Gonzalez, Instituto de Desarrollo Tecnológico para la Industria Química, Santa Fe.
CONICET Universidad Nacional del Litoral (UNL), Santa Fe, Argentina

Mirko Fiacchini, GIPSA-lab CNRS, Francia

Pipeline for producing programmable biomaterials with artificial intelligence

In the present project artificial intelligence (AI) tools and synthetic biology are combined to create programmable biomaterials using extracellular matrix (ECM) components. We hypothesize that novel ECM scaffolds and fiber-like structures could be manufactured driven by machine learning algorithms and controlled biopolymerization of elastin and collagen in *Escherichia coli*. The well-known “molecular glue” based on spy-tag and spy-catcher self-assembly peptides are used to conjugate collagen and elastin biopolymers. Programmable genetic circuits are assembled to produce on-demand controlled levels of collagen and elastin as building block units that will turn on molecularly attached fiber-like structures. In our design an iteration system allows continuous biomaterial evolution. To simplify studies on biopolymer texture and densities, we propose a pipeline directed by AI as the pathway to create a set of biomaterials that could be used as scaffold in biomedical applications and as a support for mammalian cell cultures.

Synthetic biology allows programming biomaterials and machine learning provides mathematical modeling for quantitative structure. The combination of both fields provides a unique pipeline of AI-driven assembly of synthetic scaffolds. We intend to characterize such biomaterials with analytical chemistry techniques such as infrared spectroscopy (FTIR), differential scanning calorimetry (DSC), and Thermal gravimetric analysis (TGA) for structure determination, and atomic force microscopy (AFM) for determine topography biomaterials properties. Finally, the establishment of genetically programmable ECM aided by AI contributes as a high-throughput system allowing a fast-track platform for testing mechanical properties in biocompatible materials for medical applications.

Project coordinators

Pierre Sens, Sorbonne University - CNRS / Delys Team

Alberto J. Donayre, UTEC, Perú

Martín Gutiérrez, Universidad Diego Portales, Chile