STIC AmSud
2021 call for proposal approved projects

AICODA
Artificial Intelligence COllaborative Decision making Agriculture

APCoRe
An Algebrization Program for Concurrent Realizability

CLANN
Cerebellum-Like Artificial Neural Networks bioinspired on cerebellum neural architecture at multiple levels of complexity

DAWMaL
Domain adaptation for cell segmentation and classification using weakly supervised machine learning

DODAM
Declarative and Ontology-Enhanced Data Analytics and Machine Learning

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Hybrid Algorithms based on Models And Data in Industry 4.0

IAMOP
Image Analysis for the MOnitoring of marine mammals and seabirds Populations

RSA
Solving the Routing and Spectrum Assignment Problem

RSM
Robust and Stochastic Modelling of Engineering Problems

AICODA
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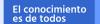
Knowledge acquisition is a key step to understand the domain in order to make proposals to obtain better results. Natural Language Processing tools in combination with Machine Learning (both from the Artificial Intelligence field) can be used to analyse the narrative descriptions captured, in order to obtain an ontology representation of the knowledge acquired. Considering the agricultural context and the use of technology, knowledge acquisition should be done with tools that suit the characteristics of the stakeholders and provide the accuracy of knowledge description needed in a technological environment. We consider three aspects to be taken into account. Collaborative Knowledge Management (CKM) is considered as a process of collective resolution of problems where it is useful to memorize the process of making collective decisions and to structure the group interactions to facilitate problem solving and sharing of ideas. Then scenarios are widely used to capture the knowledge from the stakeholders. Finally, conflict resolution is a step to be considered in knowledge acquisition. It is crucial making the group decision process interactive, iterative, collaborative and participatory. Thus, a multi-criteria decision support system arises as a tool to support this process.

Project coordinators

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APCoRe
An Algebrization Program for Concurrent Realizability

This project is part of the research program started by UdelaR researchers together with Jonas Frey dedicated to giving an algebraic presentation to Realizability and its categorical models. This program has several accomplished steps for Sequential Realizability: the remarkable feature of this program is that we found algebraic ordered structures whose elements can be seen both as truth values and as realizers. These ordered structures induce a (set-based) tripos, using a construction which is similar to the construction of a Realizability Tripos from a Partial Combinatory Algebra (PCA). On the other hand, the Concurrent Realizability developed by Beffara transposes the ideas of Classical Realizability in a context of interacting concurrent processes. Inspired by the phase sematics of Linear Logic, he replaces the Combinatory Algebra with a polarized variant of the π-calculus, endowed with a structure of abelian monoid defined by the operation of parallel composition. The pole of Classical Realizability plays the role of the orthogonal relation on Phases Spaces. The main idea we have is to develop the ideas of the algebrization program we have done for Sequential Realizability but now applied to Concurrent Realizability.

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CLANN
Cerebellum-Like Artificial Neural Networks bioinspired on cerebellum neural architecture at multiple levels of complexity
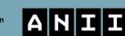
Understanding how the human brain evolved to its present complex state is a fascinating topic for neuroscience, engineering, genetics, bioinformatics, and comparative biology. At present, the enormous ability of biological neural networks to process information has produced a sizeable bio-inspiring effect on artificial signal processing. The impact of the increase in neuronal numbers, connectivity and brain regions specialization on the emergence of associative cognitive repertoires is believed to be a key to the success of animals. Conserved, divergent and convergent evolutionary mechanisms account for many anatomical, circuitry and functional solutions observed across species. We consider this concept a significant contribution to information technologies (ITs) since these evolutionary adaptations represent a natural way of optimizing information processing serving animal life. Increasing knowledge of the organization, function, development, and evolution of biological neural information processing networks would represent an opportunity to develop new AI technologies. In this grant application, we propose to join efforts and expertise in developing an interdisciplinary program to shed light on the application of cerebellum bio-inspired networks. We will reach that goal by moving through different phylogenetic, temporal and structural scales to generate several integrative platforms to explore new strategies for data analysis. We will also begin to map potential ethical issues raised by the proposed research and its potential applications.

Project coordinators

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DAWMaL
Domain adaptation for cell segmentation and classification using weakly supervised machine learning

Cell segmentation and classification share a central common problem: the lack of labelled images for training automatic methods. In this regard, adequately addressing the shortcomings of current computational approaches and enabling the clinical use of decision support tools requires training and validation of models on large-scale datasets representative of the wide variability of cases encountered every day in the clinic. At that scale, it is impossible to rely on costly and time-consuming manual annotations. Therefore, to strengthen the application of state-of-the-art segmentation and classification methods in biomedical applications, two strategies are proposed: domain adaptation and weakly supervised machine learning.

Motivated by the promising prospects of deep learning-based segmentation and classification and fuelled by the lack of fully annotated training data, in this project, we are interested in studying domain adaptation and weakly supervised methods to train neural networks for cell segmentation and classification. In this sense, we will investigate how to leverage self-training and co-training to train high-quality cell segmentation algorithms using weak labels taking advantage of domain adaptation techniques. Therefore, we will explore weak supervision (extremely one-point annotation per cell), aiming to obtain segmentation performance close to full supervision (mask annotation for each cell) but with the lowest human annotation effort. On the other hand, we will investigate strategies for domain adaptation for cell classification using weak labels. Our focus will be on applications in human sperm cells, cancer biopsies, blood parasites, and neuronal morphologies.

Project coordinators

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DODAM
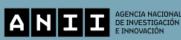# Declarative and Ontology-Enhanced Data Analytics and Machine Learning

Machine Learning (ML) and Data Analytics (DA) are showing impressive results in these days. Much can be learned from data, and new tools have emerged to analyze data and take advantage of them. However, both areas, and mainly ML, show shortcomings in relation to the use of additional knowledge that does not come as plain, flat and raw data. That additional knowledge may come in the form of knowledge bases, logic programs (most prominently, answer-set programming), formal ontologies, and knowledge graphs, in particular. This project aims at developing research and tools that help bridge this gap between traditional ML&DA methods and domain knowledge, in such a way that the former can take advantage of the domain or application semantics embodied in the latter. Among other goals, we expect to enable, improve and increase accuracy, interpretability, explainability, fairness analysis, and performance. Applications will be made in the domain of biological data analytics.

Project coordinators

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The objective of the project is to propose hybrid machine-learning approaches to address supervision, predictive maintenance, and process optimization problems occurring in Industry 4.0. This project will highlight the synergies between supervised, unsupervised and reinforcement learning approaches as well as model-based approaches. The benefits and limits of each approach will be analysed and the best of each approach will be used in the combinations (ensemble learning approaches). These combinations will be exemplified in the context of Industry 4, using each partner in-house tools representative of each category of problem.

Project coordinators

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IAMOP
Image Analysis for the MOnitoring of marine mammals and seabirds Populations

Monitoring marine mammals and colonial seabirds is an important topic in South America, especially to monitor the long-term impact of climate change. Today, the populations of seals, sea lions and Peruvian boobies are monitored, i.e. estimate the number of animals in a given population, based on manual annotation of population images from time-lapse or drone cameras. Annotating the images consists in counting manually the number of animals present on the image. Annotation is particularly time consuming and thus limits the number of images that are analysed. In the last years, computer vision techniques, especially ones based on Convolutional Neural Networks (CNN), have been applied in various domains such as medicine, security or more recently, in agriculture. In ecology, remotely sensed imagery has been used to survey large areas that are not easily accessible, from satellite imagery or with unmanned aerial vehicles. Although common CNN architecture can be used, using a CNN for a particular application needs to retrain the CNN based on a training set of manually annotated images. This project aims at designing an automatic image analysis method, based on CNN, that could automatically identify and count the number of animals present on the image. Based on the team experience in computer vision, a dedicated CNN will be designed and trained using the dataset of annotated images from the team. This project will strengthen the collaboration between the team members and allows to organize computer vision trainings and workshops in Chile and Peru.

Project coordinators

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RSA
Solving the Routing and Spectrum Assignment Problem

One of the most promising solutions to deal with huge data traffic demands in large communication networks is given by flexible optical networking, in particular the flexible grid (flexgrid) technology specified in the ITU-T standard G.694.1. In this specification, the frequency spectrum of an optical fiber link is divided into narrow frequency slots. Any sequence of consecutive slots can be used as a simple channel, and such a channel can be switched in the network nodes to create a lightpath. In this kind of networks, the problem of establishing lightpaths for a set of end-to-end demands that compete for spectrum resources is called the Routing and Spectrum Assignment problem (RSA). Due to its relevance, this problem has been intensively studied in the last years. It has been shown to be NP-hard, so nontrivial computational techniques are to be applied in order to tackle the solution of practical instances. In this project we propose to further the exploration of such an issue, by applying integer linear programming (ILP) techniques to RSA. We plan to study different ILP formulations of RSA in order to understand their properties, strengths, and weaknesses, taking combinatorial properties and symmetry aspects into account. Based on these explorations, we propose to develop ILP-based computational procedures for RSA, with the final objective of solving to optimality or near-optimality real-world instances of RSA.

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RSM
Robust and Stochastic Modelling of Engineering Problems

Many engineering applications can be modelled using optimization formulations. Nevertheless, the deterministic response of these models can be unsatisfactory for real world applications, principally because they don't take into account the stochastic nature of the data involved. Recently, several model formulations have appeared to deal with the uncertainty presented in the data. In many cases these models can be written as convex optimization problems with some particular structure (therefore can be numerically solved efficiently), known as conic programming. This structure has been shown to be useful to obtain robust formulations of deterministic models, providing results less sensible to random perturbations of the data. Therefore, conic structure suits perfectly to be applied in the realm of Data Science and in Structural Optimization. Additionally, there are several engineering applications models that must deal with uncertainty, some of them have appeared in the modelling of consumer behavior related to Supply Chain problems, and also in models in Production Planning. It is not clear that conic programming can be used in these case and other alternatives should be explored.

Additionally, recent technological improvements allow us to address bigger problems with larger amounts of data, but also these large-scale problems are increasingly complex. Therefore, we need to develop more powerful algorithms in order to deal with the overwhelming amount of complex data and complex problems. Recently, some mathematical alternatives have appeared with acceptable theoretical complexity that deal with this issue, which, with the best of our knowledge, have not yet been applied in the areas addressed by this project.

Our purpose is twofold. Firstly, to propose robust models as an alternative to deterministic models that appear in the areas of Machine Learning, Neuroscience, Product Design, Production Planning and Structural Engineering. Secondly, to adapt algorithms to deal directly with chance constraints problems (instead of robust and deterministic formulations) and to apply them to the studied engineering problems.

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