WIVACE 2022

XVI International Workshop on Artificial Life and Evolutionary Computation

Gaeta (LT), Italy,
14-16 September 2022

BOOKLET

of the

16th International Workshop on Artificial Life and Evolutionary Computation

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2 Keynote Speakers

2.1 Giovanni Iacca, University of Trento, Italy

When Explainable AI and Evolutionary Computation meet

Abstract: Motivated by the need for explanations in safety-critical applications, the field of Explainable Artificial Intelligence (XAI) has recently attracted a great interest in the AI community. Interestingly, some of the advances in XAI are based on Evolutionary Computation (EC). For instance, Genetic Programming has been extensively used to induce various kinds of white-box models, such as decision trees or rule-based systems. On the other hand, also within the EC field there is now a growing concern about explainability, since one may often need to explain how a population-based method conducted its search process and reached a certain outcome. In this talk, first I will give a general overview on the connection between EC and XAI. Then, I will highlight some recent works where EC has been used, also in connection with Reinforcement Learning, to create systems capable of solving in an interpretable way a variety of tasks, e.g., in medical imaging and pandemic control. Finally, I will discuss what I believe are the most interesting challenges and opportunities that lie at the intersection of the two fields.

Short Bio: Giovanni Iacca is an Associate Professor in Computer Engineering at the Department of Information Engineering and Computer Science of University of Trento, Italy, where he founded the Distributed Intelligence and Optimization Lab (DIOL). Previously, he worked as postdoctoral researcher in Germany (RWTH Aachen, 2017-2018), Switzerland (University of Lausanne and EPFL, 2013-2016) and The Netherlands (INCAS3, 2012-2016), as well as in industry in the areas of software engineering and industrial

automation. He was co-PI of the FET-Open project "PHOENIX" (2015-2019), and currently is co-PI of the PATHFINDER-CHALLENGE project "SUSTAIN" (2022-2026). He has received two best paper awards (EvoApps 2017 and UKCI 2012). His research focuses on computational intelligence, stochastic optimization, and distributed systems. In these fields, he co-authored more than 100 peer-reviewed publications, and he is actively involved in the organization of tracks and workshops at some of the top conferences in the field of computational intelligence. He also regularly serves as reviewer for several journals and conference committees.

2.2 Leonardo Vanneschi, NOVA IMS, Universidade Nova de Lisboa, Portugal

Genetic Programming: Introduction and Applications. A Perspective after thirty years from the first John Koza's book

Abstract: In 1992, John R. Koza published his first book on Genetic Programming (GP): "Genetic Programming: On the Programming of Computers by Means of Natural Selection". This ground-breaking book paved the way for the establishment of a new field of study. It influenced the work of thousands of researchers and practitioners worldwide, many of whom aimed to continue the exploration, formalization and improvement of the original formulation of GP and/or to apply GP to challenging problems. In this presentation, GP is introduced both recalling Koza's original ideas, as well as new variants that, although inspired from that idea, have been published along the years, re-injecting novelty in the field. Then, existing successful applications of GP are discussed, pointing out some potential competitive advantages of GP, compared to other existing Machine Learning methods. Finally, the idea of using GP

as a meta-learner is presented, opening the door to a discussion of future perspectives.

Short Bio: Leonardo Vanneschi is a Full Professor at the NOVA University of Lisbon, Portugal. His main research interests involve Machine Learning, Data Science, Complex Systems, and in particular Evolutionary Computation. His work can be broadly partitioned into theoretical studies on the foundations of Evolutionary Computation, and applicative work. He has published more than 200 contributions and he has led several research projects in the area. His work has been consistently recognized and appreciated by the international community from 2000 to nowadays. In 2015, he was honoured with the Award for Outstanding Contributions to Evolutionary Computation in Europe, in the context of EvoStar, the leading European Event on Bio-Inspired Computation.

3 Wednesday, September 14, 2022

3.1 Morning Session M1

3.1.1 The role of dynamical regimes of online adaptive BN-robots in noisy environments

Michele Braccini, Edoardo Barbieri and Andrea Roli

Abstract: Experiments involving evolution and adaptation of artificial agents allow us to speculate about the prerequisites and general principles enabling the appearance (or the very existence) of living organisms with levels of capabilities comparable or superior to those attained in artificial contexts. BNs (BNs) provide a viable and promising way to start addressing this question. Recently a novel online adaptation mechanism, inspired by the phenotypic plasticity property present in biological organisms, which exploits the intrinsic computational capabilities of the BN controlling the robot has been introduced. In these robots, the BN is coupled with sensors and actuators and plays the role of the control system. The coupling is dynamically changed so as to increase a utility function. Preliminary results have shown that this mechanism can yield robots accomplishing collision avoidance tasks and that critical networks attain the best performance compared to the other dynamical regimes, namely ordered and chaotic. An analysis of this mechanism in noisy environments is needed to assess its performance in more realistic scenarios and to reduce the so-called reality gap. This work aims to start studying the possibilities offered by this mechanism in tasks with gradually increasing complexity and with environments characterised by noise in the form of perturbations on the dynamics of the BN that controls the robots.

3.1.2 Online adaptation of robots controlled by nanowire networks: A preliminary study

Paolo Baldini and Andrea Roli

Abstract: In this work we present a study on the viability of using nanowire networks to control robots subject to an online adaptive mechanism. This work is a first step towards the deployment of small robots capable of adapting their behaviour to the environment in which they operate.

3.1.3 Impact of Morphology Variations on Evolved Neural Controllers for Modular Robots

Eric Medvet and Francesco Rusin

Abstract: Modular robots, in particular those in which the modules are physically interchangeable, are suitable to be evolved because they allow for many different designs. Moreover, they can constitute ecosystems where "old" robots are disassembled and the resulting modules are composed together, either within an external assembling facility or by self-assembly procedures, to form new robots. However, in practical settings, self-assembly may result in morphologies that are slightly different from the expected ones: this may cause a detrimental misalignment between controller and morphology. Here, we characterize experimentally the robustness of neural controllers for Voxel-based Soft Robots, a kind of modular robots, with respect to small variations in the morphology. We employ evolutionary computation for optimizing the controllers and assess the impact of morphology variations along two axes: kind of morphology and size of the robot. Moreover, we quantify the advantage of performing a re-optimization of the controller for the varied morphology. Our results show that small variations in the morphology are in general detrimental for the performance of the evolved neural controller. Yet, a short re-optimization is often sufficient for aligning back the performance of the modified robot to the original one.

3.2 Morning Session M2

3.2.1 Network Creation During Agglomeration Processes of Polydisperse and Monodisperse Systems of Droplets

Johannes Josef Schneider, Alessia Faggian, Aitor Patino Diaz, Jin Li, Silvia Holler, Federica Casiraghi, Lorena Cebolla Sanahuja, Hans-Georg Matuttis, Martin Hanczyc, David Barrow, Mathias Weyland, Dandolo Flumini, Peter Eggenberger Hotz, Pantelitsa Dimitriou, William David Jamieson, Oliver Castell, Patrik Eschle and Rudolf M. Füchslin

Abstract: We simulate the movement and agglomeration of oil droplets in water under constraints, using a simplified stochastic-hydrodynamic model. We analyze the properties of the networks formed by the agglomerations of droplets. We focus on the differences of these properties for monodisperse and polydisperse systems of droplets.

3.2.2 Computational investigation of the clustering of droplets in widening pipe geometries

Hans-Georg Matuttis and Johannes Josef Schneider

Abstract: Experimentally, periodically released droplets in systems of widening pipes show clustering. This is surprising, as purely hydrodynamic interactions, are repulsive so that agglomeration should be prevented. In the main part of this paper, we investigate the clustering of droplets under the influence of phenomenological hydrostatic forces and some hypothetical attraction. In two appendices, we explain why a direct numerical simulation for this system is rather more difficult (and probably not possible with current methods) than the "simple" geometry would suggest.

3.2.3 Artificial Chemistry Performed in an Agglomeration of Droplets with Restricted Molecule Transfer

Johannes Schneider, Alessia Faggian, William David Jamieson, Mathias Weyland, Jin Li, Oliver Castell, Hans-Georg Matuttis, David Barrow, Aitor Patino Diaz, Lorena Cebolla Sanahuja, Silvia Holler, Federica Casiraghi, Martin Hanczyc, Dandolo Flumini, Peter Eggenberger Hotz and Rudolf M. Füchslin

Abstract: Within the scope of the European Horizon 2020 project ACDC – Artificial Cells with Distributed Cores to Decipher Protein Function, we aim at the development of a chemical compiler governing the three-dimensional arrangement of droplets, which are filled with various chemicals. Neighboring droplets form bilayers with pores which allow chemicals to move from one droplet to its neighbors. With an appropriate three-dimensional configuration of droplets, we can thus enable gradual biochemical reaction schemes for various purposes, e.g., for the production of macromolecules for pharmaceutical purposes. In this paper, we demonstrate with artificial chemistry simulations that the ACDC technology is excellently suitable to maximize the yield of desired reaction products or to minimize the relative output of unwanted side products.

3.3 Afternoon Session A1

3.3.1 Chemical Neural Networks and Semantic Information investigated through Synthetic Cells

Lorenzo Del Moro, Beatrice Ruzzante, Maurizio Magarini, Pier Luigi Gentili, Giordano Rampioni, Andrea Roli, Luisa Damiano and Pasquale Stano

Abstract: In a previous contribution we briefly sketched novel topics that lie at the interface between synthetic biology (SB) and artificial intelligence (AI). In particular, we discussed (a) the possibility of engrafting chemical AI-like tools in bottom-up synthetic cell systems, and (b) the investigation of fundamental concepts of information theory – such as

the "semantic" information – by means of synthetic cells. Here we intend to report on the progress done by our groups in these fields and shortly devise future steps for theoretical and experimental approaches.

3.3.2 On the growth of chemical diversity

Federica Senatore, Marco Villani and Roberto Serra

Abstract: In complex systems that host evolutionary processes, in which entirely new entities may enter the scene, some variables can sometimes show a "hockey-stick" behavior, that is a long period of slow growth followed by an "explo-sive" increase. The TAP equation was proposed with the aim of describing the growth of the number of different types of entities in systems where new entities (e.g., artifacts) can be created, supposing that they derive from trans-formations of pre-existing ones. It shows a very interesting divergence in fi-nite times, different from the usual exponential growth where divergence takes place in the infinite time limit. The TAP equation does not deal with the growth of the number of actual types, but rather with the number of the pos-sible ones (the members of the so-called set of Adjacent Possible), and it can therefore overestimate the actual rate of growth. In this paper, we introduce a model (called BPSM, focused on systems that may be relevant for the origin of life) that takes into account the difference between the Adjacent Possible and the set of types that are actually created. Using simulations, it has been observed that the growth of the number of chemical species in the system re-sembles that of the corresponding TAP equation. Since in this case only combinations of at most two entities can be considered at each time, the TAP equation can be analytically integrated. Its behavior can be then compared to the (necessarily finite) behavior of model simulations; their behaviors turn out to be quite similar, and proper tests are introduced, which show that they differ from the familiar exponential growth. Therefore, the BPSM model provides a description of the rapid increase of diversity which resembles TAP, while based upon the growth of the actual entities rather than on the Adjacent Possible.

3.3.3 Modelling wet-dry cycles in the binary polymer model

Federica Senatore, Roberto Serra and Marco Villani

textbfAbstract: A key question concerning the origin of life is whether polymers, such as nucleic acids and proteins, can spontaneously form in prebiotic conditions. Several studies have shown that, by alternating (i) a phase in which a system is in a water-rich condition and (ii) one in which there is a relatively small amount of water, it is possible to achieve polymerization. It can be argued that such "wet-dry" cycles might have actually taken place in the primordial Earth, for example in volcanic lakes. In this paper, using a version of the bi-nary polymer model without catalysis, we have simulated wet and dry cycles to determine the effectiveness of polymerization under these conditions. By observing the behavior of some key variables (e.g., the number of different chemical species which appeared at least once and the maximum length of the species currently present in the system) it is possible to see that the alter-nation of wet and dry conditions can indeed allow a wider exploration of different chemical species when compared to constant condition.

3.4 Afternoon Session A2

3.4.1 Flow Lenia: Mass conservation for the study of virtual creatures in continuous cellular automata

Erwan Plantec, Bert Wang-Chak Chan, Gautier Hamon, Mayalen Etcheverry, Clément Moulin-Frier and Pierre-Yves Oudeyer

Abstract: Lenia is a family of cellular automata (CAs) generalizing Conway's Game of Life (GoL) to continuous space, time and states. Lenia has attracted interest because of the emerging patterns we can observe. More particularly, the emergence of life-like spatially localized patterns (SLPs), also called creatures, has made Lenia a wonderful system for studying the emergence of life-like phenomenon and even sensori-motor capabilities. However, those patterns represent a very small subsets of possible patterns in Lenia and

can be quite difficult to find necessitating fine-tuned search algorithm. We think that conservation laws could be key constraints for facilitating the search for interesting capabilities and also opening a lot of perspectives like adding environmental features and constraints to creatures. Thus, we propose in this work a mass-conservative extension to Lenia called Flow Lenia. First we present formally this new model, and then demonstrate preliminary observations showing the value of this system.

3.4.2 Collaborative learning over Cellular Automata

Franco Cicirelli, Emilio Greco, Antonio Guerrieri, Giandomenico Spezzano and Andrea Vinci

Abstract: There are many real scenarios in which some correlated complex problems have to be addressed by different autonomous learners working in parallel. In such a scenario, the collaboration among the learners can be extremely useful since they can share acquired knowledge so as to reach a reduction in the learning time, an increase in the learning quality, or both of them. Anyway, in some cases, it is not always feasible to collaborate with other learners. This is because the problems to solve are not compatible or they can have dissimilar boundary conditions leading to very different problem solutions. In this paper, we propose an approach to collaborative learning which leverages cellular automata for efficiently solving a set of compatible and sufficiently similar problems. In this direction, the notion of compatibility and similarity between problems is also given and discussed. A case study based on the maze problem will show the effectiveness of the proposed approach.

4 Thursday, September 15, 2022

4.1 Morning Session M3

4.1.1 Kernel-based early fusion of structure and attribute information for detecting communities in attributed networks

Clara Pizzuti and Annalisa Socievole

Early fusion methods are a category of community detection methods for attributed networks which merge attributes and structure before the method is executed. Typically, a weighted network, where the edge between two nodes includes both the structure information (i.e. the weight of the existing link) and the similarity of the attributes, is obtained and then, classical community detection algorithms can be applied. In this paper, we investigate the role of kernels on such methods. When measuring similarity, kernels are able to provide a more suitable and meaningful form for the similarity matrix in order to facilitate data analysis. Through simulations on both synthetic and real-world attributed networks, we first apply different kernels to @NetGA, a genetic algorithm we proposed for attributed networks which embeds into edges both the structure and the attribute information through the unified distance measure. Then, we compare the kernel-based @NetGA to other early fusion methods that we extend with kernel-based similarity.

4.1.2 An efficient implementation of Flux Variability Analysis for metabolic networks

Bruno Galuzzi and Chiara Damiani

Abstract: Flux Variability Analysis (FVA) is an important method to analyze the range of fluxes of a metabolic network. FVA consists in performing a large number of independent optimization problems, to obtain the maximum and minimum flux through each reaction in the network. Although several strategies to make the computation more efficient have been

proposed. the computation time of an FVA can still be limiting. We present a two-step procedure to accelerate the FVA computation time that exploits the large presence within metabolic networks of sets of reactions that necessarily have an identical optimal flux value or only differ by a multiplication constant. The fist step identifies such sets of reactions. The second step computes the maximum and minimum flux value for just one element of each of set, reducing the total number of optimization problems compared to the classical FVA. We show that, when applied to any metabolic network model included in the BiGG database, our FVA algorithm reduces the total number of optimization problems of about 35%, and the computation time of FVA of about 30%.

4.1.3 Spread of perturbations in supply chain networks: the effect of the bow-tie organization on the resilience of the global automotive system

Elisa Flori, Yi Zhu, Sandra Paterlini, Francesco Pattarin and Marco Villani

Abstract: Many real-world systems are subject to external perturbations, damages, or attacks with potentially ruinous consequences. The internal organization of a system allows it to effectively resist to such perturbations with more or less success. In this work, we study the resilience properties of the global auto-motive supply-chain by considering the bow-tie structure of the directed network stemming from customer-supplier relationships. Data have been re-trieved by Bloomberg supply chain database between 2018 to 2020. Our analysis involves 3,323 companies connected by 11,182 trade links and spanning 135 economic sectors. Our results indicate that the size of propaga-tion of a perturbation depends on the area of the bow-tie structure in which it initially originates. Also, it is possible to identify resistance structures within some bow-tie areas. Thus, we provide insights into the fragility and resilience of different network components and the diffusion paths of perturbations across the system. Interestingly, the level of abstraction used allows our re-sults to generalize beyond the case in question to many systems that can be represented through directed graphs.

4.2 Morning Session M4

4.2.1 Fine-Grained Agent-Based Modeling to Predict Covid-19 Spreading and Effect of Policies in Large-Scale Scenarios

Gianfranco Lombardo, Mattia Pellegrino, Michele Tomaiuolo, Stefano Cagnoni, Monica Mordonini, Mario Giacobini and Agostino Poggi

Abstract: There are several reasons why modeling and forecasting the spread of COVID-19 remains an open problem. One of these is the difficulty of developing complex system models fine-grained enough to simulate the spread taking into account individual features such as the social structure, the effects of the governments' policies, age-related sensitivity to Covid-19, mask-wearing habits, and geographical distribution of susceptible people. The social modeling approach we propose can be easily adapted for modeling future epidemics at their early stage in scenarios where little prior knowledge is available. We describe a new way to use millions of agents on an HPC facility to simulate a pathogen spread (Covid-19) at a high level of detail.

4.2.2 JGEA: a Modular Java Framework for Experimenting with Evolutionary Computation

Eric Medvet, Giorgia Nadizar, Luca Manzoni

Abstract: We present the Java General Evolutionary Algorithm (JGEA) framework, a modular Java framework for experimenting with Evolutionary Computation (EC). We designed JGEA to be (a) aimed at providing a general interface to potentially all Evolutionary Algorithms (EAs), yet (b) solid and easy to use for people who rely on EC as a tool. To this extent, we developed JGEA including a range of ready-to-use EAs, backed by a modular architecture, comprising diverse layers of abstraction, which simplifies the implementation of new EAs and the addition of new features. Here, we detail the general structure of JGEA, focusing on its high-level components, and present the use case of the

introduction of a new EA in the framework. To complete the picture, we illustrate the application of JGEA for solving a real world problem, from its formal definition in the framework to the saving and processing of results. The source code of JGEA is available at `https://github.com/ericmedvet/jgea`.

4.2.3 Pseudo-attractors in Random Boolean Network Models (and possible approaches to Single-Cell Data)

Marco Villani, Gianluca D'Addese, Stuart A. Kauffman and Roberto Serra

Abstract: Random Boolean Networks (RBNs for short) are strongly simplified models of gene regulatory networks (GRNs), which have also been widely studied as abstract models of complex systems and have been used to simulate different phenomena. For each dynamic attractor of a RBN, we find a pseudo-attractor whose components synthesize the information of the corresponding dynamic attractor. We therefore define the "common sea" (CS) as the set of nodes that take the same value in all the attractors of a given network realization, and the "specific part" (SP) as the set of all the other nodes, and we study their properties in different ensembles, generated with different parameter values. Both the CS and of the SP can be composed of one or more weakly connected components, which are emergent intermediate-level structures. We show that the study of these sets provides very important information about the behavior of the model. In particular, we show how the notion of a "common sea" of genes can be used to analyze data from single-cell experiments.

4.3 Afternoon Session A3

4.3.1 WanDa: A Mobile Application to Prevent Wandering

Berardina De Carolis, Vincenzo Gattulli, Donato Impedovo and Giuseppe Pirlo

Abstract: The nature of Big Data tends to collect a huge quantity of useful information about human life. Implementing Artificial Life applications inherent to health could

improve and sensitize individuals to the future. In fact, would be useful to implement an application that monitors people with neurodegenerative diseases when they are away from home to monitor Wandering. In this paper, an application called "WanDa" is proposed that monitors and prevents deviations from the usual path in real-time and, if wandering is detected, can guide the elderly person to a safe place and alert caregivers or relatives. The application uses the sensors and technologies of a generic Android smartphone and has a very simple interface to manage wandering behaviors. We tested the application from two perspectives: the accuracy of the algorithm in detecting wandering behaviors and the user experience. In both cases, WanDa was judged positively, showing that it can be a useful support for managing, monitoring, and reporting wonder episodes.

4.3.2 Vectorial GP for Alzheimer's Disease Prediction Through Handwriting Analysis

Irene Azzali, Nicole Dalia Cilia, Claudio De Stefano, Francesco Fontanella, Mario Giacobini and Leonardo Vanneschi

Abstract: Alzheimer's Disease (AD) is a neurodegenerative disease which causes a continuous cognitive decline. This decline has a strong impact on daily life of the people affected and on that of their rela- tives. Unfortunately, to date there is no cure for this disease. However, its early diagnosis helps to better manage the course of the disease with the treatments currently available. In recent years, AI researchers have become increasingly interested in developing tools for early diagnosis of AD based on handwriting analysis. In most cases, they use a feature en- gineering approach: domain knowledge by clinicians is used to define the set of features to extract from the raw data. In this paper, we present a novel approach based on vectorial genetic programming (VE GP) to recognize the handwriting of AD patients. VE GP is a recently defined method that enhances Genetic Programming (GP) and is able to directly manage time series in such a way to automatically extract informative features, without any need of human intervention. We

applied VE GP to handwriting data in the form of time series consisting of spatial coordinates and pressure. These time series represent pen movements collected from people while performing handwriting tasks. The presented exper- imental results indicate that the proposed approach is effective for this type of application. Furthermore, VE GP is also able to generate rather small and simple models, that can be read and possibly interpreted. These models are reported and discussed in the last part of the paper.

4.3.3 Exploring the solution space of cancer evolution inference frameworks for single-cell sequencing data

Davide Maspero, Fabrizio Angaroni, Lucrezia Patruno, Daniele Ramazzotti, David Posada and Alex Graudenzi

Abstract: In recent years, many algorithmic strategies have been developed to exploit single-cell mutational profiles generated via sequencing experiments of cancer samples, to return reliable models of cancer evolution. Here, we introduce the COB-tree algorithm, which summarizes the solutions explored by state-of-the-art methods for clonal tree inference, to return a unique consensus optimum branching tree. The method proves to be highly effective in detecting pairwise temporal relations between genomic events, as demonstrated by extensive tests on simulated datasets. We also provide a new method to visualize and quantitatively inspect the solution space of the inference methods, via Principal Coordinate Analysis. Finally, the application of our method to a single-cell dataset of patient-derived melanoma xenografts shows significant differences between the COB-tree solution and the maximum likelihood ones.

4.4 Afternoon Session A4

4.4.1 Cultural Innovation Triggers Inequality in a Sharing Economy

Elpida Tzafestas

Abstract: In this work, we are studying the dynamics of wealth inequality in a simulated primitive economy of producer agents with the possibility of food sharing. In our previous work, we have identified the conditions that define a strong tendency for emergence of sharing, namely environmental instability, low technological ability and especially much higher public storage capacity than private storage capacity, where these capacities express actual technological advances but also cultural values and processes. We now show through agent-based modelling that wealth inequality between agents follows an initially upward and then downward trend before stabilizing around its final value. This trend is reminiscent of swings identified by economists. We study it in cases of "shocks", where after stabilization one of the parameters of the system is reinitialized (technology, environment, birth model and others). In all cases, the after-shock inequality movement shows the same overall trend but it is smaller in size, and this is true irrespective of the sharing outcome. We formulate the hypothesis that the size of the emerging maximum inequality is due to cultural reinitialization or innovation, where because of the shock the agents reinitialize their stances toward sharing, i.e. they innovate culturally. This hypothesis is supported by a series of experiments with varying degrees of cultural innovation as well as by an experiment with generalized cultural evolution. The global conclusion is that it is the cognitive/cultural lever of the economic relations, here the disposition toward sharing, that is responsible for the type and breadth of inequality that emerges.

4.4.2 An agent-based model for crowd simulation

Carolina Crespi, Georgia Fargetta, Rocco Alessandro Scollo and Mario Pavone

Abstract: Simulating crowd behavior has become one of the most challenging topics of

the last few years. Indeed, in emergency management, it is crucial to know in advance how people would behave, in order to establish efficient escape plans. In this research work, an agent-based model for crowd's simulations has been developed, made up of N agents that starting from one or more entrances must reach one or more exits as quickly as possible, crossing the most convenient routes (in term of path costs), and maximizing the number of agents that reach the exit points. From the investigation performed on several scenarios and at different complexities, emerges how a mixed crowd, in which are present different behaviors of agents, is more efficient in obtaining best overall performances, as well as the transmission of the information from one group to another.

4.4.3 Evolutionary Stitching of Plot Units with Character Threads

Pablo Gervás

Abstract: Ideation of novel narrative plots is often achieved by recombination of elements from prior plots. This approach presents two challenges: what elements to select from prior narratives, and how to find a new combination that makes sense without replicating any of the originals. The present paper relies on prior results for representing elementary narrative units for plot representation that both respect connectivity across a plot and allow a high degree of abstraction from previous instances of plot. An evolutionary procedure is applied to search the space of possible combinations, driven by metrics on coherent connectivity across plot units.

5 Friday, September 16, 2022

5.1 Morning Session M6.

5.1.1 Magnetic Devices Behavioral Modeling based on Genetic Programming and Neural Networks

Giulia Di Capua, Mario Molinara, Francesco Fontanella, Claudio De Stefano, Nicola Femia and Nunzio Oliva

Abstract: This abstract compares two models for AC power loss prediction in Ferrite-Core Power Inductors (FCPIs) used in Switch-Mode Power Supply (SMPS) applications. A first model has been identified by means of a genetic programming algorithm and a multi-objective optimization technique. The resulting AC power loss model uses the voltage and switching frequency imposed to the FCPI as input variables, while the DC inductor current is used as a parameter expressing the impact of saturation on the magnetic device. A second model relies on a multilayer perceptron with a single hidden layer. The resulting AC power loss model uses the voltage, switching frequency and DC inductor current all as input variables. A 10 µH FCPI has been adopted as case study and a large sets of power loss experimental measurements have been adopted as training and test sets, including operations in partial saturation conditions. The higher reliability and flexibility of the FCPI behavioral modeling based on genetic programming is eventually proved.

5.1.2 Single and Multi-objective Genetic Programming Methods for Prediction Intervals

Karina Brotto Rebuli, Niccolò Tallone, Mario Giacobini and Leonardo Vanneschi

Abstract: A PI is the range of values in which the real target value of a supervised learning task is expected to fall into, and it should combine two contrasting properties: to be as narrow as possible, and to include as many data observations as possible. This article

presents an study on modelling Prediction Intervals (PI) with two Genetic Programming (GP) methods. The first proposed GP method is called CWC-GP, and it evolves simultaneously the lower and upper boundaries of the PI using a single fitness measure. This measure is the Coverage Width-based Criterion (CWC), which combines the width and the probability coverage of the PI. The second proposed GP method is called LUBE-GP, and it evolves independently the lower and upper boundaries of the PI. This method applies a multi-objective approach, in which one fitness aims to minimise the width and the other aims to maximise the probability coverage of the PI. Both methods were applied both with the Direct and the Sequential approaches. In the former, the PI is assessed without the crisp prediction of the model. In the latter, the method makes use of the crisp prediction to find the PI boundaries. The proposed methods showed to have good potential on assessing PIs and the results pave the way to further investigations.

5.1.3 EGSGP: an Ensemble System Based on Geometric Semantic Genetic Programming

Liah Rosenfeld and Leonardo Vanneschi

This work is inspired by the idea of seeding Genetic Programming (GP) populations with trained models from a pool of different Machine Learning (ML) methods, instead of using randomly generated individuals. If one considers standard GP, tackling this problem is very challenging, because each ML method uses its own representation, typically very different from the others. However, the task becomes easier if we use Geometric Semantic GP (GSGP). In fact, GSGP allows us to abstract from the representation, focusing purely on semantics. Following this idea, we introduce EGSGP, a novel method that can be seen either as a new initialization technique for GSGP, or as an ensemble method, that uses GSGP to combine different Base Learners (BLs). To counteract overfitting, we focused on the study of elitism and Soft Target (ST) regularization, studying several variants of EGSGP. In particular, systems that use or do not use elitism, and that use (with different

parameters) or do not use ST were investigated. After an intensive study of the new parameters that characterize EGSGP, those variants were compared with the used BLs and with GSGP on three real-life regression problems. The presented results indicate that EGSGP outperforms the BLs and GSGP on all the studied test problems. While the difference between EGSGP and GSGP is statistically significant on two of the three test problems, EGSGP outperforms all the BLs in a statistically significant way only on one of them.

5.2 Morning Session M7

5.2.1 A novel evolutionary approach for Neural Architecture Search

Alessandro Bria, Tiziana D'Alessandro, Paolo De Ciccio and Francesco Fontanella

Abstract: Deep Neural Networks (DNNs) have become a standard as machine learning-based tool in many applications. The main problem of DNNs is the lack of a well-defined and largely shared set of criteria for the choice of the architecture to use for a given problem. This lack represents a drawback for this kind of approach since the choice of architecture plays a crucial role in DNNs' performance. Usually, these architectures are manually designed by experts. However, such a design process is labour intensive because of the trial-and-error process, and also not easy to realize due to the level of expertise required to achieve good performance. Neural Architecture Search (NAS) is a type of technology that can design DNN architectures automatically. Among the many methods available for NAS, Evolutionary Computation (EC) methods have recently gained much attention and success. In this paper, we present a novel approach based on evolutionary computation to optimize DNNs. The proposed approach is based on a newly devised structure which encodes both network hyperparameters and architecture. The presented experimental results indicate that the proposed approach allows us to achieve better performance than that achieved by human experts on a real-world problem. Furthermore, the proposed approach is also able

to generate smaller networks than the state-of-the-art DNNs used for the comparison.

5.2.2 Real-time monitoring tool for spike activity in a SIMD architecture

Mireya Zapata, Vanessa Vargas, Ariel Cagua, Daniela Alvarez, Bernardo Vallejo and Jordi Madrenas

Abstract: Spiking Neural Networks are characterized by their brain-inspired biological computing paradigm. Large-scale hardware platforms are reported, where computational cost, connectivity, number of neurons and synapses, speed, configurability, monitoring restriction, are some of the main concerns. Analog approaches are limited by their low flexibility and the amount of time and resources spent on prototype development design and implementation. On the other hand, digital SNN platform based on SoC offers the advantage of the FPGAs technology, along with a powerful ARM processor in the same chip, that can be used to peripheral control and high-bandwidth direct memory Access. This paper presents a monitoring tool developed in Python that receives spike data from a large-scale SNN architecture called HEENS in order to on-line display in a dynamic raster plot in real-time. It also posible creates a file plain text with the entire spike activity with the aim to be analyzed offline. Overall, the monitoring tool and the HEENS functionalities working together show great potential for an end-user to bring up a neural application and monitor its evolution introducing a low delay, since a FIFO is used to temporarily store the incoming spikes to give the processor time to transmit data to the PC though ethernet bus, without affecting the neural network execution.

5.2.3 Green design of Single Frequency Networks by Multiband Robustness and a hybrid metaheuristic

Fabio D'Andreagiovanni, Hicham Lakhlef and Antonella Nardin

Abstract: The passage to a second generation of broadcasting Single Frequency Networks has generated the need for reconfiguring and redesigning existing networks. In this work,

we present a robust optimization model for the green design of such networks based on the digital television DVB-T2 standard. Our robust model pursues protection against uncertainty of signal propagation in a complex real-world environment. As reference model, we adopt Multiband Robustness and we propose to solve the resulting model by a hybrid metaheuristic that combines mathematically strong formulations of the optimization model, with an exact large neighborhood search. We report computational tests based on realistic instances, showing that the multiband model grants highly protected solutions without reducing service coverage and without leading to a high price of robustness.