EvoStar Programme Final

EuroGP
EvoBIO
EvoCOP
EvoMUSART
EvoAPPLICATIONS

EuroGP Programme

Wednesday 23 April

Wed 1120-1300 **Session 1: Applications**
Chair: Atif Azad

Enhancing Branch-and-Bound Algorithms for Order Acceptance and Scheduling with Genetic Programming *Su Nguyen, Mengjie Zhang, Mark Johnston*
Order acceptance and scheduling (OAS) is an important planning activity in make-to-order manufacturing systems. Making good acceptance and scheduling decisions allows the systems to utilise their manufacturing resources better and achieve higher total profit. Therefore, finding optimal solutions for OAS is desirable. Unfortunately, the exact optimisation approaches previously proposed for OAS are still very time consuming and usually fail to solve the problem even for small instances in a reasonable computational time. In this paper, we develop a new branch-and-bound (B&B) approach to finding optimal solutions for OAS. In order to design effective branching strategies for B&B, a new GP method has been proposed to discover good ordering rules. The results show that the B&B algorithms enhanced by GP can solve the OAS problem more effectively than the basic B&B algorithm and the CPLEX solver on the Mixed Integer Linear Programming model.

Building a Stage 1 Computer Aided Detector for Breast Cancer using Genetic Programming *Conor Ryan, Krzysztof Krawiec, Una-May O'Reilly, Jeannie Fitzgerald, David Medernach*
We describe a fully automated workflow for performing stage1 breast cancer detection with GP as its cornerstone. Mammograms are by far the most widely used method for detecting breast cancer in women, and its use in national screening can have a dramatic impact on early detection and survival rates. With the increased availability of digital mammography, it is becoming increasingly more feasible to use auto- mated methods to help with detection. A stage 1 detector examines mammograms and highlights suspicious areas that require further investigation. A too conservative approach degenerates to marking every mammogram (or segment of) as suspicious, while missing a cancerous area can be disastrous. Our workflow positions us right at the data collection phase such that we generate textural features ourselves. These are fed through our system, which performs PCA on them before passing the most salient ones to GP to generate classifiers. The classifiers give results of 100% accuracy on true positives and a false positive per image rating of just 1.5, which is better than prior work. Not only this, but our system can use GP as part of a feedback loop, to both select and help generate further features.

Exploring the Search Space of Hardware/Software Embedded Systems by Means of GP *Milos Minarik, Lukas Sekanina*
This paper presents a new platform for development of small application-specific digital embedded architectures based on a data path controlled by a microprogram. Linear genetic programming is extended to evolve a program for the controller together with suitable hardware architecture. Experimental results show that the platform can automatically design general solutions as well as highly optimized specialized solutions to benchmark problems such as maximum, parity or iterative division.

Wed 1430-1610 **Session 2: Operators**
Chair: Sara Silva

Semantic Crossover based on the Partial Derivative Error *Mario Graff, Ariel Graff-Guerrero, Jaime Cerda-Jacobo*
There is great interest for the development of semantic genetic operators to improve the performance of genetic programming. Semantic genetic operators have traditionally been developed employing experimentally or theoretically-based approaches. Our current work proposes a novel semantic crossover developed amid the two traditional approaches. Our proposed semantic crossover operator is based on the use of the derivative of the error propagated through the tree. This process decides the crossing point of the second parent. The results show that our procedure improves the performance of genetic programming on rational symbolic regression problems.

Measuring Mutation Operators' Exploration-Exploitation Behaviour and Long-term Biases *James McDermott*
We propose a simple method of directly measuring a mutation operator's short-term exploration-exploitation behaviour, based on its transition matrix. Higher values for this measure indicate a more exploitative operator. Since operators also differ in their degree of long-term bias towards particular areas of the search space, we propose a simple method of directly measuring this bias, based on the Markov chain stationary state. We use these measures to compare numerically the behaviours of two well-known mutation operators, the genetic algorithm per-gene bitflip mutation and the genetic programming subtree mutation.

NEAT, There's no Bloat *Leonardo Trujillo, Luis Muñoz, Enrique Naredo, Yuliana Martinez*
The Operator Equalization (OE) family of bloat control methods have achieved promising results in many domains. In particular, the Flat-OE method, that promotes a flat distribution of program sizes, is one of the simplest OE methods and achieves some of the best results. However, Flat-OE, like all OE variants, can be computationally expensive. This work proposes a simplified strategy for bloat control based on Flat-OE. In particular, bloat is studied in the NeuroEvolution of Augmenting Topologies (NEAT) algorithm. NEAT includes a very simple diversity preservation technique based on speciation and fitness sharing, and it is hypothesized that with some minor tuning, speciation in NEAT can promote a flat distribution of program size. Results indicate that this is the case in two benchmark problems, in accordance with results for Flat-OE. In conclusion, NEAT provides a worthwhile strategy that could be extrapolated to other GP systems, for effective and simple bloat control.

Wed 1745-1900 **EuroGP posters**

Asynchronous Evolution by Reference-based Evaluation: Tertiary Parent Selection and its Archive *Tomohiro Harada, Keiki Takadama*
This paper proposes a novel asynchronous reference-based evaluation (named as ARE) for an asynchronous EA that evolves individuals independently unlike general EAs that evolve all individuals at the same time. ARE is designed for an asynchronous evolution by tertiary parent selection and its archive. In particular, ARE asynchronously evolves individuals through a comparison with only three of individuals (i.e., two parents and one reference individual as the tertiary parent). In addition, ARE builds an archive of good reference individuals. This differ from synchronous evolution in EAs in which selection involves comparison with all population members. In this paper, we investigate the effectiveness of ARE, by applying it to some standard problems used in Linear GP that aim being to minimize the execution step of machine-code programs. We compare GP using ARE (ARE-GP) with steady state (synchronous) GP (SSGP) and our previous asynchronous GP (Tierra-based Asynchronous GP: TAGP). The experimental results have revealed that ARE-GP not only asynchronously evolves the machine-code programs, but also outperforms SSGP and TAGP in all test problems.

Behavioral Search Drivers for Genetic Programing *Krzysztof Krawiec, Una-May O'Reilly*
Synthesizing a program with the desired input-output behavior by means of genetic programming is an iterative process that needs appropriate guidance. That guidance is conventionally provided by a fitness function that measures the conformance of program output with the desired output. Contrary to widely adopted stance, there is no evidence that this quality measure is the best choice;

alternative search drivers may exist that make search more effective. This study proposes and investigates a new family of behavioral search drivers, which inspect not only final program output, but also program behavior meant as the partial results it arrives at while executed.

Cartesian Genetic Programming: Why No Bloat? *Andrew Turner, Julian Miller*
For many years now it has been known that Cartesian Genetic Programming (CGP) does not exhibit program bloat. Two possible explanations have been proposed in the literature: neutral genetic drift and length bias. This paper empirically disproves both of these and thus, reopens the question as to why CGP does not suffer from bloat. It has also been shown for CGP that using a very large number of nodes considerably increases the effectiveness of the search. This paper also proposes a new explanation as to why this may be the case.

On Evolution of Multi-Category Pattern Classifiers Suitable for Embedded Systems
Zdenek Vasicek, Michal Bidlo
This paper addresses the problem of evolutionary design of classifiers for the recognition of handwritten digit symbols by means of Cartesian Genetic Programming. Two different design scenarios are investigated - the design of multiple-output classifier, and design of multiple binary classifiers. The goal is to evolve classification algorithms that employ substantially smaller amount of operations in contrast with conventional approaches such as Support Vector Machines. Even if the evolved classifiers do not reach the accuracy of the tuned SVM classifier, it will be shown that the accuracy is higher than 93% and the number of required operations is a magnitude lower.

The Best Things Don't Always Come in Small Packages: Constant Creation in Grammatical Evolution *R. Muhammad Atif Azad, Conor Ryan*
This paper evaluates the performance of various methods to constant creation in Grammatical Evolution (GE), and validates the results against those from Genetic Programming (GP). Constant creation in GE is an important issue due to the disruptive nature of {\em ripple crossover}, which can radically remap multiple terminals in an individual, and we investigate if more compact methods, which are more similar to the GP style of constant creation ({\em Ephemeral Random Constants} (ERCs), perform better. The results are surprising. The GE methods all perform significantly better than GP on unseen test data, and we demonstrate that the standard GE approach of {\em digitconcatenation} does not produce individuals that are any larger than those from methods which are designed to use less genetic material.

Thursday 24 April

Thurs 0930-1110 **Session 3: Software Engineering and Software Frameworks**
Chair: Evelyne Lutton

Genetically Improved CUDA C++ Software *William B. Langdon, Mark Harman*
Genetic Programming (GP) may dramatically increase the performance of software written by domain experts. GP and autotuning are used to optimise and refactor legacy GPGPU C code for modern parallel graphics hardware and software. Speed ups of more than six times on recent nVidia GPU cards are reported compared to the original kernel on the same hardware.

Using Genetic Improvement and Code Transplants to Specialise a C++ Program to a Problem Class *Justyna Petke, Mark Harman, William B. Langdon, Westley Weimer*
Genetic Improvement (GI) is a form of Genetic Programming that improves an existing program. We use GI to evolve a faster version of a C++ program, a Boolean satisfiability (SAT) solver called MiniSAT, specialising it for a particular problem class, namely Combinatorial Interaction Testing (CIT), using automated code transplantation. Our GI-evolved solver achieves overall 17% improvement, making it comparable with average expert human performance. Additionally, this automatically evolved solver is faster than any of the human-improved solvers for the CIT problem.

Flash: A GP-GPU Ensemble Learning System for handling Large Datasets *Ignacio Arnaldo, Kalyan Veeramachaneni, Una-May O'Reilly*
The Flash system runs ensemble-based Genetic Programming (GP) symbolic regression on a shared memory desktop. To significantly reduce the high time cost of the extensive model predictions required by symbolic regression, its fitness evaluations are tasked to the desktop's GPU. Successive GP "instances" are run on different data subsets and randomly chosen objective functions. Best models are collected after a fixed number of generations and then fused with an adaptive, output-space method. New instance launches are halted once learning is complete. We demonstrate that Flash's ensemble strategy not only makes GP more robust, but it also provides an informed online means of halting the learning process. Flash enables GP to learn from a dataset composed of 370K exemplars and 90 features, evolving a population of 1000 individuals over 100 generations in as few as 50 seconds.

Thurs 1135-1315 **Session 4: Theory and Analysis**
Chair: Mengjie Zhang

Higher Order Functions for Kernel Regression *Alexandros Agapitos, James McDermott, Michael O'Neill, Ahmed Kattan, Anthony Brabazon*
Kernel regression is a well-established nonparametric method, in which the target value of a query point is estimated using a weighted average of the surrounding training examples. The weights are typically obtained by applying a distance-based kernel function, which presupposes the existence of a distance measure. This paper investigates the use of Genetic Programming for the evolution of task-specific distance measures as an alternative to Euclidean distance. Results on seven real-world datasets show that the generalisation performance of the proposed system is superior to that of Euclidean-based kernel regression and standard GP.

A Multi-dimensional Genetic Programming Approach for Multi-class Classification Problems *Vijay Ingalalli, Sara Silva, Mauro Castelli, Leonardo Vanneschi*
Classification problems are of profound interest for the machine learning community as well as to an array of application fields. However, multi-class classification problems can be very complex, in particular when the number of classes is high. Although very successful in so many applications, GP was never regarded as a good method to perform multi-class classification. In this work, we present a novel algorithm for tree based GP, that incorporates some ideas on the representation of the solution space in higher dimensions. This idea lays some foundations on addressing multi-class classification problems using GP, which may lead to further research in this direction. We test the new approach on a large set of benchmark problems from several different sources, and observe its competitiveness against the most successful state-of-the-art classifiers.

On Diversity, Teaming and Hierarchical Policies: Observations from the Keepaway Soccer Task *Stephen Kelly, Malcolm Heywood*
The 3-versus-2 Keepaway soccer task represents a widely used benchmark appropriate for evaluating approaches to reinforcement learning, multi-agent systems, and evolutionary robotics. To date most research on this task has been described in terms of developments to reinforcement learning with function approximation or frameworks for neuro-evolution. This work performs an initial study using a recently proposed algorithm for evolving teams of programs hierarchically using two phases of evolution: one to build a library of candidate meta policies and a second to learn how to deploy the library consistently. Particular attention is paid to diversity maintenance, where this has been demonstrated as a critical component in neuro-evolutionary approaches. A new formulation is proposed for fitness sharing appropriate to the Keepaway task. The resulting policies are observed to benefit from the use of diversity and perform significantly better than previously reported. Moreover, champion individuals evolved and selected under one field size generalize to multiple field sizes without any additional training.

Thurs 1430-1610 **Session 5: EuroGP best paper nominations**
Chairs: Miguel Nicolau and Krzysztof Krawiec

ESAGP - A Semantic GP Framework Based on Alignment in the Error Space (EuroGP best paper candidate) *Stefano Ruberto, Leonardo Vanneschi, Mauro Castelli, Sara Silva*

This paper introduces the concepts of error vector and error space, directly bound to semantics, one of the hottest topics in genetic programming. Based on these concepts, we introduce the notions of optimally aligned individuals and optimally coplanar individuals. We show that, given optimally aligned, or optimally coplanar, individuals, it is possible to construct a globally optimal solution analytically. Thus, we introduce a genetic programming framework for symbolic regression called Error Space Alignment GP (ESAGP) and two of its instances: ESAGP-1, whose objective is to find optimally aligned individuals, and ESAGP-2, whose objective is to find optimally coplanar individuals. We also discuss how to generalize the approach to any number of dimensions. Using two complex real-life applications, we provide experimental evidence that ESAGP-2 outperforms ESAGP-1, which in turn outperforms both standard GP and geometric semantic GP. This suggests that ``adding dimensions'' is beneficial and encourages us to pursue the study in many different directions, that we summarize in the final part of the manuscript.

Generalisation Enhancement via Input Space Transformation: A GP Approach (EuroGP best paper candidate) *Ahmed Kattan, Michael Kampouridis, Alexandros Agapitos*

This paper proposes a new approach to improve generalisation of standard regression techniques when there are hundreds or thousands of input variables. The input space X is composed of observational data of the form $(x_i, y(x_i)), i = 1... n$ where each x_i denotes a k-dimensional input vector of design variables and y is the response. Genetic Programming (GP) is used to transform the original input space X into a new input space $Z = (z_i, y(z_i))$ that has smaller input vector and is easier to be mapped into its corresponding responses. GP is designed to evolve a function that receives the original input vector from each x_i in the original input space as input and return a new vector z_i as an output. Each element in the newly evolved z_i vector is generated from an evolved mathematical formula that extracts statistical features from the original input space. To achieve this, we designed GP trees to produce multiple outputs. Empirical evaluation of 20 different problems revealed that the new approach is able to significantly reduce the dimensionality of the original input space and improve the performance of standard approximation models such as Kriging, Radial Basis Functions Networks, and Linear Regression, and GP (as a regression techniques). In addition, results demonstrate that the new approach is better than standard dimensionality reduction techniques such as Principle Component Analysis (PCA). Moreover, the results show that the proposed approach is able to improve the performance of standard Linear Regression and make it competitive to other stochastic regression techniques.

Learning Dynamical Systems Using Standard Symbolic Regression (EuroGP best paper candidate) *Sébastien Gaucel, Maarten Keijzer, Evelyne Lutton, Alberto Tonda*

Symbolic regression has many successful applications in learning free-form regular equations from data. Trying to apply the same approach to differential equations is the logical next step: so far, however, results have not matched the quality obtained with regular equations, mainly due to additional constraints and dependencies between variables that make the problem extremely hard to tackle. In this paper we propose a new approach to dynamic systems learning. Symbolic regression is used to obtain a set of first-order Eulerian approximations of differential equations, and mathematical properties of the approximation are then exploited to reconstruct the original differential equations. Advantages of this technique include the de-coupling of systems of differential equations, that can now be learned independently; the possibility of exploiting established techniques for standard symbolic regression, after trivial operations on the original dataset; and the substantial reduction of computational effort, when compared to existing ad-hoc solutions for the same purpose. Experimental results show the efficacy of the proposed approach on an instance of the Lotka-Volterra model.

EvoBIO Programme

Wednesday 23 April

Wed 1120-1300 **Session 1: Genomics**
Chair: Federico Divina

What Do We Learn from Network-Based Analysis of Genome-Wide Association Data? *Marzieh Ayati, Sinan Erten, Mehmet Koyuturk*
Network based analyses are commonly used as powerful tools to interpret the findings of genome-wide association studies (GWAS) in a functional context. In particular, identification of disease-associated functional modules, i.e., highly connected protein-protein interaction (PPI) subnetworks with high aggregate disease association are shown to be promising in uncovering the functional relationships among disease-associated genes and proteins. An important issue in this regard is the scoring of subnetworks by integrating two quantities that are not readily compatible: disease association of individual gene products and network connectivity among proteins. Current scoring schemes either disregard the level of connectivity and focus on the aggregate disease association of connected proteins or use a linear combination of these two quantities. However, such scoring schemes may produce arbitrarily large subnetworks which are often not statistically significant, or require tuning of parameters that are used to weigh the contributions of network connectivity and disease association. Here, we propose a parameter-free scoring scheme that aims to score subnetworks by assessing the disease association of pairwise interactions and incorporating the statistical significance of network connectivity and disease association. We test the proposed scoring scheme on a GWAS dataset for type II diabetes (T2D). Our results suggest that subnetworks identified by commonly used methods may fail tests of statistical significance after correction for multiple hypothesis testing. In contrast, the proposed scoring scheme yields highly significant subnetworks, which contain biologically relevant proteins that cannot be identified by analysis of genome-wide association data alone.

Benefits Of Accurate Imputations In GWAS *Shefali Setia, Peggy Peissig, Deanna Cross, Carol Waudby, Murray Brilliant, Catherine McCarty, Marylyn Ritchie*
Imputation methods have been suggested as an efficient way to increase both utility and coverage in genome-wide association studies, especially when combining data generated from different genotyping arrays. We aim to demonstrate that imputation results are extremely accurate and the association analysis from imputed data does not over-inflate the results. Instead imputation leads to an increase in the power of the dataset without introducing any systematic biases. The majority of common variants can be imputed with very high accuracy (r 2 >0.9) and we validated the accuracy of imputations by comparing actual genotypes from low-throughput genotyping assays against imputed genotypes. Imputation was performed using IMPUTE2 and the 1000. Genomes cosmopolitan reference panel, which results in about 38 million SNPs. After quality control and filtering we performed case-control associations with 3,159,556 markers. We show a comparison of results from genotyped and imputed data and also determine how accurate ancestry is determined by imputations.

Genotype Correlation Analysis Reveals Pathway-Based Functional Disequilibrium and Potential Epistasis in the Human Interactome *William Bush, Jonathan Haines*
Epistasis is thought to be a pervasive part of complex phenotypes due to the dynamics and complexity of biological systems, and a further understanding of epistasis in the context of biological pathways may provide insight into the etiology of complex disease. In this study, we use genotype data from the International HapMap Project to characterize the functional dependencies between alleles in the human interactome as defined by KEGG pathways. We performed chi-square tests to identify non-independence between functionally-related SNP pairs within parental Caucasian and Yoruba samples. We further refine this list by testing for skewed transmission of pseudo-haplotypes to offspring using a haplotype-based TDT test. From these analyses, we identify pathways enriched for functional disequilibrium, and a set of 863 SNP pairs (representing 453 gene pairs) showing consistent non-independence and transmission distortion. These results represent gene pairs with strong evidence of epistasis within the context of a biological function.

An Integrated Analysis Of Genome-Wide Dna Methylation And Genetic Variants Underlying Etoposide-Induced Cytotoxicity In European And African Populations *Ruowang Li, Dokyoon Kim, Scott Dudek, Marylyn Ritchie*

Genetic variations among individuals account for a large portion of variability in drug response. The underlying mechanism of the variability is still not known, but it is expected to comprise of a wide range of genetic factors that interact and communicate with each other. Here, we present an integrated genome-wide approach to uncover the interactions among genetic factors that can explain some of the inter-individual variation in drug response. The International HapMap consortium generated genotyping data on human lymphoblastoid cell lines of (Center d'Etude du Polymorphisme Humain population – CEU) European descent and (Yoruba population - YRI) African descent. Using genome-wide analysis, Huang et al. identified SNPs that are associated with etoposide, a chemotherapeutic drug, response on the cell lines. Using the same lymphoblastoid cell lines, Fraser et al. generated genome-wide methylation profiles for gene promoter regions. We evaluated associations between candidate SNPs generated by Huang et al and genome-wide methylation sites. The analysis identified a set of methylation sites that are associated with etoposide related SNPs. Using the set of methylation sites and the candidate SNPs, we built an integrated model to explain etoposide response observed in CEU and YRI cell lines. This integrated method can be extended to combine any number of genomics data types to explain many phenotypes of interest.

Wed 1430-1610 **Session 2: Proteins and Proteomics**

Chair: William Bush

Determining Positions Associated With Drug Resistance On HIV-1 Proteins: A Computational Approach *Gonzalo Nápoles, Isel Grau, Ricardo Pérez-García, Rafael Bello*

The computational modeling of HIV-1proteins has become a useful framework allowing understanding the virus behavior (e.g. mutational patterns, replication process or resistance mechanism). For instance, predicting the drug resistance from genotype means to solve a complicated sequence classification problem. In such kind of problems proper feature selection could be essential to increase the classifiers performance. Several sequence positions that have been previously associated with resistance are known, although we believe that other positions could be discovered. More explicitly, we observed that using positions reported in the literature for the reverse transcriptase protein, the final decision system exhibited inconsistent mutations. However, finding a minimal subset of features characterizing the whole sequence involve a challenging combinatorial problem. This research proposes a model based on Variable Mesh Optimization and Rough Sets Theory for computing those sequence positions associated with resistance, leading to more consistent decision systems. Finally, our model is validated across eleven well-known reverse transcriptase inhibitors.

GPMS: A Genetic Programming Based Approach to Multiple Alignment of Liquid Chromatography-Mass Spectrometry Data *Soha Ahmed, Mengjie Zhang, Lifeng Peng*

Alignment of samples from Liquid chromatography-mass spectrometry (LC-MS) measurements has a significant role in the detection of biomarkers and in metabolomic studies. The machine drift causes differences between LC-MS measurements, and an accurate alignment of the shifts introduced to the same peptide or metabolite is needed. In this paper, we propose the use of genetic programming (GP) for multiple alignment of LC-MS data. The proposed approach consists of two main phases. The first phase is the peak matching where the peaks from different LC-MS maps (peak lists) are matched to allow the calculation of the retention time deviation. The second phase is to use GP for multiple alignment of the peak lists with respect to a reference. In this paper, GP is designed to perform multiple-output regression by using a special node in the tree which divides the output of the tree into multiple outputs. Finally, the peaks that show the maximum correlation after dewarping the retention times are selected to form a consensus aligned map.The proposed approach is tested on one proteomics and two metabolomics LC-MS datasets with different number of samples. The method is compared to several benchmark methods and the results show that the proposed approach outperforms these methods in three fractions of the protoemics dataset and the metabolomics dataset with a larger number of maps. Moreover, the results on the rest of the datasets are highly competitive with the other methods.

Wed 1745-1900 **EvoBIO poster**

Replication of SCN5A Associations with Electrocardiographic Traits in African Americans from Clinical and Epidemiologic Studies
Janina Jeff, Kristin Brown-Gentry, Robert Goodloe, Marylyn Ritchie, Joshua Denny, Abel Kho, Loren Armstrong, Bob McClellan, Jr, Ping Mayo; Melissa Allen; Hailing Jin; Niloufar B. Gillani; Nathalie Schnetz-Boutaud; Holli H. Dilks; Melissa A. Basford; Jennifer A. Pacheco; Gail P. Jarvik; Rex L. Chisholm; Dan M. Roden; M. Geoffrey Hayes; Dana C. Crawford
The NAv1.5 sodium channel α subunit is the predominant α-subunit expressed in the heart and is associated with cardiac arrhythmias. We tested five previously identified SCN5A variants (rs7374138, rs7637849, rs7637849, rs7629265, and rs11129796) for an association with PR interval and QRS duration in two unique study populations: the Third National Health and Nutrition Survey (NHANES III,n=552) accessed by the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) as part of the Population Architecture using Genomics and Epidemiology (PAGE) I study and a combined dataset (n=455) from two biobanks linked to electronic medical records from Vanderbilt University (BioVU) and Northwestern University (Nugene) as part of the electronic Medical Records & Genomics (eMERGE) network. A meta-analysis including all three study populations (n~4,000) suggests that eight SCN5A associations were significant for both QRS duration and PR interval (p<5.0E-3). There was little evidence for heterogeneity across the study populations for either trait. These results suggest that published SCN5A associations replicate across different study designs in a meta-analysis and represent an important first step in utility of multiple study designs for genetic studies and the identification/characterization of genetic variants associated with ECG traits in African-descent populations.

EvoCOP Programme

Thursday 24 April 2014

Thurs 0930-1110 **Session 1: Swarm Intelligence Algorithms**
Chair: Christian Blum

The Influence of Correlated Objectives on Different Types of P-ACO Algorithms
Ruby L. V. Moritz, Enrico Reich, Matthias Bernt and Martin Middendorf
The influence of correlated objectives on different types of P-ACO algorithms for solutions of multi objective optimization problems is investigated. Therefore, a simple method to create multi objective optimization problems with correlated objectives is proposed. Theoretical results show how certain correlations between the objectives can be obtained. The method is applied to the Traveling Salesperson problem. The influence of the correlation type and strength on the optimization behavior of different P-ACO algorithms is analyzed empirically. A particular focus is given on P-ACOs with ranking methods.

Gaussian Based Particle Swarm Optimisation and Statistical Clustering for Feature Selection *Mitchell C. Lane, Bing Xue, Ivy Liu and Mengjie Zhang*
Feature selection is an important but difficult task in classification, which aims to reduce the number of features and maintain or even increase the classification accuracy. This paper proposes a new particle swarm optimisation (PSO) algorithm using statistical clustering information to solve feature selection problems. Based on Gaussian distribution, a new updating mechanism is developed to allow the use of the clustering information during the evolutionary process of PSO based on which a new algorithm (GPSO) is developed. The proposed algorithm is examined and compared with two traditional algorithms and a PSO based algorithm which does not use clustering information on eight benchmark datasets of varying difficulty. The results show that GPSO can be successfully used for feature selection to reduce the number of features and achieve similar or even better classification performance than using all features. Meanwhile, it achieves better performance than the two traditional feature selection algorithms. It maintains the classification performance achieved by the standard PSO for feature selection algorithm, but significantly reduces the number of features and the computational cost.

Modeling an Artificial Bee Colony with inspector for clustering tasks *Cosimo Birtolo, Giovanni Capasso, Davide Ronca and Gennaro Sorrentino*
Artificial Bee Colony (ABC) is a recent meta-heuristic approach. In this paper we face the problem of clustering by ABC and we model a further bee role in the colony, performed by inspector bee. This model conforms with real honey bee colony, indeed, in nature some bees among the foraging ones are called inspectors because they preserve the colony's history and historical information related to food sources. We experiment inspector behavior in ABC and compare the solution to traditional clustering algorithm. Finally, the effect of colony size is investigated and experimental results are discussed.

The Firefighter Problem: Application of Hybrid Ant Colony Optimization Algorithms *Christian Blum, Maria J. Blesa, Carlos García-Martínez, Francisco J Rodríguez and Manuel Lozano*
The firefigther problem is a deterministic discrete-time model for the spread (and the containment) of fire on an undirected graph. Assuming that the fire breaks out at a predefined set of vertices, the goal is to save as many vertices as possible from burning. The same model has also been used in the literature for the simulation of the spreading of deseases. In this work we present, to our knowledge, the first metaheuristics for tackling this problem. In particular, a pure ant colony optimization approach and a hybrid variant of this algorithm are proposed. The results show that the hybrid ant colony optimization variant is superior to the pure ant colony optimization version and to a mathematical programming solver, especially when the graph size and density grows.

Thurs 1135-1315 **Session 2: Fitness Landscapes and Adaptive Algorithms**
Chair: Francisco Chicano

Phase Transition and Landscape Properties of the Number Partitioning Problem *Khulood Alyahya and Jonathan E. Rowe*
This paper empirically studies basic properties of the fitness landscape of random instances of number partitioning problem, with a focus on how these properties change with the phase transition. The properties include number of local and global optima, number of plateaus, basin size and its correlation with fitness. The only two properties that were found to change when the problem crosses the phase transition are the number of global optima and the number of plateaus, the rest of the properties remained oblivious to the phase transition. This paper, also, studies the effect of different distributions of the weights and different neighbourhood operators on the problem landscape.

Global Optimization of Multimodal Deceptive Functions *David Iclanzan*
Local search algorithms operating in high-dimensional and multimodal search spaces often suffer from getting trapped in a local optima, therefore requiring many restarts. Even with multiple restarts, their search efficiency critically depends on the choice of the neighborhood structure. In this paper we propose an approach in which the need for the restarts is exploited to improve the neighborhood definitions. Namely, a graph clustering based linkage detection method is used to mine the information from several runs, in order to extract variable dependencies and update the neighborhood structure, variation operators accordingly. We show that the adaptive neighborhood structure approach enables the efficient solving of challenging global optimization problems that are both deceptive and multimodal.

An Analysis of Parameters of irace *Leslie Pérez Cáceres, Manuel López-Ibáñez and Thomas Stützle*
The irace package implements a flexible tool for the automatic configuration of algorithms. However, irace itself has specific parameters to customize the search process according to the tuning scenario. In this paper, we analyze five parameters of irace: the number of iterations, the number of instances seen before the first elimination test, the maximum number of elite configurations, the statistical test and the confidence level of the statistical test. These parameters define some key aspects of the way irace identifies good configurations. Originally, their values have been set based on rules of thumb and an intuitive understanding of the configuration process. This work aims at giving insights about the sensitivity of irace to these parameters in order to guide their setting and further improvement of irace.

Elementary Landscape Decomposition of the Hamiltonian Path Optimization Problem *Darrell Whitley and Francisco Chicano*

There exist local search landscapes where the evaluation function is an eigenfunction of the graph Laplacian that corresponds to the neighborhood structure of the search space. Problems that display this structure are called Elementary Landscapes and they have a number of special mathematical properties. The problems that are not elementary landscapes can be decomposed in a sum of elementary ones. This sum is called the elementary landscape decomposition of the problem. In this paper, we provide the elementary landscape decomposition for the Hamiltonian Path Optimization Problem under two different neighborhoods.

Thurs 1430-1610 **Session 3: Real World and Routing Problems**

Chair: Bin Hu

Personalized Multi-Day Trips to Touristic Regions: A hybrid GA-VND approach

Ali Divsalar, Pieter Vansteenwegen, Masoud Chitsaz, Kenneth Sörensen and Dirk Cattrysse

When a tourist is visiting a large region with many attractions, frequently there is not enough time to reach all of them. Moreover when the journey takes more than a day, at the end of each day an accomodation place should be selected to continue the trip the next day. In this research, we introduce the Orienteering Problem with Hotel Selection and Time Windows (OPHS-TW) in order to model this real application. A set of 395 benchmark instances with known optimal solution are created and a hybrid Genetic Algorithm with a Variable Neighborhood Descent (GA-VND) phase is developed to efficiently solve the instances in a reasonable time.

An Improved Multi-Objective Algorithm for the Urban Transit Routing Problem

Matthew P. John, Christine L. Mumford and Rhyd Lewis

The determination of efficient routes and schedules in public transport systems is complex due to the vast search space and multiple constraints involved. In this paper we focus on the Urban Transit Routing Problem concerned with the physical network design of public transport systems. Historically, route planners have used their local knowledge coupled with simple guidelines to produce network designs. Several major studies have identified the need for automated tools to aid in the design and evaluation of public transport networks. We propose a new construction heuristic used to seed a multi-objective evolutionary algorithm. Several problem specific mutation operators are then combined with an NSGAII framework leading to improvements upon previously published results.

Dynamic Period Routing for a Complex Real-World System: A Case Study in Storm Drain Maintenance *Yujie Chen, Peter Cowling and Stephen Remde*

This paper presents a case study of a real world storm drain maintenance problem where we must construct daily routes for a maintenance vehicle while considering the dynamic condition and social value of drains. To represent our problem, a dynamic period vehicle routing problem with profit (DPVRPP) model is proposed. This differs from the classical period routing problem in a number of ways. Firstly, it is dynamic: during the planning horizon, the demands from damaged drains and residents reports arrive continuously. In addition, the drains condition is changing over time. Secondly, our objective is maximizing the profit, defined here as the drains condition with respect to its social value. This study is based on large-scale data provided by Gaist Solutions Ltd. and the council of a UK town (Blackpool). We propose an adaptive planning heuristic (APH) that produces daily routes based on our model and an estimation of changing drain condition in the future. Computational results show that the APH approach can, within reasonable CPU time, produce much higher quality solutions than the scheduling strategy currently implemented by Blackpool council.

Metaheuristics for the Pick-up and Delivery Problem with Contracted Orders

Philip Mourdjis, Peter Cowling and Martin Robinson

Contracted orders represent a novel extension to the Pick-up and Delivery Problem (PDP) with soft time windows. This extension to the multiple depot problem has depots managed by separate, competing haulage companies ``carriers''. Orders may be assigned to a specific carrier ``contracted'', ``allocated'' to a specific carrier but allowed to swap if this improves the solution or free to use any carrier ``spot hired''. Soft time windows lead to a multi-objective problem of minimising distance travelled and delay incurred. In this paper we use real order data supplied by 3 large distributors and 220 carriers. Additional, randomised, orders are generated to match the distributions observed in this data, representing backhaul orders for which no data is available. We compare a manual scheduling technique based on discussions with industry partners to popular metaheuristics for similar problems namely Tabu Search (TS), Variable Neighbourhood Search (VNS) and Hybrid Variable Neighbourhood

Tabu Search (HVNTS), using our modified local search operators. Results show that VNS and HVNTS produce results which are 50% shorter than greedy approaches across test instances of 300 orders in a one week period.

Thurs 1630-1810 **Session 4: Cooperative and Meta-heuristic Search**

Chair: Darrel Whitley

A Survey of Meta-Heuristics used for Computing Maximin Latin Hypercube

Arpad Rimmel and Fabien Teytaud

Finding maximin latin hypercube is a discrete optimization problem believed to be NP-hard. In this paper, we compare different meta-heuristics used to tackle this problem: genetic algorithm, simulated annealing and iterated local search. We also measure the importance of the choice of the mutation operator and the evaluation function. All the experiments are done using a fixed number of evaluations to allow future comparisons. Simulated annealing is the algorithm that performed the best. By using it, we obtained new highscores for a very large number of latin hypercubes.

Cooperative Selection: Improving Tournament Selection via Altruism *Juan Luis Giménez Laredo, Sune S. Nielsen, Grégoire Danoy, Pascal Bouvry and Carlos M. Fernandes*

This paper analyzes the dynamics of a new selection scheme based on altruistic cooperation between individuals. The scheme, which we refer to as cooperative selection, extends from tournament selection and imposes a stringent restriction on the mating chances of an individual during its lifespan: winning a tournament entails a depreciation of its fitness value. We show that altruism minimizes the loss of genetic diversity while increasing the selection frequency of the fittest individuals. An additional contribution of this paper is the formulation of a new combinatorial problem for maximizing the similarity of proteins based on their secondary structure. We conduct experiments on this problem in order to validate cooperative selection. The new selection scheme outperforms tournament selection for any setting of the parameters and is the best trade-off, maximizing genetic diversity and minimizing computational efforts.

An Iterated Greedy heuristic for simultaneous lot-sizing and scheduling problem in production flow shop environments *Harlem M. M. Villadiego, José Elias C. Arroyo, and André Gustavo dos Santos*

In this work, we consider the integrated lot-sizing and sequencing problem in a permutation flow shop with machine sequence-dependent setups. The problem is to determine the lot sizes and the production sequence in each period of a planning horizon such that the customer demands must be met and the capacity of the machines must be respected. The objective is to determine the sum of the setup costs, the production costs and the inventory costs over the planning horizon. Due to the complexity of the problem, we propose a heuristic based on Iterated Greedy metaheuristic which uses sequencing and lot-sizing decisions. The proposed method is compared against the best heuristics available in the literature in a large set of problem instances. Comprehensive computational and statistical analyses are carried out in order to validate the performance of the proposed heuristic.

A Parametric Framework for Cooperative Parallel Local Search *Danny Munera, Daniel Diaz, Salvador Abreu, and Philippe Codognet*

In this paper we address the problem of parallelizing local search. We propose a general framework where different local search engines cooperate (through communication) in the quest for a solution. Several parameters allow the user to instantiate and customize the framework, like the degree of intensification and diversification. We implemented a prototype in the X10 programming language based on the adaptive search method. We decided to use X10 in order to benefit from its ease of use and the architectural independence from parallel resources which it offers. Initial experiments prove the approach to be successful, as it outperforms previous systems as the number of processes increases.

Friday 25 April

Fri 0930-1110 **Session 5: EvoCOP Best-paper Nominations**
Chair: Gabriela Ochoa

Diversity-Driven Selection of Multiple Crossover Operators for the Capacitated Arc Routing Problem (EvoCOP best paper candidate) *Pietro Consoli and Xin Yao*
The Capacitated Arc Routing Problem (CARP) is a NP-Hard routing problem with strong connections with real world problems. In this work we aim to enhance the performance of MAENS, a state-of-the-art algorithm, through a self-adaptive scheme to choose the most suitable operator and a diversity-driven ranking operator. Experimental results on 181 problem instances show how these techniques can both improve the results of the current state-of-the-art algorithms and provide good directions to develop EAs with a more robust approximation ratio.

Learning Inherent Networks from Stochastic Search Methods (EvoCOP best paper candidate) *David Iclanzan, Fabio Daolio and Marco Tomassini*
Analysis and modeling of search heuristics operating on complex problems is a difficult albeit important research area. Inherent networks, i.e. the graphs whose vertices represent local optima and the edges describe the weighted transition probabilities between them, enable a network characterization of combinatorial fitness landscapes. Methods revealing such inherent structures of the search spaces in relation to deterministic move operators, have been recently developed for small problem instances. This work proposes a more general, scalable, data-driven approach, that extracts the transition probabilities from actual runs of metaheuristics, capturing the effect and interplay of a broader spectrum of factors. Using the case of NK landscapes, we show that such an unsupervised learning approach is successful in quickly providing a coherent view of the inherent network of a problem instance.

Balancing Bicycle Sharing Systems: An Approach for the Dynamic Case (EvoCOP best paper candidate) *Christian Kloimüllner, Petrina Papazek, Bin Hu and Günther R. Raidl*
Operators of public bicycle sharing systems (BSSs) have to regularly redistribute bikes across their stations in order to avoid them getting overly full or empty. We consider the dynamic case where this is done while the system is in use. There are two main objectives: On the one hand it is desirable to reach particular target fill levels at the end of the process so that the stations are likely to meet user demands for the upcoming day(s). On the other hand operators also want to prevent stations from running empty or full during the rebalancing process which would lead to unsatisfied customers. We extend our previous work on the static variant of the problem by introducing an efficient way to model the dynamic case as well as adapting our previous greedy and PILOT construction heuristic, variable neighborhood search and GRASP. Computational experiments are performed on instances based on real-world data from Citybike Wien, a BSS operator in Vienna, where the model for user demands is derived from historical data.

A Hybrid Ant Colony Optimization Algorithm for the Far From Most String Problem (EvoCOP best paper candidate) *Christian Blum and Paola Festa*
The far from most string problem belongs to the family of string selection and comparison problems known as sequence consensus problems, where a finite set of sequences is given and one is interested in finding their consensus, that is, a new sequence that represents as much as possible all the given sequences. Among the consensus problems, the far from most string problem is computationally one of the hardest ones with applications in several fields, including molecular biology where one is interested in creating diagnostic probes for bacterial infections or in discovering potential drug targets. This paper comes with several contributions. On one side, the first linear integer programming formulation for the considered problem is introduced. On the other side, a hybrid ant colony optimization approach for finding good approximate solution to the problem is proposed. Both approaches are compared to the current state of the art, which is a recently proposed hybrid GRASP with path-relinking. Computational results on a large set of randomly generated test instances indicate that the hybrid ACO is very competitive.

EvoMUSART Programme

Wed 1745-1900 **EvoMUSART posters**

An Indirect Fitness Scheme for Automated Evolution of Aesthetic Images *Gary Greenfield*

Recently, the question of whether artifacts obtained from a generative art system can be judged as creative based on the characteristics of their offspring has received considerable attention. Here, we focus on the question of whether aesthetic images can be evolved by considering characteristics of their offspring. We introduce a formal model for designing fitness functions for use in automated evolution of aesthetic images whereby genotypes are evaluated relative to certain characteristics of their offspring. We describe the results of an experiment using such an indirect fitness scheme that promotes offspring diversity in order to help select for parent phenotypes with desired symmetry and complexity properties. We use as our image generation platform a variant of the Sims' classical Evolving Expressions generative art system.

Genomic: Evolving Sound Treatments Using Genetic Algorithms *Thomas Stoll*

There are many systems for the evolution of creative musical material, that create and/or manipulate musical score data or synthesis parameters with a variety of techniques. This paper aims to add the technique of corpus-based sound sampling and processing to the list of applications used in conjunction with genetic algorithms. Genomic, a simple system for evolving sound treatment parameters, is presented, along with two simple use cases. Finally, a more complex process is outlined where sound treatment parameters are evolved and stored in a database with associated metadata for further organization and compositional use.

Size Does Not Matter: Evolving Parameters for a Cayley Graph Visualiser using 64 bits *Miguel Nicolau, Dan Costelloe*

In this paper, an Interactive Evolutionary system is described, which generates visually appealing 3D projections of mathematical constructs. This system uses a combination of the Grammatical Evolution paradigm and Jenn3d, a visualiser of Cayley graphs of finite Coxeter groups. A very compact representation is used for the genotype strings, using only 64 bits. The resulting visualisations, albeit somewhat restricted, still exhibit a large degree of complexity and evolvability, and are well representative of the domain.

Thursday 24 April

Thurs 1135-1315 **Session 1: Aesthetics**
Chair: Jon McCormack

Feature Construction using Genetic Programming for Classification of Images by Aesthetic Value *Andrew Bishop, Vic Ciesielski and Karen Trist*

Classification or rating of images according to their aesthetic quality has applications in areas such as image search, compression and photography. It requires the construction of features that are predictive of the aesthetic quality of an image. Constructing features manually for aesthetics prediction is challenging. We propose an approach to improve on manually designed features by constructing them using genetic programming and image processing operations implemented using OpenCV. We show that this approach can produce features that perform well. Classification accuracies of up to 81% on photographs and 92% on computationally generated images have been achieved. Both of these results significantly improve on existing manually designed features.

A complexity approach for identifying aesthetic composite landscapes *Adrian Carballal, Rebeca Perez, Antonino Santos and Luz Castro*

The present paper describes a series of features related to complexity which may allow to estimate the complexity of an image as a whole, of all the elements integrating it and of those which are its focus of attention. Using a neural network to create a classifier based on those features an accuracy over 85% in an aesthetic composition binary classification task is achieved. The obtained network seems to be useful for the purpose of assessing the Aesthetic Composition of landscapes. It could be

used as part of a media device for facilitating the creation of images or videos with a more professional aesthetic composition.

Authorship and aesthetics experiments. Comparison of results between Human and Computational Systems *Luz Castro, Rebeca Perez, Antonino Santos and Adrian Carballal*

This paper presents the results of two experiments comparing the functioning of a computational system and a group of humans when performing tasks related to art and aesthetics. The first experiment consists of the identification of a painting, while the second one uses the Maitland Graves's aesthetic appreciation test. The proposed system employs a series of metrics based on complexity estimators and low level features. These metrics feed a learning system using neural networks. The computational approach achieves similar results to those achieved by humans, thus suggesting that the system captures some of the artistic style and aesthetics features which are relevant to the experiments performed.

1430-1610 **Session 2: Interaction**

Chair: James McDermott

Probabilistic Decision Making for Interactive Evolution with Sensitivity Analysis (EvoMUSART best paper candidate) *Jonathan Eisenmann, Matthew Lewis and Rick Parent*

Recent research in the area of evolutionary algorithms and interactive design tools for ideation has investigated how sensitivity analysis can be used to enable region-of-interest selection on design candidates. Even though it provides more precise control over the evolutionary search to the designer, the existing methodology for this enhancement to evolutionary algorithms does not make full use of the information provided by sensitivity analysis and may lead to premature convergence. In this paper, we describe the shortcomings of previous research on this topic and introduce an approach that mitigates the problem of early convergence. A discussion of the trade-offs of different approaches to sensitivity analysis is provided as well as a demonstration of this new technique on a parametric model built for character design ideation.

An Interface for Fitness Function Design

(EvoMUSART best paper candidate) *Penousal Machado, Tiago Martins, Hugo Amaro and Pedro H. Abreu*

Fitness assignment is one of the biggest challenges in evolutionary art. Interactive evolutionary computation approaches put a significant burden on the user, leading to human fatigue. On the other hand, autonomous evolutionary art systems usually fail to give the users the opportunity to express and convey their artistic goals and preferences. Our approach empowers the users by allowing them to express their intentions through the design of fitness functions. We present a novel responsive interface for designing fitness function in the scope of evolutionary ant paintings. Once the evolutionary runs are concluded, further control is given to the users by allowing them to specify the rendering details of selected pieces. The analysis of the experimental results highlights how fitness function design influences the outcomes of the evolutionary runs, conveying the intentions of the user and enabling the evolution of a wide variety of images.

1630-1810 **Session 3: Miscellaneous**

Chair: Gary Greenfield

Evolving an Aircraft Using a Parametric Design System *Jonathan Byrne, Philip Cardiff, Anthony Brabazon and Michael O'Neill*

Traditional CAD tools generate a static solution to a design problem. Parametric systems allow the user to explore many variations on that design theme. Such systems make the computer a generative design tool and are already used extensively as a rapid prototyping technique in architecture and aeronautics. Combining a design generation tool with an evolutionary algorithm provides a methodology for optimising designs. This works uses NASA's parametric aircraft design tool (OpenVSP) and an evolutionary algorithm to evolve a range of aircraft that maximise lift and reduce drag while remaining within the framework of the original design. Our approach allows the designer to automatically optimise their chosen design and to generate models with improved aerodynamic efficiency.

A Novelty Search and Power-Law-Based Genetic Algorithm for Exploring Harmonic Spaces in J.S. Bach Chorales *Bill Manaris, David Johnson and Yiorgos Vassilandonakis*

We present a novel, real-time system, called Harmonic Navigator, for exploring the harmonic space in J.S. Bach Chorales. This corpus-based environment explores trajectories through harmonic space. It supports visual exploration and navigation of harmonic transition probabilities through interactive gesture control. These probabilities are computed from musical corpora (in MIDI format). Herein we utilize the 371 J.S. Bach Chorales of the Riemenschneider edition. Our system utilizes a hybrid novelty search approach combined with power-law metrics for evaluating fitness of individuals, as a search termination criterion. We explore how novelty search can aid in the discovery of new harmonic progressions through this space as represented by a Markov model capturing probabilities of transitions between harmonies. Our results demonstrate that the 371 Bach Chorale harmonic space is rich with novel aesthetic possibilities, possibilities that the grand master himself never realized.

Balancing Act: variation and utility in Evolutionary Art *Jon McCormack*

Evolutionary Art typically involves a tradeoff between the size and flexibility of genotype space and its mapping to an expressive phenotype space. Ideally we would like a genotypic representation that is terse but expressive, that is, we want to maximise the useful variations the genotype is capable of expressing in phenotype space. Terseness is necessary to minimise the size of the overall search space, and expressiveness can be loosely interpreted as phenotypes that are useful (of high fitness) and diverse (in feature space). In this paper I describe a system that attempts to maximise this ratio between terseness and expressiveness. The system uses a binary string up to any maximum length as the genotype. The genotype string is interpreted as building instructions for a graph, similar to the cellular programming techniques used to evolve artificial neural networks. The graph is then interpreted as a form-building automaton that can construct animated 3-dimensional forms of arbitrary complexity. In the test case the requirement for expressiveness is that the resultant form must have recognisable biomorphic properties and that every possible genotype must fulfil this condition. After much experimentation, a number of constraints in the mapping technique were devised to satisfy this condition. These include a special set of geometric building operators that take into account morphological properties of the generated form. These methods were used in the evolutionary artwork 'Codeform', developed for the Ars Electronica museum. The work generated evolved virtual creatures based on genomes acquired from the QR codes on museum visitor's entry tickets.

EvoAPPLICATIONS Programme

Wednesday 23 April

Wed 1120-1300 **EvoCOMNET 1**
Chair: Domenico Maisto

Evolving a Trust Model for Peer-To-Peer Systems Using Genetic Programming *Ugur Eray Tahta, Ahmet Burak Can, Sevil Sen*

Peer-to-peer (P2P) systems have attracted significant interest in recent years. In P2P networks, each peer act as both a server or a client. This characteristic makes peers vulnerable to a wide variety of attacks. Having robust trust management is very critical for such open environments to exclude unreliable peers from the system. This paper investigates the use of genetic programming to asses the trustworthiness of peers without a central authority. A trust management model is proposed in which each peer ranks other peers according to local trust values calculated automatically based on the past interactions and recommendations. The experimental results have shown that the model could successfully identify malicious peers without using a central authority or global trust values and, improve the system performance.

A hybrid primal heuristic for Robust Multiperiod Network Design (EvoCOMNET best paper candidate) *Fabio D'Andreagiovanni, Jonatan Krolikowski, Jonad Pulaj*

We investigate the Robust Multiperiod Network Design Problem, a generalization of the classical Capacitated Network Design Problem which additionally considers multiple design periods and

provides solutions protected against traffic uncertainty. Given the intrinsic difficulty of the problem, we propose a hybrid primal heuristic based on the combination of ant colony optimization and an exact large neighborhood search. Computational experiments on a set of realistic instances from the SNDlib show that our heuristic can find solutions of extremely good quality with low optimality gap.

A Trajectory-based Heuristic to Solve a Three-Objective Optimization Problem for Wireless Sensor Network Deployment (EvoCOMNET best paper candidate)
Jose M. Lanza-Gutierrez, Juan A. Gomez-Pulido, Miguel A. Vega-Rodríguez
Nowadays, wireless sensor networks (WSNs) are widely used in more and more fields of application. However, there are some important shortcomings which have not been solved yet in the current literature. This paper focuses on how to add relay nodes to previously established static WSNs with the purpose of optimizing three important factors: energy consumption, average coverage and network reliability. As this is an NP-hard multiobjective optimization problem, we consider two well-known genetic algorithms (NSGA-II and SPEA2) and a multiobjective approach of the variable neighborhood search algorithm (MO-VNS). These metaheuristics are used to solve the problem from a freely available data set, analyzing all the results obtained by considering two multiobjective quality indicators (hypervolume and set coverage). We conclude that MO-VNS provides better performance on average than the standard algorithms NSGA-II and SPEA2.

Wed 1430-1610 **EvoCOMNET 2**
Chair: Domenico Maisto

Optimizing AEDB Broadcasting Protocol with Parallel Multi-objective Cooperative Coevolutionary NSGAII *Bernabe Dorronsoro, Patricia Ruiz, El-Ghazali Talbi, Pascal Bouvry, Apivadee Piyatumrong*
Due to the highly unpredictable topology of ad hoc networks, most of the existing communication protocols rely on different thresholds for adapting their behavior to the environment. Good performance is required under any circumstances. Therefore, finding the optimal configuration for those protocols and algorithms implemented in these networks is a complex task. We propose in this work to automatically fine tune the AEDB broadcasting protocol for MANETs thanks to the use of cooperative coevolutionary multi-objective evolutionary algorithms. AEDB is an advanced adaptive protocol based on the Distance Based broadcasting algorithm that acts differently according to local information to minimize the energy and network use, while maximizing the coverage of the broadcasting process. In this work, it will be fine tuned using multi-objective techniques in terms of the conflicting objectives: coverage, energy and network resources, subject to a broadcast time constraint. Because of the few parameters of AEDB, we defined new versions of the problem in which variables are discretized into bit-strings, making it more suitable for cooperative coevolutionary algorithms. Two versions of the proposed method are evaluated and compared versus the original NSGA-II, providing highly accurate tradeoff configurations in shorter execution times.

Improving Extremal Optimization in Load Balancing by Local Search *Ivanoe de Falco, Eryk Laskowski, Richard Olejnik, Umberto Scafuri, Ernesto Tarantino, Marek Tudruj*
The paper concerns the use of Extremal Optimization (EO) technique in dynamic load balancing for optimized execution of distributed programs. EO approach is used to periodically detect the best candidates for task migration leading to balanced execution. To improve the quality of load balancing and decrease time complexity of the algorithms, we have improved EO by a local search of the best computing node to receive migrating tasks. The improved guided EO algorithm assumes a two-step stochastic selection based on two separate fitness functions. The functions are based on specific program models which estimate relations between the programs and the executive hardware. The proposed load balancing algorithm is compared against a standard EO-based algorithm with random placement of migrated tasks and a classic genetic algorithm. The algorithm is assessed by experiments with simulated load balancing of distributed program graphs and analysis of the outcome of the discussed approaches.

Studying the Reporting Cells Planning with the Non-dominated Sorting Genetic

Algorithm II *Víctor Berrocal-Plaza, Miguel A. Vega-Rodríguez and Juan M. Sánchez-Pérez*
This manuscript addresses a vital task in any Public Land Mobile Network, the mobile location management. This management task is tackled following the Reporting Cells strategy. Basically, the Reporting Cells planning consists in selecting a subset of network cells as Reporting Cells with the aim of controlling the subscribers' movement and minimizing the signaling traffic. In previous works, the Reporting Cells Planning Problem was optimized by using single-objective metaheuristics, in which the two objective functions were linearly combined. This technique simplifies the optimization problem but has got several drawbacks. In this work, with the aim of avoiding such drawbacks, we have adapted a well-known multiobjective metaheuristic: the Non-dominated Sorting Genetic Algorithm II (NSGAII). Furthermore, a multiobjective approach obtains a wide range of solutions (each one related to a specific trade-off between objectives), and hence, it gives the possibility of selecting the solution that best adjusts to the real state of the signaling network. The quality of our proposal is checked by means of an experimental study, where we demonstrate that our version of NSGAII outperforms other algorithms published in the literature.

Wed 1120-1300 **EvoFIN 1**
Chair: Ahmed Kattan

On PBIL, DE and PSO for Optimization of Reinsurance Contracts *Omar Andres Carmona Cortes, Andrew Rau-Chaplin, Duane Wilson, Jürgen Gaiser-Porter*
In this paper, we study from the perspective of an insurance company the Reinsurance Contract Placement problem. Given a reinsurance contract consisting of a fixed number of layers and a set of expected loss distributions (one per layer) as produced by a Catastrophe Model, plus a model of current costs in the global reinsurance market, identifying optimal combinations of placements (percent shares of sub-contracts) such that for a given expected return the associated risk value is minimized. Our approach is to explore the use evolutionary algorithms with the goal of determining which evolutionary optimization approach leads to the best results for this problem, while being executable in a reasonable amount of time of realistic industrial sized problems. Our approach evaluates the performance of the algorithms solving larger "real world" problem instances than previous methods.

Algebraic level-set approach for the segmentation of financial time series *Rita Palivonaite, Kristina Lukoseviciute, Minvydas Ragulskis*
Adaptive algebraic level-set time segmentation algorithm of financial time series is presented in this paper. The proposed algorithm is based on the algebraic one step-forward predictor with internal smoothing, which is used to identify a near optimal algebraic model. Particle swarm optimization algorithm is exploited for the detection of a base algebraic fragment of the time series. A combinatorial algorithm is used to detect intervals where predictions are lower than a predefined level. Moreover, the combinatorial algorithm does assess the simplicity of the identified near optimal algebraic model. Automatic adaptive identification of quasi-stationary segments can be employed for complex financial time series.

Dynamic Index Trading using a Gene Regulatory Network Model *Miguel Nicolau, Michael O'Neill, Anthony Brabazon*
This paper presents a realistic study of applying a gene regulatory model to financial prediction. The combined adaptation of evolutionary and developmental processes used in the model highlight its suitability to dynamic domains, and the results obtained show the potential of this approach for real-world trading.

Geometric Semantic Genetic Programming for Financial Data *James McDermott, Alexandros Agapitos, Anthony Brabazon, Michael O'Neill*
We cast financial trading as a symbolic regression problem on the lagged time series, and test a state of the art symbolic regression method on it. The system is geometric semantic genetic programming, which achieves good performance by converting the fitness landscape to a cone landscape which can be searched by hill-climbing. Two novel variants are introduced and tested also, as well as a standard

hill-climbing genetic programming method. Baselines are provided by buy-and-hold and ARIMA. Results are promising for the novel methods, which produce smaller trees than the existing geometric semantic method. Results are also surprisingly good for standard genetic programming. New insights into the behaviour of geometric semantic genetic programming are also generated.

Wed 1430-1610 **EvoFIN 2**

Chair: Michael Kampouridis

Analysis of Dynamic Properties of Stock Market Trading Experts Optimized with Evolutionary Algorithm *Krzysztof Michalak*

This paper concerns optimization of trading experts that are used for generating investment decisions. A population of trading experts is optimized using dynamic evolutionary algorithm. In the paper a new method is proposed which allows analyzing and visualizing the behaviour of optimized trading experts over a period of time. The application of this method resulted in an observation that during certain intervals of time the behaviour of the optimized trading experts becomes more stable. The trading experts that remain unchanged for a long time seem to be well adapted and their fitness does not deteriorate with time.

A Comparative Study on the Use of Classification Algorithms in Financial Forecasting *Fernando Otero, Michael Kampouridis*

Financial forecasting is a vital area in computational finance, where several studies have taken place over the years. One way of viewing financial forecasting is as a classification problem, where the goal is to find a model that represents the predictive relationships between predictor attribute values and class attribute values. In this paper we present a comparative study between two bio-inspired classification algorithms, a genetic programming algorithm especially designed for financial forecasting, and an ant colony optimization one, which is designed for classification problems. In addition, we compare the above algorithms with two other state-of-the-art classification algorithms, namely C4.5 and RIPPER. Results show that the ant colony optimization classification algorithm is very successful, significantly outperforming all other algorithms in the given classification problems, which provides insights for improving the design of specific financial forecasting algorithms.

Pattern Mining in Ultra-High Frequency Order Books with Self-Organizing Maps *Piotr Lipinski, Anthony Brabazon*

This paper addresses the issue of discovering frequent patterns in order book shapes, in the context of the stock market depth, for ultra-high frequency data. It proposes a computational intelligence approach to building frequent patterns by clustering order book shapes with Self-Organizing Maps. An experimental evaluation of the approach proposed on the London Stock Exchange Rebuild Order Book database succeeded with providing a number of characteristic shape patterns and also with estimating probabilities of some typical transitions between shape patterns in the order book.

On evolving multi-agent FX traders *Alexander Loginov, Malcolm Heywood*

Current frameworks for identifying trading agents using machine learning are able to simultaneously address the characterization of both technical indicator and decision tree. Moreover, multi-agent frameworks have also been proposed with the goal of improving the reliability and trust in the agent policy identified. Such advances need weighing against the computational overhead of assuming such flexibility. In this work a framework for evolutionary multi-agent trading is introduced and systematically benchmarked for FX currency trading; including the impact of FX trading spread. It is demonstrated that simplifications can be made to the `base' trading agent that do not impact on the quality of solutions, but provide considerable computational speedups. The resulting evolutionary multi-agent architecture is demonstrated to provide significant benefits to the profitability and improve the reliability with which profitable policies are returned.

Wed 1120-1300 **EvoGAMES 1**
Chair: Paolo Burrelli

Multi-Criteria Comparison of Coevolution and Temporal Difference Learning on Othello *Wojciech Jaśkowski, Marcin Szubert, Paweł Liskowsk*

We compare Temporal Difference Learning (TDL) with Coevolutionary Learning (CEL) on Othello. Apart from using three popular single-criteria performance measures: i) generalization performance or expected utility, ii) average results against a hand-crafted heuristic and iii) result in a head to head match, we compare the algorithms using performance profiles. This multi-criteria performance measure characterizes player's performance in the context of opponents of various strength. The multi-criteria analysis reveals that although the generalization performance of players produced by the two algorithms is similar, TDL is much better at playing against strong opponents, while CEL copes better against weak ones. We also find out that the TDL produces less diverse strategies than CEL. Our results confirms the usefulness of performance profiles as a tool for comparison of learning algorithms for games.

Evolving Evil: Optimizing Flocking Strategies through Genetic Algorithms for the Ghost Team in the Game of Ms. Pac-Man *Federico Liberatore, Antonio Mora, Pedro Castillo, Juan Julián Merelo*

Flocking strategies are sets of behavior rules for the interaction of agents that allow to devise controllers with reduced complexity that generate emerging behavior. In this paper, we present an application of genetic algorithms and flocking strategies to control the Ghost Team in the game Ms. Pac-Man. In particular, we define flocking strategies for the Ghost Team and optimize them for robustness with respect to the stochastic elements of the game and effectivity against different possible opponents by means of genetic algorithm. The performance of the methodology proposed is tested and compared with that of other standard controllers. The results show that flocking strategies are capable of modeling complex behaviors and produce effective and challenging agents.

Procedural Content Generation Using Patterns as Objectives *Steve Dahlskog, Julian Togelius*

In this paper we present a search-based approach for procedural generation of game levels that represents levels as sequences of micro-patterns and searched for meso-patterns. The micro-patterns are "slices" of original human-designed levels from an existing game, whereas the meso-patters are abstractions of common design patterns seen in the same levels. This method generates levels that are similar in style to the levels from which the original patterns were extracted, while still allowing for considerable variation in the geometry of the generated levels. The evolutionary method for generating the levels was tested extensively to investigate the distribution of micro-patterns used and meso-patterns found.

Wed 1430-1610 **EvoGAMES 2**
Chair: Antonio M Mora Garcia

Micro and Macro Lemmings simulations based on ants colonies *Antonio Gonzalez-Pardo, Fernando Palero, David Camacho*

Ant Colony Optimization (ACO) has been successfully applied to a wide number of complex and real domains. From classical optimization problems to video games, these kind of swarm-based approaches have been adapted, to be later used, to search for new meta-heuristic based solutions. This paper presents a simple ACO algorithm that uses a specifically designed heuristic, called common-sense, which has been applied in the classical video game Lemmings. In this game a set of lemmings must reach the exit point of each level, using a subset of finite number of skills, taking into account the contextual information given from the level. The paper describes both the graph model and the context-based heuristic, designed to implement our ACO approach. Afterwards, two different kind of simulations have been carried out to analyse the behaviour of the ACO algorithm. On the one hand, a micro simulation, where each ant is used to model a lemming, and a macro simulation where a swarm of lemmings is represented using only one ant. Using both kind of simulations, a complete experimental comparison based on the number and quality of solutions found and the levels solved, is carried out to study the behaviour of the algorithm under different game configurations.

Fast Evolutionary Adaptation for Monte Carlo Tree Search *Simon Lucas, Spyridon Samothrakis, Diego Perez*

This paper describes a new adaptive Monte Carlo Tree Search (MCTS) algorithm that uses evolution to rapidly optimise its performance. An evolutionary algorithm is used as a source of control parameters to modify the behaviour of each iteration (i.e. each simulation or roll-out) of the MCTS algorithm; in this paper we largely restrict this to modifying the behaviour of the random default policy, though it can also be applied to modify the tree policy. This method of tightly integrating evolution into the MCTS algorithm means that evolutionary adaptation occurs on a much faster time-scale than has previously been achieved, and addresses a particular problem with MCTS which frequently occurs in real-time video and control problems: that uniform random roll-outs may be uninformative. Results are presented on the classic mountain car reinforcement learning benchmark and also on a cut-down version of Space Invaders. The results clearly demonstrate the value of the approach, significantly outperforming ``standard'' MCTS in each case. Furthermore, the adaptation is almost immediate, with no perceptual delay as the system learns: the agent frequently performs well from its very first game.

Automatic Virtual Cinematography: a Dynamic Multi-Objective Optimisation Perspective *Paolo Burelli, Mike Preuss*

Automatically generating computer animations is a challenging and complex problem with applications in games and film production. In this paper, we investigate how to translate a shot list for a virtual scene (e.g. a game replay) into a series of camera configurations. We approach this problem by modelling it as a dynamic multi-objective optimisation problem and show how this metaphor allows a much richer expressiveness than a classical single objective approach. Finally, we showcase the application of a multi-objective evolutionary algorithm to generate a shot for a sample game replay and we analyse the results.

Wed 1745-1900 **EvoAPPS posters**

A hybrid swarm algorithm for post enrollment based course timetabling problem *Cheng Weng Fong, Hishammuddin Asmuni, Way Shen Lam, Barry McCollum, Paul McMullan*

The hybridization of metaheuristic approaches in solving optimization problems is increasingly the subject of many research projects. An Important objective of hybridizing two or more metaheuristic approaches is to attain a balance between global exploration and local exploitation within the overall search process. This paper presents such an approach, hybridising the population based approach Artificial Bee Colony (ABC) algorithm with a Hill Climbing (HC) local search and applying to the post enrollment-based course timetabling problem. In addition, the global best concept inspired from Particle Swarm Optimization (PSO) is used to improve the exploration ability of the basic ABC algorithm. The proposed hybrid approach is tested on Socha's course timetabling datasets and is compared against state-of-the-art approaches from the literature. Experimental results demonstrate that the proposed hybrid approach outperforms the basic artificial bee colony algorithm and is comparable to other approaches published in the literature.

Adaptive Genetic Algorithm to Select Training Data for Support Vector Machines *Jakub Nalepa, Michal Kawulok*

This paper presents a new adaptive genetic algorithm (AGA) to select training data for support vector machines (SVMs). SVM training data selection strongly influences the classification accuracy and time, especially in the case of large and noisy data sets. In the proposed AGA, a population of solutions evolves with time. The AGA parameters, including the chromosome length, are adapted according to the current state of exploring the solution space. We propose a new multi-parent crossover operator for an efficient search. A new metric of distance between individuals is introduced and applied in the AGA. It is based on the fast analysis of the vectors distribution in the feature space obtained using principal component analysis. An extensive experimental study performed on the well-known benchmark sets along with the real-world and artificial data sets, confirms that the AGA outperforms a standard GA in terms of the convergence capabilities. Also, it reduces the number of support vectors and allows for faster SVM classification.

A Multi-objective Evolutionary Approach for Cloud Service Provider Selection Problems with Dynamic Demands *Hsin-Kai Chen, Cheng-Yuan Lin, Jianhung Chen*

This paper describes a multi-objective evolutionary approach for solving cloud computing service provider selection problems with dynamic demands. In this investigated problem, not only the service purchase costs and transmission costs of service providers are different, but the demands of service requests also change over the given periods. The objective of this problem is to select a number of cloud service provider while optimizing the total service distance, the total number of serviced demand points, the total service purchase costs, and total transmission costs simultaneously in the given continuous time periods. A multi-objective genetic approach with a seeding mechanism is proposed to solve the investigated problems. Four trail benchmark problems are designed and solved using the proposed multi-objective evolutionary algorithm. The results indicate that the proposed approach is capable of obtaining a number of non-dominated solutions for decision makers.

An Effective Nurse Scheduling by a Parameter Free Cooperative GA *Makoto Ohki*

This paper describes a technique of penalty weight adjustment for the Cooperative Genetic Algorithm applied to the nurse scheduling problem. In this algorithm, coefficients and thresholds for each penalty function are automatically optimized. Therefore, this technique provides a parameter free algorithm of nurse scheduling. The nurse scheduling is very complex task, because many requirements must be considered. These requirements are implemented by a set of penalty function in this research. In real hospital, several changes of the schedule often happen. Such changes of the shift schedule yields various inconveniences, for example, imbalance of the number of the holidays and the number of the attendance. Such inconvenience causes the fall of the nursing level of the nurse organization. Reoptimization of the schedule including the changes is very hard task and requires very long computing time. We consider that this problem is caused by the solution space having many local minima. We propose a technique to adjust penalty weights and thresholds through the optimization to escape from the local minimal area.

An Improved Multiobjective Electromagnetism-like Mechanism Algorithm *Pedro Carrasqueira, Maria João Alves, Carlos Henggeler Antunes*

Electromagnetism-like Mechanism (EM) is a population based optimization approach, which has been recently adapted to solve multiobjective (MO) problems (MOEM). In this work, an enhanced multiobjective Electromagnetism-like Mechanism algorithm is proposed (EMOEM). To assess this new algorithm, a comparison with MOEM algorithm is performed. Our aim is to assess the ability of both algorithms in a wide range of continuous optimization problems including benchmark problems with two and three objective functions. Experiments show that EMOEM performs better in terms of convergence and diversity when compared with the MOEM algorithm.

An object-oriented library in JavaScript to build modular and flexible cross-platform evolutionary algorithms *Victor Manuel Rivas Santos, Maria Isabel Garcia Arenas, Juan Julian Merelo Guervos, Antonio Mora Garcia, Gustavo Romero Lopez*

This paper introduces jsEO, a new evolutionary computation library that is executed in web browsers, as it is written in Javascript. The library allows the rapid development of evolutionary algorithm, and makes easier the collaboration between different clients by means of individuals stored in a web server. In this work, jsEO has been tested against two simple problems, such as the Royal Road function and a 128-terms equation, and analysing how many machines and evaluations it yields. This paper attempts to reproduce results of older papers using modern browsers and all kind of devices that, nowadays, have JavaScript integrated in the browser, and is a complete rewrite of the code using the popular MooTools library. Results show that the system makes easier the development of evolutionary algorithms, suited for different chromosomes representations and problems, that can be simultaneously executed in many different operating systems and web browsers, sharing the best solutions previously found.

Automated Framework for General-Purpose Genetic Algorithms in FPGAs *Liucheng Guo, David Thomas, Wayne Luk*

FPGA-based Genetic Algorithms (GAs) have been effective for optimisation of many real-world applications, but require extensive customisation of the hardware GA architecture. To promote these accelerated GAs to potential users without hardware design experience, this paper proposes an

automated framework for creating and executing general-purpose GAs in FPGAs. The framework contains a scalable and customisable hardware architecture, which provides a unified platform for both binary and real-valued chromosomes. At compile-time, a user only needs to provide a high-level specification of the target application, without writing any hardware-specific code in low-level languages such as VHDL or Verilog. At run-time, a user can tune application inputs and GA parameters without time-consuming recompilation, in order to find a good configuration for further GA executions. The framework is demonstrated on a high performance FPGA platform to solve six problems and benchmarks, including a locating problem and the NP-hard set covering problem. Experiments show our custom GA is more flexible and easier to use compared to existing FPGA-based GAs, and achieves an average speed-up of 30 times compared to a multi-core CPU.

Automatic Selection of GA Parameters for Fragile Watermarking *Marco Botta, Davide Cavagnino, Victor Pomponiu*

Genetic Algorithms (GAs) are known to be valuable tools for optimization purposes. In general, GAs can find good solutions by set ting their configuration parameters, such as mutation and crossover rates, population size, etc., to standard (i.e., widely used) values. In some application domains, changing the values of these parameters does not improve the quality of the solution, but m ight influence the ability of the algorithm to find such solution. In other application domains, fine tuning these parameters co uld result into a significant improvement of the solution quality. In this paper we present an experimental study aimed at findin g how fine tuning the parameters of a GA used for the insertion of a fragile watermark into a bitmap image influences the quality of the resulting digital object. However, when proposing a GA based new tool to non-expert users, selecting the best parameter s etting is not an easy task. Therefore, we will suggest how to automatically set the GA parameters in order to meet the quality an d/or running time performances requested by the user.

Classification of Potential Multiple Sclerosis Lesions through Automatic Knowledge Extraction by means of Differential Evolution *Ivanoe De Falco*

In this paper a classifi er, designed by taking the user-friendliness issue into account, is described and is used to tackle the problem of classification of potential lesions in Multiple Sclerosis. This tool is based on the idea of making use of Di_fferential Evolution (DE) to extract explicit knowledge from a database under the form of a set of IF-THEN rules, can use this set of rules to carry out the classi fication task, and can also provide clinicians with this knowledge, thus explaining the motivation for each of the proposed diagnoses. Each DE individual codes for a set of rules. The tool is compared over a database of Multiple Sclerosis potential lesions against a set of nine classi fication tools widely used in literature. Furthermore, the usefulness and the meaningfulness of the extracted knowledge have been assessed by comparing it against that provided by Multiple Sclerosis experts. No great diff_erences have turned out to exist between these two forms of knowledge.

Co-Evolutionary Optimization of Autonomous Agents in a Real-Time Strategy Game *Antonio J. Fernández Ares, Antonio M. Mora, Maribel García Arenas, Pablo García Sánchez, Juan Julian Merelo Guervós, Pedro A. Castillo*

This paper presents an approach based in an evolutionary algorithm, aimed to improve the behavioral parameters which guide the actions of an autonomous agent (bot) inside the real-time strategy game, Planet Wars. The work describes a co-evolutionary implementation of a previously presented method (ANONYMOUSBot), which yielded successful results, but focused in 4 vs 4 matches this time. Thus, there have been analyzed the effects of considering several individuals to be evolved (improved) at the same time in the algorithm, along with the use of three different fitness functions measuring the goodness of each bot in the evaluation. They are based in turns and position, and also in mathematical computations of linear regression and area regarding the number of ships belonging to the bot/individual to be evaluated. In addition, the variance of using an evolutionary algorithm with and without previous knowledge in the co-evolution phase is also studied, i.e., respectively using specific rivals to perform the evaluation, or just considering to this end individuals in the population being evolved. The aim of these co-evolutionary approaches are mainly two: first, reduce the computational time; and second find a robust fitness function to be used in the generation of evolutionary bots optimized for 4 vs 4 battles.

Impact of the Topology on the Performance of Distributed Differential Evolution

Ivanoe De Falco, Antonio Della Cioppa, Domenico Maisto, Umberto Scafuri, Ernesto Tarantino

Migration topology plays a key role in designing effective distributed evolutionary algorithms. In this work we investigate the impact of several network topologies on the performance of a stepping-stone structured Differential Evolution model. Although some issues on the control parameters of the migration process and the way they affect the efficiency of the algorithm and the solution quality deserve further evaluative study, the influence of the topology on the performance both in terms of solution quality and convergence rate emerges from the empirical findings carried out on a set of test problems.

Modeling the offloading of different types of mobile applications by using evolutionary algorithms

Gianluigi Folino, Francesco Pisani

Modern smartphones permit to run a large variety of applications, i.e. multimedia, games, social network applications, etc. However, that considerably reduces the battery life of these devices. A possible solution to alleviate this problem is to offload part of the application or the whole computation to remote servers, i.e. Cloud Computing. The offloading cannot be performed without considering the issues derived from the nature of the application (i.e. multimedia, games, etc.), which can considerably change the resources necessary to the computation and the type, the frequency and the amount of data to be exchanged with the network. This work shows a framework for automatically building models for the offloading of mobile applications based on evolutionary algorithms and how it can be used to simulate different kinds of mobile applications and to analyze the rules generated. To this aim, a tool for generating mobile datasets, presenting different features, is designed and experiments are performed in different usage conditions in order to demonstrate the utility of the overall framework.

Multi-material compositional pattern-producing networks for form optimisation

Ralph Evins, Ravi Vaidyanathan, Stuart Burgess

CPPN-NEAT (Compositional Pattern Producing Networks and NeuroEvolution for Augmented Topologies) is a representation and optimisation approach that can generate and optimise complex forms without any pre-defined structure by using indirect, implicit representations. CPPN is based on an analogy to embryonic development; NEAT is based on an analogy to neural evolution. We present new developments that extend the approach to include multi-material objects, where the material distribution must be optimised in parallel with the form. Results are given for a simple problem concerning PV panels to validate the method. This approach is applicable to a large number of problems concerning the design of complex forms. There are many such problems in the field of energy saving and generation, particularly those areas concerned with solar gain.

Multiobjective Approach to Optimize Cantilever Walls Cost in Civil Engineering

Jesus Torrecilla-Pinero, Fernando Torrecilla-Pinero, Juan A. Gomez-Pulido, Carlos Uruena-Fernandez

A cantilever wall is a structure very used in civil engineering to retain earth and save different ground levels. There is a huge collection of possible designs of cantilever walls, where several restrictions must be considered to guarantee some limit states established by governmental laws in order to ensure a proper stability of the structure. We can define these limit states as situations that, if reached, suppose some kind of failure in the structure: sliding, settlement, flexural breaking, etc. In addition, we must impose a certain design factor for each limit state, so that, if all bad effects would be multiplied by such factor, the wall would still be stable. The wall design is defined by geometrical variables that suppose an economic cost, and several methods select their values to obtain a feasible wall. Some of these attempts configure a monoobjetive optimization problem to minimize the economic cost. In this paper we tackle a novel approach configuring a multiobjective optimization problem where the different design factors are objectives to be maximized. We have observed the optimum design lies in a region of the design space where small increments of the cost drives to a much safer design.

Objective Dimension and Problem Structure in Multiobjective Optimization Problems

Ramprasad Joshi, Bharat Deshpande, Paritosh Gote

Multiobjective optimization seeks simultaneous minimization of multiple scalar functions on R^n. Unless weighted sums are made to replace the vector functions arising thus, such an optimization

requires some partial- or quasi-ordering of points in the search space based on comparisons between the values attained by the functions to be optimized at those points. Many such orders can be defined, and search-based (mainly heuristic) optimization algorithms make use of such orders implicitly or explicitly for refining and accelerating search. In this work, such relations are studied by modeling them as graphs. Information apparent in the structure of such graphs is studied in the form of degree distribution. It is found that when the objective dimension grows, the degree distribution tends to follow a power-law. This can be a new beginning in the study of escalation of hardness of problems with dimension, as also a basis for designing new heuristics.

Searching for Risk in Large Complex Spaces *Kester Clegg, Rob Alexander*

ASHiCS (Automating the Search for Hazards in Complex Systems) uses evolutionary search on air traffic control simulations to find scenario configurations that generate high risk for a given air sector. Weighted heuristics are able to focus on specific events, flight paths or aircraft so that the search can effectively target incidents of interest. We describe how work on the characterization of our solution space suggests that destructive mutation operators perform badly in sensitive, high dimensional spaces. Finally, our work raises some issues about using collective risk assessment to discover significant safety events and whether the results are useful to safety analysts.

Sharing Information in Adversarial Bandit *David L. St-Pierre, Olivier Teytaud*

2-Player games in general provide a popular platform for research in Artificial Intelligence (AI). One of the main challenges coming from this platform is approximating a Nash Equilibrium (NE) over zero-sum matrix games. While the problem of computing such a Nash Equilibrium is solvable in polynomial time using Linear Programming (LP), it rapidly becomes infeasible to solve as the size of the matrix grows; a situation commonly encountered in games. This paper focuses on improving the approximation of a NE for matrix games such that it outperforms the state-of-the-art algorithms given a finite (and rather small) number T of oracle requests to rewards. To reach this objective, we propose to share information between the different relevant pure strategies. We show both theoretically by improving the bound and empirically by experiments on artificial matrices and on a real-world game that information sharing leads to an improvement of the approximation of the NE.

The structure of a probabilistic 1-state transducer representation for Prisoner's Dilemma *Jeffrey Tsang*

In the study of evolutionary game theory, a tool called the fingerprint was developed. This mathematical technique generates a functional summary of an arbitrary game-playing strategy independent of representational details. Using this tool, this study expands the boundaries of investigating an entire small state space of strategies, to wit the probabilistic 1-state tranducers, as a representation for playing iterated Prisoner's Dilemma. A sampled grid of 35,937 strategies out of the continuous cube was used: they are fingerprinted and pairwise distances computed. A subsampled grid of 4,913 strategies was analyzed using metric multidimensional scaling. The results show that the known 3-dimensional manifold can be embedded into around 4--5 Euclidean dimensions without self-intersection, and the curvature of the fingerprint metric with respect to standard distance is not too extreme; there is also similarity with analogous results on other state spaces.

Tree depth influence in Genetic Programming for generation of competitive agents for RTS games *Pablo García-Sánchez, Antonio Fernández-Ares, Antonio Miguel Mora, Pedro Ángel Castillo, Juan Julián Merelo, Jesús González*

This work presents the results obtained from comparing different tree depths in a Genetic Programming Algorithm to create agents that play the Planet Wars game. Three different maximum levels of the tree have been used (3, 7 and Unlimited) and two bots available in the literature, based on human expertise, and optimized by a Genetic Algorithm have been used for training and comparison. Results show that in average, the bots obtained using our method equal or outperform the previous ones, being the maximum depth of the tree a relevant parameter for the algorithm.

Unreliable Heterogeneous Workers in a pool-based evolutionary algorithm *Mario Garcia-Valdez, Juan-J. Merelo, Francisco FernÃ¡ndez-de-Vega*

In this paper the effect of node unavailability in algorithms using EvoSpace, a pool-based evolutionary

algorithm, is assessed. EvoSpace is a framework for developing evolutionary algorithms (EAs) using heterogeneous and unreliable resources. It is based on Linda's tuple space coordination model. The core elements of EvoSpace are a central repository for the evolving population and remote clients, here called EvoWorkers, which pull random samples of the population to perform on them the basic evolutionary processes (selection, variation and survival), once the work is done, the modified sample is pushed back to the central population. To address the problem of unreliable EvoWorkers, EvoSpace uses a simple re-insertion algorithm using copies of samples stored in a global queue which also prevents the starvation of the population pool. Using a benchmark problem from the P-Peaks problem generator we have compared two approaches: (i) the re-insertion of previous individuals at the cost of keeping copies of each sample, and a common approach of other pool based EAs, (ii) inserting randomly generated individuals. We found that EvoSpace is fault tolerant to highly unreliable resources and also that the re-insertion algorithm is only needed when the population is near the point of starvation.

Using a stochastic method to calibrate a vehicle emissions model *Neil Urquhart, Emma Hart, Wafaa Saleh*

This paper examines the use of a stochastic technique (Evolutionary Algorithms) to lean the how to calibrate a vehicle emissions model that can be used to predict CO_2 emissions within a micro simulation. The model relies on the accurate calibration of parameters which represent quantities, such as rolling resistance and the relation between fuel consumption and energy for a particular vehicle, that are not readily available to the model user. We investigate whether a stochastic technique (an evolutionary algorithm) can be used to learn appropriate parameter values to predict CO_2 emissions. The learning is based upon data sets collected from instrumented vehicles driven in two UK cities. The experiments conducted show that the model can be successfully calibrated for both vehicles, with the error between predicted and actual outputs, typically $<\% . The process is compared to non-linear regression analysis, results show that the proposed process produces a more accurate emissions prediction mechanism over each observation point within a drive cycle. The authors demonstrate that complex emissions models may be successfully calibrated to individual characteristics of vehicles, in order that they can be used in activities such as micro modelling or more general vehicle routing applications. It is believed that this is the first time that stochastic methods have been utilised to calibrate vehicle emissions models.

What You Choose to See is What You Get: An Experiment with Learnt Sensory Modulation in a Robotic Foraging Task *Tiago Rodrigues, Miguel Duarte, Sancho Oliveira, Anders Christensen*

In evolutionary robotics, the mapping from raw sensory input to neural network input is typically decided by the experimenter or encoded in the genome. Either way, the mapping remains fixed throughout a robot’s lifetime. Inspired by biological sensory organs and the mammalian brain’s capacity for selective attention, we evaluate an alternative approach in which a robot has active, real-time control over the mapping from sensory input to neural network input. We augment the neural controllers with additional output neurons that control key sensory parameters and evolve solutions for a single-robot foraging task. The results show that the capacity to control the mapping from raw input to neural network input is exploited by evolution and leads to novel solutions with higher fitness compared to traditional approaches.

Thursday 24 April

Thurs 0930-1110 **EvoENERGY**
Chair: Paul Kaufmann

Customizable Energy Management in Smart Buildings using Evolutionary Algorithms *Florian Allerding, Ingo Mauser, Hartmut Schmeck*

Various changes in energy production and consumption lead to new challenges for design and control mechanisms of the energy system. In particular, the intermittent nature of power generation from renewables asks for significantly increased load flexibility to support local balancing of energy demand and supply. This paper focuses on a flexible, generic energy management system for Smart Buildings in real-world applications, which is already in use in households and office buildings. The major

contribution is the design of a "plug-and-play"-type Evolutionary Algorithm for optimizing distributed generation, storage and consumption using a sub-problem based approach. Relevant power consuming or producing components identify themselves as sub-problems by providing an abstract specification of their genotype, an evaluation function and a back transformation from an optimized genotype to specific control commands. The generic optimization respects technical constraints as well as external signals like variable energy tariffs. The relevance of this approach to energy optimization is evaluated in different scenarios. Results show significant improvements of self-consumption rates and reductions of energy costs.

Dynamic Programming Based Metaheuristic for Energy Planing Problems

Sophie Jacquin, Laetitia Jourdan, El-Ghazali Talbi

In this article, we propose DYNAMOP (DYNAmic program- ming using Metaheuristic for Optimization Problems) a new dynamic programming based on genetic algorithm to solve a hydro-scheduling problem. The representation which is based on a path in the graph of states of dynamic programming is adapted to dynamic structure of the problem and it allows to hybridize easily evolutionary algorithms with dynamic programming. DYNAMOP is tested on two case studies of hydro-scheduling problem with different price scenarios. Experiments indicate that the proposed approach performs considerably better than classical genetic algorithms and dynamic programming. Keywords : Genetic Algorithm, Dynamic Programming , Hybrid method, Hydro scheduling problem

Looking for Alternatives: Optimization of Energy Supply Systems without Superstructure

Mike Preuss, Philip Voll, André Bardow, Günter Rudolph

We investigate different evolutionary algorithm (EA) variants for structural optimization of energy supply systems and compare them with a deterministic optimization approach. The evolutionary algorithms enable structural optimization avoiding to use an underlying superstructure model. As result of the optimization, we are interested in multiple good alternative designs, instead of the one single best solution only. This problem has three levels: On the top level, we need to fix a structure; based on that structure, we then have to select facility sizes; finally, given the structure and equipment sizing, on the bottom level, the equipment operation has to be specified to satisfy given energy demands. In the presented optimization approach, these three levels are addressed simultaneously. We compare EAs acting on the top level (the lower levels are treated by a mixed-integer linear programming (MILP) solver) against an MILP-only-approach and are highly interested in the ability of both methods to deliver multiple different solutions and the time required for performing this task. Neither state-of-the-art EA for numerical optimization nor standard measures or visualizations are applicable to the problem. This lack of experience makes it difficult to understand why different EA variants perform as they do (e.g., for stating how different two structures are), we introduce a distance concept for structures. We therefore introduce a short code, and, based on this short code, a distance measure that is employed for a multidimensional scaling (MDS) based visualization. This is meant as first step towards a better understanding of the problem landscape. The algorithm comparison shows that deterministic optimization has advantages if we need to find the global optimum. In contrast, the presented EA variants reliably find multiple solutions very quickly if the required solution accuracy is relaxed. Furthermore, the proposed distance measure enables visualization revealing interesting problem properties.

Thurs 0930-1110 **EvoNUM**

Chair: Anna I Esparcia-Alcázar

A Novel Genetic Algorithmic Approach for Computing Real Roots of a Nonlinear Equation

Vijaya Lakshmi V. Nadimpalli, Rajeev Wankar, Raghavendra Rao Chillarige

Novel Pre-processing and Post-processing methodologies are designed to enhance the performance of the classical Genetic Algorithms (GA) approach so as to obtain efficient interval estimates in finding the real roots of a given nonlinear equation. The Pre-processing methodology suggests a mechanism that adaptively fixes the parameter-'length of chromosome' in GA. The proposed methodologies have been implemented and demonstrated through a set of benchmark functions to illustrate the effectiveness.

A Multi-Objective Relative Clustering Genetic Algorithm with Adaptive Local/ Global Search based on Genetic Relatedness *Iman Gholaminezhad, Giovanni Iacca*

This paper describes a new evolutionary algorithm for multi-objective optimization, namely Multi-Objective Relative Clustering Genetic Algorithm (MO-RCGA), inspired by concepts borrowed from gene relatedness and kin selection theory. The proposed algorithm clusters the population into different families based on individual kinship, and adaptively chooses suitable individuals for reproduction. The idea is to use the information on the position of the individuals in the search space provided by such clustering schema to enhance the convergence rate of the algorithm, as well as improve its exploration. The proposed algorithm is tested on ten unconstrained benchmark functions proposed for the special session and competition on multi-objective optimizers held at IEEE CEC 2009. The Inverted Generational Distance (IGD) is used to assess the performance of the proposed algorithm, in comparison with the IGD obtained by state-of-the-art algorithms on the same benchmark.

Noisy Optimization: Convergence with a Fixed Number of Resamplings *Marie-Liesse Cauwet*

It is known that evolution strategies in continuous domains might not converge in the presence of noise. It is also known that, under mild assumptions, and using an increasing number of resamplings, one can mitigate the effect of additive noise and recover convergence. We show new sufficient conditions for the convergence of an evolutionary algorithm with constant number of resamplings; in particular, we get fast rates (log-linear convergence) provided that the variance decreases around the optimum slightly faster than in the so-called multiplicative noise model. Keywords: Noisy optimization, evolutionary algorithm, theory.

A Differential Evolution Framework with Ensemble of Parameters and Strategies and Pool of Local Search Algorithms *Giovanni Iacca, Ferrante Neri, Fabio Caraffini, Ponnuthurai Nagaratnam Suganthan*

The ensemble structure is a computational intelligence supervised strategy consisting of a pool of multiple operators that compete among each other for being selected, and an adaptation mechanism that tends to reward the most successful operators. In this paper we extend the idea of the ensemble to multiple local search logics. In a memetic fashion, the search structure of an ensemble framework co- operatively/competitively optimizes the problem jointly with a pool of diverse local search algorithms. In this way, the algorithm progressively adapts to a given problem and selects those search logics that appear to be the most appropriate to quickly detect high quality solutions. The resulting algorithm, namely Ensemble of Parameters and Strategies Differential Evolution empowered by Local Search (EPSDE-LS), is evaluated on multiple testbeds and dimensionality values. Numerical results show that the proposed EPSDE-LS robustly displays a very good performance in comparison with some of the state-of-the-art algorithms.

Thurs 0930-1110 **EvoROBOT & EvoHOT**

Chair: Giovanni Squillero

Speeding up Online Evolution of Robotic Controllers with Macro-neurons *Fernando Silva, Luís Correia, Anders Christensen*

In this paper, we introduce a novel approach to the online evolution of robotic controllers. We propose accelerating and scaling online evolution to more complex tasks by giving the evolutionary process direct access to behavioural building blocks prespecified in the neural architecture as \emph{macro-neurons}. During task execution, both the structure and the parameters of macro-neurons and of the entire neural network are under evolutionary control. We perform a series of simulation-based experiments in which an e-puck-like robot must learn to solve a deceptive and dynamic phototaxis task with three light sources. We show that: (i) evolution is able to progressively \emph{complexify} controllers by using the behavioural building blocks as a substrate, (ii) macro-neurons, either evolved or preprogrammed, enable a significant reduction in the adaptation time and the synthesis of high performing solutions, and (iii) evolution is able to inhibit the execution of detrimental task-unrelated behaviours and adapt non-optimised macro-neurons.

HyperNEAT versus RL PoWER for Online Gait Learning in Modular Robots
Massimiliano D'Angelo, Berend Weel, A.E. Eiben
This paper addresses a principal problem of in vivo evolution of modular multi-cellular robots, where robot `babies' can be produced with arbitrary shapes and sizes. In such a system we need a generic learning mechanism that enables newborn morphologies to obtain a suitable gait quickly after `birth'. In this study we investigate and compare the reinforcement learning method RL PoWeR with HyperNEAT. We conduct simulation experiments using robot morphologies with different size and complexity. The experiments give insights into the differences in solution quality and algorithm efficiency, suggesting that reinforcement learning is the preferred option for this online learning problem.

Diagnostic Test Generation for Statistical Bug Localization using Evolutionary Computation *Marco Gaudesi, Maksim Jenihhin, Jaan Raik, Ernesto Sanchez, Giovanni Squillero, Valentin Tihomirov, Raimund Ubar*
Verification is increasingly becoming a bottleneck in the process of designing electronic circuits. While there exists a wide range of verification tools that assist in detecting occurrences of design errors, or bugs, there is a lack of solutions for accurately pin-pointing the root causes of these errors. Statistical bug localization has proven to be an approach that scales up to large designs and is widely utilized both in debugging hardware and software. However, the accuracy of statistical localization is highly dependent on the diagnostic quality of the test stimuli. In this paper we formulate diagnostic test set generation as a task for an evolutionary algorithm and propose dedicated fitness functions that closely correlate with the bug localization capabilities of statistical approaches. We perform experiments on the register-transfer level design of the Plasma microprocessor implementing µGP (MicroGP) for evolutionary test pattern generation and the zamiaCAD tool's bug localization infrastructure for fitness evaluation. As a result, the diagnostic resolution of the tests is significantly improved.

Thurs 1430-1610 **EvoIASP 1 : Best EvoIASP paper candidates**
Chair: Stefano Cagnoni

Evolutionary algorithm for dense pixel matching in presence of distortions (EvoIASP best paper candidate) *Ana Carolina dos Santos Paulino, Jean-Christophe Nebel, Francisco Flórez-Revuelta*
Dense pixel matching is an essential step required by many computer vision applications. While a large body of work as addressed quite successfully the rectified scenario, accurate pixel correspondence between an image and a distorted version remains very challenging. Exploiting an analogy between sequences of genetic material and images, we propose a novel genetics inspired algorithm where image variability is treated as the product of a set of image mutations. As a consequence, correspondence for each scanline of the initial image is formulated as the optimisation of a path in the second image minimising a fitness function penalising mutations. This optimisation is performed by a evolutionary algorithm which, in addition to provide fast convergence, implicitly ensures consistency between successive scanlines. Performance evaluation on locally and globally distorted images validates our bio-inspired approach.

Is a Single Image Sufficient for Evolving Edge Features by Genetic Programming? (EvoIASP best paper candidate) *Wenlong Fu, Mark Johnston, Mengjie Zhang*
Typically, a single natural image is not sufficient to train a program to extract edge features in edge detection when only training images and their ground truth are provided. However, a single training image might be considered as proper training data when domain knowledge, such as used in Gaussian-based edge detection, is provided. In this paper, we employ Genetic Programming (GP) to automatically evolve Gaussian-based edge detectors to extract edge features based on training data consisting of a single image only. The results show that a single image with a high proportion of true edge points can be used to train edge detectors which are not significantly different from rotation invariant surround suppression. When the programs separately evolved from eight single images are considered as weak classifiers, the combinations of these programs perform better than rotation invariant surround suppression.

Improving Graph-Based Image Segmentation Using Automatic Programming (EvoIASP best paper candidate) *Lars Vidar Magnusson, Roland Olsson*
This paper investigates how Felzenszwalb's and Huttenlocher's graph-based segmentation algorithm can be improved by automatic programming. We show that computers running Automatic Design of Algorithms Through Evolution (ADATE), our system for automatic programming, have induced a new graph-based algorithm that is 12 percent more accurate than the original without affecting the runtime efficiency. The result shows that ADATE is capable of improving an effective image segmentation algorithm and suggests that the system can be used to improve image analysis algorithms in general.

Thurs 1630-1810 **EvoIASP 2**
Chair: Stefano Cagnoni

New Representations in PSO for Feature Construction in Classification *Yan Dai, Bing Xue, Mengjie Zhang*
Feature construction can improve the classification performance by constructing high-level features using the original low-level features and function operators. Particle swarm optimisation (PSO) is an powerful global search technique, but it can not be directly used for feature construction because of its representation scheme. This paper proposes two new representations, pair representation and array representation, which allow PSO to direct evolve function operators. Two PSO based feature construction algorithms (PSOFCPair and PSOFCArray) are then developed. The two new algorithms are examined and compared with the first PSO based feature construction algorithm (PSOFC), which employs an inner loop to select function operators. Experimental results show that both PSOFCPair and PSOFCArray can increase the classification performance by constructing a new high-level feature. PSOFCArray outperforms PSOFCPair and achieves similar results to PSOFC, but uses significantly shorter computational time. This paper represents the first work on using PSO to directly evolve function operators for feature construction.

GPU-based Point Cloud Recognition using Evolutionary Algorithms *Roberto Ugolotti, Giorgio Micconi, Jacopo Aleotti, Stefano Cagnoni*
In this paper, we describe a method for recognizing objects in the form of point clouds acquired with a laser scanner. This method is fully implemented on GPU and uses bio-inspired metaheuristics, namely PSO or DE, to evolve the rigid transformation that best aligns some references extracted from a dataset to the target point cloud. We compare the performance of our method with an established method based on Fast Point Feature Histograms (FPFH). The results prove that FPFH is more reliable under simple and controlled situations, but PSO and DE are more robust with respect to common problems as noise or occlusions.

A New Binary Particle Swarm Optimisation Algorithm for Feature Selection *Bing Xue, Su Nguyen, Mengjie Zhang*
Feature selection aims to select a small number of features from a large feature set to achieve similar or better classification performance than using all features. This paper develops a new binary particle swam optimisation (PSO) algorithm (named PBPSO) based on which a new feature selection approach (PBPSOfs) is developed to reduce the number of features and increase the classification accuracy. The performance of PBPSOfs is compared with a standard binary PSO based feature selection algorithm (BPSOfs) and two traditional feature selection algorithms on 14 benchmark problems of varying difficulty. The results show that PBPSOfs can be successfully used for feature selection to select a small number of features and improve the classification performance over using all features. PBPSOfs further reduces the number of features selected by BPSOfs and simultaneously increases the classification accuracy, especially on datasets with a large number of features. Meanwhile, PBPSOfs achieves better performance than the two traditional feature selection algorithms. In addition, the results also show that PBPSO as a general binary optimisation technique can achieve better performance than standard binary PSO and uses less computational time.

Thurs 1430-1610 **EvoPAR 1**
Chair : Francisco Fernández

Hybrid MPI/OpenMP Parallel Evolutionary Algorithms for Vehicle Routing Problems

Raul Banos, Julio Ortega, Consolacion Gil

The traditional fields of improvement in parallelism have been orientated to experimentation on high-budget equipment, such as clusters of computers or shared memory machines thanks to their high-performance and scalability. In recent years, the generalization of multi-core microprocessors in almost all the computing platforms makes it possible to take advantage of parallel processing even for the desktop computer user. This paper analyzes how to improve the performance of population-based meta-heuristics using MPI, OpenMP, and hybrid MPI/OpenMP implementations in a workstation having a multi-core processor. The results obtained when solving large scale instances of the Capacitated Vehicle Routing Problem with hard Time Windows (VRPTW) show that, in all cases, the parallel implementations produce better quality solutions for a given amount of runtime than the sequential algorithm, and also solutions of similar quality in less runtime.

Dynamic and Partially Connected Ring Topologies for Evolutionary Algorithms with Structured Populations

Carlos Fernandes, Juan Laredo, Juan Merelo, Carlos Cotta, Agostinho Rosa

This paper investigates dynamic and partially connected ring topologies for cellular Evolutionary Algorithms (cEA). We hypothesize that these structures maintain population diversity at a higher level and reduce the risk of premature convergence to local optima on deceptive and NP-hard fitness landscapes. A general framework for modelling partially connected topologies is proposed and three different schemes are tested. The results show that the structures improve the rate of convergence to global optima when compared to cEAs with standard topologies (ring, rectangular and square) on quasi-deceptive, deceptive and NP-hard problems. Optimal population size tests demonstrate that the proposed topologies require smaller populations when compared to traditional cEAs.

Systolic Genetic Search for Software Engineering: The Test Suite Minimization Case

Martín Pedemonte, Francisco Luna, Enrique Alba

The Test Suite Minimization Problem (TSMP) is a NP-hard real-world problem that arises in the field of software engineering. It lies in selecting the minimal set of test cases from a large test suite, ensuring that the test cases selected cover a given set of elements of a computer program under test. In this paper, we propose a Systolic Genetic Search (SGS) algorithm for solving the TSMP. We use the global concept of SGS to derive a particular algorithm to explicitly exploit the high degree of parallelism available in modern GPU architectures. The experimental evaluation on seven real-world programs shows that SGS is highly effective for the TSMP, as it obtains the optimal solution in almost every single run for all the tested software. It also outperforms two competitive Genetic Algorithms. The GPU-based implementation of SGS has achieved a high performance, obtaining runtime reductions of up to 40X compared to its sequential implementation, and solving all the instances considered in less than nine seconds.

Thurs 1630-1810 **EvoPAR 2**
Chair: Ignacio Hidalgo

Optimization of Application Placement towards a Greener Cloud Infrastructure

Tania Lorido-Botran, Jose Antonio Pascual, Jose Miguel-Alonso, Jose Antonio Lozano

Cloud infrastructures are designed to simultaneously service many, diverse applications that consist of collections of Virtual Machines (VMs). The policy used to map applications onto physical servers (placement policy) has important effects in terms of application performance and resource efficiency. This paper proposes enhancing placement policies with network-aware optimizations trying to simultaneously improve application performance, resource efficiency and, as a consequence, power efficiency. The per-application placement decision is formulated as a bi-objective optimization problem (minimizing communication cost and minimizing the number of physical servers assigned to the application) whose solution is searched using an evolutionary algorithm with problem-specific crossover and mutation operators. Experiments carried out with a simulator demonstrate how a low-

cost optimization technique results in improved placements that achieve all the target objectives.

GridVis: Visualisation of Island-Based Parallel Genetic Algorithms *Evelyne Lutton, Hugo Gilbert, Waldo Cancino, Benjamin Bach, Pierre Parrend, Pierre Collet*

Island Model parallel genetic algorithms rely on various migration models and their associated parameter settings. A fine understanding of how the islands interact and exchange informations is an important issue for the design of efficient algorithms. This article presents GridVis, an interactive tool for visualising the exchange of individuals and the propagation of fitness values between islands. We performed several experiments on a grid and on a cluster to evaluate GridVis' ability to visualise the activity of each machine and the communication flow between machines. Experiments have been made on the optimisation of a Weierstrass function using the EASEA language, with two schemes: a scheme based on uniform islands and another based on specialised islands (Exploitation, Exploration and Storage Islands).

Friday 25 April

Fri 1000-1140 **EvoCOMPLEX**
Chair: Carlos Cotta

Common Developmental Genomes Revisited - Evolution through Adaptation *Konstantinos Antonakopoulos*

Artificial development has been widely used for designing complex structures and as a means to increase the complexity of an artifact. One central challenge in artificial development is to understand how a mapping process could work on a class of architectures in a more general way by exploiting the most favorable properties from each computational architecture or by combining efficiently more than one computational architectures (i.e., a true multicellular approach). Computational architectures in this context comprise structures with connected computational elements, namely, cellular automata and boolean networks. The ability to develop and co-evolve different computational architectures has previously been investigated using common developmental genomes. In this paper, we extend a previous work that studied their evolvability. Here, we focus on their ability to evolve when the goal changes over evolutionary time (i.e., adaptation), utilizing a more fair fitness assignment scheme. In addition, we try to investigate how common developmental genomes exploit the underlying architecture in order to build the phenotypes. The results show that they are able to find very good solutions with rather simplified solutions than anticipated.

Investigation of Genome Parameters and Sub-Transitions to Guide Evolution of Artificial Cellular Organisms *Stefano Nichele, Håkon Hjelde Wold, Gunnar Tufte*

Artificial multi-cellular organisms develop from a single zygote to complex morphologies, following the instructions encoded in their genomes. Small genome mutations can result in very different developed phenotypes. In this paper we investigate how to exploit genotype information in order to guide evolution towards favorable areas of the phenotype solution space, where the sought emergent behavior is more likely to be found. Lambda genome parameter, with its ability to discriminate different developmental behaviors, is incorporated into the fitness function and used as a discriminating factor for genetic distance, to keep resulting phenotype’s developmental behavior close by and encourage beneficial mutations that yield adaptive evolution. Genome activation patterns are detected and grouped into genome parameter sub-transitions. Different sub-transitions are investigated as simple genome parameters, or composed to integrate several genome properties into a more exhaustive composite parameter. The experimental model used herein is based on 2-dimensional cellular automata.

Training Complex Decision Support Systems with Differential Evolution Enhanced by Locally Linear Embedding *Piotr Lipinski*

This paper aims at improving the training process of complex decision support systems, where evolutionary algorithms are used to integrate a large number of decision rules in a form of a weighted average. It proposes an enhancement of Differential Evolution by Locally Linear Embedding to process objective functions with correlated variables, which focuses on detecting local dependencies among variables of the objective function by analyzing the manifold in the search space that contains the current population and transforming it to a reduced search space. Experiments performed on some popular benchmark functions as well as on a financial decision support system confirm that the method may significantly improve the search process in the case of objective functions with a large number of variables, which usually occur in many practical applications.

A Memetic Framework for Solving Difficult Inverse Problems *Maciej Smolka, Robert Schaefer*

The paper introduces a multi-deme, memetic global optimization strategy Hierarchic memetic Strategy (HMS) especially well-suited to the solution of a class of parametric inverse problems. This strategy develops dynamically a tree of dependent populations (demes) searching with the various accuracy growing from the root to the leaves. The search accuracy is associated with the accuracy of solving direct problems by hpâ€“adaptive Finite Element Method. Throughout the paper we describe details of exploited accuracy adaptation and computational cost reduction mechanisms, an agent-based architecture of the proposed system, a sample implementation and preliminary benchmark results.

Fri 1000-1140 **EvoINDUSTRY & EvoRISK**

Chairs: Kevin Sim & Anna I Esparcia-Alcázar

Reducing the Number of Simulations in Operation Strategy Optimization for Hybrid Electric Vehicles

Christopher Bacher, Thorsten Krenek, Günther Raidl

The fuel consumption of a simulation model of a real Hybrid Electric Vehicle is optimized on a standardized driving cycle using metaheuristics (PSO, ES, GA). Search space discretization and metamodels are considered for reducing the number of required, time-expensive simulations. Two hybrid metaheuristics for combining the discussed methods are presented. In experiments it is shown that the use of hybrid metaheuristics with discretization and metamodels can lower the number of required simulations without significant loss in solution quality.

Hybridisation Schemes for Communication Satellite Payload Configuration Optimisation *Apostolos Stathatkis, Gregoire Danoy, El-Ghazali Talbi, Pascal Bouvry, Gianluigi Morelli*

The increasing complexity of current telecommunication satellite payloads has made their manual management a difficult and error prone task. As a consequence, efficient optimisation techniques are required to help engineers to configure and reconfigure the payload. Recent works focusing on exact approaches faced scalability issues while metaheuristics provided unsatisfactory solution quality. This work therefore proposes three hybridisation schemes that combine both metaheuristics and an exact method. Experimental results on realistic payload sizes demonstrate the advantage of those approaches in terms of efficiency and scalability within a strict operational time constraint of ten minutes on a single CPU core.

Hyper-Heuristics for Online UAV Path Planning under Imperfect Information

Engin Akar, Haluk Topcuoglu, Murat Ermis

Hyper-heuristic techniques are problem independent meta-heuristics that automate the process of selecting a set of given low-level heuristics. Online path planning in an uncertain or unknown environment is one of the challenging problems for autonomous unmanned aerial vehicles (UAVs). This paper presents a hyper-heuristic approach to develop a 3-D online path planning for unmanned aerial vehicle (UAV) navigation under sensing uncertainty. The information regarding the state of a UAV is obtained from on-board sensors during the execution of a navigation plan. The trajectory of a

UAV at each region is represented with B-spline curves, which is constructed by a set of dynamic control points. Experimental study performed on various terrains with different characteristics validates the usage of hyper-heuristics for online path planning. Our approach outperforms related work with respect to the quality of solutions and the number of feasible solutions produced.

Fri 1000-1140 **EvoSTOC**
Chair: Anabela Simões

Co-evolution of sensory system and signal processing for optimal wing shape control *Olga Smalikho, Markus Olhofer*

This paper demonstrates the applicability of evolutionary computation methods to co-evolve a sensor morphology and a suitable control structure to optimally adjust a virtual adaptive wing structure. In contrast to approaches in which the structure of a sensor configuration is fixed early in the design stages, we target the simultaneous generation of information acquisition and information processing based on the optimization of a target function. We consider two aspects as main advantages. First the ability to generate optimal environmental sensors in the sense that the control structure can optimally utilize the information provided and secondly the abdication of detailed prior knowledge about the problem at hand. In this work we investigate the expected high correlation between the sensor morphology and the signal processing structures as well the quantity and quality of the information gathered from the environment.

Infeasibility Driven Evolutionary Algorithm with Feed-Forward Prediction Strategy for Dynamic Constrained Optimization Problems *Patryk Filipiak, Piotr Lipinski*

This paper proposes a modification of Infeasibility Driven Evolutionary Algorithm that applies the anticipation mechanism following Feed-forward Prediction Strategy. The presented approach allows reacting on environmental changes more rapidly by directing some individuals into the areas of most probable occurrences of future optima. Also a novel population segmentation on exploring, exploiting and anticipating fractions is introduced to assure a better diversification of individuals and thus improve the ability to track moving optima. The experiments performed on the popular benchmarks confirmed the significant improvement in Dynamic Constrained Optimization Problems when using the proposed approach.

Identifying the Robust Number of Intelligent Autonomous Vehicles in Container Terminals *Shayan Kavakeb, Trung Thanh Nguyen, Zaili Yang, Ian Jenkinson*

The purpose of this research is to provide an improved Evolutionary Algorithm (EA) in combination with Monte Carlo Simulation (MCS) to identify the robust number of a new type of intelligent vehicles in container terminals. This type of vehicles, named Intelligent Autonomous Vehicles (IAVs), has been developed in a European project. This research extends our previous study on combining MCS with EAs. This paper has three main contributions: first, it proposes a dynamic strategy to adjust the number of samples used by MCS to improve the performance of the EA; second, it incorporates different robustness measures into the EA to produce different robust solutions depending on user requirements; and third, it investigates the relation between different robust solutions using statistical analyses to provide insights into what would be the most appropriate robust solutions for port operators. These contributions have been verified using empirical experiments. Keywords: Robust optimisation, Uncertainty, Evolutionary Algorithms, Monte Carlo Simulation, Fleet Sizing