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in this issue

Editorial

Welcome to the first 2019 newsletter! Our cover illustrates part of the collaboration network for EuroGP (European Conference on Genetic Programming), featuring a large group of connected authors. We start this Spring issue with a manifesto by **Darrell Whitley** in favor of "Gray Box" optimization. He stresses that in other to be competitive and solve real-world problems, evolutionary algorithms should consider more informed and deterministic alternatives to random mutation and recombination. Coming back to the cover, the second article in the issue by **Mila Goranova**, **Gabriela Ochoa** and **Marco Tomassini**, analyzes and contrasts the co-authorship networks of the the two main EvoStar (the leading European event on Bio-Inspired Computation) conferences: EurpGP and EvoCOP. In these networks two authors are connected if they have coauthored one or more papers appearing in these conferences. The networks are analyzed and visualized, revealing interesting insights into the collaboration patterns of these communities. We continue with a recount by **Dennis Wilson** of the inaugural workshop on Developmental Neural Networks, held in conjunction with PPSN (Parallel Problem Solving from Nature) 2018 in Coimbra. The workshop encourages approaches that focus on the development of artificial neural networks. The next edition of the workshop will take place this summer in conjunction with the Conference on Artificial Life (ALIFE 2019), Newcastle, UK.

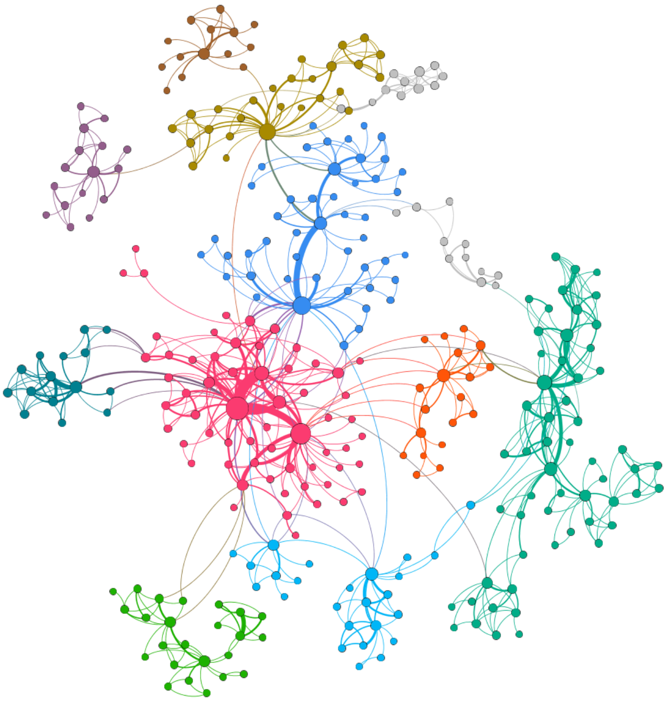
We take the opportunity to remind our members that the SIGEVO's election goes live on April 15th . The election notices go out on the 15th and throughout the election. In some cases when members go to vote they realize their membership is not up to date and therefore they will not be able to vote because they were not active members on the eligible voter cut-off date of April 1st .

As ever, please get in touch if you would like to contribute an article for a future issue or have suggestions for the newsletter.

Gabriela Ochoa, Editor.

About the Cover

The cover illustrates a subset of the co-authorship network for EuroGP (European Conference on Genetic Programming). Each node in the network is an author, and two authors are connected if they have co-authored one or more papers appearing in EuroGP since its inception until 2018. Edge widths are proportional to number of papers co-authored. Node sizes are proportional to their centrality. Node colours identify clusters or communities detected with a modularity minimization algorithm. You can visually explore the EuroGP and EvoCOP (Evolutionary Computation in Combinatorial Optimization) collaboration networks by following these links:
EuroGP Network | EvoCOP Network



A Gray Box Manifesto for Evolutionary Combinatorial Optimization

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It is almost an article of faith that most evolutionary algorithms utilize random mutation and random recombination operators. Often the mutation is uniform random and sometimes the recombination operator is also a type of “Uniform Crossover.” However when solving classic combinatorial optimization problems, random mutation and recombination operators are often both unnecessary and unproductive.

Another recent trend is to characterize all evolutionary algorithms as “Black Box” optimizers where nothing is known about the objective function. Unfortunately, Black Box optimizers are subject to the restrictions of No Free Lunch theorems. This is especially a concern because recent Focused No Free Lunch proofs hold over finite and tractable sets of functions [9, 8].

Black Box optimizers using random operators are doom to fail in any competition against more intelligent forms of search. Today, all competitive MAXSAT and Graph Coloring heuristic search methods deterministically compute the location of improving moves in constant time. For MAXSAT, this result has been known since 1992 [6]. Algorithms such as GSAT and Walksat (and their modern descendents) do not enumerate bit flip neighborhoods or use random sampling; instead, these algorithms can compute the location of improving moves and can track equal moves while also targeting variables that appear in specific unsatisfied clauses [2]. Again this does **not** involve the enumeration of the bit flip neighborhood; instead, the exact location of improving moves can be determined analytically, on average in O(1) time. Under these conditions, random mutation is hopelessly inefficient. Mathematical proofs now exists which show that these same results hold over all k-bounded pseudo Boolean functions for “next improving move” local search; it is possible to compute which bits can yield an improving move in constant time [10]. For some classes of functions, such as MAXSAT, one can also (almost always) identify the best improving moves in constant time [13].

The requirement that the functions be k-bounded is also not as restrictive as it might at first seem. Just as all SAT problems can be reduced to a MAX-3SAT instance, all problems that have a bit representation can be transformed into a k-bounded pseudo Boolean function [1]. This raises an important challenge to all researchers working in evolutionary computation. Why does the field ignore these advances and continue to use random and blind Black Box operators?

Advances have also made in the realm of recombination operators. In domains such as MAXSAT and NK-Landscapes [7] as well as the Traveling Salesman Problem [5, 12] we can also prove that deterministic forms of recombination can offer new performance guarantees. *Partition Crossover* operators deterministically use problem decomposition to perform intelligent guided recombination. Given q properly chosen crossover points, partition crossover operators are proven to return the best of 2^q possible offspring. If the parents are known to be local optima, all of the offspring are proven to also be locally optimal in largest hyperplane subspace that contains both parents [7]. An example is given in Figure 1. This is a large industrial MAXSAT instance from a recent SAT competition designed to solve an air traffic controller shift scheduling problem (instance atco_enc3_opt1_13_48). Partition crossover decomposes the problem into 1087 subgraphs, and returns the best of 2^{1087} possible offspring in linear time. A more detailed discussion of deterministic operators can be found in the tutorial “Next Generation Genetic Algorithms” [14].

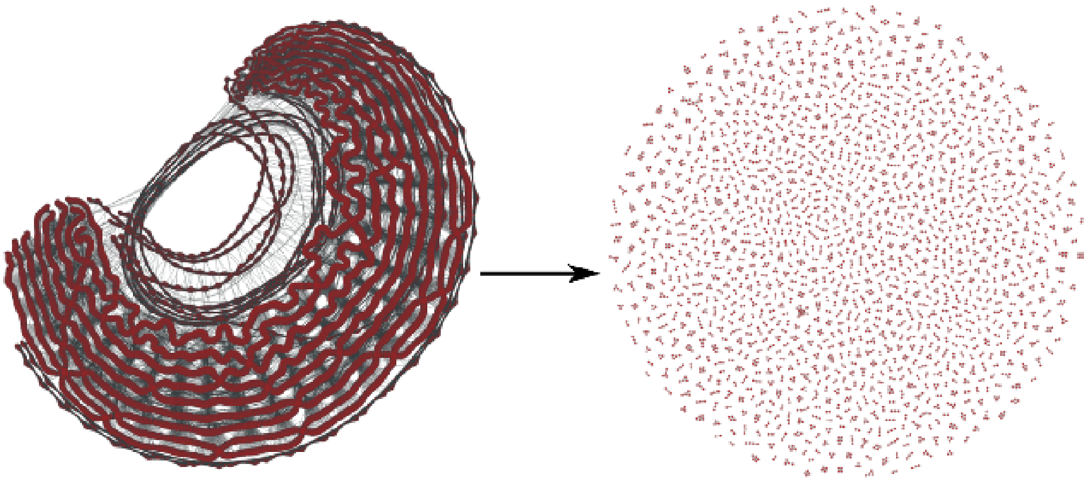

Figure 1: These images represent the variable interactions for a large industrial MAXSAT instance. On the left is the “Variable Interaction Graph” (VIG) where the vertices are variables and the edges represent nonlinear interactions between the variables. On the right, is the “Recombination Graph.” Given two parents that had been improved using local search, all of the variables that have the same assignment have been removed from the VIG to create the recombination graph. This decomposes the variable interaction graph into 1087 linearly independent subgraphs. Partition Crossover, which is a form of intelligent greedy crossover, can now return the best of 2^{1087} offspring in linear time by simply picking the best partial solution from each of the 1087 subgraphs.

I would argue that the only way for evolutionary algorithms to be competitive on many classic NP Hard combinatorial optimization problems is to abandon “Black Box” optimization and adopt more intelligent search methods. The result is a form of Gray Box optimization where knowledge about problem structure is actively and explicitly exploited [11]. And in many cases, there is an enormous amount of problem structure that is readily available, particularly when working with problems in combinatorial optimization. This line of research can also be described as a form of “Landscape Aware Heuristic Search” [3]. There have been several workshops on Landscape Aware Heuristic Search at the recent GECCO conferences.

Theory also needs to catch up. The (1+1)ES and Holland’s Simple Genetic Algorithm are more than fifty years old and yet most theory is still applied to these ancient algorithms in a Black Box scenario. Runtime analysis is also overly focused on test problems that have polynomial complexity. But this isn’t surprising: performing runtime analysis on NP-Hard problems means that one must deal with exponential runtimes in the worst case unless N=NP. Furthermore, assuming that runtime results on simple linear problems like ONEMAX can tell us anytime about how to apply evolutionary algorithms to nonlinear NP-hard problems is like a physicist assuming that atoms are just like ping pong balls. Finally, under a Gray Box scenario, simple test problems (such as ONEMAX, Trap functions, Leading Ones, and JUMP functions) become trivial to solve in linear time because the problems are separable and/or the order 1 hyperplanes all exactly point to the global optimum [11].

One might argue that “Evolutionary Algorithms” are based on natural selection and natural variation, and that random mutations and random recombination drive natural evolution. But this argument does not hold up to closer examination. In the mini-review article published in the *Journal of Bacteriology* in 2000, Barbara Wright describes DNA “Hot-Spots” where different parts of the DNA can have very different mutation rates. She also discusses mechanisms that can can cause mutation rates to vary. At the most basic level, mutations are more frequent on the non-transcripted parts of DNA. Wright also states there exists “an impressive array of circumstances that enhance background mutation rates in response to environmental stress ....” and that this can target specific genes [15]. Wright suggests several ways in which natural evolution is also “landscape aware.” In a paper in *Nature* in 2012, Martincorena et al. showed that mutation rates across genes in *E. Coli* can vary by an order of magnitude and that the variation is not random: the mutation rate was lower in highly expressed genes and those undergoing strong selection [4]. They go on to suggest that the mutation rate maybe adapted to reduce the risk of deleterious mutations.

For anyone interested in solving real world optimization problems, Gray Box optimization offers too many advantages to be ignored. And even natural evolution displays features that appear to be "Landscape Aware." This is good news. And it also open the door to new forms of theory that actively model problem structure in a useful fashion.

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EuroGP vs EvoCOP:
Contrasting the Colloboration Networks

By **Mila Goranova** [1] (✉), **Gabriela Ochoa** [1], and **Marco Tomassini** [2]

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Abstract. Using an online database with bibliographic information on major computer science publications we have constructed collaboration networks for the two main EvoStar (the he leading European event on Bio-Inspired Computation) conferences: EuroGP (European Conference on Genetic Programming) and EvoCOP (Evolutionary Computation in Combinatorial Optimisation). In these networks two authors are connected if they have coauthored one or more papers appearing in these conferences since their inception until 2018. The networks are then visualised and analysed using a number of network statistics. Our main focus is to reveal and contrast the patterns of collaboration and the most active researchers in both conferences. EuroGP's network shows a large central component of connected authors, wherease EvoCOP authors appear to work in small groups without direct interaction between groups. This could be explained by the different origins and composition of these two communities.

1 Introduction

Coauthorship of a scientific paper can be considered as an evidence of a collaboration between two or more authors. These collaborations form a ‘coauthorship network’, in which nodes represent authors, and two authors are linked if they have coauthored one or more papers. The study of such networks reveals interesting features of academic communities such as the number of collaborators of scientists, the numbers of papers they write, the distance between scientists and other features describing the patterns of collaboration. Coautorship networks have been studied, especially in the field of physics, mathematics, and other scientific disciplines notably by M. Newman [1]–[3]. A similar approach has subsequently been used in the field of evolutionary computation (EC). Merelo and Cotta in [4], [5], have investigated the coauthorship network for authors who have published in the main EC conferences in the five years previous to the articles publication. Using online bibliographic data, they searched publications by this list of authors on both journal and conferences in EC and other venues having terms relevant to EC in the paper title. Tomassini et al. [6] have focused only on collaboration data in the field of Genetic Programming (GP) with data containing most of the papers published in several venues since the inception of the field up until 2006. Both groups of authors compare the EC networks with the collaboration networks from Newman's paper[3].

Previous studies focused on collaboration networks of a given scientific field or sub-field across several publication venues (including both journal and conference publications), and covering a fixed number of years (up to 5 years in most cases). The EC studies published so far consider publication data up to 2006. In this paper we look instead into the collaboration network of particular conferences within EC, from the conference inception until the most recent proceedings in 2018. Specifically, we look into the publication data of the leading European event on bio-inspired computation EvoStar, of which the two main conferences are EuroGP and EvoCOP. EuroGP is devoted specifically to the branch of Genetic Programming, while EvoCOP focuses on evolutionary computation methods and metaheuristics applied to combinatorial optimisation. The data source for the authors and their publications was the bibliography server DBLP (Database Systems and Logic Programming). The resulting networks are built, visualised and analysed in the coming sections. We are interested in revealing the global structure of these collaboration networks and identifying the most central authors in each conference, as well as several other measures.

2 Methodology

A collaboration network is a graph in which there are two types of nodes: actors of some kind and groups to which actors belong. For example, actors could be researchers and groups could be equated to projects or publications in which researchers are connected through their participation in the project or the article. We describe below the steps of our methodological approach.

Data source. The bibliographical data was gathered from the DBLP website, an online reference for bibliographic information on major computer science publications, including more than 32000 journal volumes, 31000 conference or workshop proceedings, and 23000 monographs. It is updated promptly after a new event or conference has taken place, which makes it a reliable source for the data used in this work. The entries are structured and tagged with HTML tags which makes the data scraping process precise.

Data collection. The data were collected with a Python script using the *lxml* library. The data for each conference proceedings have clearly indicated HTML tags for each author name and paper title. The Python script scraped the data and then saved it into two spreadsheets, one for authors and one for papers, keeping the relevant data on each. Some data cleaning was required as author names varied in entries with people that have multiple middle names or had their surname changed.

Network construction and visualisation. The coauthorship network is the projection of the original bipartite graph in which there are two disjoint sets of nodes: author nodes and publication nodes. In this bipartite view, authors have connections to all the publication nodes in which they are coauthors. In the author projection network examined here, there is a connection between two authors if they have coauthored at least one paper. Edges are weighted with the strength of the collaboration, that is, the number of co-authored articles between each pair of authors. The freeware package Gephi [7] was subsequently used to construct the networks from the collected datasheets. Visualisation was also conducted with Gephi using a combination of the graph layout algorithms provided; (mainly force-directed algorithms) which simulate repulsive and attractive forces between the adjacent nodes when building the network, similar to an electrical force. The main idea is to minimise the energy of the network by changing the places of the nodes and adjusting the forces between them. These algorithms produce aesthetically-pleasing images, cluster nodes that are connected, and minimal edges crossing. The igraph package [8] within the R statistical language was also used to compute network metrics and produce the degree distribution plot.

3 Results

3.1 Visualisation

Visualising networks is a powerful and accessible way of gaining insight into their structure if they are not too large. *Figure 1* illustrate the collaboration networks for EuroGP (top) and EvoCOP (bottom). To improve visibility, instead of the full network, a subset of each network is visualised [1]. *Figure 1* includes the nodes and edges that belong to the 14 largest communities. The colour of nodes represent community membership. Communities in networks are set of nodes which are more closely connected among themselves than across different groups. *Community detection* is a method of graph partitioning. The goal is to search for a partition of a graph's nodes which optimises a given cost function. A typical cost function is the number of links that connect between the partitions. Community detection is an exploratory method in the sense that there are no pre-formulated constraints to the problem of choosing a partition of a graph. Instead, a community detection algorithm is free in determining the number of communities or the number of nodes per community. The definition of a community depends

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[1] Interactive web-based visualisation of the collaboration networks: EuroGP Network | EvoCOP Network

on the discipline applied and there exists a variety of algorithms that have been validated for different purposes [9]. Here we use the community detection algorithm provided in Gephi, proposed by Blondel et. al. [10] . This method is a fast heuristic approach based on minimising a metric called modularity that measures the density of links inside communities as compared to links between communities.

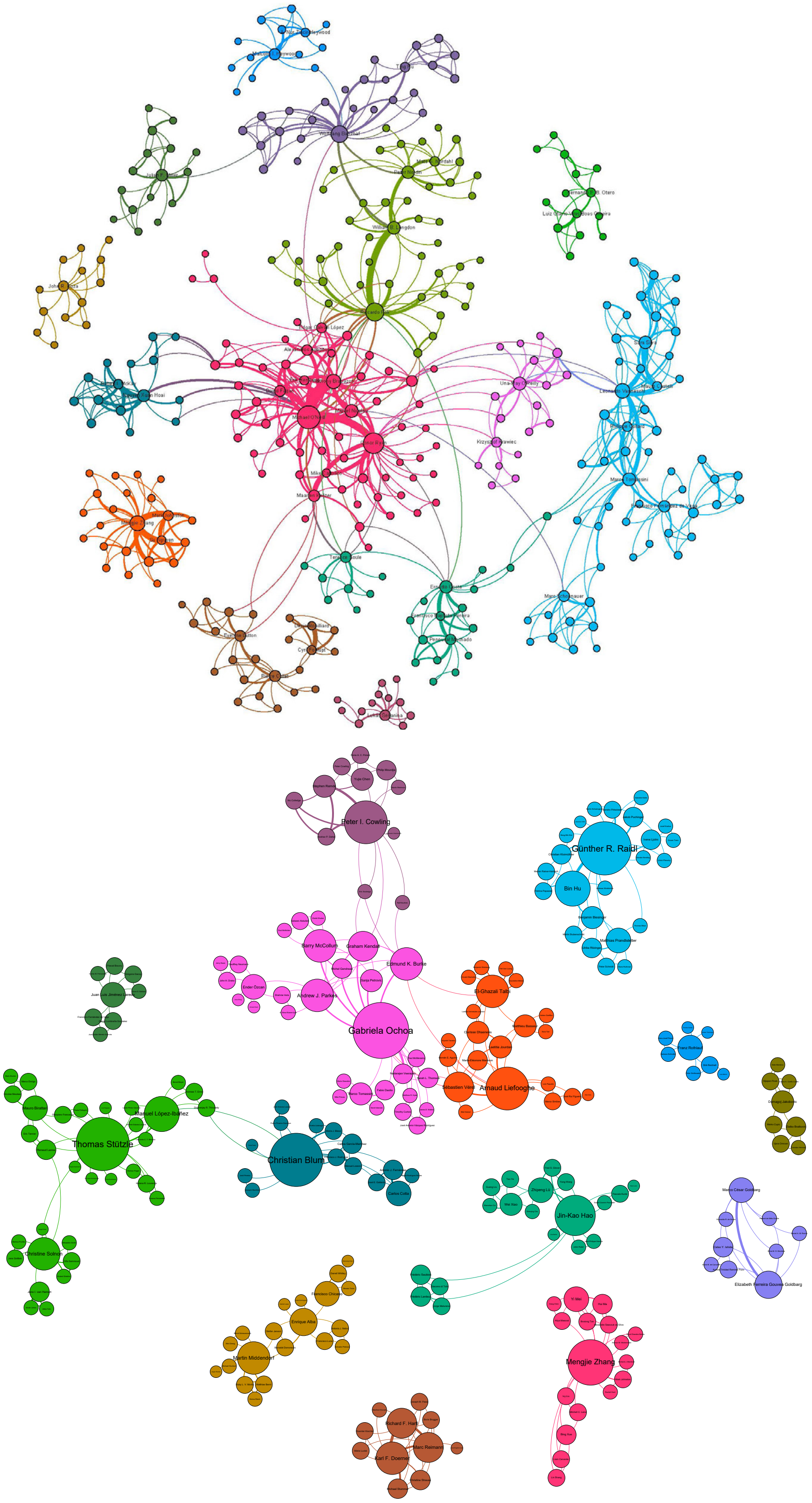

Figure 1. Subset of the coautorhisp networks for EuroGP (top) and EvoCOP (bottom). Edge widths are proportional to number of papers co-authored. Node sizes are proportional to their centrality (PageRank). Node colours identify communities.T

3.2 Metrics

A summary of the basic statistics of the two networks is given in *Table 1* EuroGP has the largest network with 577 publications over a 21-year period. EvoCOP has produced 372 papers over 18 years. The average number of publications per author, and the average number of authors per publication are higher for EuroGP. Even though the two conferences produce a similar number of papers per year and the number of authors difference is 109, EuroGP authors produce more papers on average. This might indicate that the EvoCOP authors are less productive and less likely to collaborate.

The most striking difference between the two networks is the size of the largest connected component. A connected component is a subgraph in which any two vertices are connected to each other by paths. In the realm of collaboration networks, a component is a set of authors connected via coauthorship, such that any node in the set can be reached from any other For the EuroGP network the percentage of nodes included in the largest component is close to half of the authors (40.02%). This implies that EuroGP authors are connected in a type of linked research enterprise. This metric is much lower for EvoCOP with only about 9%, which implies that people are working within their own smaller component, in isolation, rather than having more varied collaborations. This can be seen as a worrying sign for this community. An increased collaboration among authors would tend to increase the size of the largest component, and promote a more collective research effort. The average distance between two authors, as well as the diameter in EvoCOP are rather short, reflecting the small size of the separated connected components (see EvoCOP network in *Figure 1*).

	EuroGP	**EvoCOP**
Years Running	21	18
Total Number of Publications	577	372
Average Publications Per Year	21.4	20.6
Nodes (Number of Authors)	812	703
Edges (Number of Collaborations)	1264	880
Average Publication per Author	3.11	2.50
Average Authors per Publication	4.53	2.92
Largest Component	325 (40.02%)	63 (8.96%)
Average Distance (Path Length)	4.83	2.86
Diameter	11	7
Connected Components	163	163
Average Clustering Coefficient	0.854	0.795

Table 1. Statistical Properties for EuroGP's and EvoCOP's networks

As a remarkable coincidence, the two networks have the same number of connected components, although their distribution of sizes is rather different as indicated by the large difference in the size of the largest component (40% vs. 9%). Finally, the clustering coefficient, which measures the probability that two of a researchers' coauthors have themselves coauthored a paper, is higher for EuroGP. This is in line with the stronger pattern

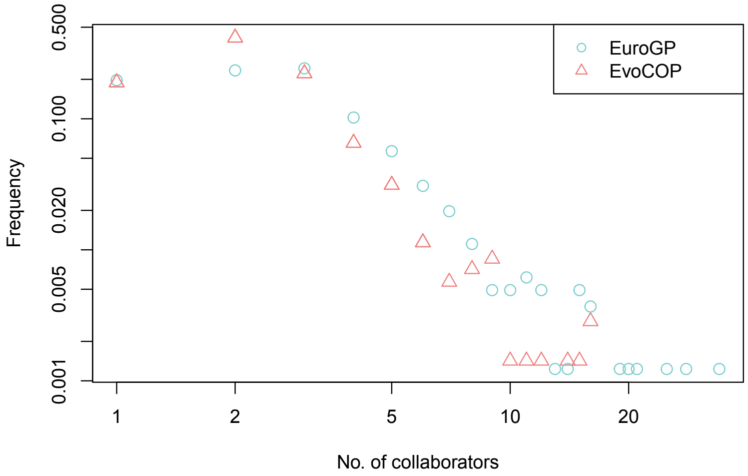

Figure 2. Degree distribution (number of collaborators per author) in log-log scale

Figure 2 shows the degree distribution for both networks in log-log scale. The distributions are similar, both being fat-tailed as is generally the case for collaboration networks [2], [6]. We can observe that EuroGP has a higher number of larger hubs, that is, several authors with more than 20 collaborators, whereas in EvoCOP the largest number of collaborators of an author is 18.

3.3 Most Central Authors

Another aim of this work is to find out who are the most active researchers in EuroGP and EvoCOP. There are multiple ways in which the centrality of the authors could be measured, but here we will focus on three of them - degree, PageRank and betweeness centrality.

Degree. The degree of a node is simply the number of edges connected to it, which here corresponds the number of the collaborating authors. It is a purely local measure.

PageRank. According to this metric authors are considered central if they are highly connected and the co-authors are themselves central [11]. So it is a more global metric of centrality. Note that when calculating the PageRank, the weight of the edges signifies the number of papers coauthored by the two connected authors.

Betweenness. This is defined as the number of shortest paths between other pairs of nodes that pass through that node. This metric is regarded as a measure of the influence that the authors have over the collaboration flow between other [12]. The authors who act as a link between other authors will have the highest betweenness scores and could be considered hubs for information flow. The calculations provided are normalised in [0,1].

Degree		PageRank		Betweenness	
Michael O'Neill	40	Michael O'Neill	0.01393	Wolfgang Banzhaf	0.06281
Conor Ryan	34	Conor Ryan	0.01039	Miguel Nicolau	0.04984
Riccardo Poli	28	Riccardo Poli	0.00982	Conor Ryan	0.03875
Wolfgang Banzhaf	25	Wolfgang Banzhaf	0.00866	Riccardo Poli	0.03742
Mengjie Zhang	21	Mengjie Zhang	0.00760	Michael O'Neill	0.03449
Leonardo Vanneschi	20	William B. Langdon	0.00677	Leonardo Vanneschi	0.03157
Anthony Brabazon	19	Anthony Brabazon	0.00635	William B. Langdon	0.02763
Una-May O'Reilly	16	Leonardo Vanneschi	0.00579	Maarten Keijzer	0.02340
Miguel Nicolau	16	Malcolm I. Heywood	0.00552	James McDermott	0.02255
Marco Tomassini	16	Peter Nordin	0.00547	Evelyne Lutton	0.01773

Table 2. Most central authors in the EuroGP network

Table 2 shows the results for the top ten authors for the EuroGP conference in reference to the three chosen metrics. We can see that **Michael O'Neill** heavily influences the network being the author with the highest degree and PageRank score. However, the betweenness centrality highest scoring author is **Wolfgang Banzhaf** as he connects authors with bigger distance in the network, while **Michael O'Neill** is heavy connected more locally in the network.

Degree		PageRank		Betweenness	
Gabriela Ochoa	18	Günther R. Raidl	0.008118	Christian Blum	0.023732
Christian Blum	17	Gabriela Ochoa	0.007367	Manuel López-Ibáñez	0.022538
Günther R. Raidl	17	Thomas Stützle	0.00682	Gabriela Ochoa	0.018147
Thomas Stützle	17	Christian Blum	0.005869	Bin Hu	0.014975
Mengjie Zhang	14	Mengjie Zhang	0.00522	Martin Middendorf	0.014973
Arnaud Liefooghe	13	Jin-Kao Hao	0.004752	Jin-Kao Hao	0.013528
Peter I. Cowling	13	Arnaud Liefooghe	0.004578	Peter I. Cowling	0.012998
Jin-Kao Hao	12	Peter I. Cowling	0.004522	Thomas Stützle	0.011700
Bin Hu	10	Bin Hu	0.004508	Arnaud Liefooghe	0.010848
Manuel López-Ibáñez	10	Karl F. Doerner	0.003863	Günther R. Raidl	0.009895

Table 3. Most central authors in the EvoCOP network

Table 3 shows the ten authors with highest centrality for the EvoCOP conference. The degree differences between the top four authors is rather small. An interesting observation is that **Manuel López-Ibáñez** does not feature in the PageRank ranking and is number ten in the degree metric, however, he scores second in the betweenness centrality. This indicates, that he serves as a connector allowing the information flow between authors in the two communities within the second largest connected component in the network (see *Figure 1*). There are not global connectors in the EvoCOP collaboration network, which is worrying.

4 Conclusions

Collaboration networks provide a convenient way of analysing how scientists work and exchange information between each other. In this work, we have discussed the structure of the two networks representing the collaborations in the EuroGP and EvoCOP conferences under the form of coauthored papers. Network visualisation techniques greatly contribute to the understanding of their structures in the present case due to their relatively small size.

Not surprisingly, EuroGP represents a larger network as it has been active for 21 years as opposed to 18 years of EvoCOP. There are, however, some differences between the patterns of collaboration in the two conferences. Both conferences have a broad distribution of the number of authors per publication, but EuroGP has a higher number of larger hubs. Although the average number of publications per year is similar in both events, EuroGP authors are on average more productive and interact more widely with each other. The EvoCOP collaboration pattern indicates that authors collaborate within small groups, whith no interaction between groups. This could be explained in part by the different origins of the two communities. EuroGP unites researchers working sepecifically on Evolutionary Computation and Genetic Programming, whereas EvoCOP reunites researchers from Evolutionary Computation, Metaheuristics and Operational Research as well as application oriented research groups.

The results explored in this paper are a small portion of the information we can discover from such data and have been purposely limited due to space constraints. Possible future use of the data is to aim at the title of the publications alone and establish trends within the subjects of interest within the evolutionary computation community. As well, it would be interesting to investigate the nature of the clusters or communities in each network.

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Workshop on Developmental Neural Networks

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The inaugural workshop on Developmental Neural Networks was held at PPSN (Parallel Problem Solving from Nature) 2018 in Coimbra, Portugal. The aim of this workshop is to encourage approaches which focus on the development of artificial neural networks (ANN). In nature, brains are built through a process of biological development in which many aspects of the network of neurons and connections change, shaped by external information received through sensory organs. However, many modern artificial neural networks do not include developmental mechanisms and regard learning as the adjustment of connection weights, while some that do use development restrain it to a period before the ANN is used. The first edition of the workshop demonstrated a broad interest in this nascent topic.

The workshop started with a keynote address on biological neural development by **Sophie Pautot**, a neuroscientist from the Institute for Advanced Technology in Life Science in Toulouse, France. She detailed the process of in vivo development, focusing on cellular interactions in the developing human brain, and then related these concepts to her own work on in vitro development of 3D neural cultures. The second presentation of the workshop was given by **Julian Miller** on the evolution of programs that build neural networks. In this work, evolved soma and dendrite programs coordinate to grow different ANNs for multiple tasks.This was followed by a presentation on a surrogate objective function for neuroevolution by **Jörg Stork** which can be used to reduce the evaluation of an ANN's performance. This is especially important for developmental programs, where individuals could be selected before devoting resources to development and evaluation.

The final two presentations of the workshop focused on computational models of ANNs inspired by computational neuroscience. In the first, presented by **Will Browne**, an artificial rat was tasked with navigating through different mazes, learning with Spike Timing Dependent Plasticity. Both the model, which uses biological neural models and learning rules, and the application of maze navigation are relevant for neural development, as they relate the computational models to known developmental neuroscience. The last presentation of the workshop, given by **Dennis Wilson**, demonstrated that an evolved controller for axon guidance used neural activity in creating a desired topology. In the brain, axon guidance is responsible for the complex wiring of the brain and has also been shown to rely on neural activity in experiments on the visual cortex.

The workshop was concluded with a panel discussion with many interesting questions from the audience. We discussed how the presented works relate to existing deep neural network and neuroevolution methods. The general conclusion was that a focus on ontogeny, ie lifetime development, is currently lacking in the neural network literature, with deep learning often using static architectures and neuroevolutionary methods focusing on phylogeny, ie evolutionary development. It is worthwhile to understand therefore how computational models of neural ontogeny can improve ANNs.

The second edition of the workshop will be held at the 2019 Conference on Artificial Life (ALIFE 2019), Newcastle, UK, on Monday July 29th, 2019. As in the first edition, we will explore existing and future approaches that aim to incorporate development into ANNs. We welcome anyone to participate and encourage the submission of extended abstracts of 2-4 pages (MIT Press format). We are open to submissions concerning a variety of neural development topics, from hand-written rules to evolved systems, and from conceptual work to experimental results. Accepted submissions will be distributed online and presented during the workshop. Abstracts must be submitted via email by June 3, 2019. For more information, see https://www.irit.fr/devonn/.

Developmental Neural Network Organizers
Julian F. Miller
Sylvain Cussat-Blanc
Dennis G. Wilson

About the Author

Dennis G. Wilson is currently a postdoctoral researcher at the Institut de Recherche en Informatique de Toulouse (IRIT). He obtained his PhD at IRIT in 2019 on the evolution of principles of artificial neural networks. He is interested in learning in ANNs at the intersection of computational neuroscience and artificial intelligence, bringing principles of biological learning into artificial models. He is equally interested in the evolution of learning, how learning evolved, and how artificial evolution can support learning discovery.

Dennis previously worked in the Anyscale Learning For All group in CSAIL, MIT, applying evolutionary strategies and developmental models to the problem of wind farm layout optimization, a topic on which he organized two GECCO competitions. He was selected as a SIGEVO student representative to the Turing Award ceremony and as a winner of the SIGAI student essay competition on ethics and AI. He is a former chair of the Emergent Researchers in Alife group and a current editor of the student games studies journal Press Start.

Forthcoming Conferences

FOGA XV

The 15th ACM/SIGEVO Workshop on Foundations of Genetic Algorithms. Potsdam, Germany. 26-29 August 2019.

The FOGA workshop series aims at advancing our understanding of the working principles behind evolutionary algorithms and related randomized search heuristics, such as local search algorithms, differential evolution, ant colony optimization, particle swarm optimization, artificial immune systems, simulated annealing, and other Monte Carlo methods for search and optimization. Connections to related areas, such as Bayesian optimization and direct search, are of interest as well. FOGA is the premier event to discuss advances on the theoretical foundations of these algorithms, tools needed to analyze them, and different aspects of comparing algorithms' performance.

Important Dates (all dates AoE)
- **Deadline for paper submission**: April 17, 2019 (non-extensible)
- Author rebuttal phase: May 21-23, 2019 Notification of authors: June 5, 2019
- Conference: 26-29 August 2019

Organizers
- **Tobias Friedrich**, Hasso Plattner Institute, Potsdam, Germany (General Chair)
- **Carola Doerr**, CNRS and Sorbonne University, Paris, France (Program co-Chair)
- **Dirk Arnold**, Dalhousie University, Halifax, Nova Scotia, Canada (Program co-Chair)

http://www.hpi.de/foga2019

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SIGEVOlution is the newsletter of SIGEVO, the ACM Special Interest Group on Genetic and Evolutionary Computation. To join SIGEVO, please follow this link: [WWW]

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We solicit contributions in the following categories:

Art: Are you working with Evolutionary Art? We are always looking for nice evolutionary art for the cover page of the newsletter.

Short surveys and position papers: We invite short surveys and position papers in EC and EC related areas. We are also interested in applications of EC technologies that have solved interesting and important problems.

Software: Are you are a developer of an EC software and you wish to tell us about it? Then, send us a short summary or a short tutorial of your software.

Lost Gems: Did you read an interesting EC paper that, in your opinion, did not receive enough attention or should be rediscovered? Then send us a page about it.

Dissertations: We invite short summaries, around a page, of theses in EC-related areas that have been recently discussed and are available online.

Meetings Reports: Did you participate to an interesting EC-related event? Would you be willing to tell us about it? Then, send us a short summary, around half a page, about the event.

Forthcoming Events: If you have an EC event you wish to announce, this is the place.

News and Announcements: Is there anything you wish to announce, such as an employment vacancy? This is the place.

Letters: If you want to ask or to say something to SIGEVO members, please write us a letter!

Suggestions: If you have a suggestion about how to improve the newsletter, please send us an email.

Contributions will be reviewed by members of the newsletter board.

We accept contributions in LATEX, MS Word, and plain text.

Enquiries about submissions and contributions can be emailed to editor@sigevolution.org

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