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Organisations

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18/02/2013 → present
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Publications:

**A Runtime Analysis of Parallel Evolutionary Algorithms in Dynamic Optimization**
A simple island model with (Formula presented.) islands and migration occurring after every (Formula presented.) iterations is studied on the dynamic fitness function Maze. This model is equivalent to a (Formula presented.) EA if (Formula presented.), i.e., migration occurs during every iteration. It is proved that even for an increased offspring population size up to (Formula presented.), the (Formula presented.) EA is still not able to track the optimum of Maze. If the migration interval is chosen carefully, the algorithm is able to track the optimum even for logarithmic (Formula presented.). The relationship of (Formula presented.), and the ability of the island model to track the optimum is then investigated more closely. Finally, experiments are performed to supplement the asymptotic results, and investigate the impact of the migration topology.

**General information**
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Sheffield
Authors: Lissovoi, A. (Ekstern), Witt, C. (Intern)
Pages: 641–659
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Algorithmica
Volume: 78
Issue number: 2
ISSN (Print): 0178-4617
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.11 SJR 0.685 SNIP 1.338
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.77 SNIP 1.354 CiteScore 1.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.921 SNIP 1.347 CiteScore 1.2
Lower bounds on the run time of the univariate marginal distribution algorithm on OneMax

The Univariate Marginal Distribution Algorithm (UMDA), a popular estimation of distribution algorithm, is studied from a run time perspective. On the classical OneMax benchmark function, a lower bound of $\Omega(\mu \sqrt{n} + n \log n)$, where $\mu$ is the population size, on its expected run time is proved. This is the first direct lower bound on the run time of the UMDA. It is stronger than the bounds that follow from general black-box complexity theory and is matched by the run time of many evolutionary algorithms. The results are obtained through advanced analyses of the stochastic change of the frequencies of bit values maintained by the algorithm, including carefully designed potential functions. These techniques may prove useful in advancing the field of run time analysis for estimation of distribution algorithms in general.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, Hasso Platter Institute, Postdam
Authors: Krejca, M. S. (Ekstern), Witt, C. (Intern)
Pages: 65-79
Publication date: 2017

Host publication information
Title of host publication: 14th ACM/SIGEVO Workshop on Foundations of Genetic Algorithms
The (1+λ) evolutionary algorithm with self-adjusting mutation rate

We propose a new way to self-adjust the mutation rate in population-based evolutionary algorithms. Roughly speaking, it consists of creating half the offspring with a mutation rate that is twice the current mutation rate and the other half with half the current rate. The mutation rate is then updated to the rate used in that subpopulation which contains the best offspring. We analyze how the (1 + A) evolutionary algorithm with this self-adjusting mutation rate optimizes the OneMax test function. We prove that this dynamic version of the (1 + A) EA finds the optimum in an expected optimization time (number of fitness evaluations) of O(nA/log A + n log n). This time is asymptotically smaller than the optimization time of the classic (1 + A) EA. Previous work shows that this performance is best-possible among all A-parallel mutation-based unbiased black-box algorithms. This result shows that the new way of adjusting the mutation rate can find optimal dynamic parameter values on the fly. Since our adjustment mechanism is simpler than the ones previously used for adjusting the mutation rate and does not have parameters itself, we are optimistic that it will find other applications.
of the optimum with overwhelming probability. Experimentally, we show that very frequent migration on a ring topology is
not an effective diversity mechanism, while a lower migration rate allows the ring topology to track the optimum for a wider
range of oscillation patterns. When migration occurs only rarely, we prove that dense migration topologies of small
diameter may be advantageous. Combined, our results show that the sparse migration topology is able to track the
optimum through a wider range of oscillation patterns, and cope with a wider range of migration frequencies.

General information
State: Published
Organisations: Algorithms and Logic, Department of Applied Mathematics and Computer Science
Authors: Lissovoi, A. (Intern), Witt, C. (Intern)
Number of pages: 24
Pages: 1-24
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Algorithmica
ISSN (Print): 0178-4617
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.11 SJR 0.685 SNIP 1.338
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.77 SNIP 1.354 CiteScore 1.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.921 SNIP 1.347 CiteScore 1.2
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.023 SNIP 1.572 CiteScore 1.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.872 SNIP 1.228 CiteScore 0.99
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.862 SNIP 1.166 CiteScore 0.91
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.99 SNIP 1.356
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.019 SNIP 1.397
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.174 SNIP 1.248
Scopus rating (2007): SJR 1.052 SNIP 1.466
Scopus rating (2006): SJR 1.241 SNIP 1.76
Scopus rating (2005): SJR 0.865 SNIP 1.45
Scopus rating (2004): SJR 1.129 SNIP 1.55
Scopus rating (2003): SJR 0.989 SNIP 1.317
Scopus rating (2002): SJR 0.993 SNIP 1.545
Scopus rating (2001): SJR 1.296 SNIP 1.141
Scopus rating (2000): SJR 0.49 SNIP 1.086
The Impact of Parametrization on Randomized Search Heuristics

In this work we present runtime analyses of randomized search heuristics (RSH) in various settings that are determined by parameters of the problems, the algorithms and also exogenous parameters like noise. In the process we provide new techniques for the theoretical analysis of RSH as well as new optimization algorithms. We consider the following topics.

Escaping local optima using local search. We analyze memetic algorithms, i.e. evolutionary algorithms equipped with a local search after mutation. To this end we consider the (1+1) EA equipped with Standard Local Search (SLS) and Variable-Depth Search (VDS) on an artificial test function. We determine features of the fitness landscape that lead to the (1+1) EA using SLS outperforming the (1+1) EA using VDS with an exponential performance gap. Moreover, we present a new local search operator, Opportunistic Local Search (OLS), that can deal with such features in the landscape and show that the (1+1) EA with OLS can efficiently optimize a discretized Rastrigin function. Stochastic fitness functions. We analyze the role of populations in stochastic optimization. We assume that the objective function is subject to noise, introducing stochastic errors in its evaluation. On classical test functions, such noise makes optimization by the simple (1+1) EA hillclimber infeasible even in exponential time. Interestingly, the use of parent and offspring populations of only logarithmic size turns the algorithm into an efficient one. The results are obtained by drift analysis. An asymptotic expansion of the expected runtime of the (1+λ) EA on ONE MAX. We consider the (1+λ) EA with mutation probability c/n, where c > 0 is a constant on ONE MAX. We give an asymptotic expansion for the expected runtime depending on both c and λ. Our results show that c = 1 is the optimal mutation rate for λ = o(log log n log log log n) and that c only has an impact on the lower-order terms of the expected runtime, i.e. c = 1 is no longer the only optimal mutation rate. Our methods are strongly based on variable drift theorems for upper and lower bounds and a precise analysis of order statistics of the binomial distribution. To the best of our knowledge this is the first tight runtime analysis of a population-based EA, up to lower-order terms. Furthermore, we develop helpful stochastic tools for runtime analyses. Optimal mutation rates for the (1+λ) EA on ONE MAX. We consider the (1+λ) EA with mutation probability c/n on ONE MAX, where c > 0 and λ are constant. We present an improved variable drift theorem that weakens the requirement that no large steps towards the optimum may occur in the process to a stochastic one, reducing the analysis of the expected optimization time to finding an exact expression for the drift. We formalize an exact closed-form expression for the drift and provide small error approximations that are very efficient to compute. Self-adjusting mutation rates for the (1+λ) EA on ONE MAX. We propose a new mechanism to self-adjust the mutation rate in population-based evolutionary algorithms. It consists of creating half the offspring with a higher and the rest with a lower mutation rate. The mutation rate is then adjusted, based on the success of the subpopulations. We show that the (1+λ) EA optimizes ONE MAX in an expected optimization time of $O(n/\lambda + n \log n)$ which has been shown to be best-possible among all λ-parallel mutation-based unbiased black-box algorithms.
The Interplay of Population Size and Mutation Probability in the (1+λ) EA on OneMax

The \((\text{Formula presented.})\) EA with mutation probability \(c/n\), where \((\text{Formula presented.})\) is an arbitrary constant, is studied for the classical OneMax function. Its expected optimization time is analyzed exactly (up to lower order terms) as a function of \(c\) and \((\text{Formula presented.})\). It turns out that \(1/n\) is the only optimal mutation probability if \((\text{Formula presented.})\), which is the cut-off point for linear speed-up. However, if \((\text{Formula presented.})\) is above this cut-off point then the standard mutation probability \(1/n\) is no longer the only optimal choice. Instead, the expected number of generations is (up to lower order terms) independent of \(c\), irrespectively of it being less than 1 or greater. The theoretical results are obtained by a careful study of order statistics of the binomial distribution and variable drift theorems for upper and lower bounds. Experimental supplements shed light on the optimal mutation probability for small problem sizes.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic
Authors: Gießen, C. (Intern), Witt, C. (Intern)
Pages: 587–609
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Algorithmica
Volume: 78
Issue number: 2
ISSN (Print): 0178-4617
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.11 SJR 0.685 SNIP 1.338
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.77 SNIP 1.354 CiteScore 1.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.921 SNIP 1.347 CiteScore 1.2
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.023 SNIP 1.572 CiteScore 1.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.872 SNIP 1.228 CiteScore 0.99
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.862 SNIP 1.166 CiteScore 0.91
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.99 SNIP 1.356
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.019 SNIP 1.397
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.174 SNIP 1.248
Scopus rating (2007): SJR 1.052 SNIP 1.466
Scopus rating (2006): SJR 1.241 SNIP 1.76
Scopus rating (2005): SJR 0.865 SNIP 1.45
Scopus rating (2004): SJR 1.129 SNIP 1.55
Upper bounds on the runtime of the univariate marginal distribution algorithm on OneMax

A runtime analysis of the Univariate Marginal Distribution Algorithm (UMDA) is presented on the OneMax function for wide ranges of the parameters $\mu$ and $\lambda$. If $\mu \geq c \log n$ for some constant $c > 0$ and $\lambda = (1 + O(1))\mu$, a general bound $O(\mu n)$ on the expected runtime is obtained. This bound crucially assumes that all marginal probabilities of the algorithm are confined to the interval $[1/n, 1 - 1/n]$. If $\mu \geq c'\sqrt{n \log n}$ for a constant $c' > 0$ and $\lambda = (1 + O(1))\mu$, the behavior of the algorithm changes and the bound on the expected runtime becomes $O(\mu \sqrt{n})$, which typically even holds if the borders on the marginal probabilities are omitted. The results supplement the recently derived lower bound $\Omega(\mu \sqrt{n} + n \log n)$ by Krejca and Witt (FOGA 2017) and turn out as tight for the two very different values $\mu = c \log n$ and $\mu = c'\sqrt{n \log n}$. They also improve the previously best known upper bound $O(n \log n \log \log n)$ by Dang and Lehre (GECCO 2015).
Migration Topology in Island Models. We investigate the impact of the migration topology on the performance of an island model optimizing a Maze-like dynamic function, demonstrating that in some cases, a less-dense migration topology is preferable to a complete migration topology.

(1+1) EA on Generalized Dynamic OneMax. We analyze the (1 + 1) EA on dynamically changing OneMax, re-proving known results on first hitting times using modern drift analysis, and providing a new anytime analysis showing how closely the EA can track the dynamically moving optimum over time. These results are also extended to a finite-alphabet search space.

Detecting structural breaks in time series via genetic algorithms
Detecting structural breaks is an essential task for the statistical analysis of time series, for example, for fitting parametric models to it. In short, structural breaks are points in time at which the behaviour of the time series substantially changes. Typically, no solid background knowledge of the time series under consideration is available. Therefore, a black-box optimization approach is our method of choice for detecting structural breaks. We describe a genetic algorithm framework which easily adapts to a large number of statistical settings. To evaluate the usefulness of different crossover and mutation operations for this problem, we conduct extensive experiments to determine good choices for the parameters and operators of the genetic algorithm. One surprising observation is that use of uniform and one-point crossover together gave significantly better results than using either crossover operator alone. Moreover, we present a specific fitness function which exploits the sparse structure of the break points and which can be evaluated particularly efficiently. The experiments on artificial and real-world time series show that the resulting algorithm detects break points with high precision and is computationally very efficient. A reference implementation with the data used in this paper is available as an applet at the following address: http://www.imm.dtu.dk/~pafi/TSX/. It has also been implemented as package SBRect for the statistics language R.
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.724 SNIP 1.179 CiteScore 1.53
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.793 SNIP 1.518 CiteScore 2.01
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.857 SNIP 1.454 CiteScore 2
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.805 SNIP 1.232 CiteScore 1.94
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.892 SNIP 1.817 CiteScore 2.38
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.736 SNIP 1.303
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.744 SNIP 1.417
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.776 SNIP 1.228
Scopus rating (2007): SJR 0.459 SNIP 0.742
Scopus rating (2006): SJR 0.466 SNIP 0.968
Scopus rating (2005): SJR 0.382 SNIP 0.876
Scopus rating (2004): SJR 0.227 SNIP 0.63
Scopus rating (2003): SJR 0.275 SNIP 0.297
Scopus rating (2002): SJR 0.235 SNIP 0.585
Scopus rating (2001): SJR 0.131 SNIP 0.783
Original language: English
Break points, Experimentation, Genetic Algorithms, Range trees, Statistics, Time series
DOIs:
10.1007/s00500-016-2079-0
Source: FindIt
Source-ID: 2292430854
Publication: Research - peer-review › Journal article – Annual report year: 2016

**Guest Editorial: Theory of Evolutionary Computation**

**General information**
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, Ecole Polytechnique
Authors: Doerr, B. (Ekstern), Witt, C. (Intern)
Pages: 425-427
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Algorithmica
Volume: 75
Issue number: 3
ISSN (Print): 0178-4617
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.11 SJR 0.685 SNIP 1.338
We study the \( (1+\lambda) \) EA with mutation probability \( c/n \), where \( c > 0 \) is a constant, on the ONEMAX problem. Using an improved variable drift theorem, we show that upper and lower bounds on the expected runtime of the \( (1+\lambda) \) EA obtained from variable drift theorems are at most apart by a small lower order term if the exact drift is known. This reduces the analysis of expected optimization time to finding an exact expression for the drift.

We then give an exact closed-form expression for the drift and develop a method to approximate it very efficiently, enabling us to determine approximate optimal mutation rates for the \( (1+\lambda) \) EA for various parameter settings of \( c \) and \( \lambda \) and also for moderate sizes of \( n \). This makes the need for potentially lengthy and costly experiments in order to optimize the parameters unnecessary.

Interestingly, even for moderate \( n \) and not too small \( \lambda \) it turns out that mutation rates up to 10% larger than the asymptotically optimal rate \( 1/n \) minimize the expected runtime. However, in absolute terms the expected runtime does not change by much when replacing \( 1/n \) with the optimal mutation rate.

**Optimal mutation rates for the \( (1+\lambda) \) EA on OneMax**

We study the \( (1 + \lambda) \) EA with mutation probability \( c/n \), where \( c > 0 \) is a constant, on the ONEMAX problem. Using an improved variable drift theorem, we show that upper and lower bounds on the expected runtime of the \( (1+\lambda) \) EA obtained from variable drift theorems are at most apart by a small lower order term if the exact drift is known. This reduces the analysis of expected optimization time to finding an exact expression for the drift.

We then give an exact closed-form expression for the drift and develop a method to approximate it very efficiently, enabling us to determine approximate optimal mutation rates for the \( (1+\lambda) \) EA for various parameter settings of \( c \) and \( \lambda \) and also for moderate sizes of \( n \). This makes the need for potentially lengthy and costly experiments in order to optimize the parameters unnecessary.

Interestingly, even for moderate \( n \) and not too small \( \lambda \) it turns out that mutation rates up to 10% larger than the asymptotically optimal rate \( 1/n \) minimize the expected runtime. However, in absolute terms the expected runtime does not change by much when replacing \( 1/n \) with the optimal mutation rate.

**General information**

State: Published
The impact of migration topology on the runtime of island models in dynamic optimization

We introduce a simplified island model with behavior similar to the $\lambda$ (1+1) islands optimizing the Maze fitness function, and investigate the effects of the migration topology on the ability of the simplified island model to track the optimum of a dynamic fitness function. More specifically, we prove that there exist choices of model parameters for which using a unidirectional ring as the migration topology allows the model to track the oscillating optimum through $n$ Mazelike phases with high probability, while using a complete graph as the migration topology results in the island model losing track of the optimum with overwhelming probability. Additionally, we prove that if migration occurs only rarely, denser migration topologies may be advantageous. This serves to illustrate that while a less-dense migration topology may be useful when optimizing dynamic functions with oscillating behavior, and requires less problem-specific knowledge to determine when migration may be allowed to occur, care must be taken to ensure that a sufficient amount of migration occurs during the optimization process.

Update Strength in EDAs and ACO: How to Avoid Genetic Drift

We provide a rigorous runtime analysis concerning the update strength, a vital parameter in probabilistic model-building GAs such as the step size $1/K$ in the compact Genetic Algorithm (cGA) and the evaporation factor $\rho$ in ACO. While a large update strength is desirable for exploitation, there is a general trade-off: too strong updates can lead to genetic drift and poor performance. We demonstrate this trade-off for the cGA and a simple MMAS ACO algorithm on the OneMax function. More precisely, we obtain lower bounds on the expected runtime of $\Omega(K\sqrt{n + \log n})$ and $\Omega(\sqrt{n}/\rho + \log n)$, respectively, showing that the update strength should be limited to $1/K, \rho = O(1/(\sqrt{n} \log n))$. In fact, choosing $1/K, \rho \sim 1/(\sqrt{n} \log n)$ both algorithms efficiently optimize OneMax in expected time $O(n \log n)$. Our analyses provide new insights into the stochastic behavior of probabilistic model-building GAs and propose new guidelines for setting the update strength in global optimization.
(1+1) EA on Generalized Dynamic OneMax

Evolutionary algorithms (EAs) perform well in settings involving uncertainty, including settings with stochastic or dynamic fitness functions. In this paper, we analyze the (1+1) EA on dynamically changing OneMax, as introduced by Droste (2003). We re-prove the known results on first hitting times using the modern tool of drift analysis. We extend these results to search spaces which allow for more than two values per dimension.

Furthermore, we make an anytime analysis as suggested by Jansen and Zarges (2014), analyzing how closely the (1+1) EA can track the dynamically moving optimum over time. We get tight bounds both for the case of bit strings, as well as for the case of more than two values per position. Surprisingly, in the latter setting, the expected quality of the search point maintained by the (1+1) EA does not depend on the number of values per dimension.

Improved time complexity analysis of the Simple Genetic Algorithm

A runtime analysis of the Simple Genetic Algorithm (SGA) for the OneMax problem has recently been presented proving that the algorithm with population size $\mu n^{1/8-\epsilon}$ requires exponential time with overwhelming probability. This paper presents an improved analysis which overcomes some limitations of the previous one. Firstly, the new result holds for population sizes up to $\mu n^{1/4-\epsilon}$ which is an improvement up to a power of 2 larger. Secondly, we present a technique to bound the diversity of the population that does not require a bound on its bandwidth. Apart from allowing a stronger result,
we believe this is a major improvement towards the reusability of the techniques in future systematic analyses of GAs. Finally, we consider the more natural SGA using selection with replacement rather than without replacement although the results hold for both algorithmic versions. Experiments are presented to explore the limits of the new and previous mathematical techniques.

**General information**
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Sheffield
Authors: Oliveto, P. S. (Ekstern), Witt, C. (Intern)
Pages: 21-41
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Theoretical Computer Science
Volume: 605
ISSN (Print): 0304-3975
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 0.97 SJR 0.569 SNIP 1.006
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.623 SNIP 1.212 CiteScore 1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.708 SNIP 1.228 CiteScore 1.08
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.739 SNIP 1.38 CiteScore 1.17
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.844 SNIP 1.288 CiteScore 1.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.81 SNIP 1.289 CiteScore 1.17
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.91 SNIP 1.329
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.948 SNIP 1.475
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.188 SNIP 1.638
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.997 SNIP 1.65
Scopus rating (2006): SJR 0.911 SNIP 1.49
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.821 SNIP 1.486
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.804 SNIP 1.366
Web of Science (2004): Indexed yes
MMAS Versus Population-Based EA on a Family of Dynamic Fitness Functions

We study the behavior of a population-based EA and the Max–Min Ant System (MMAS) on a family of deterministically-changing fitness functions, where, in order to find the global optimum, the algorithms have to find specific local optima within each of a series of phases. In particular, we prove that a (2+1) EA with genotype diversity is able to find the global optimum of the Maze function, previously considered by Kötzing and Molter [9], in polynomial time. This is then generalized to a hierarchy result stating that for every μ, a (μ + 1) EA with genotype diversity is able to track a Maze function extended over a finite alphabet of μ symbols, whereas population size μ−1 is not sufficient. Furthermore, we show that MMAS does not require additional modifications to track the optimum of the finite-alphabet Maze functions, and, using a novel drift statement to simplify the analysis, reduce the required phase length of the Maze function.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic
Authors: Lissovoi, A. (Intern), Witt, C. (Intern)
Pages: 554-576
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Algorithmica
Volume: 75
Issue number: 3
ISSN (Print): 0178-4617
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.11 SJR 0.685 SNIP 1.338
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.77 SNIP 1.354 CiteScore 1.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.921 SNIP 1.347 CiteScore 1.2
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.023 SNIP 1.572 CiteScore 1.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.872 SNIP 1.228 CiteScore 0.99
ISI indexed (2012): ISI indexed yes
On the Runtime of Randomized Local Search and Simple Evolutionary Algorithms for Dynamic Makespan Scheduling

Evolutionary algorithms have been frequently used for dynamic optimization problems. With this paper, we contribute to the theoretical understanding of this research area. We present the first computational complexity analysis of evolutionary algorithms for a dynamic variant of a classical combinatorial optimization problem, namely makespan scheduling. We study the model of a strong adversary which is allowed to change one job at regular intervals. Furthermore, we investigate the setting of random changes. Our results show that randomized local search and a simple evolutionary algorithm are very effective in dynamically tracking changes made to the problem instance.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Adelaide
Authors: Neumann, F. (Ekstern), Witt, C. (Intern)
Pages: 3742-3748
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 24th International Conference on Artificial Intelligence (IJCAI '15)
Publisher: AAAI Press
Article number: 3742
ISBN (Print): 978-1-57735-738-4
BFI conference series: International Joint Conference on Artificial Intelligence (5000155)
Main Research Area: Technical/natural sciences
Conference: 24th International Joint Conference on Artificial Intelligence, Buenos Aires, Argentina, 25/07/2015 - 25/07/2015
Electronic versions:
makespan.pdf
Source: PublicationPreSubmission
Source-ID: 118051538
On the Utility of Island Models in Dynamic Optimization

A simple island model with \( \lambda \) islands and migration occurring after every \( \tau \) iterations is studied on the dynamic fitness function Maze. This model is equivalent to a \((1+\lambda)\) EA if \( \tau=1 \), i.e., migration occurs during every iteration. It is proved that even for an increased offspring population size up to \( \lambda=O(n^{1-\varepsilon}) \), the \((1+\lambda)\) EA is still not able to track the optimum of Maze. If the migration interval is increased, the algorithm is able to track the optimum even for logarithmic \( \lambda \). Finally, the relationship of \( \tau, \lambda \), and the ability of the island model to track the optimum is investigated more closely.

**General information**

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic
Authors: Lissovoi, A. (Intern), Witt, C. (Intern)
Pages: 1447-1454
Publication date: 2015

**Host publication information**

Title of host publication: Proceedings of the Genetic and Evolutionary Computation Conference (GECCO '15)
Publisher: Association for Computing Machinery
ISBN (Print): 978-1-4503-3472-3
BFI conference series: Genetic and Evolutionary Computation Conference (5000582)
Main Research Area: Technical/natural sciences
Conference: Genetic and Evolutionary Computation Conference (GECCO 2015), Madrid, Spain, 11/07/2015 - 11/07/2015
Evolutionary Algorithm, Island Models, Dynamic Problems, Populations, Runtime Analysis
DOIs:
10.1145/2739480.2754734

**Part E: Evolutionary Computation**

Part E, Evolutionary Computation, edited by Professors Frank Neumann, Carsten Witt, Peter Merz, Carlos A. Coello Coello, Oliver Schütze, Thomas Bartz-Beielstein, Jörn Mehnen, and Günther Raidl, concerns the third fundamental element of what is traditionally being considered to be the core of Computational Intelligence.

First, comprehensive surveys of genetic algorithms, genetic programming, evolution strategies, parallel evolutionary algorithms are presented, which are readable and constructive so that a large audience might find them useful and – to some extent – ready to use. Some more general topics like the estimation of distribution algorithms, indicator-based selection, etc., are also discussed.

An important problem, from a theoretical and practical point of view, of learning classifier systems is presented in depth.

Multiobjective evolutionary algorithms, which constitute one of the most important group, both from the theoretical and applied points of view, are discussed in detail, followed by an account of parallel multiobjective evolutionary algorithms, and then a more general analysis of many multiobjective problems.

Considerable attention has also been paid to a presentation of hybrid evolutionary algorithms, such as memetic algorithms, which have emerged as a very promising tool for solving many real-world problems in a multitude of areas of science and technology. Moreover, parallel evolutionary combinatorial optimization has been presented.

Search operators, which are crucial in all kinds of evolutionary algorithms, have been prudently analyzed. This analysis was followed by a thorough analysis of various issues involved in stochastic local search algorithms.

An interesting survey of various technological and industrial applications in mechanical engineering and design has been provided. Then, an account of the use of evolutionary combinatorial optimization in bioinformatics is given.

An analysis of a synergistic integration of metaheuristics, notably evolutionary computation, and constraint satisfaction, constraint programming, graph coloring, tree decomposition, and similar relevant problems completes the part.

**General information**

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Adelaide, University of Applied Sciences and Arts Hildesheim, CINVESTAV-IPN, Cologne University of Applied Sciences, Cranfield University, Vienna University of Technology
Pages: 823-1288
Population Size vs. Mutation Strength for the (1+µ) EA on OneMax

The (1+1) EA with mutation probability c/n, where c>0 is an arbitrary constant, is studied for the classical OneMax function. Its expected optimization time is analyzed exactly (up to lower order terms) as a function of c and µ. It turns out that 1/n is the only optimal mutation probability if µ=O(ln n ln ln n/ln ln ln n), which is the cut-off point for linear speed-up. However, if µ is above this cut-off point then the standard mutation probability 1/n is no longer the only optimal choice. Instead, the expected number of generations is (up to lower order terms) independent of c, irrespectively of it being less than 1 or greater. The results are obtained by a careful study of order statistics of the binomial distribution and variable drift theorems for upper and lower bounds.

Runtime analysis of ant colony optimization on dynamic shortest path problems

A simple ACO algorithm called lambda-MMAS for dynamic variants of the single-destination shortest paths problem is studied by rigorous runtime analyses. Building upon previous results for the special case of 1-MMAS, it is studied to what extent an enlarged colony using lambda ants per vertex helps in tracking an oscillating optimum. It is shown that easy cases of oscillations can be tracked by a constant number of ants. However, the paper also identifies more involved oscillations that with overwhelming probability cannot be tracked with any polynomial-size colony. Finally, parameters of dynamic shortest-path problems which make the optimum difficult to track are discussed. Experiments illustrate theoretical findings and conjectures.
COMPUTER, Ant colony optimization, Shortest paths, Dynamic problems, Runtime analysis

Electronic versions:

ants_dynamic_sp_journal.pdf

DOIs:

10.1016/j.tcs.2014.06.035
**Bioinspired computation in combinatorial optimization - Algorithms and their computational complexity**

**General information**
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic
Authors: Neumann, F. (Ekstern), Witt, C. (Intern)
Number of pages: 40
Pages: 647-686
Publication date: 2014

**Host publication information**
Title of host publication: Proceedings of the sixteenth conference on genetic and evolutionary computation
Publisher: Association for Computing Machinery
ISBN (Print): 9781450328814
BFI conference series: Genetic and Evolutionary Computation Conference (5000582)
Main Research Area: Technical/natural sciences
Conference: Genetic and Evolutionary Computation Conference (GECCO 2014), Vancouver, Canada, 12/07/2014 - 12/07/2014
Computational Theory and Mathematics, Applied Mathematics
DOIs: 10.1145/2598394.2605353
Source: FindIt
Source-ID: 2201121295
Publication: Research - peer-review › Article in proceedings – Annual report year: 2014

**Concentrated Hitting Times of Randomized Search Heuristics with Variable Drift**
Drift analysis is one of the state-of-the-art techniques for the runtime analysis of randomized search heuristics (RSHs) such as evolutionary algorithms (EAs), simulated annealing etc. The vast majority of existing drift theorems yield bounds on the expected value of the hitting time for a target state, e. g., the set of optimal solutions, without making additional statements on the distribution of this time. We address this lack by providing a general drift theorem that includes bounds on the upper and lower tail of the hitting time distribution. The new tail bounds are applied to prove very precise sharp-concentration results on the running time of a simple EA on standard benchmark problems, including the class of general linear functions. The usefulness of the theorem outside the theory of RSHs is demonstrated by deriving tail bounds on the number of cycles in random permutations. All these results handle a position-dependent (variable) drift that was not covered by previous drift theorems with tail bounds. Moreover, our theorem can be specialized into virtually all existing drift theorems with drift towards the target from the literature. Finally, user-friendly specializations of the general drift theorem are given.

**General information**
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Nottingham
Authors: Lehre, P. K. (Intern), Witt, C. (Intern)
Pages: 686-697
Publication date: 2014

**Host publication information**
Title of host publication: Proceedings of the 25th International Symposium on Algorithms and Computation, ISAAC 2014
Publisher: Springer
Editors: Ahn, H., Shin, C.
ISBN (Print): 978-3-319-13074-3
ISBN (Electronic): 978-3-319-13075-0
Series: Lecture Notes in Computer Science
Number: 8889
ISSN: 0302-9743
BFI conference series: International Symposium on Algorithms and Computation (5000486)
Main Research Area: Technical/natural sciences
DOIs:
Fitness levels with tail bounds for the analysis of randomized search heuristics

The fitness-level method, also called the method of f-based partitions, is an intuitive and widely used technique for the running time analysis of randomized search heuristics. It was originally defined to prove upper and lower bounds on the expected running time. Recently, upper tail bounds were added to the technique; however, these tail bounds only apply to running times that are at least twice as large as the expectation. We remove this restriction and supplement the fitness-level method with sharp tail bounds, including lower tails. As an exemplary application, we prove that the running time of randomized local search on OneMax is sharply concentrated around $n \ln n - 0.1159\ldots n$.

General information

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic
Authors: Witt, C. (Intern)
Pages: 38-41
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information

Journal: Information Processing Letters
Volume: 114
Issue number: 1-2
ISSN (Print): 0020-0190
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 0.57 SNIP 0.967 CiteScore 1.02
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.602 SNIP 1.167 CiteScore 0.93
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.593 SNIP 0.934 CiteScore 0.94
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.609 SNIP 1.047 CiteScore 0.95
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.603 SNIP 1.037 CiteScore 0.92
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.612 SNIP 0.929 CiteScore 0.85
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.625 SNIP 1.016
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.708 SNIP 1.062
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.837 SNIP 1.161
MMAS vs. Population-based EA on a family of dynamic fitness functions
We study the behavior of a population-based EA and the Max-Min Ant System (MMAS) on a family of deterministically-changing fitness functions, where, in order to find the global optimum, the algorithms have to find specific local optima within each of a series of phases. In particular, we prove that a (2+1) EA with genotype diversity is able to find the global optimum of the Maze function, previously considered by Kötzing and Molter (PPSN 2012, 113--122), in polynomial time. This is then generalized to a hierarchy result stating that for every $\mu$, a ($\mu$+1) EA with genotype diversity is able to track a Maze function extended over a finite alphabet of $\mu$ symbols, whereas population size $\mu-1$ is not sufficient. Furthermore, we show that MMAS does not require additional modifications to track the optimum of the finite-alphabet Maze functions, and, using a novel drift statement to simplify the analysis, reduce the required phase length of the Maze function.

On the runtime analysis of the Simple Genetic Algorithm
For many years it has been a challenge to analyze the time complexity of Genetic Algorithms (GAs) using stochastic selection together with crossover and mutation. This paper presents a rigorous runtime analysis of the well-known Simple Genetic Algorithm (SGA) for OneMax. It is proved that the SGA has exponential runtime with overwhelming probability for population sizes up to $\mu^{1/8-\varepsilon}$ for some arbitrarily small constant $\varepsilon$ and problem size $n$. To the best of our knowledge, this is the first time non-trivial lower bounds are obtained on the runtime of a standard crossover-based GA for a standard benchmark function. The presented techniques might serve as a first basis towards systematic runtime analyses of GAs.
Revised analysis of the (1+1) EA for the minimum spanning tree problem

We revisit the classical analysis of the (1+1) EA for the minimum spanning tree problem in the case that nothing is known about the weights of the underlying graph. Here the original upper bound on the expected running time by Neumann and Wegener [Theor. Comput. Sci. 378(1), 32-40, 2007], which depends on the largest weight of the graph, is of no use. The best upper bound available before in this case is due to Reichel and Skutella [FOGA 2009, 21-28] and is of order \( O(m^3 \log n) \), where \( m \) is the number of edges and \( n \) the number of vertices. Using an adaptive drift analysis, we show the improved bound \( O(m^2 (\sqrt{c(G)} + \log n)) \), where \( c(G) \) is the circumference (length of the longest cycle) of the graph. This is only by an asymptotic factor of at most \( \sqrt{n}/\log n \) away from the classical lower bound. Furthermore, an alternative fitness function leading to the bound \( O(m^2 \log n) \) is proposed, and limitations of the adaptive drift analysis are pointed out.

A method to derive fixed budget results from expected optimisation times

At last year's GECCO a novel perspective for theoretical performance analysis of evolutionary algorithms and other randomised search heuristics was introduced that concentrates on the expected function value after a pre-defined number of steps, called budget. This is significantly different from the common perspective where the expected optimisation time is analysed. While there is a huge body of work and a large collection of tools for the analysis of the expected optimisation time the new fixed budget perspective introduces new analytical challenges. Here it is shown how results on the expected optimisation time that are strengthened by deviation bounds can be systematically turned into fixed budget results. We demonstrate our approach by considering the (1+1) EA on LeadingOnes and significantly improving previous results. We prove that deviating from the expected time by an additive term of \( \omega(n^{3/2}) \) happens only with probability \( o(1) \). This is turned into tight bounds on the function value using the inverse function. We use three, increasingly strong or general approaches to proving the deviation bounds, namely via Chebyshev's inequality, via Chernoff bounds for geometric random variables, and via variable drift analysis.
Bioinspired computation in combinatorial optimization - Algorithms and their computational complexity

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Adelaide
Authors: Neumann, F. (Ekstern), Witt, C. (Intern)
Pages: 567-590
Publication date: 2013

Host publication information
Title of host publication: Proceeding of the fifteenth annual conference companion on Genetic and evolutionary computation
Publisher: Association for Computing Machinery
ISBN (Print): 978-1-4503-1964-5
BFI conference series: Genetic and Evolutionary Computation Conference (5000582)
Main Research Area: Technical/natural sciences
Conference: Genetic and Evolutionary Computation Conference (GECCO 2013), Amsterdam, Netherlands, 06/07/2013 - 06/07/2013
Electronic versions:
p567_neumann.pdf
DOIs:
10.1145/2464576.2466738

Bibliographical note
Tutorial at GECCO 2013.
Source: dtu
Source-ID: n::oai:DTIC-ART:compendex/391006656::31786
Publication: Research - peer-review › Article in proceedings – Annual report year: 2013

Evolutionary Algorithms for the Detection of Structural Breaks in Time Series
Detecting structural breaks is an essential task for the statistical analysis of time series, for example, for fitting parametric models to it. In short, structural breaks are points in time at which the behavior of the time series changes. Typically, no solid background knowledge of the time series under consideration is available. Therefore, a black-box optimization approach is our method of choice for detecting structural breaks. We describe a evolutionary algorithm framework which easily adapts to a large number of statistical settings. The experiments on artificial and real-world time series show that the algorithm detects break points with high precision and is computationally very efficient.
A reference implementation is available at the following address: http://www2.imm.dtu.dk/~pafi/SBX/launch.html

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, Max Planck Institute, Linnaeus University
Authors: Doerr, B. (Ekstern), Fischer, P. (Intern), Hilbert, A. (Ekstern), Witt, C. (Intern)
Pages: 119-120
Publication date: 2013

Host publication information
Title of host publication: Proceeding of the fifteenth annual conference companion on Genetic and evolutionary computation
Publisher: Association for Computing Machinery
ISBN (Print): 978-1-4503-1964-5
Improved Runtime Analysis of the Simple Genetic Algorithm

A runtime analysis of the Simple Genetic Algorithm (SGA) for the OneMax problem has recently been presented proving that the algorithm requires exponential time with overwhelming probability. This paper presents an improved analysis which overcomes some limitations of our previous one. Firstly, the new result holds for population sizes up to $\mu = n^{1/4 - \epsilon}$ which is an improvement up to a power of 2 larger. Secondly, we present a technique to bound the diversity of the population that does not require a bound on its bandwidth. Apart from allowing a stronger result, we believe this is a major improvement towards the reusability of the techniques in future systematic analyses of GAs. Finally, we consider the more natural SGA using selection with replacement rather than without replacement although the results hold for both algorithmic versions. Experiments are presented to explore the limits of the new and previous mathematical techniques.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, University of Birmingham
Authors: Oliveto, P. S. (Ekstern), Witt, C. (Intern)
Pages: 1621-1628
Publication date: 2013

Runtime analysis of ant colony optimization on dynamic shortest path problems

A simple ACO algorithm called $\lambda$-MMAS for dynamic variants of the single-destination shortest paths problem is studied by rigorous runtime analyses. Building upon previous results for the special case of 1-MMAS, it is studied to what extent an enlarged colony using $\lambda$ ants per vertex helps in tracking an oscillating optimum. It is shown that easy cases of oscillations can be tracked by a constant number of ants. However, the paper also identifies more involved oscillations that with overwhelming probability cannot be tracked with any polynomial-size colony. Finally, parameters of dynamic shortest-path problems which make the optimum difficult to track are discussed. Experiments illustrate theoretical findings and conjectures.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic
Authors: Lissovoi, A. (Intern), Witt, C. (Intern)
Pages: 1605-1612
Publication date: 2013
Tight Bounds on the Optimization Time of a Randomized Search Heuristic on Linear Functions

The analysis of randomized search heuristics on classes of functions is fundamental to the understanding of the underlying stochastic process and the development of suitable proof techniques. Recently, remarkable progress has been made in bounding the expected optimization time of a simple evolutionary algorithm, called (1+1) EA, on the class of linear functions. We improve the previously best known bound in this setting from \((1.39+o(1))en \ln n + \ln n + O(n)\) in expectation and with high probability, which is tight up to lower-order terms. Moreover, upper and lower bounds for arbitrary mutation probabilities \(p\) are derived, which imply expected polynomial optimization time as long as \(p = O((\ln n)/n)\) and \(p = \Omega(n^{-C})\) for a constant \(C > 0\), and which are tight if \(p = c/n\) for a constant \(c > 0\). As a consequence, the standard mutation probability \(p = 1/n\) is optimal for all linear functions, and the (1+1) EA is found to be an optimal mutation-based algorithm. Furthermore, the algorithm turns out to be surprisingly robust since the large neighbourhood explored by the mutation operator does not disrupt the search.
When do evolutionary algorithms optimize separable functions in parallel?

Separable functions are composed of subfunctions that depend on mutually disjoint sets of bits. These subfunctions can be optimized independently, however in black-box optimization this direct approach is infeasible as the composition of subfunctions may be unknown. Common belief is that evolutionary algorithms make progress on all subfunctions in parallel, so that optimizing a separable function does not take too much longer than optimizing the hardest subfunction-subfunctions are optimized "in parallel." We show that this is only partially true, already for the simple (1+1) evolutionary algorithm (1+1) EA. For separable functions composed of \( k \) Boolean functions indeed the optimization time is the maximum optimization time of these functions times a small \( O(\log k) \) overhead. More generally, for sums of weighted subfunctions that each attain non-negative integer values less than \( r = o(\log^{1/2} n) \), we get an overhead of \( O(r \log n) \).

However, the hoped for parallel optimization behavior does not always come true. We present a separable function with \( k \leq \sqrt{n} \) subfunctions such that the (1+1) EA is likely to optimize many subfunctions sequentially. The reason is that standard mutation leads to interferences between search processes on different subfunctions. Under mild assumptions, we show that such a sequential optimization behavior is worst possible. Copyright © 2013 ACM.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Algorithms and Logic, Max Planck Institute, University of Sheffield
Authors: Doerr, B. (Ekstern), Sudholt, D. (Ekstern), Witt, C. (Intern)
Pages: 51-64
Publication date: 2013

Host publication information
Title of host publication: Proceedings of the 12th ACM Workshop on Foundations of Genetic Algorithms (FOGA 2013)
Publisher: The Association for Computing Machinery
ISBN (Print): 9781450319904
BFI conference series: Foundations of Genetic Algorithms (5010308)
Main Research Area: Technical/natural sciences
Genetic algorithms, Optimization, Boolean functions
DOIs:
10.1145/2460239.2460245
Source: dtu
Source-ID: n:doi:DTIC-ART:compendex/385605264::28081
Publication: Research - peer-review » Article in proceedings – Annual report year: 2013

Analysis of an iterated local search algorithm for vertex cover in sparse random graphs

Recently, various randomized search heuristics have been studied for the solution of the minimum vertex cover problem, in particular for sparse random instances according to the \( G(n,c/n) \) model, where \( c > 0 \) is a constant. Methods from statistical physics suggest that the problem is easy if \( c < e \). This work starts with a rigorous explanation for this claim based
on the refined analysis of the Karp–Sipser algorithm by Aronson et al. (1998) [1]. Subsequently, theoretical supplements
are given to experimental studies of search heuristics on random graphs. For c<1, an iterated local search heuristic finds
an optimal cover in polynomial time with a probability arbitrarily close to 1. This behavior relies on the absence of a giant
component. As an additional insight into the randomized search, it is shown that the heuristic fails badly also on graphs
consisting of a single tree component of maximum degree 3.

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling
Authors: Witt, C. (Intern)
Pages: 117-125
Publication date: 2012
Main Research Area: Technical/natural sciences

Publication information
Journal: Theoretical Computer Science
Volume: 425
ISSN (Print): 0304-3975
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 0.97 SJR 0.569 SNIP 1.006
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.623 SNIP 1.212 CiteScore 1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.708 SNIP 1.228 CiteScore 1.08
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.739 SNIP 1.38 CiteScore 1.17
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.844 SNIP 1.288 CiteScore 1.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.81 SNIP 1.289 CiteScore 1.17
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.91 SNIP 1.329
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.948 SNIP 1.475
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.188 SNIP 1.638
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.997 SNIP 1.65
Scopus rating (2006): SJR 0.911 SNIP 1.49
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.821 SNIP 1.486
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.804 SNIP 1.366
Bioinspired computation in combinatorial optimization: algorithms and their computational complexity

Bioinspired computation methods, such as evolutionary algorithms and ant colony optimization, are being applied successfully to complex engineering and combinatorial optimization problems, and it is very important that we understand the computational complexity of these algorithms. This tutorial explains the most important results achieved in this area.

The presenters show how runtime behavior can be analyzed in a rigorous way, in particular for combinatorial optimization. They present well-known problems such as minimum spanning trees, shortest paths, maximum matching, and covering and scheduling problems. Classical single objective optimization is examined first. They then investigate the computational complexity of bioinspired computation applied to multiobjective variants of the considered combinatorial optimization problems, and in particular they show how multiobjective optimization can help to speed up bioinspired computation for single-objective optimization problems.

The tutorial is based on a book written by the authors with the same title. Further information about the book can be found at www.bioinspiredcomputation.com.

Black-Box Search by Unbiased Variation

The complexity theory for black-box algorithms, introduced by Droste, Jansen, and Wegener (Theory Comput. Syst. 39:525–544, 2006), describes common limits on the efficiency of a broad class of randomised search heuristics. There is an obvious trade-off between the generality of the black-box model and the strength of the bounds that can be proven in such a model. In particular, the original black-box model provides for well-known benchmark problems relatively small lower bounds, which seem unrealistic in certain cases and are typically not met by popular search heuristics. In this paper, we introduce a more restricted black-box model for optimisation of pseudo-Boolean functions which we claim captures the working principles of many randomised search heuristics including simulated annealing, evolutionary algorithms, randomised local search, and others. The key concept worked out is an unbiased variation operator. Considering this
class of algorithms, significantly better lower bounds on the black-box complexity are proved, amongst them an \( \Omega(n \log n) \) bound for functions with unique optimum. Moreover, a simple unimodal function and plateau functions are considered. We show that a simple (1+1) EA is able to match the runtime bounds in several cases.
On the Analysis of the Simple Genetic Algorithm

For many years it has been a challenge to analyze the time complexity of Genetic Algorithms (GAs) using stochastic selection together with crossover and mutation. This paper presents a rigorous runtime analysis of the well-known Simple Genetic Algorithm (SGA) for OneMax. It is proved that the SGA has exponential runtime with overwhelming probability for population sizes up to $\mu \leq n^{1/8-\varepsilon}$ for some arbitrarily small constant $\varepsilon$ and problem size $n$. To the best of our knowledge, this is the first time non-trivial lower bounds are obtained on the runtime of a standard crossover-based GA for a standard benchmark function. The presented techniques might serve as a first basis towards systematic runtime analyses of GAs.

Optimizing Linear Functions with Randomized Search Heuristics - The Robustness of Mutation

The analysis of randomized search heuristics on classes of functions is fundamental for the understanding of the underlying stochastic process and the development of suitable proof techniques. Recently, remarkable progress has been made in bounding the expected optimization time of the simple $(1+1)$ EA on the class of linear functions. We improve the best known bound in this setting from $(1.39+o(1))(en \ln n)$ to $(en \ln n) + O(n)$ in expectation and with high probability, which is tight up to lower-order terms. Moreover, upper and lower bounds for arbitrary mutations probabilities $p$ are derived, which imply expected polynomial optimization time as long as $p = O((\ln n)/n)$ and which are tight if $p = c/n$ for a constant $c$. As a consequence, the standard mutation probability $p=1/n$ is optimal for all linear functions, and the $(1+1)$ EA is found to be an optimal mutation-based algorithm. Furthermore, the algorithm turns out to be surprisingly robust since large neighborhood explored by the mutation operator does not disrupt the search.
Bioinspired algorithms, such as evolutionary algorithms and ant colony optimization, are widely used for different combinatorial optimization problems. These algorithms rely heavily on the use of randomness and are hard to understand from a theoretical point of view. This paper contributes to the theoretical analysis of ant colony optimization and studies this type of algorithm on one of the most prominent combinatorial optimization problems, namely the traveling salesperson problem (TSP). We present a new construction graph and show that it has a stronger local property than one commonly used for constructing solutions of the TSP. The rigorous runtime analysis for two ant colony optimization algorithms, based on these two construction procedures, shows that they lead to good approximation in expected polynomial time on random instances. Furthermore, we point out in which situations our algorithms get trapped in local optima and show where the use of the right amount of heuristic information is provably beneficial.
Theory of Randomized Search Heuristics

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Algorithms and Logic, University of Paris
Authors: Auger, A. (Ekstern), Witt, C. (Intern)
Pages: 621-622
Publication date: 2012
Main Research Area: Technical/natural sciences

Publication information
Journal: Algorithmica
Volume: 64
Issue number: 4
ISSN (Print): 0178-4617
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.11 SJR 0.685 SNIP 1.338
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.77 SNIP 1.354 CiteScore 1.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.921 SNIP 1.347 CiteScore 1.2
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.023 SNIP 1.572 CiteScore 1.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.872 SNIP 1.228 CiteScore 0.99
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.862 SNIP 1.166 CiteScore 0.91
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.99 SNIP 1.356
BFI (2009): BFI-level 2
Edge-Matching Problems with Rotations

Edge-matching problems, also called puzzles, are abstractions of placement problems with neighborhood conditions. Pieces with colored edges have to be placed on a board such that adjacent edges have the same color. The problem has gained interest recently with the (now terminated) Eternity II puzzle, and new complexity results. In this paper we consider a number of settings which differ in size of the puzzles and the manipulations allowed on the pieces. We investigate the effect of allowing rotations of the pieces on the complexity of the problem, an aspect that is only marginally treated so far. We show that some problems have polynomial time algorithms while others are NP-complete. Especially we show that allowing rotations in one-row puzzles makes the problem NP-hard. We moreover show that many commonly considered puzzles can be emulated by simple puzzles with quadratic pieces, so that one can restrict oneself to investigating those.

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling, Technical University of Denmark
Authors: Ebbesen, M. (Ekstern), Fischer, P. (Intern), Witt, C. (Intern)
Pages: 114-125
Publication date: 2011

Host publication information
Title of host publication: Fundamentals of Computation Theory : 18th International Symposium, FCT 2011 Oslo, Norway, August 22-25, 2011 Proceedings
Publisher: Springer
ISBN (Print): 978-3-642-22952-7
ISBN (Electronic): 978-3-642-22953-4

Series: Lecture Notes in Computer Science
Number: 6914
ISSN: 0302-9743
Main Research Area: Technical/natural sciences
Conference: International Symposium on Fundamentals of Computation Theory, Oslo, Norway, 01/01/2011

Runtime analysis of the 1-ANT ant colony optimizer
The runtime analysis of randomized search heuristics is a growing field where, in the last two decades, many rigorous results have been obtained. First runtime analyses of ant colony optimization (ACO) have been conducted only recently. In these studies simple ACO algorithms such as the 1-ANT are investigated. The influence of the evaporation factor in the pheromone update mechanism and the robustness of this parameter w.r.t. the runtime behavior have been determined for...
the example function OneMax. This work puts forward the rigorous runtime analysis of the 1-ANT on the example functions LeadingOnes and BinVal. With respect to Evolutionary Algorithms (EAs), such analyses were essential to develop methods for the analysis on more complicated problems. The proof techniques required for the 1-ANT, unfortunately, differ significantly from those for EAs, which means that a new reservoir of methods has to be built up. Again, the influence of the evaporation factor is analyzed rigorously, and it is proved that its choice has a crucial impact on the runtime. Moreover, the analyses provide insight into the working principles of ACO algorithms. Our theoretical results are accompanied by experimental results that give us a more detailed impression of the 1-ANT’s performance. Furthermore, the experiments also deal with the question whether using many ant solutions in one iteration can decrease the total runtime.
Sharp Bounds by Probability-Generating Functions and Variable Drift

We introduce to the runtime analysis of evolutionary algorithms two powerful techniques: probability-generating functions and variable drift analysis. They are shown to provide a clean framework for proving sharp upper and lower bounds. As an application, we improve the results by Doerr et al. (GECCO 2010) in several respects. First, the upper bound on the expected running time of the most successful quasirandom evolutionary algorithm for the OneMax function is improved from $1.28n\ln n$ to $0.982n\ln n$, which breaks the barrier of $n\ln n$ posed by coupon-collector processes. Compared to the classical $(1+1)$ EA, whose runtime will for the first time be analyzed with respect to terms of lower order, this represents a speedup by more than a factor of $e = 2.71$.

Simplified Drift Analysis for Proving Lower Bounds in Evolutionary Computation

Drift analysis is a powerful tool used to bound the optimization time of evolutionary algorithms (EAs). Various previous works apply a drift theorem going back to Hajek in order to show exponential lower bounds on the optimization time of EAs. However, this drift theorem is tedious to read and to apply since it requires two bounds on the moment-generating (exponential) function of the drift. A recent work identifies a specialization of this drift theorem that is much easier to apply. Nevertheless, it is not as simple and not as general as possible. The present paper picks up Hajek’s line of thought to prove a drift theorem that is very easy to use in evolutionary computation. Only two conditions have to be verified, one of which holds for virtually all EAs with standard mutation. The other condition is a bound on what is really relevant, the drift. Applications show how previous analyses involving the complicated theorem can be redone in a much simpler and clearer way. In some cases even improved results may be achieved. Therefore, the simplified theorem is also a didactical contribution to the runtime analysis of EAs.
Randomized search heuristics, Computational complexity, Drift analysis, Runtime analysis

DOIs:
10.1007/s00453-010-9387-z
Theory of Randomized Search Heuristics in Combinatorial Optimization

The rigorous mathematical analysis of randomized search heuristics (RSHs) with respect to their expected runtime is a growing research area where many results have been obtained in recent years. This class of heuristics includes well-known approaches such as Randomized Local Search (RLS), the Metropolis Algorithm (MA), Simulated Annealing (SA), and Evolutionary Algorithms (EAs) as well as more recent approaches such as Ant Colony Optimization (ACO) and Particle Swarm Optimization (PSO). Such heuristics are often applied to problems whose structure is not known or if there are not enough resources such as time, money, or knowledge to obtain good specific algorithms. It is widely acknowledged that a solid mathematical foundation for such heuristics is needed. Most designers of RSHs, however, rather focused on mimicking processes in nature (such as evolution) rather than making the heuristics amenable to a mathematical analysis. This is different to the classical design of (randomized) algorithms which are developed with their theoretical analysis of runtime (and proof of correctness) in mind. Despite these obstacles, research from the last about 15 years has shown how to apply the methods for the probabilistic analysis of randomized algorithms to RSHs. Mostly, the expected runtime of RSHs on selected problems is analyzed. Thereby, we understand why and when RSHs are efficient optimizers and, conversely, when they cannot be efficient. The tutorial will give an overview on the analysis of RSHs for solving combinatorial optimization problems. Starting from the first toy examples such as the OneMax function, we approach more realistic problems and arrive at analysis of the runtime and approximation quality of RSHs even for NP-hard problems. Our studies treat not only simple RLS algorithms and SA but also more complex population-based EAs. The combinatorial optimization problems that we discuss include the maximum matching problem, the partition problem and, in particular, the minimum spanning tree problem as an example where Simulated Annealing beats the Metropolis algorithm in combinatorial optimization. Important concepts of the analyses will be described as well.
Approximating covering problems by randomized search heuristics using multi-objective models

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling
Authors: Friedrich, T. (Ekstern), He, J. (Ekstern), Hebbinghaus, N. (Ekstern), Neumann, F. (Ekstern), Witt, C. (Intern)
Pages: 617-633
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Evolutionary Computation
Volume: 18
Issue number: 4
ISSN (Print): 1063-6560
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.924 SNIP 2.023 CiteScore 3.07
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.005 SNIP 2.559 CiteScore 3.29
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.149 SNIP 3.277 CiteScore 4.21
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.164 SNIP 3.251 CiteScore 4.38
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.936 SNIP 2.44 CiteScore 2.78
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.666 SNIP 2.09 CiteScore 2.96
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.254 SNIP 3.081
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.047 SNIP 2.533
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Bioinspired Computation in Combinatorial Optimization: Algorithms and Their Computational Complexity

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling
Authors: Neumann, F. (Ekstern), Witt, C. (Intern)
Publication date: 2010

Publication information
Publisher: Springer
ISBN (Print): 978-3-642-16543-6
Original language: English
Series: Natural Computing Series
Main Research Area: Technical/natural sciences
Links:
http://www.bioinspiredcomputation.com
Source: orbit
Source-ID: 274282
Publication: Research - peer-review › Book – Annual report year: 2011

Black-Box Search by Unbiased Variation

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling
Authors: Lehre, P. K. (Intern), Witt, C. (Intern)
Pages: 1441-1448
Publication date: 2010

Host publication information
Title of host publication: GECCO 2010: Portland, Oregon, USA
ISBN (Print): 978-1-4503-0072-5
Main Research Area: Technical/natural sciences
Conference: Genetic and Evolutionary Computation Conference 2010, Portland, OR, United States, 07/07/2010 - 07/07/2010
Links:
http://doi.acm.org/10.1145/1830483.1830747
Source: orbit
Source-ID: 265793
Publication: Research - peer-review › Article in proceedings – Annual report year: 2010
Quasirandom evolutionary algorithms

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling
Authors: Doerr, B. (Ekstern), Fouz, M. (Ekstern), Witt, C. (Intern)
Pages: 1457-1464
Publication date: 2010

Host publication information
Title of host publication: GECCO 2010: Portland, Oregon, USA
ISBN (Print): 978-1-4503-0072-5
Main Research Area: Technical/natural sciences
Conference: Genetic and Evolutionary Computation Conference 2010, Portland, OR, United States, 07/07/2010 - 07/07/2010
Links:
http://doi.acm.org/10.1145/1830483.1830749
Source: orbit
Source-ID: 265792
Publication: Research - peer-review › Article in proceedings – Annual report year: 2010

Runtime analysis of a binary particle swarm optimizer

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling, International Computer Science Institute
Authors: Sudholt, D. (Ekstern), Witt, C. (Intern)
Pages: 2084-2100
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Theoretical Computer Science
Volume: 411
Issue number: 21
ISSN (Print): 0304-3975
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2016): CiteScore 0.97 SJR 0.569 SNIP 1.006
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.623 SNIP 1.212 CiteScore 1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.708 SNIP 1.228 CiteScore 1.08
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.739 SNIP 1.38 CiteScore 1.17
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.844 SNIP 1.288 CiteScore 1.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Theoretical properties of two ACO approaches for the traveling salesman problem

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling
Authors: Kötzing, T. (Ekstern), Neumann, F. (Ekstern), Röglin, H. (Ekstern), Witt, C. (Intern)
Publication date: 2010

Host publication information
Title of host publication: Ant Colony Optimization and Swarm Intelligence - ANTS 2010
Series: Lecture Notes in Computer Science
Number: 6234
Main Research Area: Technical/natural sciences

Theory of randomised search heuristics in combinatorial optimisation

General information
State: Published
Organisations: Algorithms and Logic, Department of Informatics and Mathematical Modeling
Authors: Witt, C. (Intern)
Analysis of Diversity-Preserving Mechanisms for Global Exploration

Maintaining diversity is important for the performance of evolutionary algorithms. Diversity-preserving mechanisms can enhance global exploration of the search space and enable crossover to find dissimilar individuals for recombination. We focus on the global exploration capabilities of mutation-based algorithms. Using a simple bimodal test function and rigorous runtime analyses, we compare well-known diversity-preserving mechanisms like deterministic crowding, fitness sharing, and others with a plain algorithm without diversification. We show that diversification is necessary for global exploration, but not all mechanisms succeed in finding both optima efficiently. Our theoretical results are accompanied by additional experiments for different population sizes.
Greedy Local Search and Vertex Cover in Sparse Random Graphs

Recently, various randomized search heuristics have been studied for the solution of the minimum vertex cover problem, in particular for sparse random instances according to the $G(n, c/n)$ model, where $c > 0$ is a constant. Methods from statistical physics suggest that the problem is easy if $c < e$. This work starts with a rigorous explanation for this claim based on the refined analysis of the Karp-Sipser algorithm by Aronson et al. Subsequently, theoretical supplements are given to experimental studies of search heuristics on random graphs. For $c < 1$, a greedy and randomized local-search heuristic finds an optimal cover in polynomial time with a probability arbitrarily close to 1. This behavior relies on the absence of a giant component. As an additional insight into the randomized search, it is shown that the heuristic fails badly also on graphs consisting of a single tree component of maximum degree 3.
Projects:

Algorithms for Compressed Computation
Department of Applied Mathematics and Computer Science
Period: 01/11/2014 → 30/11/2017
Number of participants: 6
Phd Student:
Christiansen, Anders Roy (Intern)
Supervisor:
Gørtz, Inge Li (Intern)
Main Supervisor:
Bille, Philip (Intern)
Examiner:
Witt, Carsten (Intern)
Grossi, Roberto (Ekstern)
Puglisi, Simon J. (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet

Relations
Publications:
Compressed and Practical Data Structures for Strings
Project: PhD

Bridging the Gap Between Theory and Practice in Nature-inspired algorithms
Department of Applied Mathematics and Computer Science
Period: 01/10/2014 → 30/09/2017
Number of participants: 5
Phd Student:
Gießen, Christian (Intern)
Main Supervisor:
Witt, Carsten (Intern)
Examiner:
Bille, Philip (Intern)
Lehre, Per Kristian (Intern)
Sudholt, Dirk (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Forskningsrådsfinansiering

Relations
Publications:
The Impact of Parametrization on Randomized Search Heuristics
Project: PhD

Matching and Compression of Strings with Automata and Word Packing
Department of Applied Mathematics and Computer Science
Period: 01/03/2014 → 14/06/2017
Number of participants: 7
Phd Student:
Skjoldjensen, Frederik Rye (Intern)
Supervisor:
Gørtz, Inge Li (Intern)
Thomassen, Carsten (Intern)
Main Supervisor:
Bille, Philip (Intern)
Examiner:
Witt, Carsten (Intern)
Landau, Gad M. (Ekstern)
Pagh, Rasmus (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Forskningsrådsfinansiering

Relations
Publications:
Matching and Compression of Strings with Automata and Word Packing
Project: PhD

Logical and Computational Aspects of Infinite Games
Department of Applied Mathematics and Computer Science
Period: 01/05/2013 → 23/11/2016
Number of participants: 6
Phd Student:
Vester, Steen (Intern)
Supervisor:
Goranko, Valentin (Intern)
Main Supervisor:
Hansen, Michael Reichhardt (Intern)
Examiner:
Witt, Carsten (Intern)
Larsen, Kim Guldstrand (Ekstern)
Olderog, Ernest-Rüdiger (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)

Relations
Publications:
Game-based verification and synthesis
Project: PhD

Algorithms for Metadata
Department of Applied Mathematics and Computer Science
Period: 01/10/2012 → 20/05/2015
Number of participants: 6
Phd Student:
Vind, Søren Juhl (Intern)
Supervisor:
Bille, Philip (Intern)
Main Supervisor:
Gertz, Inge Li (Intern)
Examiner:
Witt, Carsten (Intern)
Clifford, Raphael (Ekstern)
Italiano, Giuseppe F. (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Exploring the boundaries of nature-inspired algorithms

Department of Applied Mathematics and Computer Science
Period: 01/10/2012 → 31/03/2016
Number of participants: 5
PhD Student:
Lissovoi, Andrei (Intern)
Main Supervisor:
Witt, Carsten (Intern)
Examiner:
Fischer, Paul (Intern)
Lehre, Per Kristian (Intern)
Prügel-Bennett, Adam (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

Approximate Text Indexing and String Matching Algorithms

Department of Applied Mathematics and Computer Science
Period: 15/09/2011 → 19/12/2014
Number of participants: 6
PhD Student:
Vildhøj, Hjalte Wedel (Intern)
Supervisor:
Bille, Philip (Intern)
Main Supervisor:
Gertz, Inge Li (Intern)
Examiner:
Witt, Carsten (Intern)
Farach-colton, Martin (Ekstern)
Lewenstein, Moshe (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD