Benchmarking Algorithms from the platypus Framework on the Biobjective bbob-biobj Testbed

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ABSTRACT

One of the main goals of the COCO platform is to produce, collect, and make available benchmarking performance data sets of optimization algorithms and, more concretely, algorithm implementations. For the recently proposed biobjective bbob-biobj test suite, less than 20 algorithms have been benchmarked so far but many more are available to the public. We therefore aim in this paper to benchmark several available multiobjective optimization algorithms on the bbob-biobj test suite and discuss their performance. We focus here on algorithms implemented in the platypus framework (in Python) whose main advantage is its ease of use without the need to set up many algorithm parameters.

CCS CONCEPTS

•**Computing methodologies → Continuous space search;**

KEYWORDS

Benchmarking, Black-box optimization, Bi-objective optimization

ACM Reference format:
Dimo Brockhoff and Tea Tušar. 2019. Benchmarking Algorithms from the platypus Framework on the Biobjective bbob-biobj Testbed. In *Proceedings of Genetic and Evolutionary Computation Conference Companion, Prague, Czech Republic, July 13–17, 2019 (GECCO '19 Companion),* 7 pages.
DOI: 10.1145/3319619.3326896

1 INTRODUCTION

Among the most difficult tasks when solving a black-box optimization problem in practice is to choose an appropriate optimization algorithm from the vast amount of available ones. Making such a decision based on experimental data from numerical benchmarking experiments is the most viable alternative. The Comparing Continuous Optimizers platform (COCO, [7], github.com/numbbo/coco/) assists in this task by automatizing the benchmarking experiments and, more importantly, by freely providing the data of many such experiments to the public.

Since 2016, COCO also offers a biobjective benchmark suite (called bbob-biobj, [12]) with 55 objective functions that are composed of the original single-objective bbob functions. Compared to the 190+ algorithm data sets for the original bbob suite, only few algorithms have been compared on the bbob-biobj suite so far—despite the huge amount of available multiobjective optimization algorithms in the literature.

In this paper, we contribute to COCO's bbob-biobj data set by running experiments with several multiobjective optimization algorithms from the platypus library (in Python).[1] These algorithms are well-known in the evolutionary multiobjective optimization community and have performed well in several previous algorithm comparisons. The platypus library already provides default values for the algorithms' internal parameters, making it easy to use for practitioners. The next section gives more details on the algorithms compared here.

2 ALGORITHMS IN THE COMPARISON

In the following, we compare the platypus implementation of the algorithms NSGA-II [5], IBEA [14], MOEA/D [13], SPEA2 [15] and GDE3 [10], as well as of the recently proposed NSGA-III [4]. It will be especially interesting to see how the platypus implementation of NSGA-II compares with the one in Matlab from the gamultiobj library that has been benchmarked on the bbob-biobj suite before [1]. We denote the latter algorithm as NSGA-II-MATLAB in the remainder of the paper.

Not contained in our comparison are the lesser known algorithms OMOPSO, SMPSO, and EpsMOEA as well as the CMAES algorithm from platypus for which preliminary experiments with the default setup showed significantly worse results than the available UP-MO-CMA-ES data set of [9].

3 EXPERIMENTAL PROCEDURE

All algorithm implementations have been taken from the platypus framework (https://github.com/Project-Platypus/Platypus) with the version "4 - beta" as of November 2017[2].

Let n denote the problem dimension. GDE3, IBEA, and NSGA-II have been run for $10^5 n$ function evaluations, SPEA2 and NSGA-III for $10^4 n$ function evaluations (due to slower internal computations). Note here that the experimental setup of COCO does not impose a concrete number of function evaluations and that COCO's target-based performance assessment allows naturally to compare data

GECCO '19 Companion, Prague, Czech Republic

978-1-4503-6748-6/19/07…$15.00
DOI: 10.1145/3319619.3326896

[1] The source code is available from https://github.com/Project-Platypus/Platypus.

[2] Until then, only a callback functionality was added and the documentation was updated such that the current platypus version at the time of the paper submission shall be the same as the version used for the experiments.

	2-D	3-D	5-D	10-D	20-D	40-D
SPEA2	43	46	44	40	43	46
NSGA-III-11	4.7	4.7	4.7	5.1	5.7	7.2
NSGA-III-111	7.1	7.1	7.1	7.4	8.1	9.5
MOEA/D	4.1	4.0	4.0	4.4	5.1	6.5
IBEA	54	53	51	50	50	52
GDE3	5.7	5.7	5.7	5.9	6.5	7.5
NSGA-II	7.1	7.1	7.1	7.4	8.1	9.5

Table 1: CPU timing of all algorithms in milliseconds per function evaluation for the standard `bbob-biobj` dimensions 2 to 40.

from experiments that have been run with different numbers of function evaluations.

For NSGA-III, we have run two versions, one with 11 and one with 111 reference points, denoted by N-III-11 and N-III-111 in the following. [3] Besides this one parameter, all algorithms have been run with `platypus`' standard settings and a population size of 100 in particular, except for the initialization. In our experiments, we first evaluate the search space origin $[0, \ldots, 0] \in \mathbb{R}^n$ following the recommendation in the (Python) example experiment of COCO and then initialize the actual `platypus` algorithm by sampling the first population uniformly at random within $[-5, 5]^n$, according to the `bbob-biobj` test suite which guarantees that the extreme solutions of the Pareto front are contained in this box. For NSGA-II, we also consider other initializations later when comparing it with the Matlab version from [1].

4 CPU TIMING

In order to evaluate the CPU timing of the algorithms, we have collected the runtimes per function evaluation of all experiments according to [8] for a budget of $1000n$ on the first three instances. The Python code was run on a Linux machine with 64 Intel(R) Xeon(R) CPU E5-2683 v4 @ 2.10GHz processors but with other load on the machine. The time per function evaluation for dimensions 2, 3, 5, 10, 20, and 40 is given in Table 1.

We can observe that there are two groups of algorithms in terms of cpu timing: SPEA2 and IBEA need about 5–10 times as much time per function evaluation than the other tested `platypus` algorithms. Over dimension, the cpu timing results are rather stable with slightly increased times in dimensions 20 and 40 for the latter (faster) group of algorithms.

5 RESULTS

Results from experiments according to [8], [6] and [3] on the benchmark functions given in [12] are presented in Figures 1, 2, 3 and 4. For more details, in particular the tabular data, we refer to the supplementary material at http://randopt.gforge.inria.fr/ppdata-archive/2019-platypus/. The experiments were performed with COCO [7], version 2.0 or 2.2.x depending on the algorithm. The plots were produced with COCO version 2.3.1 that explicitly turns of simulated restarts for the empirical runtime distribution plots (as indicated by always flat curves after the cross).

The **average runtime (aRT)**, used in the tables, depends on a given quality indicator value, $I_{\text{target}} = I_{\text{ref}} + \Delta I_{\text{HV}}^{\text{COCO}}$, and is computed over all relevant trials as the number of function evaluations executed during each trial while the best indicator value did not reach I_{target}, summed over all trials and divided by the number of trials that actually reached I_{target} [8, 11]. **Statistical significance** is tested with the rank-sum test for a given target I_{target} using, for each trial, either the number of needed function evaluations to reach I_{target} (inverted and multiplied by -1), or, if the target was not reached, the best $\Delta I_{\text{HV}}^{\text{COCO}}$-value achieved, measured only up to the smallest number of overall function evaluations for any unsuccessful trial under consideration.

From the graphs and tables, the following main observations can be made.

Overall performance. Surprisingly, the `platypus` algorithms are all relatively similar in performance, in particular when compared to the already existing data sets of COCO, which are more diverse, see for example http://coco.gforge.inria.fr/ppdata-archive/bbob-biobj/2016-all/. The `platypus` algorithms included in this comparison can be found in the middle performance range similar to an algorithm like SMS-EMOA, but are definitely outperformed in the larger dimensions by the hybrid HMO-CMA-ES and for larger budgets also by RM-MEDA and UP-MO-CMA-ES.

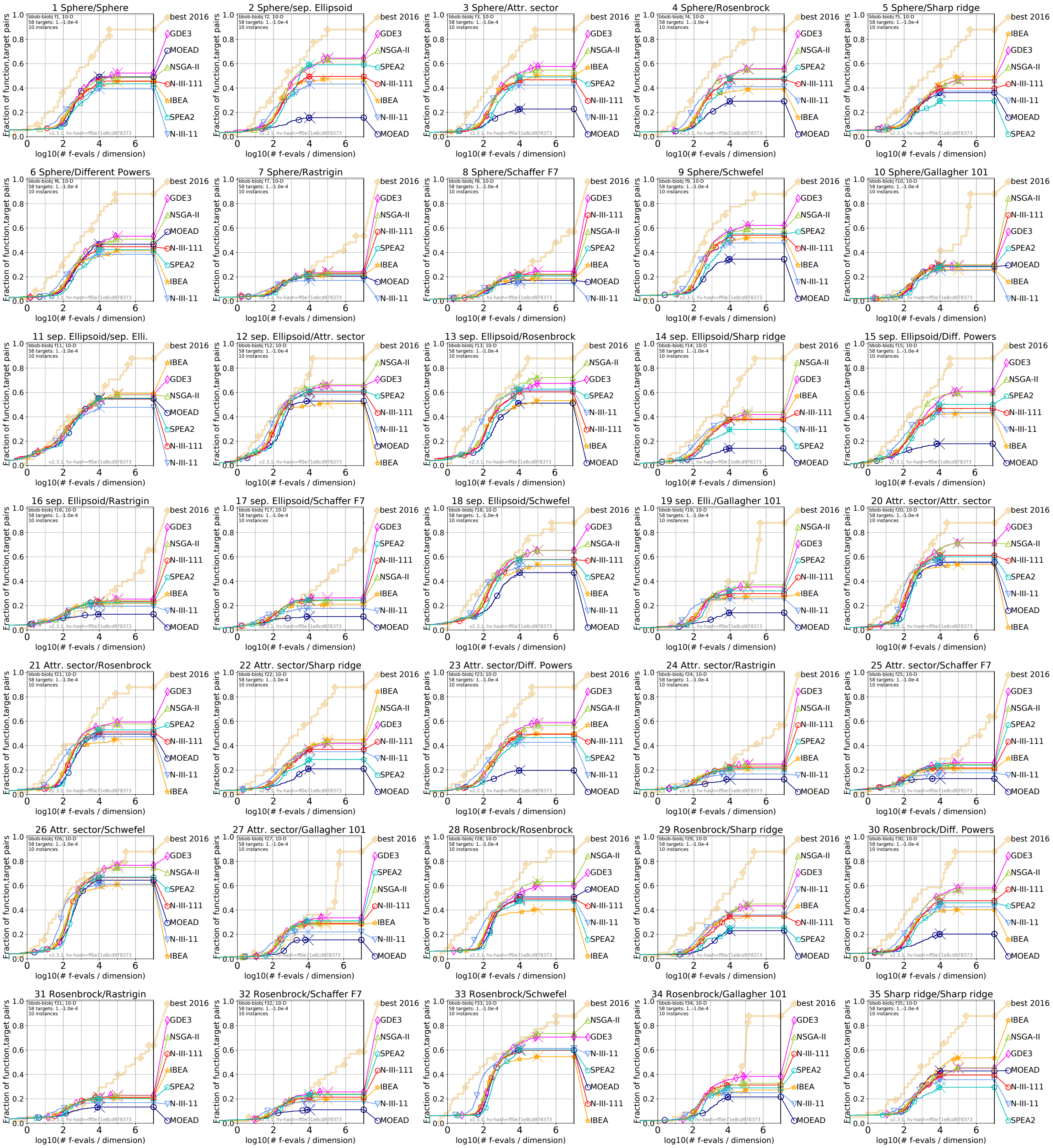
The few trends among the `platypus` algorithms that can be reported is that MOEA/D falls short after some time and that NSGA-III with 11 reference vectors is outperforming the other algorithms around $100n$ function evaluations (the improvement over the second-best algorithm, however, is only about a factor of 1.5–2). Exceptions where MOEA/D is not falling behind in dimension 5–20 are the following 26 of the 55 `bbob-biobj` functions: F_1 (where for large budgets in dimension 20, MOEA/D is here even the best algorithm), F_5–F_8, F_{10}, F_{11}, F_{20}, F_{21}, F_{26} (not in dimension 20), F_{28}, F_{33}, F_{35}–F_{37}, F_{41}–F_{43}, F_{45}–F_{47}, F_{49}, F_{50}, F_{52}, F_{53} and F_{55}. Similar observations can be made in lower dimensions where the differences, however, are smaller.

Over all functions, in particular in the higher dimensions, GDE3 is the best algorithm for the larger budgets, followed almost immediately by the performance of NSGA-II. In the lower dimension and for larger budgets, it is NSGA-II that is outperforming GDE3. This good performance of GDE3 and NSGA-II can be mostly attributed to problems where the objectives come from the separable, moderate, and ill-conditioned function classes of the original `bbob` test suite—in the higher dimensions, in particular in 20-D, GDE3 and NSGA-II are often the best algorithms among the tested ones for a large range of budgets.

6 COMPARISON BETWEEN NSGA-II IMPLEMENTATIONS

Benchmarking algorithms is a non-trivial task, especially when it comes to different *implementations* of one and the same (theoretical) algorithm. Here, we would like to make the point that, in practice, we can only compare algorithm *implementations* and that they may *differ quite significantly*.

[3] Note that platypus does not provide a default value here such that we run two variants with (arbitrary) numbers of reference points in the order of magnitude of the default population size of 100.


1 Sphere/Sphere

2 Sphere/sep. Ellipsoid

3 Sphere/Attr. sector

4 Sphere/Rosenbrock

5 Sphere/Sharp ridge

6 Sphere/Different Powers

7 Sphere/Rastrigin

8 Sphere/Schaffer F7

9 Sphere/Schwefel

10 Sphere/Gallagher 101

11 sep. Ellipsoid/sep. Elli.

12 sep. Ellipsoid/Attr. sector

13 sep. Ellipsoid/Rosenbrock

14 sep. Ellipsoid/Sharp ridge

15 sep. Ellipsoid/Diff. Powers

16 sep. Ellipsoid/Rastrigin

17 sep. Ellipsoid/Schaffer F7

18 sep. Ellipsoid/Schwefel

19 sep. Elli./Gallagher 101

20 Attr. sector/Attr. sector

21 Attr. sector/Rosenbrock

22 Attr. sector/Sharp ridge

23 Attr. sector/Diff. Powers

24 Attr. sector/Rastrigin

25 Attr. sector/Schaffer F7

26 Attr. sector/Schwefel

27 Attr. sector/Gallagher 101

28 Rosenbrock/Rosenbrock

29 Rosenbrock/Sharp ridge

30 Rosenbrock/Diff. Powers

31 Rosenbrock/Rastrigin

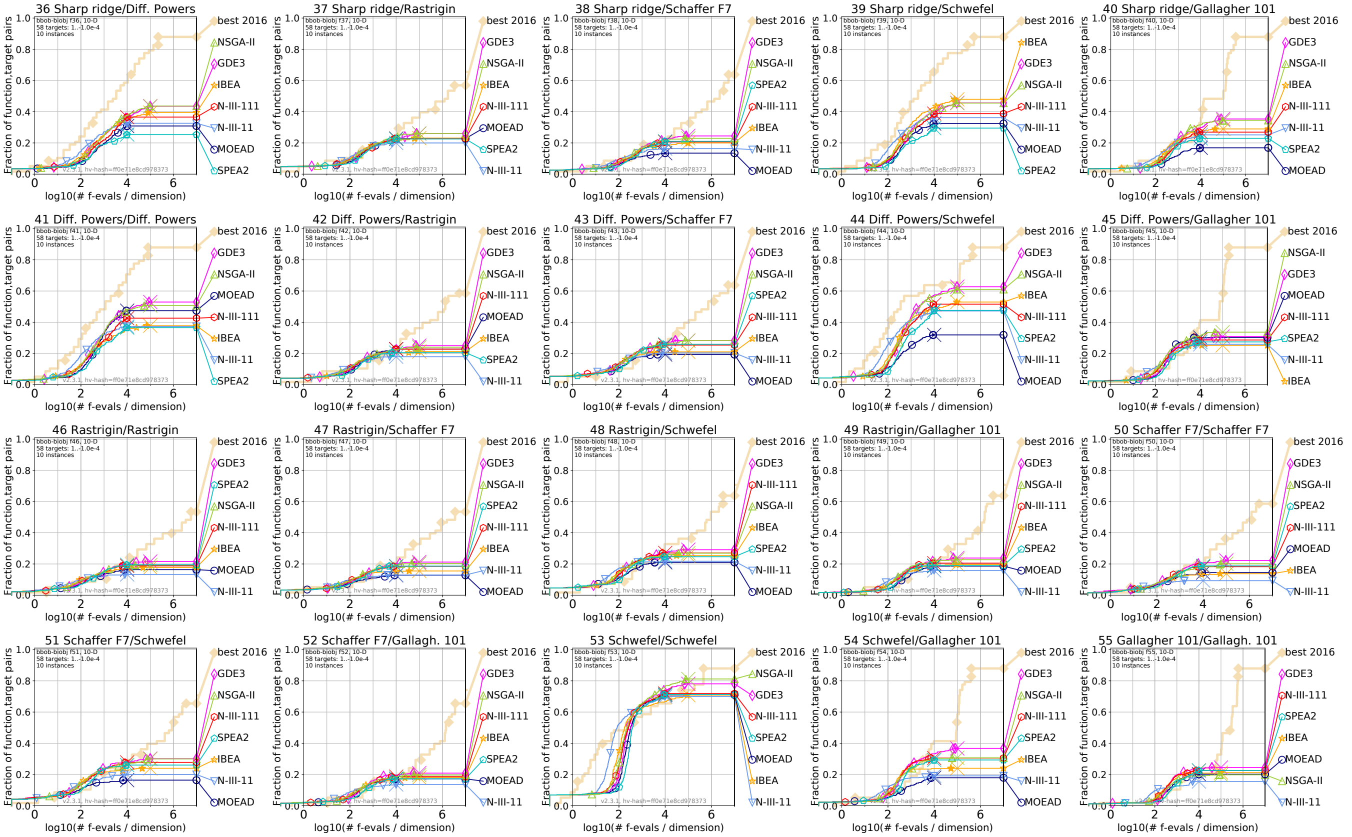
32 Rosenbrock/Schaffer F7

33 Rosenbrock/Schwefel

34 Rosenbrock/Gallagher 101

35 Sharp ridge/Sharp ridge

Figure 1: Empirical cumulative distribution of simulated (bootstrapped) runtimes, measured in number of objective function evaluations, divided by dimension (FEvals/DIM) for the 58 targets $\{-10^{-4}, -10^{-4.2}, -10^{-4.4}, -10^{-4.6}, -10^{-4.8}, -10^{-5}, 0, 10^{-5}, 10^{-4.9}, 10^{-4.8}, \ldots, 10^{-0.1}, 10^{0}\}$ in dimension 10.



36 Sharp ridge/Diff. Powers · 37 Sharp ridge/Rastrigin · 38 Sharp ridge/Schaffer F7 · 39 Sharp ridge/Schwefel · 40 Sharp ridge/Gallagher 101

41 Diff. Powers/Diff. Powers · 42 Diff. Powers/Rastrigin · 43 Diff. Powers/Schaffer F7 · 44 Diff. Powers/Schwefel · 45 Diff. Powers/Gallagher 101

46 Rastrigin/Rastrigin · 47 Rastrigin/Schaffer F7 · 48 Rastrigin/Schwefel · 49 Rastrigin/Gallagher 101 · 50 Schaffer F7/Schaffer F7

51 Schaffer F7/Schwefel · 52 Schaffer F7/Gallagh. 101 · 53 Schwefel/Schwefel · 54 Schwefel/Gallagher 101 · 55 Gallagher 101/Gallagh. 101

Fraction of function,target pairs
log10(# f-evals / dimension)
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
bbob-biobj f36, 10-D
58 targets: 1..-1.0e-4
10 instances
v2.3.1, hv-hash=ff0e71e8cd978373
36: best 2016, NSGA-II, GDE3, IBEA, N-III-111, N-III-11, MOEAD, SPEA2
37: best 2016, GDE3, NSGA-II, IBEA, N-III-111, MOEAD, SPEA2, N-III-11
38: best 2016, GDE3, NSGA-II, SPEA2, N-III-111, IBEA, N-III-11, MOEAD
39: best 2016, IBEA, GDE3, NSGA-II, N-III-111, N-III-11, MOEAD, SPEA2
40: best 2016, GDE3, NSGA-II, IBEA, N-III-111, N-III-11, SPEA2, MOEAD
41: best 2016, GDE3, NSGA-II, MOEAD, N-III-111, IBEA, N-III-11, SPEA2
42: best 2016, GDE3, NSGA-II, N-III-111, MOEAD, IBEA, SPEA2, N-III-11
43: best 2016, GDE3, NSGA-II, SPEA2, N-III-111, IBEA, N-III-11, MOEAD
44: best 2016, GDE3, NSGA-II, IBEA, N-III-111, SPEA2, N-III-11, MOEAD
45: best 2016, NSGA-II, GDE3, MOEAD, N-III-111, SPEA2, N-III-11, IBEA
46: best 2016, GDE3, SPEA2, NSGA-II, N-III-111, IBEA, MOEAD, N-III-11
47: best 2016, GDE3, NSGA-II, SPEA2, N-III-111, IBEA, N-III-11, MOEAD
48: best 2016, GDE3, N-III-111, NSGA-II, IBEA, SPEA2, N-III-11, MOEAD
49: best 2016, GDE3, NSGA-II, N-III-111, IBEA, SPEA2, MOEAD, N-III-11
50: best 2016, GDE3, NSGA-II, SPEA2, N-III-111, MOEAD, IBEA, N-III-11
51: best 2016, GDE3, NSGA-II, N-III-111, SPEA2, IBEA, N-III-11, MOEAD
52: best 2016, GDE3, NSGA-II, N-III-111, IBEA, SPEA2, MOEAD, N-III-11
53: best 2016, NSGA-II, GDE3, N-III-111, SPEA2, MOEAD, IBEA, N-III-11
54: best 2016, GDE3, NSGA-II, N-III-111, SPEA2, IBEA, N-III-11, MOEAD
55: best 2016, GDE3, N-III-111, SPEA2, IBEA, MOEAD, NSGA-II, N-III-11

Figure 2: Bootstrapped empirical cumulative distribution of the number of objective function evaluations divided by dimension (FEvals/DIM) as in Fig. 1 but for functions F_{36} to F_{55} in 10-D.

To showcase this, we provide a comparison between the `platypus` implementation of the well-known NSGA-II algorithm [5] with the already benchmarked Matlab version of the same algorithm [1]. More specifically, we run the NSGA-II algorithm of `platypus` with different initializations in order to see differences and to match the setup of the previous BBOB-2016 benchmarking result [1] as much as possible without changing the `platypus` code. We distinguish in the following between four NSGA-II variants:

- The original data set from BBOB-2016 [1] as the default Matlab implementation of the algorithm which initializes its population of size 100 by a uniform random sample of 99 search points in $[-100, 100]^n$ and a very first search point, drawn from a multivariate normal distribution with variance 1 and mean in the search space origin. We denote this algorithm variant as NSGA-II-MATLAB,
- The above described `platypus` implementation with initialization in $[-5, 5]^n$ and the search space origin as the very first evaluation, denoted again as NSGA-II here.
- The `platypus` version with initialization in $[-100, 100]^n$ for the entire population, i.e. without evaluating the search space origin, denoted as m100p100 strategy and, finally,
- as the closest version to NSGA-II-MATLAB we can get, the `platypus` implementation with a standard normally distributed search point (with 0^n as mean) as initial search point and a subsequent random population of 100 random points from $[-100, 100]$, denoted as randn1st variant.

Figure 5 shows the empirical runtime distributions over all 55 `bbob-biobj` functions in dimensions 2 and 10 for all four versions. The entire postprocessed data can be found at http://randopt.gforge.inria.fr/ppdata-archive/2019-nsga2-comp/. Already from the aggregated results, we observe that the investigated NSGA-II implementations are very different in performance.

Three main differences can be observed. The most obvious difference is coming from the different sample volumes in the algorithm variants' initialization: a large sample volume of $[-100, 100]^n$ has naturally disadvantages (especially in the beginning of the search) due to the curse of dimensionality and the fact that the `bbob-biobj` functions' single objectives have their optima always within the hyperbox $[-4, 4]$.

Second, adding the search space origin as the first search point or adding the normally distributed first search point shifts the empirical runtime distribution slightly upwards for the first evaluations (until the first population is filled), but the actual shape of the runtime distribution is not affected for larger budgets as we can see when comparing m100p100 with randn1st.

And third, we can observe that having the normally distributed first search point within the first population (for NSGA-II-MATLAB) or not (for randn1st) makes a big difference in the later stages of

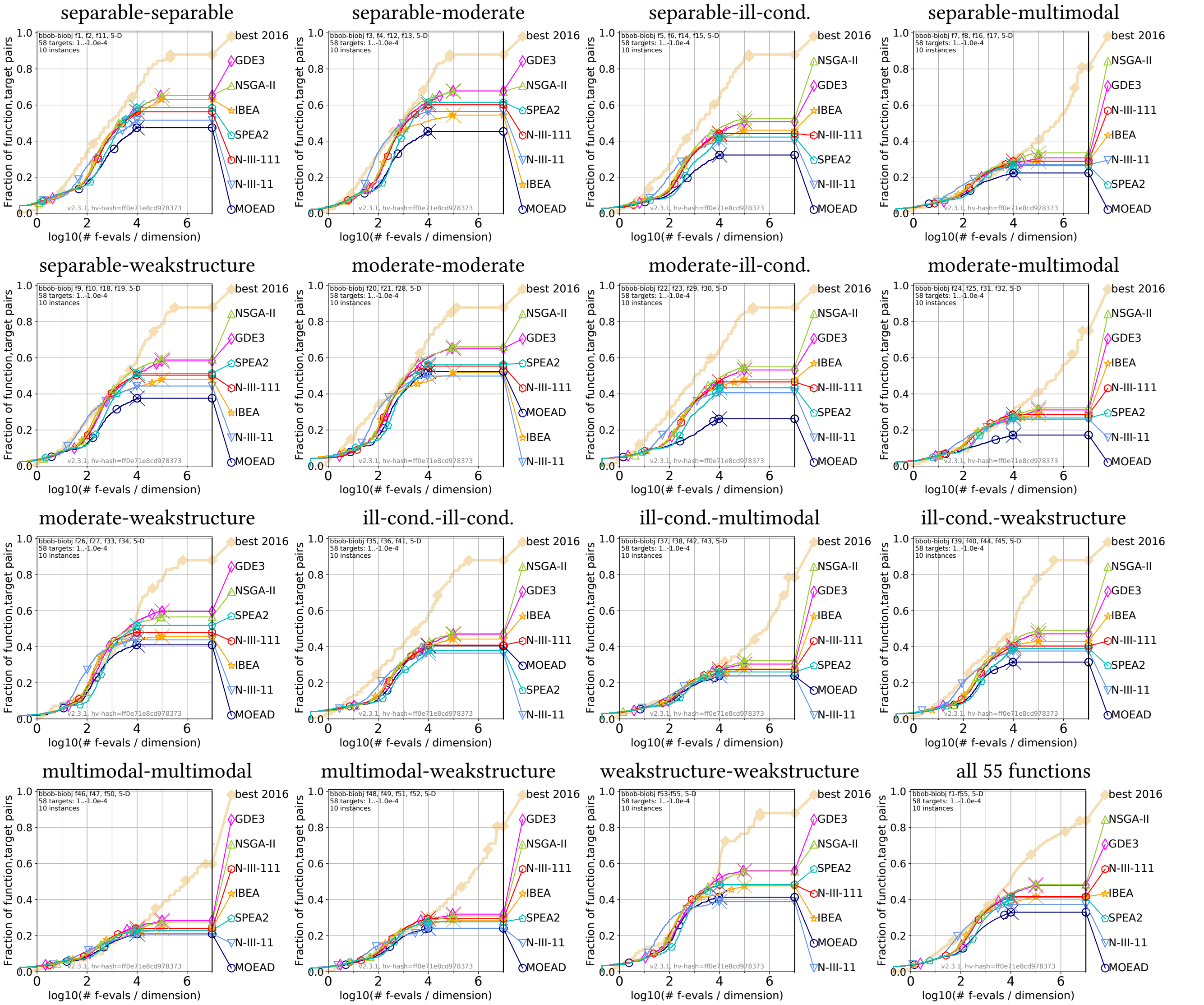


Figure 3: Bootstrapped empirical cumulative distribution of the number of objective function evaluations divided by dimension (FEvals/DIM) for 58 targets with target precision in $\{-10^{-4}, -10^{-4.2}, -10^{-4.4}, -10^{-4.6}, -10^{-4.8}, -10^{-5}, 0, 10^{-5}, 10^{-4.9}, 10^{-4.8}, \ldots, 10^{-0.1}, 10^{0}\}$ for all functions and subgroups in 5-D. As reference algorithm, the best algorithm from BBOB 2016 is shown as light thick line with diamond markers.

the optimization. In lower dimension, we observe an advantage of NSGA-II-MATLAB over randn1st for all budgets. In higher dimensions, the randn1st variant becomes better than NSGA-II-MATLAB from around $10^3 n$ function evaluations onwards in dimensions 10 and 20. Note here that we do not know whether there are other differences in the Matlab and Python implementations of NSGA-II. But we can imagine that the recombination can take advantage of the potentially good first search point[4]—an advantage that the randn1st variant does not have because the normally distributed first search point is not integrated into the initial population. [5]

Finally, it is interesting to note that the Matlab implementation of NSGA-II and the platypus implementation, despite the slightly different initialization, show the same performance for large budgets in dimension 2. With increasing dimension, we can observe a larger and larger difference between the Matlab and Python versions in favor of the platypus implementation.

[4] We know that a solution, chosen closely to the search space origin, has likely better objective function values for some functions than a random search point, see [2].

[5] The implementation of platypus did not allow for a quick implementation of non-uniform initial populations as needed to fully recover the variant from [1].

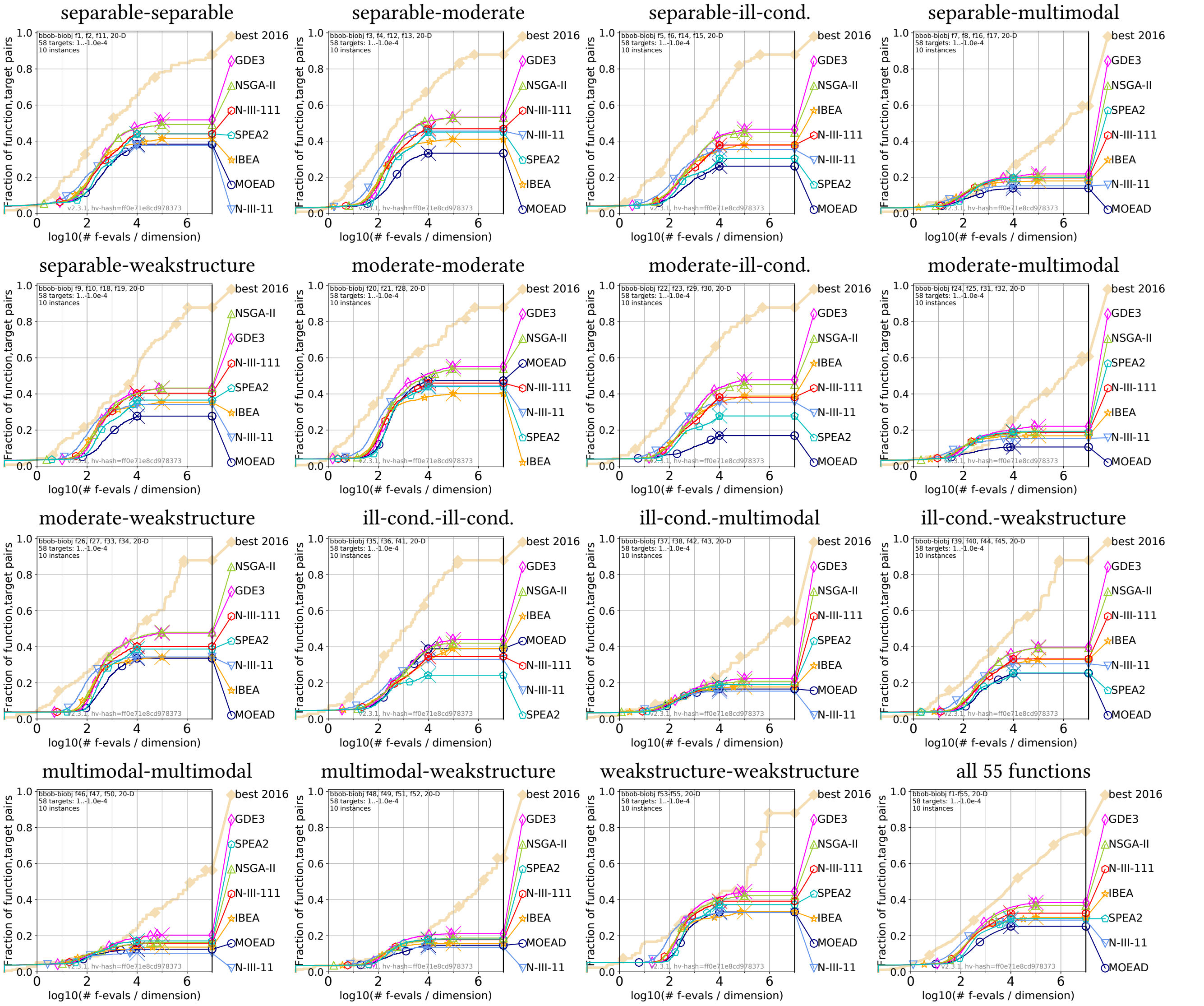


Figure 4: Bootstrapped empirical cumulative distribution of the number of objective function evaluations divided by dimension (FEvals/DIM) for 58 targets with target precision in $\{-10^{-4}, -10^{-4.2}, -10^{-4.4}, -10^{-4.6}, -10^{-4.8}, -10^{-5}, 0, 10^{-5}, 10^{-4.9}, 10^{-4.8}, \ldots, 10^{-0.1}, 10^{0}\}$ for all functions and subgroups in 20-D. As reference algorithm, the best algorithm from BBOB 2016 is shown as light thick line with diamond markers.

7 CONCLUSIONS

We benchmarked six multiobjective algorithms from the `platypus` framework on the `bbob-biobj` test suite with the help of the COCO platform. Five of them are well-known but have not yet been tested with COCO and thus also no reference data sets had been available to the public for them. Over all `bbob-biobj` functions, the two algorithms GDE3 and NSGA-II stood out with the best performance. As a surprise, MOEA/D fell behind the other tested algorithms on about half of the `bbob-biobj` test functions in all dimensions while in previous benchmarking studies on other well-known test suites, such as the DTLZ and ZDT suites, MOEA/D has been performing quite well. Note that in most of the comparisons where MOEA/D shows good performance on DTLZ and ZDT problems, a fixed budget and the quality of a fixed size Pareto set approximation (typically the algorithm's population) is used as a performance criterion. With COCO, on the contrary, we measure the quality of an algorithm based on the time to achieve certain hypervolume target values for an *unbounded archive* of all non-dominated solutions ever evaluated—a scenario where algorithms that actually converge to a fixed-size Pareto set approximation have disadvantages over algorithms that might not converge to a fixed set of solutions but instead sample close to the Pareto set in a larger region.

We furthermore showed exemplarily for NSGA-II in a comparison with already available data from a Matlab implementation of

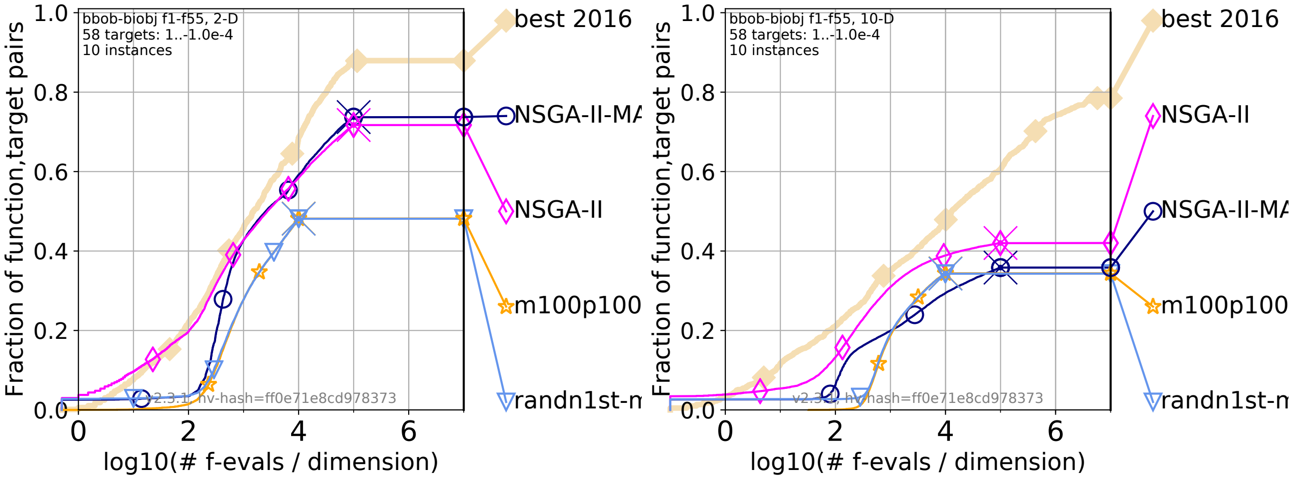


Figure 5: Comparison of four different variants of the well-known NSGA-II algorithm. Shown are the empirical runtime distributions over all 55 `bbob-biobj` test functions for the Matlab implementation of [1] (denoted NSGA-II-MATLAB) and the `platypus` variants with different initializations (NSGA-II: initial 100 search points uniformly sampled at random in $[-5, 5]^n$, m100p100: first 100 search points uniformly chosen in $[-100, 100]$, and randn1st-m100p100: 1st search point normally distributed around the origin and first population of 100 points chosen at random in $[-100, 100]$). Left: dimension 2. Right: dimension 10.

the same algorithm, that different implementations of the same algorithm can perform quite differently and that it is crucial to set the internal parameters and the initialization in a comparable way.

ACKNOWLEDGEMENTS

This work was supported by a public grant as part of the Investissement d'avenir project, reference ANR-11-LABX-0056-LMH, LabEx LMH, in a joint call with Gaspard Monge Program for optimization, operations research and their interactions with data sciences.

Tea Tušar furthermore acknowledges the financial support from the Slovenian Research Agency (project No. Z2-8177).

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