

Research Article

Benchmarking RCGAu on the Noiseless BBOB Testbed

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RCGAu is a hybrid real-coded genetic algorithm with “*uniform random direction*” search mechanism. The *uniform random direction* search mechanism enhances the local search capability of RCGA. In this paper, RCGAu was tested on the BBOB-2013 noiseless testbed using restarts till a maximum number of function evaluations (#FEs) of $10^5 \times D$ are reached, where D is the dimension of the function search space. RCGAu was able to solve several test functions in the low search dimensions of 2 and 3 to the desired accuracy of 10^8 . Although RCGAu found it difficult in getting a solution with the desired accuracy 10^8 for high conditioning and multimodal functions within the specified maximum #FEs, it was able to solve most of the test functions with dimensions up to 40 with lower precisions.

1. Introduction

The simple genetic algorithm (GA) introduced by Holland is a probabilistic algorithm based on the theory of natural selection by Charles Darwin. GA mimics the evolutionary process through the creation of variations in each generation and the survival of the fittest individuals through the blending of genetic traits. Individuals with genetic traits that increase their probability of survival will be given more opportunities to reproduce and their offspring will also profit from the heritable traits. Over the period of time these individuals will eventually dominate the population [1, 2].

GA consists of a set of potential solutions called chromosomes, a selection operator, a crossover operator, and a mutation operator. A chromosome is a string of zeros (0s) and ones (1s). It is a metaphor of the biological chromosome in living organisms. The zeros (0s) and ones (1s) are called genes. A gene is the transfer unit of heredity. It contains genetic traits or information that is passed on from a parent solution to its offspring. The selection operator selects solutions for mating based on the principle of “*survival of the fittest*.” The crossover operator generates new solution pairs called children by

combining the genetic materials of the selected parents. The mutation operator is an exploratory operator that is applied, with low probability, to the population of chromosomes to sustain diversity. Without the mutation operator, GAs can easily fall into premature convergence [1, 3].

The simple GA was designed to work on binary strings and it is directly applicable to pseudoboolean objective functions. However, most real life problems are represented as continuous parameter optimization problems. A decoding function was designed to map the solutions from binary space to the real-valued space. This decoding process can become prohibitively expensive for binary string GAs especially when the problem dimension increases [1, 3]. To tackle this problem real-coded genetic algorithms were introduced [4].

Real-coded genetic algorithms (RCGAs) use real-valued vectors to represent individual solutions. Surveys show that several variants of RCGAs have been proposed and used to solve a wide range of real life optimization problems. Some recent examples can be found in [1, 4–10].

Over the last three decades, researchers have continuously improved the performance of RCGAs through hybridization. RCGAs have been hybridized with other

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(1) Initialize  $P_{t=0}, P_t = \{x_{1,t}, x_{2,t}, \dots, x_{N,t}\}$  from  $X$ 
(2)  $f(x_{i,t}) = \text{evaluate}(P_t), \{1 \leq i \leq N\}$ 
(3) While not stopping condition, do Steps 4–12
(4) Calculate  $\sigma(f(P_t))$ , if  $\sigma(f(P_t)) \leq \epsilon$  do Step 5 else do Step 6
(5)  $\hat{P}_t = \text{perturb}(P_t)$ 
(6)  $\hat{P}_t = \text{tournamentSelection}(P_t)$ 
(7)  $C_t = \text{blend-}\alpha\text{Crossover}(\hat{P}_t, p_c)$ 
(8)  $M_t = \text{non-uniformMutation}(C_t, p_m)$ 
(9)  $Y_t = \text{ulsearch}(M_t)$ 
(10)  $f(x_{i,t}) = \text{evaluate}(Y_t)$ 
(11)  $P_{t+1} = \text{replace}(P_t, Y_t)$ 
(12)  $t = t + 1$ 
(13) end while

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ALGORITHM 1: The RCGAu Algorithm.

optimizers such as Nelder-Mead algorithms [11], simplex method [12], quadratic approximation [13], and pattern search [14–16].

In this paper, a set of noiseless testbed from the black-box optimization benchmarking (BBOB) 2013 workshop is used to benchmark RCGAu, a hybrid real-coded genetic algorithm that consists of “uniform random direction” local search technique.

The RCGAu algorithm is presented in Section 2, Section 3 provides the CPU timing for the experiments, Section 4 presents the results and discussion, and finally Section 5 concludes the paper with some recommendations.

2. The RCGAu Algorithm

RCGAu is a hybrid RCGA with a simple derivative-free local search technique called “uniform random direction” local search method. The local search technique operates on all individuals after the mutation operator has been applied to the population of individuals.

The RCGAu used in this work is a modified version of the RCGAu used in [16, 17]. It consists of five major operators, namely, tournament selection, blend- α crossover, nonuniform mutation, uniform random direction local search method, and a stagnation alleviation mechanism. Algorithm 1 shows the RCGAu algorithm.

The notations used in this paper are defined as follows.

P_t denotes the population of individual solutions $x_{i,t}$ at time t , N is the size of P_t , $\sigma(f(P_t))$ represents the standard deviation of the fitness values $f(P_t)$ of all solutions $x_{i,t} \in P_t$, \hat{P}_t is the mating pool containing the parent solutions, C_t is the population of offspring solutions obtained after applying crossover on the parents in \hat{P}_t , p_c is the crossover probability, M_t is the resultant population of solutions after applying mutation on C_t , p_m is the mutation probability, and Y_t is the population of solutions obtained after ulsearch has been applied to M_t , where ulsearch denotes the uniform random direction local search. Also, $\epsilon = 10^{-12}$, a very small positive value [18].

The evolutionary process in Algorithm 1 starts by initializing $P_{t=0}$ from the search space $X \subset \mathfrak{R}^n$. The domain of X is

defined by specifying upper (u^j) and lower (l^j) limits of each j th component of x ; that is, $l^j \leq x^j \leq u^j$ and $l^j, u^j \in \mathfrak{R}$, $j = 1, 2, \dots, n$. Next, the fitness value $f(x_{i,t})$, $\forall x_{i,t} \in P_0$, is calculated and the population diversity of P_t is measured by calculating the standard deviation $\sigma(f(P_t))$ of $f(x_{i,t})$.

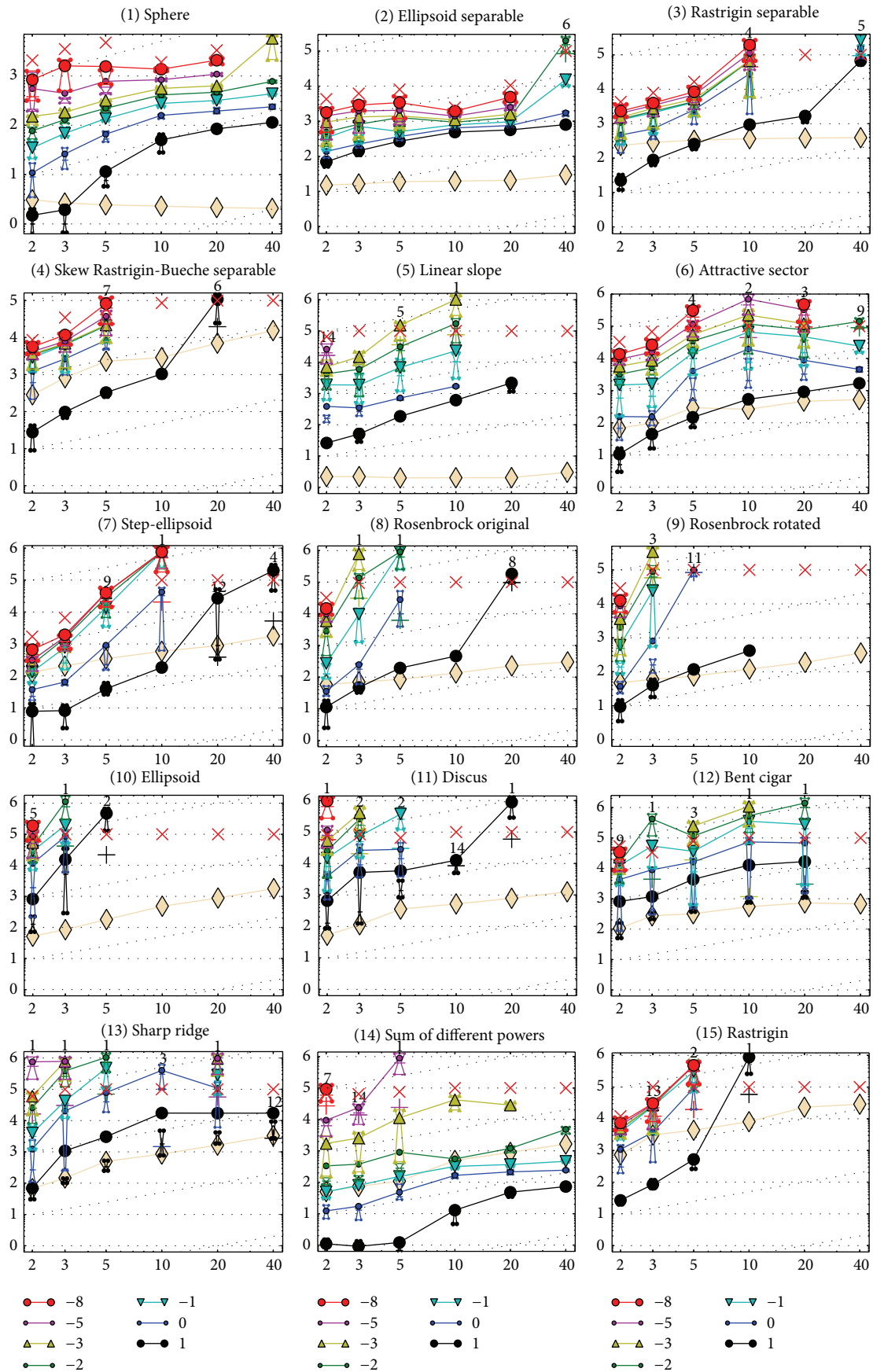
If $\sigma(f(P_t)) \leq \epsilon$ and the global optimum has not been found, then 90% of P_t is refreshed with newly generated solutions using the function perturb (P_t). P_t is refreshed by sorting the solutions according to their fitness values and preserving the top 10% of P_t . The remaining 90% of P_t are replaced with uniformly generated random values from the interval $[-4, 4]^D$ and the resultant population; $\hat{P}_t = \{x_{1,t}, x_{2,t}, \dots, x_{m,t}\}$ is created. m is the size of the mating pool \hat{P}_t and $m \leq N$. If, on the other hand, $\sigma(f(P_t)) > \epsilon$ then tournament selection is applied on P_t to create an equivalent mating pool \hat{P}_t .

The tournament selection scheme works by selecting r number of solutions uniformly at random from P_t , where r is the tournament size and $r < N$. The selected r individuals are compared using their fitness values and the best individual is selected and assigned to \hat{P}_t . This procedure is repeated m times to populate \hat{P}_t .

After the mating pool has been created, blend- α crossover is applied to a pair of parent solutions ($x_{i,t}, x_{k,t}$) if a randomly generated number τ drawn uniformly from the interval $[0, 1]$ is greater than the specified crossover probability threshold p_c . Blend- α crossover creates a pair of offspring ($c_{1,t}, c_{2,t}$) from the interval $[\min(x_{i,t}^j, x_{k,t}^j) - \alpha * d^j, \max(x_{i,t}^j, x_{k,t}^j) + \alpha * d^j]$ as follows:

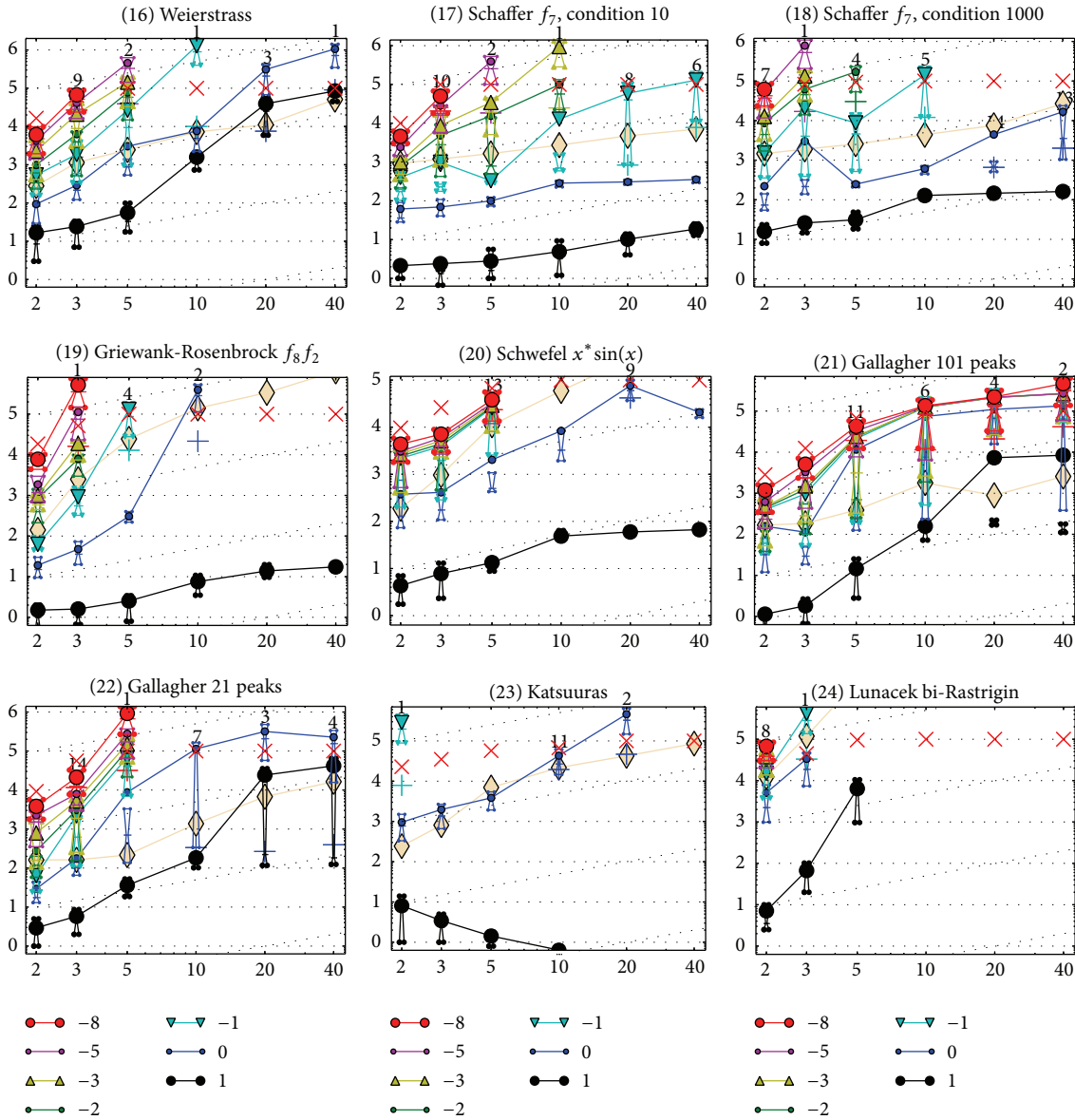
$$\begin{aligned}
 c_{1,t}^j &= \left(\min(x_{i,t}^j, x_{k,t}^j) - \alpha * d^j, \max(x_{i,t}^j, x_{k,t}^j) + \alpha * d^j \right) \\
 c_{2,t}^j &= \left(\min(x_{i,t}^j, x_{k,t}^j) - \alpha * d^j, \max(x_{i,t}^j, x_{k,t}^j) + \alpha * d^j \right),
 \end{aligned} \tag{1}$$

where $(1 \leq k \leq N)$, $\alpha = 0.3 + 0.2 * z$, z is a uniform random number drawn from the interval $[0, 1]$, and $d^j = |x_{i,t}^j - x_{k,t}^j|$. The new pair ($c_{1,t}, c_{2,t}$) is then copied to the set C_t ; otherwise the pair ($x_{i,t}, x_{k,t}$) is copied to C_t .



(a)

FIGURE 1: Continued.



(b)

FIGURE 1: Expected number of f -evaluations (ERT, lines) to reach $f_{\text{opt}} + \Delta f$; median number of f -evaluations (+) to reach the most difficult target that was reached not always but at least once; maximum number of f -evaluations in any trial (\times); interquartile range with median (notched boxes) of simulated run lengths to reach $f_{\text{opt}} + \Delta f$; all values are divided by dimension and plotted as \log_{10} values versus dimension. Also, $\Delta f = 10^{\{1,0,-1,-2,-3,-5,-8\}}$ are shown. Numbers above ERT-symbols (if appearing) indicate the number of trials reaching the respective targets. The light thick line with diamonds indicates the respective best results from BBOB-2009 for $\Delta f = 10^{-8}$. Horizontal lines mean linear scaling and slanted grid lines depict quadratic scaling.

Then the nonuniform mutation [4] is applied to the components of each member of C_t with probability, p_m , as follows :

$$m_{i,t}^j = \begin{cases} c_{i,t}^j + \Delta(t, u^j - c_{i,t}^j) & \text{if } u \leq 0.5, \\ c_{i,t}^j - \Delta(t, c_{i,t}^j - l^j) & \text{otherwise,} \end{cases} \quad (2)$$

where u is a uniformly distributed random number in the interval $[0, 1]$. u^j and l^j are the upper and lower boundaries

of $x \in X$, respectively. The function $\Delta(t, u^j - c_{i,t}^j)$ given below takes a value in the interval $[0, y]$:

$$\Delta(t, y) = y(1 - r^{(1-(t/T))^\beta}), \quad (3)$$

where r is a uniformly distributed random number in the interval $[0, 1]$, T is the maximum number of generations, and β is a parameter that determines the nonuniform strength of the mutation operator. The mutated individual $m_{i,t}$ is then copied to the set M_t ; otherwise $c_{i,t}$ is copied to M_t .

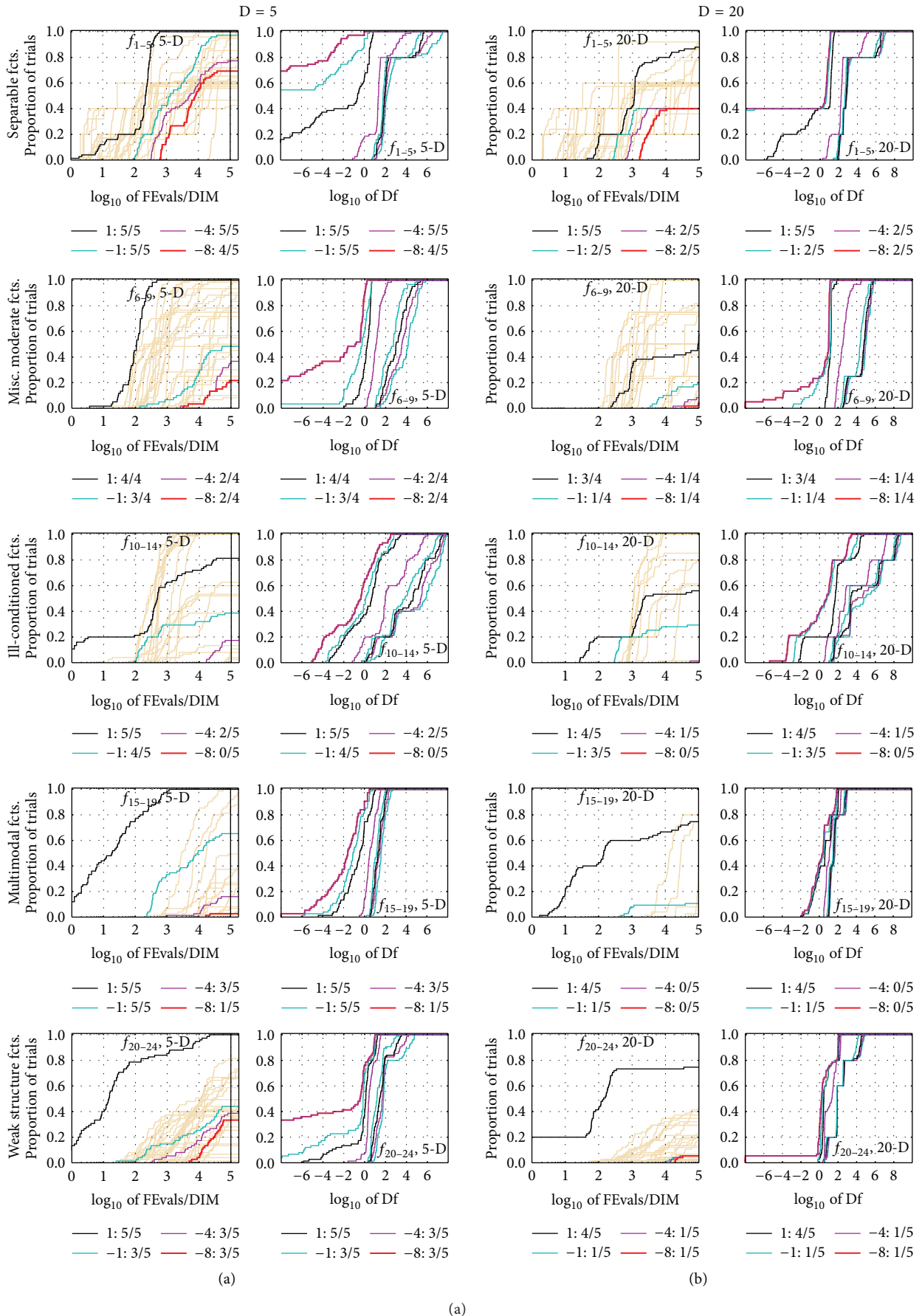


FIGURE 2: Continued.

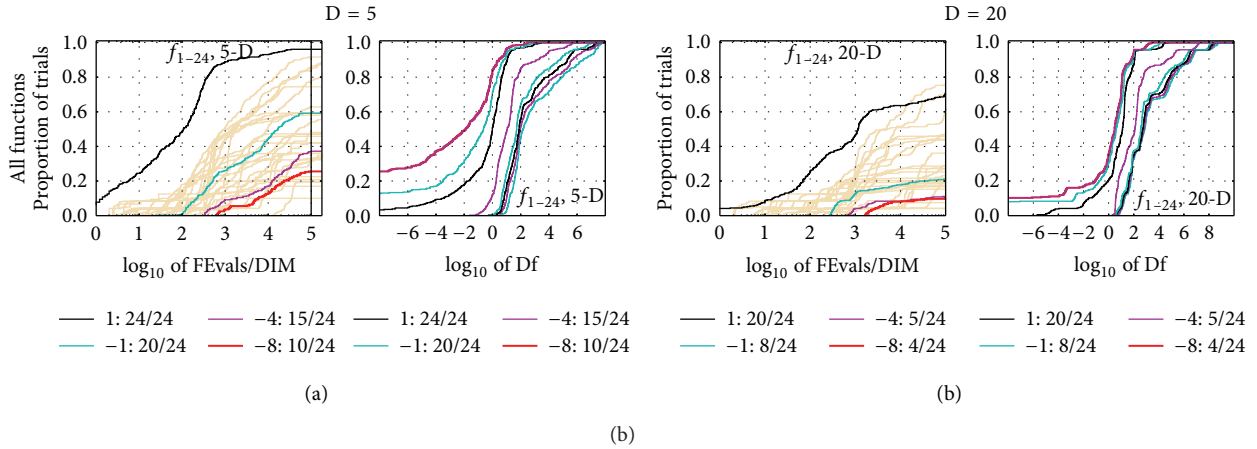


FIGURE 2: Empirical cumulative distribution functions (ECDF), plotting the fraction of trials with an outcome not larger than the respective values on the x-axis. Left subplots: ECDF of the number of function evaluations (FEvals) divided by search space dimension D , to fall below $f_{\text{opt}} + \Delta f$ with $\Delta f = 10^k$, where k is the first value in the legend. The thick red line represents the most difficult target value $f_{\text{opt}} + 10^{-8}$. Legends indicate for each target the number of functions that were solved in at least one trial within the displayed budget. Right subplots: ECDF of the best achieved Δf for running times of $0.5D, 1.2D, 3D, 10D, 100D, 1000D, \dots$ function evaluations (from right to left cycling cyan-magenta-black...) and final Δf -value (red), where Δf and Df denote the difference to the optimal function value. Light brown lines in the background show ECDF for the most difficult target of all algorithms benchmarked during BBOB-2009.

Then ulsearch is applied on each solution $m_{i,t} \in M_t$ with the aim of performing local searches around the neighborhood of each solution. ulsearch works by randomly selecting a solution $m_{i,t} \in M_t$ and creating a trial point $y_{i,t}$ using

$$y_{i,t} = m_{i,t} + \Delta_t U, \quad (4)$$

where Δ_t is a step size parameter and $U = (U_1, U_2, \dots, U_n)^T$ is a directional cosine with random components

$$U_j = \frac{R_j}{(R_1^2 + \dots + R_n^2)^{1/2}}, \quad j = 1, 2, \dots, n, \quad (5)$$

where $R_j \sim \text{Unif}([-1, 1])$. There are cases when the components of the trial point $y_{i,t} = (y_{i,t}^1, y_{i,t}^2, \dots, y_{i,t}^n)$ generated by (4) fall outside the search space X during the search. In these cases, the components of $y_{i,t}$ are regenerated using

$$y_{i,t}^j = \begin{cases} m_{i,t}^j + \lambda(u^j - m_{i,t}^j), & \text{if } y_{i,t}^j > u^j \\ m_{i,t}^j + \lambda(m_{i,t}^j - l^j), & \text{if } y_{i,t}^j < l^j, \end{cases} \quad (6)$$

where $\lambda \sim \text{Unif}([0, 1])$ and $m_{i,t}^j$ is the corresponding component of the randomly selected solution $m_{i,t} \in M_t$.

The step size parameter, Δ_t , is initialized at time $t = 0$ according to [15, 16] by

$$\Delta_0 = \tau \times \max \{u^j - l^j \mid j = 1, 2, \dots, n\}, \quad (7)$$

where $\tau \in [0, 1]$. The idea of using (7) to generate the initial step length is to accelerate the search by starting with a suitably large step size to quickly traverse the search space and as the search progresses the step size is adaptively adjusted at the end of each generation, t , by

$$\Delta_{t+1} = \frac{1}{K} \sum_{i=1}^K \gamma^i, \quad (8)$$

where K is the number of Euclidean distances $\{\gamma^1, \gamma^2, \dots, \gamma^K\}$ between K nearest points to the mean \bar{x} and \bar{x} of a set of randomly selected distinct points $\Omega = \{x_1, x_2, \dots, x_q\} \subset P_t$.

After the trial point $y_{i,t} \in Y$ has been created, it is evaluated and compared with $m_{i,t}$. If $y_{i,t} < m_{i,t}$, then $y_{i,t} \in Y$ is used to replace $m_{i,t} \in M_t$; otherwise the search direction is changed by changing the sign of the step length. The new step length is used to recalculate a new trial point. After a new trial point has been recalculated and evaluated, it is used to replace $m_{i,t} \in M_t$ with $y_{i,t}$, if $y_{i,t} < m_{i,t}$; otherwise $m_{i,t} \in M_t$ is retained.

At the end of ulsearch, P_t is updated with M_t to form P_{t+1} and elitism is used to replace the worst point in P_{t+1} with the best point in P_t because the generational model is the replacement strategy adopted in this work [19].

3. Experimental Procedure and Parameter Settings

The experimental setup was carried out according to [20] on the benchmark functions provided in [21, 22]. Two independent restart strategies were used to restart RCGAu whenever P_t stagnates or when the maximum number of generations is exceeded and f_{target} is not found. For each restart strategy, the experiment is reinitialized with an initial population P_0 which is uniformly and randomly sampled from the search space $[-4, 4]^D$ [6, 18].

Two stopping conditions used for the restart strategies are as follows.

- (i) A test for stagnation is carried out to check if the best solution obtained so far did not vary by more than 10^{-12} during the last $(50 + 25 \times D)$ generations as in [6].

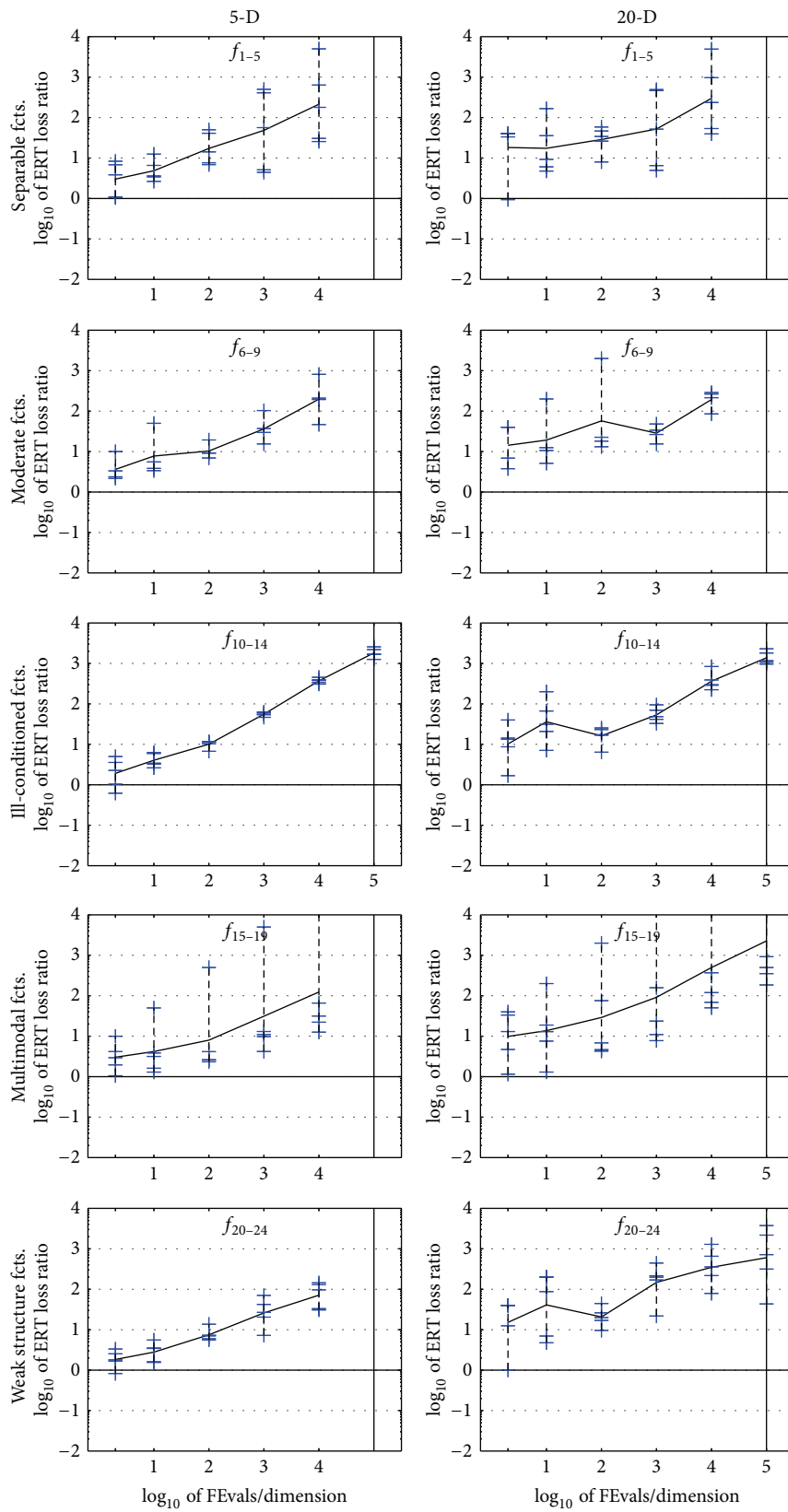
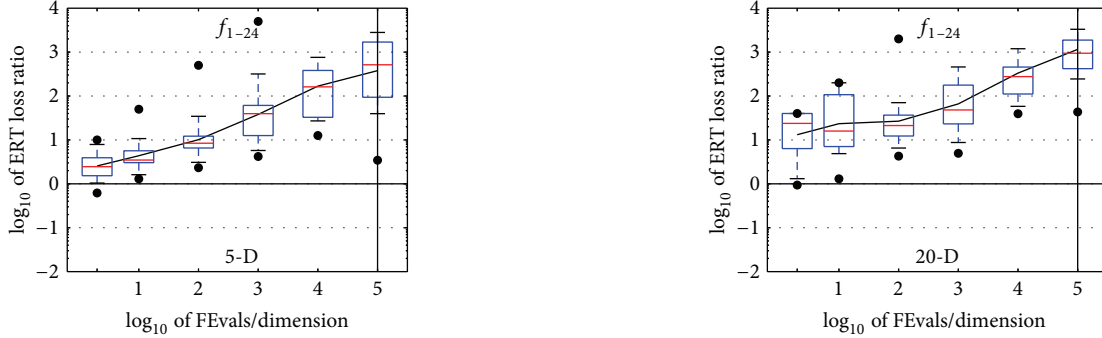


FIGURE 3: ERT loss ratios (see Table 2 for details). Each cross (+) represents a single function and the line is the geometric mean.

TABLE 1: Expected running time (ERT in number of function evaluations) divided by the best ERT measured during BBOB-2009. The ERT and, in braces, as dispersion measure, the half difference between 90 and 10 percentile of bootstrapped run lengths appear in the second row of each cell, the best ERT in the first. The different target Δf -values are shown in the top row. #succ is the number of trials that reached the (final) target $f_{\text{opt}} + 10^{-8}$.

Δf	5D										20D									
	1e+1	1e+0	1e-1	1e-2	1e-3	1e-5	1e-7	#succ	Δf	1e+1	1e+0	1e-1	1e-2	1e-3	1e-5	1e-7	#succ			
f_1	11 5.2(6)	12 27(15)	12 56(15)	12 91(22)	12 131(29)	12 319(193)	12 580(800)	15/15	f_1	43 39(7)	43 90(17)	43 148(19)	43 218(28)	43 294(36)	43 506(112)	43 787(173)	15/15			
f_2	83 16(3)	87 21(6)	88 29(10)	89 71(118)	90 79(118)	92 112(180)	94 155(176)	15/15	f_2	385 29(5)	386 39(8)	387 50(8)	388 66(17)	390 81(30)	391 128(41)	393 189(78)	15/15			
f_3	716 1.8(1)	1622 7.8(9)	1637 13(15)	1642 13(15)	1646 16(16)	1650 21(20)	1654 24(19)	15/15	f_3	5066 6.6(6)	7626 7626	7635 7635	7637 7637	7643 7643	7646 7646	7651 7651	15/15			
f_4	809 2.0(0.9)	1633 26(26)	1688 62(83)	1758 60(79)	1817 60(63)	1886 99(109)	1903 129(134)	15/15	f_4	4722 459(473)	7628 7666	7666 7666	7686 7686	7700 7700	7758 7758	1.4e5 cool.1e6	9/15			
f_5	10 93(20)	10 359(112)	10 3404(3910)	10 15683(18516)	10 76807(77456)	10 1075(273)	10 1075(273)	15/15	f_5	41 1075(273)	41 41	41 41	41 41	41 41	41 41	41 41	15/15			
f_6	114 6.5(6)	214 95(217)	281 263(443)	404 432(351)	580 470(459)	1038 552(489)	1332 749(685)	15/15	f_6	1296 14(3)	2343 75(28)	3413 277(325)	4255 365(470)	5220 465(474)	6728 971(1056)	8409 1110(1193)	15/15			
f_7	24 8.4(6)	324 14(22)	1171 58(89)	1451 98(114)	1572 126(139)	1572 126(133)	1597 125(134)	15/15	f_7	1351 402(507)	1351 402(507)	1351 402(507)	1351 402(507)	1351 402(507)	1351 402(507)	1351 402(507)	15/15			
f_8	73 13(4)	273 517(732)	336 13503(15418)	372 12258(13199)	391 12258(13199)	410 12258(13199)	422 12258(13199)	15/15	f_8	2039 1796(1474)	3871 1796(1474)	4040 1796(1474)	4148 1796(1474)	4219 1796(1474)	4371 1796(1474)	4484 1796(1474)	15/15			
f_9	35 17(7)	127 3920(3354)	214 3920(3354)	263 3920(3354)	300 3920(3354)	335 3920(3354)	369 3920(3354)	15/15	f_9	1716 1716	3102 3102	3277 3277	3379 3379	3455 3455	3594 3594	3727 3727	15/15			
f_{10}	349 67.25(7986)	500 698(864)	574 2442(2575)	607 2442(2575)	626 2442(2575)	829 2442(2575)	880 2442(2575)	15/15	f_{10}	7413 17715(19470)	8661 17715(19470)	10735 17715(19470)	13641 17715(19470)	14920 17715(19470)	17073 17715(19470)	17476 17715(19470)	15/15			
f_{11}	143 205(236)	202 698(864)	763 2442(2575)	977 2442(2575)	1177 2442(2575)	1467 2442(2575)	1673 2442(2575)	15/15	f_{11}	1002 17715(19470)	2228 17715(19470)	6278 17715(19470)	8586 17715(19470)	9762 17715(19470)	12285 17715(19470)	14831 17715(19470)	15/15			
f_{12}	108 201(576)	268 303(585)	371 490(704)	413 1392(1453)	461 2674(2913)	1303 2674(2913)	1494 2674(2913)	15/15	f_{12}	1042 320(961)	1938 706(1035)	2740 2024(2557)	3156 8893(9507)	4140 18749	12407 24455	13827 30201	15/15			
f_{13}	132 115(216)	195 2009(2341)	250 9467(10306)	319 16356(17378)	1310 16356(17378)	1752 16356(17378)	2255 16356(17378)	15/15	f_{13}	652 529(907)	2021 1072(1477)	2751 2052(2407)	3507 5467(5911)	18749 1026(1134)	24455 792(852)	30201 cool.2e6	15/15			
f_{14}	10 0.62(0.6)	41 5.9(5)	58 13(5)	90 50(23)	139 406(473)	251 17736(19499)	476 17736(19499)	15/15	f_{14}	75 13(6)	239 18(3)	304 24(5)	451 53(29)	932 612(196)	1648 4.5e5	15661 cool.2e6	15/15			
f_{15}	511 5.1(4)	9310 50(60)	19369 81(91)	19743 120(151)	20073 118(142)	20769 115(142)	21359 114(130)	14/15	f_{15}	30378 30378	1.5e5 1.5e5	3.1e5 3.1e5	3.2e5 3.2e5	3.2e5 3.2e5	4.5e5 4.5e5	4.6e5 4.6e5	15/15			
f_{16}	120 2.3(2)	612 25(7)	2662 50(79)	10163 38(49)	10449 69(80)	11644 196(217)	12095 196(217)	15/15	f_{16}	1384 569(695)	27265 227(268)	77015 77015	1.4e5 1.4e5	1.9e5 1.9e5	2.0e5 2.0e5	2.2e5 2.2e5	15/15			
f_{17}	5.2 2.7(3)	215 2.3(0.8)	899 1.8(0.6)	2861 27(33)	3669 47(57)	6351 308(353)	7934 308(353)	15/15	f_{17}	63 3.2(3)	1030 6.0(2)	4005 294(397)	12242 28555	30677 67569	56288 1.3e5	80472 cool.1e6	15/15			
f_{18}	103 1.5(1)	378 3.3(0.8)	3968 11(11)	8451 101(106)	9280 101(106)	10905 101(106)	12469 101(106)	15/15	f_{18}	621 4.7(2)	3972 22(3)	19561 22(3)	28555 28555	67569 67569	1.3e5 1.3e5	1.5e5 cool.1e6	15/15			
f_{19}	1 13(15)	1 1532(999)	242 2682(3069)	1.0e5 51362	1.2e5 54470	1.2e5 54470	1.2e5 54470	15/15	f_{19}	1 277(139)	1 277(139)	3.4e5 3.4e5	4.7e6 4.7e6	6.2e6 6.2e6	6.7e6 6.7e6	6.7e6 6.7e6	15/15			
f_{20}	16 4.2(3)	851 12(21)	3811 3.4(3)	51362 2.7(3)	54470 2.7(3)	54861 3.0(3)	55313 3.4(3)	14/15	f_{20}	82 15(3)	46150 33(33)	3.1e6 33(33)	5.6e6 5.6e6	5.6e6 5.6e6	5.6e6 5.6e6	5.6e6 5.6e6	14/15			

TABLE 2: ERT loss ratio versus the budget (both in number of f -evaluations divided by dimension). The target value f_t for a given budget FEvals is the best target f -value reached within the budget by the given algorithm. Shown is the ERT of the given algorithm divided by best ERT seen in GECCO-BBOB-2009 for the target f_t , or, if the best algorithm reached a better target within the budget, the budget divided by the best ERT. Line: geometric mean. Box-Whisker error bar: 25–75%-ile with median (box), 10–90%-ile (caps), and minimum and maximum ERT loss ratio (points). The vertical line gives the maximal number of function evaluations in a single trial in this function subset. See also Figure 3 for results on each function subgroup.



#FEs/ D	$f_1 - f_{24}$ in 5-D, maxFE/ $D = 100018$					
	best	10%	25%	med	75%	90%
2	0.62	1.0	1.4	2.5	4.0	8.5
10	1.3	1.6	2.9	3.5	5.8	16
100	2.3	2.6	6.4	8.4	13	42
1e3	4.2	5.0	12	40	62	4.2e2
1e4	13	25	32	1.6e2	3.9e2	1.2e3
1e5	3.4	35	83	5.1e2	1.7e3	3.0e3
1e6	3.4	35	1.4e2	8.6e2	1.2e4	2.2e4
RL _{US} / D	3e4	4e4	5e4	5e4	7e4	1e5
#FEs/ D	$f_1 - f_{24}$ in 20-D, maxFE/ $D = 100004$					
	best	10%	25%	med	75%	90%
2	0.94	1.1	5.8	24	40	40
10	1.3	4.8	7.0	16	1.3e2	2.0e2
100	4.3	6.2	11	21	39	2.7e2
1e3	5.0	7.6	23	48	1.8e2	4.7e2
1e4	39	53	1.0e2	2.8e2	5.2e2	1.7e3
1e5	43	2.3e2	4.0e2	9.4e2	1.9e3	8.3e3
1e6	2.4e2	4.2e2	9.9e2	3.9e3	1.1e4	6.8e4
RL _{US} / D	4e4	5e4	5e4	6e4	1e5	1e5

(ii) A test is carried out to check if the maximum number of generations is satisfied and f_{target} is not found.

The parameters used for RCGAu on all functions are

- (i) population size = $\min(100, 10 \times D)$, where D is the problem dimension;
- (ii) maximum number of evaluations #FEs = $10^5 \times D$;
- (iii) tournament size $r = 3$;
- (iv) crossover rate $p_c = 0.8$;
- (v) mutation rate $p_m = 0.15$;
- (vi) nonuniformity factor for the mutation $\beta = 15$;
- (vii) elitism $E = 1$;

(viii) crafting effort CrE = 0 [20].

4. CPU Timing Experiment

The CPU timing experiment was conducted for RCGAu using the same independent restart strategies on the function f_8 for a duration of 30 seconds on an AMD Turion (tm) II Ultra Dual-Core Mobile M620 CPU processor, running at 2.50 GHz under a 32-bit Microsoft Windows 7 Professional service pack 1 with 2.75 GB RAM usable and Matlab 7.10 (R2010a).

The time per function evaluation was 2.5, 2.6, 2.9, 3.0, 3.2, and 3.5 times 10^{-4} seconds for RCGAu in dimensions 2, 3, 5, 10, 20, and 40, respectively.

5. Results

The results of the empirical experiments conducted on RCGAu according to [20] on the benchmark functions given in [21, 22] are presented in Figures 1, 2, and 3 and in Tables 1 and 2.

Figure 1 shows the performance of RCGAu on all the noiseless problems with the dimensions 2, 3, 5, 10, 20, and 40. RCGAu was able to solve many test functions in the low search dimensions of 2 and 3 to the desired accuracy of 10^8 . It is able to solve most test functions with dimensions up to 40 at lowest precision of 10^1 .

Although RCGAu found it difficult in getting a solution with the desired accuracy 10^8 for high conditioning and multimodal functions within the specified maximum #FEs it was able to solve f_{21} with dimensions up to 40, f_1 and f_2 with dimensions up to 20, f_3 and f_7 with dimensions up to 10, and f_4 , f_6 , f_{15} , f_{20} , and f_{22} with dimensions up to 5.

In Figure 2, the left subplot graphically illustrates the empirical cumulative distribution function (ECDF) of the number of function evaluations divided by the dimension of the search space, while the right subplot shows the ECDF of the best achieved Δf . This figure graphically shows the performance of RCGAu in terms of function evaluation.

Table 1 presents the performance of RCGAu in terms of the expected running time (ERT). This measure estimates the run time of RCGAu by using the number of function evaluations divided by the best ERT measured during BBOB 2009 workshop. This benchmark shows that RCGAu needs some improvement in terms of performance.

6. Conclusion

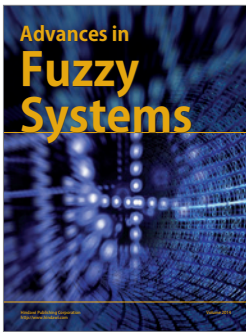
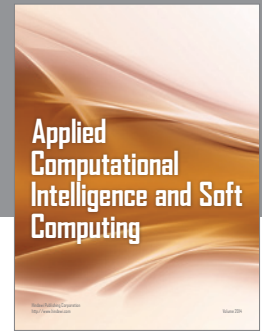
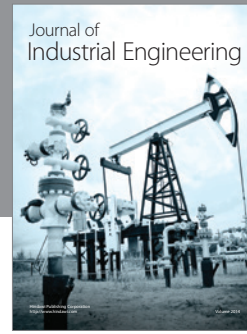
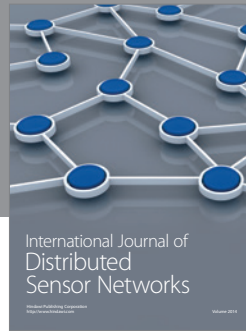
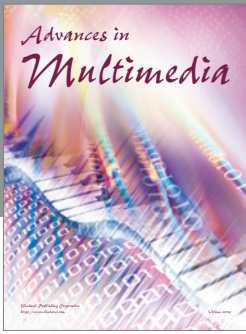
The performance of RCGAu on the suite of noiseless black-box optimization testbed has been average on a number of problems but it has excelled in solving functions f_1 , f_2 , f_3 , f_7 , and f_{21} . Studies have currently been carried out to find out why RCGAs do not efficiently solve highly conditioned problems. Further modifications to RCGAs are needed to exploit the full strength of evolutionary processes.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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