M2 AIC

TC2: Introduction to Optimization

Black-Box Optimization Benchmarking with the COCO platform - Multiobjective Optimizer adaptive IBEA (ϵ-indicator)

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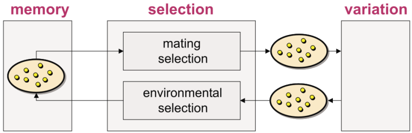
IBEA: Indicator-Based Evolutionary Algorithm

- optimization: find decision space vectors leading to objective space minima
- multiobjective: the objective space is multidimensional
- evolutionary: decision space candidates follows an natural selection-like evolution
- indicator-based: binary quality indicators to compare two Pareto set approximations

Successive steps of IBEA:

1. Initialization
2. Fitness assignment
3. Environmental selection
4. Termination
5. Mating selection
6. Variation



[1]

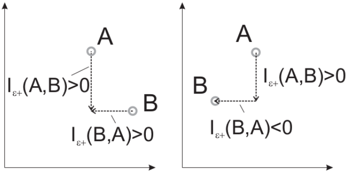
[1] Illustration from:
A Tutorial on Evolutionary Multiobjective Optimization - E. Zitzler, M. Laumanns, and S. Bleuler

- Binary quality indicators:

$$I_{\epsilon^+(A,B)} = min_\epsilon\{\forall x^2 \in B\ \exists x^1 \in A : f_i(x^1) - \epsilon \leq f_i(x^2)\ for\ i \in \{1, ..., n\}\} \tag{1}$$

- Fitness values:

$$F(x^1) = \sum_{x^2 \in P \setminus \{x^1\}} -e^{-\frac{I(\{x^1\},\{x^2\})}{ck}} \tag{2}$$



[2]

[2] Illustration from:
Indicator-Based Selection in Multiobjective Search - E. Zitzler and S. Künzli

Mating selection

Binary tournament selection

- Two individuals randomly chosen from the population
- Best individual kept in mating pool
- Repeated until mating pool filled

[3] *A Tutorial on Evolutionary Multiobjective Optimization* - E. Zitzler, M. Laumanns, and S. Bleuler

Recombination

For recombination, Simulated Binary Crossover (SBX) operator was chosen. A random number u created within $[0, 1]$, as follows:

- if $u \leq 0.5$:

$$\beta_q = (2u)^{\frac{1}{\eta_c + 1}} \tag{3}$$

- else:

$$\beta_q = \left(\frac{1}{2(1-u)} \right)^{\frac{1}{\eta_c + 1}} \tag{4}$$

[1] *K. Deb and R. B. Agrawal. Simulated binary crossover for continuous search space. Complex Systems, 9(2):115–148, 1995.*

Recombination

Thus, we can compute the children's coordinates:

- first child:

$$child0[j] = 0.5((1 + \beta_q)parent0[j] + (1 - \beta_q)parent1[j]) \quad (5)$$

- second child:

$$child1[j] = 0.5((1 - \beta_q)parent0[j] + (1 + \beta_q)parent1[j]) \quad (6)$$

[3] *K. Deb and R. B. Agrawal. Simulated binary crossover for continuous search space. Complex Systems, 9(2):115–148, 1995.*

Mutation

Polynomial mutation operator: this mutation operator modifies individuals by changing small parts in the associated vectors according to a given mutation rate.

- if $u \leq 0.5$:

$$\sigma_L = (2u)^{\frac{1}{\eta_m+1}} - 1 \tag{7}$$

$$p_{mut}[j] = ind[j] + \sigma_L(ind[j] - Lo) \tag{8}$$

- else:

$$\sigma_R = (2(1-u))^{\frac{1}{\eta_m+1}} \tag{9}$$

$$p_{mut}[j] = ind[j] + \sigma_R(Up - ind[j]) \tag{10}$$

[4] *K. Deb and S. Agrawal. A niched-penalty approach for constraint handling in genetic algorithms. In Parallel Problem Solving from Nature (PPSN-VI), pages 365–374, 2000.*

- Code built for the most general case
- The IBEA code is in the class IBEA, where each method implements one step of the algorithm
- No difficulty to get to the best asymptotic complexity

- Good data structures choices
- The Indicator function was the key
- Execution time improvement : 59.6s to 12.7s per execution (divided by 4.6)

Computer specifications and batch options

- Intel(R) Core(TM) i7-7500U CPU @ 2.70GHz
- Quad core CPU with 16GB RAM

Everything ran with a budget of 100

- Three batchs for dimensions 2, 3, 5, 10, 20
- First batch running alone, and two others together
- One batch for dimensions 40

Options chosen to run the algorithm

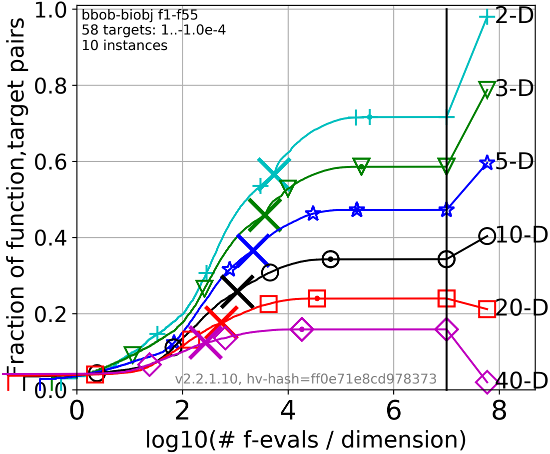
- Population size : 100
- Maximum number of generation : 100
- Scaling factor : 0.05
- Mutation rate : 0.01
- Recombination and mutation η_m & η_c : 1
- Population initialization in range (-5, 5)

Batch \ Dimension	2	3	5
Batch 1 on 3	6.0e-04	6.3e-04	8.1e-04
Batch 2 and 3 on 3 run simultaneously	8.6e-04	8.6e-04	9.1e-04
	8.3e-04	8.4e-04	8.9e-04

Batch \ Dimension	10	20
Batch 1 on 3	8.3e-04	1.1e-03
Batch 2 and 3 on 3 run simultaneously	1.1e-03	1.3e-03
	1.0e-03	1.3e-03

Batch \ Dimension	40
Whole test suite	4.2e-03

Results


bbob-biobj f1-f55
58 targets: 1..-1.0e-4
10 instances
v2.2.1.10, hv-hash=ff0e71e8cd978373
2-D
3-D
5-D
10-D
20-D
40-D
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
8

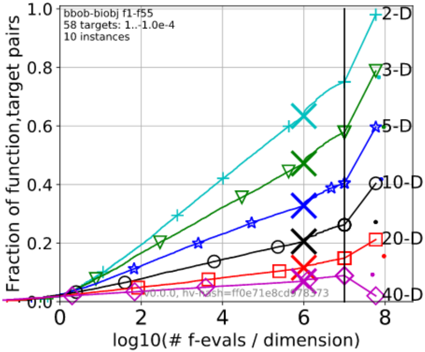
Results analysis

- Comparatively better in higher dimensions
- Results globally good for a MOEA

- More budget could have given better results
- A better initialization of population could lead to a sharper increase at the beginning

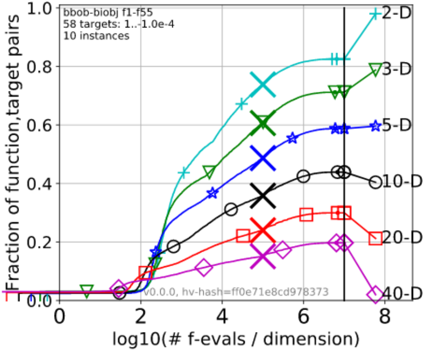
Random Search

- Its ECDF looks like linear functions
- It doesn't work well when the dimension is too high
- Globally worse than our algorithm



NSGA-II

Algorithm faster, although budget is much higher.
It has slightly better results.



- Overall satisfaction with our results.
- Parameter tuning could be further studied.
- Modification of small modules of MOEA.

Non-exhaustive bibliography

- *Indicator-Based Selection in Multiobjective Search* - Zitzler, E. and Künzli, S.
- *A Tutorial on Evolutionary Multiobjective Optimization* - Zitzler, E. and Laumanns, M. and Bleuler, S.
- *Biobjective Performance Assessment with the COCO Platform* - Brockhoff, D. and Tušar, T. and Tušar, D. and Wagner, T. and Hansen, N. and Auger, A.