

Sim-EDA: A Multipopulation Estimation of Distribution Algorithm Based on Problem Similarity

Krzysztof Michalak¹⁾

¹⁾ Wroclaw University of Economics, Poland [krzysztof.michalak@ue.wroc.pl]

The Sim-EDA algorithm

- ❑ A multipopulation algorithm...
- ❑ ...but each subpopulation tackles a slightly different instance of the problem
- ❑ Island model + migration
- ❑ Migration influenced by similarities of problem instances
- ❑ Each subpopulation processed using an Estimation of Distribution Algorithm

Main steps

1. Initialize probabilistic models
2. The main loop
 - 2.1. Generate new specimens
 - 2.2. Select source populations and specimens for migration
 - 2.3. Migrate specimens
 - 2.4. Update probabilistic models

❑ Details: [proceedings, page 239](#)

Problem similarity

❑ Problem instance similarity matrix:

$$S_{[N_{prob} \times N_{prob}]}$$

where:

N_{prob} – the number of problem instances

higher values = more similar instances

❑ Similarity between the i -th and j -th problem instances is expressed numerically as $S_{i,j}$

❑ In this paper problem instances are represented as weighted graphs

❑ The i -th problem instance has a cost matrix:

$$C_{[N \times N]}^{(i)}$$

❑ Similarity between i -th and j -th problem instance:

$$S_{i,j} = - \sum_{p=1}^N \sum_{q=1}^N (C_{p,q}^{(i)} - C_{p,q}^{(j)})^2.$$

Migration

❑ For each destination population i select the source population j based on values of $S_{i,j}$

❑ Migration strategies:

- Nearest – Migrate specimens from the most similar subproblem (largest $S_{i,j}$ for $j \neq i$)
- Rank - Rank all subpopulations from the largest $S_{i,j}$ to the smallest (for $j \neq i$) and apply roulette-wheel selection
- Uniform – Migrate specimens from a subproblem chosen at random with uniform probability (from $j \neq i$)
- None – No migration

❑ Incoming specimens are added one by one

- x – incoming specimen
- w – the weakest specimen in target population
- binary tournament between x and w
- if x wins it replaces w

Test Problems – The Max-Cut

❑ Find a partition of a graph $G = \langle V, E \rangle$ with N vertices

$$V' \cup V'' = V \quad V' \cap V'' = \emptyset$$

❑ Lengths of edges given in a cost matrix

❑ Each solution is a binary vector

❑ Minimization problem:

$$\begin{aligned} \text{maximize } f(V') &= \sum_{i \in V', j \in (V-V')} c_{ij}, \\ \text{subject to } V' &\in 2^V, \end{aligned}$$

Test Problems – The TSP

❑ Find the shortest route through N cities, visiting each city only once

❑ Distances given in a cost matrix

❑ Each solution is a permutation

❑ Minimization problem:

$$\text{minimize } f(\pi) = C_{\pi(N)\pi(1)} + \sum_{i=1}^{N-1} C_{\pi(i)\pi(i+1)}$$

subject to $\pi \in \Pi(N)$

where:

$\Pi(N)$ - the set of all permutations of numbers $1, \dots, N$

Generating similar problem instances

❑ $N_{sub} = 20$ cost matrices:

$$C_{[N \times N]}^{(1)}, \dots, C_{[N \times N]}^{(20)}$$

❑ In $C_{[N \times N]}^{(i)}$ the elements were drawn from $U[0, 100]$

❑ $C_{[K \times K]}^{(j)}$ was generated from $C_{[K \times K]}^{(j-1)}$ by replacing $1 / N_{prob}$ ($1/20 = 5\%$) of elements by random values

❑ To ensure symmetry the elements above and below the diagonal kept identical

Problem-specific EDAs

The Max-Cut

❑ Model: a vector $P \in [0, 1]^N$

➢ p_i – how probable it is that i -th element equals 1?

❑ Initially: $P = [0.5, 0.5, \dots, 0.5]$

❑ Model update from Population-Based Incremental Learning (PBIL) is used

The TSP

❑ Model: a matrix $Q_{[N \times N]}$ with $q_{ij} \in [0, 1]^N$

➢ q_{ij} – how probable it is that j is placed right after i

❑ Initially:

$$q_{i,j} = \begin{cases} 0 & \text{for } i = j \\ \frac{1}{N-1} & \text{for } i \neq j \end{cases}$$

❑ Model update from Population-Based Incremental Learning (PBIL) is used

❑ Best and worst permutations converted to Q_{best} and Q_{worst} by setting 1 iff i follows j in the permutation

❑ Obtaining permutations from $Q_{[N \times N]}$:

Algorithm 2. Initialization of a genotype for a new specimen for the TSP based on the probabilistic model Q .

```

IN:  Q - the probabilistic model
      N - genotype length
OUT: X - a new genotype
X[1] = UniformSelection({1, ..., N})
for k = 2, ..., N do
  U = [1, ..., N] - {X[1], ..., X[k-1]}
  i = X[k-1]
  S = sum_{j in U} Q[i,j]
  if S > 0 then
    X[k] = RouletteWheelSelection(U, {Q[i,j]}_{j in U})
  else
    X[k] = UniformSelection(U)
end if
end for
    
```

Experiments and Results

❑ Aimed at comparing the migration strategies

❑ Problem instances:

- The Max-Cut Problem with $N = 12, 25, 50, 100, 250$ and 500 nodes
- The Travelling Salesman Problem (TSP) with $N = 12, 25, 50, 100, 150, 200$ and 250 cities

❑ 30 runs for each instance and migration strategy

❑ Results compared at the common time limit (a time in which the None strategy completed 200 generations)

❑ Comparison performed using the Wilcoxon statistical test

❑ Max-Cut results

- Nearest vs. None: $N = 12$: Insignificant $N > 12$: Significant
- Rank & Uniform vs. None: $N \leq 100$: Significant $N \geq 250$: Worse

❑ TSP results:

- Nearest vs. None: $N \leq 50$: Insignificant $N \geq 100$: Significant
- Rank & Uniform vs. None: In most cases Insignificant

❑ The strategy of migrating specimens solely from the nearest subpopulation

- Consistently produced better results than those obtained when no migration was used for larger instances
- Was not significantly different from no migration for some smaller instances