

ComposedTrapOneMax

Objective function

binary

`Gevol.evolution.objective.binary`

Description

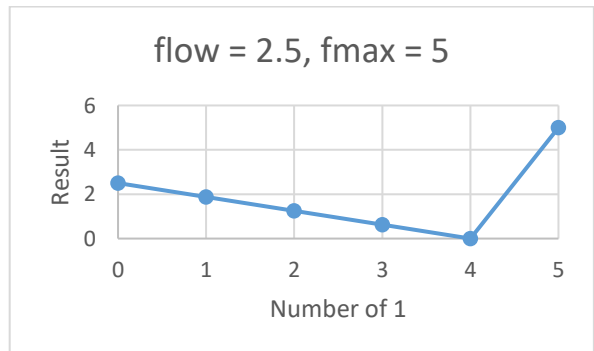
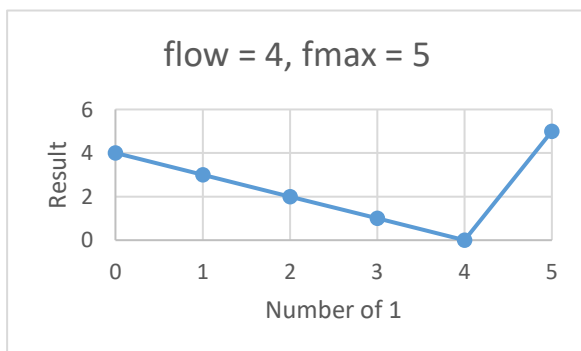
This is a trap function divided into blocks. Chromosome with the length of k-blocks multiplied by size of each block. For the each block is calculated a trap function. Final result is sum of values from every block.

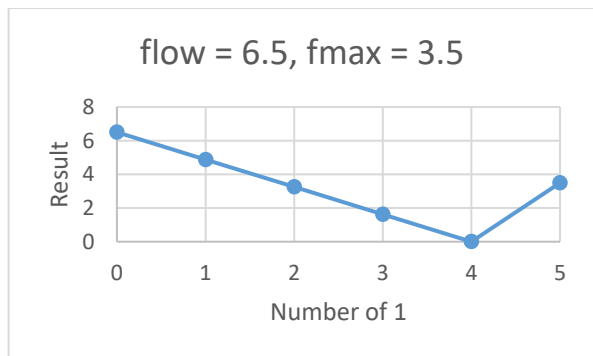
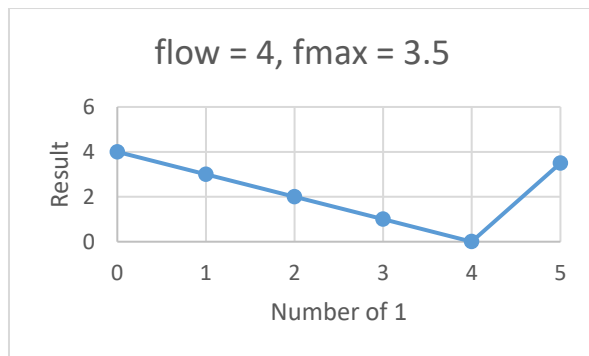
$$f_{trap}(x, k) = \sum_{i=0}^{\frac{n}{k}-1} trap(x_{i \cdot k} + \dots + x_{i \cdot k + k - 1}, k)$$
$$trap(u, k) = \begin{cases} f_{high}, & \text{if } u = k \\ f_{low} - u \frac{f_{low}}{k-1}, & \text{otherwise} \end{cases}$$

Where

- f_{trap} - calculate final result for the chromosome
- $trap$ - calculate value of each block
- x - chromosome, genes
- $x_{ik} + \dots + x_{ik+k-1}$ - calculates how many times appears 1 in each block
- n - chromosome length
- k - block length
- u - how many times genes are 1 in the block
- f_{high} - value if genes are 1
- f_{low} - maximum value otherwise (all genes are 0)

Parameters f_{high} and f_{low} may change the gap between global optimum ($u=5$) and local one ($u=0$). The most common usage is $f_{high} = k$, $f_{low} = k-1$, but other variances are possible, few examples are shown in the charts below.





Parameters

Parameters with description.

Pseudocode

Code .

Implementation details

Source codes with explanations.

References

1. Updating the probability vector using MRF technique for a Univariate EDA, S. K. Shakya, J. A. W. McCall, D. F. Brown, School of Computing, The Robert Gordon University, St. Andrew Street, Aberdeen, AB25 1HG, UK
2. Bayesian Optimization Algorithm: from single level to hierarchy, Martin Pelikan, DIPL., Comenius University, 1998, thesis submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Computer Science in the Graduate College of the University of Illinois at Urbana-Champaign, 2002