

Introduction: the FP-QIEA- $\mathbb{R}$ model implements and evaluates a new quantum inspired evolutionary algorithm based on the concept of quantum superposition for initialization. This model is based on a QIEA- $\mathbb{R}$, but instead of just using quantum individuals based on uniform probability density functions, where the update consists on change the width and mean of each pdf; this proposal uses a combined mechanism inspired in particle filter and pdf(probability density function) using rewarding criteria to sample with higher probability the best individuals and update pdf during the iterations. To evaluate this proposal, were performed experiments with theoretical problems: benchmark functions and some real applications. The results shows the potential of the proposal.

Objectives

- Study QIEA- $\mathbb{R}$.
- To model a efficient mechanism inspired in Particle Filter.
- To implement FP-QIEA- $\mathbb{R}$ and experiment with benchmark functions and real applications .

QIEA- $\mathbb{R}$

The QIEA- $\mathbb{R}$ model, proposed by [da Cruz et al., 2010] is composed by the following steps: generation of quantum population, generation of classic population by observing quantum population, and update of quantum population.

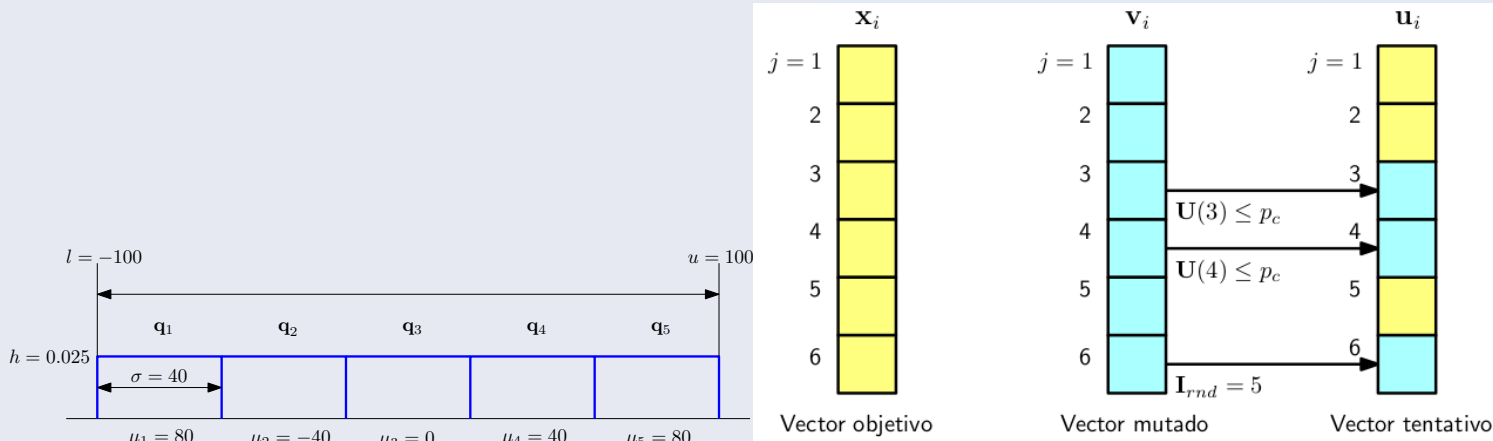


Figure 1: QIEAR steps

FP-QIEA- $\mathbb{R}$

The proposal follow the proposal [Chire and Tupac, 2015] with modifications is described below:

Initialization

- Classical population X generated using QIEA- $\mathbb{R}$.
- Evaluate X , use NRN(normalization, reward criteria, normalization) to get Y .

Create PDF and CDF For every dimension:

- Create a vector X_{id}, Y_i to get pdf and cdf.
- Sampling using Akima interpolation cdf_{f_i}, X_{id} to get X_{est} .

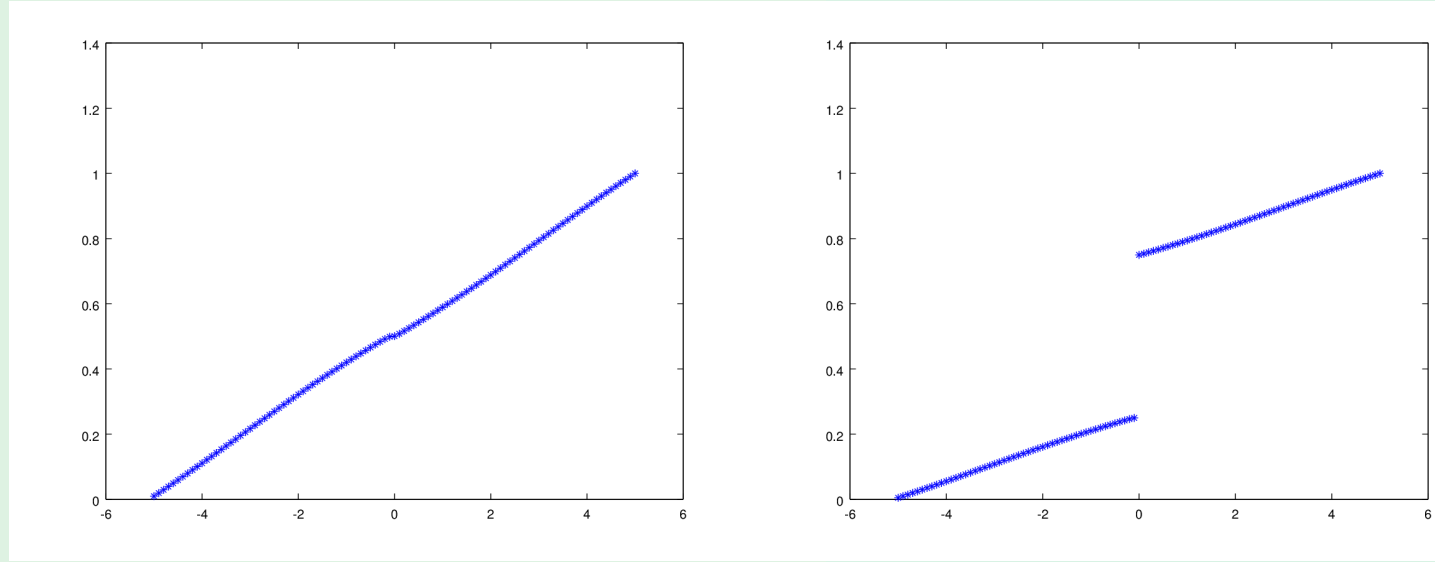


Figure 2: Pdf, cdf

Update

- Take the best of $X + X_{est}$ and update X .
- Evaluate X , use NRN(normalization, reward criteria, normalization) to get Y .

Replacing the worst

- Use crossover between the best individual x_{best} and the 2nd best to get new individual.
- Replace it for worst individual add it to the population X .

The next figure shows the evolution of cdf during iterations for dimension 1.

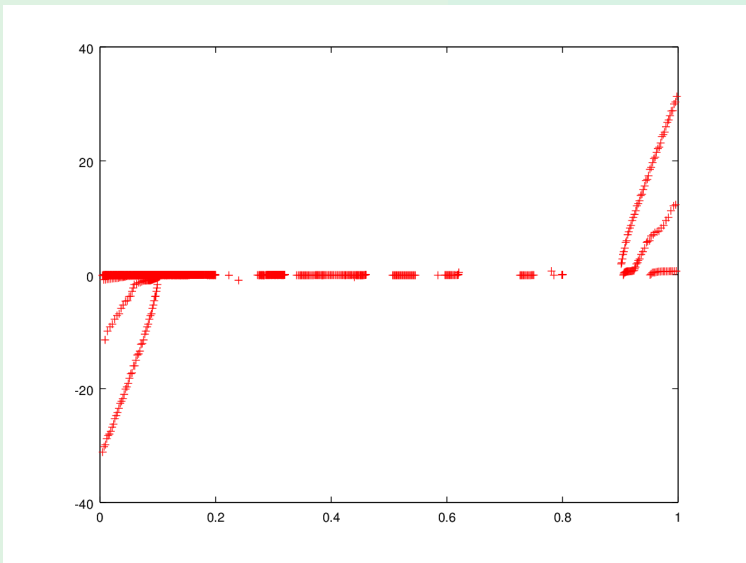


Figure 3: Cdf during iterations

Experiments

Benchmark functions Dimension = 30, iterations = 75.

Table 1: QIEA-R, FP-QIEA-R,FP-AK-QIEAR, MV = minimal value y SD = standard deviation

Function	QIEAR	FP-AK-QIEAR	f*
Ackley	4.770E-04	4.4409E-16	0
Rastrigin	3.0888E-05	0	0
Rosenbrock	7.9276E-02	27.3909	0
Schweffel	10660.4	10694.8	10660
Sphere	1.9560E-05	2.8629E-30	0

Function	QIEAR	FP-AK-QIEAR
Ackley	5.7468E-03	2.47024e-13
Rastrigin	2.5537E-03	0
Rosenbrock	7.48339	0.4473
Schweffel	5.90742	5.86587
Sphere	4.0369E-03	1.0588E-22

Experiments

Training MLP Replace random initialization for FP-QIEA $\mathbb{R}$ initialization.

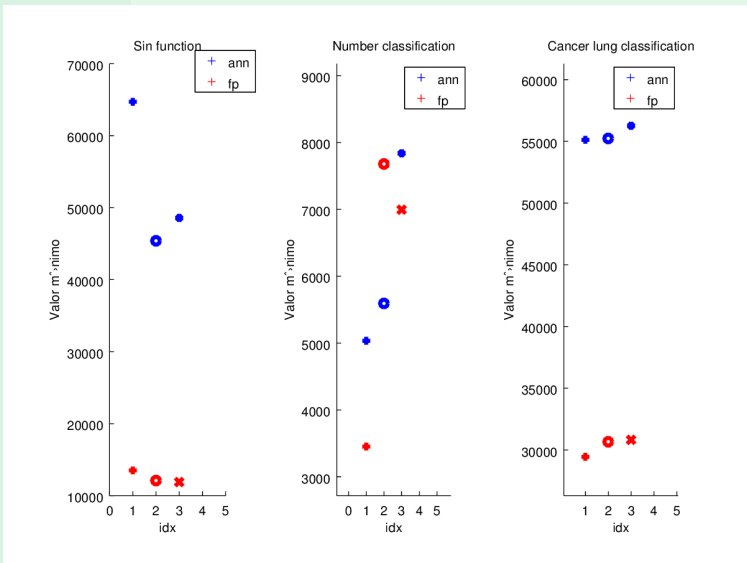


Figure 4: Random initialization vs FP-QIEAR initialization

Protein Folding For experiments with protein folding we used 24 experiments and we got the best, median and standard deviation to compare with the results obtained using PSO, GSA, BAT, ABC [Parpinelli et al., 2014], the best performance was using PSO. The dimensionality is $2n - 5$.

Table 2: Comparison using Protein folding

N	PSO E_{avg}	E_{best}	FP-QIEAR E_{avg}	E_{best}
13	-23.102 $\pm$ 0.93	-24.888	-22.1814 $\pm$ 0.813222	-23.9409
21	-43.047 $\pm$ 2.34	-46.611	-41.9036 $\pm$ 2.74061	-46.0356
34	-70.866 $\pm$ 5.95	-80.409	-68.9528 $\pm$ 3.63282	-75.9811
55	-87.715 $\pm$ 19.27	-115.758	-107.276 $\pm$ 8.86613	-119.652

Comparison of random initialization and FP-QIEAR initialization in PECO(Parallel Ecological Algorithm) [Benítez et al., 2013].

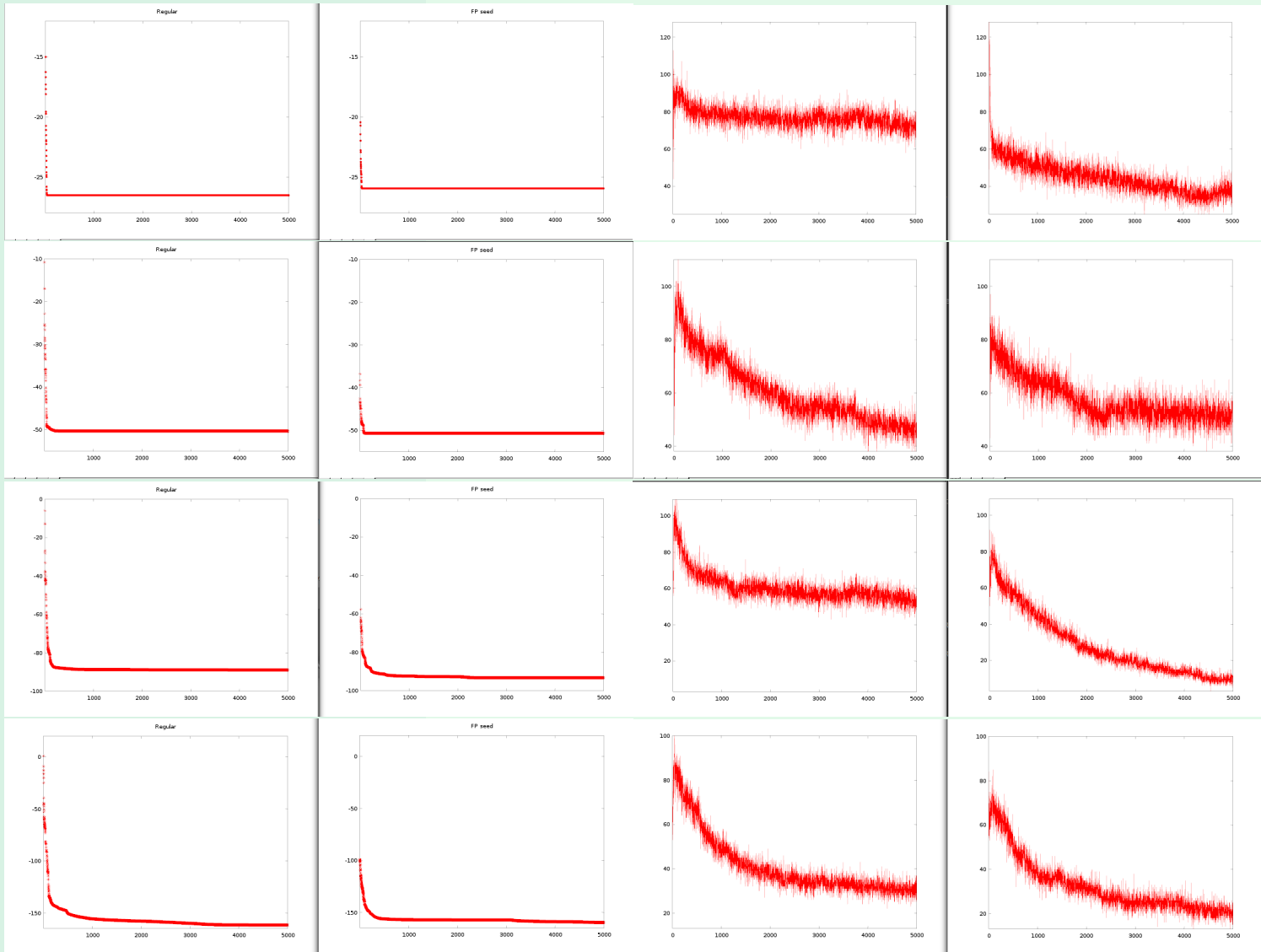


Figure 5: The best ever and number of habitats

Knapsack Problem Using sigmoid function to have binary values 0 , 1.

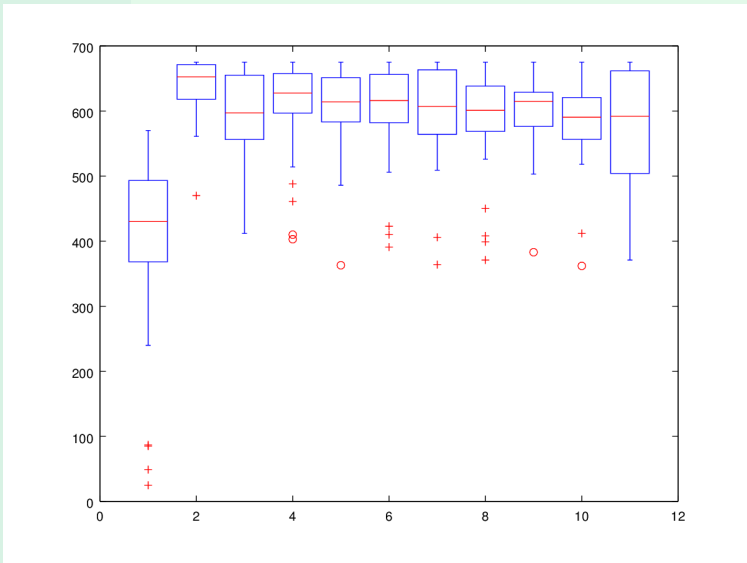


Figure 6: Pdf, cdf

Conclusions

- The proposal FP-QIEA- $\mathbb{R}$ is based on probability density function that follows the best individuals.
- The results in the experiments shows good performance.
- There is a promissory way for FP-QIEA- $\mathbb{R}$ in binary and real domain problems.

References

- Benítez, C. M. V., Parpinelli, R. S., and Lopes, H. S. (2013). A heterogeneous parallel ecologically-inspired approach applied to the 3d-ab off-lattice protein structure prediction problem. In *2013 BRICS Congress on Computational Intelligence and 11th Brazilian Congress on Computational Intelligence*, pages 592–597.
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