Stationary Multivariate Probabilities Estimation for Intelligent MCMC Algorithms

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Abstract

The purpose of this paper is to get theoretical and empirical results for stationary multivariate probabilities estimation of any clonal selection or genetic algorithm by new presented proposed algorithm. The estimation proposed formula is true for any regular Markov Chain to get the desirable multivariate distribution.

Keywords:
Evolutionary Algorithms; Evolutionary-Like Algorithms; Regular Markov Chains; Multivariate Distribution.

1. Introduction

Genetic and clonal selection algorithms have been proved as MCMC by El-Nady et al. [3-4]. Abou El-Enien estimation theorems for stationary joint and triple probabilities for mathematical programming problems have been proposed by Abou El-Enien [1-2]. We develop estimation theorem for stationary multivariate probabilities for clonal selection or genetic algorithms and this theorem is true for mathematical programming problems . Our purpose also for carrying out the study is stationary multivariate probabilities estimation of any regular Markov Chain by using one chain only and proposed original estimation formula.

2. Problem Formulation

Proposition 2.1. For u-iterations, where u is a large number, we apply clonal selection or genetic algorithms on any randomly picked state, count for each $Y = (y_{h-1} = s_1, y_h = s_2, y_{h+1} = s_{i+1}, ...) \ \forall \ h \geq 1$ and $\forall$

$i \geq 2$ times number it appeared and calculate probability of each Y such that $y_0, y_1,....$ are outcome functions and $s_1, s_2, s_{i+1},.....$ are any possible sequence of outcomes.

3. Main theorem

We have the probability W of each Y, where

$$W = \frac{\text{number of times } (y_{h-1} = s_1, y_h = s_2, y_{h+1} = s_{i+1}, ...) \text{ appeared}}{u - i}$$

, by applying clonal selection or genetic algorithms and have, for any regular Markov Chain, stationary multivariate probabilities.

4. Main theorem proof

1- We clench clonal selection or genetic algorithms on any randomly picked state.

2- We count appeared times number and figure probability respecting each *Y*.

5. Proposed algorithm

By using MATLAB 7.5, we prepared our programs. Proposed name for the algorithm is Abou El-Enien Estimation of Stationary Multivariate Probabilities (**Abou El-Enien ESMP**):

1. Put in bits number.

2. Procure all unique chromosomes.

3. Put in chromosomes number.

4. Procure states number.

5. Produce all prospective unique chromosomes combinations states and award each state a number.

6. Randomly, Pick one state.

7. Apply genetic or clonal selection algorithms on the randomly picked state for *u* -iterations.

8. For each *Y*, count times number it appeared.

9. Calculate *W* of each *Y*.

10. Procure stationary multivariate probabilities.

6. Numerical results

For $y(d) = d \cdot \sin(10\Pi \cdot d) + 1, d \in [-1, 2]$, mutation probability = 0.9, crossover probability = 0.6, chromosomes number = 2 and bits number = 5, we apply genetic algorithm on the picked state 1006 and calculate one of the stationary quartet probabilities *W* (1006, 17, 1006, 17) =0.0000100003 for this chain only,

 u = 100000 iterations (for stability),   (1006,17,1006,17,972,......,63,960,30,977,55).

In past studies, the obtained results have been for stationary joint and triple probabilities [1-2].

7. Conclusions

The new proposed method is Abou El-Enien ESMP to estimate stationary multivariate probabilities and we get Abou El-Enien ESMP theorem by using one chain only. For any regular Markov Chain, the original estimation formula is true to get stationary multivariate probabilities of the desirable multivariate distribution (triple distribution, quartet distribution and ......).

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