Estimation of First Passage Time Probabilities at Second Transition respecting Evolutionary MCMC Algorithms

Dr. Usama Hanafy Abou El-Enien

Administrative Information Systems Department the High Institute for Tourism, Hotels & Computer, El-Seyouf, Alexandria, Egypt.

https://orcid.org/0000-0001-9640-7320

ossama.hanafy77@gmail.com

Abstract

With regard to genetic algorithms with bit mutation, the target is to offer novel algorithm to obtain experiential and theoretic results for first passage time probabilities estimation at second transition. The estimating proposed formula is true to get the desirable conditional bivariate distribution with regard to any regular Markov Chain.
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Keywords: Evolutionary Algorithms; First Passage Time; Regular Markov Chain; Conditional Bivariate Distribution.

1. Introduction

Genetic algorithms have been proved like MCMC by El-Nady et al. [4].

First passage time probabilities, at first transition, estimation method has been proposed by Abou El-Enien [1].

For stationary joint probabilities, Abou El-Enien estimation procedure has been proposed by Abou El-Enien [2].

Estimation algorithm respecting first passage time transition probabilities with regard to transient states, concerning genetic algorithms **without** bit mutation, has been proposed by Abou El-Enien [3].

Our purpose else for carrying out the study is first passage time probabilities estimation at second transition of any regular Markov Chain via using one and only chain and proposed original estimation formula.

2. Problem Formulation

Proposition 2.1. For each $A = (a_{p+1} = z, a_p = y | a_{p-1} = x) \forall p \geq 1$ and $a_p \neq z$ and x, y, z are any

outcomes possible sequence, we tick off appeared times number and reckon probability.

3. Theorem

For each A, if we enforce genetic algorithms with bit mutation then we possess probability L (conditional bivariate probabilities formula), where

$$L = \frac{(a_{p+1} = z, a_p = y | a_{p-1} = x) \; appeared \; times \; number}{appeared \; times \; number \; of \; any \; joint \; states \; given \; state \; x}$$

, and first passage time probabilities at second transition.

4. Theorem Proof

1- As for h-iterations on any randomly picked state, where h is a large number, we enforce genetic

algorithms with bit mutation.

2- We tick off appeared times number and reckon probability respecting each *A*.

5. The proposed Algorithm

We utilized MATLAB 7.5 and designed our programs. The suggested name for algorithm is Abou El-Enien First Passage Time Probabilities Estimation at Second Transition (**Abou El-Enien FPTPEST**):

1. Let in bits number.

2. Procure commonalty unique chromosomes.

3. Let in chromosomes number.

4. States number, obtain.

5. Produce commonalty prospective unique chromosomes combinations states and confer each state a number.

6. Randomly, elect one state.

7. Genetic algorithms with bit mutation on the randomly elected state for *h* –iterations, apply.

8. For each *A*, tick off appeared times number.

9. For each *A*, reckon *L*.

10. Angle first passage time probabilities at second transition.

6. Numerical Example

As for function $w(j) = j \cdot \sin(10\Pi \cdot j) + 1, j \in [-1,2]$. Insomuch as probability of mutation = 0.9, probability of crossover = 0.6, number concerning chromosomes = 2 and number concerning bits = 5, via applying genetic algorithm on the elected state 1006 and calculating one of the first passage time probabilities at second transition

$L(972,17|1006)$ = 0.033898305 in connection with the chain (1006,17,1006,17,972,......,63,960,30,977,55) and *h* = 100000 iterations (with regard to stability).

In past study, the obtained results have been for first passage time probabilities, at first transition [1].

7. Conclusions

The offered method is Abou El-Enien FPTPEST to estimate first passage time probabilities at second transition and for this **conditional bivariate probabilities** formula, we possess Abou El-Enien FPTPEST theorem via using one and only chain. For any regular Markov Chain, the original suggested estimation formula is true to get first passage time probabilities at second transition of desirable **conditional** bivariate distribution.

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