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A Proposed Bayesian Estimation of Transitional Probability for a Markov Chain with Random Times via Swarm Algorithm

Alaa F. Ahmed	Muthanna S. Sulaiman
alaa.21csp99@student.uomosul.edu.iq	muthanna.sulaiman@uomosul.edu.iq
Department of Statistics and Informatics, College of Computer Science and Mathematics, University of Mosul, Mosul, Iraq.	

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Abstract

The transition matrix estimators of the Markov chain are not accurate and the transition matrix is considered given. There are many methods that are used to estimate the transition probabilities matrix for different cases, the most famous of which is the Maximum Likelihood Method, in order to find a good and new estimator for the transition probabilities matrix of the Markov chain, a method was proposed, which is a modification of the Bayes method, to reach the transition probabilities with the least variance. This method assumes that the values of α_{ij} in the initial probability are estimated by two methods: Maximum Likelihood Method (MLE), and the algorithm of particle swarm (PSO), The Escherichia Coli (E.Coli) gene chain was chosen as an applied aspect of the study due to its importance in medical research and for the purpose of discovering and manufacturing treatments by knowing the final form of its gene chain. After testing the E.Coli gene chain, it was found that is represents a Markov chain, and then both the transition probabilities matrix and the transition probabilities variance were estimated, and it was found that the proposed method for transitional probabilities is better than the method of greatest possibility depending on the variance.

Correspondence:
Muthanna S. Sulaiman
muthanna.sulaiman@uomosul.edu.iq

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1. Introduction

Markov chains are considered one of the most important stochastic processes, as the scientist Andrei Markov published a set of scientific papers in 1907. These papers represented the development of the Calton-Watson process, as it is considered the beginning of Markov chains. Through these papers presented by Markov, he set a condition for the use of Markov chains. This condition represents the Markovian property, which states: “The future states of the process depend only on the current state of the process and are independent of the previous states” [1]. There are four cases of Markov chains, as is the case in stochastic operations, where both time and state space can be continuous or discontinuous, and among the most widely applied and famous Markov chains

are those in which both state space and time are discontinuous. So the elements of the state space can be sign with integers $(1,2,3,\dots)$. If the discontinuous random variable X_n represents a state seen at time n , the stochastic process can be sign in a discontinuous state space in the form $\{ X_n ; n = 0,1,2,3,\dots\}$, where the index n sign to time or location somewhere, and it can be any other index. Since the index n represents time, it represents the present, and $n - c$ represents the past before c units of time, and $n + c$ represents the future after c units of time.

The stochastic process X_n is called the Markov process, as it achieves the following[2]:

$$P_r\{ X_n = j \mid X_{n-1} = i , X_{n-2} = c , \dots , X_k = k \} = P_r\{ X_n = j \mid X_{n-1} = i \} \quad (1)$$

Where this conditional probability shows that the process in case (i) will move to case (j)after one step and with a probability of P_{ij}, and the researcher G. Wang in the date of 2010 published a research on estimating transitional probabilities[3], and the researchers Junsheng Ma, and others in 2014 published a paper on the Bayes method in estimating the transition probabilities matrix for discontinuous-time data of the Markov process[4], and Lee, and others in 1968 published a paper on the Bayes estimator and the greatest possibility of transitional probabilities[5],and KALBFLEISCH and LAWLESS were also presented in 1984 Least squares estimation of transitional probabilities from data collection[6].

2. The theoretical side

Building a model of a Markov chain by assuming a chain of observations. The first thing that is observed is the observations of that chain, which may be letters or integers. From these observations, the transitions from one state to another are calculated to form a matrix that includes these transitions, called the iterations matrix and denoted by the symbol F. Assuming that the case space $s = \{ 1, 2, 3, \dots , n \}$,the iterations matrix is as follows:

$$F = \begin{array}{c} \\ 1 \\ 2 \\ \vdots \\ n \end{array} \begin{array}{c} \begin{array}{ccccc} 1 & 2 & 3 & \cdots & n \end{array} \\ \begin{bmatrix} f_{11} & f_{12} & f_{13} & \cdots & f_{1n} \\ f_{21} & f_{22} & f_{23} & \cdots & f_{2n} \\ \vdots & & \vdots & \cdots & \vdots \\ f_{n1} & f_{n2} & f_{n3} & \cdots & f_{nn} \end{bmatrix} \end{array} \quad (2)$$

Since the state space is discontinuous and finite, it is possible to express the probabilities of transitions to and from different states after one step in the form of a matrix called the Transition Matrix and denoted by the symbol P, and the element (i, j) of this matrix is represented by the probability of transitions from state i to state j with a probability $P_{ij} = (X_n = j | X_{n-1} = i)$. Also, the transition matrix P is a stochastic matrix and it must fulfill the two conditions:

- All of its elements are non-negative and greater than zero (being probability values).
- The sum of each of its rows is equal to one (since the sum of the total probabilities is equal to one).

2.1 Estimating the Transition Probability Matrix

There are many methods that are used to estimate the transition probabilities matrix for different cases, and in this research the method of greatest possibility was used and a proposed method for estimating the transition probabilities matrix.

2.2 Estimating transition matrix using MLE method

Let $x_1, x_2, x_3, \dots , x_n$ be the observations of a random sample drawn from collection with a probability density function $f(x, P)$. Then the possibility function of the sample observations can be defined as the joint distribution of those observations. Let $L(P)$ be a symbol for the possibility function, then this function takes the form[7, 8]:

$$L(P) = \prod_{i=1}^{n} f(x_i, P)$$

$$L(P) = P(x_1) \prod_{t=2}^{n} P(x_t | x_{t-1})$$

$$L(P) = P(x_1) \prod_{t=2}^{n} P_{x_{t-1} x_t} \quad (3)$$

After rewriting the transition probabilities to obtain the possibility function of the transition matrix

$$L(P) = P(x_1) \prod_{i=1}^{k} \prod_{j=1}^{k} P_{ij}^{n_{ij}} \quad (4)$$

Where n_{ij} is the number of transitions from i to j.

By maximizing the above equation by taking the natural logarithm, we get:

$$\ln L(P) = \ln P(x_1) + \sum_{i,j} n_{ij} \ln P_{ij} \quad (5)$$

For the purpose of finding transition probabilities from the equation of greatest possibility above, we follow the Lagrange multiples method

$$\mathcal{L}(P,\lambda) = \ln P(x_1) + \sum_{i,j} n_{ij} \ln P_{ij} - \left(\sum_{i=1}^{j} \lambda_i \left(\sum_j P_{ij} - 1\right)\right) \quad (6)$$

λ_{ij} : Lagrange multiples,P_{ij}: transition probabilities

where: $\sum_j P_{ij} = 1$

and by taking the partial derivation of equation (6) with respect to $P_{ij}$and λ_i, we get:

$$\frac{\partial \mathcal{L}}{\partial \lambda_i} = \sum_j P_{ij} - 1 \quad (7)$$

since $\sum_j P_{ij} = 1$, that is $\frac{\partial \mathcal{L}}{\partial \lambda_i} = 0$.

$$\frac{\partial \mathcal{L}}{\partial P_{ij}} = \frac{n_{ij}}{P_{ij}} - \lambda_i \quad (8)$$

by equating the above equation to zero, we get:

$\frac{n_{ij}}{P_{ij}} - \lambda_i = 0$, $\lambda_i = \frac{n_{ij}}{P_{ij}}$

$$P_{ij} = \frac{n_{ij}}{\lambda_i} \quad (9)$$

and by taking the sum of both sides of the equation above to (n) with respect to (j) , we get:

$$1 = \sum_j \frac{n_{ij}}{\lambda_i} \quad (10)$$

$$\lambda_i = \sum_j n_{ij} \quad (11)$$

substituting equation (11) into equation (9), we get:

$$P_{ij}^{(MLE)} = \frac{n_{ij}}{\sum_j n_{ij}} \quad (12)$$

Therefore, formula (12) represents an estimator for the transition probabilities matrix of the Markov chain using the method of greatest possibility.

2.3 Proposed method for estimating transition matrix

It was proposed to use the Bayes method to estimate the transition matrix by estimating parameters based on a traditional method MLE and an intelligent method PSO, so that we have $D = (x_1, x_2, \dots, x_n)$ representing the observed data, so Bayes theory can be written in the following form:

$$P(\theta|D) = \frac{P(D|\theta)P(\theta)}{P(D)} \quad (13)$$

Where $P(\theta|D)$ is the subsequent distribution which represents the probability of the model parameters (θ) conditioned by the observed data. The value $P(D|\theta)$ is the conditional probability of the data given the parameters of the model, and this value represents the possibility function. Whereas $P(D)$ is the probability of the model data. The value P(θ) represents the initial probability and the initial probability reflects our belief about the parameters before we see the data. In our case, the initial probability for each row of the transition matrix is the Dirichlet distribution.

Let us have the variables ($x_1, x_2, \dots, x_k$) and these variables must satisfy $x_i \in [0,1]$ and $\sum_{i=1}^{k} x_i = 1$, and the distribution parameters ($\alpha_1, \alpha_2, \dots, \alpha_k$), $\alpha_0 = \sum_{i=1}^{k} \alpha_i$,so the Dirichlet distribution is in the form [9, 10]:

$$f(x_1, x_2, \dots, x_k; \alpha_1, \alpha_2, \dots, \alpha_k) = \frac{\Gamma(\sum_{i=1}^{k} \alpha_i)}{\prod_{i=1}^{k} \Gamma(\alpha_i)} \prod_{i=1}^{k} x_i^{\alpha_i - 1} \quad (14)$$

the expected value of the Dirichlet distribution is:

$$E(x_i) = \frac{\alpha_i}{\alpha_0} \quad (15)$$

the variance of the Dirichlet distribution is:

$$Var(x_i) = \frac{\alpha_i(\alpha_0 - \alpha_i)}{\alpha_0^2(\alpha_0 + 1)} \quad (16)$$

This method assumes that the α_{ij} values in the initial probability (which follows the Dirichlet distribution) are estimated by the Dirichlet distribution, so the initial probability is of the form:

$$P(\theta) = \prod_i \frac{\Gamma(\sum_j \alpha_{ij})}{\prod_j \Gamma(\alpha_{ij})} \prod_j P_{ij}^{\alpha_{ij}-1} \quad (17)$$

and the conditional probability of the data given the parameters of the model is of the form:

$$P(D|\theta) = P(x_1) \prod_i \prod_j P_{ij}^{n_{ij}} \quad (18)$$

and the probability of the model data is in the form:

$$P(D) = \int P(D|\theta)\, P(\theta)\, d\theta \quad (19)$$

substituting equation (17) and equation (18) into equation (19), we get:

$$P(D) = \int P(x_1) \prod_i \prod_j P_{ij}^{n_{ij}} \prod_i \frac{\Gamma(\sum_j \alpha_{ij})}{\prod_j \Gamma(\alpha_{ij})} \prod_j P_{ij}^{\alpha_{ij}-1} d\theta$$

since

$$\int \prod_j P_{ij}^{n_{ij}+\alpha_{ij}-1}\, d\theta = \frac{\prod_j \Gamma(n_{ij}+\alpha_{ij})}{\Gamma(\sum_j (n_{ij}+\alpha_{ij}))}$$

$$P(D) = P(x_1) \prod_i \frac{\Gamma(\sum_j \alpha_{ij}) \prod_j \Gamma(n_{ij}+\alpha_{ij})}{\prod_j \Gamma(\alpha_{ij}) \Gamma(\sum_j (n_{ij}+\alpha_{ij}))} \quad (20)$$

The subsequent distribution of the proposed method in estimating the transition probabilities matrix is obtained by substituting equation (17), equation (18), and equation (20) into equation (13), we get:

$$P(\theta|D) = \prod_i \prod_j P_{ij}^{n_{ij}+\alpha_{ij}-1} \frac{\Gamma(\sum_j (n_{ij}+\alpha_{ij}))}{\prod_j \Gamma(n_{ij}+\alpha_{ij})} \quad (21)$$

Equation (10) represents the subsequent distribution of the proposed method in estimating the transition probabilities matrix, and by analogy with equation (10) to the Dirichlet distribution with parameters $(n_{ij} + \alpha_{ij})$ and therefore the rate and variance of the subsequent distribution is:

$$E[P_{ij}] = \frac{n_{ij}+\alpha_{ij}}{\sum_j (n_{ij}+\alpha_{ij})} \quad (22)$$

$$Var[P_{ij}] = \frac{(n_{ij}+\alpha_{ij})(\sum_j (n_{ij}+\alpha_{ij}) - (n_{ij}+\alpha_{ij}))}{(\sum_j (n_{ij}+\alpha_{ij}))^2 (\sum_j (n_{ij}+\alpha_{ij})+1)} \quad (23)$$

When the value of α_{ij} approaches the value of n_{ij}, therefore, the variance of the proposed method approaches from the variation of the method of greatest possibility MLE, and it is in the form[8]:

$$Var[P_{ij}] = \frac{2n_{ij}\,(2n_{i.} - 2n_{ij})}{(2n_{i.})^2\,(2n_{i.}+1)} \quad (24)$$

Therefore, then the proposed method estimator for the Markov chain transition matrix is:

$$P_{ij}^{(\hat{\alpha})} = \frac{n_{ij} + \alpha_{ij}}{\sum_j (n_{ij} + \alpha_{ij})} \quad (25)$$

It has been proposed to use two methods to estimate the Dirichlet distribution parameter α_{ij} , the first is traditional and the second is intelligent, as follows:

2.3.1 *Estimation of α_{ij} using MLE*

Let's have the variables $x_i = \{x_1, x_2, \dots, x_k\}$, and the distribution parameters $\alpha_i = \{\alpha_1, \alpha_2, \dots, \alpha_k\}$ So the Dirichlet distribution function is of the form[11]:

$$f(x;\alpha) = \frac{\Gamma(\sum_{i=1}^k \alpha_i)}{\prod_{i=1}^k \Gamma(\alpha_i)} \prod_{i=1}^k x_i^{\alpha_i - 1}$$

The possibility function for this distribution is:

$$L = \frac{\left[\Gamma(\sum_{i=1}^k \alpha_i)\right]^N}{\left[\prod_{i=1}^k \Gamma(\alpha_i)\right]^N} \prod_{i,j}^N x_{i,j}^{\alpha_i - 1} \quad (26)$$

and by maximizing equation (15) by taking the natural logarithm, we get:

$$\ln L = N\, \ln\left(\Gamma(\sum_{i=1}^k \alpha_i)\right) - N\, \ln\left(\prod_{i=1}^k \Gamma(\alpha_i)\right) + N \sum_{i=1}^k (\alpha_i - 1)\, \ln x_i \quad (27)$$

and by taking the derivative of equation (16) with respect to α_i , we get:

$$\frac{d\ln L}{d\alpha_i} = N\frac{d\ln\left(\Gamma(\sum_{i=1}^{k}\alpha_i)\right)}{d\alpha_i} - N\frac{d\ln\left(\prod_{i=1}^{k}\Gamma(\alpha_i)\right)}{d\alpha_i} + N\sum_{i=1}^{k}\frac{d((\alpha_i-1)\ln x_i)}{d\alpha_i} \quad (28)$$

Equation (28) is an equation for estimating the values of α_{ij} using the Maximum Likelihood estimator method, and a program in R language has been used to estimate the parameter $\hat{\alpha}_{ij}$.

2.3.2 *Estimation of α_{ij} using PSO*

The (PSO) algorithm was proposed in 1995 by researchers James Kennedy and Russel Eberhart to solve the unconstrained continuous improvement problem [12].

The particle swarm algorithm is inspired by biological examples of the natural and collective behavior of a community of animals, insects, and creatures that live in groups, such as wasps, bees, termites, and geese, and from the animal community, groups of fish and flocks of birds. Swarm intelligence is used to describe systems to achieve an optimal state, whereby decisions in a swarm are made decentralized by individuals on the basis of information obtained from their environment [13].

The PSO algorithm aims to find the optimal solution by repeatedly updating the position and speed of each particle based on the movement of the particles in the swarm. The basis for the work of this algorithm is the particles, as it simulates the natural behavior of swarms of particles in a computer program, where the particles are initially configured and each of these particles has its own speed and position, and those particles fly in the search space, and the speed of the particles is modified by controlling their current location and speed, and they are updated in each iteration of the algorithm, so those particles have a tendency to fly towards the best solution in the search space, and the update equations for the particle position and speed are as follows:

$$V_i^{t+1} = \omega V_i^t + c_1 r_1(P_{best} - X_i^t) + c_2 r_2(g_{best} - X_i^t) \quad (29)$$

$$X_i^{t+1} = X_i^t + V_i^{t+1} \quad (30)$$

where: $X_i^0 \sim U(X_{Min}, X_{Max})$

that is

$$X_i^0 = X_{Min} + r_i(X_{Max} - X_{Min}) \ , \ r_i \sim U(0,1) \quad (31)$$

where that

V_i^{t+1} : is the particle speed at k repetitions

X_i^{t+1}: the particle position at k repetitions

ω : is a positive constant representing the inertial weight

c_1, c_2 : Acceleration coefficients regulate how far a particle can move in one repetition

r_1, r_2: Random numbers from the regular distribution

So the main steps of the PSO algorithm can be summarized as follows:

- Initializing the position by assigning a random position to each particle
- Computing an appropriate value for each particle within the swarm
- The local best position is updated if it is better than the previous
- The global best position is updated if it is better than the previous one
- Calculate the speed of each particle using equation (29)
- Update the particle position using equation (30)
- Steps (2-6) are repeated until the completion condition is met

3. Discuss the results

Bioinformatics is widely used in the study of the genomes of living organisms in the determination of Deoxyribonucleic acid DNA sequences. And that the science of bioinformatics depends on each of the sciences of statistics, mathematics, computer, chemistry and medicine in data analysis. Bioinformatics was used to determine Deoxyribonucleic acid DNA sequences, and nucleic acid is a complex chemical compound responsible for determining genetic traits and is present in all living organisms. Deoxyribonucleic acid (DNA) is found in the cell nucleus within the chromosomes that consist of the chromatin network. In 1900, deoxyribonucleic acid was defined as a long strand consisting of four nitrogenous bases, which are of two types:

- Purines rules, which are:

a. Adenine and symbolized by the symbol A
b. Guanine and symbolized by the symbol G

- Pyrimidines rules, which are:
  a. Cytosine and symbolized by the symbol C
  b. Thiamin and symbolized by the symbol T

The DNA strand consists of the linking of nitrogenous bases with each other, as thymine binds with adenine, and cytosine binds with guanine. Data for Escherichia Coli (E.Coli) were obtained from the website of the National Center for Biotechnology Information through the link https://www.ncbi.nlm.nih.gov,as this website provides a database that is available For researchers for the purposes of development and scientific research, the gene chain of E.Coli with a length of 1039 nitrogenous bases was chosen as an applied aspect of the study due to its importance in medical research and for the purpose of discovering and manufacturing treatments by knowing the final form of its gene chain.

And using the program prepared for this purpose in the MATLAB R2021a programming language, a matrix of repeats was formed for the E.Coli gene chain, which includes the number of transitions between the four nitrogenous bases.

$$F = \begin{array}{c} \\ A \\ T \\ C \\ G \\ f_{.j} \end{array} \begin{array}{c} \begin{array}{cccc} A & T & C & G \end{array} \\ \begin{bmatrix} 86 & 65 & 68 & 46 \\ 47 & 76 & 42 & 81 \\ 74 & 49 & 65 & 73 \\ 57 & 56 & 86 & 68 \end{bmatrix} \\ \begin{array}{cccc} 264 & 246 & 261 & 268 \end{array} \end{array} \begin{array}{c} f_{i.} \\ 265 \\ 246 \\ 261 \\ 267 \\ N = 1039 \end{array}$$

The E.Coli gene chain was tested under both the null hypothesis and the alternative hypothesis, which states:

H_0: The E.Coli gene chain is not a Markov chain

H_1: The E.Coli gene chain is represents a Markov chain

And that the statistical laboratory that tests whether the E.Coli gene chain represents a Markov chain or not follows χ_n with a degree of freedom $(s-1)^2$, where:

S : represents the number of cases in the iterations matrix

n_{ij}: represents the observation i, j in the iterations matrix

$n_{i.}$: represents the sum of the row in the iterations matrix

$n_{.j}$: represents the sum of the column in the iterations matrix

N : represents the sum of the iterations matrix

By comparing the calculated value of χ_n which is equal to (1361.4) with the value of the tabular χ_n which is equal to (27.88), we reject the null hypothesis and accept the alternative hypothesis, that is, the E.Coli gene chain represents a Markov chain.

Translational probabilities matrix estimation of the E.Coli gene chain

The transitional probabilities matrix of the E.Coli gene chain was estimated using the method of Maximum Likelihood Method and the proposed method of using the PSO algorithm and the MLE method to estimate the values of the parameter $\hat{\alpha}_{ij}$, and the following table shows the elements of the transitional probabilities matrix.

Table (1): Transitional probabilities of the E.Coli gene chain using different estimation methods.

Transition	probability of Transition		
	MLE	Proposed Method (PM)	
		PSO to estimate $\hat{\alpha}_{ij}$	MLE to estimate $\hat{\alpha}_{ij}$
AA	0.3245	0.3225	0.3035
AT	0.2453	0.2460	0.2474
AC	0.2566	0.2573	0.2556
AG	0.1736	0.1743	0.1936
TA	0.1911	0.1918	0.208
TT	0.3089	0.3109	0.2928
TC	0.1707	0.1715	0.1925
TG	0.3293	0.3258	0.3067
CA	0.2835	0.2818	0.2743
CT	0.1877	0.1884	0.2043
CC	0.249	0.2496	0.2497
CG	0.2797	0.2802	0.2716
GA	0.2135	0.2141	0.2237
GT	0.2097	0.2105	0.2209
GC	0.3221	0.3201	0.3015
GG	0.2547	0.2554	0.2539

Table (2): Comparison of the estimation methods used for the transition matrix depending on the minimum of variance.

Transition	Variance of Transition			MOV
	Method			
	MLE	Proposed method (PM)		
		PSO to estimate $\hat{\alpha}_{ij}$	MLE to estimate $\hat{\alpha}_{ij}$	
AA	0.00041282	0.0003907	0.00035739	PM
AT	0.00034862	0.00033167	0.00031481	PM
AC	0.00035924	0.00034169	0.0003217	PM
AG	0.00027016	0.00025738	0.00026392	PM
TA	0.0003135	0.00028806	0.0002885	PM
TT	0.00043306	0.00039811	0.00036258	PM
TC	0.00028719	0.00026403	0.00027214	PM
TG	0.00044797	0.00040816	0.00037233	PM
CA	0.00038841	0.00033898	0.00033837	PM
CT	0.00029157	0.00025607	0.0002763	PM
CC	0.00035759	0.0003137	0.00031848	PM
CG	0.00038521	0.00033775	0.00033628	PM
GA	0.00031385	0.00030031	0.00029229	PM
GT	0.00030981	0.00029664	0.00028967	PM
GC	0.00040813	0.0003885	0.0003545	PM
GG	0.0003548	0.00033944	0.00031888	PM

4. Conclusions

In recent years, the study of Bioinformatics is one of the important topics that researchers have been interested in, especially DNA data. Therefore, the aim of the research was to choose one of the types of E.Coli bacteria as an applied aspect of the research.

A new method was proposed to estimate the transition probabilities matrix by estimating the Dirichlet distribution parameter α_{ij} using the MLE method and the PSO intelligence method, and comparing the results with the Maximum Likelihood Method to estimate the transition probabilities matrix.

It was concluded that the proposed method for estimating the transitional matrix is better than the Maximum Likelihood Method, and the proposed method gave a simpler way to estimate the transitional probabilities matrix using the PSO algorithm.

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تقدير الاحتمالات الانتقالية لسلسلة ماركوف المشاهدة في أوقات عشوائية مع التطبيق

علاء فرحان احمد	مثنى صبحي سليمان
alaa.21csp99@student.uomosul.edu.iq	muthanna.sulaiman@uomosul.edu.iq

قسم الإحصاء والمعلوماتية، كلية علوم الحاسوب والرياضيات، جامعة الموصل، موصل، العراق.

المستخلص

إن مقدرات مصفوفة الاحتمالات الانتقالية لسلسلة ماركوف ليست دقيقة ويتم اعتبار المصفوفة الانتقالية معطاة. هناك العديد من الطرق التي تستخدم لتقدير مصفوفة الاحتمالات الانتقالية لحالات مختلفة، ومن أشهرها طريقة الإمكان الاعظم، ومن أجل إيجاد مقدر جيد وجديد لمصفوفة الاحتمالات الانتقالية لسلسلة ماركوف، تم استخدام طريقة مقترحة وهو اجراء تعديل لطريقة بيز للوصول إلى احتمالات انتقالية بأقل تباين. تفترض هذه الطريقة أن قيم α_{ij} في الاحتمال الأولي يتم تقديرها بطريقتين: طريقة الإمكان الاعظم (MLE)، وخوارزمية سرب الجسيمات (PSO)، وتم اختيار سلسلة الجينات الإشريكية القولونية (E.Coli) كجانب تطبيقي للدراسة نظراً لأهميتها في الأبحاث الطبية ولغرض اكتشاف وتصنيع العلاجات من خلال معرفة الشكل النهائي لسلسلة الجينات الخاصة بها. وبعد اختبار سلسلة جينات E.Coli تبين أنها تمثل سلسلة ماركوف، ومن ثم تم تقدير كل من مصفوفة الاحتمالات الانتقالية وتباين الاحتمالات الانتقالية، وتبين أن الطريقة المقترحة لتقدير الاحتمالات الانتقالية أفضل من طريقة الإمكان الأعظم بالاعتماد على التباين.

معلومات البحث

تواريخ البحث:

تاريخ تقديم البحث: 25/2/2024
تاريخ قبول البحث: 12/4/2024
تاريخ رفع البحث على الموقع: 31/12/2024

الكلمات المفتاحية:

الاحتمالات الانتقالية، سلسلة ماركوف، MLE، بيز، PSO، DNA.

للمراسلة:

د. مثنى صبحي سليمان
muthanna.sulaiman@uomosul.edu.iq

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