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The Time Evolution of the Random Genetic Drift Equation and the Computational Proof of Galton's Theory

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Abstract: This paper focuses in studying the genetic diffusion process of a finite population in the absence of mutation, migration and immigration. In this paper, we aim to numerically solve the modified Kimura model in order to mathematically and computationally prove the Galton's theory of hereditary genius. There are two steps to the proof. Assuming that the number of diploid individuals varies randomly over generations is the first step. In the second step, the classical random genetic drift equation with selection is extended to the time-fractional random genetic drift equation to include the memory effect on the diffusion process. The fourth order compact finite difference is implemented to derive the approximate solutions of the studied partial differential equation. For the purpose of determining the discrete scheme of the time-fractional operator, the Grünwald-Letnikov scheme is implemented. The simulations of the approximate solutions, the stationary approximate solution, the stability of the difference scheme and the total sum of the approximate solutions are all calculated and interpreted computationally. The discrete convergence of the approximate solutions is numerically studied and its asymptotic behaviors are compared with the Mittag-Leffler function.

Keywords: Random genetic drift equation with selection, fourth order compact finite difference method, Grünwald- Letnikov scheme, Caputo-time fractional operator, Galton's theory of genius inheritance, random number of individuals.

1 Introduction

The history book of any individual is carried on his, or its, DNA as it carries the genetic inheritance of the individual. The population genetics is the genetic study whose aim is to interpret the factors influencing the population genetic variables. The changes of genes of populations or species are scientifically affected by many factors such as mutation, natural selection, immigration and emigration. The first big steps on this field are done by the following pioneer researchers: Darwin [1], Gregor Mendel [2], Francis Galton [3], William Bateson [4], and not finally G. H. Hardy [5]. Francis Galton [3] was the first to apply statistical methods to discuss how intelligence is inherited and how people differ from one another. He got the fact that the Laplace-Gauss distribution, the normal distribution, could be applied to human psychological attributes including intelligence. Galton [3] invented in his book *Hereditary Genius*, the term *positive and negative eugenics*, for families having good talents and families with bad characteristics, respectively. He statistically proved that most of the talents, intelligence, diseases and physical characteristics were inherited from the big families. That means the child inherit his characteristics, that are carried on the DNA, from his parents, grand parents, ancestors and so on. In other words he concluded that the inheritance process has a memory.

Ronald Fisher and Sewall Wright mathematically formulated the genetic evolution and studied the basis for population of genetics. Their works leaded to the known mathematical Wright–Fisher model, *WF model* for genetic drift, see [6] and [7]. Later in (1945), Sewall Wright [8] derived the partial differential equation (pde) describing the distribution of the gene

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frequencies among populations under the interaction of the natural selection, mutation, migration and genetic random drift, see [9] and [10].

Feller [11,12] is also one of the pioneers of the genetic diffusion studies. He built his mathematical model on the simple Markov branching process. As a mathematical consequence of Mendelian inheritance, Haldane re-established the contribution of the natural selection on the genetic diffusion, see [13],[14] and [15].

Kimura derived the classical pde being mathematically modelled the diffusion process with selection by using the discrete Markov transition probabilities and Kolmogorov forward equation, see [16], [17], [18] and [19]. He assumed a fixed finite population.

Hossjer et. al. [20] studied the analytical solution of the diffusion equation of the WF model with one-way mutation rate and with no selection, by implementing the Kolmogorov forward equation or the Fokker–Planck equation [18].

Zhao et. al. [21] numerically discussed the classical diffusion equation of random genetic till the fifth generation by implementing the finite volume method.

The history of the inheritance process was not discussed in any of the old or new literatures, which focused only on the traditional case in which children inherit their traits (genes) from their parents, see WF model [6,7]. Most of the literature also fix the number of individuals in all the successive generations. Therefore, the studied pde are far away from the real life problem. As in the real life problem the offspring, the new born individual, may have a physical character or a talent that is not one of his parents characteristics and exist on his grandparents or ancestors, etc.. Also the number of individuals are changed randomly through generations. That is because the pioneer researchers studied only the continuous Markov process that is mathematically modelled in the classical genetic drift pdes of Markov-Type with non constant coefficients. Kimura, [18], [19] and [22] , studied the influences of the selection on the genetic diffusion process. He mathematically formulated the genetic diffusion with two allele A and a in which they take part with respective frequencies x and $1-x$. It is also assumed that the population size N of the diploid adults is large and *constant* and there is no generational overlap. It is supposed that $u(p,x;t)$ be the conditional probability with the initial frequency p at $t=0$. $u(p,x;t)$ represents the transition probability that the gene will move from p to x after t time, namely

$$\frac{\partial u(p,x;t)}{\partial t} = \frac{1}{2}\frac{\partial^2}{\partial x^2}\{V(x,t)u(p,x;t)\} - \frac{\partial}{\partial x}\{M(x,t)u(p,x;t)\}\,. \tag{1}$$

This equation is subjected to the initial condition

$$u(p,x;0) = \delta(x-p). \tag{2}$$

If p is fixed, $u(p,x;t) \approx u(x,t)$. In other words, the conditional probability of finding allele A with frequency x, $0<x<1$, is represented by $u(x,t)$ at the generation t, $t \in \mathbb{N}$, and it must satisfy

$$\int_0^1 u(x,t)dx = 1\ , \tag{3}$$

at any generation t.

The points $x=0,1$ are lateral singular points. Assuming the general case of Zygotic natural selection by letting s and $s\varepsilon$ to be the selective advantages of the mutant homo-zygote AA and the hetero-zygote aa. Here s is the selective rate and ε represents the mutation rate. Then the general average rate of change in x per generation of the selective advantage on the random mating of A and a alleles is represented by

$$M(\Delta x) = sx(1-x)(x+\varepsilon(1-2x))\,. \tag{4}$$

The values $s=\{0,0.5,1\}$ in equation (4) represent the no dominant, the semi dominant and the fully dominant cases, respectively. Kimura assumed that the diploid population consisting of fixed N_e individuals (genes) at any generation t. That means there are N_e of genes at each locus. The only constraint imposed on s is that $|sN_e| \le 1$, see [21]. This condition means that the selection effect is weak. For the semi dominant case, i.e. $\varepsilon = 0.5$, the drift term is represented by

$$M(x,t) = \frac{1}{2}sx(1-x)\,, \tag{5}$$

while the fully dominant case is represented by

$$M(x,t) = sx(1-x)^2\,. \tag{6}$$

The variance of the change in gene frequency $V(x,t)$ is defined as

$$V(x,t) = \frac{x(1-x)}{2N_e}\,, \tag{7}$$

then the classical genetic drift equation (gde) with fixed number of individuals (Kimura model) reads

$$\frac{\partial u(p,x;t)}{\partial t} = \frac{1}{4N_e(t)}\frac{\partial^2}{\partial x^2}\{x(1-x)u(p,x;t)\} - s\frac{\partial}{\partial x}\{x(1-x)u(p,x;t)\}\,. \tag{8}$$

The explicit approximate solutions of this model represent the conditional probability of obtaining the studied allele with specific frequency at a certain generation. According to the condition (3), the summation of the approximate solution must be one at any number of generation. Abdel-Rehim et. al. [23] computationally proved by using the finite difference method (*FDM*) that the solutions of the Markov-Type genetic equations loose this property on the long Run. The sum of the approximate solution of the classical diffusion genetic with fixed number of individuals, N_e is plotted at Fig[1]. The biologists explain this phenomenon by the occurring of sudden death of the individuals of the community, the huge migration or the huge immigration. All these factors can have effects on the diffusion of the genes but it takes many years.

Our aim in this paper is to solve this problem by modifying the classical equation (8) to make it more reality. We aim also to maintain the normalization condition (3). In other words the approximate solution must maintain the conservation of the probability to be sure that nothing flow out through the lateral points. Unfixing the number of individuals to make it randomly varies through generations is the first step. The classical random gde with random individuals number reads

$$\frac{\partial u(p,x;t)}{\partial t} = \frac{1}{4N_e(t)}\frac{\partial^2}{\partial x^2}\{x(1-x)u(p,x;t)\} - \frac{s_1}{N_e(t)}\frac{\partial}{\partial x}\{x(1-x)u(p,x;t)\}\,. \tag{9}$$

Here s_1 is the random selection. We aim also to computationally prove the Galton's theory. To do so, one has to replace the first order time derivative operator $\frac{\partial}{\partial t}$ at equation (9) by the Caputo time–fractional operator as

$${}^{\mathrm{C}}_{0}\mathrm{D}^{\beta}_{t}\,u(x,t) = \frac{1}{4N_e(t)}\frac{\partial^2}{\partial x^2}\{x(1-x)u\} - \frac{s_1}{N_e(t)}\frac{\partial}{\partial x}\{x(1-x)u\}\,,0<\beta<1\,,0<x<1\,. \tag{10}$$

The Caputo-time derivative operator reflects the memory of the stochastic processes. The memory-dependent processes are called the *Non-Markov processes* and the time–fractional Caputo derivative operator of order β reads

$${}^{\mathrm{C}}_{0}\mathrm{D}^{\beta}_{t}\,f(t) = \begin{cases} \frac{1}{\Gamma(m-\beta)}\{\int_0^t f^{(m)}(\tau)K_\beta(t-\tau)d\tau\} & \text{for } m-1<\beta<m\,, \\ \frac{d^m}{dt^m}f(t) & \text{for } \beta=m\,, \end{cases} \tag{11}$$

where the kernel

$$K_\beta(t-\tau) = \frac{(t-\tau)^{\beta+1-m}}{\Gamma(m-\beta)}\,,$$

is called the memory function and it is responsible for reflecting the memories of several physical, biological, etc. , processes [24]. For further information about time–fractional Caputo operator and its relation to the Riemann-Liouville Integral operators, see also [25].

D. Baleanu et. al. [26] introduced a new and general Caputo fractional derivative ${}^{C}_{t}\mathrm{D}^{\beta}_{T}f(t)$ to investigate the complex behaviours of a capacitor microphone dynamical system that reads

$${}^{C}_{t}\mathrm{D}^{\beta}_{T}f(t) = \int_t^T f'(\tau)K_\beta(t-\tau)d\tau\,, \tag{12}$$

where

$$K_\beta(t-\tau) = \sum_{k=1}^{n} a_k\frac{(t-\tau)^{-\beta_k}}{\Gamma(1-\beta_k)}\,,\ 0<\beta_1<\cdots<\beta_n<1\,.$$

The general Caputo fractional formulation has also been used successfully to investigate the asymptotic behavior of immunogenic tumor dynamics, see [27]. A new mathematical model of cholera disease including the general form of the Caputo fractional operator was recently studied by the same research group [28].

Abdel-Rehim et. al. [23], studied the time-fractional genetic diffusion models with fixed number of individuals by using the common rules of the *FDM* besides the Grünwald- Letnikov scheme. In this paper, the fourth-order compact finite difference method *FOCFDM* is used to get more accurate approximate solutions. The FOCFDM has been successfully implemented to solve numerically lots of pdes, specially those with non constant coefficients, i.e. the diffusion convection pdes. The stability of all the studied schemes will be investigated by implementing the matrix method.

Therefore, the paper is organized as follows: section 1 is devoted to the introduction. Section 2, is devoted to derive the approximate solutions of the classical random genetic diffusion equation with fixed N_e by FOCFDM. Section 3 is devoted to derive the approximate solution corresponds to unfixed number of genes $N_e(t)$. Section 4 is to prove the Galton's Theory by implementing the Grüwald-letnikov scheme. In section 5, the stationary approximate solution, the reversibility property are driven. The discrete convergence is estimated and compared with the Mittag-Leffler function for different values of the fractional order β. In section 6, simulations of the time evolution of the studied model's approximations are given and interpreted for different values of the time-fractional order β.

2 The Approximate Solutions of the Classical GDE with Constant Number of Individuals by the FOCFDM

In this section, we begin by driving the difference scheme of the gde (8) in which the population is consisting of a fixed number of individuals at any generation. Therefore, let $N_e(t=0)=N_e^{(0)}=N_e$. Define the grids of the independent variables (x,t) as

$$x_j = jh,\ h>0,\ j\in\mathbb{N}\,, \tag{13}$$

where $j\in(2,R-2)$, $h=\frac{1}{R-2}$ and $R\in\mathbb{N}$. Let the time grid be $\tau>0$ and

$$t_n = n\tau,\ \tau>0,\ n\in\mathbb{N}_0\,. \tag{14}$$

Introduce the clump $y^{(n)}$ as

$$y^{(n)} = \{y_2^{(n)},\cdots,y_{R-2}^{(n)}\}^T\,, \tag{15}$$

where $y^{(n)}=y(t_n)$ represents the discrete probability column vector to find the A allele with frequency x_j at generation t_n. This choice makes us avoid the lateral frequencies, $(x=0,x=1)$, to be sure that there is out flow of the probability. The initial value $y^{(0)}$ must satisfy $\sum_{j=2}^{R-2} y_j^{(0)}=1$, $\forall n\in\mathbb{N}_0$, see [29]. Regarding the initial condition (2), let p is fixed at $p=0.5$. That means each one of the random mating couple is carrying half the initial number of genes N_e. Therefore, $y^{(0)}$ reads

$$y^{(0)} = \{0\cdots,1,\cdots,0\}^T\,. \tag{16}$$

To derive the boundary conditions, substitute $x=0$ and $x=1$ at equation (9), one gets

$$\frac{\partial u(0,t)}{\partial t} = \frac{\partial u(1,t)}{\partial t} = 0\,,$$

and let $f(t)$ and $g(t)$ be any functions. Then one can generally write $u(0,t)=f(t)$ and $u(1,t)=g(t)$. In this paper, we numerically investigate the Kimura model, in which he assumed the boundary conditions

$$u(0,t)=u(1,t)=0\,. \tag{17}$$

We derive the approximate solutions $y_j^{(n)}$ for $2\le j\le R-2$, as we are interested only on the frequencies $0<x<1$.

The FOCFDM approximately approaches the exact solutions of the diffusion equations than by using the common FDM. The basic idea of the FOCFDM is that more nodes are added and smaller mesh mesh sizes are defined to get more exact numerical results. Turkel and Singer [30], defined fixed grid sizes to improve high-order compact finite difference schemes to calculate more better solutions. In order to simplify the implementation of the central difference schemes and facilitate accurate solution of convection-diffusion equations, the FOCFDM is later discussed in [31]. For further information on the benefits and drawbacks of the compact finite difference methods, see [32], [33], [34], [35] and [36]. It is known that the first $\delta_x y_j^{(n)}$ and the second $\delta_x^2 y_j^{(n)}$ classical spatial discrete central finite difference operators are defined as

$$\delta_x y_j^{(n)} = \frac{y_{j+1}^{(n)}-y_{j-1}^{(n)}}{2h},\ \delta_x^2 y_j^{(n)} = \frac{y_{j+1}^{(n)}-2y_j^{(n)}+y_{j-1}^{(n)}}{h^2}\,. \tag{18}$$

To implement the FOCFDM, one has to use 1st derivative operator that is defined as, see [31,34],

$$\left(\frac{\partial y}{\partial x}\right)_j^{(n)} = \frac{\delta_x y_j^{(n)}}{2h(1+\frac{1}{6}\delta_x^2)}\,, \tag{19}$$

and the 2nd derivative operator is defined as

$$(\frac{\partial^2 y}{\partial x^2})_j^{(n)} = \frac{\delta_x^2 y_j^{(n)}}{h^2(1+\frac{1}{12}\delta_x^2)} . \tag{20}$$

To implement the FOCFDM on the random gde (8) of fixed number of individuals, rewrite equation (8) as

$$\frac{y_j^{(n+1)} - y_j^{(n)}}{\tau} = \frac{1}{4N_e}\frac{\delta_x^2[x(1-x)y_j^{(n)}]}{h^2(1+\frac{1}{12}\delta_x^2)} - s\frac{\delta_x[x(1-x)y_j^{(n)}]}{2h(1+\frac{1}{6}\delta_x^2)} . \tag{21}$$

Then apply $(1+\frac{1}{12}\delta_x^2)$ to both sides of equation (21), to get

$$(1+\frac{1}{12}\delta_x^2)(y_j^{(n+1)} - y_j^{(n)}) = \frac{\tau}{4N_e h^2}\delta_x^2[x(1-x)y_j^{(n)}] - \frac{s\tau}{2h}\frac{(1+\frac{1}{12}\delta_x^2)(\delta_x[x(1-x)y_j^{(n)}])}{(1+\frac{1}{6}\delta_x^2)} , \tag{22}$$

and apply $\delta_x y_j^{(n)}$, and $\delta_x^2 y_j^{(n)}$ defined in equation (18), to get

$$\begin{aligned}
&\frac{5}{6}y_j^{(n+1)} + \frac{1}{12}y_{j-1}^{(n+1)} + \frac{1}{12}y_{j+1}^{(n+1)} - (\frac{5}{6} - \frac{2x_j(1-x_j)\tau}{4N_e h^2})y_j^{(n)} - (\frac{1}{12} + \frac{x_{j-1}(1-x_{j-1})\tau}{4N_e h^2})y_{j-1}^{(n)} \\
&-(\frac{1}{12} + \frac{x_{j+1}(1-x_{j+1})\tau}{4N_e h^2})y_{j+1}^{(n)} = \frac{-s\tau}{2h(1+\frac{1}{6}\delta_x^2)}\{[\frac{5}{6}x_{j+1}(1-x_{j+1})]y_{j+1}^{(n)} - [\frac{5}{6}x_{j-1}(1-x_{j-1})]y_{j-1}^{(n)} \\
&\qquad + [\frac{1}{12}x_{j+2}(1-x_{j+2})]y_{j+2}^{(n)} - [\frac{1}{12}x_{j-2}(1-x_{j-2})]y_{j-2}^{(n)}\} + O(h^4+\tau) .
\end{aligned} \tag{23}$$

Again apply operator $(1+\frac{1}{6}\delta_x^2)$ to both sides of equation (23), and use the central difference operators $\delta_x y_j^{(n)}$, and $\delta_x^2 y_j^{(n)}$, to get

$$\begin{aligned}
&[\frac{7}{12}y_j^{(n+1)} + \frac{7}{36}y_{j-1}^{(n+1)} + \frac{7}{36}y_{j+1}^{(n+1)} + \frac{1}{72}y_{j-2}^{(n+1)} + \frac{1}{72}y_{j+2}^{(n+1)}] = [\frac{7}{12} - \frac{\mu j}{4RN_e}(1-\frac{j}{R})]y_j^{(n)} + [\frac{7}{36} + \\
&(\frac{\mu}{12N_e} + \frac{5sh\mu}{12})(\frac{j-1}{R})(1-\frac{j-1}{R})]y_{j-1}^{(n)} + [\frac{7}{36} + (\frac{\mu}{12N_e} - \frac{5sh\mu}{12})(\frac{j+1}{R})(1-\frac{j+1}{R})]y_{j+1}^{(n)} + [\frac{1}{72} + \\
&(\frac{\mu}{24N_e} + \frac{sh\mu}{24})(\frac{j-2}{R})(1-\frac{j-2}{R})]y_{j-2}^{(n)} + [\frac{1}{72} + (\frac{\mu}{24N_e} - \frac{sh\mu}{24})(\frac{j+2}{R})(1-\frac{j+2}{R})]y_{j+2}^{(n)} + O(h^4+\tau) ,
\end{aligned} \tag{24}$$

where μ is the scaling relation being defined as $\mu = \frac{\tau}{h^2}$. The non-negativity condition of equation (24) requires that

$$0 < \mu \le \frac{7N_e}{3\max[jh(1-jh)]} = \frac{28N_e}{3} , \tag{25}$$

and to get a good result of the term $\max[jh(1-jh)]$, one has to choose the mid point $jh = \frac{r}{2}\times\frac{1}{r} = \frac{1}{2}$. In other words, $\max[jh(1-jh)]$ is replaced by $\frac{1}{4}$. At the program code, the population size is fixed at $N_e = 100$. This means the scaling parameter fulfills the condition

$$0 < \mu \le \frac{2800}{3} . \tag{26}$$

Again, rewrite equation (24) in the matrix form as

$$K^T . y^{(n+1)} = P^T . y^{(n)} , n \ge 0 , 2 \le j \le R-2 , \tag{27}$$

where $P = (p_{ij})$, $K = (k_{ij})$ are $R-2 \times R-2$ fifth-diagonal matrices with $i, j = 2, \ldots, R-2$ and are respectively defined as follows

$$P_{ij} = \begin{cases}
P_{ij}^{(1)} = \frac{1}{72} + (\frac{\mu}{24N_e} + \frac{sh\mu}{24})(\frac{j-2}{R})(1-\frac{j-2}{R}), & i = j-2, j = 2, \cdots, R-2 \\
P_{ij}^{(2)} = \frac{7}{36} + (\frac{\mu}{12N_e} + \frac{5sh\mu}{12})(\frac{j-1}{R})(1-\frac{j-1}{R}), & i = j-1, j = 2, \cdots, R-2 \\
P_{ij}^{(3)} = \frac{7}{12} - \frac{\mu j}{4RN_e}(1-\frac{j}{R}), & i = j, j = 2, \cdots, R-2 \\
P_{ij}^{(4)} = \frac{7}{36} + (\frac{\mu}{12N_e} - \frac{5sh\mu}{12})(\frac{j+1}{R})(1-\frac{j+1}{R}), & i = j+1, j = 2, \cdots, R-2 \\
P_{ij}^{(5)} = \frac{1}{72} + (\frac{\mu}{24N_e} - \frac{sh\mu}{24})(\frac{j+2}{R})(1-\frac{j+2}{R}), & i = j+2, j = 2, \cdots, R-2 ,
\end{cases} \tag{28}$$

and

$$K_{ij}=\begin{cases}K_{ij}^{(1)}=\frac{1}{72}, & i=j-2,\, j=2,\cdots,R-2\\ K_{ij}^{(2)}=\frac{7}{36}, & i=j-1,\, j=2,\cdots,R-2\\ K_{ij}^{(3)}=\frac{7}{12}, & i=j,\, j=2,\cdots,R-2\\ K_{ij}^{(4)}=\frac{7}{36}, & i=j+1,\, j=2,\cdots,R-2\\ K_{ij}^{(5)}=\frac{1}{72}, & i=j+2,\, j=2,\cdots,R-2\ .\end{cases} \tag{29}$$

The sum of all the rows of the matrix $(P.K^{-1})$ is 1 proving once more that it is a stochastic matrix. With the aid of the scaling relation condition (25) and equation (26), the matrix P is an M-Matrix and a non-negative diagonally dominating matrix. Therefore the obtained approximate solutions are stable, see [37] and [38]. It is recommended to transpose each side of equation (27) for computation purposes, to get

$$z^{(n+1)}=\left(z^{(n)}.P\right).K^{-1}, n\geq 0, 2\leq j\leq R-2. \tag{30}$$

It is more suitable for the numerical calculation, by Mathematica soft ware, to write the matrix $P^T=(K^T+\mu H^T)$, then equation (27), is rewritten as

$$K^T.y^{(n+1)}=(K^T+\mu H^T).y^{(n)}, 2\leq j\leq R-2, \tag{31}$$

where H is $R-2\times R-2$ fifth diagonal matrix H defined as

$$H_{ij}=\begin{cases}H_{ij}^{(1)}=(\frac{1}{24N_e}+\frac{sh}{24})(\frac{j-2}{R})(1-\frac{j-2}{R}), & i=j-2,\, j=2,\cdots,R-2\\ H_{ij}^{(2)}=(\frac{1}{12N_e}+\frac{5sh}{12})(\frac{j-1}{R})(1-\frac{j-1}{R}), & i=j-2,\, j=2,\cdots,R-2\\ H_{ij}^{(3)}=-\frac{j}{4RN_e}(1-\frac{j}{R}), & i=j,\, j=2,\cdots,R-2\\ H_{ij}^{(4)}=(\frac{1}{12N_e}-\frac{5sh}{12})(\frac{j+1}{R})(1-\frac{j+1}{R}), & i=j+1,\, j=2,\cdots,R-2\\ H_{ij}^{(5)}=(\frac{1}{24N_e}-\frac{sh}{24})(\frac{j+2}{R})(1-\frac{j+2}{R}), & i=j+2,\, j=2,\cdots,R-2\ .\end{cases} \tag{32}$$

Then (30) is rewritten as

$$z^{(n+1)}=z^{(n)}.\left(I+\mu H.K^{-1}\right), 2\leq j\leq R-2, n\geq 0, \tag{33}$$

where I is $R-2\times R-2$ unit matrix. The $H.K^{-1}$ matrix has the property that the sum of all of its rows is zero.

The matrix method is used to prove the stability of the matrix equation (30). To do so, let us calculate the infinity norm of the matrix $(I+\mu H.K^{-1})$, which is defined as

$$||(I+\mu H.K^{-1})||_\infty=\max_{1\leq i\leq j}\sum_{j=2}^{R-2}|(I+\mu H.K^{-1})|_{i,j}\ .$$

For all the values of the matrix $(I+\mu H.K^{-1})$ to be positive, one has to be sure that he uses the scaling relation (26). Then constitute a vector row η whose length is $R-2$ elements and is defined as

$$\eta=\{1,\cdots,1,\cdots,1\}\ ,\ 0=\{0,\cdots,0,\cdots,0\}\ . \tag{34}$$

The row vector η is called the good vector. It is widely used in the theory of the stochastic processes. It satisfies with the stochastic matrix $(I+\mu H.K^{-1})$ that $\eta.(I+\mu H.K^{-1})=\eta$. This is natural as the matrix $(I+\mu H.K^{-1})$ represents the transition probabilities of a Markov chain, see [17]. Also $\eta.(H.K^{-1})=0$, in other words, the summation over the rows of the matrix $(H.K^{-1})$ is zero because its elements represent the diffusion process.

Suppose that the spectral radius of the matrix $(I+\mu H.K^{-1})^T.(I+\mu H.K^{-1})$ is ρ. By using MATHEMATICA, one can easily calculate the set of eigenvalues $\{\lambda\}$ of the matrix $(I+\mu H.K^{-1})^T.(I+\mu H.K^{-1})$ and one gets

$$||(I+\mu H.K^{-1})||_2=\sqrt{\rho((I+\mu H.K^{-1})^T.(I+\mu H.K^{-1}))}=\lambda_{\max}=1$$

Then the matrix $(I+\mu H.K^{-1})$ is stable and henceforth its corresponding approximate solution is stable. For more details about the conservative schemes, see [37] and [38] .

In the section (6), the time evolution of the approximate solution of the genetic diffusion with drift solution for successive generations are simulated and compared, and the $\sum_{j=2}^{R-2} y_j^{(n)}\, n \in \mathbb{N}_0$ is also plotted in Fig[1]. The figure shows that there is a loss of unity as $t >> 1$, for this Markov case. While $y^{(n)}$ should represent the conditional probability of finding the specific allele at the generation t with frequency x and $0 < x < 1$. Therefore its $\sum_{j=2}^{R-2} y_j^{(n)}\, n \in \mathbb{N}_0$ must be one at any t_n. According to Biologists, dramatic death, migration and immigration may responsible about this loose. In the next sections, we mathematically try to solve this still open problem by firstly randomly change the number of individuals at any generations and secondly use the time-fractional operator.

3 Discretization of the Classical Random GDE with Variable Number of Genes Using the FOCFDM

The discrete scheme of equation (9) is derived in this section. Equation (9) represents the genetic drift with the number of individuals randomly varies through generations. To imitate the natural random genetic diffusion, it is important to have random variable number of individuals $N_e(t)$ at any generation. Since $|sN_e(t)| \leq 1$, i.e. $s \leq \frac{1}{N_e(t)}$, then the selection rate will also be randomly changed from generation to generation. Generate λ_1, λ_2 as two uniform random variables representing two successive rates of growth in the population at any generation. Then the random average number of increasing is $m_i = \frac{1}{\lambda_i}\, , i = 1,2$. For more details about the stochastic processes, see [17]. Now, suppose $N_e(t=0) = N_e^{(0)} = N_e$, then generate

$$N_e(t) = N_e^{(n)} = \text{Random Integer} \in [N_e^{(n-1)}, N_e^{(n-1)} + m_r]\, , n \geq 1\, , \tag{35}$$

where $m_r = \text{Random Integer} \in (\frac{1}{\lambda_1}, \frac{1}{\lambda_2})$. To implement the FOCFDM on the random gde (9) having random number of individuals, rewrite equation (9) as

$$\frac{y_j^{(n+1)} - y_j^{(n)}}{\tau} = \frac{1}{4N_e^{(n)}} \frac{\delta_x^2[x(1-x)y_j^{(n)}]}{h^2(1+\frac{1}{12}\delta_x^2)} - \frac{s_1}{N_e^{(n)}} \frac{\delta_x[x(1-x)y_j^{(n)}]}{2h(1+\frac{1}{6}\delta_x^2)}\, . \tag{36}$$

Then apply $(1+\frac{1}{12}\delta_x^2)$ to both sides of equation (36), and then apply operator $(1+\frac{1}{6}\delta_x^2)$ to the resultant equation. Rearrange the result and solve for $y^{(n+1)}$, to have

$$K^T.y^{(n+1)} = (K^T + \frac{\mu}{N_e^{(n)}} H^T).y^{(n)}\, , n \geq 0\, , 2 \leq j \leq R-2\, , \tag{37}$$

where the Matrix K is the same defined matrix at equation (29), and the matrix H is defined as

$$H_{ij} = \begin{cases} H_{ij}^{(1)} = (\frac{1}{24} + \frac{s_1 h}{24})(\frac{j-2}{R})(1-\frac{j-2}{R}), & i = j-2,\, j = 2,\cdots,R-2 \\ H_{ij}^{(2)} = (\frac{1}{12} + \frac{5s_1 h}{12})(\frac{j-1}{R})(1-\frac{j-1}{R}), & i = j-1,\, j = 2,\cdots,R-2 \\ H_{ij}^{(3)} = -\frac{j}{4R}(1-\frac{j}{R}), & i = j,\, j = 2,\cdots,R-2 \\ H_{ij}^{(4)} = (\frac{1}{12} - \frac{5s_1 h}{12})(\frac{j+1}{R})(1-\frac{j+1}{R}), & i = j+1,\, j = 2,\cdots,R-2 \\ H_{ij}^{(5)} = (\frac{1}{24} - \frac{s_1 h}{24})(\frac{j+2}{R})(1-\frac{j+2}{R}), & i = j+2,\, j = 2,\cdots,R-2\, . \end{cases} \tag{38}$$

For computational purposes, rewrite the transpose of the matrix equation (37) as

$$z^{(n+1)} = z^{(n)}.\left(I + \frac{\mu}{N_e^{(n)}} H.K^{-1}\right),\, 2 \leq j \leq R-2, n \geq 0\, , \tag{39}$$

where μ is same defined scaling relation and $\eta.(H.K^{-1}) = 0$. This scheme is convergent and stable as $\eta.(I + \frac{\mu}{N_e^{(n)}} H.K^{-1}) = \eta$. furthermore $\sum_{j=2}^{R-2} y_j^{(n)} \to 1\, n \in \mathbb{N}_0$ and is also plotted in Fig[2]. Again the spectral radius of the matrix $(I + \frac{\mu}{N_e^{(n)}} H.K^{-1})^T.(I + \mu H.K^{-1})$ is $\lambda_{\max} = 1$. The matrix $(I + \frac{\mu}{N_e^{(n)}} H.K^{-1})$ is a stochastic matrix as its elements are the transition probabilities of this Markov chain. Henceforth we approximately satisfies the normalization condition (3). In the following step we try to keep $\sum_{j=2}^{R-2} y_j^{(n)} = 1$ at any number of generation and on the long run by adding the effect of the memory on the genetic diffusion process. In the same time, this will prove the Galton's theory

4 Extending the Classical Random GDE and the Computational Proof of Galton's Theory

The simulation of $\sum_{j=2}^{R-2} y_j^{(n)}, n \in \mathbb{N}_0$ of the approximate solution $y^{(n)}$, $n \in \mathbb{N}$, of the previous classical case, along the successive 30 generations of the genetic drift is plotted at Figure [2]. The figure shows that there is still some lose of the unity on the long run. The fundamental reason is that the early pioneer researchers relied on the Markov chain for their mathematical manipulation. The Markov chain is independent of the genetic inheritance history of the human population. Random genetic drift Markov process means that children inherit their characteristics from their parents regardless of whether the parents' characters (genes) come from relatives outside of their own or from their grandparents and ancestors. The reason is that the models of Markov process have an exponential waiting time between each pair of succeeding generations. That means the influence of the earlier generations on the transition of the gene between the parents to their offspring is neglected. Furthermore, the exponential distribution possesses the memoryless property. In other words, the generation t_{n+1} relies only on the generation t_n and not on t_{n-1}, or on any earlier generations.

The mathematical proof is quite simple regarding the L. H. S. of the discrete schemes of the classical genetic equations (8) and (9), in which $\frac{\partial u(x,t)}{\partial t} = \frac{y_j^{(n+1)} - y_j^{(n)}}{\tau}$. Suppose that the approximate solution at the next time step is represented by $y_j^{(n+1)}$. Here $y_j^{(n+1)}$ represents the conditional probability of finding the studied allele at the offspring generation t_{n+1} with frequency $x_j = jh$. The conditional probability at the parents generation is represented by $y_j^{(n)}$. Then to study the genetic history through the family, one needs the grandparents generation, i.e. $y_j^{(n-1)}$, and the grand grandparents generation $y_j^{(n-2)}$ and back in the past till you add $y_j^{(1)}$ and $y_j^{(0)}$. Only the Caputo time-fractional operator (11) reflects the memory of the stochastic processes. So far,the Caputo time–fractional operator must be used in place of the first order time derivative on the studied equations. Researchers have successfully implemented the Caputo time-fractional operator to represent the memory of enormous diffusion processes in many fields. The used Caputo–time fractional operator ${}^{C}_{0}\mathrm{D}_t^{\beta}$ on equation (10) has been applied in modeling many processes in chemistry, physics, medicine, biology, and etc., see [24], and [25] for more details. The Grünwald-Letnikov scheme of the Caputo–time fractional operator reads

$$ {}^{C}_{0}\mathrm{D}_t^{\beta}\, y_j(t_{n+1}) = \tau^{-\beta} \sum_{k=0}^{n+1} (-1)^k \binom{\beta}{k} \left(y_j^{(n+1-k)} - y_j^{(0)} \right), \; 0 < \beta < 1 \, , \; n \geq 1 \, . \tag{40} $$

This scheme has been applied successfully by several authors, see for examples [25], [29], [39] and [40] and the references therein. Applying this Grünwald–Letnikov scheme on equation (10) and rearrange its terms, one gets

$$ \begin{aligned} & y_j^{(n+1)} - \beta y_j^{(n)} - \sum_{m=2}^{n+1} (-1)^m \binom{\beta}{m} y_j^{(n+1-m)} - \sum_{m=0}^{n+1} (-1)^m \binom{\beta}{m} y_j^{(0)} = \\ & \frac{\tau^{\beta}}{4N_e^{(n)} h^2} \frac{\delta_{x^2}(x_j(1-x_j)y_j^{(n)})}{(1+\frac{1}{12}\delta_x^2)} - \frac{s_1}{N_e^{(n)}} \frac{\tau^{\beta}}{2h} \frac{\delta_x(x_j(1-x_j)y_j^{(n)})}{(1+\frac{1}{6}\delta_x^2)} \, , \; n \geq 1 \, . \end{aligned} \tag{41} $$

Let's recall the coefficients $b_n = \sum_{m=0}^{n} (-1)^m \binom{\beta}{m}$, and $c_m = (-1)^{m+1} \binom{\beta}{m}$, which were defined by Gorenflo et. al. [40], in order to satisfy the relation

$$ b_n + \sum_{m=1}^{n} c_m = 1 \, , $$

where $b_0 = c_1 = \beta$. The scaling relation is defined as $\mu = \frac{\tau^{\beta}}{h^2}$, and equation(41), has to be rewritten as

$$ \begin{aligned} & y_j^{(n+1)} - \beta y_j^{(n)} - \sum_{m=2}^{n+1} c_m y_j^{(n+1-m)} - b_n y_j^{(0)} = \frac{\tau^{\beta}}{4N_e^{(n)} h^2} \times \\ & \frac{\delta_{x^2}(x_j(1-x_j)y_j^{(n)})}{(1+\frac{1}{12}\delta_x^2)} - \frac{s_1}{N_e^{(n)}} \frac{\tau^{\beta}}{2h} \frac{\delta_x(x_j(1-x_j)y_j^{(n)})}{(1+\frac{1}{6}\delta_x^2)} \, , \; n \geq 1 \, . \end{aligned} \tag{42} $$

Now by applying the difference operators $(1+\frac{1}{12}\delta_x^2)$ and $(1+\frac{1}{6}\delta_x^2)$ on both sides with taking into consideration the initial clump (16), one gets $(1+\frac{1}{12}\delta_x^2)y^{(0)} = y^{(0)}$ because all $y_{j\pm k}^{(0)} = 0\ \forall k \geq 1$. After some mathematical manipulations, one gets

$$\begin{aligned}
&\frac{7}{12}y_j^{(n+1)} + \frac{7}{36}y_{j-1}^{(n+1)} + \frac{7}{36}y_{j+1}^{(n+1)} + \frac{1}{72}y_{j-2}^{(n+1)} + \frac{1}{72}y_{j+2}^{(n+1)} = b_n y_j^{(0)} + \sum_{m=2}^{n} c_m(\frac{7}{12}y_j^{(n+1-m)} + \\
&\frac{7}{36}y_{j-1}^{(n+1-m)} + \frac{7}{36}y_{j+1}^{(n+1-m)} + \frac{1}{72}y_{j-2}^{(n+1-m)} + \frac{1}{72}y_{j+2}^{(n+1-m)}) + [\frac{7\beta}{12} - \frac{\mu j}{4RN_e^{(n)}}(1-\frac{j}{R})]y_j^{(n)} + \\
&[\frac{7\beta}{36} + (\frac{\mu}{12N_e^{(n)}} + \frac{5s_1h\mu}{12N_e^{(n)}})(\frac{j-1}{R})(1-\frac{j-1}{R})]y_{j-1}^{(n)} + [\frac{7\beta}{36} + (\frac{\mu}{12N_e^{(n)}} - \frac{5s_1h\mu}{12N_e^{(n)}})(\frac{j+1}{R})(1- \\
&\frac{j+1}{R})]y_{j+1}^{(n)} + [\frac{\beta}{72} + (\frac{\mu}{24N_e^{(n)}} + \frac{s_1h\mu}{24N_e^{(n)}})(\frac{j-2}{R})(1-\frac{j-2}{R})]y_{j-2}^{(n)} + [\frac{\beta}{72} + (\frac{\mu}{24N_e^{(n)}} - \frac{s_1h\mu}{24N_e^{(n)}})\times \\
&(\frac{j+2}{R})(1-\frac{j+2}{R})]y_{j+2}^{(n)} + O(h^4+\tau)\ ,\ n \geq 1\ .
\end{aligned} \tag{43}$$

The positivity and the stability of this difference scheme required that the scaling relation μ must satisfy the following condition

$$0 < \mu \leq \frac{2800}{3}\beta\ . \tag{44}$$

The matrix form of the difference scheme (43) is written as

$$K^T.y^{(n+1)} = b_n y^{(0)} + \sum_{m=2}^{n} c_m K^T.y^{(n+1-m)} + (\beta K^T + \frac{\mu}{N_e^{(n)}}H^T).y^{(n)}\ ,n \geq 1 \tag{45}$$

For the numerical calculations, it is better to rewrite equation (45), after taking the transpose of each sides, as

$$z^{(n+1)} = b_n(z^{(0)}.K^{-1}) + \sum_{m=2}^{n} c_m z^{(n+1-m)} + z^{(n)}.(\beta I + \frac{\mu}{N_e^{(n)}}H.K^{-1})\ ,n \geq 1. \tag{46}$$

As $n = 0$, and with the initial condition (16), the memory term $b_n(z^{(0)}.K^{-1}) + \sum_{m=2}^{n} c_m z^{(n+1-m)}$ is vanished, then

$$z^{(1)} = z^{(0)}(\beta I + \frac{\mu}{N_e})H.K^{-1}\ , 2 \leq j \leq R-2\,, \tag{47}$$

with the same matrices H and K defined at (38) and (29).

Again this difference scheme is convergent and stable if the scaling relation μ satisfies the condition (44). Taking into consideration that the time fractional random gde is not representing the diffusion limit of Markov process as we have a memory. Then use the same good row vector (34), to get

$$\eta.(\beta I + \frac{\mu}{N_e^{(n)}}H.K^{-1}) = \beta\eta\ , \tag{48}$$

and $\eta.(H.K^{-1}) = 0$. Let $Q^{(n)} = (\beta I + \frac{\mu}{N_e^{(n)}}H.K^{-1})$, then it is non stochastic matrix for a Non-Markov process, the sum of all of its rows is β at each time step n. Therefore, the infinity norm of the matrix $Q^{(n)}$ is β. Again its spectral radius $\rho = \lambda_{\max} = \beta$, where β is the maximum eigenvalue of the matrix $Q^{(n)}$. Our difference scheme (43) is therefore stable, and once more with the help of the scaling relation condition (44), one has a diagonally dominant non-negative matrix and M-Matrix, which ensures the stability of the approximate solutions, see [37].

In section (6), the approximate solutions for the Markov case with $(\beta = 1)$ and the Non-Markov case with $(0 < \beta < 1)$ are compared for various numbers of generations. Also, the comparison of the total sum of the approximate solutions for different values of β. The comparison of the classical and time-fractional genetic drift are given for constant number of generations that could be calculated from the matrix equation (46) and its defined matrices H and K by fixing $N_e^{(n)}$ at its initial value N_e.

The simulation shows that the extension to the time-fractional order maintains the allele within the same big family for longer number of generations. This explains why the individuals of the isolated trips have the same physical and mental characteristics.

5 The Stationary Discrete Approximate Solution, Approximate Solution Convergence and the Reversibility Property of the GDEs

The classical and the time-fractional pdes being discussed here have the same continuous stationary approximate solutions. To get their stationary solutions, let

$$\frac{\partial u(x,t)}{\partial t} = \frac{\partial^{\beta} u(x,t)}{\partial t^{\beta}} = 0 \,, \forall \beta \,, 0 < \beta \leq 1 \,,$$

and ignore any terms that depend on t. Apply this approach here, on the equations (8), (9), and (10), leading to analytic stationary solutions that are given in terms of hyper-geometric functions.

The alternative method is calculating the discrete stationary approximations, $\bar{y}$, of the above discussed equations. By neglecting the time-dependent t at the discrete schemes, $\bar{y}$ is given. The process of calculating $\bar{y}$ is as follows: Replace all $y_{j\pm k}^{(n+1)}$ by $y_{j\pm k}^{(n)}$, $k = 0,1,2$ on the classical schemes (24) and on the time-fractional schemes (43), all $y^{(0)}$, y^{n+1} and y^{n+1-m} have to be replaced by y^n and more precisely by y. Then for $n \to \infty$, the discrete schemes of the gdes (8), (9) and (10) converge to $z.(P-K) = 0$, which is identical to

$$(P-K)^T.y = 0 \,.$$

The matrices P,K are defined in equations (28,29). The classical and the time-fractional gdes also has the same stationary approximate solution $\bar{y}$, where their P,K matrices are specified in equations (28,29). Then find the eigenvector corresponds to the eigenvalue zero of the matrix $(P-K)^T$, and call it y^*. Constitute the $\bar{y} = cy^*$ vector with $c = 1/\sum_{j=2}^{R-2} y_j^*$. The column vector $\bar{y}$ is also a vector of probability, i.e. it satisfies $\sum_{j=2}^{R-2} \bar{y}_j = 1$. The simulation of stationary approximate solution of the gdes are plotted at figure [7].

Now to discuss the discrete convergence of the clump $y^{(n)}$, constitute the column vector $d = d_0, d_1, d_2, \cdots, d_n$, whose elements are defined as

$$d_n = d(t_n) = \sum_{j=2}^{R-2} |y_j(t_n) - \bar{y}_j|, \; n = 1,2,\cdots \,. \tag{49}$$

The simulation for $\beta = 1$, for the classical gdes (8) and (9), demonstrates that the row vector d approximates an exponential function

$$d(t) \approx e^{-wt} \,,$$

where w is called the convergence rate. While the numerical results indicate that the row vector d behaves like the Mittag-Leffler function $E_{\beta}(-t^{\beta})$ for $0 < \beta < 1$, for the time-fractional random gde (10). The Mittag-Leffler function $E_{\beta}(-t^{\beta})$ is a special form of the Mittag–Leffler function of two fractional parameters (γ, ζ) being defined as

$$E_{\gamma,\zeta} = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\gamma + \zeta k)} \,, \; \gamma, \zeta \in \mathbb{R}, z \in \mathbb{C} \,. \tag{50}$$

We need here to use the asymptotic behavior of $E_{\beta}(-t^{\beta})$ being defined as,

$$E_{\beta}(-t^{\beta}) \begin{cases} = 1 - \frac{t^{\beta}}{\Gamma(\beta+1)} \approx exp\{-t^{\beta}/\Gamma(\beta+1)\} \,, & 0 \ll t \ll 1 \,, \\ \approx \frac{\sin \beta\pi}{\pi} \frac{\Gamma(\beta)}{t^{\beta}} \,, & t \to \infty \,, \end{cases} \tag{51}$$

and for further information on how the Mittag-Leffler is implemented in the time-fractional diffusion processes, see [29] and [39]. The simulations of the Mittag-Leffler function (51) are plotted at Figures[15] and [16]. It is worth to say that as $\beta = 1$, one gets the fastest decay function e^{-t}. The simulation of $\ln(d(t_n))$ of the genetic drift is plotted at Figure[8], to be compared with the the Mittag-Leffler function formulae that are plotted at Figures [15] and [16].

The Diffusion Processes Reversibility are defined according to Kelly[41] as: If $X(t_1), X(t_2), \cdots, X(t_n)$ have the same distribution as $X(\tau - t_1), X(\tau - t_2), \cdots, X(\tau - t_n)\{X_n, n \in \mathbb{N}\}$, then $\{X_n, n \in \mathbb{N}\}$ is said to be reversible if it is a two-sided extension of a non-negative recurrent Markov state, see also Ross[17]. The matrix of the classical processes P are given in equations (28). While the time fractional diffusion processes' non-stochastic matrices Q is defined as $Q^{(n)} = (\beta I + \frac{\mu}{N_e^{(n)}} H.K^{-1})$. This reversible property is mathematically formulated as

$$\bar{y}_j.P_{ij}^{(n)} = \bar{y}_j P_{ji}^{(n)} \,, \tag{52}$$

where the time-reversibility is represented by the equation (52), see [17], [29], [41], and [42]. Abdel-Rehim [29] has shown that

$$\sum_{j=2}^{R-2} P^T . \bar{y_j} = 1 \,, \tag{53}$$

for the classical cases. While for the time-fractional cases, one has

$$\sum_{j=2}^{R-2} (Q^{(n)})^T . \bar{y} = \beta \,, 0 < \beta < 1 \,, n \geq 0 \,, \tag{54}$$

as the discrete stationary solution is valid for all values of n. One can use the MATHEMATICA software, to prove the conditions of reversibility defined in equation (53) for the classical processes and equation (54) for the time-fractional processes.

6 The Numerical Results and Their Interpretations

In this section, the approximate solutions of the discussed pde are compared numerically. The Markov, classical case, and the Non-Markov, the time-fractional or the non-classical case, chains and and the loss of unity in the conditional probability summing of obtaining the gene with frequency x at the generation t are also discussed.

In this numerical analysis, Boundary conditions are set for the models (8), (9) and (10) according to equations (17) to zeros as $t \geq 5$, i.e. $u(x,p,0) = u(1,p,t) = 0 \; \forall t \leq T$, where T is the number of generations. Singularities occur at $x = 0$ and $x = 1$ points in the solutions, which must be provided separately. The initial condition is $u(x,p,0) = \delta(x-p)$, where the genes frequency is p, and $0 < x < 1$. While the initial condition for $x_0 = p = 0.5$ is $u(x,p;0) = \delta(x_0 - p) = \delta(0)$ is $y^{(0)} = \{0, \cdots, 1, \cdots, 0\}^T$. Let $R = 100$ and the single step number per generation $n = 1/\tau$. Then use the condition imposed on the scaling relations to calculate the proper value of μ to ensure the stability and the convergence of the studied difference schemes.

For the numerical calculation of $y^{(n)}$ of the gdes (9) and (10), by using the MATHEMATICA software, we fix the seed at seed $= 200$, and use equation (35) to generate the random number of individual $N_e^{(n)}$ at each time step t_n.

To do so, first choose m_r as integer random number $\in (10, 20)$. That means, we suppose that the random average of increasing is between 10 to 20 percent of the initial number of individuals $N_e^{(0)}$. This choice is coincide with the average of increasing of populations all over the world.

In this numerical computations, we fix the initial number of individuals to $N_e = 100$, and since we restrict the selection rate to $sN_e < 1$, then we fix $s = 0.01$ for equation(8).

For the random variable number of individuals represented by equations (9) and (42), we replace s by $\frac{s_1}{N_e^{(n)}}$.

The plot of $\sum_{j=2}^{R-2} y_j^{(n)} \; n \in \mathbb{N}_0$, up to 30 generations of the $y^{(n)}$ of equation(8) is represented at Figure[1] and that of equation (9) is plotted at Figure[2]. The figures show that changing the random number of individuals at each time step, even for $\beta = 1$, satisfies the normalization condition more than $N_e(t)$ is fixed.

Now the diffusion processes of the $y^{(n)}$ of the classical gde (8) and of the non-classical gde, with constant number of individuals, for different values of β and t are plotted at Figures[3- 5]. Figure[6] represents the comparison of the classical and time-fractional gdes, with constant number of individuals, for different β and t. The comparison shows that the diffusion away from the initial frequency $x_0 = 0.5$ is slower in the time-fractional than the classical.

That partially proves Galton's theory in which the effect of the inheritance, memory, from the big family makes the conditional probability to find the allele on the long run generations does not much smaller than its first generation. In other words $y_j^{(n)}$ diffuses near to $p = 0.5$.

The discrete stationary solution of the gdes, all the studied equations have the same stationary solution, is represented at Fig[7]. The convergence of the stationary solution $d(t)$ of the gdes for fixed number of individuals, being called also the first norm, is calculated by using equation (49). In Figure[8], we plotted $\ln[d(t)]$ against $t : 1 \to 50$. The figure shows that $\ln[d(t)]$ asymptotically converges as e^{-t} as $\beta = 1$ and behaves as the Mittag-Leffler function for $0 < \beta < 1$.

The diffusion of $y^{(n)}$ of the classical random gde (9), having random variable individuals number at each time step is plotted at Figure[9] for different values of t. Figures[10, 11] represent the simulation of the diffusion of the approximate solutions of the time-fractional gde (10), for $\beta = 0.85$ and $\beta = 0.75$ respectively. In these figures, the number of individuals

is represented by an integer random variable that is varying from a generation to generation. Figure[12] represents the comparison between the diffusion of the approximate solutions for different values of β at the third generation and at the generation number 20. The simulation shows that the approximations for $\beta < 1$ is more slower than that of Figure[9] and more more slower than the previous case. That means changing the number of individuals beside adding the memory effect make the conditional probability to find the allele on the long run is much close to its initial frequency $p = 0.5$. That is exactly the proof of the Galton's. The gene that carries the physical characteristic or the talent in the early generation remains strong and still exist with approximately the same frequency in the coming generations on the future.

Figures[13, 14] represent the proof of the normalization condition (3), that is computationally proved by the plot of $\sum_{j=2}^{R-2} y_j^{(n)}$, $n \in \mathbb{N}_0$. The figures show that the fractional order beside using random number of individuals make $\sum_{j=2}^{R-2} y_j^{(n)} = 1$, $n \in \mathbb{N}_0$ even till the 30^{th} generation. while using only fractional order with fixed number of individuals makes $\sum_{j=2}^{R-2} y_j^{(n)} \approx 1$, $n \in \mathbb{N}_0$ till the 30^{th} generation.

Finally, the modifications that we made to the classical gde (8), Kimura model, improve its numerical results, make it more reality, and prove Galton's theory.

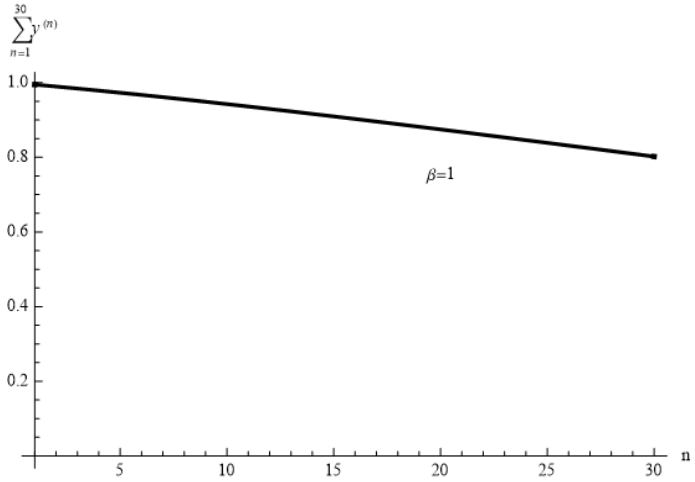

Fig. 1: $\sum_{j=2}^{R-2} y_j^{(n)}$ of the *random gde* (8) as N_e fixed.

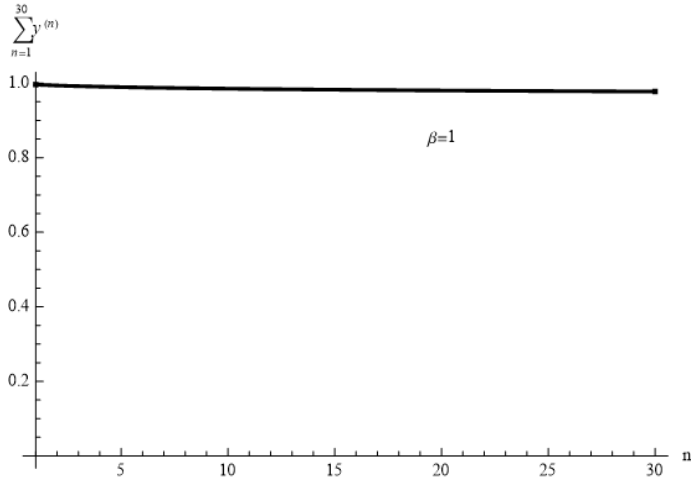

Fig. 2: $\sum_{j=2}^{R-2} y_j^{(n)}$ of the *gde* (8) as N_e randomly changed.

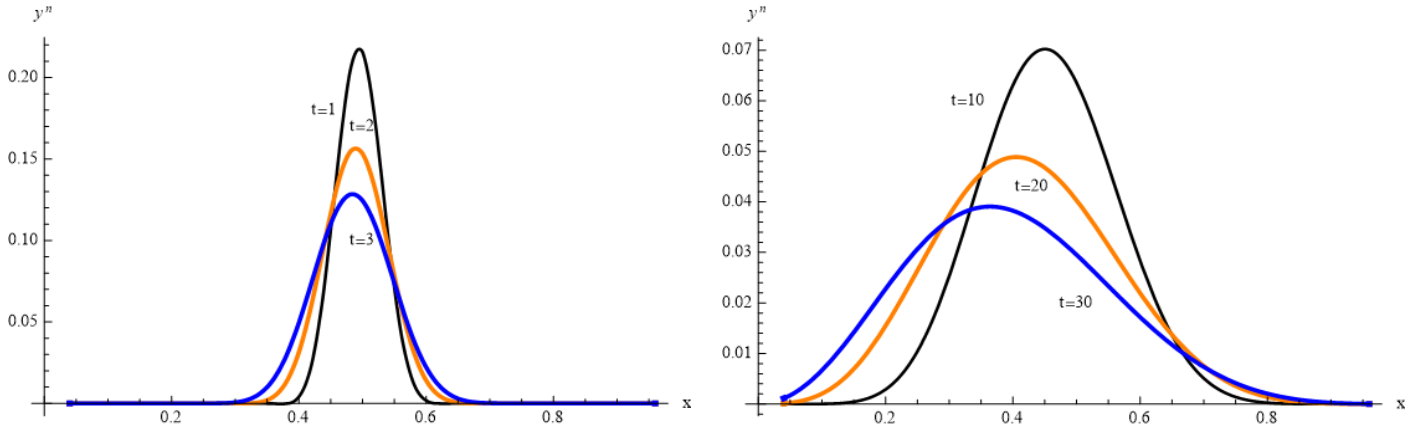

Fig. 3: Simulation of the classical *gde* (8), for N_e fixed, within different generations.

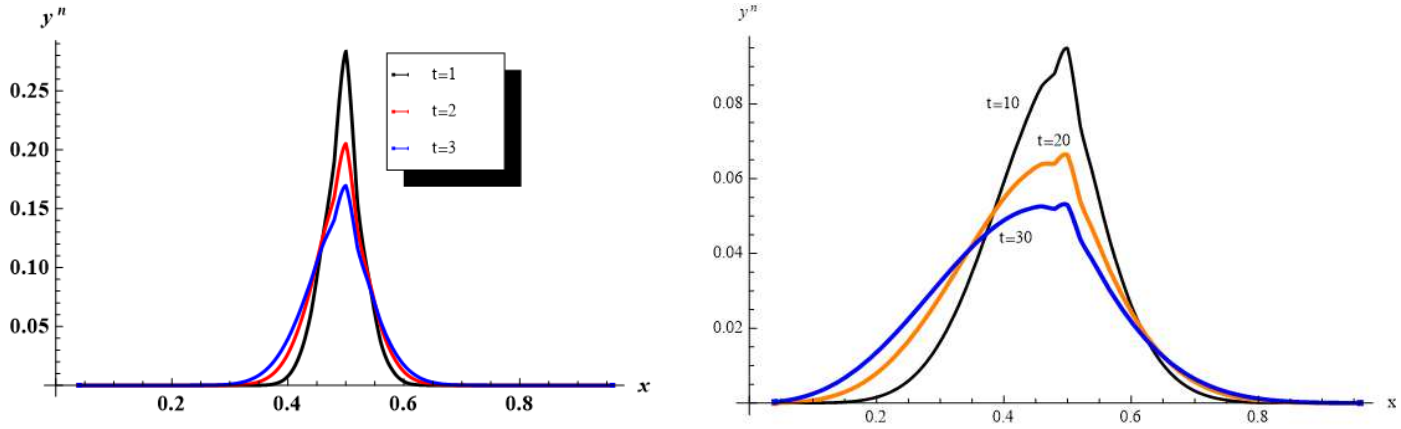

Fig. 4: Simulation of the non–classical *gde* (10, with fixed number of individuals, for $\beta = 0.85$.

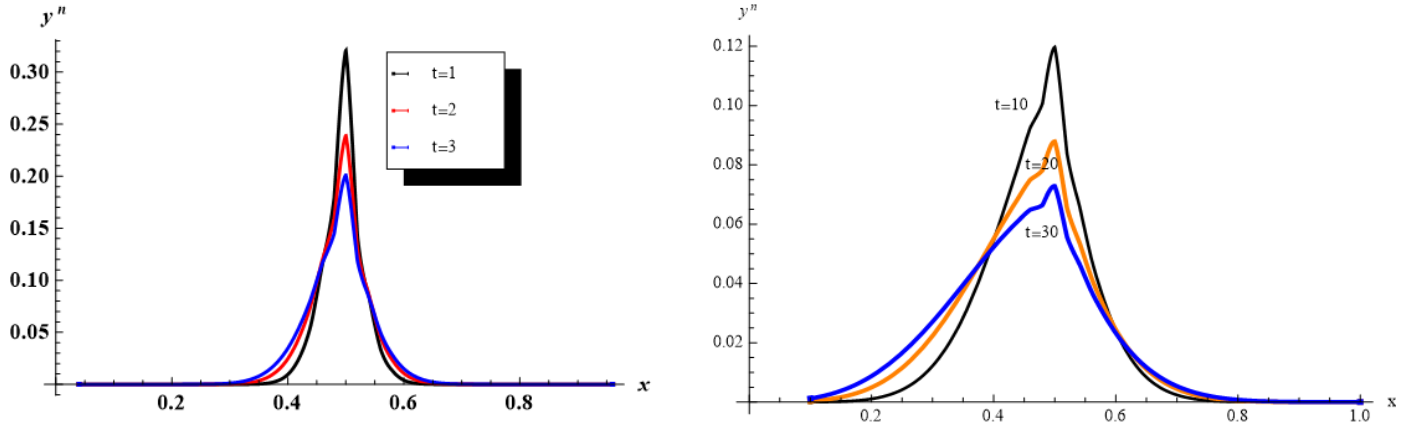

Fig. 5: Simulation of the non–classical *gde* (10, with fixed number of individuals, for $\beta = 0.75$.

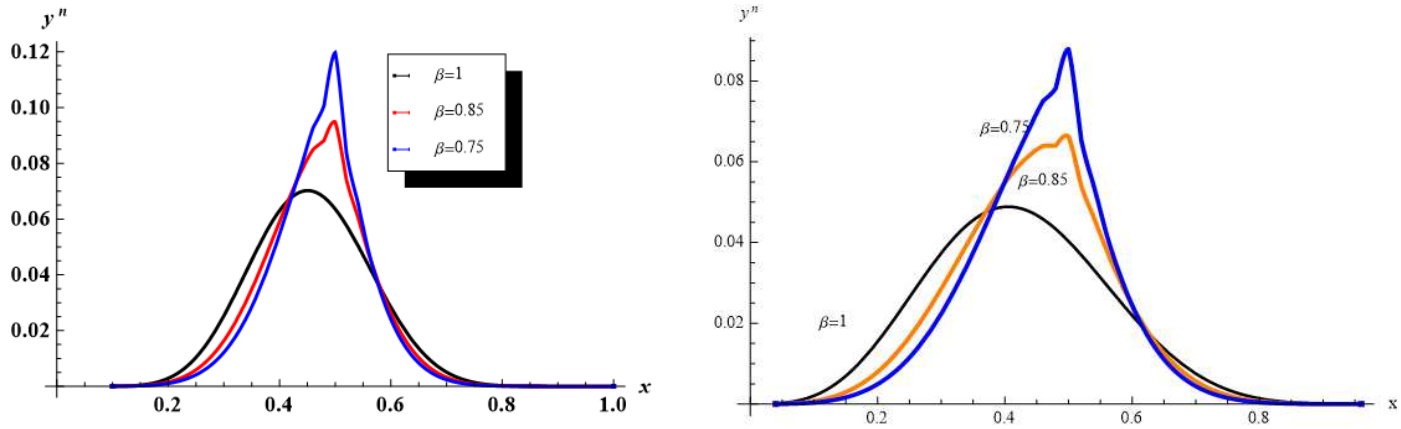

Fig. 6: Comparison of the classical and the time–fractional *gde* (8),(10), with fixed number of individuals, and for $t = 10, 20$, respectively.

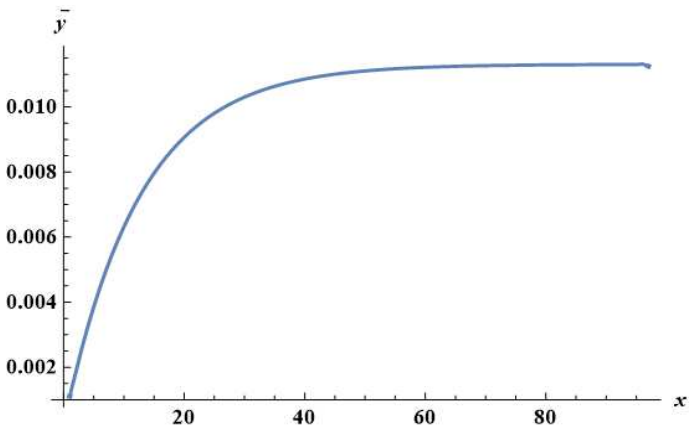

Fig. 7: $\bar{y}$ of the gdes.

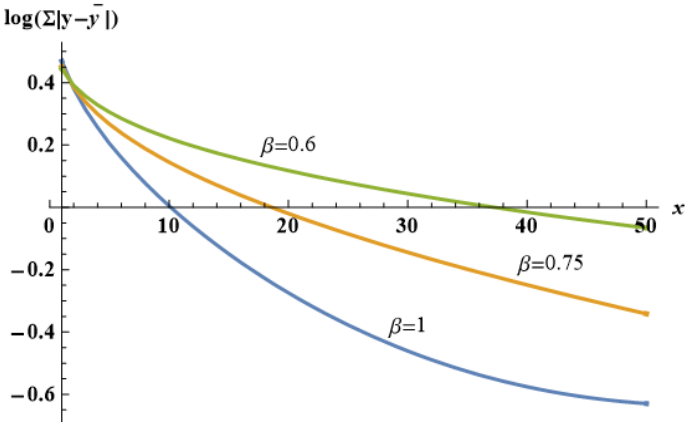

Fig. 8: The convergence of the discrete scheme of the non–classical *gde* (10) for N_e fixed.

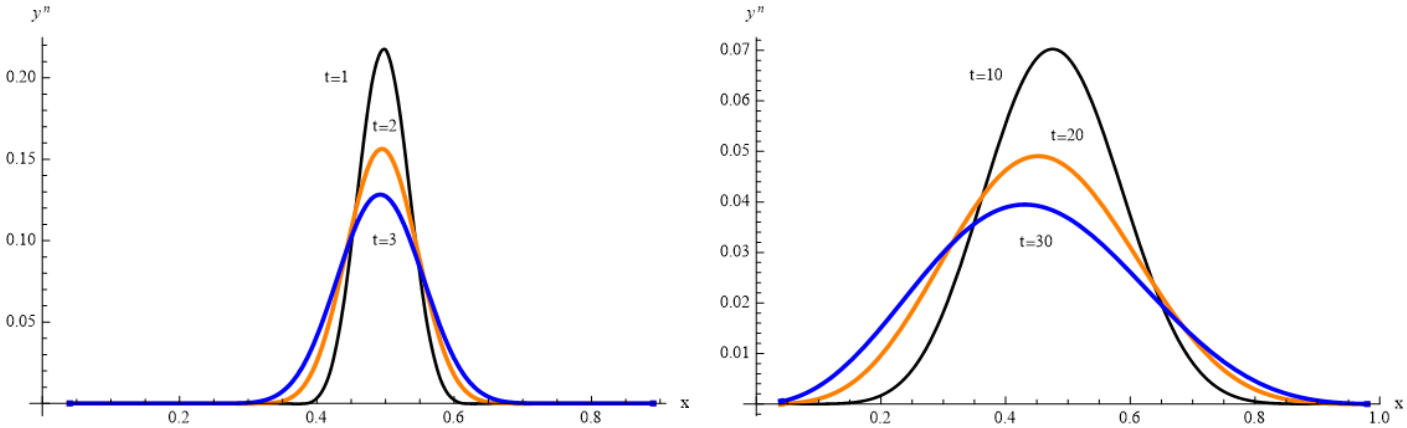

Fig. 9: Simulation of the classical *gde* (9), for random variable number of individuals at each time step, for different generations.

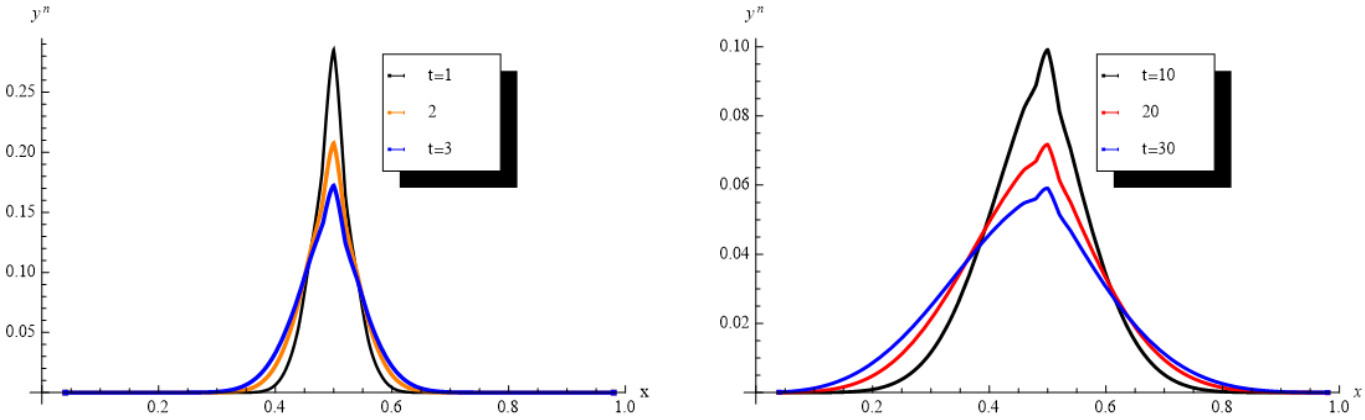

Fig. 10: Simulation of the non-classical *gde* (10), for random variable number of individuals at each time step, for different generations, and for $\beta = 0.85$.

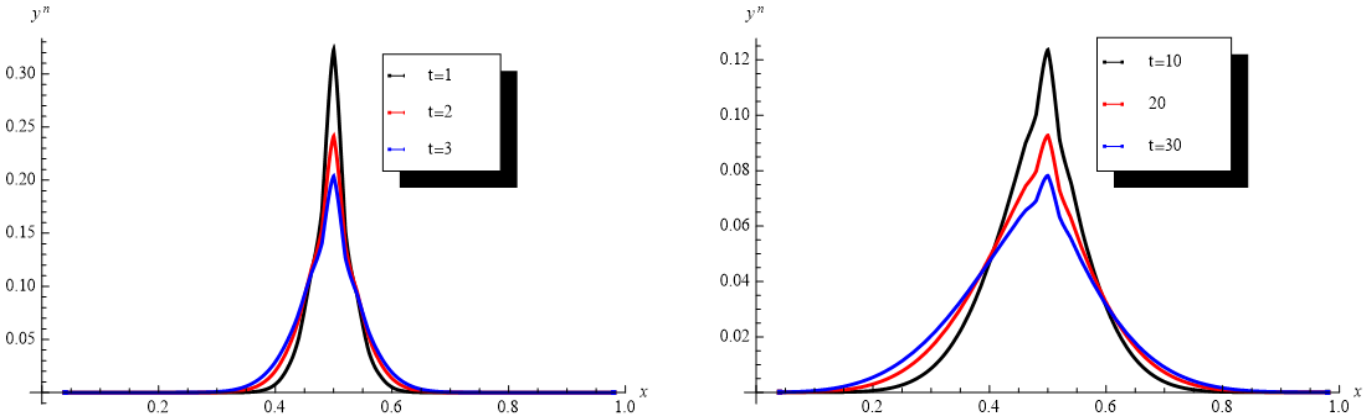

Fig. 11: Simulation of the non-classical *gde* (10), for N_e unfixed at each time step, for different generations, and for $\beta = 0.75$.

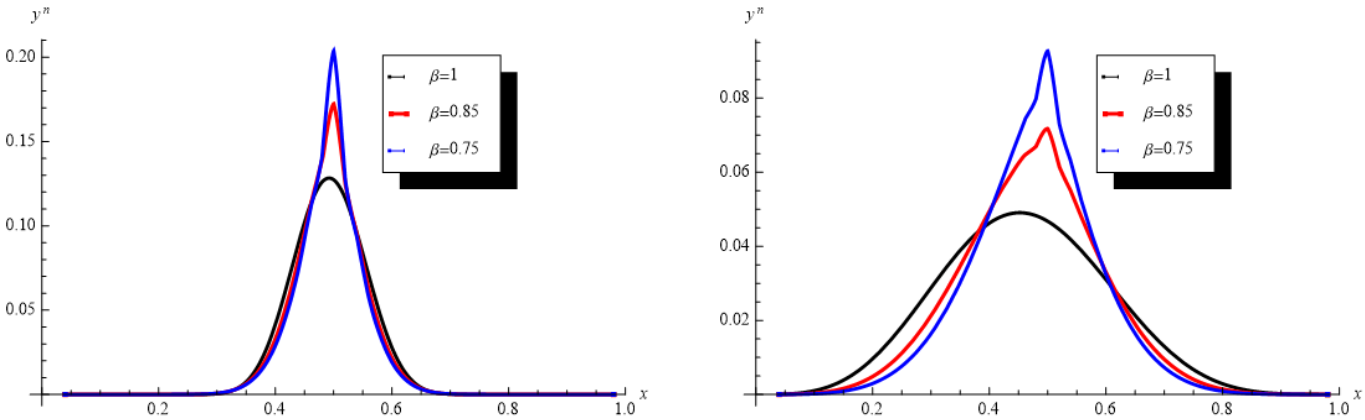

Fig. 12: Comparison of the classical and the non–classical *gdes* (9),(10), with the number of individuals is represented by integer random variable, for different values of β, and for $t = 3, 20$, respectively.

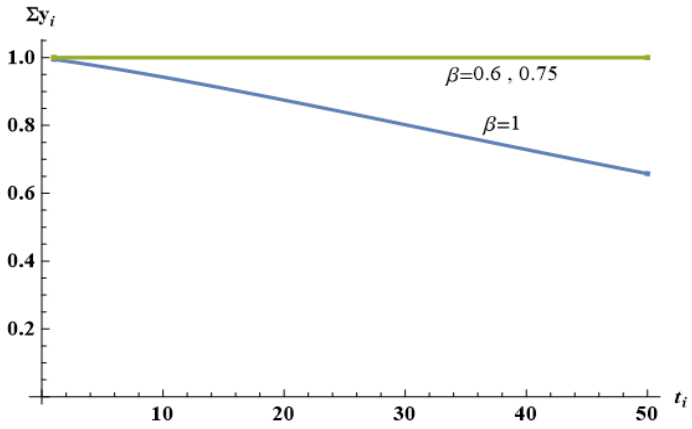

Fig. 13: $\sum_{j=2}^{R-2} y_j^{(n)}$ of the gde, with constant number of individuals at each generation, for different values of β

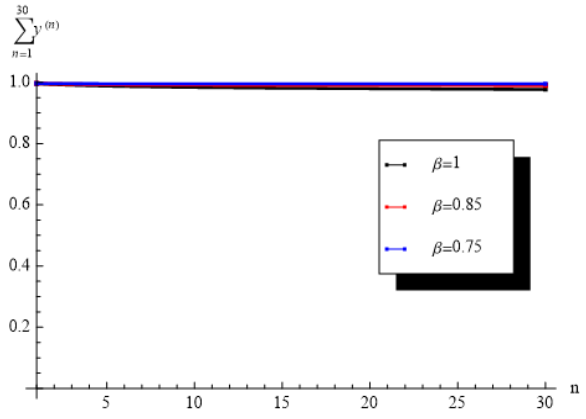

Fig. 14: $\sum_{j=2}^{R-2} y_j^{(n)}$ of the genetic drift equation, with random variable number of individuals at each generation, for different values of β

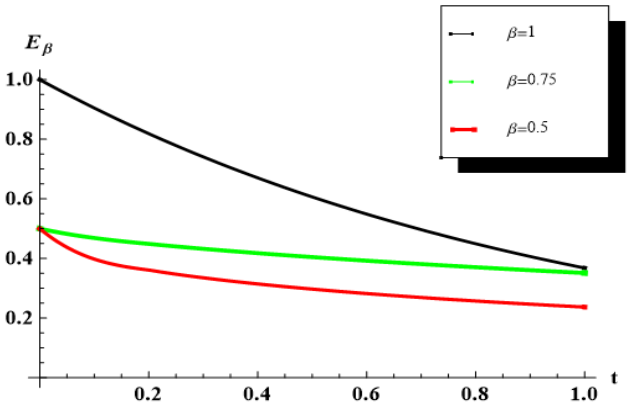

Fig. 15: The simulation of the Mittag-Leffler as $t : 0 \to 1$, for different values of β

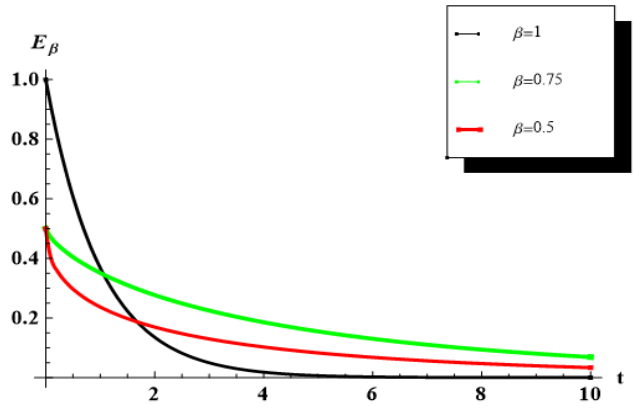

Fig. 16: The simulation of the Mittag-Leffler as $t : 0 \to 10$, for different values of β

7 Conclusion

In this paper, the classical gde is computationally proved to be not relevant to model the hereditary process on human beings. The influence of the memory, the history of the diffusion of the studied allele through the random mating individuals, should be add and studied. Therefore, the modification of the classical gde by the time-fractional gde has been computationally proved. Changing randomly the number of individuals through generations, also modifies Kimura model to make it more realistic. In section (6), we demonstrate that memory dependence causes the time-fractional diffusion processes to be slower compared to the classical cases. That means the human talents and characteristics remains very longer, for many generations, in the same family. According to time-fractional gdes, the numerical results show that the conditional probability cumulative summation to find the genes after many generations, is very near to 1, but those corresponding to the classical cases behave very far than 1. That means approximations of the classical pdes lose their efficiency as conditional probabilities.

Finally, after all these numerical results one can say that the time-fractional gde with random variable number of individuals at each time step is more effective at simulating the processes of genetic diffusion, and the hereditary processes than the classical ones. These numerical results are consistent with the Galton's theory of inheritance.

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