

A model extending from Goldstein-Kac Telegraphic Equation that describe numerically the population dynamics problem

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Abstract. In this work we consider a particles motion modeling into 2D domain. The motion happens by particles' decision which is modeled from parameters like territorial occupation and populational value, both at the domain. We used an equations' system to create our model from extending the well-known Goldstein-Kac telegraphic equation. Specifically, the particles could be animals, virus, cells, the property concentration and anything of engineering as well. This model describes the population's density behavior at the space and time in a two dimensional space. Also, the model lets the particles to have different spreading properties in each dimension. Besides, the model is solved by quasi linear numerical method (QLNM). The QLNM is a novel smart finite difference technique that solves complex nonlinear partial differential equations. The quality of solutions is guaranteed by numerical analysis tools. Moreover, in this work, the population dynamics of the spreading is gotten and analyzed yet.

Keywords: Telegraph equation, Population Dynamics, Quasi linear numerical method

1 Introduction

Population dynamics is a subject of great mathematical relevance. From Malthus [1] works in 1798 describing the population growth in unrestricted environments to more recent findings, like the effect of aggregation in population survival made by Allee and Bowen [2] in 1938, this topic is far from exhausted. Besides, the importance of the spatial dimensions occupied by such populations and its impact on the population dynamics is also a topic of mathematical interest [3]. Recent works are still exploring both theoretical properties of spatio temporal models, i.g. Alharbi and Petrovskii [4] investigated the effects of a complex landscape from a reaction-diffusion model. Morozov et al. [5] studied more complex spatial patterns from predator-prey reaction-diffusion models using Allee and Bowen [2] population model. Cirilo et al. [6] worked on the critical domain problem for the Goldstein-Kac model, i.g. Ganesan and Lingeshwaran [7] worked on a tumor growing mathematical model using the reaction-diffusion equation in realistic 3D domains and Mammeri [8] used a reaction-diffusion system to analyze the COVID-19 spread in France. In this context we explore the Goldstein-Kac model, which is a improve of reaction-diffusion equation, called as Telegraphic Equation, to describe the two dimensional population dynamics model. We aim to introduce the particles motion at the plane, for future we will use it in biological problems. As noted by Holmes [9] the Telegraphic Equation can have a positive impact, justifying its use over the more widely-known reactive-diffusive model. Since this model results in a non-linear equation system, the quasi linear numerical method, proposed by Cirilo et al. [6], will be used in order to solve the model.

2 Materials and Methods

This section presents the model governing equation deduction and the considerations made to extend it to the two dimensional domain. The quasi linear numerical method will also be presented, already applied to the model equation.

2.1 Model Description

Suppose that a group of particles are moving and reproducing on a two dimensional plane. Also, suppose that the movement is independent in each plane axis. Besides that, the movement follows a correlated random walk pattern in each axis, i.e the particles decision to keep the movement direction or reverse it depends on the last step. The newly created particles will have equal chance to start its movement going north, south, east or west.

So, considering that the particles move in the x axis with steps of δ_x size at a constant speed of γ_x , with steps of δ_y size and constant speed of γ_y in the y axis, and have a probability $p = 1 - \lambda\epsilon$ of keeping its movement direction and probability $q = \lambda\epsilon$ of inverting its movement direction in any axis for small time lapses ϵ , where λ is the rate of inversion, the particles that arrive at any point at a given time should be, as illustrated in Fig 1, $S = \alpha_x + \beta_x + \alpha_y + \beta_y$,

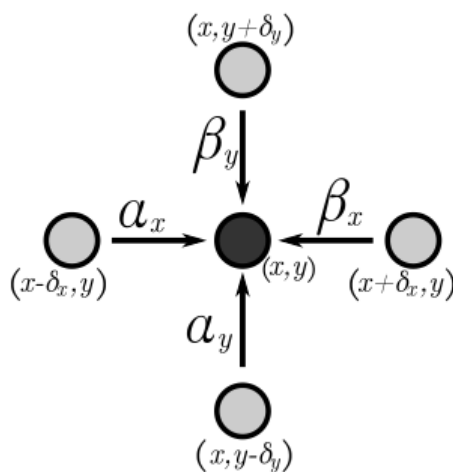


Figure 1. Particles movement to the point (x, y)

with $\epsilon F(S)$ being the particles generated by reproduction in the time step ϵ ,

$$\alpha_\kappa(\kappa, t + \epsilon) = p\alpha_\kappa(\kappa - \delta_\kappa, t) + q\beta_\kappa(\kappa - \delta_\kappa, t) + \frac{1}{4}\epsilon F(S(\kappa - \delta_\kappa, t)) \quad (1)$$

and

$$\beta_\kappa(\kappa, t + \epsilon) = p\beta_\kappa(\kappa + \delta_\kappa, t) + q\alpha_\kappa(\kappa + \delta_\kappa, t) + \frac{1}{4}\epsilon F(S(\kappa + \delta_\kappa, t)), \quad (2)$$

for $\kappa = x$ or y .

Just as done in [9], to obtain our differential equation we will expand eq. (1) and eq. (2) using Taylor Series and getting up the limit of ϵ and δ_κ to 0, so we have

$$\alpha_\kappa + \epsilon \frac{\partial \alpha_\kappa}{\partial t} + O(\epsilon^2) = p(\alpha_\kappa - \delta_\kappa \frac{\partial \alpha_\kappa}{\partial \kappa} + O(\delta_\kappa^2)) + q(\beta_\kappa - \delta_\kappa \frac{\partial \beta_\kappa}{\partial \kappa} + O(\delta_\kappa^2)) + \frac{1}{4}\epsilon(F(S) - \delta_\kappa \frac{\partial F(S)}{\partial \kappa} + O(\delta_\kappa^2)) \quad (3)$$

and

$$\beta_\kappa + \epsilon \frac{\partial \beta_\kappa}{\partial t} + O(\epsilon^2) = p(\beta_\kappa + \delta_\kappa \frac{\partial \beta_\kappa}{\partial \kappa} + O(\delta_\kappa^2)) + q(\alpha_\kappa + \delta_\kappa \frac{\partial \alpha_\kappa}{\partial \kappa} + O(\delta_\kappa^2)) + \frac{1}{4}\epsilon(F(S) + \delta_\kappa \frac{\partial F(S)}{\partial \kappa} + O(\delta_\kappa^2)). \quad (4)$$

Substituting $p = 1 - \lambda\epsilon$ and $q = \lambda\epsilon$ in eq. (3) and eq. (4), dividing it by ϵ and taking the limit as δ_κ and ϵ go to zero, we get

$$\frac{\partial \alpha_\kappa}{\partial t} + \gamma_\kappa \frac{\partial \alpha_\kappa}{\partial \kappa} = \lambda\beta_\kappa - \lambda\alpha_\kappa + \frac{1}{4}F(S) \quad (5)$$

and

$$\frac{\partial\beta_\kappa}{\partial t} - \gamma_\kappa \frac{\partial\beta_\kappa}{\partial\kappa} = \lambda\alpha_\kappa - \lambda\beta_\kappa + \frac{1}{4}F(S). \quad (6)$$

The results of eq. (5) and eq. (6) are possible considering that

$$\lim_{\substack{\delta_\kappa \rightarrow 0 \\ \epsilon \rightarrow 0}} \frac{\delta_\kappa}{\epsilon} = \gamma_\kappa, \quad (7)$$

which is justifiable by the definition of instant velocity by limit. Since ϵ is the time the particle use to traverse a distance δ_κ then $\gamma_\kappa = \frac{\delta_\kappa}{\epsilon}$ is the mean speed of the particle in this interval. If the limit is taken maintaining this relation, and the particle velocity is constant, then we have (7). Note that the same result may be achieved without the truncated Taylor expansion but using a difference equation before taking the limits, but the consideration shown in (7) is still necessary [10].

Taking the sum of eq. (5) and eq. (6) and the and subtraction of eq. (6) from eq. (5) we have

$$\frac{\partial(\alpha_\kappa + \beta_\kappa)}{\partial t} + \gamma_\kappa \frac{\partial(\alpha_\kappa - \beta_\kappa)}{\partial\kappa} = \frac{1}{2}F(S) \quad (8)$$

and

$$\frac{\partial(\alpha_\kappa - \beta_\kappa)}{\partial t} + \gamma_\kappa \frac{\partial(\alpha_\kappa + \beta_\kappa)}{\partial\kappa} = -2\lambda(\alpha_\kappa - \beta_\kappa). \quad (9)$$

Differentiating eq. (8) with respect to t and differetiating eq. (11) with respect to κ and multipling it by γ_κ we get

$$\frac{\partial^2(\alpha_\kappa + \beta_\kappa)}{\partial t^2} + \gamma_\kappa \frac{\partial^2(\alpha_\kappa - \beta_\kappa)}{\partial\kappa\partial t} = \frac{1}{2} \frac{\partial F(S)}{\partial t} \quad (10)$$

and

$$\gamma_\kappa \frac{\partial^2(\alpha_\kappa - \beta_\kappa)}{\partial\kappa\partial t} + \gamma_\kappa^2 \frac{\partial^2(\alpha_\kappa + \beta_\kappa)}{\partial\kappa^2} = -2\gamma_\kappa\lambda \frac{\partial(\alpha_\kappa - \beta_\kappa)}{\partial\kappa}. \quad (11)$$

Considering that eq. (10) also gives us the relation

$$-\gamma_\kappa \frac{\partial(\alpha_\kappa - \beta_\kappa)}{\partial\kappa} = \frac{\partial(\alpha_\kappa + \beta_\kappa)}{\partial t} - \frac{1}{2}F(S), \quad (12)$$

we may rewrite eq. (11) as

$$\gamma_\kappa \frac{\partial^2(\alpha_\kappa - \beta_\kappa)}{\partial\kappa\partial t} + \gamma_\kappa^2 \frac{\partial^2(\alpha_\kappa + \beta_\kappa)}{\partial\kappa^2} = 2\lambda \frac{\partial(\alpha_\kappa + \beta_\kappa)}{\partial t} - \lambda F(S). \quad (13)$$

Summing eq. (10) and eq. (13), and considering $S_\kappa = \alpha_\kappa + \beta_\kappa$ we have

$$\frac{\partial^2 S_\kappa}{\partial t^2} + 2\lambda \frac{\partial S_\kappa}{\partial t} - \frac{1}{2} \frac{\partial F(S)}{\partial t} = \gamma_\kappa^2 \frac{\partial^2 S_\kappa}{\partial\kappa^2} + \lambda F(S). \quad (14)$$

The amount of particles S reaching the point (x, y) should be $S_x + S_y$. We can already write equations for S_x and S_y from eq. (14) by assuming $\kappa = x$ and $\kappa = y$, having, respectively

$$\frac{\partial^2 S_x}{\partial t^2} + 2\lambda \frac{\partial S_x}{\partial t} - \frac{1}{2} \frac{\partial F(S)}{\partial t} = \gamma_x^2 \frac{\partial^2 S_x}{\partial x^2} + \lambda F(S), \quad (15)$$

and

$$\frac{\partial^2 S_y}{\partial t^2} + 2\lambda \frac{\partial S_y}{\partial t} - \frac{1}{2} \frac{\partial F(S)}{\partial t} = \gamma_y^2 \frac{\partial^2 S_y}{\partial y^2} + \lambda F(S). \quad (16)$$

In order to sum eq. (15) and eq. (16) to obtain S we will remind that the movement is independent in each axis, so the movement over the x axis do not interfere in the movement over the y axis, and the contrary is also true. So we may assume that

$$\frac{\partial^2 S_x}{\partial y^2} = \frac{\partial^2 S_y}{\partial x^2} = 0, \quad (17)$$

and therefore

$$\frac{\partial^2 S}{\partial x^2} = \frac{\partial^2(S_x + S_y)}{\partial x^2} = \frac{\partial^2 S_x}{\partial x^2} + \frac{\partial^2 S_y}{\partial x^2} = \frac{\partial^2 S_x}{\partial x^2}, \quad (18)$$

$$\frac{\partial^2 S}{\partial y^2} = \frac{\partial^2(S_x + S_y)}{\partial y^2} = \frac{\partial^2 S_x}{\partial y^2} + \frac{\partial^2 S_y}{\partial y^2} = \frac{\partial^2 S_y}{\partial y^2}. \quad (19)$$

Finally, we can sum eq. (15) and eq. (16) obtaining

$$\frac{\partial^2 S}{\partial t^2} + 2\lambda \frac{\partial S}{\partial t} - \frac{\partial F(S)}{\partial t} = \gamma_x^2 \left(\frac{\partial^2 S}{\partial x^2} \right) + \gamma_y^2 \left(\frac{\partial^2 S}{\partial y^2} \right) + 2\lambda F(S). \quad (20)$$

Considering that

$$\frac{\partial F(S)}{\partial t} = \frac{dF}{dS} \frac{\partial S}{\partial t}, \quad (21)$$

dividing eq. (20) by 2λ , taking $\tau = \frac{1}{2\lambda}$, $D_x = \frac{\gamma_x^2}{2\lambda}$ and $D_y = \frac{\gamma_y^2}{2\lambda}$ we get

$$\tau \frac{\partial^2 S}{\partial t^2} + \left[1 - \tau \frac{dF}{dS} \right] \frac{\partial S}{\partial t} = D_x \left(\frac{\partial^2 S}{\partial x^2} \right) + D_y \left(\frac{\partial^2 S}{\partial y^2} \right) + F(S), \quad (22)$$

the governing equation of our model.

For a rectangular domain $\Omega = [0, L] \times [0, M]$, considering a Dirichlet boundary condition, a initial state S_I for S and a ending time t_f , we have the following initial value problem for our model

$$\begin{cases} \tau \frac{\partial^2 S}{\partial t^2} + \left[1 - \tau \frac{dF}{dS} \right] \frac{\partial S}{\partial t} = D_x \left(\frac{\partial^2 S}{\partial x^2} \right) + D_y \left(\frac{\partial^2 S}{\partial y^2} \right) + F(S) & \text{int}\Omega \times (0, t_f] \\ S(x, y, 0) = S_I; \quad \frac{\partial S(x, y, 0)}{\partial t} = 0 & \Omega \\ S(0, y, t) = S(L, y, t) = S(x, 0, t) = S(x, M, t) = 0 & \partial\Omega. \end{cases} \quad (23)$$

From (23) it's possible to model the problems with diffusion and reproduction at the bidimensional domain. Additionally, here the parameter τ means a delay over the movement, and this is more realistic to biological problems. This work is being developed together with a cellular invasion problem called Wound Healing Assay (as in [11]) where the invasion speed and reproduction rate may be affected by the use of specific drugs.

2.2 Numerical Modeling

For the numerical resolution of the model (23) we will discretize the two dimensional domain $[0, L] \times [0, M]$ with the sets $(x_i, i = 1, 2, \dots, ni \in \mathbb{N})$ and $(y_i, i = 1, 2, \dots, mj \in \mathbb{N})$, respectively, to create a two dimensional grid. Since our model describe the density of particles in the domain, we will calculate the value of S in the center of each cell.

Numerically, at a point $(x, y, k + 1)$, eq. (22) may be written as

$$\tau \frac{\partial^2 S}{\partial t^2} \Big|_P^{k+1} + \left[1 - \tau \frac{dF}{dS} \right] \Big|_P^{k+1} \frac{\partial S}{\partial t} \Big|_P^{k+1} = D_x \frac{\partial^2 S}{\partial x^2} \Big|_P^{k+1} + D_y \frac{\partial^2 S}{\partial y^2} \Big|_P^{k+1} + F(S) \Big|_P^{k+1}, \quad (24)$$

where $k + 1$ is a single step in time. Additionally, we employed the labels $P = (x, y)$, $N = (x, y + 1)$, $E = (x + 1, y)$, $W = (x - 1, y)$ and $S = (x, y - 1)$ as well.

Applying the Finite Difference Method to eq. (24) we have

$$\begin{aligned} \frac{\tau}{(\Delta t)^2} (S_P^{k+1} - 2S_P^k + S_P^{k-1}) + \left[1 - \tau \frac{dF}{dS} \right] \Big|_P^{k+1} \left(\frac{S_P^{k+1} - S_P^k}{\Delta t} \right) = \\ = \frac{D_x}{(\Delta x)^2} (S_W^{k+1} - 2S_P^{k+1} + S_E^{k+1}) + \frac{D_y}{(\Delta y)^2} (S_S^{k+1} - 2S_P^{k+1} + S_N^{k+1}) + F \Big|_P^{k+1}, \end{aligned} \quad (25)$$

which may be rewritten as

$$\left(C_P + \tau \tilde{C}_P \right) S_P^{k+1} - C_W S_W^{k+1} - C_E S_E^{k+1} - C_S S_S^{k+1} - C_N S_N^{k+1} = \bar{b}_P + \tau \tilde{b}_P, \quad (26)$$

with

$$\begin{aligned}
 C_P &= \frac{1}{\Delta t} + \frac{2D_x}{(\Delta x)^2} + \frac{2D_y}{(\Delta y)^2}, \quad \tilde{C}_P = \frac{1}{(\Delta t)^2} - \frac{1}{\Delta t} \frac{dF}{dS} \Big|_P^{k+1}, \\
 C_W &= C_E = \frac{D_x}{(\Delta x)^2}, \quad C_S = C_N = \frac{D_y}{(\Delta y)^2}, \\
 \bar{b}_P &= \frac{1}{\Delta t} S_P^k + F \Big|_P^{k+1}, \quad \tilde{b}_{\kappa_P} = \left(\frac{2}{(\Delta t)^2} - \frac{1}{\Delta t} \frac{dF}{dS} \Big|_P^{k+1} \right) S_P^k - \frac{1}{(\Delta t)^2} S_P^{k-1}.
 \end{aligned} \tag{27}$$

The discrete boundary condition and the initial values of S will be taken as

$$\begin{aligned}
 S(x, y, 0) &= S_I^0 && \implies S_I^0 = S_I, \\
 \frac{\partial S(x, y, t)}{\partial t} \Big|_P^0 &= \frac{S(x, y, 0) - S(x, y, -\delta t)}{\Delta t} = 0 && \implies S_I^{-1} = S_I^0, \\
 S(0, y, t) \Big|^{k+1} &= S(L, y, t) \Big|^{k+1} = S(x, 0, t) \Big|^{k+1} = S(x, M, t) \Big|^{k+1} = 0.
 \end{aligned} \tag{28}$$

With the conditions described in (28) we can numerically solve eq. (26) for all points in the domain as a system of equations, with

$$S_P^{k+1} = \frac{1}{(C_P + \tau \tilde{C}_P)} \left(C_W S_W^{k+1} + C_E S_E^{k+1} + C_S S_S^{k+1} + C_N S_N^{k+1} + \bar{b}_P + \tau \tilde{b}_P \right), \tag{29}$$

but we note that \tilde{C}_P , \bar{b}_P and \tilde{b}_P depend on S_P^{k+1} , so the system of equations is not linear.

There are many ways to linearize an equations' system which can be solved by linear system methodology, but we will apply the quasi linear numerical method, as proposed by Cirilo et al. [6] in order to avoid to making further changes to the equation, which would result in a bigger mathematical workload.

2.3 Quasi Linear Numerical Method Approach to Solution

The quasi linear numerical method uses a iterative approach to approximate the value of the non-linear terms of a system of equations. To calculate the value of $^{(IT)}S_P^{k+1}$, i.e. the value of S_P^{k+1} at iteration IT , with $IT = 1, 2, \dots, IT_{max}$ we may first calculate all non-linear terms using $^{(IT-1)}S_P^{k+1}$. In our model, this results in

$$\begin{aligned}
 ^{(IT)}\tilde{C}_P &= \frac{1}{(\Delta t)^2} - \frac{1}{\Delta t} \frac{^{(IT-1)}dF}{dS} \Big|_P^{k+1}, \\
 ^{(IT)}\bar{b} &= \frac{1}{\Delta t} S_P^k + ^{(IT-1)}F \Big|_P^{k+1}, \\
 ^{(IT)}\tilde{b}_{\kappa} &= \left(\frac{2}{(\Delta t)^2} - \frac{1}{\Delta t} \frac{^{(IT-1)}dF}{dS} \Big|_P^{k+1} \right) S_P^k - \frac{1}{(\Delta t)^2} S_P^{k-1}.
 \end{aligned} \tag{30}$$

Since $^{(IT-1)}S_P^{k+1}$ is a known value, using it to solve \tilde{C}_P , \bar{b}_P and \tilde{b}_P transforms eq. (29) in a linear system in the current iteration. From there we may solve $^{(IT)}S_P^{k+1}$ with any available numerical method for linear systems. An advantage of this approach is that if the numerical method for solving linear systems is already a iterative process, like the Gauss-Seidel method or the successive over-relaxation method, the quasi linear method iteration is done alongside the linear system method iteration adding only an insignificant amount of computational time to each iteration.

3 Preliminary Conclusions

This work isn't close yet. But, here we showed that two dimensional population dynamics can be modeled by Goldstein-Kac telegraphic equation. This modeling is important, because the invasion problems' pattern can be described more realistic.

About numerical result, considering the assumption $\lim_{\lambda \rightarrow \infty} \tau = \lim_{\lambda \rightarrow \infty} \frac{1}{2\lambda} = 0$, the equation (22) can be rewrite at the form

$$\frac{\partial S}{\partial t} = D_x \left(\frac{\partial^2 S}{\partial x^2} \right) + D_y \left(\frac{\partial^2 S}{\partial y^2} \right) + F(S), \quad (31)$$

which is called two dimensional reaction-diffusion equation. In fact, there are analytical solution of the equation (31) to some specific $F(S)$ functions. Because this mathematical evidence, we use it to validate our numerical procedure through numerical analysis.

Besides, in collaboration with other researchers, we are working on numerical code to obtain new applied results. Come soon, we will show numerical results of the cellular invasion problem, known as Wound Healing Assay [11], which is an important biological phenomena. About it, from of ongoing experiments, some quantities of the drug are tested to check how it affects carcinogenic cells ability to move, reproduce and invade new areas. Therefore, we intent to compare our results with experiments and provide a new biological analysis tools.

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