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# Time-fractional numerical modelling applied to diffusion-wave processes of bacterial biomass growth

A time-fractional model of diffusion-wave processes is considered to describe the bacterial growth phenomenon. The 2D model is specified as an initial boundary value problem for a system of semilinear time-fractional partial differential equations. A computational scheme is based on a combination of a splitting finite difference method and an iterative procedure. Simulations are performed with the use of Matlab programming. Computational experiments allow one to examine the interactions of nutrient availability and biomass production under variation of dynamical modes of the biological system.

**Key words:** *diffusion-wave equation, fractional derivative, splitting finite difference method, model of bacterial biomass growth.*

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## Introduction

Modelling of many reactive-diffusive phenomena, representing spatial and temporal changes in concentrations of substances or accompanying transfer processes often do not agree with real observations for a number of amorphous structures, porous media, liquid crystals, biopolymers, proteins, biosystems, ecosystems, etc. Such processes can be accompanied by significant gradient changes in analyzed characteristics or a very long waiting time for aftereffects. One of the promising approaches to derive models of nonstandard diffusion and transport phenomena in heterogeneous, complex-structured, and hereditary systems is based on the apparatus of fractional calculus [1].

Mostly, biological objects exhibit heterogeneity and self-similarity of structures, formation of fractal patterns, irregularity and scalability properties, nonlinear, stochastic, and time-delay dynamics [2–6]. For example, time-fractional differential equations allow one to describe time memory effects which are common for different bacterial species [5, 7–9]. In addition, bacterial biofilms as complex self-similar structures can be under consideration. Biofilms are aggregations of microorganisms growing at interfaces

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embedded in a polymer matrix. The formation of such structures plays a vital role in medicine, because biofilms involved in bacterial infections can become resistant to antibiotics [10, 11].

A well-known deterministic approach has been successfully applied to explore bacterial population dynamics [13]. Specifically, a model of growth of microorganisms formalized by a system of ordinary differential equations has been proposed by J. Monod, considering the saturation of the growth rate of a culture on a nutrient substrate. Further, M. Droop has described the dependence of biomass on the cell quota growth of microalgae cultivated in a photobioreactor based on the logistic model. Later, various modifications of the model of bacterial biomass growth have been developed. Nowadays, models also consider the spatial heterogeneity of biofilms and can be formalized with partial differential equations (PDEs). Moreover, for modeling biofilms growth, a hybrid approach has been proposed that combines a stochastic – cellular automaton model and a deterministic model to estimate nutrient concentration [2].

For instance, the model proposed in [10, 12] can be considered as a modification of the Monod model, taking into account space-time distributions of the biomass as well as the nutrient concentration. For this study, due to bacterial dynamics exhibiting self-similar character and time memory effects, it was of interest to investigate the capability of a time-fractional modification of the reaction-diffusion model to explore the complex dynamics of bacterial biomass. It should be mentioned that a fractional approach has also been previously applied to modify the chemostatic model to describe time memory effects in bacterial populations [7]. The overall goal of the present study is to develop the 2D time-fractional reaction-diffusion model of bacterial biomass growth with a focus on the application of numerical methods.

## 1 The mathematical model

As above, the considered model describing the dynamics of nutrient concentration and bacterial biomass density is governed by an initial-boundary value problem for a system of semilinear PDEs [10, 12]. In the framework of this study, we suggest modifying this model by means of the introduction of the time-fractional differential operators to mathematically generalize the complex dynamics of the bacterial biomass as well as the nutrient concentration:

$$\frac{\partial^\alpha c}{t^* \partial t^\alpha} = D_c \Delta c - k_1 \frac{cm}{k_2 + c}, \tag{1}$$

$$\frac{\partial^\beta m}{t^* \partial t^\beta} = D_m(m) \Delta m + k_3 \frac{k_1 cm}{k_2 + c} - k_3 k_4 m, \tag{2}$$

$$c\big|_{t=t_0/t^*} = c_0, \quad m\big|_{t=t_0/t^*} = m_0, \quad 0 < x < L_x, \quad 0 < y < L_y, \tag{3}$$

$$c\big|_{x=L_x} = C, \quad \left.\frac{\partial c}{\partial \mathbf{n}}\right|_{\partial\Omega \setminus \{x=L_x\}} = 0, \quad \left.\frac{\partial m}{\partial \mathbf{n}}\right|_{\partial\Omega} = 0, \quad t_0/t^* \le t \le T/t^*, \tag{4}$$

where $0 < \alpha,\ \beta \le 2$ are the orders of time-fractional derivatives in the Riemann – Liouville sense, $c(x, y, t)$ is the nutrient concentration in g/m$^3$; $m(x, y, t)$ is the biomass density in g/m$^3$ ; $D_c$, $D_m$, $k_1$, $k_2$, $k_3$, $k_4$, $c_0$, $m_0$, $C$ are the model parameters; $L_x$, $L_y$ define the size of a solution domain in m; $\partial\Omega$ is the boundary of the solution domain;

$\theta = t \cdot t^*$ is the time in days; $t^*$ is the characteristic time in days; $t_0$ and $T$ are the initial and the observation time in days.

The solvability of considered types of problems is rather well studied in the classical case. Notably, existence and uniqueness of solution for nonlocal nonlinear evolution equations arising in population dynamics has been supported by [14]. In [15], the Monod model for biochemically reacting contaminant transport in the subsurface regarding higher order regularity of solutions has been analyzed. Basically, a specific model (1)–(4) requires further additional theoretical study. As far as the construction of analytical solutions for fractional PDEs results in serious difficulties, using numerical methods is justified. In particular, to solve 2D problem, here we apply a finite difference splitting method.

## 2 Computational scheme

The computational scheme for implementing the 2D anomalous diffusion model is based on the Grunwald– Letnikov formula and a finite difference splitting method (namely, the Yanenko scheme). Let us introduce a rectangular space-time mesh for two space coordinates $\Omega^{\tau}_{\overline{h_1,h_2}} = \{x_i = (i-1)h_1,\ i = \overline{1, N+1},\ y_j = (j-1)h_2,\ j = \overline{1, M+1},\ t^k = (k-1)\tau,\ k = \overline{1, K+1}\}$. Further, we can apply a two-layer scheme for equations (1)–(2). For the first equation for $k+1/2$ layer, we have

$$-R_x c^{k+1/2}_{i-1,j} + [1+2R_x]\, c^{k+1/2}_{i,j} - R_x c^{k+1/2}_{i+1,j} = -\sum_{p=1}^{k} g_p c^{k-p+1}_{i,j} - t^* \tau^{\alpha} F^k_{i,j} + \psi^{k+1/2}_{i,j}. \quad (5)$$

For the first equation at $k+1$ layer, we obtain

$$-R_y c^{k+1}_{i,j-1} + [1+2R_y]\, c^{k+1}_{i,j} - R_y c^{k+1}_{i,j+1} = c^{k+1/2}_{i,j}. \quad (6)$$

Here we use the following notations

$$R_x = \frac{D_c \tau^{\alpha} t^*}{h_1^2},\ R_y = \frac{D_c \tau^{\alpha} t^*}{h_2^2},\ \psi^{k+1/2}_{i,j} = \sum_{v=0}^{\lfloor \alpha \rfloor} \frac{t^* \tau^{\alpha} t^{k+1/2}}{\Gamma(v+1-\alpha)} \left(c^1_{i,j}\right)^{(v)},\ F^k_{i,j} = \frac{k_1 c^k_{i,j} m^k_{i,j}}{k_2 + c^k_{i,j}}.$$

The weights are specified as follows $g_p = \dfrac{\Gamma(p-\alpha)}{\Gamma(-\alpha)\Gamma(p+1)}$. It is known that the Grunwald – Letnikov formula can be correctly applied only for problems with homogeneous initial conditions. In our case we should take into account a correction term $\psi$ added to the scheme (5). Since we have a nonlinear function $F^k_{i,j}$ depending on the functions $c^k_{i,j}$ and $m^k_{i,j}$, the general scheme should be supplemented by the iterative procedure

$$\left\{c^{(s)}_{i,j}\right\} \to c^{k+1/2}_{i,j}, \quad s = 1, 2, \ldots,\ c^{(1)}_{i,j} = c^k_i.$$

We can construct the computational scheme for the equation (2) in similar way. For $k+1/2$ time-layer, we have

$$-\widetilde{R}^k_{x\,i,j} m^{k+1/2}_{i-1,j} + \left[1 + 2\widetilde{R}^k_{x\,i,j} - t^* \tau^{\beta} \Phi^{k+1/2}_{i,j}\right] m^{k+1/2}_{i,j} - \widetilde{R}^k_{x\,i,j} m^{k+1/2}_{i+1,j} =$$

$$= -\sum_{p=1}^{k} q_p m^{k-p+1}_{i,j} + \widetilde{\psi}^{k+1/2}_{i,j}.$$

Table 1: Model parameters for problem (1)–(4)

| Name | Parameter | Numerical value | Unit |
|---|---|---|---|
| $\mu$ | Parameter for the biomass concentration | 10000 | g/m$^3$ |
| $c_0$ | Initial value of nutrient medium concentration | 1 | g/m$^3$ |
| $D_c$ | Diffusion coefficient for the substrate | $8 \cdot 10^{-5}$ | m$^2$/day |
| $D_m^*$ | Diffusion parameter for bacterial cells | $10^{-12}$ | m$^2$/day |
| $k_1$ | Power consumption rate | 9.52 | 1/day |
| $k_2$ | Monod saturation constant | 4 | g/m$^3$ |
| $k_1k_3$ | Maximum specific growth rate | 6 | 1/day |
| $k_3k_4$ | Bacteria outflow rate | 0.4 | 1/day |
| $L_x = L_y$ | Linear size of the domain | 0.1 | mm |

Hence, for $k+1$ time-layer, we obtain

$$-\widetilde{R}^{k+1/2}_{y\,i,j} m^{k+1}_{i,j-1} + \left[1 + 2\widetilde{R}^{k+1/2}_{y\,i,j}\right] m^{k+1}_{i,j} - \widetilde{R}^{k+1/2}_{y\,i,j} m^{k+1}_{i,j+1} = m^{k+1/2}_{i,j},$$

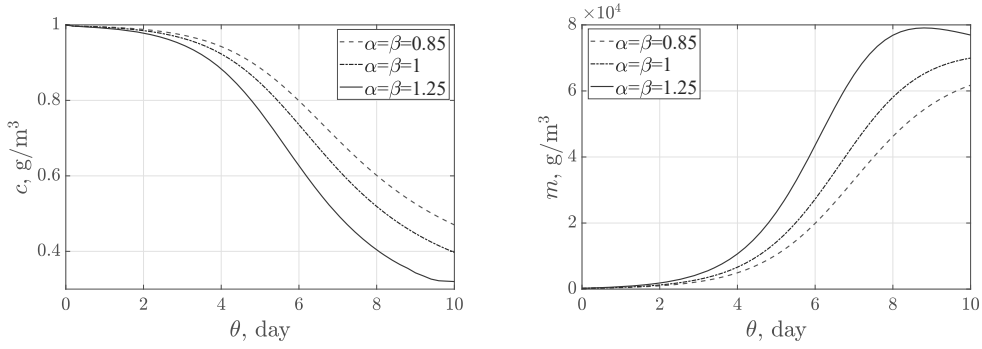
where $\widetilde{R}^{k}_{x\,i,j} = \dfrac{D^{k}_{m\,i,j}\tau^{\beta}t^{*}}{h_1^2}$, $\widetilde{R}^{k}_{y\,i,j} = \dfrac{D^{k}_{m\,i,j}\tau^{\beta}t^{*}}{h_2^2}$, $q_p = \dfrac{\Gamma(p-\beta)}{\Gamma(-\beta)\Gamma(p+1)}$, the correction term is set to be $\widetilde{\psi}^{k+1/2}_{i,j} = \sum\limits_{v=0}^{\lfloor\beta\rfloor} \dfrac{t^{*}\tau^{\beta}t^{k+1/2}}{\Gamma(v+1-\beta)} \left(m^{1}_{i,j}\right)^{(v)}$, $\Phi^{k+1/2}_{i,j} = \dfrac{k_3k_1c^{k+1/2}_{i,j}}{k_2 + c^{k+1/2}_{i,j}} - k_3k_4$.

Diffusion coefficient for bacterial biomass is defined as $(D_m)^{k}_{i,j} = \overline{D}_m(m^{k}_{i,j}) = D^{*}_m\left(m^{k}_{i,j}\right)^4/\left(\mu - m^{k}_{i,j}\right)^4$, for $m^{k}_{i,j} \le 0.8\mu$ and $(D_m)^{k}_{i,j} = \overline{D}^{*}_m(0.8\mu)$ otherwise. Let us assume that only one bacterial colony is located in the center of the computational domain at the initial moment $m^{1}_{i,j} = \kappa \exp\left(-r^2/\sigma\right)$ for $r \le \widetilde{r}$ and $m^{1}_{i,j} = 0$ otherwise, where $r^2 = \left(x_i - 0.5L_x\right)^2 + \left(y_j - 0.5L_y\right)^2$; $\sigma$, $\kappa$, and $\widetilde{r}$ are the parameters empirically estimated. In the same way, an iterative procedure is introduced into the computational algorithm for each time layer. Noted also that the Yanenko scheme is characterized by $O(h_1^2 + h_2^2 + \tau)$ order of accuracy. We also applied nonsymmetric approximations of the second order of accuracy for the Neumann boundary conditions.

## 3 Numerical experiments

To perform numerical experiments we initialize a set of model parameters listed in Table 1 previously specified for the "intege" model [12]. Figure 1 shows the time-dependent distributions of the nutrient concentration and biomass density at the central point of the computational domain under varying dynamical regimes. We set the boundary value of the nutrient concentration $C = 1$ g/m$^3$, the observation time equals 10 days. The empirical parameters are set to be $\sigma = 10^{-11}$m$^2$, $\kappa = 0.05\mu$ g/m$^3$, and $\widetilde{r} = 0.05L_x$ m.

In terms of the anomalous diffusion process, we can explore the implementation of three different dynamical regimes of the biosystem: the subdiffusion at $\alpha = 0.85$, the classical diffusion at $\alpha = 1$, and the superdiffusion at $\alpha = 1.25$. Computational experiments indicate direct dependence of the velocity of bacteria growth as well of the bacterial nutrient consumption on the order of the time-fractional derivative. When the superdiffusion




**a** **b**

Fig. 1: The temporal profiles of the nutrient concentration — a and biomass density — b calculated at the central position for different values of orders of fractional derivatives.

regime is realized, the observed processes occur with greater intensity and the absolute values of the key characteristics reach values deviating by $20 - 30\%$ compared to the classical case. On the contrary, the implementation of the subdiffusion regime leads to a slowdown in the dynamics of both growth and nutrient consumption.

## Conclusion

In summary, in order to describe the complex growth dynamics of the bacterial biomass, a time-fractional modification of the 2D model was considered. An implicit computational scheme was constructed based on the Grunwald – Letnikov formula and an iterative procedure. The computational algorithm was implemented using Matlab programming. The considered approach enables one to generalize and significantly expand the class of deterministic models used to model a bacterial population due to the possibility of varying dynamic regimes.

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*Мороз Л. И.* Численное дробно-дифференциальное моделирование диффузионно-волновых процессов роста бактериальной биомассы. *Дальневосточный математический журнал.* 2022. Т. 22. № 2. С. 207–212.

## АННОТАЦИЯ

Рассматривается дробно-дифференциальная модель диффузионно-волновых процессов в приложении к описанию явления бактериального роста. Двумерная модель формализуется в виде начально-краевой задачи для системы полулинейных дифференциальных уравнений в частных производных с дробной производной по времени. Вычислительная схема основана на комбинации метода расщепления и итерационной процедуры. Компьютерное моделирование проведено в Matlab. Вычислительные эксперименты позволяют исследовать взаимодействие концентрации питательных веществ и роста биомассы при варьировании динамических режимов функционирования биосистемы.

Ключевые слова: *диффузионно-волновое уравнение, производная дробного порядка, конечно-разностная схема расщепления, модель роста бактериальной биомассы.*