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Decomposition Solution of a Mathematical Model for Capillary Formation

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Abstract: We compare the numerically calculated solution of a mathematical model for capillary formation in tumor angiogenesis with the one that is obtained by Adomian's decompostion method. This methods requires no additional assumptions and linearization. Numerical comparison indicates that there is a close agreement between the two solutions.

Keywords: Adomian's decomposition method, capillary formation, tumor angiogenesis.

1 Introduction

In this paper, we consider the Endothelial Cell (EC) equation

$$\frac{\partial \eta}{\partial t} = D_\eta \frac{\partial}{\partial x}\left(\eta \frac{\partial}{\partial x}\left(\ln \frac{\eta}{\tau}\right)\right) \tag{1}$$

originally presented in [10]. Here $\eta = \eta(x,t)$ is the concentration of EC, D_η is the EC diffusion coefficient in the capillary, and τ is the so called transition probability function. This function has the effect of biasing the random walk of endothelial cells. In this case, it is known that [7,8] the walk is influenced by the proteolytic enzyme (c) it produces in response to the angiogenic factor that has made its way to the cell receptors and by the fibronectin (f) in the basement lamina, i.e., we write

$$\tau(x) = \tau(c(x), f(x)). \tag{2}$$

A simple transition probability which reflects the influence of enzyme and fibronectin on the motion of endothelial cells is $\tau(c(x), f(x)) = \tau_1(c(x))\tau_2(f(x))$ where

$$\tau_1(c(x)) = \left(\frac{a_1 + c(x)}{a_2 + c(x)}\right)^{\gamma_1}, \quad \tau_2(f(x)) = \left(\frac{b_1 + f(x)}{b_2 + f(x)}\right)^{\gamma_2}. \tag{3}$$

Here the a_i, b_i are constants such that $0 < a_1 << 1 < a_2$ and $b_1 > 1 >> b_2 > 0$, and γ_1, γ_2 are positive constants. We impose zero flux boundary conditions for the cells in the capillary:

$$D_\eta \eta \frac{\partial}{\partial x} \ln\left(\frac{\eta}{\tau(c(x), f(x))}\right) = 0 \quad (\text{at } x = 0, 1). \tag{4}$$

Initially we assume that there is a constant amount of EC along the capillary, i.e, we take

$$\eta(x, 0) = \eta_0 > 0. \tag{5}$$

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It is easy to see that

$$\frac{\partial}{\partial x}\left(\ln\frac{\eta}{\tau}\right)=\frac{\eta_x}{\eta}-\frac{\tau_1'(c)}{\tau_1(c)}c_x-\frac{\tau_2'(f)}{\tau_2(f)}f_x, \tag{6}$$

since $\tau(c,f)=\tau_1(c)\tau_2(f)$. If we set

$$\Omega(c)=\frac{\tau_1'(c)}{\tau_1(c)},\quad \Psi(f)=\frac{\tau_2'(f)}{\tau_2(f)}, \tag{7}$$

Eqs.(1) and (4) become

$$\frac{\partial\eta}{\partial t}=D_\eta\frac{\partial}{\partial x}\Big[\eta_x-\eta S(x)\Big] \tag{8}$$

and

$$\eta_x-\eta S(x)=0,\quad \text{at } x=0,1 \tag{9}$$

respectively, where

$$S(x)=\Omega(c)c_x+\Psi(f)f_x. \tag{10}$$

In fact, Eq.(8) can be written as

$$\frac{\partial\eta}{\partial t}=D_\eta\Big[\eta_{xx}-\eta_x S(x)-\eta S'(x)\Big]. \tag{11}$$

2 The Decomposition Method

In this section we consider Eq.(11) in an operator form

$$L_t(\eta)=D_\eta\Big[L_{xx}(\eta)-S(x)L_x(\eta)-S'(x)\eta\Big], \tag{12}$$

with the initial and boundary conditions, where the notations $L_t=\frac{\partial}{\partial t}$, $L_x=\frac{\partial}{\partial x}$ and $L_{xx}=\frac{\partial^2}{\partial x^2}$ symbolize the linear differential operators. We assume the integration inverse operator ${L_t}^{-1}$ exist, and it is defined as ${L_t}^{-1}=\int_0^t(.)du$. Therefore, we can write the solution [1-4]

$$\eta(x,t)=\eta(x,0)+D_\eta{L_t}^{-1}\Big[L_{xx}(\eta)-S(x)L_x(\eta)-S'(x)\eta\Big]. \tag{13}$$

One can write the solution in series form [1] as

$$\eta(x,t)=\sum_{n=0}^{\infty}\eta_n(x,t). \tag{14}$$

To find the solution, one solves the recursive relations

$$\eta_0=\eta(x,0),\quad \eta_{n+1}=D_\eta{L_t}^{-1}\Big[L_{xx}(\eta_n)-S(x)L_x(\eta_n)-S'(x)\eta_n\Big],\ n\geq 0. \tag{15}$$

Let $\phi_n(x,t)$ be the partial sum

$$\phi_n(x,t) = \sum_{k=0}^{n} \eta_k(x,t) \ , \quad n \geq 0, \tag{16}$$

so that the desired solution of Eq.(8) will be

$$\eta(x,t) = \lim_{n\to\infty} \phi_n(x,t). \tag{17}$$

3 Application

In Eq.(3) we take

$$c(x) = Ax^n(1-x)^n, \quad 0 \leq x \leq 1, \tag{18}$$

for enzyme where A and n are positive constants. This simple form is chosen to form a unimodal enzyme distrubition as in [9] & [11]. Since proteolytic enzyme acts as a catalyst for fibronectin degradation we approximate the fibronectin by the function

$$f(x) = 1 - Bx^n(1-x)^n, \quad 0 \leq x \leq 1, \tag{19}$$

where B is positive constant.

The sensitivity parameters a_i, b_i, γ_i in (3) were chosen for illustrative purposes. We therefore take $a_1 = 0.1, a_2 = 2, b_1 = 10, b_2 = 0.1, \gamma_1 = 1, \gamma_2 = 1$. We also take $A = 28 \times 10^7, n = 16, B = 0.22 \times 10^9$ and $\eta_0 = 1$. In [9] & [10] we estimated the scaled diffusion coefficient $D_\eta = 0.00025$.

For this choices of $c(x)$ and $f(x)$, the function $S(x)$ in (10) becomes

$$S(x) = \frac{(a_2 - a_1)}{(a_1 + c(x))(a_2 + c(x))} c'(x) + \frac{(b_2 - b_1)}{(b_1 + f(x))(b_2 + f(x))} f'(x). \tag{20}$$

Therefore, from (15) we have

$$\eta_0(x,t) = 1, \tag{21}$$

$$\eta_1(x,t) = -D_\eta S'(x)t, \tag{22}$$

$$\eta_2(x,t) = D_\eta^2 \left[-S'''(x) + S(x)S''(x) + S'(x)^2 \right] \frac{t^2}{2!}, \tag{23}$$

$$\eta_3(x,t) = D_\eta^3 \Big[-S(x)^V + 2S(x)S^{IV}(x) + 3S'(x)S'''(x) - \ldots$$
$$S(x)^2 S'''(x) - 2S(x)S(x)'S''(x) + \ldots (S''(x))^2 - (S'(x))^3 \Big] \frac{t^3}{3!}$$

and so on. Therefore, the series solution will be approximated by

$$\eta(x,t) = \eta_0(x,t) + \eta_1(x,t) + \eta_2(x,t) + \eta_3(x,t) + \cdots. \tag{24}$$

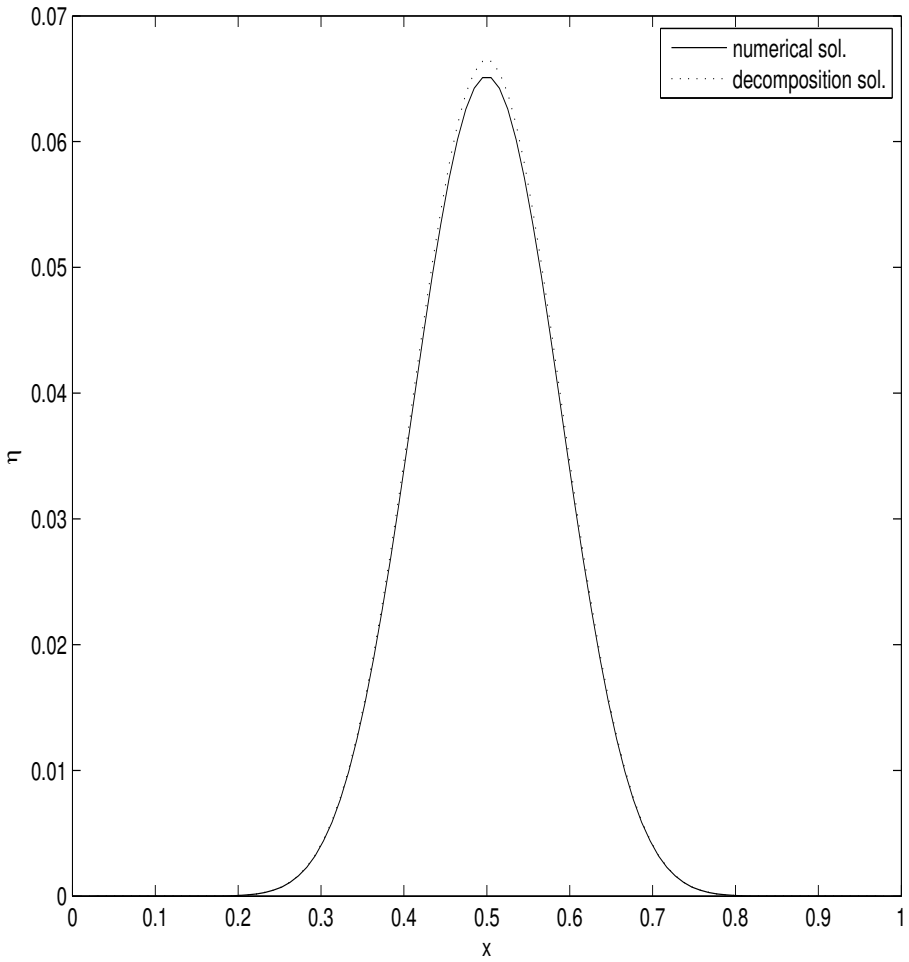

Fig. 1: EC at $t = 0.6$.

4 Conclusion and results

Figure 1 shows the comparison between the numerical (obtained by the method of lines [9]) and decomposition solutions of Eq.(1) at $t = 0.6$ while Figure 2 shows the comparison at $t = 0.9$.

It is clear from the two figures that there is a very close agreement between the numerically calculated solution and the one obtained by the Adomian's decomposition method. A very good approximation to the numerical solution can be achieved by adding new terms to the decomposition series although it is kind of tedious to compute these terms in this case.

In conclusion, the decomposition method provides very accurate approximate solutions to linear and nonlinear problems [5,6]. It also does not require large computer memory, and avoids biologically unrealistic assumptions.

Competing interests

The authors declare that they have no competing interests.

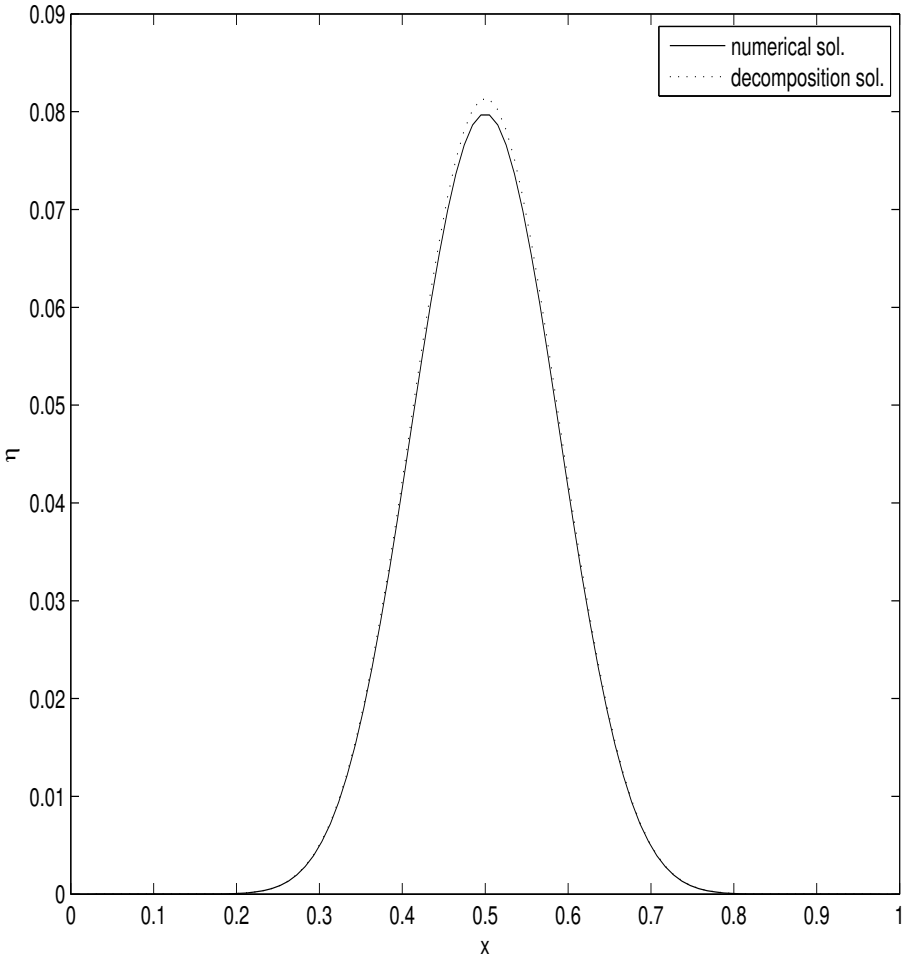

Fig. 2: EC at $t = 0.9$.

Authors' contributions

All authors have contributed to all parts of the article. All authors read and approved the final manuscript.

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