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Engineering Mathematics

Bachelor-Thesis

Continuous Modeling of Extracellular Matrix Invasion by Tumor Growth

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Zusammenfassung

Krebszellen können sich vom Primärtumor lösen und das umgebende Gewebe abbauen. Kontinuierliche mathematische Modelle wurden in der Vergangenheit mehrmals verwendet, um diesen Prozess besser zu verstehen. In diesem Zusammenhang basiert ide Modelle in der Regel auf mindestens drei Schlüsselkomponenten: den Tumorzellen, dem umgebenden Gewebe oder der extrazellulären Matrix (ECM) und den matrixabbauenden Enzymen (MDE). Das hier verwendete Modell beschreibt die obigen drei genannten Parameter, wobei Nullstrom Randbedingungen verwendet werden.

Die Analyse dieses Modells wird in der Literatur größtenteils in $1D$ durchgeführt, und einzelne Beispiele wurden in $2D$ gemacht. Allerdings zeigen vorläufige Reproduktionen des Modells, dass höhere Dimensionen signifikant unterschiedliche Ergebnisse liefern. Daher stellt sich die Frage, ob die Parameter für dieses Modell für Simulationen in $2D$ oder $3D$ unterschiedlich ausgewählt werden müssen oder ob die Ergebnisse und Analysen für den eindimensionalen Fall inkorrekt sind.

Darüber hinaus wurde in der Literatur die heterogene Struktur der extrazellulären Matrix (ECM) bereits behandelt. Die Struktur der epithelialen Schicht und der benachbarten extrazellulären Matrix ist jedoch in biologischem Gewebe organisierter als in den gezeigten Simulationen und anderen Beispielen. Daher könnten einfachere Unterteilungen der Geometrie in ECM-Gewebe aussagekräftigere Ergebnisse liefern.

Das Ziel dieser Arbeit ist es, einerseits die Parameter und das Modell für höhere Dimensionen zu untersuchen und andererseits eine einfache Heterogenität der ECM-Struktur in Betracht zu ziehen.

Abstract

Cancer cells can migrate from the primary tumor and degrade the surrounding tissue. Continuous mathematical models have been used several times in the past to better understand this process. In this context, the model is usually based on at least three key species, the tumor cells, the surrounding tissue or extracellular matrix (ECM) and the matrix degradative enzymes (MDE). The investigated model in this work describes the above mentioned 3 parameters, with zero-flux boundry conditions.

The analysis of this models is mostly done in $1D$ in the literature and individual examples were done in 2D. However, reproductions of the model show that higher dimensions produce significantly different results. The question therefore arises as to whether the parameters for this model need to be selected differently for simulations in 2D or 3D, or whether the results and analysis for the one dimensional case is incorrect.
Ergebnis einfuegen

Furthermore, the heterogeneous ECM structure has been addressed in the literature. However, the structure of the epithelial layer and the adjacent extracellular matrix is more organized in biological tissue than in the simulations shown in and, for example. Therefore, simpler subdivisions of the geometry into ECM tissue could provide more meaningful results.

The aim of this work is to investigate the parameters and the model for higher dimensions on the one hand, and to consider a simple heterogeneity of the ECM structure on the other hand.

Contents

1 Introduction

Modelling tumor growth plays a key role in understanding the complex mechanisms, governing development and progression of cancer diseases. Since cancer is one of the leading death causes worldwide and many of its forms are incurable, challenges in the area of Oncology require researchers to have a deep understanding in as well the biological foundation, which lead to malignant cell mutation and factors for tumor growing and spreading, as well as the mathematical models used for simulating these events. This Bachelorthesis is dedicated to analyse Anderson et al.'s [1, 2] model for tumor modelling. The dynamics of tumerous growth are an intricate system, which is influenced by numerous biological and chemical factors, as well as genetic pre-dispostitions, the surrouding tissue of cancer cells, angiogene processes an interactions with the immune system. The integration of these factors in mathematical models allow us to decode these complex interactions with quantification and help us understand the fundamental mechanisms, which surroud cancerous diseases, as the last year's experience has shown.
Mathematical models are a very important part in Oncology. They are used to quantify biological phenomena and therefore help to predict and understand tumor development and treatment response. In Mathematical Oncology we differentiate between continuous, discrete and hybrid models. For the continuous type, cells and tissue are described over time with differential equations modelling continuous quantities like in our case the cell or extracellular matrix density. In the discreate case, a entity based model is used, pursued with the goal to better understand the phenoma on cell level. This approach allows the researcher to better implement biological effects a cell has with its outer circumstances, like interaction with other cells, nutrients or other microorganisms. As the name implies do these models use discrete values to describe the temporal course of events. Hybrid models try to combine both approaches, to offer efficient systems capturing cell level events as well as continuous changes in outer circumstances.
In this work we are investigating how a continuous model proposed by Anderson et al. [1, 2] to analyse tumur development in the early stages performs in the case of different dimensions and free parameter values. The model examines the first two stages of a cancer disease; tumor initiaition, where the tumor cells are localized to a small area and have not yet spread throughout the body; and tumor promotion, with the tumor cells growing and proliferating, invading the surrounding tissue. From examples of the original paper we can already see that the model's results vary with the dimensionality of the space we are modelling the partial differential equations in. Our main focuse lies on comparing simulations of two dimensions with those of three dimensions of extracellular matrix invasion by the tumor growth. Additionally to the variation of dimensions we will have a closer look on how the geometry of the extracellular matrix will influence the tumor development.
Another point fo interest is the investigation of how the model's free parameters influence the tumor dynamics growth. An important task is to give those parameters a biological meaning and to eventually gain insight to how to adjust them to make the simulation more realistic.

2 Theoretical Basics

2.1 Basics of Tumor Biology

The body of a living creature is made up of more than 200 different types of cells, the coordination between the cells and their surroundings keep the body running. Each of these cells is built from the genetic information encoded in the DNA, located in the cells' nuclei. Though the nucleotide sequence of DNA is well checked and maintained throughout the cell's life, mutations still occur that cause the changes in the DNA of a cell. These mutations may be of a positive, negative or neutral nature. In the case of a negative mutation this alternation of the DNA may cause diseases, with cancer being one of them. The failure of the complex system managing cell birth, proliferation, and cell death (apoptosis) causes cancer, resulting in an uncontrolled cell proliferation in a at first local area. An conglomeration of cancer cells is called a tumor.
A cancer disease typically follows five stages. First the tumor initiation phase where it comes to the above explained genetic mutations of normal cells. The next stage is the tumor promotion stage, in which the mutated cells of phase one may experience further genetic alterations, with the result of uncontrolled growth and proliferation of the cancerous cells. The third stage is the tumor progression stage, where the cancerous cells progress in growing and proliferating, reaching a critical mass, they form a tumor at a local site of the body. Fourth comes the invasion stage, here the tumor is able to invade surrouding tissue and enter the blood circulation system or the lymphatic system. Next the tumor cells which have invaded the blood circulation of lymphatic system spread throughout the body and form new tumors. This stage is called Metastization. To further grow the tumors need to have access to nutrient and oxygen supply. During angiogensis a tumor develops blood vessels of its own securing its nutritional provision. At this stage first symptoms of host may appear, enabling medical treatment.
In our model the focus lies on the first two stages; tumor invasion and tumor progression, so we are going to have a deeper look at those two phases.The tumor invasion stage is characterized by the malignant cells gaining the ability to penetrate and invade the surrouding tissuse. The tumor cells break through the normal tissue barrier and infiltrate neigbhoring structures. In order to do so the cancer cells produce so called matrix-degrading enzymes which break down the extracellular-matrix. This not only helps local spreading but also destroys otherwise healthy tissue and cells in the affected area. In the next phase the tumor progresssion stage, the tumor has grown larger and the cancerous cells take on more aggressive behaviour, by invading the surrounding area further. Whilst they keep growing uncontrolled they are also affected by further genetic instabilities, which lead to more mutations among the tumor cells, resulting possibly in the development of resistent cancer cells. Already in this stage the affected area is exposed to heavy tissue damage and functional disabilities.
The most important factors influencing those two phases are the genetic dispoistions of the tumor cells towards proliferation and the evasion of apoptosis, which increase the invasive potential. Another important factor is geometry of the extracellular matrix, as well as the exact macromolcules which make it up. A strong immune biological defense reaction also helps the body defend against the spreading of the cancer cells, so evasion

of detection and destruction of the tumor cells plays a key role for the first stages. To invade the affected area the malignant cells need to be able to move freely and fastly. In order to do so cancer cells can gain the ability to lose adhestion properties which healthy cells have, to allow migrating into surrouding tissue.

2.2 Mathematical Methods in Oncology

Mathematical Methods and Models in Oncology play a cruical role in analysing, understanding and predicting cancer development. Since the obejctive of this research underlies complex and intricate biological systems and mechanisms, there exist many models, which find their repsective application in many distinct areas of this research field. These methods can be coarsely divided into three sections; continuous, discrete and hybrid models. For describing tumor growth, exponential and logisitc growth models are often used, the later allowing limiting factors to play a role during modelling. These methods are a subclass of the differential equations approach which base their functionality on a ordinary or partial differential equation, studying the continuous approach. Like in our model they are not limited to consist of one equation but can of many, therefore also incorporating limiting or accellerating factors. These models in generals deal with continuous parameters like densities, or fluid concentrations, for example spacial and temporal nutritional supply or drug concentration, as well as their effects on the affected area over time. Discrete models use a agent-based approach, where the participating individual entities are modeled as objects which can interact on their environment, this means for example cell-cell interaction or cell-tissue interaction. This enables researchers to focus on biological effects during modelling. With these approaches we can also simulate genetic and evolutionary events. For example studying the genetic alternations of tumor cells.
Hybid models combine both aforementioned methods, of using continuous and discrete models. Like in the model proposed by Franssen et al. [3], these apporoaches allow to incorporate the exactness of continuous models with the wide range of biological effects of discrete models.
But no all models try to model tumor growth, there others concerning for example optimality regarding drug dossages or radition exposition, offering personalized treatment, or Machine Learining and Data Mining methods analysing large datasets, to identify patters and predict outcomes. The later method may be used in all kinds of applications, for example spacial or temporal cancer development but also for drug dosage optimization for individual patients. Putting all these methods together gives us an powerful toolbox to simulate and understand cancer biology. Like the last years have shown they are applied in a wide range, offering insight for all areas of cancer research. Therefore it is important not only to come up with methods but to also evaluate their usefulness and meaningfulness regarding different areas of research.

3 Modelling

3.1 Mathematical Formulation

The model propsed by Anderson et al. [1, 2] and Chaplain et al. [1, 3, 4], extended with terms for cell modelling cell proliferation consists of a system of linearly coupled partial differential equations:

$$\frac{\partial c}{\partial t} = D_c \Delta c - \chi \nabla \cdot (c \nabla e) + \mu_1 c \left(1 - \frac{c}{c_0} - \frac{e}{e_0}\right) \tag{1}$$

$$\frac{\partial e}{\partial t} = -\delta m e + \mu_2 c \left(1 - \frac{c}{c_0} - \frac{e}{e_0}\right) \tag{2}$$

$$\frac{\partial m}{\partial t} = D_m \Delta c + \mu_3 c - \lambda m \tag{3}$$

with zero-flux boundary conditions,

$$n \cdot (-D_c \nabla c + c \chi \nabla e) = 0 \tag{4}$$

$$n \cdot (-D_m \nabla m) = 0 \tag{5}$$

where the free parameters are D_c, D_m, χ, δ, μ_1, μ_2, μ_3 and λ.
The variable c describes the tumor cell density, e the density of the extracellular matrix and m the matrix-degrading enzyme concentration. All of those functions are mathematically defined to be mapping a 1,2 or 3 dimensional spacial value and a point in time to a scalar value describing the concentration at a specific point in space and time, $\{c, e, m\} : \mathbb{R}^3 \times \mathbb{R} \to \mathbb{R}$.
To derive at the expression for the tumor cell concentration c we are going to assume that the tumor cell's moement is subject to two influences, haptotaxis and random movement. Haptotaxis is a directed migratory response of cells to gradients of fixed or bound chemicals [1] and random movement is influenced by for example mechanical stress, electric voltage or other such physical effects. To get an expression for how much or how fast the tumor cells move, we need to define what flux is, flux is defined to be the amount of a substance which crosses a unit area in unit time. Incorporating the two assumed influencing factors into our mathematical model we define the haptotatic flux $J_{hapto} = \chi c \nabla e$, where χ is the haptotactic flux coefficient, and the random flux $J_{random} = -D_c \nabla c$, where D_c is random mobility constant. In general this parameter could also be a function of both extracellular matrix and matrix-degrading enzyme concentration $D_c \to D(e, m)$. As we know cells proliferate and grow over time, so we want to respect this in our model with a term for tumor cell proliferation: $\mu_1 c(1 - \frac{c}{c_0} - \frac{e}{e_0})$. The idea is that this term describes the cell proliferation with a logisitic growth model, μ_1 describing the proliferation rate. In the inital model proposed by Anderson et al. [1, 2] and Chaplain et al. [1, 3–5], they did not respect proliferation of tumor cells and extracellular matrix and therefore applied a conservation equation for the tumor cells $\frac{\partial c}{\partial t} + \nabla \cdot (J_{hapto} + J_{random}) = 0$, in our model we extend this conservation formula with a proliferation rate. Explicitly inserting the flux formulas and logisitc growth function for the tumor cells gives us: $\frac{\partial c}{\partial t} + \nabla(J_{hapto} + J_{random}) + \mu_1 c(1 - \frac{c}{c_0} - \frac{e}{e_0}) = \frac{\partial c}{\partial t} + \chi \nabla(c \nabla e) - D_c \Delta c + \mu_1 c(1 - \frac{c}{c_0} - \frac{e}{e_0})$.

Which is equivalent to equation 1.
To model the extracellular-matrix concentration e, we asssume that the enzymes degrade the extracellular matrix upon contact. This assumption is simply modeled by the equation $\frac{\partial e}{\partial t} = -\delta m e$, δ is a positive constant describing this annihilation process. To this we also add a term describing the proliferation process: $\frac{\partial e}{\partial t} = -\delta m e + \mu_2 c(1 - \frac{c}{c_0} - \frac{e}{e_0})$.
Modelling the matrix-degrading enzyme concentration m, we combine a diffusion term with production and decay terms. The diffusion term is described like in tumor cell concentration, with the addition that haptotatic fluxes are neglected and only random mobility is assumed, $J_{random} = -D_m \nabla m$. The production term depends on the tumor cell concentration and the decay term on the extracellular matrix concentration. This results in the term: $\frac{\partial m}{\partial t} = \nabla J_{random} + \mu c - \lambda e = D_m \Delta m + \mu_3 c - \lambda m$, μ and δ describing production and decay rates.

3.2 Numerical Model and Parameters

To make solving the model easier we are first going to non-dimensionalise all the equations 1 to 5 in a standard way, with the goal to rescale the space domain onto unit size. For one space dimension this results in the unit interval $[0, 1]$, for two dimensions the unit square $[0, 1] \times [0, 1]$ and for three dimensions the unit cube $[0, 1] \times [0, 1] \times [0, 1]$. We start with rescaling the distance with an appropriate length scale L and the time with $\tau = \frac{L^2}{D}$ (D being a chemical diffusion coefficient). The three variables are being rescaled with their initial values respectively c_0, e_0, m_0, which gives us this:

$$\tilde{c} = \frac{c}{c_0}; \tilde{e} = \frac{e}{e_0}; \tilde{m} = \frac{m}{m_0}$$

Next we modify the system's free parameters $D_c, \chi, \delta, D_m, \mu_3, \lambda$:

$$d_c = \tfrac{D_c}{D}, \quad \gamma = \chi \tfrac{e_0}{D}, \quad \eta = \tau m_0 \delta, \quad d_m = \tfrac{D_m}{D}, \quad \alpha = \tau \mu_3 \tfrac{c_0}{m_0}, \quad \beta = \tau \lambda.$$

with D being a refrence chemical diffusion coeffizcient.
These modifications make the new system of linearly coupled partial differential equations, where the tildes are dropped for simplicitie's sake:

$$\frac{\partial c}{\partial t} = d_c \Delta c - \gamma \nabla \cdot (c \nabla e) + \mu_1 c \left(1 - \frac{c}{c_0} - \frac{e}{e_0}\right) \tag{6}$$

$$\frac{\partial e}{\partial t} = -\eta m e + \mu_2 c \left(1 - \frac{c}{c_0} - \frac{e}{e_0}\right) \tag{7}$$

$$\frac{\partial m}{\partial t} = d_m \Delta c + \alpha c - \beta m \tag{8}$$

with also updated zero-flux boundary conditions,

$$\zeta \cdot (-d_c \nabla c + c \gamma \nabla e) = 0 \tag{9}$$

$$\zeta \cdot (-d_m \nabla m) = 0 \tag{10}$$

where ζ is an appropriate outward unit normal vector.
In order to use the finite element method we will change to the variational formulation.

If we assume each species to be in the Hilbert space $H^1(\Omega)$, the variational formulation can be derived by multiplying with a test function, integrating over the domain Ω and use integration by parts and the Gauss theorem. This will give us a broader solution space and reduces the requirements of the solution regarding differentiability. With $(\cdot,\cdot)$ denoting the L^2-scalar product on Ω the following equation system results

$$\left(\frac{\partial c}{\partial t},\varphi_c\right) = -D_c\left(\nabla c,\nabla\varphi_c\right) + \chi\left(c\nabla e,\nabla\varphi_c\right) + \mu_1\left(c\cdot\left(1-\frac{c}{c_0}-\frac{e}{e_0}\right),\varphi_c\right) \tag{11}$$

$$\left(\frac{\partial e}{\partial t},\varphi_e\right) = -\delta\left(me,\varphi_e\right) + \mu_2\left(e\left(1-\frac{c}{c_0}-\frac{e}{e_0}\right),\varphi_e\right) \tag{12}$$

$$\left(\frac{\partial m}{\partial t},\varphi_m\right) = -D_m\left(\nabla m,\nabla\varphi_m\right) + \mu_e\left(c,\varphi_m\right) - \lambda\left(m,\varphi_m\right) \tag{13}$$

For the initial conditions we will assume that at dimensionless time $\tau = 0$, there is already a nodule of cells present centered around the origin in every dimension. For example in one dimension c is having the initial density distribution, $c(x,0) = \begin{cases}\exp(\frac{-x^2}{\epsilon}), x\in[-0.25,0.25]\\ 0, x\notin[-0.25,0.25]\end{cases}$, with ϵ being a postive constant. The tumor will have degraded some of its surrounding tissue in every experiment and hence we take the inital profile of the extracellular matrix to be $e(x,0) = 1-0.5c(x,0)$. At last we assume the initial matrix-degrading enzyme concentration to be proportional to the initial tumor cell density and therefore take $m(x,0) = 0.5c(x,0)$. These inital values are displayed in figure 3.2.

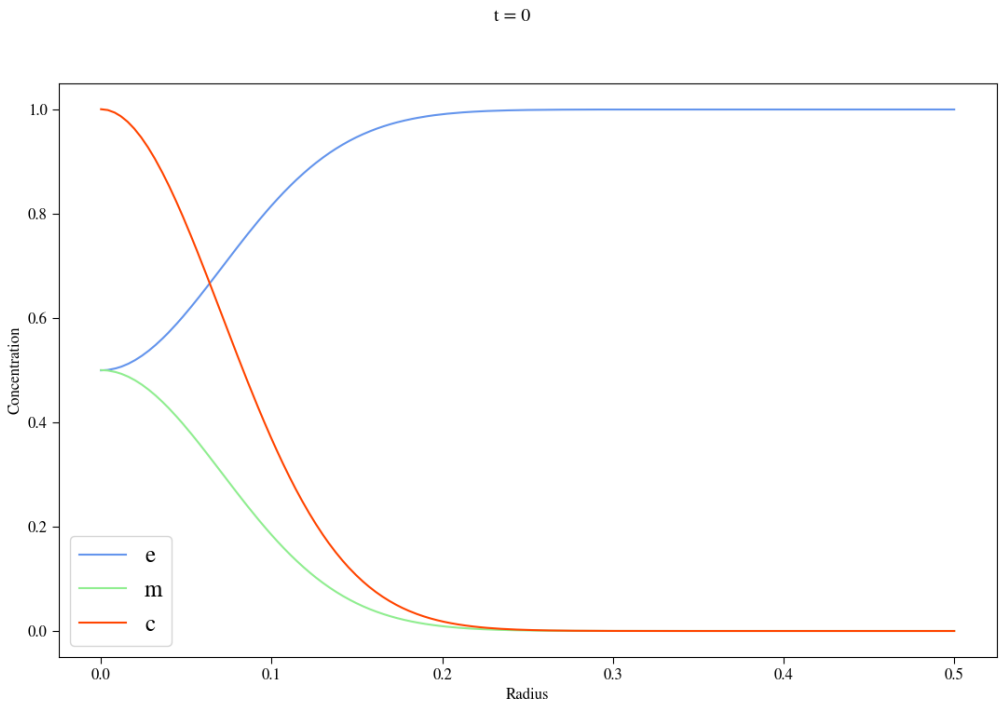

Figure 1: Visualization of the initial value distribution for an experiment in two space dimensions, radially symmetrical

4 Method

This work will investigate how the free parameters of the model given by the equations 6 - 10 will affect the spatial temporal progress of the numerical simulation. For the numerical simulation we will use the weak form given with equations 11 - 13 and solve it using HiFlow. To study the results of the numerical simulation ParaView is used, producing informative plots to compare the evolution of the simulation in time. For this we rely on the tool Plot Over Line to give radially symmetrical reulsts of the three variables of tumour and extracellular matrix density and matrix-degrading enzymes, an example for this can be seen in figure 3.2 showing the initial conditions. In figure 2 you can see the configuraion for the Plot Over Line tool, since we are consider the experiments on the unit squre in 2D dimensional case, the line starts at $x = 0.5, y = 0.5$ and ends at $x = 0.5, y = 1$.
For the three dimensional experiments a different tool was used *explain3Dexperientsmethodology*

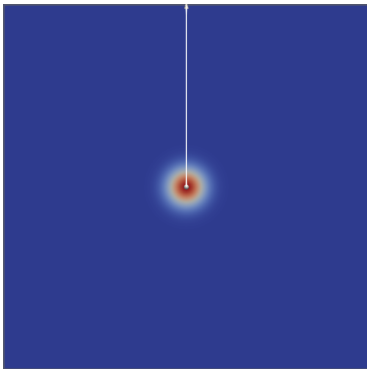

Figure 2: Plot Over Line Tool Configuration

All experiments that consider the ECM to be homogenous start with the same initial values as seen in figure 3.2. Experiments observing the effects of a heterogenous ECM use different initial values, like seen in *initialvaluesheterogenousECM*
This work starts with trying to replicate/replicating numerical simulations done by other papers. Since there were only 1D simulations done previously, the model will be adjusted in such a way, that the Plot Over Line graphs mimick the plots given by the previous experiments. This will serve two purposes, first and minor it will verify a correct implemntation of the model and second this will give us a starting point by which we can vary the parameters, investigating the phenomena this model exhibits.
We will start with exmaining 2D experiments with homogenous ECMs, using our model with the parameters mu_1 and mu_2 both set to zero, considering a case with no proliferation, after this we will introduce proliferation, varying also mu_1 and mu_2. The same will be done for the 3D cases, also at first neglecting proliferation to apply it in a later stage. Our focus here lies on investigating the effects of the parameters, but also on how the dimension changes results, with fixed free parameters. At last we will have a brief outlook on how a heterogenous ECM influences our results
The results of the above experiments will be summarized and discussed in the Conclusion and Discussion part, pointing out the important characteristics of the simulations and disucssing the sensitivity of each of the parameters and the influence of the dimension.

At this point we will have an outlook on how to extend the model with more continuous and or discrete adaptations.

Looking at the parameter estimates from [2] to non-dimensionalise the time, we see that with $L \in [0.1cm, 1cm]$ and $D \approx 10^{-6} \frac{cm^2}{s}$, $\tau = \frac{L^2}{D}$ gives a relative big temporal range, $\tau_{min} = 1000s = 16.66min$ and $\tau_{max} = 1000000s = 16666.66min$, which makes it hard, to find the correct time step value to compare our simulation results with the one from [2] and [6]. Another challenge are the diffusion coefficients, since they are dependent on the dimension we are in, we have to find our own estimate as a baseline value.
For our experiments we will use a set of baseline parameters, which will be evaluated experimentally, and from there vary one parameter at a time to get a overview of their effects and later we will incorporate variation of multiple paramters in accordance with the numerical model.

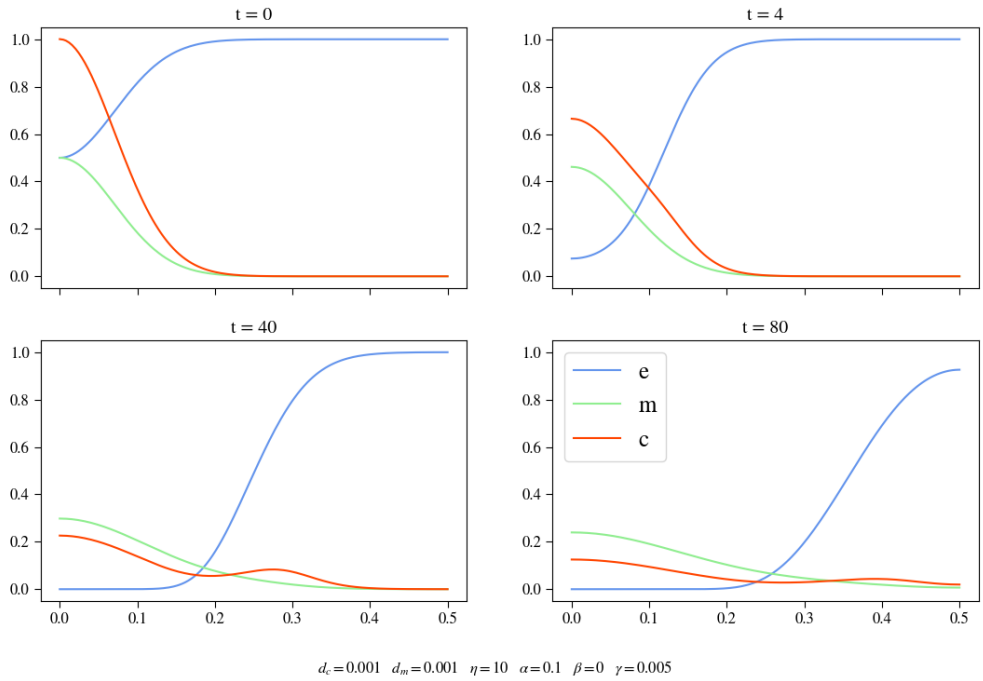

Figure 3: Caption

5 Experiments and Results

For all the plots of the experiments the red curve indicates the tumour cell density, the blue curve the ECM density and the green curve the MDE concentration. In all of the experiments we used the value of $\epsilon = 0.01$ to match the inital conditions from [2] and [6].

5.1 Two dimensional Results

5.1.1 Replicating results

We will start with replicating previous results from Anderson et al.[2], Figure 1, making our curves fit the findings in their diagramms.

In the first simulation the same parameter were used as in Anderson et al. first one dimensional experiment; $d_c = 0.001, d_m = 0.001, \gamma = 0.005, \eta = 10, \alpha = 0.1, \beta = 0, \mu_1 = 0, \mu_2 = 0$. Figure 3 shows 4 snapshots of different points in time of tumour cell density, extracellular matrix density and matrix degrading enzymes concentration. In the conducted experiments it was shown that for every step in time done in the original paper we have done 4 steps, this is the reason for our time scale. Starting from the inital values seen at $t = 0$ we see that after four time steps a very small unevenness has formed for the tumour cell density at $x \approx 0.1$. Both concentrations of MDEs and ECM have decreased as expected, looking at the model, MDEs have also invaded into the surrouding tissue, stretching the initial concentration around the origin. In the next image showing

the simulation after 40 timesteps we see that this unevenness has been propagated to form a hill at the leading edge of the tumour cells invading the surrounding tissue, at $x \approx 0.28$. MDEs also continued their diffusion into the area, decaying the ECM in their wake, decreasing them further. The last image, after 80 simulation time steps, we see that as well the hill that has formed at the leading edge of the tumour cells as well as the concentration of tumour cells at the origin, has decreased, due to the diffusion factor and the haptotactic flux. If we were to look at the simulation at later points in time, this curve will flatten even more, since with more time the ECM will be decayed and therefore the haptotactic flux coefficient γ will lose its influence, leaving the movement of the cells to diffusion only. The curve for the MDEs has also flattened, yet not as strongly as the tumour cells concentration and as the observed before the ECM decayed where the MDEs were previously.
Comparing 3 to figure 1 in [2], we can see major differences. The first image showing $t = 0$ looks the same, which confirms that both experiments start with the same initial values. In the images showing the simulation at the second time checkpoint we see that though the tumour concentration and ECM density values are approximately the same, the MDE concentration is slightly lower in our experiment, which will get more pregnant in the later images. The unevenness having formed at the leading edge of the tumour cell concentration also looks to be slightly smaller. The differences in the third image are more strikingly, both c and m have considerably lower concentrations, yet the ECM value looks to in line. In our case the diffusion of the tumour cells into the tissue also seems to happen a littel bit too fast. The last time checkpoints manifest our findings, showing the same behaviour with ECM being approximately the same, tumour cell density and MDE concentration being clearly lower in our experiment and invasion of tissue happening too fast, leaving the lump at the origin $x = 0$ too small.
This first of all confirms the initial supposition that with changing the dimension for the simulations the results also vary. We will now adjust the parameters iteratively to align our results with above compared experiment. For this we will now start with varying the MDE production coefficient α, to get higher concentration values, and also change the diffusion terms d_c and d_m, to adjust the pace of the invasion of tumour cells and MDEs into the area.

Figure 4 shows a comparison of different values set for α and their effect on the curve of the MDE concentration. To determine the correct value for α to replicate the result we can look at the later points in time, $t = 40$ and $t = 80$ and see that with the value of α between 0.3 and 0.4 we will get a good approximation. The value of the original paper is at this point in time about 0.7 at $x = 0$. Fine tuning this parameter led us to $\alpha = 0.35645$.

The next main difference was that the tumour cell invasion of the tissue looked slightly different, for this we also conducted a set experiments regarding the parameters d_c and γ, seen in 5 and 6, showing in each comparison only the curve for the tumour cell concentration. Here we see that changing d_c with equally distanced parameters does not give us an as regular result as it did regarding α. Looking at the two later points in time, we see that the dashed curve with $d_c = 0.0005$ resembles the original experiment really well. For the comparison of the parameter γ we see that with increasing it form 0.005 to 0.007

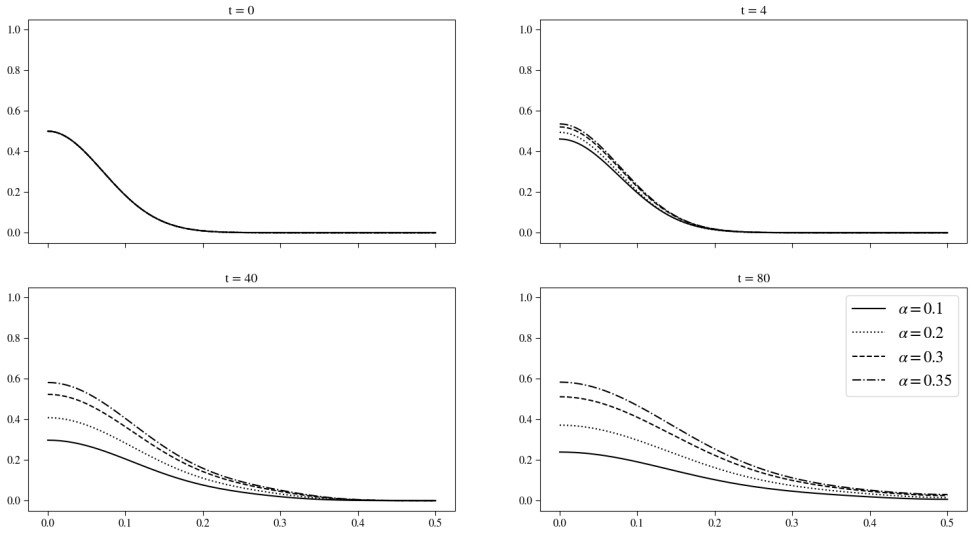

Figure 4: Caption

the initial value was already really close to the to be replicated experiment, yet a slight adjustment to $\gamma = 0.0055$ worked better since we want the small hill at the leading edge of the tumour cell concentration in the latter two points in time to ber a little farther out, yet not as steep as for example $\gamma = 0.007$.

These adjustments leave with the final configuration for replicating the system with the curves in figure 7 and the parameter settings also seen in the same figure. Slightly adjusting the haptotatic flux to $\gamma = 0.0055$ yields the following results, seen in figure 7. comparing our final version with the original one we can see that in the second point in time, at $t = 4$ in our case, the values of the three curves at the $x = 0$ are nearly the same. In the original experiment the bump in the curve for the tumour concentration looks more pregnant, but this is only due to the fact, that this experiment was most likely done on the unit line, not the unit cube, and therefore the x-scale has been streched to $y_{max} = 1$ where in our case it is $x_{max} = 0.5$. The two later points in time confirm the similarity with having also nealy the same values for the three curves at $x = 0$ but also their respective propagations in time look to be in line with the original experiment.

5.1.2 Parameter Analysis

From the replicated results shown in figures **??**-*insertcorrectlastreplicatedresult* we saw variation across all parameters except d_c since this one is assumed to be constant, as described in Anderson et al. [2]. We are now going to take the baseline values of $(d_c, \gamma, \mu_1, \eta, \mu_2, d_m, \alpha, \beta) = (0.001, 0.005, 0.3, 10, 0.3, 0.001, 0.1, 0.1)$ and start experimenting with it as seen in table **??**, for this.

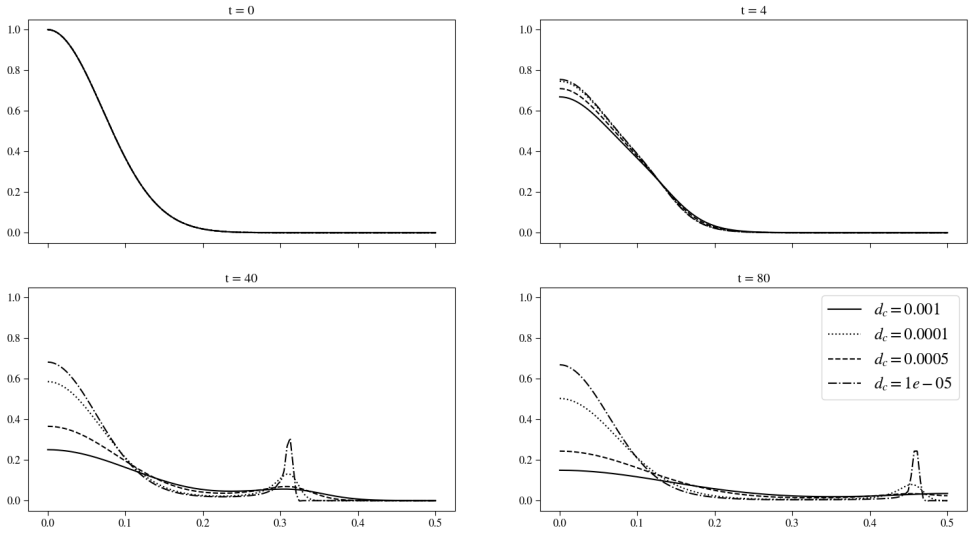

Figure 5: Caption

5.2 Three Dimensional Results

5.2.1 Replicating Results

5.2.2 Parameter Analysis

5.3 Three Dimensional Simulations with Heterogenous ECM Structure

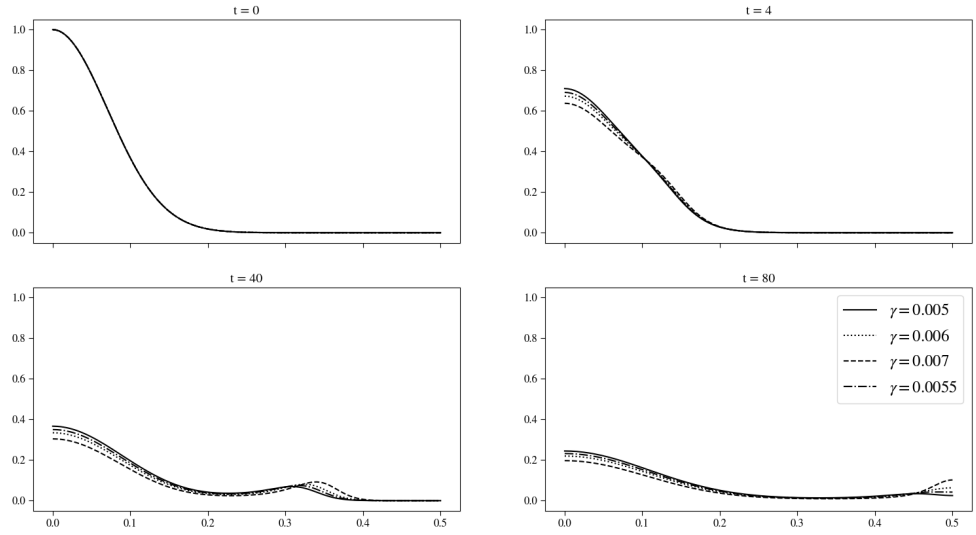

Figure 6: Caption

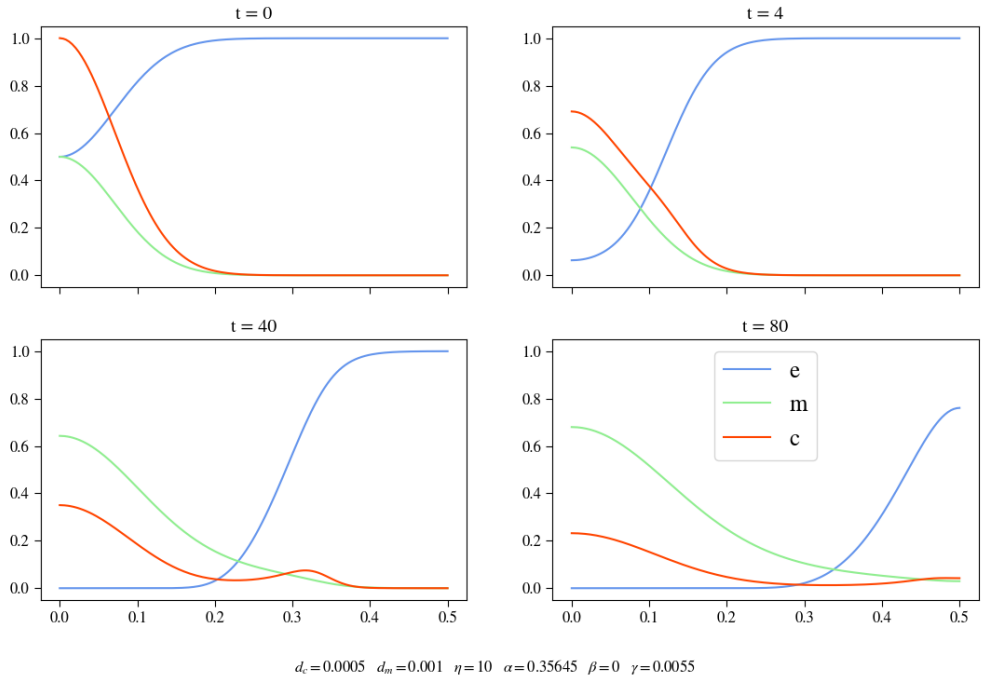

Figure 7: Caption

6 Conclusion and Discussion

6.1 Extra-Dimension Evaluation

Ergebnisse reporuzieren und vergleichen.

6.2 Inter-Dimension Evaluation

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