

A Moving Mesh Approach to Avascular Tumour Growth

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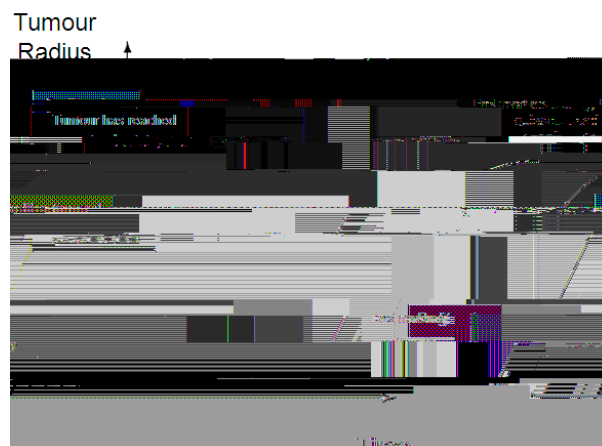


Figure 1. The growth of a spherical tumour

growth of cancerous cells. The process by which the tumour obtains its own blood supply is called ANGIOGENESIS and preventing this from occurring is of particular interest to drug development. This is especially true once the tumour has obtained its own blood supply the tumours can evade its primary location in the circulatory system, metastasise and settle in multiple regions of the body. The METASTATIC stage is the final stage of tumour growth and the most difficult to treat.

From the onset of cancer cells up to cancer cells there are three distinct stages to cancer. The different stages have different characteristics so require individual investigation. We shall study the primary stage – spherical tumour growth.

1.1. A spherical tumour

As previously mentioned the later stages of tumour growth are more critical since it is usually not until after angiogenesis that cancer is detrimental to the host's health. During the spherical stage the tumour is significant. Indeed following a study of human cancers in mice [1] there is recent controversial hypothesis that the host's body does not kill spherical tumours in our bodies.

Regardless of this critical point spherical tumour growth remains the interest of scientists. It is essential to understand the simple system and its components prior to attempting analysis of more complex systems. Spherical tumours have many of the same characteristics as spherical tumours but

the quantity and quality of data on securitours is of higher standard. This is because it is comparatively easier and cheaper to reproduce high quality securitour experience evidence in intro for

In summary, the investigation mode for securitours (see Figure 2) is they're supposed to code and help give an insight into the mechanisms of securitour growth.



Figure 2 An securitour

Chapter

The role of the tics in cancer research

Ever since co-polymer life evolved it has been susceptible to cancer. The oldest description of cancer in humans is found in an Egyptian papyrus written between 1600-1700 BC. Today specialists are still interested

the perimeters but not the areas. Through the development and solution of the metric models that describe different aspects of solid tumor growth, applied the metrics has the potential to prevent excessive experimentation.

Identifying perimeters and modeling growth are hard to handle. The perimeters can not only provide the cost but the subtleties of the many intricate processes can easily be overlooked. By modeling tumor growth to indicate that

Chapter

Acrophase mode of solid tor growth

Byrne et al. formulated acrophase mode of solid tor growth as more general version of two different pre-existing modes for solid tor growth and . Although fundamental aspects of the modeling are not given in this paper the logic reasoning and assumptions that contribute to the mode are explicitly described. This is the mode that we are discussing and solving numerically in this report.

Our first task is to nondimensionalise the mode. This involves the partitioning of units by suitable substitution of variables. Nondimensionalisation simplifies problem by reducing the number of variables. It simplifies analysis of the behaviour of system by recovering characteristic properties. In our case the requirement to nondimensionalising the system is to enable us to take advantage of parameters studied elsewhere.

In this report we shall propose the nondimensionalised modeling boundary problem by applying modeling approach to the mesh in three different ways by ensuring that assumptions in need are constant over time by using the mesh with the cell velocity by driving mesh to equilibrium in proportion to that of the modeling boundary.

The results generated from these methods are discussed and compared with previous results.

Mode for tion

In it is assumed that tor consists of cells and tor with respect to our fractions α and β with $\alpha + \beta = 1$. The acrophases have associated

here

- $\psi_c(\alpha)$ is the pressure difference between the top phases and only include contributions due to force per particle interactions and external stress. It is defined by

$$\psi_c(\alpha) = \begin{cases} \frac{\hat{\Sigma}_c |\mathbf{x} - \mathbf{x}^*|^{r-1}}{(1-\alpha)^q} (\alpha - \alpha^*) & \alpha_{min} \leq \alpha < \alpha^* \\ 0 & \alpha^* \leq \alpha < \alpha_{max} \end{cases}$$

for positive constants $q, r, \alpha_{min} < \alpha^* < \alpha_{max}$ and $\hat{\Sigma}_c$

When specifying $\psi_c(\alpha - \alpha^*)$ denotes a turbulent packing density if $\alpha > \alpha^*$ cells move to reduce their stress. Here if $\alpha < \alpha^*$ they aggregate if they are not too sparsely populated, $\alpha \geq \alpha_{min}$. By definition we have

ψ_c

These equations are defined on Ω including domain Ω and in the whole domain $\mathbb{R}^2$ subject to the boundary conditions and initial conditions as follows

$$\begin{aligned} \mathbf{v}_c &= \mathbf{v}_w + \frac{\partial \mathbf{C}}{\partial \mathbf{x}} \quad \text{at } \mathbf{x} \in \Gamma, \quad \forall \mathbf{x} \in \mathbb{R}^2 \\ p &= 0, \quad \mu_c = \lambda_c \frac{\partial v_c}{\partial x} = \mu_c \alpha \quad \text{at } \mathbf{x} \in \mathbf{x}_N, \quad \forall \mathbf{x} \in \mathbb{R}^2 \\ \alpha &= \alpha_0 \quad \text{at } \mathbf{x} \in \mathbf{x}_0 \quad \text{at } t = 0. \quad \forall \mathbf{x} \in \mathbb{R}^2 \end{aligned}$$

Equations (1) ensure symmetry about $\mathbf{x} = 0$. In (1) $\mathbf{C}_\infty$ denotes the nutrient concentration at the far field.

etittyreeurdi

$$\mathbf{x}_N(\cdot), \alpha \in \alpha_0 \quad t \in \mathbb{R}^+$$

$$\mathbf{v} = \frac{\partial \mathbf{C}}{\partial \mathbf{x}} \quad t \in \mathbb{R}$$

$$\Rightarrow \mu \frac{\partial \mathbf{v}}{\partial \mathbf{x}} = \chi(\alpha), \quad \frac{\partial \mathbf{x}_N}{\partial t} = \mathbf{v}, \quad \mathbf{C} \in \mathbb{R}^+ \quad t \in \mathbb{R}$$

In equations (1) to (3) we have introduced the parameters

$$\mathbf{s}_1 = \mathbf{s}_1 \mathbf{C}_\infty, \quad \mathbf{s}_2 = \frac{\mathbf{s}_1 \mathbf{C}_\infty}{\mathbf{s}_1 \mathbf{C}_\infty} \mathbf{s}_2, \quad \mathbf{s}_3 = \frac{\mathbf{s}_1 \mathbf{C}_\infty}{\mathbf{s}_0} \mathbf{s}_3, \quad \mathbf{s}_4 = \mathbf{s}_4 \mathbf{C}_\infty,$$

$$\mathbf{k} = \frac{\mathbf{k}_0 \mathbf{x}_N^2}{\mathbf{s}_1 \mathbf{C}_\infty}, \quad \mu = \mu_c, \quad \lambda_c = \frac{\mathbf{s}_0 \mathbf{C}_\infty}{\mathbf{s}_1 \mathbf{C}_\infty},$$

$$\chi(\alpha) = \begin{cases} \frac{\hat{\mathbf{z}}_c |\hat{\alpha} - \alpha^*|^{r-1}}{(1-\hat{\alpha})^q} & \alpha_{min} \leq \alpha < \alpha_{min} \\ \leq \alpha < \alpha_{min} & \alpha_{min} \leq \alpha < \alpha_{min} \end{cases},$$

$$\mathbf{Q} = \mathbf{Q}_0 \mathbf{x}_N^2, \quad \mathbf{Q}_1 = \mathbf{Q}_1 \mathbf{C}_\infty.$$

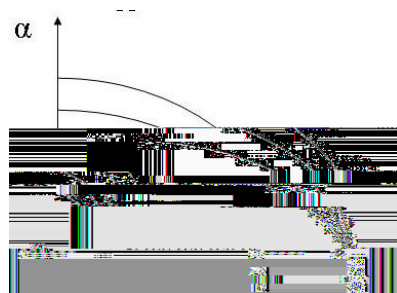
In this paper the terms (4) are dropped from the series and parameters

In this study we shall solve this problem numerically using three different methods

Chapter 4

Moving Meshes

Generality for the numerical solution of time dependent di



4. **Di erent methods to o e the esh**

e i investigate three strategies for o ing the esh i.e. di erent ys to de ne the esh e ocity **x**. The three esh e ocities i e

A: sed on conser ing ss fr ctions

B: the ce e ocity **v**

C: proportion to the ound ry o e ent $\underline{dx_N}$

Chapter

hich c n e ritten s

$$\mathbf{T}_j^l \mathbf{C}_{j-1} \mathbf{T}_j^d \mathbf{C}_j \mathbf{T}_j^u \mathbf{C}_{j+1} = \mathbf{w}_j \mathbf{C}_j \quad (j = 1, 2, \dots, N-2), \quad (1)$$

the function is symmetric about $\mathbf{x}_0$. Hence we conclude that $\mathbf{x}_1 = -\mathbf{x}_{-1}$ and hence $\mathbf{C}_1 = \mathbf{C}_{-1}$. Substituting these values into (16) for $j = 1$ gives

$$\frac{-2}{x_1^2 - x_0^2} \mathbf{C}_0 = \frac{2}{x_1^2 - x_0^2} \mathbf{C}_1 = \frac{Q \mathbf{C}_0 \alpha_0}{Q_1 \mathbf{C}_0}. \quad (17)$$

Therefore we have values for $\mathbf{T}_0^d$, $\mathbf{T}_0^u$ and $w_1 \mathbf{C}$

$$\begin{aligned} \mathbf{T}_0^d &= -\mathbf{T}_0^u = \frac{-2}{x_1^2 - x_0^2}, \\ w_1 \mathbf{C}_0 &= \frac{Q \mathbf{C}_0 \alpha_0}{Q_1 \mathbf{C}_0}. \end{aligned}$$

Boundary Conditions: $j = N - 1$

For the right boundary we return to (16) this time for $j = N - 1$ with the substitution $\mathbf{C}_N = 0$ from (18).

$$\begin{aligned} \frac{2}{(x_{N-1} - x_{N-2})(x_N - x_{N-2})} \mathbf{C}_{N-2} &= \frac{2}{(x_N - x_{N-1})(x_{N-1} - x_{N-2})} \mathbf{C}_{N-1} \\ &= \frac{Q \mathbf{C}_{N-1} \alpha_{N-1}}{Q_1 \mathbf{C}_{N-1}} = \frac{2}{(x_N - x_{N-1})(x_N - x_{N-2})}. \end{aligned}$$

So $\mathbf{T}_{N-1}^l$ and $\mathbf{T}_{N-1}^d$ are independently equated to the entry in $w_1 \mathbf{C}$ has no further due to the boundary condition.

Now we have our complete tri-system $\mathbf{T}$ to solve in $\mathbf{C}_j, j = 1, \dots, N - 1$ but note that the right hand side is nonlinear.

Numerically solving the discretized PDE

For the solution of (19) we use Newton's method where the residual vector $\mathbf{R}$ of (19) is

$$\mathbf{R} = \mathbf{T} \mathbf{C} - w_1 \mathbf{C}.$$

We seek $\mathbf{C}$ such that $\mathbf{R} = 0$ so equation (19) holds. Note that if $\mathbf{Q}_1 = 0$ the equations are linear and no iteration is needed. Otherwise we carry out Newton's Method

Finding singularity mesh

Once $\mathbf{C}$ and $\mathbf{v}$ are determined over the region of interest the solution of the time dependent PDE using moving mesh approach can be done in three different ways to solve the mesh. For these three methods the updated mesh is obtained from the mesh velocity used in the implicit time stepping scheme.

The first way of moving the mesh Method A, defines the mesh movement by keeping the cell surface fractions constant in time. The second uses the cell velocity as the mesh velocity Method B. Both these methods are implemented in the code.

It is worth noting that this corresponds to the goodness result

d

Recovering the Solution α

To find an equation that allows us to compute the solution α from the mesh, we return to $\frac{dx}{dt} = \alpha(x, t)$ and equate it to $\frac{x_{j+1}(t) - x_{j-1}(t)}{\Delta t}$ between the two points $x_{j-1}(t)$ and $x_{j+1}(t)$ as in

$$\frac{1}{\Delta t} \int_{x_{j-1}(t)}^{x_{j+1}(t)} \alpha(x, t) dx = \frac{1}{\Delta t} \int_{x_{j-1}(0)}^{x_{j+1}(0)} \alpha(x, 0) dx.$$

Applying the mean value theorem for integrals and taking the mean value to be $\alpha_j(t)$ we obtain the approximation

$$\frac{1}{\Delta t} (x_{j+1}(t) - x_{j-1}(t)) \alpha_j(t) = \frac{1}{\Delta t} (x_{j+1}(0) - x_{j-1}(0)) \alpha_j(0).$$

we now move on to Method B.

Method B

Under this strategy the velocity of the boundary is equal to the velocity of the cells at the boundary. Then

$$\frac{dx_j}{dt} = v_j \quad \text{for } j = 1, 2, \dots, N$$

Once the mesh velocity is defined, so the new mesh can be determined by the explicit time stepping scheme as in Method A.

To recover α on this new mesh, *conservative manner*, we define the partials

$$j = \frac{dx_{j+1}(t)}{dx_{j-1}(t)} \alpha \, dx. \quad \text{for } \mathbb{R}$$

Differentiating j with respect to time using Leibniz integration rule here $x_j = v_j$

$$\begin{aligned} j &= \frac{d}{dt} \int_{x_{j-1}(t)}^{x_{j+1}(t)} \alpha \, dx, \\ &= \int_{x_{j-1}(t)}^{x_{j+1}(t)} \frac{\partial \alpha}{\partial t} \, dx + \alpha x_{j+1}^{j+1} \\ &= \int_{x_{j-1}(t)}^{x_{j+1}(t)} \frac{\partial \alpha}{\partial t} \, dx + \frac{\partial}{\partial x} (\alpha v) \, dx. \end{aligned}$$

Hence the terms under the integrals are equal to one side of the PDE, so can be replaced by the source term

$$\begin{aligned} j &= \int_{x_{j-1}}^{x_{j+1}} \frac{\partial \alpha}{\partial t} \, dx + \frac{\partial}{\partial x} (\alpha v) \, dx \\ &= \int_{x_{j-1}}^{x_{j+1}} S(\alpha, C) \, dx. \end{aligned}$$

we update j at the new time by using the explicit time stepping scheme then use the new value for j and the updated solution y solve the mid-point approximation in Method A applied to $\mathbb{R}$

$$x_{j+1} = x_{j-1} + \alpha_j \Delta t$$

gi ing

α_j

Chapter 6

Bread and Butter Method

In 5, the steady two-dimensional growth problem is solved by applying the variable $\mathbf{x}(t)$ to the fixed domain $\xi \in [0, 1]$ by the transformation $\xi = \frac{x(t)}{L(t)}$ and $\tau = t$ where $\mathbf{x} = \mathbf{x}_N(\mathbf{t})$. Using the chain rule of Chapter 5, the transformed problem reads

$$\frac{\partial \alpha}{\partial \tau} - \frac{\xi}{L} \frac{dL}{d\tau} \frac{\partial \alpha}{\partial \xi} = \frac{\partial}{\partial \xi} \left(\nu \frac{\partial \alpha}{\partial \xi} - \frac{s_1 C}{s_1 C} \alpha \right) - \alpha = \frac{s_2}{s_4 C} \frac{s_3 C}{s_4 C} \alpha, \quad (6.1)$$

$$\frac{\partial}{\partial \xi} \left(\alpha \zeta \right) = \frac{k^2 \alpha \nu}{L - \alpha} = \mu \frac{\partial}{\partial \xi} \left(\alpha \frac{\partial v}{\partial \xi} \right), \quad (6.2)$$

$$\frac{\partial^2 C}{\partial \xi^2} = \frac{Q^2 \alpha C}{Q_1 C}, \quad (6.3)$$

with initial and boundary conditions

$$\alpha = 1, \quad \alpha = \alpha_0 \quad \text{at} \quad \tau = 0, \quad (6.4)$$

$$\frac{\partial C}{\partial \xi} = v = 0 \quad \text{at} \quad \xi = 0, \quad (6.5)$$

$$\mu \frac{\partial v}{\partial \xi} = \zeta \alpha, \quad C = 0 \quad \text{at} \quad \xi = 1, \quad (6.6)$$

$$\frac{dL}{d\tau} = v \quad \text{at} \quad \xi = 1, \quad (6.7)$$

here k and μ have the same definitions as before and the pressure difference between the two phases $\chi(\alpha)$ is defined in the specific sense $c = r = 1$ and

$$q^{-1/2} \leq s$$

$$\chi(\alpha) - \zeta(\alpha) \Big] \leq \alpha < \alpha_{min}$$

$$\frac{-}{(1-)^2} \alpha_{min} \leq \alpha < ^*.$$

To compare the results from the foregoing method to those in [1], we have replicated their results using the same set of equations to postulate the algorithm

Previously, Otwinowski [1] and [2]

Find **C**

h the $\mathbf{C}_{-1} \dots \mathbf{C}_1$ and $\mathbf{C}_N \dots \mathbf{C}_{N-1}$ from ξ_0 and ξ_N respectively. To correspond with these conditions the above equation for the specieses $\mathbf{j} \dots$ and $\mathbf{j} \dots \mathbf{N} - 1$ are

$$-2\mathbf{C}_0 + 2\mathbf{C}_1 \dots = \frac{Q^2_j C_0}{1+Q_1 C_0} \xi^2 \dots = \mathbf{w}_j \mathbf{C}_0$$

$$\mathbf{C}_{N-2} - 2\mathbf{C}_{N-1} \dots = \frac{Q^2_j C_{N-1}}{1+Q_1 C_{N-1}} \xi^2 \dots = \mathbf{w}_j \mathbf{C}_{N-1}$$

As in Chapter 4 we write the nonlinear systems

$$\mathbf{T}\mathbf{C} = \mathbf{w}_j \mathbf{C}$$

here

$\mathbf{C}$ is vector of $\mathbf{C}_0$ to $\mathbf{C}_{N-1}$ $\mathbf{j} \dots, \dots, \mathbf{N} - 1$

$\mathbf{w}_j \mathbf{C}$ is vector of $\mathbf{w}_j \mathbf{C}_j$ $\mathbf{j} \dots, \dots, \mathbf{N} - 1$

and

$\mathbf{T}$ is tridiagonal tri of the $\mathbf{C}_j$ coefficients

$$\mathbf{T} = \begin{pmatrix} -2 & 2 & & \dots & \\ & -2 & & \dots & \\ & & \dots & \dots & \\ \dots & \dots & & -2 & 2 \\ & & \dots & & -2 \end{pmatrix}.$$

The subalgorithm for cutting $\mathbf{C}$ is the same as in Chapter 4 namely

Preinitialization: Make an initial guess for $\mathbf{C}$.

1. Use $\mathbf{C}^p$ to find $\mathbf{w}_j \mathbf{C}^p$.

2. Find the residual $\mathbf{R}^p = \mathbf{T}\mathbf{C}^p - \mathbf{w}_j \mathbf{C}^p$.

3. Cut the column of $\mathbf{R}^p$

$$\mathbf{J}^p = \left[\frac{\partial \mathbf{R}^p}{\partial \mathbf{C}^p} \right] = \mathbf{T} - \left[\frac{\partial \mathbf{w}_i^p}{\partial \mathbf{C}_j^p} \right]$$

here $\mathbf{i}, \mathbf{j} = 1, 2, \dots, \mathbf{N} - 1$ and $-\frac{w_i^p}{C_j^p}$ is the diagonal tri

$$\frac{\partial \mathbf{w}_i}{\partial \mathbf{C}_j} = \begin{pmatrix} \frac{Q^2_0}{(1+Q_1C_0)^2} \xi^2 & \dots & \dots \\ \frac{Q^2_1}{(1+Q_1C_1)^2} \xi^2 & \dots & \vdots \\ \vdots & \dots & \dots \\ \dots & \dots & \frac{Q^2_{N-1}}{(1+Q_1C_{N-1})^2} \xi^2 \end{pmatrix}.$$

d Find $\mathbf{H}^p = \mathbf{J}^p - \mathbf{1R}^p$

e Set $\mathbf{C}^{p+1} = \mathbf{C}^p - \mathbf{H}^p$

f With the new approximation $\mathbf{C}^{p+1}$ return to c and repeat until e converges successfully $\|\mathbf{C}^{p+1} - \mathbf{C}^p\|_2 < \epsilon \times 10^{-6}$

In step c the entries to the diagonal tri $-\frac{w_i^p}{C_j^p}$ contain the factor of ξ^2 then compared to Chapter 4 to correct the different $\mathbf{w}_i \mathbf{C}_j$.

Finding the velocity v

Find the velocity in the same manner as in Chapter 2. We discretise Δz and rearrange so that

$$\mathbf{A}_j^l \mathbf{v}_{j-1} + \mathbf{A}_j^d \mathbf{v}_j + \mathbf{A}_j^u \mathbf{v}_{j+1} = \mathbf{b}_j \alpha_j \quad j = 2, \dots, \mathbf{N} - 1. \quad (6)$$

$$\text{here } \mathbf{A}_j^l = \frac{(j + j - 1)\mu}{2(\Delta z)^2} \quad \mathbf{A}_j^d = -\frac{(j + j - 1)\mu}{2(\Delta z)^2} - \frac{(j + j + 1)\mu}{2(\Delta z)^2} - \frac{k^2 j}{1 - j}$$

$$\mathbf{A}_j^u = \frac{(j + j + 1)\mu}{2(\Delta z)^2} \text{ for } j = 2, \dots, \mathbf{N} - 1 \quad \text{and}$$

$$\mathbf{b}_j \alpha_j = \frac{1}{4\Delta z} (\alpha_j + \alpha_{j+1}) \zeta \frac{1}{2} (\alpha_j + \alpha_{j+1}) - \frac{1}{4\Delta z} (\alpha_j + \alpha_{j-1}) \zeta \frac{1}{2} (\alpha_j + \alpha_{j-1})$$

As with the mesh equations $\mathbf{v}_0 = 0$. For the case when $\mathbf{j}$

Let $\mathbf{A}_j^l, \mathbf{A}_j^d$ and $\mathbf{A}_j^u, j = 1, 2, \dots, N$ be the respective entries to the lower, diagonal and upper diagonals of matrix $\mathbf{A}$ and $\mathbf{b}_j, j = 1, 2, \dots, N$. Hence Step 2 finding the cell velocity $\mathbf{v}$ is determined by solving

$$\mathbf{A}\mathbf{v} = \mathbf{b}, \quad \mathbf{v} = \mathbf{v}_j.$$

As intended, the executed $\mathbf{C}$ and $\mathbf{v}$ on the edges in the system, the executed the ongoing mesh. For the edges there is no mesh velocity to define but the still need to compute the change in the tumour radius.

Finding the solution α

Finally to obtain α on the edges, we discretise the explicit in time with central difference approximation in space

$$\begin{aligned} \frac{\alpha_j^{i+1} - \alpha_j^i}{\Delta t} &= \frac{\xi v_N}{\Delta x} \frac{\alpha_{j+1}^i - \alpha_{j-1}^i}{2 \Delta x} - \frac{v_{j+1}^i \alpha_{j+1}^i - v_{j-1}^i \alpha_{j-1}^i}{2 \Delta x} \\ &\quad - \frac{s_1 \alpha_j^i - \alpha_j^i C_j^i}{s_1 C_j^i} - \frac{s_2 s_3 C_j^i}{s_4 C_j^i} \alpha_j^i, \\ \Rightarrow \alpha_j^{i+1} &= \frac{\xi v_N}{\Delta x} \frac{\alpha_{j+1}^i - \alpha_{j-1}^i}{2 \Delta x} - \frac{v_{j+1}^i \alpha_{j+1}^i - v_{j-1}^i \alpha_{j-1}^i}{2 \Delta x} \\ &\quad - \frac{s_1 \alpha_j^i - \alpha_j^i C_j^i}{s_1 C_j^i} - \frac{s_2 s_3 C_j^i}{s_4 C_j^i} \alpha_j^i, \quad j = 1, 2, \dots, N. \end{aligned}$$

A one-sided approximation to α is used at the boundaries. This scheme is non-conservative (see Chapter 2.2) because although the α are updated in this way in

Finding the tumour radius

By the tumour radius Δ grows at the same rate as the cell velocity at the boundary v_N . Hence the tumour radius at the next time step using the explicit Euler time stepping scheme

§ 4.1 Numerical Results for Breard et al.'s Method

It is important to re-emphasize that the numerical algorithm specified in this chapter is surmise based upon the transformed profile given in 4.1. However, solving the transformed profile using this numerical process is successfully generating plots which replicate those shown in 4.1. We can therefore be reasonably confident in our preliminary calculations in Chapter 4, where we find the concentration C and cell velocity v using finite differences.

for both α and β . Nonetheless, we can reasonably be confident that the solution and the two boundary conditions converge

Chapter

Numeric results for solving mesh methods

In this section we use the solving mesh methods described earlier to present numeric simulations of the non dimensionalised code equations $\mathbb{R}$ to $\mathbb{R}$, in several parameter regimes. Our aim is to compare the three different solving mesh methods and so to compare the results with existing mesh numeric simulations in $\mathbb{R}$.

The results given here are the nondimensionalised ones. T

stepping scheme is used. In this case the number of nodes doubled the time step is quartered. This decision is made as the solution α is recovered using mid point approximation which is second order in space and the explicit Euler time stepping scheme is first order in time.

We would expect the solutions to converge quicker here using the ODE45 solver because this uses an approximation based upon Runge-Kutta 4th order which has a higher order of accuracy than Euler time stepping. However we should be careful to note that the time steps are considerably larger when using ODE45.

The relative errors for

convergence behaviour when comparing Euler time stepping and using ODE2. Yet within chosen time stepping scheme Method B and C have nearly identical convergence rates especially when using ODE2. These 2 and 3 when comparing Methods B and C with the explicit Euler time stepping. These and we see that the α convergence is fairly but the order of convergence of x for Method B. The error appears to be exhibiting erratic behaviour for the standard steps outlined here. The mesh from Method C together with Euler time stepping. The error seems to have the highest rate of convergence.

It appears that generally the mesh approaches an order of convergence greater than that of the α property of second order convergence. However we cannot be sure of the order of convergence in any of the cases without having more data and comparing the solutions to data retrieved using `N >> E`. Even so we can reasonably be confident that the solution and mesh converge for three ongoing mesh methods.

Comparison with Brendt's method
 , Comparing Figure from 4.c

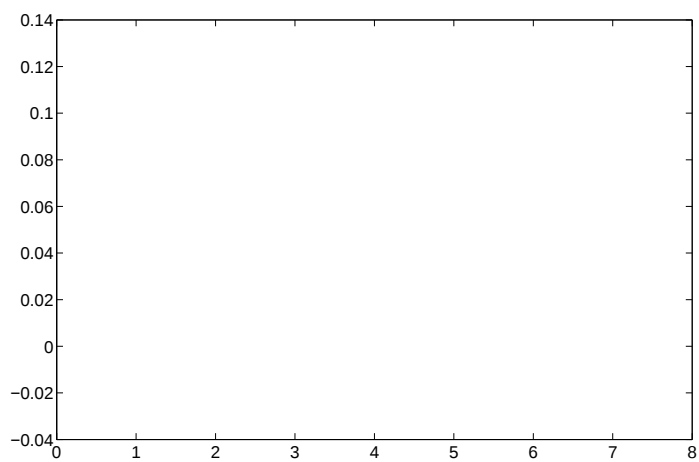
We wish to compare our numeric methods to the mesh method used in the general results using the same parameters. We compare our results with Figure 4 in [1]. A three methods were investigated using both the explicit Euler time stepping scheme and ODE2. Throughout this section we use `N` and `t` and run until `t`.

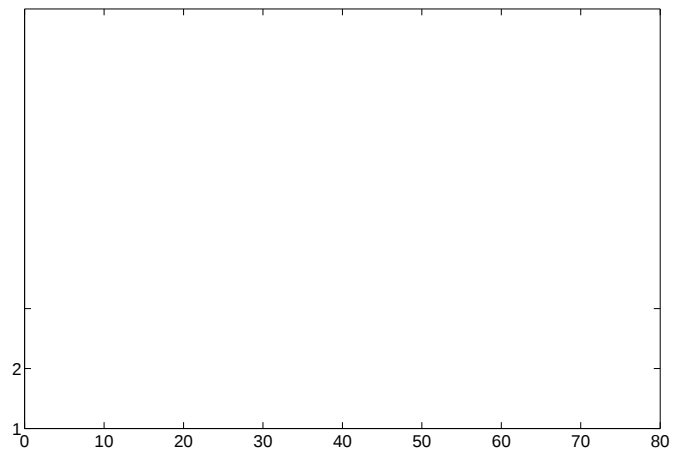
Methods A and C produce very similar plots to each other regardless of the time stepping approach. For this reason only the results from Method A are included here.

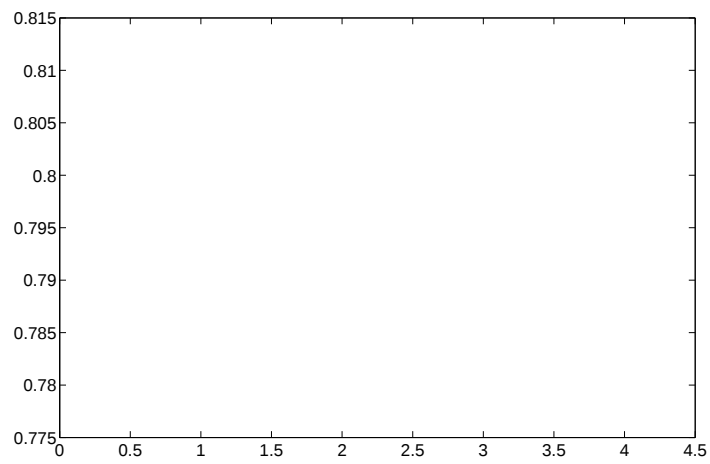
The explicit Euler time stepping scheme and ODE2 generate

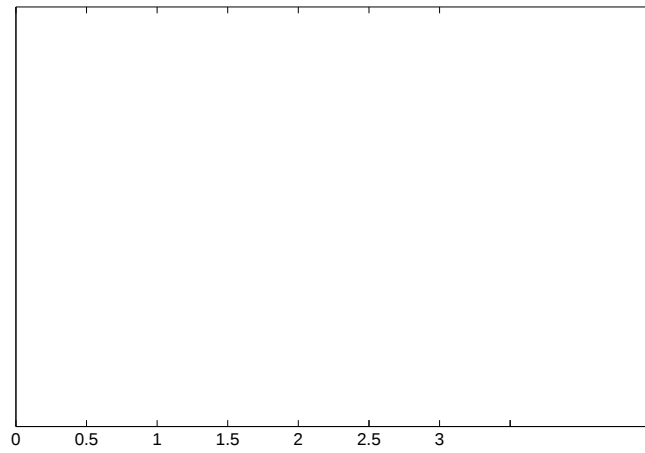
Method B appears to behave like Method A and therefore it is not after proper time t_{crit} , α appears to grow and the boundary no longer decreases to regularize the centre of the tuour. The plots from Method B are smooth despite the small number of nodes used for both methods. There is a considerable increase in α and v for t_{crit} , which appears to depend on the time step. The solution α does not drop to zero at the centre of the tuour even for t_{crit} (not shown here). The key characteristics remain the same for smaller t and so when using ODE23 suggesting that this behaviour is due to the numerical method. The processes of Method B and Method C are very similar and so Method C behaves as in Figures 4.7 and 4.8. It is reasonable to conclude that truncating the cell velocity with the mesh nodes can result in the mesh becoming too coarse in some regions. This is proven that could be compounded over time especially where the cell velocities vary between positive and negative. At this point the nodes would be moving in opposite directions meaning a considerable deficit in density. Indeed if we look at Figure 4.8 for t_{crit} we see that the velocity is mostly negative so the nodes are moving to the left.

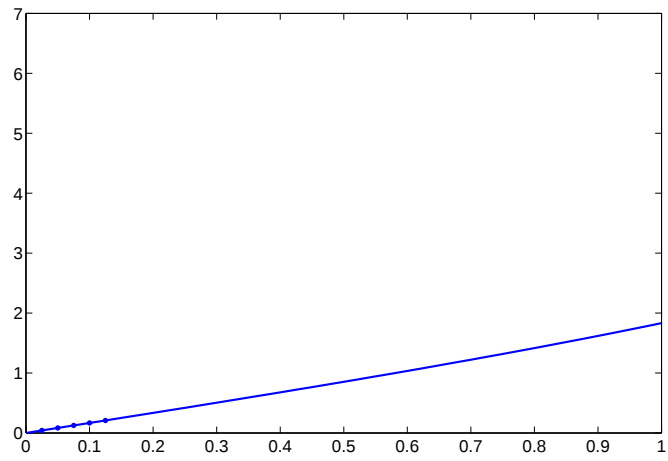
The differences between Method B and the results presented in 4.5 are more apparent in Figure 4.8. We can see more clearly that it appears to be











Chapter

Further

Attenuating the cell velocity boundary condition

Throughout this report we have not changed the mode presented in [1] and [2]. Let us consider the boundary condition on the cell velocity

$$\mathbf{v} = \mathbf{0} \quad \text{at } \mathbf{x} = \mathbf{x}_0.$$

Possible future work could include changing the left boundary condition to

$$\frac{d\mathbf{v}}{dx} = \mathbf{0} \quad \text{at } \mathbf{x} = \mathbf{x}_0,$$

depending on the internal pressure. Thus $\mathbf{v} \neq \mathbf{0}$ at the inner boundary. This would mean that the tumour would still be in symmetric about $\mathbf{x} = \mathbf{x}_0$ but the cells in the centre would have the velocity that depends on the viscosity μ and the nutrient concentration $\mathbf{C}$. When the necrotic core forms i.e. when $\alpha \rightarrow 0$ the region occupied by cells goes to zero from the origin. The profile would be based on the region occupied by $\alpha \neq 0$.

Examining the effect of

Let us return to $\chi(\alpha)$ in the form shown in Section 2.2

$$\chi(\alpha) = \begin{cases} \frac{\hat{\mathbf{z}}_c - \alpha^*}{(1 - \alpha^*)^q} (\alpha - \alpha^*) & \alpha_{min} \leq \alpha < \alpha^* \\ \alpha & \alpha_{min} \leq \alpha < \alpha^* \end{cases}$$

For $\alpha_{min} < \alpha^*$ there is discontinuity at α_{min} . This jump may cause issues when numerically approximating the derivative of $\chi(\alpha)$ used in Chapter 2.

since in this section we solved the equation for the cell velocity $\frac{d\alpha}{dx}$ by discretising in space. The right hand side of the tri-system is the vector of the numerical approximation of $\frac{d}{dx} \alpha \chi(\alpha)$

$$\begin{aligned} \frac{d}{dx} \chi(\alpha) \alpha &= \alpha_{j+\frac{1}{2}} \chi(\alpha_{j+\frac{1}{2}}) - \alpha_{j-\frac{1}{2}} \chi(\alpha_{j-\frac{1}{2}}) \\ &= \frac{1}{2} (\alpha_j^* + \alpha_{j+1}) \chi(\alpha_j^* + \alpha_{j+1}) - \frac{1}{2} (\alpha_j^* + \alpha_{j-1}) \chi(\alpha_j^* + \alpha_{j-1}). \end{aligned}$$

By approximating across the whole region in this manner we are not accounting for the jump in $\chi(\alpha)$ at $\alpha = \alpha_{min}$. This only becomes an issue if this point is high enough to account for the severe oscillations in Figures 6 to 8. These figures use $\alpha_{min} = 0$ and $\alpha^* = 1$ and show that the solution is oscillated until near the point where α drops down to 0.

To assess this error in our discretisation we identify when $\alpha = \alpha_{min}$ and use one sided approximation for $\frac{d}{dx} \alpha \chi(\alpha)$ either side of this point so as to not discretise across the jump in $\chi(\alpha)$.

As in the cell velocity calculation it is necessary to use one sided approximations at the same point $\alpha = \alpha_{min}$ when finding the solution α . This is because use α

Biography

1. Arujo R P and McE in D L S 1978 A history of the study of solid tumor growth The contribution of the elastic modeling *Definition of the elastic Deformability* **66** 1-10
2. Arujo R P and McE in D L S 1978 The nature of stresses induced during tissue growth *App Math Lett* **18** 1-10
3. B e 1978 Moving Mesh Methods for Non Linear Partial Differential Equations Ph.D Thesis *Department of Mathematics University of Reading*
4. Bre rd C 1978 Byrne H M and Le is C E 1978 The role of cell-cell interactions in topographic order for tumor growth *of Math Biol* **45(2)** 1-10

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Appendices

Appendix A

Estimating the effect of ()

Let us identify the node just to the left of the point where $\alpha = \alpha_{min}$ as the former node which we shall denote as $\mathbf{x}_m$. To account for the jump between $\mathbf{x}_m$ and $\mathbf{x}_{m+1}$ we use one sided discretisation of $\frac{\partial v}{\partial x}$ at $\mathbf{x}_m$ and $\mathbf{x}_{m+1}$.

Downwind discretisation of the velocity (3.10) at $\mathbf{x}_m$

$$\frac{\partial v}{\partial x} \bigg|_{\mathbf{x}_m - \mathbf{x}_{m-1}} = \alpha \mu \frac{\partial v}{\partial x} - \alpha \chi \bigg|_{\mathbf{x}_m} = \alpha \mu \frac{\partial v}{\partial x} - \alpha \chi \bigg|_{m-1} = \frac{k \alpha_{m-\frac{1}{2}}}{\alpha_{m-\frac{1}{2}}} v_{m-\frac{1}{2}}$$

Again we use one sided discretisation on the terms in the square brackets so as to not propagate differentials across $\mathbf{x}_m$. As so as before we use

$$\alpha_{m-\frac{1}{2}} \approx \frac{1}{2} (\alpha_m + \alpha_{m-1})$$

$$\begin{aligned} \frac{\partial v}{\partial x} \bigg|_{\mathbf{x}_m - \mathbf{x}_{m-1}} &= \mu \alpha_m \frac{v_m - v_{m-1}}{\mathbf{x}_m - \mathbf{x}_{m-1}} - \chi \bigg|_{\mathbf{x}_m} \alpha_m - \mu \alpha_{m-1} \frac{v_{m-1} - v_{m-2}}{\mathbf{x}_{m-1} - \mathbf{x}_{m-2}} - \chi \bigg|_{\mathbf{x}_{m-1}} \alpha_{m-1} \\ &= \frac{k (\alpha_m + \alpha_{m-1})}{-2 (\alpha_m + \alpha_{m-1})} (v_m - v_{m-1}) \end{aligned}$$

$$\begin{aligned} \mu \alpha_m \frac{v_m - v_{m-1}}{\mathbf{x}_m - \mathbf{x}_{m-1}} - \mu \alpha_{m-1} \frac{v_{m-1} - v_{m-2}}{\mathbf{x}_{m-1} - \mathbf{x}_{m-2}} &= \frac{k (\alpha_m + \alpha_{m-1}) (\mathbf{x}_m - \mathbf{x}_{m-1})}{-2 (\alpha_m + \alpha_{m-1})} (v_m - v_{m-1}) \\ &= \chi \bigg|_{\mathbf{x}_m} \alpha_m - \chi \bigg|_{\mathbf{x}_{m-1}} \alpha_{m-1} \end{aligned}$$

nd

$$\mathbf{b}(\boldsymbol{\alpha}) = \begin{pmatrix} \mathbf{b}(\boldsymbol{\alpha}_1) & \mathbf{b}(\boldsymbol{\alpha}_2) & \cdots & \mathbf{b}(\boldsymbol{\alpha}_m) & \mathbf{b}(\boldsymbol{\alpha}_{m+1}) & \cdots & \mathbf{b}(\boldsymbol{\alpha}_{N-1}) & \mathbf{b}(\boldsymbol{\alpha}_N) \end{pmatrix}^T$$

$$\mathbf{v} = \begin{pmatrix} \mathbf{v}_1 & \mathbf{v}_2 & \cdots & \mathbf{v}_m & \mathbf{v}_{m+1} & \cdots & \mathbf{v}_{N-1} & \mathbf{v}_N \end{pmatrix}^T.$$

Recovering $\boldsymbol{\alpha}_m$ and $\boldsymbol{\alpha}_{m+1}$ using one-sided approximations

For consistency we recover $\boldsymbol{\alpha}$ using one-sided approximation to $\mathbf{x}_m$ and $\mathbf{x}_{m+1}$. Method A:

$$\boldsymbol{\alpha}_m = \frac{\theta(\mathbf{t})}{\theta(\mathbf{t})} \frac{\mathbf{x}_{m+1}(\mathbf{t}) - \mathbf{x}_{m-1}(\mathbf{t})}{\mathbf{x}_m(\mathbf{t}) - \mathbf{x}_{m-1}(\mathbf{t})} \boldsymbol{\alpha}_m$$

$$\boldsymbol{\alpha}_{m+1} = \frac{\theta(\mathbf{t})}{\theta(\mathbf{t})} \frac{\mathbf{x}_{m+2}(\mathbf{t}) - \mathbf{x}_{m+1}(\mathbf{t})}{\mathbf{x}_{m+2}(\mathbf{t}) - \mathbf{x}_{m+1}(\mathbf{t})} \boldsymbol{\alpha}_{m+1}.$$

Methods B and C:

$$\boldsymbol{\alpha}_m = \frac{m}{\mathbf{x}_m - \mathbf{x}_{m-1}}$$

$$\boldsymbol{\alpha}_{m+1} = \frac{m+1}{\mathbf{x}_{m+2} - \mathbf{x}_{m+1}}.$$

We should note that the downwind approximation to $\mathbf{x}_m$ requires $m \geq 2$ but at the position where $\boldsymbol{\alpha} = \boldsymbol{\alpha}_{min}$ occurs at the right hand boundary so initially m is likely to be smaller than 2.