Accuracy of geometrical modelling of heat transfer from tissue to blood vessels

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Abstract. We have developed a thermal model in which blood vessels are described as geometrical objects, 3D curves with associated diameters. Here the behaviour of the model is examined for low resolutions compared with the vessel diameter and for strongly curved vessels. The tests include a single straight vessel and vessels describing the path of a helix embedded in square tissue blocks. The tests show the excellent behaviour of our discrete vessel implementation.

1. Introduction

Kotte et al (1996) presented a discrete-vessel thermal model in which vessels are described as geometrical objects, 3D curves with associated diameter, independent of the tissue grid. The vessel temperatures are maintained in structures outside the tissue voxel space and the vessels can have any position with respect to the voxels. For the calculation of the interaction between tissue and vessels an analytic result is used. This result is exact for a cylindrically symmetric stationary temperature distribution around the vessel and thermally developed flow. Heat transfer in the solid tissue itself is modelled using a finite differences method. It was shown that the model gives highly accurate results if conditions conform to the assumptions made in the calculation of the tissue–vessel interaction: straight vessels embedded in cylinders of tissue, modelled at a high resolution compared with the vessel diameter. In this paper we investigate the accuracy of the model in situations where it is not a priori clear that the model will yield good results: for low resolutions (compared with the vessel size) and for curved vessels. Those tests are a necessity because the model must be capable of describing the thermal behaviour of all thermally significant vessels in tissue grids of 1–2 mm. This includes the description of strongly curved vessels with diameters as small as 0.2 mm. The tests are done by looking at the simulated thermal equilibration of blood in vessels that are either straight or describe the path of a helix.

2. Thermal model description

Only a brief explanation of some key concepts of the model will be given here, for a more comprehensive description of the model we refer to the paper of Kotte et al (1996).

Discrete vascular trees are constructed of vessel segments, which are defined as vessel sections between branching points. The segments are described using parametrized curves
For the implementation of the heat flow between vessel and tissue two sets of voxels are employed by the vessel (see figure 1). The exchange set comprises the voxels that both have the voxel centre inside the vessel or (for small vessels) contain the heart line of the vessel, and adjoin at least one voxel of surrounding tissue. The estimation set consists of the voxels in the surrounding tissue that adjoin at least one exchange set voxel.

For all voxels in the estimation set an estimate for the heat flow rate density at the vessel wall can be calculated using an analytical solution (Kotte et al 1996). These estimates are averaged and multiplied with the vessel surface to yield the heat flow rate into the vessel. Using this heat flow rate the new vessel temperatures are calculated. The heat that is withdrawn from the tissue is removed (in equal amounts) from the exchange set voxels of the vessel.

The flow of blood in the vessel segment is modelled by means of a subdivision of the segment in small subsegments, so-called buckets (Kotte et al 1996).

3. Two-dimensional (2D) simulations

To investigate the influence of the model resolution on the calculation of the vessel–tissue heat exchange 2D simulations were performed in planes perpendicular to the vessel axis. The vessel–tissue interaction takes place in this radial plane. A geometry containing a single vessel was examined, with special attention to the position of the vessel with respect to the voxels. As in Kotte et al (1996), the rate of thermal equilibration of the vessel, as defined by the equilibration length, was determined as a test for the accuracy of the model.

A square cross section was chosen for the tissue block because this allowed fixing the boundary temperature at points that really are situated on the tissue boundary, whereas a circular boundary will be approximated increasingly crudely for decreasing resolution. The 2D simulations were performed by assigning zero conductivity to the tissue outside the plane of interest. Simulations were carried out for a block centred vessel, as well as for geometries in which the vessel was translated along one of the diagonals. For a view of some of the simulation set-ups see figure 2.
The dimensions of the tissue slice were $12 \times 12 \times 5$ mm$^3$. Because there is no conductive heat transport in the $z$-direction the accuracy of the simulated equilibration length does not depend on the blood velocity. The voxel dimensions of the tissue in the $x, y$-plane were varied between 0.25 and 3 mm.

The equilibration lengths found for various positions of the vessel using all different resolutions are pictured in figure 3. With just one exception, all simulated equilibration lengths are within 3% of the highly accurate value obtained using a very high resolution. The exception, with a discrepancy of about 10%, occurred for one of the geometries modelled with a voxel size of $3 \times 3 \times 5$ mm$^3$. This large discrepancy is caused by the fact that the vessel is placed very eccentric in the matching voxel. The heat loss from the tissue is effected in this (exchange set) voxel, and the geometry will behave somewhat like a vessel located at the voxel centre. This was verified in a $3 \times 3 \times 5$ mm$^3$ voxel simulation with the vessel really going through the centre of the voxel in question.

A surprising feature is the non-monotonic behaviour of the curves. For a central vessel the high accuracy at low resolution can be explained by the small discretization errors in the tissue. As the resolution decreases, a growing tissue annulus around the vessel is treated analytically, and in this case exactly. Because a relatively large part of the tissue thermal resistance is concentrated around the vessel (the thermal resistance per distance is inversely proportional to the radius), this analytic treatment more than compensates for the larger discretization errors produced by modelling the remaining tissue at lower resolution. For other vessel positions an explanation for the non-monotonic behaviour of the curves can be found in the irregular behaviour of the vessel position with respect to the grid (a vessel located very eccentric with respect to the voxel for one resolution may be almost centred on a lower resolution).
4. Three-dimensional (3D) simulations

4.1. Straight vessel

The important factor influencing the accuracy of the single-vessel simulations for varying $z$-resolution is the ratio between equilibration length and tissue voxel length. If this ratio is large ($>20$) the radial heat flow in the tissue and into the vessel will change just a little along the length of one voxel and the accuracy of the simulation will not be affected by the discretization in the $z$-direction. If the ratio is not large, discretization effects in the tissue and deviations due to the blood experiencing a changing interaction along its path can emerge. The latter effects are significantly reduced in our thermal model by interpolation of the radial heat flow between consecutive vessel subsegments (buckets). Before choosing a specific geometry it must be noted that, other than in 2D, a given geometry (tissue radius, vessel radius, resolution) will not be modelled with the same accuracy after scaling the geometry with an arbitrary factor; for a given grid (given numbers of voxels in the $x$, $y$ and $z$ directions) with fixed vessel radius/voxel dimensions ratio and boundary temperatures the voxel temperatures do depend on the dimensions of the voxels. This is due to the fact that the equilibration length scales with the square of $r_{ves}$ instead of linearly: small vessels
are less accurately modelled than large vessels for equal relative resolution because the ratio between equilibration length and tissue voxel length is smaller. This effect is further enhanced by lower flow velocities in smaller vessels.

The 3D simulations were performed in a volume of $12 \times 12 \times 18 \text{ mm}^3$. The voxel dimensions were equal in all directions and were varied between 0.25 and 3 mm. The vessel was subdivided in buckets with a length equal to the voxel dimensions. Just one geometry was analysed: a straight vessel running parallel to the tissue central axis, the vessel axis shifted 0.4 mm in both $x$ and $y$ directions with respect to this axis.

For a long equilibration length (diameter $\phi = 1.0 \text{ mm}$, $u_b = 0.04 \text{ m s}^{-1}$, $L_{eq} \approx 90 \text{ mm}$) it was found that simulations at different resolutions resulted in slightly different equilibration lengths. However, all simulated equilibration lengths were, within 0.1%, equal to the results found in the equivalent 2D simulations. This proves that the mutual differences are introduced by discretization in the radial plane and not by discretization in the axial direction, as was anticipated.

For a smaller vessel diameter (0.5 mm) and low blood velocity ($0.005 \text{ m s}^{-1}$, $L_{eq} \approx 4 \text{ mm}$) both $z$-discretization effects and axial conduction will induce changes with respect to the 2D results. An estimate for the effect of axial conduction can be found using the solution for a vessel embedded in a coaxial tissue cylinder, instead of the rectangular block.
Figure 5. Geometry of curved vessel simulations. Picture generated using the actual parametrized vessel description.

Figure 6. Vessel describing a helix. Simulated stationary temperature distribution in a central plane in the tissue (interpolated results of simulation with voxel size 0.5 mm).

For the equivalent tissue radius of 6.5 mm (for this radius $L_{eq}$ without axial conduction equals the 2D high-resolution simulated $L_{eq}$) $L_{eq}$ increases by a factor of 1.2 due to axial conduction (see Appendix). In figure 4 the results of the 3D simulations are shown. Also shown are the 2D results multiplied by our estimated axial conduction factor of 1.2. For most resolutions the 3D simulated results agree very well with the 2D results corrected for axial conduction. This means that the $z$-discretization effects are small, proving the efficacy of the vessel heat flow interpolation scheme. For the 3.0 mm resolution case a somewhat larger deviation is found. Here, the ratio $L_{eq} : \Delta z \approx 1.4$ is small, and the linear interpolation along the vessel of the exponentially decaying heat flow rate introduces errors. One might consider modelling the vessel at twice the resolution of the tissue. A simulation of the same geometry with 3.0 mm cubic voxels and vessel buckets with a length of 1.5 mm yielded a much improved vessel temperature profile (equilibration length correct to within 3%).
4.2. Curved vessel

In the calculation of the tissue–vessel interaction the program does not take any specific measures to account for vessel curvature: a curved vessel is treated as a series of very short cylinders. In this section we present results obtained for an artificial spiralling vessel simulated at various resolutions. The high-resolution result will be used to evaluate the accuracy of the simulations using lower resolutions.

The modelled geometry is depicted in figure 5. A vessel ($\phi = 1$ mm) enters the modelled tissue block ($24 \times 24 \times 60$ mm$^3$) along the $z$-axis and spirals slowly outward. At a distance of 5 mm to the $z$-axis, the vessel retains this distance and forms a helix having four turns with a pitch of 6 mm and a diameter of 10 mm. The end of the vessel mirrors the start by smoothly returning to the $z$-axis. The temperature of the four tissue walls parallel to the $z$-axis was set to $+8$ K, whereas the two walls perpendicular to the $z$-axis were isolated. The mixing-cup temperature of the blood entering the volume was set to 0 K. This geometry was modelled with voxel dimensions ranging between 0.5 mm and 12 mm. Simulations were continued until no change in tissue and blood temperatures could be observed. Only the stationary temperature distributions (figure 6) were evaluated.

The different voxel sizes for the 3D helix simulation were chosen such that all distances...
between opposing tissue boundaries were equal to an integer number of voxels. This was done to ensure optimal modelling of the boundary conditions. The vessel was modelled by 14 segments, three in each winding. Each segment is described by a parametric curve characterized by four points. The composite vessel curve is a nice smooth approximation of the desired helix. The bucket length was chosen as 3 mm or equal to the voxel size, whichever was smallest. The stationary mixing-cup temperature profiles of the vessel are pictured in figure 7. For voxel dimensions up to 3.0 mm the temperature profile shows very good agreement with the high-resolution result (1.0, 2.0 mm not shown for clarity). For lower resolutions, notable differences are found. It is seen that for low resolution the blood equilibrates faster. For 4.0, 6.0 and 12.0 mm the equilibration lengths are respectively roughly 10%, 20% and 40% shorter than the high-resolution result. Shorter equilibration lengths for low resolutions were indeed expected, as the number of voxels inside the helix involved in the estimation of the heat flow rate was too small compared with the number of voxels on the outside of the helix. This makes the temperatures on the outside too important and in this case results in an overestimation of the heat flow rate and an equilibration length that is too short.

5. Conclusion

For single-vessel simulations it was shown that, at low resolutions compared with the vessel size, the freedom to position the vessel anywhere with respect to the tissue grid can lead to a small loss in accuracy. For vessel segments that are not located very eccentric in their corresponding (exchange) voxels the error in the equilibration length will be just a few per cent, even if the resolution is low. Slightly larger deviations can occur if the voxel size is not small compared with the thermal equilibration length or to the curvature of the vessel.

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Appendix. Analytic solution for the equilibration length of a vessel with axial conduction in the tissue

The 3D differential equation governing the temperature field in the coaxial cylinder of tissue surrounding the vessel is

$$\frac{\partial^2 T}{\partial r^2} + \frac{1}{r} \frac{\partial T}{\partial r} + \frac{1}{r^2} \frac{\partial^2 T}{\partial \theta^2} + \frac{\partial^2 T}{\partial z^2} = \frac{1}{\alpha} \frac{\partial T}{\partial t}. \quad (1)$$

The symbol $\alpha$ denotes the thermal diffusivity ($\alpha = k_{\text{tis}}/\rho_{\text{tis}}c_{\text{tis}}$). The stationary solution must be cylindrically symmetric, because of the constant tissue boundary temperature $T_{\text{bound}}$. Without loss of generality we define this tissue outer wall temperature as zero.

The velocity and temperature profiles in the vessel are assumed to be fully developed. On top of that we also assume the cylinder segment to be sufficiently far from both faces to expect the shape of the radial temperature profile in the tissue to be independent of $z$. This suggests separation of variables. Indeed, if we substitute

$$T(r, z) = T^+(r)Z(z) \quad (2)$$
it is found that the \( z \) dependence of the temperature, considering the boundary condition on the tissue wall, is given by

\[
Z(z) = \exp(-z/L_{eq}).
\]  

(3)

Here \( L_{eq} \) is an integration constant, the value of which can only be determined if the solution to the radial differential equation (4) is known and the boundary conditions are applied. It is clear that \( L_{eq} \) must equal the equilibration length of the vessel.

The radial profile must satisfy

\[
\frac{\partial^2 T^*}{\partial r^2} + \frac{1}{r} \frac{\partial T^*}{\partial r} + \frac{T^*}{L_{eq}^2} = 0
\]

(4)

which is Bessel’s equation of order zero. Two independent solutions are the Bessel functions of first and second kind of order zero. The general solution is therefore

\[
T^*(r) = C_1 J_0(r/L_{eq}) + C_2 Y_0(r/L_{eq}).
\]

(5)

The integration constant \( C_1 \) is eliminated by imposing the boundary condition \( T(r_{tis}) = 0: \)

\[
T^*(r) = C_2 \left( \frac{-Y_0(r_{tis}/L_{eq})}{J_0(r_{tis}/L_{eq})} J_0(r/L_{eq}) + Y_0(r/L_{eq}) \right).
\]

(6)

The still unknown equilibration length features as a parameter in this solution. The solution is determined by the vessel properties. The heat flow rate in the tissue at the vessel wall can be calculated with

\[
2\pi r_{ves} \phi|_{r=r_{ves}} = -2\pi r_{ves} k_{tis} \left( \frac{dT^*}{dr} \right)|_{r=r_{ves}}.
\]

(7)

Using (e.g. Abramowitz and Stegun 1965) the relations

\[
J_1' = -J_1 \quad Y_1' = -Y_1
\]

(8)

describing the derivatives using the first-order Bessel functions \( J_1 \) and \( Y_1 \), the heat flow rate is given by

\[
\phi = k_{tis} \frac{C_2}{L_{eq}} \left( \frac{-Y_0(r_{tis}/L_{eq})}{J_0(r_{tis}/L_{eq})} J_1(r_{ves}/L_{eq}) + Y_1(r_{ves}/L_{eq}) \right)
\]

\[
\equiv k_{tis} \theta(L_{eq}).
\]

(9)

(10)

The blood mixing-cup temperature can be determined from this heat flow rate and the vessel wall temperature by using the Nusselt relation (11). The rate of change of the blood mixing-cup temperature follows from the heat flow rate (12) and must match the equilibration length in the tissue \( L_{eq} \). Combining all we get

\[
T_{ves} = T^*(r_{ves}) + \frac{2r_{ves} \phi}{N\kappa_b}
\]

(11)

\[
\frac{dT_{ves}}{dz} = -\frac{2\phi}{r_{ves} \mu_b \rho_b c_b}
\]

(12)

\[
\Rightarrow \frac{dT_{ves}}{dz} = -\frac{k_{tis} \theta(L_{eq})}{L_{eq}} \frac{1}{2r_{ves} \mu_b \rho_b c_b} T_{ves}
\]

(13)

\[
\Rightarrow L_{eq} = \frac{L_{eq}}{k_{tis} \theta(L_{eq})} \frac{1}{2r_{ves} \mu_b \rho_b c_b} T_{ves}
\]

(14)

\[
\Rightarrow T^*(r_{ves}) + \frac{\phi 2r_{ves}}{N\kappa_b} = \frac{k_{tis} \theta(L_{eq})}{2r_{ves} \mu_b \rho_b c_b}
\]

(15)
This closed form gives the exact solution of the equilibration length for an infinitely long vessel. Since the Bessel functions (appearing in both $T^*$ and $\theta$) have no inverse functions, the equation cannot be solved directly. An iterative scheme, however, can quickly yield the solution.

For a given tissue radius this solution approximates the solution derived without taking account of axial conduction (e.g. Crezee and Lagendijk 1992) more and more for increasing equilibration length:

$$L_{eq} = \frac{r_{ves}^2 \Delta T \rho_c c_b}{\frac{1}{2} \frac{k_{tis} \theta(L_{eq})}{\frac{1}{2} r_{ves} \Delta T \rho_c c_b} - \frac{1}{2} \frac{T^*(r_{ves})}{k_{tis} \theta(L_{eq})^2 r_{ves}}}.$$  

(19)

This value is taken as a first estimate in the iterative scheme solving equation (18) yielding the equilibration length accounting for axial conduction in the tissue.

References

Abramowitz M and Stegun I A 1965 *Handbook of Mathematical Functions with Formulas, Graphs and Mathematical Tables* (New York: Dover)
