Discrete vessel heat transfer in perfused tissue—model comparison

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Abstract
The aim of this paper is to compare two methods of calculating heat transfer in perfused biological tissue using a discrete vessel description. The methods differ in two important aspects: the representation of the vascular system and the algorithm for calculating the heat flux between tissue and blood vessels. The first method was developed at the University of Utrecht between 1994 and 1998 and has been used in several clinical applications. The second method has been proposed by the first author. The methods are briefly described, their assumptions and limitations are discussed. Finally, the test simulation is introduced and the results produced by both methods are compared. The test indicates that the simpler, and less computationally intensive method proposed by the present author for calculating 2D problems containing countercurrent blood vessel systems can reproduce quite well some features of the solution obtained by the more complex 3D method. The observed discrepancies could be explained on physical grounds.

1. Introduction

Transport of heat in living biological tissues is a very complex phenomenon. The tissue is invariably an inhomogeneous, anisotropic material and a scene for various processes influencing the heat balance. The most important of these is the circulation of blood.

The blood flows through the vessels forming a circulatory system. The heart supplies the pressure driving the blood through a branching system of vessels that get smaller and smaller, until they reach the level of the capillaries. At that point the blood drains into the small venous vessels that drain into larger and larger vessels, ultimately bringing the blood to the heart to complete the circulation.
Figure 1. The temperature of the blood as it traverses the generations of blood vessels. Temperature of surrounding tissue is within a range schematically indicated by the dashed line, after Chen and Holmes (1980).

There are numerous refinements and exceptions to the simple picture sketched above, but it is realistic enough to serve as a basis for the further considerations of the influence of blood flow on heat transfer in tissue. The temperature of the blood as it traverses the vessels of subsequent generations is schematically depicted in figure 1. The most important conclusion from this figure is the fact that the temperature of the blood is significantly different from that of the surrounding tissue only when the blood is in relatively large vessels. The thermal equilibration between tissue and blood vessels becomes an increasingly quicker process with decreasing vessel diameter.

The models of heat transfer in perfused tissue (bio-heat equations) available in the literature can be divided into two classes: the continuum models and the vascular models. The continuum models describe the perfused tissue by means of a single tissue temperature. The most important continuum models are the Pennes model (Pennes 1948, Stańczyk and Telega 2002, Wissler 1998), the effective conductivity models, (Weinbaum and Jiji 1985, Weinbaum et al 1992, Charny et al 1990, Stańczyk and Telega 2002), and the directed perfusion model (Wulff 1974, Stańczyk and Telega 2002). All these models rest on additional assumptions regarding the blood thermal equilibration and describe the heat transfer in terms of a single tissue temperature. Their applicability is limited to a range of vessel diameters and heat loads. Continuum models cannot predict the effects of the individual vessels on the local tissue temperature.

In a recent paper Shrivastava and Roemer (2006), using a vascular model of generic geometry, investigated the contribution of various generations of vessels to the heat transfer process. They concluded that, contrary to the common belief, thermal significance of the vessel cannot be determined on the basis of the vessel diameter but is in fact a strong function of inlet blood temperature, surrounding tissue temperature distribution and blood mass flow. Furthermore, the results obtained in Shrivastava and Roemer (2006) suggest that the absolute...
diameters and heat transfer coefficients do not affect thermal significance of the vessels much. These results lead to the conclusion that applicability of the continuum models can only be established on a case-by-case basis and the vascular model is necessary to that end.

Vascular models describe the heat transfer between the blood in individual vessels and the tissue. No assumption is made \textit{a priori}, concerning the possible relation between these two temperatures. Therefore, the full range of the thermal equilibration regimes, as depicted in figure 1, can be reproduced. Also, modelling of physiological phenomena such as vasodilation and vasoconstriction, blood viscosity changes, etc., can be done in a more straightforward manner than in the case of the continuum models.

The vascular models need detailed information about the vasculature in the region of interest and need to keep track of all the blood temperatures throughout this system in order to calculate the tissue temperature. This high level of complexity results also in high computational power needed to perform calculations on such models. In fact, the vascular model presented by Brinck and Werner (1994) could only be formulated and solved for a very small region of tissue. The vascular model devised by Baish (1994) circumvents this difficulty to a large extent by using the boundary element approach which requires only the boundary of the tissue region to be discretized. The shortcoming of such a method is the fact that only linear problems can be considered.

2. Method

In this paper a comparison between two vascular models is undertaken. A brief explanation of the basic assumptions made in each model is followed by a description of the test simulation and a discussion of the obtained results.

2.1. Unidirectional discrete vessel heat transfer model—the DIVA system

The DIVA (DIscrete VA sculation) program is a computer implementation of a vascular model based on a unidirectional vascular tree description. It has been developed at the Utrecht University in the 1990s; see e.g. Kotte et al (1996, 1999).

The DIVA model can calculate 3D temperature distributions while accounting for individual vessels in an extensive discrete vasculature perfusing the tissue region of interest. The tissue is discretized into regular cuboid voxels. Each blood vessel is divided into a prescribed number of \textit{buckets} (blood temperature samples). Each bucket is assigned an estimation set consisting of voxels that, more or less, surround the vessel segment and a sink set consisting of the tissue voxels that lie, more or less, inside the vessel. The calculation of the blood-tissue energy transfer is performed as follows.

First, the temperature around a straight vessel of radius $r_{\text{ves}}$, surrounded by a layer of tissue of constant thickness of $R - r_{\text{ves}}$, is considered. In polar coordinates the conduction equation takes on the form:

$$\rho c_t \frac{\partial T_t}{\partial t} = \frac{1}{r} \frac{\partial}{\partial r} \left( \lambda r \frac{\partial T_t}{\partial r} \right) + P$$

(1)

where $\rho$, $c$ and $\lambda$ are the density, specific heat and conductivity, respectively. Subscript $t$ denotes tissue properties. The heat flux from the blood to the inner vessel wall can be expressed as

$$q \Big|_{r=r_{\text{ves}}} = -\frac{Nu \lambda_{bl}}{2r_{\text{ves}}} (T_t(r_{\text{ves}}) - T_{bl})$$
where subscript ‘bl’ denotes properties of the blood and $Nu$ is a (prescribed) Nusselt number. $T_{bl}$ is the mixing-cup temperature of the blood. If we assume that the temperature at the surface of the tissue cylinder is constant, the problem can be solved analytically and the heat flux through the vessel wall can be expressed as a function of $T_t(R)$, $R$, $Nu$ and other known parameters.

In the DIVA system this analytical solution is used to estimate heat flux through the vessel wall. Tissue temperatures at all the voxels of the estimation set of the vessel bucket are used one by one as $T_t(R)$, with the distance $R$ being equal to the distance between the centre of the estimation voxel and the vessel centreline. The results are then averaged. The resulting heat flux is then distributed over the voxels of the sink set of the vessel bucket in form of the volumetric heat source. The procedure is approximate because the temperature distribution around any vessel in the simulation will, most probably, be different from the solution to the problem described by equation (1).

The flow of blood in the DIVA system is computationally separated from the heat transfer calculation and is modelled via the shift-and-resample method, which involves shifting the blood temperature samples along the vessel by the amount determined by flow velocity and then obtaining new samples by means of interpolation.

The details of the calculation method used in the DIVA program are described at length in Kotte et al (1996, 1999). The analysis of use of DIVA system to calculation of heat flows in countercurrent geometry can be found in van Leeuwen et al (1997). An account of the practical application of the system can be found in van Leeuwen et al (1999).

2.2. Countercurrent discrete vessel heat transfer model

In the second method, developed by the first author, the vascular system is described in terms of a single countercurrent arterio-venous tree. Rather than from single vessel segments, the vasculature is now built from pairs of arterio-venous vessel segments, cf figure 2. The numerical implementation of the method (called GRID from now on) presented in the paper is two-dimensional.

One of the first bio-heat transfer models to explore the fact that blood vessels occur in countercurrent pairs, was presented in the work of Weinbaum and Jiji (1985). These authors derived a continuum equation, in which the contributions of the blood flow in the countercurrent vessels were included in an anisotropic effective conductivity tensor. They formulated an equation for the local temperature of the tissue, assuming it to be equal to the local average blood temperature. This made the formulation of the continuum approximation possible, but was also subject to severe criticism, cf Wissler (1987). The GRID is a vascular counterpart of the continuum Weinbaum–Jiji model, where no relation between average blood and tissue temperatures is postulated a priori.
The calculation of blood temperatures in the GRID system is based on the following equation:

\[
\pi r^2 \rho_{bl} c_{bl} \frac{\partial T_{bl}}{\partial t} = \frac{2 \pi r q_w(s)}{\partial s} - \pi r^2 \frac{\partial q(s)}{\partial s} - \pi r^2 \rho_{bl} c_{bl} v \frac{\partial T_{bl}}{\partial s}
\]

where \( v \) denotes the average blood velocity in the vessel and \( s \) denotes the vessel axial coordinate.

The average velocity is assumed equal in both countercurrent vessels. This is a simplification—in reality the arteries and veins differ in structure and size. The venous vessels are larger and therefore the average venous blood velocity is expected to be smaller.

We then assume that axial conduction is negligible and that the heat flux from the vessel can be divided into two terms: one describing heat exchange with the countercurrent vessel and one describing the heat exchange between the vessel and the surrounding tissue. We then assume that the former is proportional to the temperature difference between the countercurrent vessels and the latter is proportional to the temperature difference between the vessel and the tissue. Denoting the dimensionless proportionality coefficients with \( \sigma_{cc} \) and \( \sigma_t \) respectively one can obtain the equations for the arterial and venous blood temperature (\( T_a \) and \( T_v \) respectively):

\[
\rho_{bl} c_{bl} \frac{\partial T_a}{\partial t} = \sigma_{cc} \lambda_t \pi r^2 (T_v - T_a) + \sigma_t \lambda_t \pi r^2 (T_t - T_v) - \rho_{bl} c_{bl} v \frac{\partial T_a}{\partial s}
\]

(2)

\[
\rho_{bl} c_{bl} \frac{\partial T_v}{\partial t} = \sigma_{cc} \lambda_t \pi r^2 (T_a - T_v) + \sigma_t \lambda_t \pi r^2 (T_t - T_v) - \rho_{bl} c_{bl} v \frac{\partial T_v}{\partial s}
\]

(3)

The shape coefficients \( \sigma_{cc} \) and \( \sigma_t \) can be estimated using the stationary solution of the corresponding 2D problem; see e.g. Incropera and DeWitt (1996). For two parallel cylinders of diameters \( D_1, D_2 \), lying a distance \( w \) apart the following expression can be used, after Incropera and DeWitt (1996):

\[
\sigma_{cc} = \frac{2 \pi}{\cosh^{-1}\left(\frac{4w^3 - D_1^3 - D_2^3}{2D_1D_2}\right)}
\]

If we assume that the cylinders are the same \( D_1 = D_2 \) and \( w \) is proportional to \( D_1 \), the value of \( \sigma_{cc} \) becomes constant and equal to about 2.3855. The proposition that the distance between vessels is proportional to their diameters is an assumption that is not exactly satisfied in real vessel trees, and is proposed here in order to simplify the model. It is however possible to take into account variable vessel–vessel separation, by calculating the local shape coefficient values instead of using constants, if only such data were known for the particular tree.

A similar formulation is used in Baish et al (1986) to analyse temperature fluctuations around countercurrent blood vessels.

The heat flux into the tissue from a unit length of the vessel pair is therefore

\[
q_l = -\frac{\sigma_{cc} \lambda_t}{\pi r^2} ((T_v - T_a) + (T_t - T_v)) = \frac{2 \sigma_{cc} \lambda_t}{\pi r^2} \left( \frac{T_a + T_v}{2} - T_t \right).
\]

The temperature field in the tissue obeys standard heat conduction equation:

\[
\rho_t c_t \frac{\partial T_t}{\partial t} = \lambda_t \nabla^2 T_t + q_m + q_{bl}
\]

(4)

where \( \rho_t, c_t, \phi_t \) are tissue density, specific heat and local volumetric tissue fraction; \( q_m \) is a prescribed metabolic heat generation rate (assumed zero for the calculations presented).
the equations (A) is a standard set of linear equations resulting from applying the finite element method to equation (4). The set of equations (B) consists of four finite-difference equations per segment, corresponding to four unknown temperatures in each segment (inflowing-arterial, outflowing-arterial, inflowing-venous, outflowing-venous). The equations themselves are finite difference counterparts of equations (2) and (3) plus the mixing condition (for the temperature resulting from mixing of two blood streams) plus the continuity condition (stating that the blood stream will not change temperature upon splitting in the bifurcation). Root segment is treated differently (the inflowing-arterial temperature is prescribed), as well as terminal segments (the inflowing-venous temperature is set to local tissue temperature). The equations for the general and all these special cases are given and discussed in detail in Stańczyk (2005).

The heat exchange with the blood vessels enters the tissue temperature problem as a local volumetric heat generation/sink term $q_{bl}$. This term is calculated for each finite element separately and it sums all the contributions from blood vessel pairs traversing given element.

For each $k$th finite element this source term can be expressed as

$$q_{bl}^{(k)} = \frac{1}{V^{(k)}} (\hat{q}_{l}^{(k)} + \hat{q}_{\text{term}}^{(k)}). \quad (5)$$

Here $V^{(k)}$ is the volume of the $k$th element, $\hat{q}_{l}^{(k)}$ is the heat conducted from the walls of all vessels embedded in the $k$th element to the tissue matrix, and $\hat{q}_{\text{term}}^{(k)}$ is the heat transported at the tips of all the terminal vessels embedded in the $k$th element to the tissue matrix (this heat accounts for the possible temperature difference between arterial end-of-terminal temperature and the end-of-terminal venous temperature. The first term in parentheses in equation (5) is calculated as follows:

$$\hat{q}_{l}^{(k)} = 2\sigma t \lambda t \int_{\text{start}(i)}^{\text{end}(i)} \left( \frac{T_a(l) + T_v(l)}{2} - T_t(l) \right) dl,$$

where $\text{start}(i)$ and $\text{end}(i)$ denote the starting and ending point of the $i$th segment contained within the considered element, $n_k$ is the number of vessel segments traversing the tissue element and $l$ is the local coordinate of the segment. The tissue temperature is approximated by the shape functions of the finite-element formulation and therefore the heat flow between the tissue element and the vessel pair depends on the position of the vessel pair segment inside the tissue element.

The second term in parentheses in equation (5) is obtained:

$$\hat{q}_{\text{term}}^{(k)} = \pi \rho c_b c_bl \int_{i=1}^{m_k} r^2(i) v(i) (T^e_a - T_t), \quad (6)$$

where $m_k$ denotes the number of terminal segments in the $k$th element of the tissue discretization and $r(i), v(i)$ denote radius and blood velocity in the $i$th segment. As one can see, the heat stemming from the fact, that the end-of-terminal arterial blood temperature is different than tissue temperature is exchanged with the tissue element, that the terminal occupies. Conversely, in DIVA this heat is exchanged with the set of voxels, named ‘sink set’ by the program developers; see Kotte et al (1996, 1999).

In a sense, the arterial and venous circulation form a closed system both in DIVA and in GRID—the blood massflow is preserved at terminals and no blood ‘leaks out’ out of the terminal. There is however a potential discontinuity in blood temperature at the place where arterial circulation enters the venous one. This discontinuity is caused by the fact that, upon leaving the terminal outlet, the arterial blood instantaneously equilibrates with tissue before entering the venous circulation.
Table 1. Comparison of most important features of both methods.

<table>
<thead>
<tr>
<th>Feature</th>
<th>DIVA</th>
<th>GRID</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basic building block of the tree description</td>
<td>Single vessel segment</td>
<td>Countercurrent vessel pair segment</td>
</tr>
<tr>
<td>Structure of the vasculature</td>
<td>Arbitrary number of independent arterial and/or venous trees,</td>
<td>Single tree of arterio-venous vessel pairs</td>
</tr>
<tr>
<td>Blood vessel discretization</td>
<td>Arbitrary number of blood temperature samples per segment</td>
<td>Three unknown temperatures per c-c segment</td>
</tr>
<tr>
<td>Blood vessel bifurcations</td>
<td>Multiple bifurcations of the vessels are allowed</td>
<td>Binary bifurcations only, higher-order of bifurcation can be simulated by using very short segments</td>
</tr>
<tr>
<td>Flow conservation at bifurcations</td>
<td>Not enforced, surplus flow can be used to model small-vessel bleed-off</td>
<td>Enforced</td>
</tr>
<tr>
<td>Calculation of blood-tissue heat flow</td>
<td>Averaging heat flux densities to surrounding tissue estimated using an analytical expression</td>
<td>Assumes the heat flow is proportional to the local temperature difference between the tissue temperature and the local average blood temperature</td>
</tr>
</tbody>
</table>

A detailed description of the GRID method and its numerical implementation can be found in Stańczyk (2005).

In table 1, the most important aspects of both GRID and DIVA methods are compared.

2.3. Simulation

In order to compare the two methods a simple simulation was conducted for both. Since DIVA is entirely three-dimensional and the implementation of GRID is not yet capable of full 3D simulation, the test problem was chosen in such a way as to yield an approximately 2D temperature profile. The 3D anatomy simulated with DIVA is shown in figure 3 while figure 4 depicts the corresponding 2D anatomy used with GRID.

Note that, for simplicity, only the first three bifurcations of both trees are shown in figure 3. The topology of the arterial and venous trees that were actually simulated was effectively identical to that of the tree in figure 4.

A flat vascular tree was generated using an algorithm based on that described in Schreiner and Buxbaum (1993). This tree, with segments representing countercurrent vessel pairs was used for the calculation with GRID, while two identical trees were used to form the separate arterial and venous trees in the calculations with DIVA. These were constructed by taking two flat trees (identical to that used with GRID) and placing them in parallel planes one over the other. The separation between the respective nodes of both trees was adjusted so as to be equal to twice the diameter of the vessel having the end-point at that node (this value being identical on both trees). The relocation was done in such a way that the system remained symmetrical about the plane midway between the tree planes.

Eventually both trees are no longer planar, but they are aligned with each other and the separation between the centrelines of the corresponding vessels is equal to twice the vessel diameter at each node, as assumed in GRID. It should be noted that, as the vessel diameter is constant along each vessel segment in both methods and (usually) suffers a jump at the
Figure 3. The domain of interest used in the simulation with the fully three-dimensional method DIVA.

bifurcations, the mentioned correspondence is satisfied only nodewise. The sketch in figure 3 tries to reproduce this situation.

The vascular trees used with GRID (figure 3) and DIVA included 50 terminal vessels, with all flows and diameters identical for both methods. The flows were preserved at all the bifurcations in both methods.

The root of the tree had a diameter of about 0.495 mm and the supply flow of 10.62 mm$^3$ s$^{-1}$ which corresponds to the average inlet velocity of about 56 mm s$^{-1}$. The tree generation algorithm employed assures that the terminal outflow is identical in every terminal and is equal to 0.208 mm$^3$ s$^{-1}$ (Brinck and Werner 1994). The diameters of the terminals are not constant, these also result from the generation method.

Figure 4. The domain of interest used in the simulation with GRID. The arterial and venous trees used in the simulation with DIVA have effectively the same topology. The highlighted vessel segments indicate the (return) path of the blood sample for which temperature is charted in figure 6.
The bounding plane opposite the vasculature entry was kept at a fixed temperature of 20 °C, whereas the remaining boundaries were modelled as adiabatic walls, as depicted in figure 3.

The corresponding setup is assumed for the 2D system depicted in figure 4—left, right and bottom boundaries of the region are assumed adiabatic, while the top boundary is isothermal at 20 °C.

The inlet arterial blood temperature is set at 37 °C, the temperature of the venous blood leaving the tissue region is unknown and is calculated by both methods.

Since the system in figure 3 is not invariant with respect to translation along the z-axis, the resulting temperature distribution along the tree is also expected to vary with z. However, the adiabatic boundary condition on top and bottom walls of the tissue region justify to some extent treating the tissue region as a ‘basic cell’ of a hypothetical larger blood vessel pattern.

It is assumed that the results calculated for the 2D region (GRID) can be compared with the results for 3D region as obtained by DIVA (averaged over the z-coordinate) and correspond to the representative temperature profile of the basic cell.

The steady-state temperature distribution was calculated using both methods. The initial temperature of the system was set to 20 °C and the response was iterated forward in time, until the suitable norm of the temperature change was negligible.

### 3. Results

#### 3.1. Tissue temperatures

The tissue temperature in the region perfused by discrete vessels can be conceptually seen as the sum of an average, y-dependent (see figure 3) component and the local departures from that average caused by the influence of the blood vessels. In figure 5 the average temperatures, as calculated by DIVA and GRID, are depicted as a function of the y-coordinate. The averaging was done over all voxels having the same y-coordinate (over entire tissue slices). Note that in the DIVA model a finer tissue mesh was used for the calculations.

#### 3.2. Blood temperatures

In figure 6 the temperature of a blood particle as it travels from the arterial root to the venous root via the path indicated in figure 4 is plotted against the current coordinate along path. It is noticeable that the density of the blood samples is more variable in the case of GRID system.

The agreement between these temperature profiles calculated by the two methods is not so good as it was for the average tissue temperature profiles but quite a large degree of similarity is retained. Also the discontinuous character of the blood temperature variation in the venous part of the tree, cf figure 1, is captured by both methods.

The nonuniform distribution of the blood tissue samples in figure 6 stems from the fact that the lengths of blood vessels (distances between bifurcations) are different: the samples are uniformly distributed in individual vessels in DIVA. Also, during the preprocessing stage in GRID, some vessels undergo subdivision into shorter vessels that occupy single tissue elements (so that no vessel lies in more than one tissue element).

In figure 7 the blood temperatures in the arterial and venous vessels throughout the whole model are depicted as a function of the spatial coordinate. While the average arterio-venous temperature distributions obtained by both methods seem to be quite similar, the difference between arterial and venous temperature is larger for the DIVA results for some arterio-venous pairs. Figure 6 confirms the tendency seen in figure 7: GRID underestimates the arterial
temperatures and overestimates venous ones relative to DIVA. The reason for this discrepancy most probably lies in the fact that the assumed 3D simulation setting (shown in figure 3) produces only approximately a 2D temperature field. The variation of the tissue temperature in the z-direction is small but not zero. Therefore, in the DIVA model the warmer arterial tree lies on the warmer side and the cooler venous tree—on the cooler side of the calculation domain. The tendency is more pronounced for larger vessels, since the distance between the trees is larger for these vessels.

In GRID, the basic building block of the GRID model is the countercurrent pair which models the artery-vein heat exchange internally. Also, there is no z-direction so the calculation of the heat transfer between the tissue and the arterial vessel and the tissue and the venous
vessel uses the same value of tissue temperature. This would hold even for a three-dimensional version of the GRID method, because a single geometrical description is used in this method for both arterial and venous trees, the distance between the trees being used only as a local parameter. Therefore, no tissue temperature variations on the scale of the vessel diameter can be captured by the model in the vicinity of the vessels. For applications where such resolution is needed, this can be recognized a serious drawback of the method.

Figure 7. The temperature of the blood in the arterial (filled squares) and venous (empty circles) vessels as the function of spatial coordinate, calculated with DIVA (upper panel) and GRID (lower panel).
The return venous temperature was calculated to be 34.61 °C by DIVA and 35.65 °C by GRID, the inflowing arterial blood having a prescribed temperature of 37 °C in both cases. The reason for this discrepancy is, most probably, the nonzero variation of the tissue temperature along the z-axis in the DIVA model as explained above.

The net heat flow transported between the blood and the isothermal wall is smaller in the case of GRID, due to the previously discussed effect of re-warming of the venous blood being more intensive in the GRID model.

4. Conclusions

The presented results indicate that both tested models give similar steady states for the specified scenario. It was also observed that the steady state was attained after similar periods of time in both models. The average tissue temperatures agree fairly, despite the fact that the numerical mesh of the same region in both models had different density (220 × 220 for the DIVA model and 35 × 35 for the GRID model). The agreement can also be considered acceptable in the case of the blood temperatures, the GRID model yielding lower temperature difference between the countercurrent vessels. This results from the fact that the 3D problem calculated with DIVA is not really planar. The 2D setting used in GRID is only an approximation of the 3D temperature field considered in the DIVA model.

The method employed in the GRID program is potentially much less computationally intensive than that used in DIVA. This fact is only in part explained by lower dimensionality of the problem. In GRID, entire countercurrent tree pairs are modelled, not single trees. More importantly, the method used to calculate vessel–tissue heat transfer does not require the tissue voxels to be significantly smaller than the vessel segments, as is the case in DIVA. In fact, the tissue elements may even contain multiple vessel segments. On the other hand, the method used in GRID is restricted to identical countercurrent arterio-venous tree pairs.

The method proposed by the first author in Stańczyk (2005) is designed to handle countercurrent vessel geometries and situations where tissue temperature variations, on a scale comparable to the distance between the countercurrent vessels, are not important. Under these conditions the method exhibits some advantages over the more general approach used by the designers of the DIVA system.

The latter model has already found its practical applications, cf Raaymakers (2001). The large-scale calculations are however computationally intensive since DIVA requires that the tissue mesh needs to be very fine relative to the corresponding given vasculature model. The GRID method allows the tissue mesh to be considerably sparser, in principle lowering the demands on the computational power required. Before any more direct comparisons in that respect are made, the GRID system implementation needs to be extended to handle 3D simulations which is an attractive direction for further study. It also has to be optimized with respect to the CPU time and memory requirements.

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