

AN IMPROVED BLOOD FLOW MODEL TO SIMULATE EM INDUCED HYPERTHERMIA

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Currently work is being performed at IT'IS to develop a comprehensive hyperthermia treatment planning (HTP) tool. This tool should be able to perform all required steps from tissue segmentation to field optimization. It is based on the commercial EM simulation platform SEMCAD X that uses the non-uniform FDTD method to obtain field distributions in highly detailed and inhomogeneous models within reasonable simulation time using efficient computational techniques as well as hardware acceleration. The suitability of this method has been demonstrated in previous works.

Knowing the EM induced temperature distribution and being able to optimize it would certainly benefit hyperthermia treatment planning and treatment outcome. Online monitoring of the temperature distribution in the treatment volume is still in development, costly, rarely available and only of limited use, which leaves numerical simulations as the only practical choice. However, currently temperature simulations are rarely performed, as they either require substantial time and effort to setup and execute or do not deliver results of sufficient accuracy and reliability. The most commonly used heat transfer model - the Pennes Bioheat Transfer Equation (PBTE, [1]) - can be implemented such that the simulations are easy to set up and give fast results. However, its formulation suffers from several drawbacks: it does not account for the directivity of blood flow; it neglects the discreteness of blood vessels; and its standard formulation/implementation does not account for the temperature dependence of various (tissue) parameters.

The work presented in this study therefore attempts to create a model that retains the simplicity of Pennes' approach while introducing the following improvements to overcome the above mentioned problems:

Tensorial thermal conductivity (k): This accounts for the directivity of blood flow. Having a tensorial k makes it possible to preferentially conduct heat along a bloodvessel, perpendicular to it or in any given direction. This corresponds to real tissue, where the vasculature/microvasculature is often distributed in an anisotropic way.

Discrete vessel network: The 3D temperature simulation is coupled to a pseudo-1D simulation of the blood flow in the major vessels (cp. [2,3]). In a next step the vessel tree can be used to determine the local tensor character (orientation of main axis and degree of anisotropy) of the heat conductivity, resulting in a position dependent k instead of a k that is constant throughout the organ/solid.

Temperature dependent parameters: Perfusion, thermal conductivity and electrical conductivity (and therefore SAR) can be made temperature dependent. Currently only simple dependencies have been implemented, though work is underway to extend this. A possible model for the temperature dependence has been developed that should permit fast simulations while allowing for complicated temperature dependences.

Furthermore, the metabolic heat generation rate can be time dependent to account for metabolic changes due to prolonged heating.

The new model can mostly work with tissue parameters that have already been determined for other heat transfer models.

It has been implemented as part of the SEMCAD X platform. Results from various EM simulations can be individually scaled and coherently or incoherently added before being used for heating. The scaling can be made time dependent, allowing for pulsed excitation. Various boundary conditions (fixed temperature, fixed flux, temperature dependent radiation and mixture thereof) can be separately specified for all material interfaces. A conformal subcell model has been developed to reduce staircasing errors at interfaces.

The implementation is tuned toward high speed and subsequently low memory usage. It permits simulations with sub-millimeter resolution in critical regions and millions of voxels to be performed within minutes.

The new temperature model will enable the user to generate more reliable and detailed temperature predictions without requiring unreasonable computation or setup times. The user can decide how detailed a vessel network he wants to provide - restricting the vessel segmentation task to easily available, large vessels. And each specified vessel will improve the temperature predictions not only locally but in the surrounding tissues as well by determining the k anisotropy distribution, thereby mimicking the distribution of finer vessels. In the future the model should be extended to include effects such as irreversible tissue changes (relevant, e.g., for RF ablation) and further research should be invested in the study of nonlinear temperature dependences of tissue parameters. Other numerical schemes (such as semi-implicit schemes...) will be tested to check for possible additional speed increases. The model will be extensively validated in experimental work.

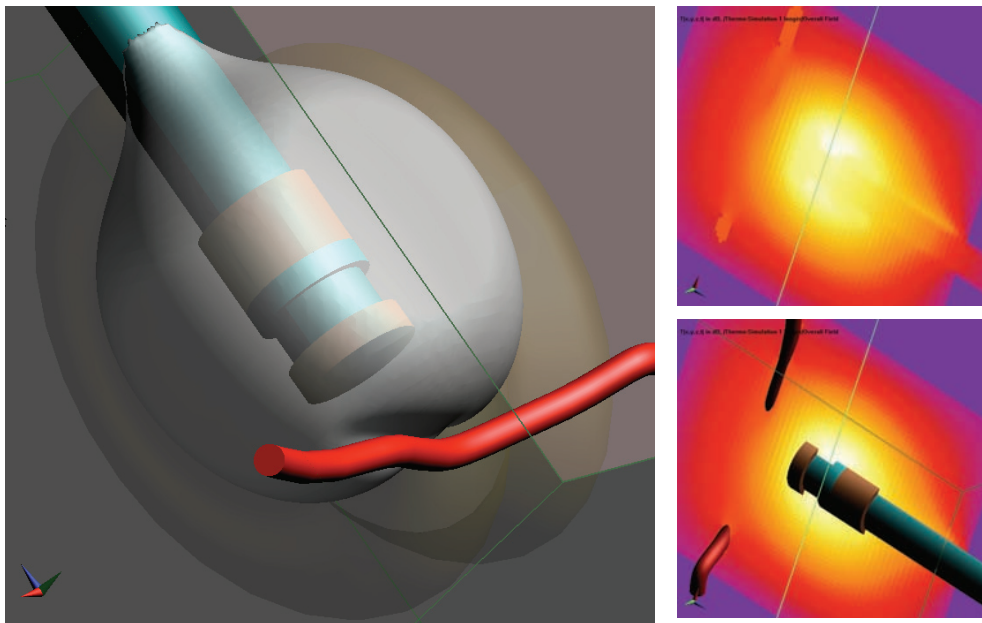


Fig. 1: Simulation of the temperature distribution as produced by an RF ablation catheter (cap-choke antenna) inside a nodular tumour next to a blood-vessel. The image on the left shows a temperature isosurface, while the pictures on the right show cross-sections of the temperature distribution.

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