GPU accelerated finite element method for radio frequency ablated cancer treatment

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Abstract

We developed a fast RFA simulation software tool to predict the lesion development for radio frequency ablated cancer treatment. We use Penne's bioheat mathematical model and finite element method for numerical discretization. Our software tool utilizes GPU technology to predict the lesion in real time. A 5 cm ablation of 26 minutes real protocol is simulated in less than 3 minutes using our fast RFA simulation software.

Mathematical Model

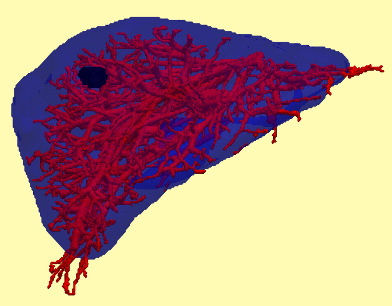
Our simulation software solves Penne's bioheat equation [1], where the source term is an approximation of the Joule heating model using Gaussian distribution. A two state model is used to predict the cell death value [2].

Penne's Bioheat:

$$\rho_b C_b \frac{\partial T}{\partial t} = k\Delta T + \omega_b \rho_b C_b (T_a - T) + Q_r \quad \text{on the domain}$$

$$h_C T + k\frac{\partial T}{\partial \vec{n}} = h_c T_\infty \quad \text{on vessels boundary}$$

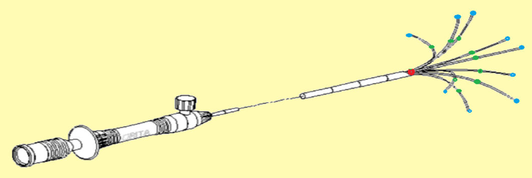
$$T = T_0 \quad \text{on the sphere}$$



Point Source:

$$Q_r(x,y,z) = \sum_{node} \frac{1}{26(\sigma\sqrt{2\pi})^3} \sum_{tip} C_{tip} e^{-\frac{(x-x_{tip})^2+(y-y_{tip})^2+(z-z_{tip})^2}{2\sigma^2}}$$

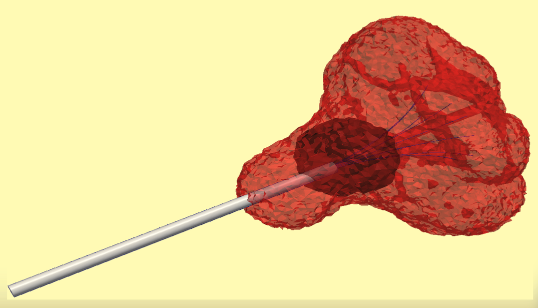
Cell Death:



$$\frac{dA}{dt} = -k_f e^{\frac{T}{T_k}}(1-A) + k_b(1-A-D)$$

$$\frac{dD}{dt} = k_f e^{\frac{T}{T_k}}(1-A)(1-A-D)$$

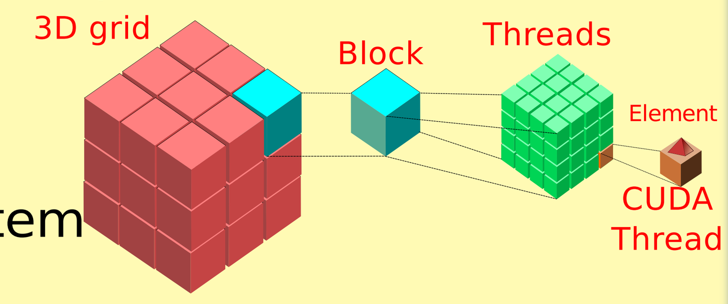
$A(0) = 0.99$ and $D(0) = 0.0$



GPU accelerated FEM

At first, the CPU reads mesh, finds the neighbours. Based on the neighbours of each node, we generate the pointer and column indices of a CSR matrix. The CPU sends node, elements, CSR matrix and other initial parameters to the GPU. In GPU, each thread computes

- each node's heat source term
- each element's shape function
- each element's local linear system
- each node's cell death values



Our optimized code avoids explicit numerical integration [3] while computing the local linear system and the GPU assembles the local matrices into the global matrices with the help of an efficient neighbour mapping algorithm. The resulting linear system is solved using *CUBLAS* and *CUSPARSE* libraries. After receiving the computed temperature and dead values from the GPU, the CPU verifies the breaking criteria and saves the lesion values in a *vtp* file at regular intervals.

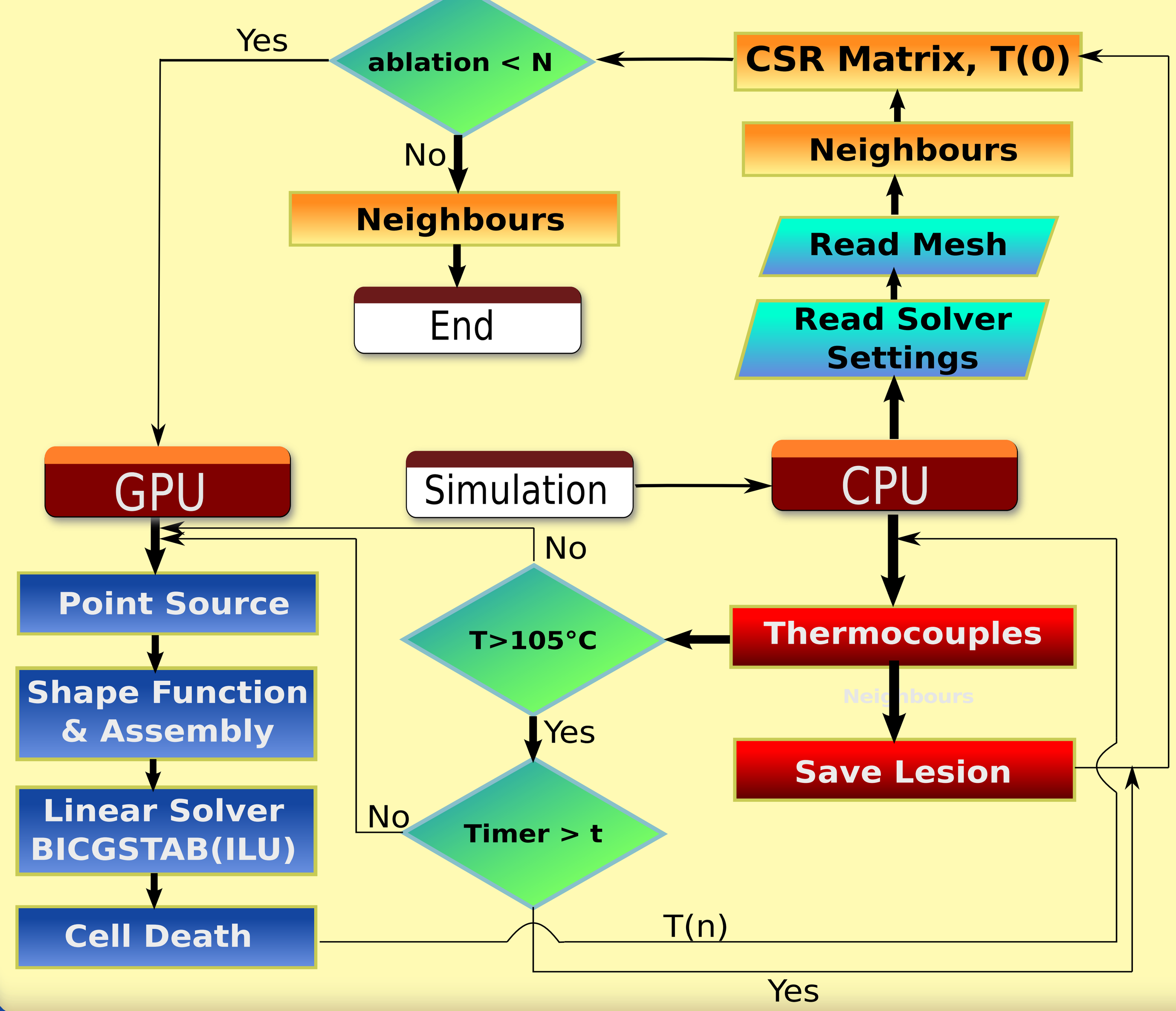
References

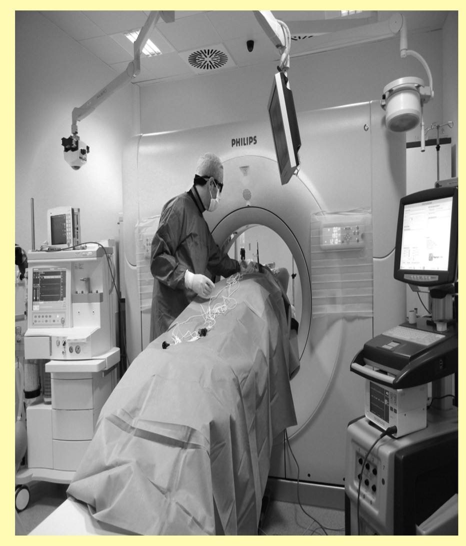
[1] Pennes, H.H., **Analysis of Tissue and Arterial Blood Temperature in the Resting Human Forearm,** *J. of Applied Physiology* , Vol. 1, pp. 93-102, 1948.

[2] Payne, S., et al, **Image-based multi-scale modelling and validation of radio frequency ablation in liver tumours**, *Phil. Trans. R. Soc. A*, 369, 4233-4254, 2011.

[3] M.A. Eisenberg and L.E. Malvern, **On finite element integration in natural coordinates**, *Int. J. Num. Meth. Eng*, Vol. 8,574-575,1973.

Flowchart

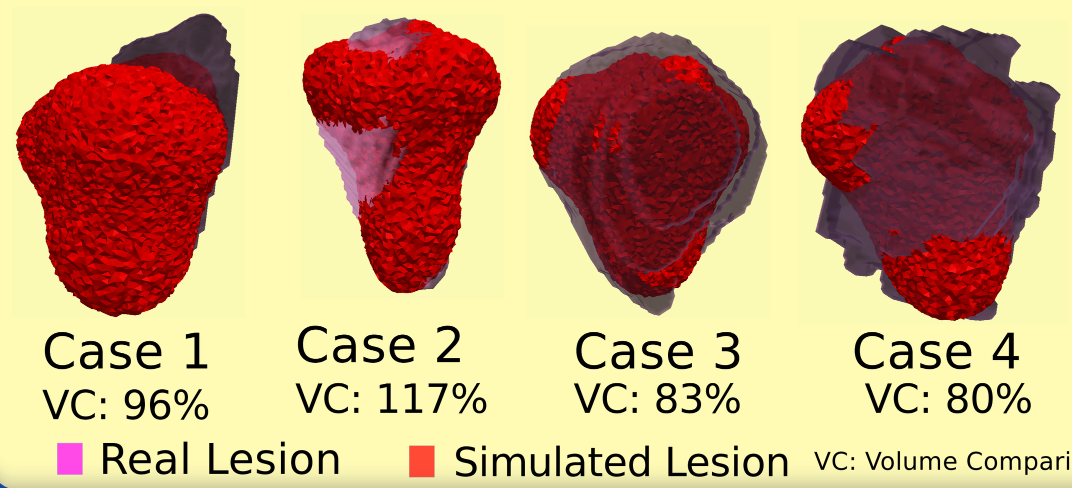




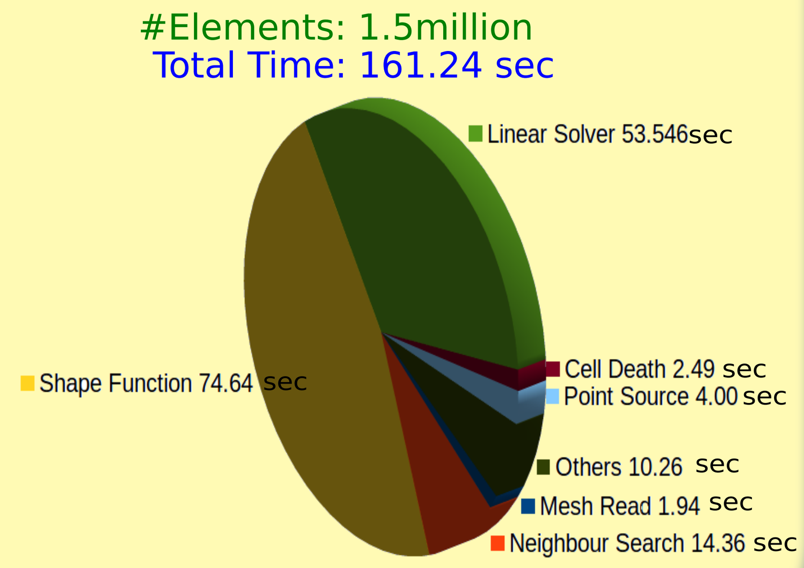
Source: http://acceleratingscience.com

Results

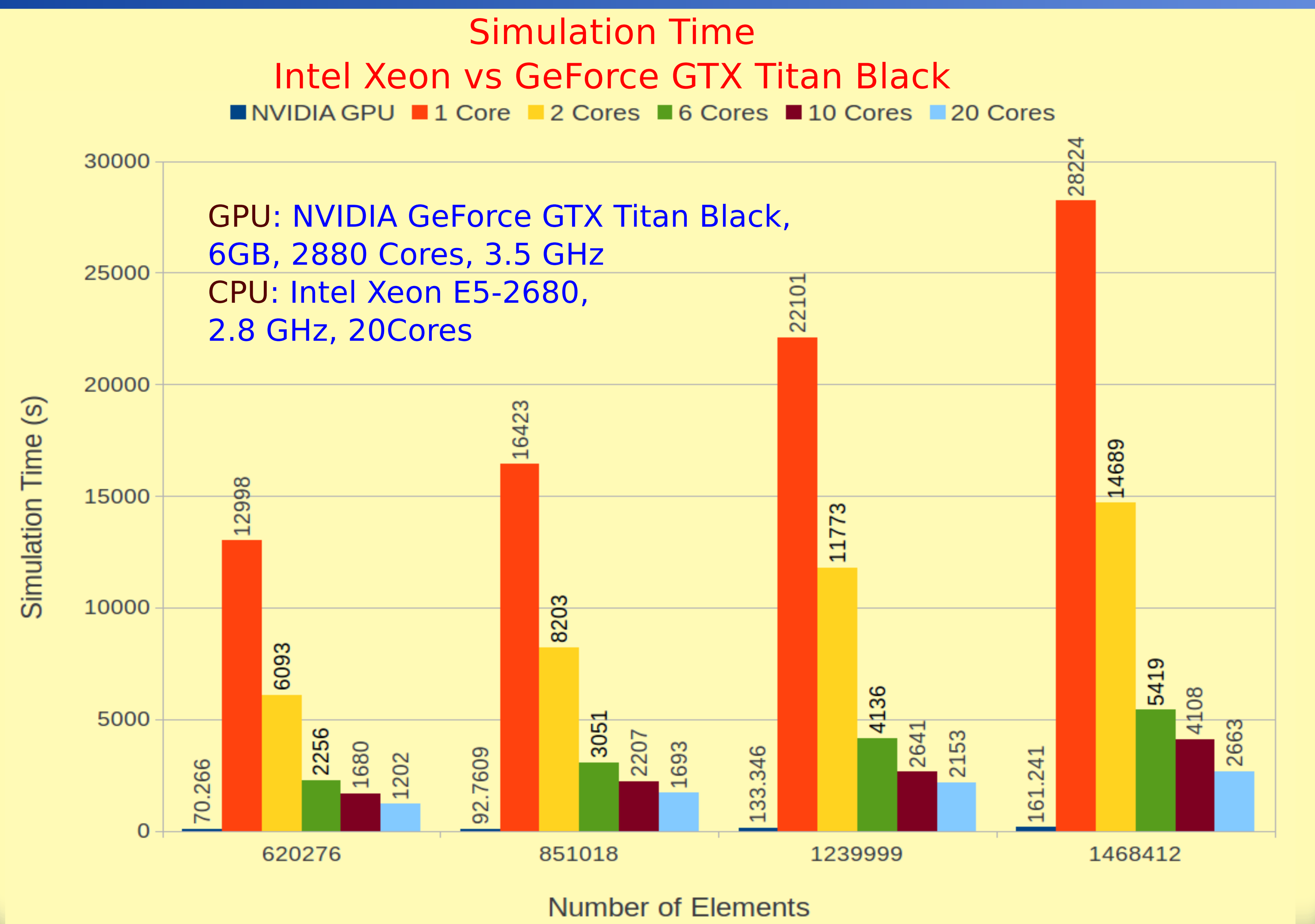
The following figure shows that real and simulated lesions match well for various cases.



VC: Volume Comparison between real and simulated lesions



Comparison



Conclusion

Our GPU accelerated RFA simulation software tool gives the results in less than 3 minutes, whereas a quad core CPU takes 2.5 hours to predict the lesion for a fine mesh. A heterogenous CPU-GPU configuration saves simulation time and cost. As our numerical tool predicts the lesion within 3 minutes, it is clinically practical to use our tool on the day of treatment.

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