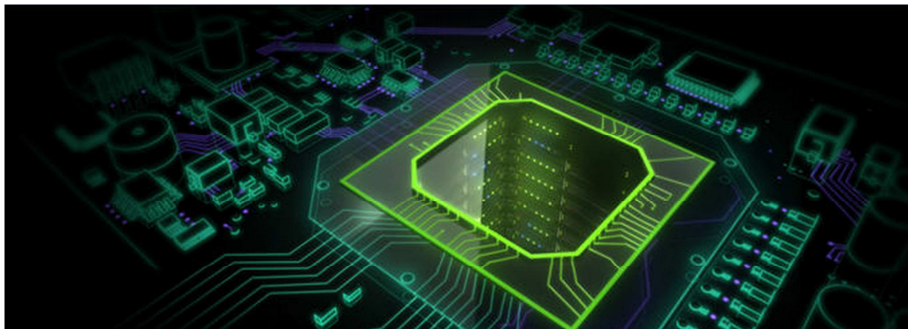


SciencePG Frontiers (News Article – an Example)

Parallel Processing is setting the Scene for New In Silico Experiments of Cancer

Numerical solutions to complex mathematical models of tumour growth dynamics are experiencing a rapid increase in execution using parallel processing techniques.



In a recent paper by author Dr P. M. Darbyshire, dramatic increases in computational speedup were obtained by implementing conventional solutions to complex tumour dynamics using parallel methods. Such increased computational efficiency clearly highlights the potential for rapid numerical solutions to highly complex compute intensive mathematical models of tumour growth, angiogenesis, vascularisation, invasion and metastasis.

“Parallelisation of such models can greatly facilitate researchers, clinicians and oncologists by performing time-saving *in silico* experiments that have the potential to highlight new cancer treatments and therapies without the need for the use of valuable resources associated with excessive pre-clinical trials”, Darbyshire said.

In the paper, Darbyshire shows how a mathematical model describing avascular tumour growth can be solved numerically using time-stepping finite difference methods treated in a parallel manner. In modelling tumour dynamics, the finite-difference scheme generally involves producing a set of discrete numerical approximations to a set of coupled nonlinear partial differential equations. In this way, explicit time-marching methods can be thought of in terms of being naturally parallel candidates for such advanced computational techniques.

Darbyshire goes on to suggest that “Progress in mathematical modelling of avascular tumour growth has largely been driven by biological and clinical observations through *in*

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1. About 25-40 words in length;
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vitro and *in vivo* experiments. By making use of parallel processing techniques it will soon be possible to develop real-time virtual laboratories running thousands of *in silico* experiments testing numerous predictions and hypotheses. Such an interconnected distributive network could never be achieved in a physical laboratory at the time scales considered here.”

The modelling of avascular tumours is often seen as a first step towards the development of more complex models of later stage tumour growth, such as angiogenesis, vascularisation and metastasis. Mathematical and computational modelling is playing an increasingly important role in helping clinical physicians and research scientists in understanding the different aspects of solid tumour dynamics. *In-silico* experiments and simulations, such as those performed in the paper, give researchers, clinicians and oncologists the tools and opportunity to observe effects of different treatments on cancerous cells in realistic time frames. This will inevitably lead to more rapid improvements in effectual therapeutic strategies as well as aiding in the discovery of new forms of treatment. Personalised healthcare, adapted to patient specific symptoms, could be used in therapy planning by suggesting irradiation regions adapted to growth dynamics or optimal temporal distribution of chemotherapy through advanced computer simulation. In fact, getting new chemotherapy and other anti-cancer drugs into pre-clinical trials will inevitably rely more and more on supportive evidence from *in silico* experiments. The ability to use advanced computational methods to simulate the virtual stages of pre-clinical trials greatly reduces time to market and use of excessive laboratory resources, as well as the huge financial costs involved.

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A paper about the study appeared recently in Computational Biology and Bioinformatics.

Paper

link:<http://www.sciencepublishinggroup.com/journal/paperinfo.aspx?journalid=112&doi=10.11648/j.cbb.20150305.11>

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