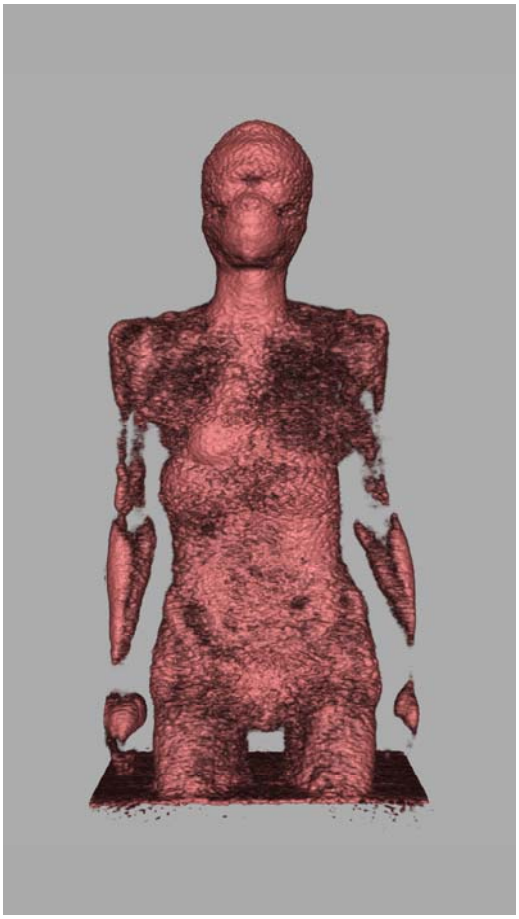
Life sciences: Simulation of a 'whole body' PET imaging examination

Interpreting data from positron emission tomography (PET) - a type of medical imaging scan increasingly used in the hospital environment - remains a complex problem. Researchers are working on computer simulation programs in support of PET, with a view to optimizing the data analysis and extracting the most relevant physiological information. The simulations are currently limited by the computation time required.
This issue led the CEA-SHFJ[1] (Frédéric Joliot Hospital) to set up the GATE[2] simulation platform, which models PET examinations, using the TERA-10 supercomputer located at the CEA centre in Bruyères-le-Châtel. The simulation can reproduce the distribution of a tracer used in PET scans performed for cancer diagnosis, in a very short time and with a high degree or realism. These initial simulation results mean that, in the medium term, a more precise use of the data provided by the images can be envisaged, as well as personalised scans for patients.



Personalising the patient's medical examination

Positron emission tomography (PET) involves using an intravenous injection to administer a molecule labelled with a radioactive isotope, a "tracer", which is then tracked using external detection tools to monitor how an organ is functioning. Using suitable detection tools, radiation emitted by the tracer is used to construct an image through which distribution of the molecule in the body can be visualised. Certain pathologies react to the molecules used: this is particularly the case for glucose, which concentrates in cancerous tumours where the metabolism is increased.

Researchers used the simulations as a corrective tool to optimise the detectability of tumours according to the radioactive dose injected in the patient and to overcome parameters that disturb the analysis (for example: patient respiration during the scans, or the reaction of other organs with naturally high metabolisms). These simulations are performed using the Monte-Carlo method, based on probability theory. The analysis is hindered, however, by the limitations of computer processing: for a standard "whole-body" PET scan, a Monte-Carlo simulation must process the emission of several billion positrons and gamma photons, equivalent to at least 10,000 hours of computation, or 400 days of analysis on a standard PC.

A promising first simulation

To reduce this computation time, SHFJ and DAM researchers conducted a simulation on the Tera-10 supercomputer. After modelling the patient's body, using data from an actual scan, researchers then simulated the injection of a tracer by selecting a realistic activity of 264 megabecquerels (MBq) and an acquisition time similar to a standard PET scan. This initial simulation required less than three hours computation time using 7,000 processors. The subsequent comparison of the real scan and its simulation showed almost identical tracer distribution. From a quantitative point of view, a comparison of the volume of a tumour located under the patient's left armpit returned a difference of 6%, considered as very low for an initial simulation.
This result constitutes a decisive first step towards the development of methods to correct real data from PET scans and, in the long term, aims to create a patient specification for PET acquisition protocols and analysis. It also demonstrates the benefits of intensive computations in the field of life sciences.

For further details, see: http://www-dsv.cea.fr/

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[1] The SHFJ is one of the 4 research platforms from the French Institute of Biomedical Imaging (CEA-I²BM). The others are NeuroSpin (Saclay), MIRCen (Fontenay-aux-Roses) and Ci-NapS (Caen).
[2] GATE: Geant4 Application for Tomographic Emission – Geant4 is an international simulation programme developed at CERN (Switzerland).