A Virtual Imaging Platform for the Virtual Physiological Human

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1 Introduction

Healthcare is being metamorphosed by pervasive digital worlds exploiting human models and medical simulations enabled by large computing infrastructures. Medical images, in particular, can be simulated from numerical models of the human body for a variety of applications including fast prototyping of new imaging devices and the evaluation of image analysis algorithms such as computer-aided detection, or segmentation. Image simulation is also used in the modeling of virtual humans by identifying model parameters leading to the most realistic images. Several image modalities, among which Magnetic Resonance Imaging (MRI), ultrasound imaging (US), Positron Emission Tomography (PET), and Computed Tomography (CT) are complementary to simulate and study the various aspects of biology, i.e., anatomy, physiology, metabolism, and function.

Currently, image simulation remains mastered only by a few due to the complexity and heaviness of most pipelines. Both the simulation code and the physical model of the imaged object can be very elaborated, and they are usually not designed by the same person or group: sharing them is thus required. In addition, computing times and the volume of produced data are potential showstoppers if no appropriate infrastructure is available. This abstract describes the Virtual Imaging Platform (VIP), an openly-accessible online platform used to share models and simulators, and to support the execution of heavy simulations. Its integration with the VPH ToolKit is also described.

2 The Virtual Imaging Platform

2.1 Support for heavy simulations

Simulators are integrated in VIP based on their workflow description. Marion et al[2] proposed a workflow template to facilitate integration. Simulation parallelization relies on data parallelism to avoid refactoring simulator codes. Simulators are iterated on subsets of the simulation scene or of input parameter sets, and the resulting partial results are eventually merged by another process. Simulations are launched on the *biomed* virtual organization (VO) of the European Grid Infrastructure (EGI).[3] This VO has access to 100+ computing clusters world-wide. The MOTEUR engine is used to enact the workflows.

VIP uses the EGI data management system to store files. Files are distributed on different storage sites supporting the *biomed* virtual organization. Resources expose a homogeneous interface to access files. A central logical file catalog provides a common indexing space for these files. 3.5 PB are available for storage, among which 2 PB are currently used.

2.2 Interface with the VPH ToolKit

Grid computing resources on EGI are abundant and easily accessed. However, they are shared among different user groups, which hampers efficiency and reliability. In particular, parallel jobs executed with the message-passing interface (MPI) are notably not well supported. Conversely, supercomputing resources available on PRACE[4] can only be accessed by a few (as a result of a specific application procedure), but resource efficiency is then guaranteed and reliability is high.
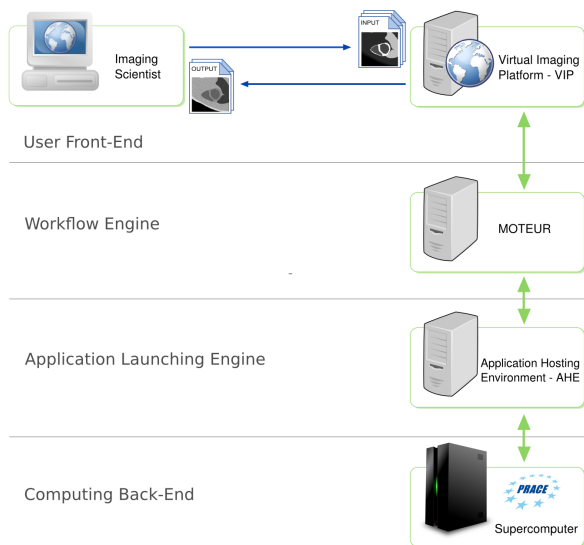

Figure 1: System architecture

We are in the process of interfacing the VIP portal with PRACE. Combining both infrastructures will provide high reliability and efficiency to support simulation challenges while keeping grid resources accessible for daily simulation activity. These developments consist of an interface between the MOTEUR workflow engine and the Application Hosting Environment.[5] AHE is an application launching engine that interfaces to a number of back end middlewares, including Globus 2/4 and Unicore 6. It manages the submission and monitoring of jobs, as well as data transfer, on behalf of a user. Here, AHE will be used as an interface between MOTEUR and the Unicore middleware running on PRACE systems. In the past, AHE has been successfully employed within DEISA DECI and Virtual Community projects to submit and manage jobs on the PRACE Tier 1 resources at SARA and EPCC.

The required steps are (i) porting of simulation codes to PRACE architectures, (ii) enabling data transfers between EGI and PRACE, and (iii) enabling AHE job submission and monitoring in MOTEUR. The figure 1 outlines the system architecture. More details are available online.[6]

2.3 Results

VIP is publicly available as a web portal[7] where users can access the model repository (browsing and importing), define a simulation scene through the 3D interface, launch new simulations, monitor performance, and transfer input/output files. Example of images simulated with VIP for various imaging modalities are shown on Figure 2.

3 Conclusion

VIP is an online platform for image simulation. It currently relies on the European Grid Infrastructure to support the computation and storage. Four medical image modalities are supported. The VPH ToolKit is being used to interface it to PRACE computing resources. VIP also offers functionality for the sharing of digital object models as presented by Forestier *et al.*[1]

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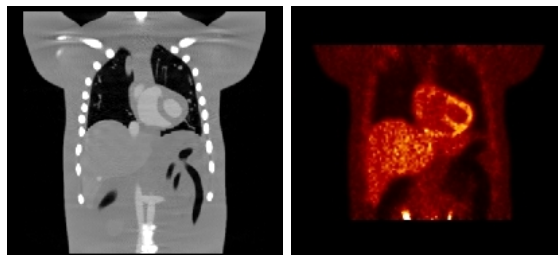
(a) Left: simulated whole-body 0.5s CT acquisition. Simulation courtesy of Carole Lartizien, and Joachim Tabary. Right: simulated whole-body static 224s FDG-PET acquisition. Simulation courtesy of Carole Lartizien and Simon Marache.
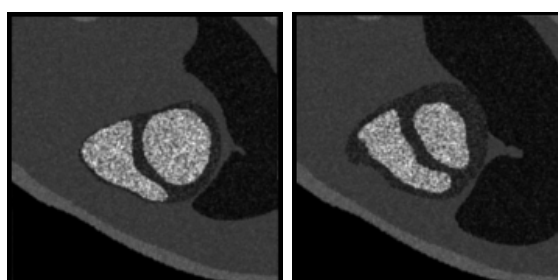
(b) Simulated cardiac short-axis MRI. Left: end diastole; right: end systole. Simulations courtesy of Patrick Clarysse, Sorina Camarasu-Pop, and Hugues Benoit-Cattin.
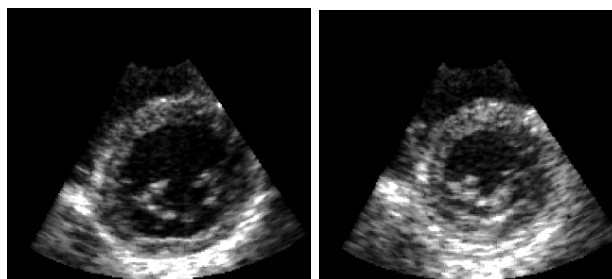
(c) End diastolic (left) and end systolic (right) instants of a simulated 2D+t echocardiography with scatterer distributions extracted from a real image. Simulation courtesy of Olivier Bernard and Martino Alessandrini.
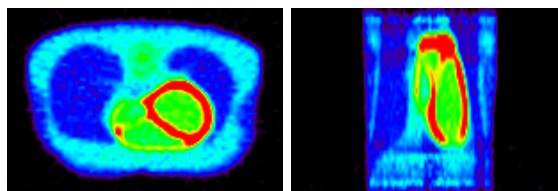
(d) Simulated cardiac FDG-PET. Left: transverse; right: coronal. Simulations courtesy of Patrick Clarysse and Frédéric Cervenansky.

Figure 2: Simulation examples computed on VIP.

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