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Calibrating models of human physiology using scientific cloud

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We developed a system to support modeling of physiological systems in the phase of calibrating model parameters and in the phase of simulating different scenarios. The loosely coupled part of the system is deployed in a remote distributed computational capacity. A significant speedup was shown in the case of the large complex physiological model computed in cloud computing infrastructure provided by Czech NGI (CESNET) resources. The system capabilities is accessible via a web application and allows user to focus on experimental data, names of parameters, visual control of the calibration computation and hide unnecessary complexity of the remote subsystems computation. The data of real experiments and simulations are stored and provided for further research.
The system is now used in these domains:
1) Acidbase balance within human body. Several main theories about acid base balance are researched and interpreted in an integrative approach using the system.
2) Haematopoiesis. The interpretation of new hemopoesis experiments are examined with mathematical formalization and simulation.
3) Heart defect and identifiyng values of parameters of mathematical models to show the effect in educational simulators.

Wider impact and conclusions

The system is developed with focus on the domain of human physiology and modeling technology based on Modelica language. However the protocol and data might be used in any modeling domain and modeling tecnology.

URL(s) for further info

www.physiovalues.org

Description of work

The web application for calibration of model integrates several technologies. The computational demanding process is designed as master worker. The identification algorithm employs the well known genetic algorithm implemented in MATLAB environment and exported as DLL library. The server (master) module manages the identification algorithm and distributes single simulation tasks to workers. Workers provides a REST interface to receive simulation task requests. We exported the models of Human physiology from Modelica langugage into standardized FMU package which is in fact DLL library with standardized API on Windows platform. The client application is developed in HTML5 utilizing AJAX technology to communicate with server services, collect data and request computation.

The parameter identification of the complex model spends some time in parallel simulation and some time in communication and synchronization procedures.

If the majority of the time is spent on simulation, then significant speedup can be achieved if the computation (workers) is distributed into remote capacity e.g. within a cloud or grid. We got about 96x speedup when identified a parameter of complex model Hummod (http://physiome.cz/hummod) on about 100 virtual CPUs of several virtual machines in the scientific cloud provided by Czech NGI CESNET.

On the other hand, the parameter identification of simpler models converges to a highly parallel computation system where time spent in parallel simulation is moreless same as in communication and synchronization procedures. Such computation is better to distribute to single machine with e.g. high number of CPU cores.

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Session Classification: Going beyond grid to enable life science data analysis

Track Classification: Success stories in using e-Infrastructures for research (Track Leaders: E. Katragkou, P. Castejon)