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Cardiac motion analysis pipeline support with the EGEE grid and MOTEUR

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Cardiovascular diseases are one of the major cause of mortality in industrialized countries. There is a thorough research effort to analyze and diagnose diseases of the heart from large volume temporal acquisitions of 3D images capturing the heart cycle. Diagnosis is assisted by the extraction of quantitative parameters such as ventricular Ejection Fraction (EF) measuring the accuracy of the cardiac beat and myocardial motion field giving insights on the proper heart function.

Impact

Complex data flows are commonly encountered in medical image analysis pipelines but there is little support in the existing tools to represent them as a high-level user-accessible framework and to control their execution on the grid infrastructure. In the context of the GWENDIA project (Grid Workflow ENactment for Data Intensive Applications), we are extending the Scufl data flow language and the MOTEUR gLite-interfaced workflow manager to represent and support complex data flows such as the cardiac motion analysis described above. The GWENDIA data flow language can represent multi-depth nested lists of data items that can be split (for processing individual data items) or gathered (for processing compound items such as volumes at once) at different steps of the workflow. The workflow engine ensures the coherency of the computation in an asynchronous, concurrent environment by processing reordering. It is fully interfaced to the gLite middleware.

URL for further information

http://gwendia.polytech.unice.fr

Conclusions and Future Work

Cardiovascular images analysis require the processing of a complex data flow. We approached the problem generically by extending the expression capability of the MOTEUR workflow engine so that the development can benefit to many different workflow-based applications. The workflow designed for the cardiac application enables the coherent processing of large amounts of temporal cardiac image sequences. The solution proposed is also generic enough to support multi-patients concurrent processing.

Keywords

Cardiovascular diseases, workflows, data flows

Detailed analysis

Extracting quantitative parameters from heart image sequences require building a complex pipeline of image pre-processing, analysis and parameters extraction. The pipeline developed includes 15 computing stages including DICOM images series sorting, region of interest identification, cropping, images interpolation and 3D reconstruction, pyramidal decomposition, gradients extraction, thresholding, gradient vector flow computation, sequences segmentation and movement vector fields computation. These steps compose a non-linear complex and heterogeneous pipeline that is represented through a workflow graph with data dependencies. Each processing step performs on different scale elements of the data flow (some process images slices individually, some process full stack of 2D image composing 3D volumes and some even require the processing of temporal series or 4D images at once). A very complex data flow with data sets splitting and merging thus has to be represented.

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