MATHEMATICAL AND COMPUTER METHODS OF DATA PROCESSING IN NUCLEAR MEDICINE STUDIES

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Abstract

Currently nuclear medicine is a high-tech field. Its development requires solutions of problems related both to the improvement of hardware and computer processing of the information obtained in the course of study. The basic types of hardware of nuclear medicine are gamma cameras and single photon emission computed tomography (SPECT) [1], positron emission tomography (PET) and hybrid scanners (SPECT/CT, PET/CT).

The methods of SPECT data processing include analysis of static, dynamic, tomographic and ECG-gated images [2-9].

The PET data reconstruction software restores the threedimensional distribution of the radiopharmaceutical in the body. Performance of iterative methods increases with the use of modern graphics processors [10]. Threedimensional imaging allows a detailed analysis of the study area. The software also implements a fusion imaging of SPECT/CT, PET/CT scans performed in the same coordinate system.

An application of data flow model in medical software development is considered. Web-based imaging front-end of storage and processing system is presented.

DATA PROCESSING

The flexible platform with batch execution support and imaging elements is required during the process of development and testing new processing algorithms.

Mathematical modelling software such as MatLab is usually used for this purpose. But it makes harder to integrate the solutions into data processing applications as it often require redevelopment for application native platform.

Dataflow Programming

An approach to efficient development of data processing algorithms on .NET Framework is considered: program is represented as dataflow graph.

Dataflow consists of set of simple processing units called activities and connections. Activities represent simple operations such as data acquisition, reconstruction, volume transformations, ROI extraction, dynamic curves computation and analysis, etc. Each activity define a list of Inputs (or Attributes), a list of Outputs (or Results) and the Execution method, which supports cancellation and progress reporting. Dataflow connections bind activities outputs to inputs. Unbound inputs' data can be set from UI or file.

Dataflow are presented as an XML files. Activities are classes implementing interface *IActivity* and marked with

Activity attribute. Its writable public properties define list of inputs, and read-only properties of generic type *ActivityResult* represent list of outputs. Sample dataflow graph is presented on fig. 1.



Figure 1: Example of dataflow application.

Basic dataflow execution environment (DEE) is developed. It supports running dataflow programs in interactive and batch modes. In interactive mode DEE dynamically loads user interface from a XAML file and binds UI components to inputs and outputs. Batch mode allows running dataflow with different input values provided from text files.

Reconstruction

Using dataflow approach we conducted series of experiments in tomographic reconstruction of PET data. Its goal was determination of correction parameters which adjust reconstructed values to physical units (Bq/ml).

Mathematical modeling of PET acquisition was performed. Cylindrical phantom (radius – 100 mm, length – 190 mm) with variable activity (10^5 , 10^6 and 10^7 Bq) was used as positron source. Time of acquisition was selected in inverse ratio to activity (1000, 100 and 10 sec).

Ring detector configuration (radius – 410 mm) with different axial field of view (FOV) (50, 100, 150 and 200 mm) and number of detectors (720, 360, 240 and 144) was used.

The above experiments were repeated with photon attenuation in phantom volume.

Total of 96 sinograms were calculated.

Tomographic reconstruction of the sinograms was performed using 15 iterations of MLEM [10]. The iterative process is described by formula

$$x_{j}^{k+1} = \frac{x^{k}}{\sum_{i} m_{i} A_{ij}} \sum_{i} \frac{A_{ij} p_{i}}{\sum_{l} A_{il} x_{l}^{k}} , \qquad (1)$$

where x – reconstructed image in vector form, p – sinogram in vector form, A – system matrix, m – correction vector.

Images were reconstructed with three different resolutions: 32x32 (pixel size -10 mm), 64x64 (5 mm) and 128x128 (2.5 mm).

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System matrix values A_{ij} were calculated as normalized intersection area of *j*-th image pixel with *i*-th line of response. Uniform images $(x^{\theta_j}=I)$ were used as initial estimation. No multiplicative correction was performed $(m_i=I)$. For each image the average pixel value was calculated in central 110 mm square region.

Data analysis shows dependency of average values on acquisition and reconstruction parameters (fig. 2, 3).



Figure 2: Quadratic dependency of reconstructed values on axial FOV and pixel size (volume activity -10^6 , 720 detectors, no attenuation).

The correction formula was derived as follows

$$m_{i} = \frac{1}{1000} \frac{X^{2} Z^{2}}{4 R N_{d}} \frac{T_{1/2}}{\ln 2} (1 - 2^{-\frac{T}{T_{1/2}}}) e^{-\int_{L_{i}} \mu dl} , \quad (2)$$

where X-pixel size (mm), Z-axial FOV(mm), Rdetector ring radius (mm), N_d -number of detectors, $T_{1/2}$ -radiopharmaceutical half-life (sec), T-time of acquisition (sec), μ -linear attenuation coefficient (1/mm), L_i -*i*-th line of response.

Reconstruction was performed second time using correction calculated by formula (2). Comparison of corrected average values with phantom activity was made (fig. 4).



Figure 3: Inverse relation of reconstructed values and number of detectors (volume activity -10^6 , axial FOV -100 mm, no attenuation).



Figure 4: Reconstructed values compared to theoretical baseline (volume activity - 10⁶, attenuation is present).

Figure 5 shows diagram of dataflow program used for reconstruction.



IMAGING TECHNIQUES

Besides data processing imaging plays important role in development of medical software. Basic imaging techniques (2D and 3D imaging, multiplanar reconstruction) have been presented in previous works [11, 12].

Fusion

Fusion is the technique of simultaneous imaging of anatomic (CT or MR) and functional (PET or SPECT) 3D data. These images have different resolution and common approach use data rescaling.

We have developed fusion imaging software which uses GPU to perform computation-heavy tasks (fig. 6).



Figure 6: SPECT/CT fusion imaging.

Software automatically aligns images using DICOM (Digital Imaging and Communications in Medicine) metadata. It is also possible to perform value alignment manually. Two fusion modes are available: constant and progressive alpha.

Web Imaging

Evolution of web-technologies (HTML5, JavaScript, AJAX and WebGL) made it possible to create rich interactive applications executed in client browser. Such applications are high-portable. It also allows constructing distributed applications: heavy data processing is performed on server backend; imaging is done by client web-application.

To access possibilities of web imaging we have developed software capable of visualization of 2D medical images, multiplanar reconstruction and basic topographic processing (fig. 7).



Figure 7: CT data imaging using WebGL.

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