

# CT–SPECT Analyzer - A Tool for CT and SPECT Data Fusion and Volumetric Visualization

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**Abstract.** Data fusion and specific visualization of CT and SPECT are important for diagnosis and research purposes. Selected problems are considered in the paper and are related to the developed CT–SPECT Analyzer software. Hierarchical mapping with SPECT priority for maximum value of rays is applied in this software. Three variants of color mappings are presented. Some practical aspects related to low quality of CT are considered also. The most promising is the rainbow gradient with gamma curve adjustment.

**Keywords:** CT · SPECT · Data fusion · Volumetric visualization

## 1 Introduction

Computer tomography (CT) is a standard medical procedure nowadays. CT allows the acquisition of volumetric data of patient body and it is the evolution of old X–ray technology. There are numerous challenging tasks related to CT due to phenomena related to patient body, limitations of X–ray exposition, synthesis of volume and data visualization, for example. Conventional X–ray imaging gives single view of patient body, so 2D image is obtained at high spatial 2D resolution. CT give access to arbitrary view of patient body with software based slicing technique. Multiple measurements are necessary for the reconstruction

(estimation) of single slice of patient. Multiple slices are combined into volume of patient body.

The visualization of 2D images is rather simple and numerous image enhancement algorithms are available, starting from simple like: global or local contrast enhancement, false color mapping, up to advanced like: machine vision algorithms for pattern (object) recognition and fitting to specific prior models of body structures.

Similar enhancement techniques are applied for volumetric data, but 3D visualization supports opacity, different data fusion algorithms and artificial light/shading, moreover.

Another standard technique that allows volumetric recording from patient body using gamma rays is SPECT (Single-Photon Emission Computed Tomography) [7]. The source of gamma rays is a radioisotope. CT-SPECT machine allows the acquisition of both volumes together, that are spatially aligned and calibrated. Combined CT-SPECT volume has two values for single voxel (3D pixel) corresponding to both measurements. The fusion algorithm is necessary for specific region body that enhances visibility, especially for medical research purposes.

### 1.1 Related Works

Data fusion of volumens is very important for medical images analysis [3,5]. There are numerous software tools for CT and SPECT data visualization. Some of them are universal and require a lot of settings, some of them are dedicated tools. The developed software is dedicated to analysis of parathyroid glands [1], so specific set of options are available, for improving interaction with operator. This set evolved during development of CT-SPECT Analyzer for improving man-machine interface toward to more intuitive and with low latency in pipeline. There are numerous variants of data visualization for volume [6] and current version of software was obtained by numerous iterations after testing visualization quality and possibilities of results interpretation.

### 1.2 Contribution of the Paper

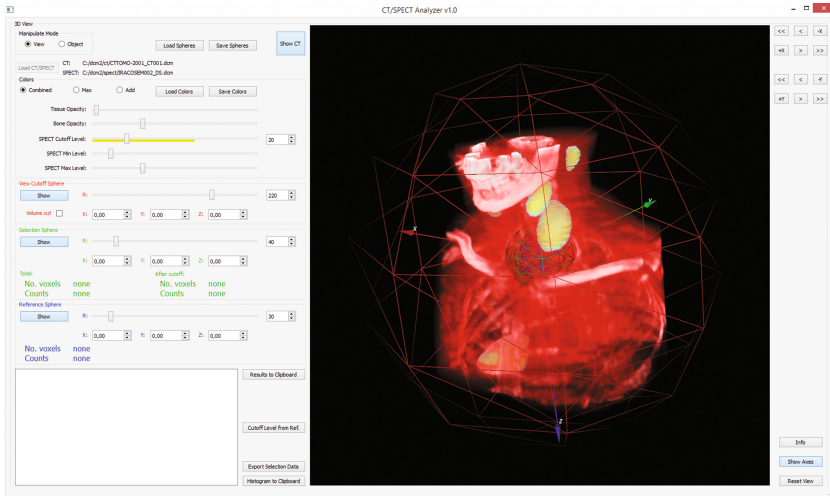
This paper considers visualization pipeline for developed CT-SPECT Analyzer software. A few variants of visualization of combined CT-SPECT volume are presented, used for improving contrast of parathyroid glands.

The processing pipeline is considered in Sect. 2. Example results of visualization are provided in Sect. 3 for maximum value mode and different color mappings. Discussion of results is provided in Sect. 4. Conclusions and further work are considered in Sect. 5.

## 2 CT-SPECT Processing Pipeline

CT-SPECT Analyzer uses a few large frameworks, that support migration of software between Linux and Windows. The first version was designed using Linux

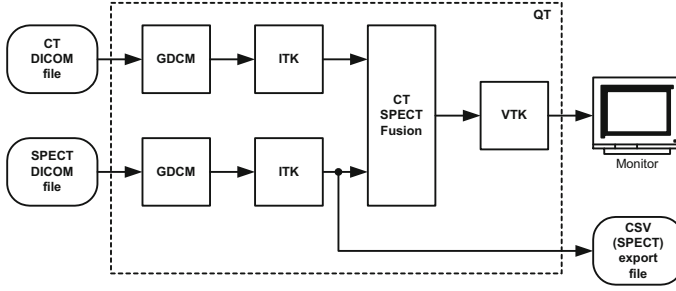
and later was converted to Windows due to portability of libraries. QT framework was selected as GUI and main framework, that forces structure of code and order of operations also. Most tools for volume visualization uses multiple windows with numerous options. CT-SPECT Analyzer is a single window application intentionally – sophisticated interface with multiple windows of the same object of interest requires long learning of operator. Blender, has a very efficient man-machine interface in single window mode was used as a reference. The control of camera view and object uses similar mouse interaction and some keyboard shortcuts are identical, also. QT supports e.g. SpaceNavigator 3D mouse that gives advanced control of view, moreover. Example screen of CT-SPECT Analyzer is shown in Fig. 1.



**Fig. 1.** Example screen of CT-SPECT Analyzer

The input data are standard DICOM files [4] that include a lot of meta-data about acquisition parameters as well as patient personal data. Such data are used by CT-SPECT Analyzer, but patient data are hidden due to privacy protection requirements. DICOM files are imported using GDCM library (Grassroots DICOM), but some additional adjustments are necessary because available DICOM files do not comply standard requirements.

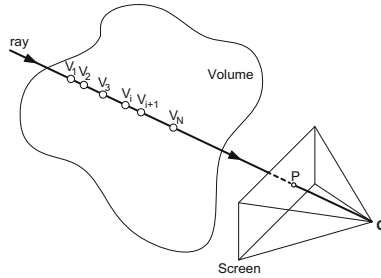
CT and SPECT volumes are processed using ITK [2] and VTK [6], and they are responsible for basic processing of volumes and visualization tasks respectively. Both are very complex and they offer a lot of options, but data fusion of both volumes must be developed separately. ITK and VTK are free libraries, well documented and with active development, so further improvements are expected. Schematic of data pipeline is shown in Fig. 2.



**Fig. 2.** Data pipeline of CT/SPECT Analyzer

## 2.1 Volume Rendering

Numerous volume rendering techniques are available and VTK supports a few of them. The maximal value and additive value are the most interesting. The additive value mode uses accumulation of values for particular screen pixel. The maximal value mode uses maximal value obtained for particular pixel (Fig. 3). There are some disadvantages of additive mode because color rendering does not work in this mode and some artifacts may be generated from voxels – maximal value could be as sum of different, not connected regions from biological point-of-view. During first tests maximal value mode was selected as most promising for analyzes of parathyroid glands.



**Fig. 3.** Computation of pixel value

CT volume is the reference for SPECT in maximal value mode, because it contains patient skeleton and tissue. SPECT volume resolution is lower and very specific. The region of interest (ROI) for SPECT, after manual selection, is exported to a text file in CSV format for further analysis using external tools.

## 2.2 Selection of ROI and Data Fusion

The selection of ROI in SPECT volume is a manual process supported by CT data. The problem of selection is related to CT-SPECT volumes fusion. VTK library

allows the assignment of RGB value and opacity to particular voxel. Rendering algorithm calculates final value for particular ray and the final pixel with RGB values are achieved on computer screen. Color mapping algorithm is applied for the assignment of voxel value to color and opacity. The VTK pipeline is very fast and memory efficient, that is necessary for interactive application, but requires proper color and opacity mapping. Rendering of two volumes in the same position is not a correct solution.

There are three spheres (they are VTK objects) that define visible region and area of analysis. The selection sphere defines ROI for further analysis, because there are multiple blobs in SPECT images.

Proposed solution in CT-SPECT Analyzer uses hierarchical mapping for visualization. The most important data are SPECT, and CT data could be overlapped by SPECT. The mapping function requires input values from 0 to 255 range for the VTK interpolation algorithm using look-up table (LUT). Values from 0 to 127 are assigned to CT data and values from 128 to 255 are used by SPECT. CT volume data are mapped to particular values. It is possible for CT, because HU (Hounsfield Unit/CT number) ranges are well defined for air, water, body tissue, bones. SPECT data are contrast enhanced for improving visibility. Automatic contrast is straightforward (128 - corresponds to value 0 of SPECT; 255 - corresponds to maximal value of SPECT). Additional manual adjustments are possible using GUI sliders, that control contrast. Following formulas are applied for contrast corrections:

$$V_{SPECT}^*(x, y, z) = 127 \frac{V_{SPECT}(x, y, z)}{V_{maxSPECT}} + 128 \quad (1)$$

$$V_{CT}^*(x, y, z) = a \cdot V_{CT}(x, y, z) + b, \quad (2)$$

where  $V_{SPECT}$  and  $V_{CT}$  denote volumens,  $a$  is the scaling coefficient, and  $b$  is the bias of HU for air, and  $V_{maxSPECT}$  is the maximal measured value of SPECT. The voxel coordinates are denoted using  $x, y, z$ .

The problem of maximum value mode for rendering is related to the overlapping of CT by SPECT. Some voxels should be assigned to 0–127 range for visibility of body and bones from CT. The solution is the threshold algorithm with level  $T$  that is used for two purposes - visualization of CT and manual segmentation of ROI:

$$V_F^*(x, y, z) = \begin{cases} V_{SPECT}^*(x, y, z) : V_{SPECT}(x, y, z) > T \\ V_{CT}^*(x, y, z) : V_{SPECT}(x, y, z) \leq T \end{cases} \quad (3)$$

A higher value of threshold reduces ROI, that is possible and necessary, and improves visibility of parathyroid glands.

## 2.3 Color Mapping for CT

There are some expectations of users related to color mapping. Typical X-ray image is grayscale with bright area related to high density body parts like bones.

Calibrated CT volumes (in HU values) give the possibility of patient's body segmentation using predefined ranges. HU value ranges are established for typical patient body and could be applied for improving the visibility of bones. The problem is that HU ranges are related to high quality CT volumes. CT-SPECT acquisition uses CT as a reference for SPECT, and high resolution is not necessary. Faster acquisition of CT reduces resolution and introduces some reconstruction artifacts, but more important for patient, it reduces X-ray dose. The HU unit ranges for such case do not correspond to expected, so multiplication by experimentally evaluated value is used (Fig. 4).

The color gradient with three colors is used: black for air, red for tissue, and white for bones. Intermediate colors are possible depending on HU value. Opacity values for tissue and bones are controlled using sliders.

## 2.4 Color Mapping for SPECT

Simple gradient was assigned with two contrast colors (opposite in HS color space) during first tests. Small differences in SPECT ROI were not well visible for untrained operator and require good quality monitor and proper light conditions in room.

Alternative mapping uses rainbow gradient, but highest value of SPECT are assigned to red and magenta. Such constraint is necessary because body tissue is also red. Low values of SPECT are assigned to blue like colors so this color gives visual boundary between red color of tissue and SPECT. It is possible to disable visibility of CT on demand.

Further improving of visual contrast is possible by the application of nonlinear mapping of colors. One of the mappings is the gamma curve:

$$V_{SPECTcorr_{norm}(x,y,z)} = V_{SPECT_{norm}}(x,y,z)^\gamma, \quad (4)$$

where  $V_{SPECT_{norm}}$  is the value from normalized range (0–1).

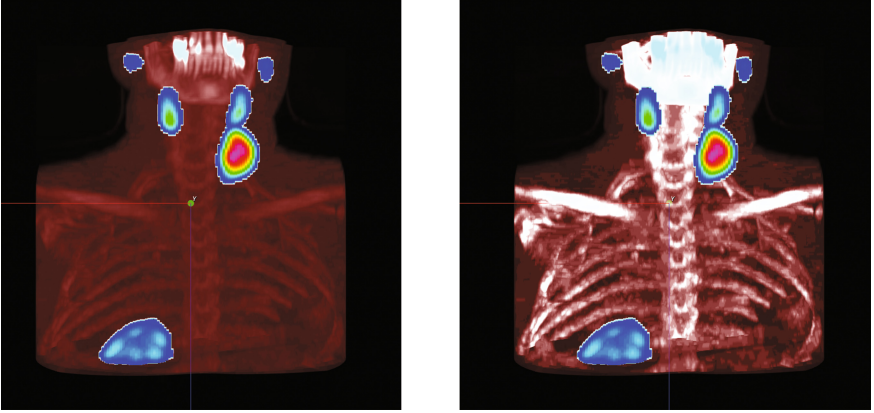
## 2.5 ROI Envelope

Additional feature that allows the better visual separation of CT and SPECT is the cyan color that is assigned to two LUT positions 127 and 128. The envelope around SPECT volume is created and is related to settings of threshold setup.

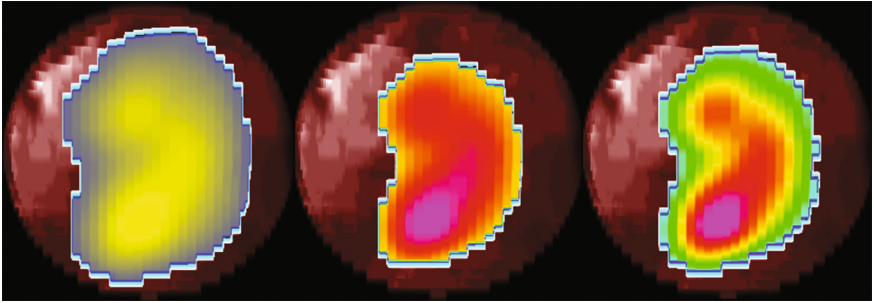
## 3 Example of Parathyroid Glands

The correction of HU due to low quality CT volume is shown in Fig. 4. The contrast is enhanced two times.

SPECT color mapping for maximal value mode is show in Fig. 5. The gamma coefficient is 0.5. Red–brown area is a part of CT after the enabling of volume cut using sphere. SPECT resolution is low so some artifacts are shown. Data fusion algorithm uses interpolation of SPECT and nearest neighborhood algorithms, so voxel/pixel structure is well visible. The regions are different due to not the same threshold value. This view is obtained from side view of patient.



**Fig. 4.** Raw (left) and HU corrected (right) volume examples



**Fig. 5.** Three different visualization techniques for parathyroid glands: gradient of two opposite colors (left), rainbow mapping (middle), rainbow mapping with gamma (right)

## 4 Discussion

Direct application of HU ranges does not provide expected visual results and most bones are low contrast for low quality CT data. Improvement of contrast gives better visual results (Fig. 4), but saturation related to high density bones is visible also (skull area). Automatic selection of HU regions is interesting alternative to experimental selection of contrast, but more different quality CT volumes are necessary.

The application of gamma curve improves visibility of details and instead a single object (mirrored C shape in Fig. 5) two or three blob regions are well visible. The application of local contrast could be applied for the further improving of details visibility, but pattern recognition approach is better for the analysis. The proposed visual contrast enhancement is sufficient for the determination of basic properties of parathyroid glands.

## 5 Conclusions and Further Work

Current version of CT-SPECT Analyzer support export of SPECT volume selection with mask for further processing of data using external tools, like Matlab or R. The second part of the project is Generalized Gaussian Distribution Mixture optimization tool. This part allows the estimation of parameters for selected parathyroid gland area using CUDA code. Further version of CT-SPECT Analyzer will merge optimization tool.

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