Quantitative Analysis of SPECT Myocardial Perfusion and Assessment of Myocardium Defect Regions through Image Processing Techniques

Rodrigo Coelho Barros[1], Lucas Ferrari de Oliveira[1], Marcus Vinicius Simões[2]
[1]*Departamento de Informática, Universidade Federal de Pelotas – UFPel*
Campus Universitário, s/nº · Caixa Postal 354 · 96010-900 Pelotas, RS
[2] *Divisão de cardiologia – Hospital das Clínicas da Faculdade de Medicina de Ribeirão Preto – USP – Ribeirão Preto, SP*
{rbarros.ifm, lucas.ferrari}@ufpel.edu.br simoesmv@yahoo.com

Abstract

In this paper we present a new approach for quantitative analysis of myocardial perfusion SPECT studies and assessment of myocardium defect regions. Myocardial perfusion SPECT is widely used in the evaluation of post-infarction patients, in order to foretell the patients' future conditions. Our approach is based on the use of polar maps, a two-dimensional plot of the reconstructed volume from the SPECT study. Using an automatic technique for polar map creation, based on image registration techniques, we were able to generate six different polar maps, allowing medical visual interpretation and analysis of myocardium defect regions.

1. Introduction

Assessment of cardiac performance is markedly enhanced by a quantitative description of the specific physiologic parameters evaluated by *single-photon computed tomography* scintigraphic images (SPECT Myocardial Perfusion) [1].

The SPECT study consists of several frames that together can sample, in three dimensions, the blood perfusion of the heart muscle [2].

Estimation of myocardium affected area is a very important achievement in patients with coronary artery disease, as those survivors of acute myocardial infarction (AMI), and it is known the close association between the SPECT study infarction size and the actual fibrosis in human hearts [3] [4].

Quantification of the SPECT studies enables objective interpersonal comparison and objective assessment of cardiac status. Furthermore, computer algorithms that enhance the images, extract parameters of cardiac performance and define criteria for normality and abnormality have the potential to be precisely described [1].

The traditional way of quantitating perfusion involves extraction of a maximal count circumferential profile from each short-axis image, and plotting this data into a single two-dimensional image, called *polar map* or *bull's eye* [5].

Our approach is based on the generation of polar maps of two distinct phases the patient undergoes in the SPECT study: rest and stress protocol. The rest protocol shows the patient's myocardium state when he is resting on a bed and the stress protocol when the patient is walking in a treadmill.

By the comparison of the stress and rest polar maps, it is possible to analyze the possible amount of myocardium tissue capable of having its perfusion restored. Moreover, by comparing the stress and rest polar maps with normality databases, it is possible to define the defect regions of the patient.

2. Polar Map Generation

The polar map generation procedure, in essence, starts from an abstraction of the heart shape in simple geometric forms. We adopted a cylinder with semi-sphere in the apex abstraction, which is a widely adopted technique [6]. In the next step, the algorithm searches the volume selecting the highest counting points. This way, it asserts that these points belong to the cardiac muscle [1]. In the last step, the Cartesian coordinates of the selected points are transformed into Polar coordinates, and then plotted into the polar map.

We use image registration as the solution to suppress the manual intervention of a medical specialist during the algorithm execution, which is by all means error-prone. We align the patient's SPECT study with a model which has pre-established criteria of sample-coordinates searching (first step of the polar map generation). The image metric used is the normalized mutual information, which provided the most accurate results in the registration of myocardial SPECT images, accordingly to previous tests.

Thus, we generate the polar maps of the patient's stress and rest protocols, as indicated in Fig. 1.

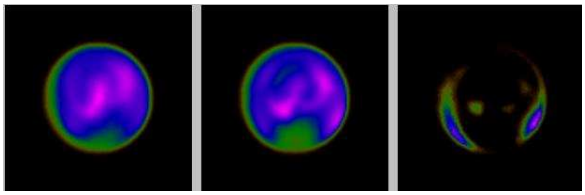

Figure 1 - Polar maps of stress (left) and rest (middle) protocols, and the reversible amount of tissue after the comparison of both images (right).

3. Quantitative Analysis and Extent of Defect Assessment

After generating the two polar maps previously discussed, we generated twenty segments of each polar map, with values in the range varying from 0 to 100, allowing the comparison of the data with gold-standard softwares which also generate these 20 segments. The segments are generated in order to evaluate the different zones of extension in the polar maps. This step is called "quantitative analysis".

To establish normality of each segment, we applied the following criteria, when comparing the polar maps generated with a normality database:

- For each segment, if the segment value is below the minimum accepted value from the database plus two standard deviations, the segment is considered abnormal, thus being "blackouted" (segmented from the image as a black spot).

This criterion is scientifically accepted by medical specialists. By running this algorithm in both polar maps, we were able to generate other two polar maps, which were referred as "defect extent polar maps". These images are exactly like the original polar maps, but having the abnormal zones segmented as a blackout zone, as shows Fig.2

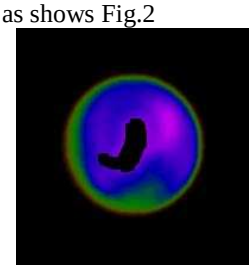

Figure 2 – "Defect Extent" polar map of a patient's stress protocol.

We were also able to generate two "reversibility" polar maps (Fig.1), which indicate, by comparing the stress and rest protocols through an arithmetic operator (based on the subtraction operation between images), the tissue of myocardium that has the highest probability of having its perfusion function restored.

It was applied in all polar maps the Gaussian smoothing filter, as well as pseudo colors, in order to provide better visualization for the specialist analysis.

4. Discussion and results

Through the use of several image processing techniques (image registration, image segmentation, image enhancement in the spatial domain, arithmetic operations among images), we were able to build a toolbox capable of assisting the specialist in the assessment of defect regions of the heart muscle.

All the tools used in the quantization of SPECT studies, like QGS and Emory Cardiac Toolbox, are proprietary software, elevating the total cost of this type of solution [6]. Our goal is to distribute the software as free software, making possible its modification according do the particular needs of each institution, reducing the total cost of the solution.

The preliminary analysis made by a specialist in nuclear medicine indicates that the approach is valid. We are working in the generation of quantitative analysis of more studies, aiming an objective comparison with data generated by gold standard tools.

5. References

[1] E. G. De Puey, E. V. Garcia, and D. S. Berman, *Cardiac SPECT Imaging*, 2.ed. Lippincott Willians & Wilkins, Philadelphia, 2001.

[2] Marcus V. Simões, J. Neverve, M. Schwaiger, Stephan G. Nekolla. "Nuclear Cardiology Core Laboratory: State of the Art". *Heart Drug*, vol.3, 2003, pp. 34-47.

[3] Raymond J. Gibbons et al. "Infarct Size Measured by Single Photon Emission Computed Tomographic Imaging With 99mTc-Sestamibi". *Circulation – Journal of the American Heart Association*, vol. 101, 2000, pp.101-108.

[4] Marcus V Simões et al. "Presence of sympathetically denervated but viable myocardium and its electrophysiologic correlates after early revascularised, acute myocardial infarction". *European Heart Journal*, vol.25, 2004, pp.551-557.

[5] Guido Germano et al. "A New Algorithm for the Quantitation of Myocardial Perfusion SPECT. I: Technical Principles and Reproducibility". *Journal of Nuclear Medicine*, vol. 41, 2000, pp.712-719.

[6] G. S. Lin et al. "Automated Quantification of Myocardial Ischemia and Wall Motion Defects by Use of Cardiac SPECT Polar Mapping and 4-Dimensional Surface Rendering", *The Journal of Nuclear Medicine*, vol. 34, n. 1, 2006, pp. 3-17.