

New Software Assistants for Cardiovascular Diagnosis

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Abstract: An important design criterion for current application development in cardiac image analysis is the applicability in clinical routine as well as in research environments. We present two novel applications dedicated to diagnosis support of the coronary heart disease. CT data of coronary arteries and cardiac function as well as MR data of myocardial perfusion are processed for quantitative anatomical and functional analysis. Semi-automatic segmentation methods are provided for a reliable representation of the coronary arteries and the left ventricular myocardium. Furthermore, quantitative parameters of the coronary vessels and the myocardium are computed. The novel approach is a standardization of the multi-parameter representation using advanced visualization techniques, that reveals possible correlations between vascular morphometry, ventricular function, and myocardial perfusion. Both prototypical applications are based on the visual programming and prototyping platform MeVisLab.

1 Introduction

The heart is seated in the center of each life. It is an autonomous muscle which automatically contracts and relaxes to provide the whole body with oxygenated blood [SS98]. It supplies two circulatory systems: the pulmonary and the systemic circulation. The heart also supplies itself with oxygenated blood via the coronary arteries, usually originating in two branches from the aorta.

Diseases of the coronary arteries (coronary heart disease, CHD) are the main cause of death in western countries. In particular, the so-called ischaemia, the undersupply of the heart muscle with blood, has the most frequent occurrence. Typically, symptoms of the partial stenosis of a coronary artery range from an insufficient supply of corresponding myocardial areas to dysfunction and a decrease of the ejected blood volume. The last stadium is the heart attack, caused by the significant destruction of myocardial cells, which can possibly kill the patient [Web]. According to the particular state, MR perfusion examinations are taken from patients with diffuse symptoms of a CHD, patients with clear symptoms but no clear intervention indication are screened via CT [RG03]. If an intervention is indispensable, catheter angiography is used immediately for imaging and possibly for therapy.

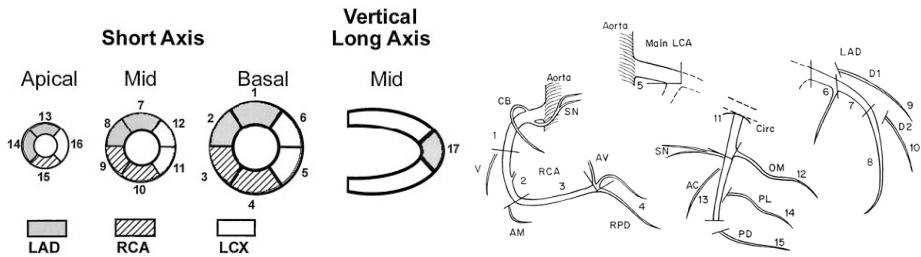


Figure 1: Left: Assignment of the 17 myocardial segments to the territories of the left anterior descending (LAD), right coronary artery (RCA), and the left circumflex coronary artery (LCX). Right: AHA-conform Coronary Tree Segments.[CWD⁺02]

The evaluation of the cardiac function requires the observation of at least two heart phases: the end-diastolic (at maximum relaxation) and the end-systolic phase (at maximum contraction). For the definition of quantitative measurements of myocardial function and perfusion in relation to the supplying coronary vessels, the 17-segment-model was established by the American Heart Association (AHA) (Fig. 1) [CWD⁺02]. Corresponding results are often displayed in a so-called bull's-eye plot (BEP). To speed up the diagnosis in case of CHD indication, all examination results must be comparable within a single workflow on a single workstation. The comparison of results from perfusion, vessel, and function analysis provides efficient contextual analysis of both cause and effect within the framework of dedicated software assistants.

Today, MR or CT cardiac function and CT coronary tree analysis are integral parts of the clinical routine, while MR and CT perfusion studies are still research subjects. Several commercial applications for cardiac diagnosis support are available, such as Easy Vision [BJK03] [Philips, Hamburg, Germany], QMass MR [Medis, Leiden, Netherlands], and syngoARGUS [Siemens Medical Solutions, Erlangen, Germany], which allow for semi-automatic segmentation of the myocardium and the extraction of relevant parameters from MR images. Software assistance for cardiac CT data analysis, for example by MxView [Philips, Hamburg, Germany], QMass CT [Medis, Leiden, Netherlands] and CIRCULATION [Siemens Medical Solutions, Erlangen, Germany], is provided, offering robust segmentation results, reliable quantitative measurements and adequate visualization. However, a combined presentation of results from different examinations, is not supported by these workstations.

Our proposed software assistants MeVisCardio, and MeVisCardioPerfusion offer a suitable platform for image analysis, including comfortable XML-based patient data management as well as an adequate workflow with easy manageable user interfaces. The combination of segmentation results of the coronary arteries and quantitative parameters of the left ventricular function provides a physician with the ability of handling different medical questions side by side in one assistant. Furthermore, advanced visualization methods allow the correlation of results from both applications.

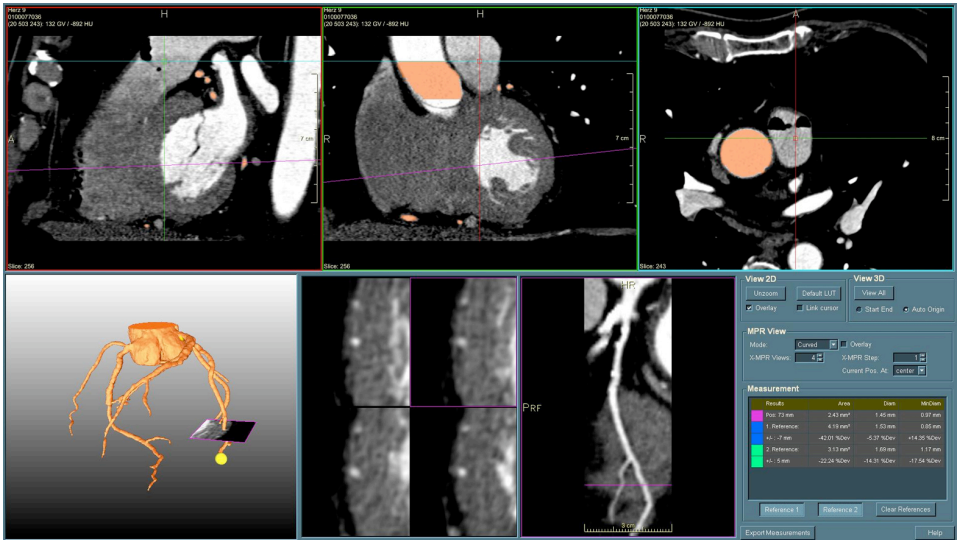


Figure 2: MeVisCardio - Coronary Tree Analysis (patient image data courtesy of University Erlangen).

2 Image Analysis and Visualization

For a reliable diagnosis, the physician needs to obtain robust and reproducible quantitative parameters at a minimal expenditure of time. The most significant quantities are vessel diameters, change in myocardial wall thickness, ventricular blood volume, and different global and local perfusion parameters [SMJ⁺00]. The first step to obtain these parameters for a quantitative analysis is to perform a robust segmentation of the relevant cardiac structures in the images, i.e. the main branches of the coronary tree, the myocardium and the blood pool of the left ventricle.

2.1 Quantitative Analysis Methods

Coronary Tree Analysis. For the analysis of the coronary artery tree, we have developed a fast and widely applicable method that detects the coronary arteries in CT angiographic images with a minimum amount of user interaction. The performed segmentation provides the basis for an analysis of the patient individual vascular structure such as measurements of vessel diameters or vascular dependencies [BHH⁺05]. In the first step, the aorta is segmented using a marker-based region growing method followed by a shape analysis of the aorta cross-sections yielding voxel clusters located at the aorta boundary which are further classified based on their size, shape, and orientation. Those clusters that are considered as possible coronary artery origins are used as seeds for a subsequent progressive 3D region growing segmentation of the coronary arteries. The progressive approach of the region growing algorithms allows for interactive adjustment without result recomputation. Undetected coronary branches can be added by interactively placing additional seed points.

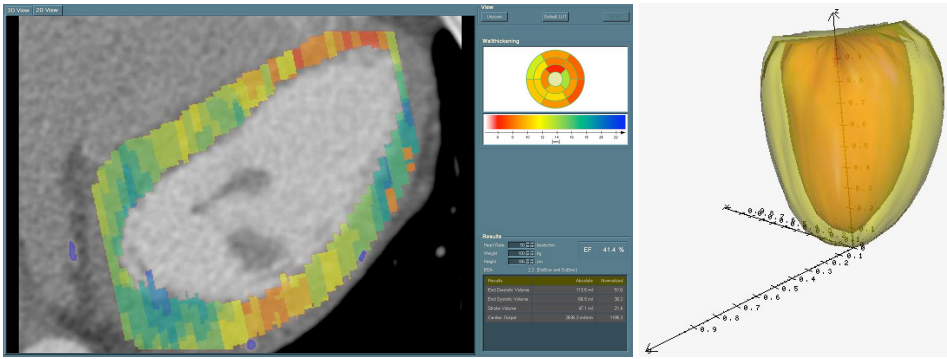


Figure 3: Left: MeVisCardio - Left Ventricular Function Analysis (patient image data courtesy of University Erlangen). Right: Mean Normalized Left Ventricular Model (patient image data courtesy of University Tuebingen, University Muenster).

In a further step an accurate skeletonization of the segmented arteries is achieved. The resulting vessel centerlines are used to define orthogonal cross-sections at arbitrary positions along the vessel path in order to measure local cross-sectional areas and diameters (Fig. 2) [SPS⁺02]. Calcified plaques are excluded by a user-defined thresholding operation.

Analysis of Left Ventricular Blood Pool and Myocardium. The most important quantities for the assessment of left ventricular function are the ejected blood volume and the change in myocardial wall thickness over the heart cycle. In order to obtain these quantities, the blood pool and the myocardium have to be segmented. Our blood pool segmentation algorithm starts with a region growing similar to the algorithm used for the coronary artery segmentation. Subsequently, the remaining gaps in the segmentation result are closed in 3D using a complementary region growing algorithm. Both algorithms are progressive, i.e. the segmentation threshold can be interactively adjusted without re-computing the segmentation.

For the extraction of the left ventricular myocardium and the quantification of wall thickness and motion over a complete cardiac cycle, an active shape model is used [CT04, BTM⁺06]. First, we defined a 3D model of the left ventricle with a variable number of feature vector components. This model is matched to training segmentations performed manually by experienced radiologists. A principal component analysis yields the statistical model representing the different shape variants present in the training data. In a second step, this model is iteratively adapted to a new dataset in order to extract the myocardial shape. This is done by defining a distance measure between the model and the data, and by optimizing the adaption by a gradient descent method. The segmentation result is represented as a winged edge mesh data structure [Bau74], suitable for visualization as well as for storing local parameters such as the wall thickness.

Perfusion Analysis. To measure the perfusion of the heart muscle, image sequences acquired after a contrast bolus injection are analyzed with respect to the intensity change caused by the wash-in and wash-out of contrast agent. The resulting time-intensity-curves are used to derive parameters describing the myocardial perfusion [aSGB⁺01].

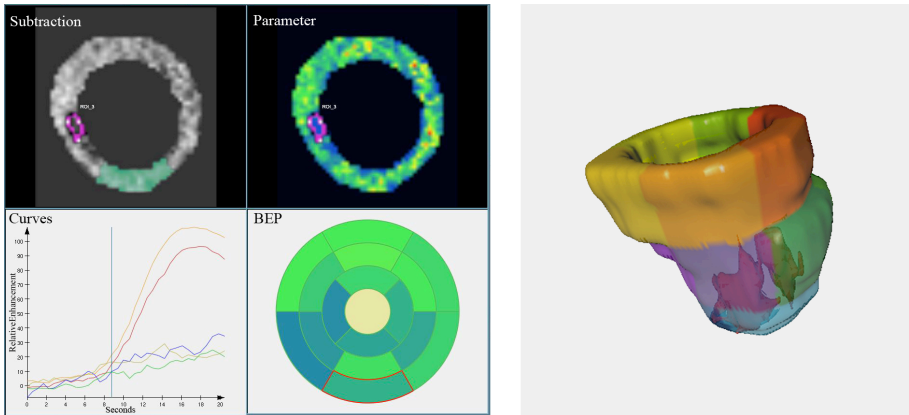


Figure 4: Left: MeVisCardioPerfusion - Segmentation in subtraction images (upper left) and parameter map-based images (upper middle) allow for more accurate analysis of suspicious regions than the BEP (bottom middle). Perfusion parameter behavior along time is shown in region-based as well as segment-based time-intensity-curves (bottom left). Right: 3D-BEP with segmented late enhancement volume (patient image data courtesy of University Tuebingen).

Various methods for segmentation and analysis of the myocardium can be performed on the motion corrected data. Two strategies exist to evaluate the regional myocardial perfusion: segment-based and voxel-based analysis. Segment-based analysis refers to the 17-segment-model developed by the AHA [CWD⁺02], which is used in DICOM Structured Reporting [Kri06] and which provides a basis for the comparison of myocardial parameters across examinations. The segment-based results are visualized in BEPs (Fig. 4 left). To get a more accurate impression of the location, shape, extent, and grade of a perfusion defect, the time-intensity-curves and derived parameters can be analyzed per voxel. The results are visualized as parameter images and used for the segmentation and quantification of suspicious regions (Fig. 4 left). The acquisition of perfusion image sequences at rest and at – pharmaceutically induced – stress allows to compare the corresponding parameters per segment, per pixel, or within user defined regions. This comparison is used to calculate the perfusion reserve [WJHW⁺97]. Necrotic tissue in a certain heart segment is characterized by delayed enhancement approximately ten minutes after the injection of the contrast agent. It can be detected by a histogram-based segmentation similar to [KCW⁺03](Fig. 4 right).

2.2 Presentation and Visualization of Results

For an integrative presentation of the perfusion analysis results, the dynamic parameters characterizing the contrast agent distribution for each myocardial region are visualized separately in a color-coded BEP (Fig. 5). The plot is augmented by a picking facility which allows the user to select individual segments. In an additional 2D-diagram, the corresponding time-intensity-curves are visualized. In a rest/stress comparison, parameters of both states are merged in a single visualization by bisecting each segment ring (Fig. 4).

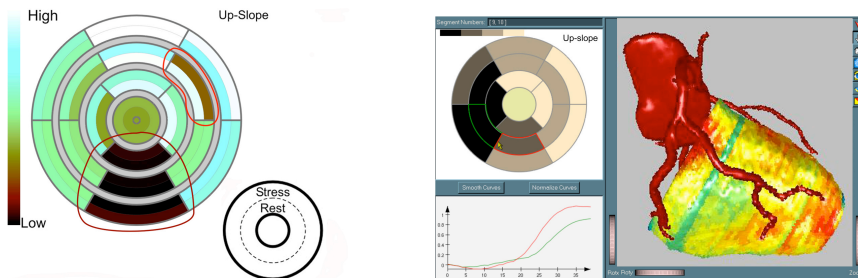


Figure 5: Left: Integrated visualization of parameter up-slope for rest and stress state. Ischemic areas are marked. Right: Bidirectional linked BEP and 3D-view with corresponding perfusion parameter curves, 3D view shows wall thickness mapped on the segmented ventricle (patient image data courtesy of University Erlangen).

According to the AHA-standards, each segment of the BEP is supplied by the respective coronary tree branch. Hence, the detection of myocardial regions exhibiting delayed and decreased perfusion or the visualization of functional wall parameters using a BEP may be accompanied by an examination of the supplying coronary arteries. For this purpose, a bidirectional link between the BEP and a 3D-view showing the coronaries, the ventricle, and the aorta was established. Furthermore, picking facilities are implemented for both. When a segment of the plot is selected interactively, the 3D-view focuses on the corresponding vessel branch (Fig. 5 right)[MBP06] and vice versa. Hereby, the associated time-intensity curves are automatically displayed. Function parameters are visualized the same way using a BEP to ensure vessel correspondence. We also merged result masks from the coronary tree segmentation and the wall thickness computation in 3D as well as in 2D to allow for local correlation of cause – a stenotic vessel – and effect – the myocardial dysfunction (Fig. 5 right).

3 Software Workflow Design

In general, the design of a medical software assistant should follow the clinical workflow. Due to the variety of existing examination methods for CHD diagnosis, this requirement is not easily fulfilled. In this work, we present two software assistants dealing with cardiac CT and MR images: MeVisCardio provides tools for the analysis of coronary arteries as well as left ventricular function in CT images (Fig. 2, Fig. 3). A further software assistant – MeVisCardioPerfusion – performs the analysis and visualization of myocardial perfusion parameters in MR images (Fig. 4 left). Common tasks required in both applications, e.g. loading and managing the patient data, are implemented in a generalized framework [RKHP06] available within the application development platform MeVisLab [MeV]. This allows simple usage due to generalization of basic steps for all applications. In order to simplify the use of the software assistants, each application step is documented by process descriptions and no complex user interactions are required. Furthermore, all interactions are designed similarly. The interaction expense is minimized by automating the algorithms as much as possible and by re-using manual initializations as, for example, in the segmen-

tation of the left ventricular blood pool in both end-diastolic and end-systolic phases. Both software assistants are designed to support the interpretation of related results from vascular, ventricular function, and perfusion analysis. In MeVisCardio, for example, the user is able to switch between coronary tree and ventricular function analysis. If a coronary tree segmentation result already exists, it is automatically added to the ventricular wall thickness display, which simplifies the detection of local relations between ventricular dysfunction and vascular stenoses (Fig. 3 left).

4 Discussion & Conclusion

The software assistants are evaluated in several clinics. In addition, the coronary analysis software was used in a multi-center study, where a high performance and a low amount of required interaction could be assessed. The presented assistants allow combined analysis of perfusion, function, and vessel parameters. The merging and animation tools as well as the BEP offer a clear parameter visualization, which guides the user to suspicious regions (Fig. 5).

A future challenge is the integration of all cardiac analysis components within a single software assistant. Appropriate workflow concepts with a clear user guidance through all possible scenarios are essential to support the usage in clinical routine as well as in studies. Furthermore, robust registration methods are required in order to allow for combined visualization of all analysis results such as segmentation masks and quantitative parameters from different imaging modalities (MR, CT, SPECT). The problem of finding adequate visualizations of multiple parameters of dynamic images sequences is an active field of research [OGH⁺06].

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