PCARDM Cardiac MR Analysis

Cardiac MR (CMR)

The PCARDM tool is a versatile solution for researches who need to analyze CMR image data. It includes two distinct workflows. The relatively straightforward FUNCTION workflow supports the analysis of cardiac cine MR images and results in measures of cardiac pumping function. The sophisticated PERFUSION workflow addresses the absolute quantification of left ventricular perfusion based on Gd first-pass perfusion images.

PCARDM combines PMOD's modeling expertise with ETH’s leading-edge MR methodology into a comprehensive package for the quantification of perfusion CMR images.

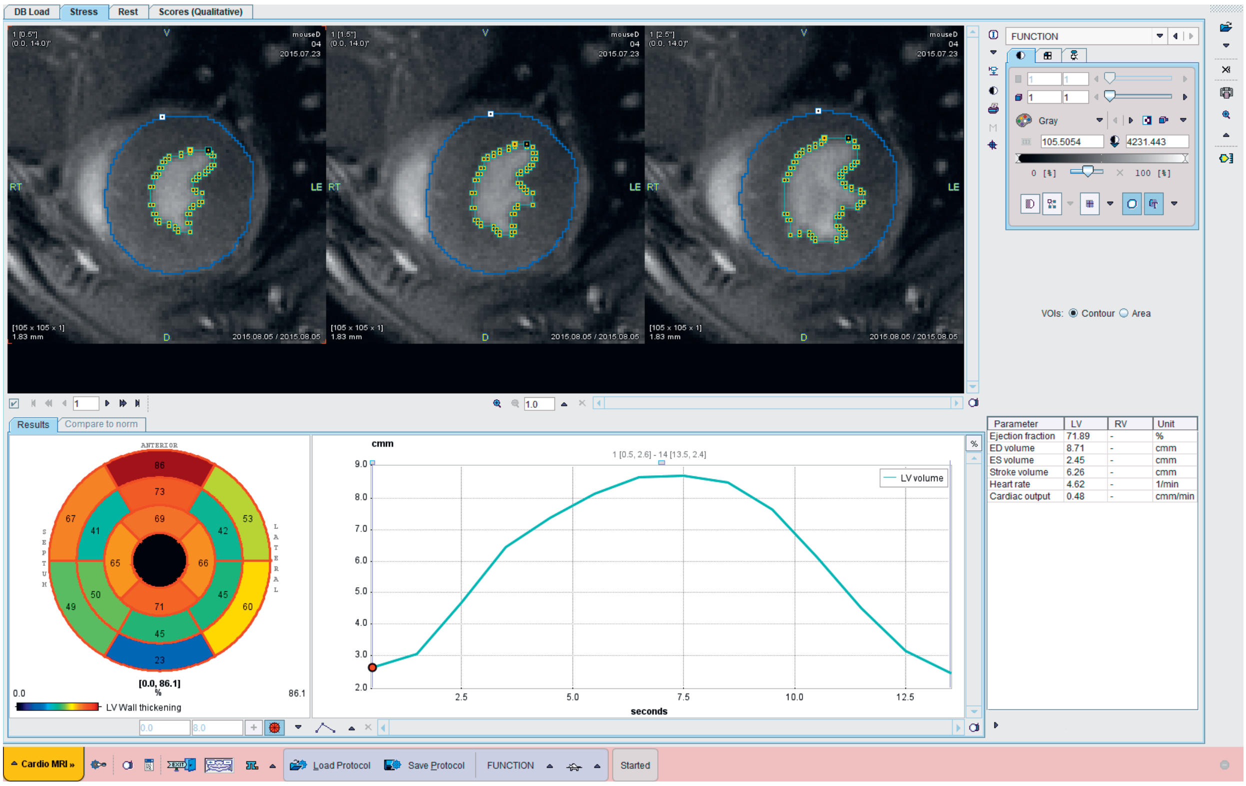
Cardiac Function Analysis with PCARDM

Cardiac cine images allow measuring the shape of the ventricles throughout the contraction cycle of a heart. By analyzing the movements of the inner and outer boundaries of the muscle the ventricular beating function can be quantified. The FUNCTION workflow supports the contour detection using manual and automatic approaches, and evaluates the functional parameters by analyzing the volume curve.

Cardiac Perfusion Modeling with PCARDM

Perfusion assessment by cardiac magnetic resonance builds on the injection of a contrast agent bolus and dynamic imaging while the bolus passes the myocardium. The contrast agent changes the MR signal of blood and is similar to the use of tracers in PET. The situation, however, is complicated by the fact that the MRI signal is not strictly proportional to the contrast agent concentration. This effect as well as field inhomogeneity have to be corrected for in order to achieve fully quantitative perfusion values. The PERFUSION workflow is a joint development with the CMR research group of ETH Zurich, Switzerland. It combines PMOD’s long-standing modeling expertise with ETH’s leading-edge MR methodology in a comprehensive package for qualitative and quantitative perfusion image analysis.

The new FUNCTION workflow provides a unique solution for the quantification of ventricular beating function from cine MR images of humans, rats and mice.



VOIs: ● Contour ○ Area

Parameter	LV	RV	Unit
Ejection fraction	71.89	-	%
ED volume	8.71	-	cmm
ES volume	2.45	-	cmm
Stroke volume	6.26	-	cmm
Heart rate	4.62	-	1/min
Cardiac output	0.48	-	cmm/min

PCARDM user interface illustrating myocardium segmentation, volume curve of the left ventricle during a heartbeat, and the functional analysis results.

Function CMR Requirements

The FUNCTION workflow requires a cardiac cine MR series in short-axis orientation which portrays the heart shape throughout an entire heartbeat. For results representing the whole ventricle, a multi-slice series is required which covers the whole axial extent of the LV. Otherwise the volumetric results have to be interpreted accordingly.

Quantification of Function

The FUNCTION workflow is easy to perform. After loading the cardiac cine MR images, the heart can optionally be cropped from the volume. The main task then consists of defining the endocardial and epicardial boundaries of the left ventricle. Three different approaches are supported:

- Fully automatic, AI-based segmentation, available for human and mouse data (PAI licensing required).
- Semi-automatic segmentation by a rough manual LV definition and subsequent fitting of an active model to the boundaries.
- Manual method using the various VOI tools within PMOD.

The blood volume during contraction is then analyzed and the percent ejection fraction calculated from the volume difference at end systole and diastole. Additional reported results are the stroke volume and cardiac output.

Perfusion CMR Requirements

The full PERFUSION workflow requires the following MR scans:

- Dynamic gadolinium first-pass scan: A 3D sequence which is able to acquire contrast images covering the left ventricle within a breath hold. Utilizing ECG triggers, contrast images can be reconstructed which are practically devoid of motion.
- B_1 scan: Volumetric sequence for assessing the B_1 field inhomogeneity of the surface coils.
- T_1 scan: Single-slice sequence measuring global T_1 relaxation time in blood and myocardium for conversion of the MR signal to contrast agent concentration.

If these requirements are not fully met, only a partial analysis can be performed

Full Quantification of Perfusion

In the PERFUSION workflow, the user is guided in a step-by-step manner as follows:

- Loading of the perfusion series and cropping of the heart volume.
- Loading of the B_1 map and inhomogeneity correction of the perfusion series.
- Definition of the LV segments and blood volume.
- Calculation of the average signal time course in the LV segments and blood.
- Loading of the T_1 series and T_1 averaging in the LV segments and blood.
- Conversion of the resulting signal curves to contrast concentration.
- Model-based quantification of the segment perfusion in [ml/min/g] using blood concentration as the arterial input function.
- Calculation of the segmental perfusion reserves.

Perfusion Quantification Models

PMOD's PKIN modeling tool is leveraged for the quantification of the segmental concentration curves, offering the following quantification methods:

- Fermi function
- Basis function method
- Model-independent approach

Reduced Quantification of Perfusion

If no B_1 and T_1 data are available, simplified processing can still be applied. Assuming similar signal distortions in stress/rest studies, the ratio of their outcome can be considered as a measure of the coronary flow reserve.

Qualitative Perfusion Analysis

Non-quantitative perfusion analysis can also be performed in PCARDM. A separate panel supports interactive reviewing of the rest and stress images side by side with the sectors in the overlay. Three different grading schemes can be employed for assigning defect scores to the sectors.