

Workshop on Reconstruction Schemes for MR Data
17th August 2016

Magnetic Resonance MicroImaging of a Swine Infarcted Heart: Performing Cardiac Virtual Histologies

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17th August 2016

This is a presentation of the work exhibited in the 37th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC'15) in Milan, Italy (August 25th-29th, 2015).

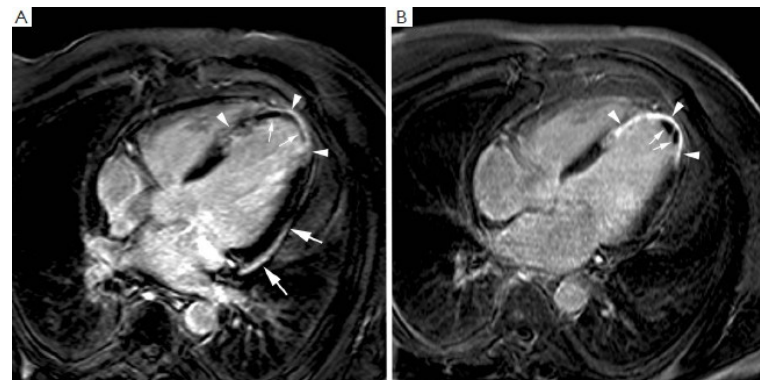
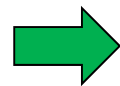
R. Ortiz, J. M. Morales, S. Ruiz-España, V. Bodí, D. Monleón and D. Moratal,
"Magnetic resonance microimaging of a swine infarcted heart: Performing cardiac
virtual histologies," *2015 37th Annual International Conference of the IEEE
Engineering in Medicine and Biology Society (EMBC)*, Milan, 2015, pp. 1584-1587.

DOI: 10.1109/EMBC.2015.7318676

Introduction

The myocardial infarction

- ⌘ The myocardial infarction (MI) is the leading cause of death in developed countries.
 - MI occurs when blood flow stops to part of the heart, causing damage to the heart muscle.
- ⌘ Nowadays around a 70% of patients hospitalised with MI survive the hospital phases.
 - It is necessary to control the evolution of these patients' hearts and prevent and identify future cardiovascular risks → **CARDIAC IMAGING**



Introduction

Swine as model in cardiovascular research

⌘ APPROACH → Study of medical images of a swine's infarcted heart

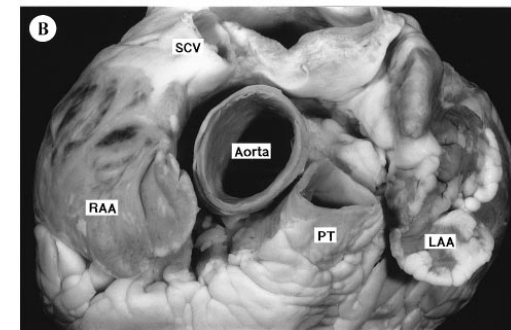
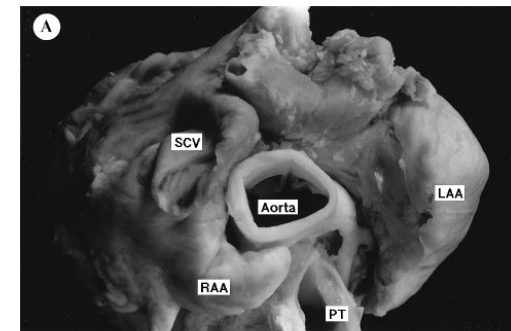
⌘ Swine are commonly used in cardiovascular research because porcine and human hearts share important anatomic and physiologic characteristics:

- Similar size and shape
- Similar distribution of blood supply by the coronary artery

⌘ Magnetic Resonance Imaging (MRI):

- Non-invasive technique
- Strong control over the data acquisition and how it can be managed.
- Image with high precision and reliability.

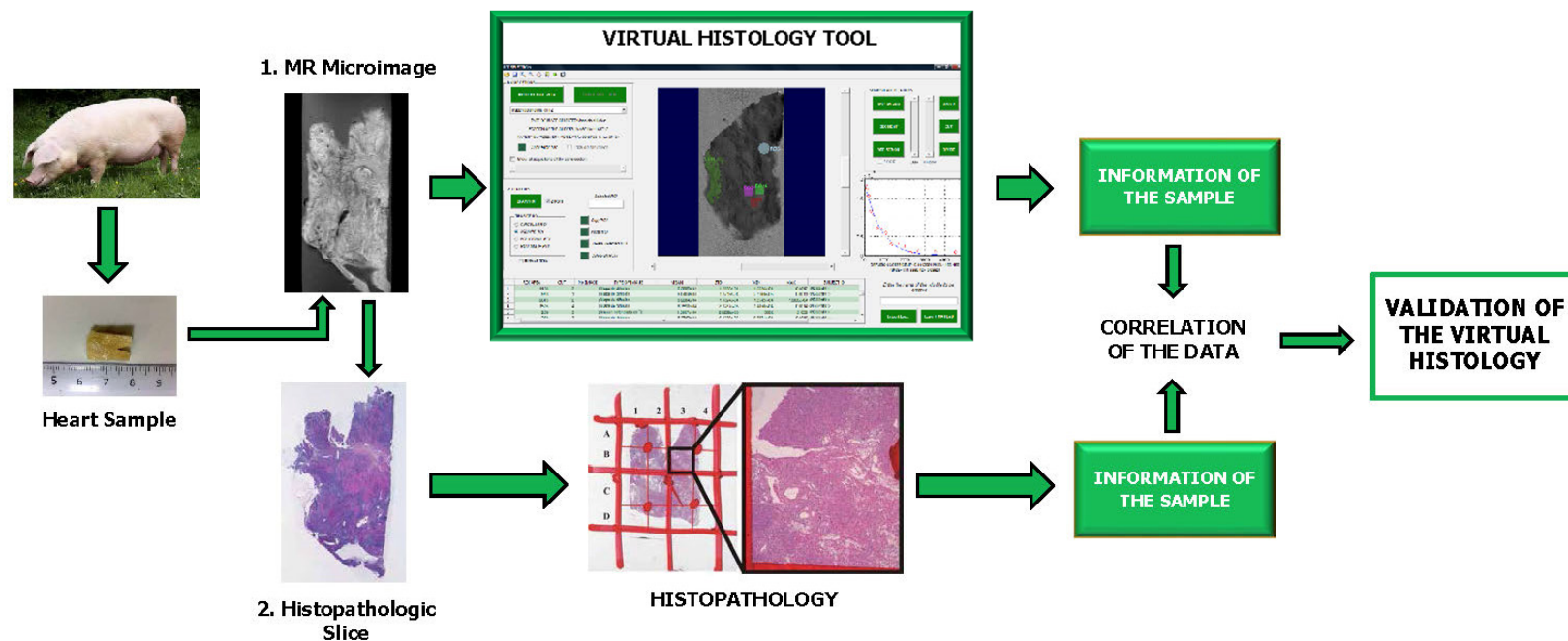
Porcine Heart



Human Heart

Objectives

- ⌘ Development of an intuitive software tool in MATLAB that allows a detailed study of the magnetic properties of infarcted hearts tissue by the mathematical processing of a set of Magnetic Resonance (MR) microimages of that tissue.
 - Recreation of a virtual histology of infarcted heart tissue.
- ⌘ Preliminary stage: Work with a swine's hearts and establish a complete analysis of the conditions of the heart after an infarction
 - Compare the results of the virtual histology with the results of the histopathology
 - Relate the study, as a last resort, to human hearts.

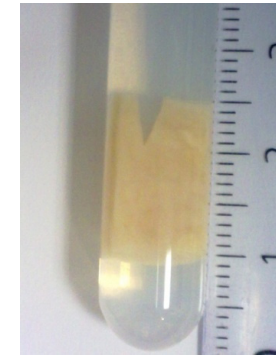


Materials and Methods

⌘ Two small samples (size 1 cm × 1.6 cm) of the infarcted heart of two different young female domestic pigs.

➤ Obtaining the images:

1. The samples are introduced in an agarose matrix inside a tube.
2. These tubes with the heart samples are introduced one by one in the NMR tube of the spectrometre (1 cm wide) and correctly positioned in the inside of the coil
3. Run the required sequences in order to obtain the MR microimages.



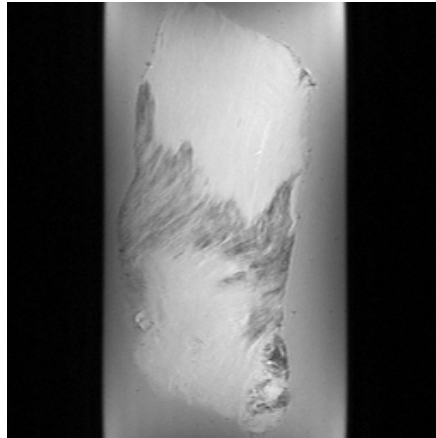
⌘ Bruker Spectrometre ADVANCE 14 Teslas

- Acquisition of 5 types of weighted images (matrix size = 256 × 256):
- T1-weighted reference image (TR = 500 ms; TE = 9,3 ms)
 - T2-weighted reference image (TR = 4000 ms; TE = 57,6 ms)
 - Diffusion-Weighted Images (DWI) (16 b-values)
 - T2-weighted images (TR = 2000 ms; 16 TE values)
 - T2*-weighted images (TR = 1500 ms; 12 TE values)

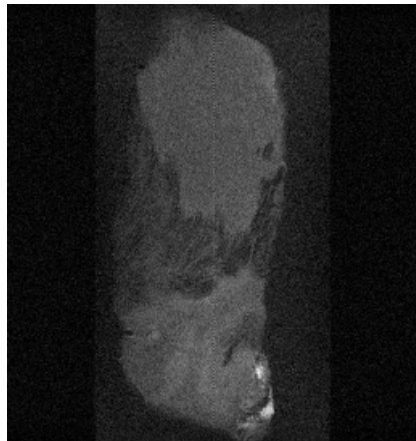
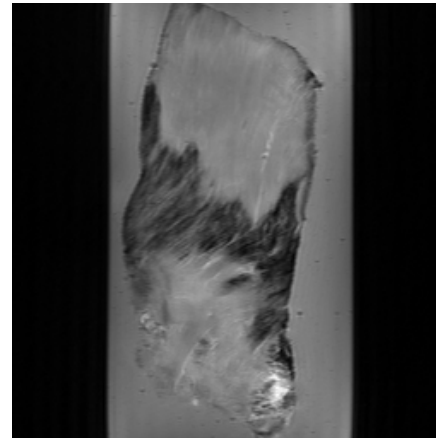


Materials and Methods

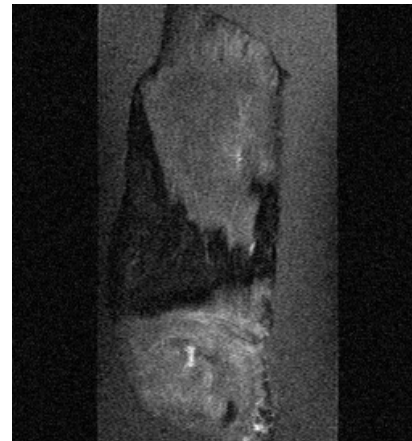
T1-weighted Image



T2-weighted Image



DWI
Acquisition num. 8
 $b\text{-value}=822.297 \text{ s/mm}^2$



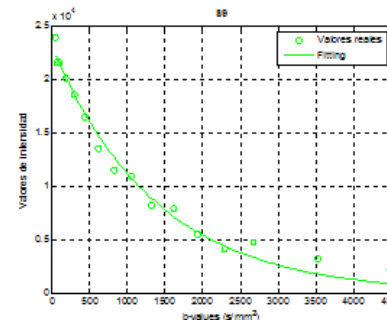
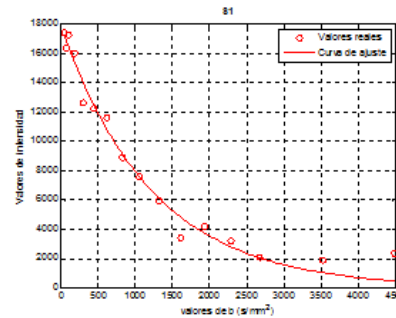
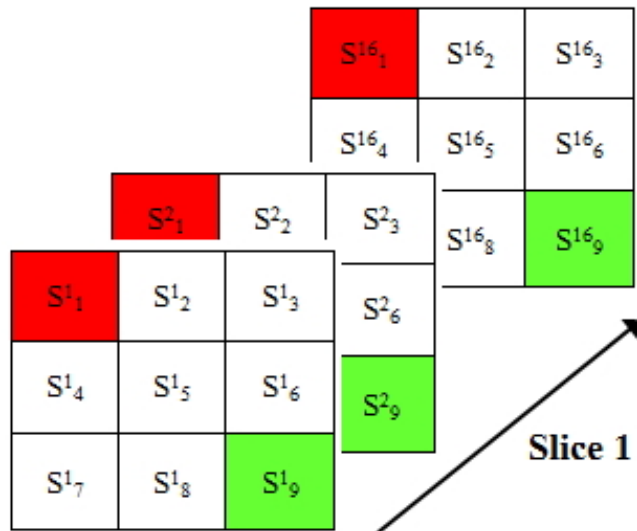
T2-weighted Image
Acquisition num. 8
TE=78.19 ms



T2*-weighted Image
Acquisition num. 8
TE=34 ms

⌘ The process to generate the maps consists on:

1. Analyse pixel by pixel every acquisition of each slice of the sample and store the values of the pixels.
2. Execute the fitting process of the set of values of the pixels using the values of the variable parameter, previously known.
3. Generate the map with the ADC, T2 or T2* value obtained for each pixel



ADC ¹ ₁	ADC ¹ ₂	ADC ¹ ₃
ADC ¹ ₄	ADC ¹ ₅	ADC ¹ ₆
ADC ¹ ₇	ADC ¹ ₈	ADC ¹ ₉

⌘ ADC map: the variable parameter is the *b-value* (s/mm²)

➤ Mono-Exponential

$$S(b) = S_0 e^{-bD}$$

➤ Bi-exponential

$$S(b) = S_0 [\xi e^{-bD_f} + (1 - \xi) e^{-bD_s}]$$

⌘ T2 and T2* maps: the variable parameter is the Time of Echo TE (s)

➤ Mono-exponential

$$S(TE) = S_0 e^{-\frac{TE}{T_2}}$$

Results

Structure of the Graphical User Interface

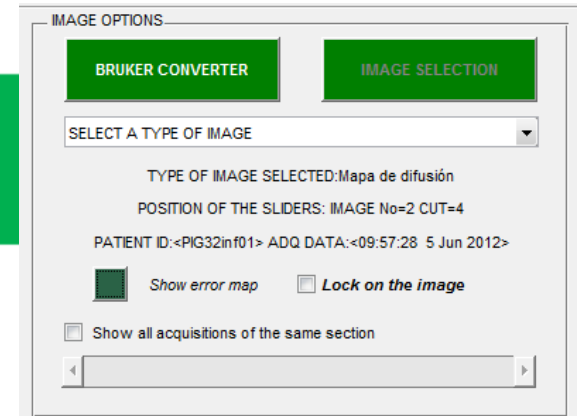
The screenshot displays the 'ROI SELECTION' software interface. It is divided into several functional areas:

- IMAGE OPTIONS:** Contains buttons for 'BRUKER CONVERTER' and 'IMAGE SELECTION'. It shows 'Imagen potenciada en T2' as the selected image type. Other details include 'TYPE OF IMAGE SELECTED: Mapa de difusión', 'POSITION OF THE SLIDERS: IMAGE No=1 CUT=3', and 'PATIENT ID: <PIG32inf01> ADQ DATA: <09:57:28 5 Jun 2012>'. There are checkboxes for 'Show error map', 'Lock on the image', and 'Show all acquisitions of the same section'.
- ROI OPTIONS:** Features a 'DRAW ROI' button and a 'LOCK' checkbox. It lists 'TIPOS DE ROI' (CIRCULAR ROI, SQUARE ROI, POLIGONAL ROI, HANDMADE ROI) and actions like 'Copy ROI', 'Paste ROI', 'Delete selected ROI', and 'Delete all ROIs'. A 'Hide all ROIs' checkbox is also present.
- SEGMENTATION OPTIONS:** Includes buttons for 'NEW REGION', 'MERGE', 'SEGMENT', 'CUT', 'ADD REGION', and 'DIVIDE'. It also has a 'LOCK' checkbox and sliders for 'AREA' and 'WINDOW'.
- Central Image:** A grayscale diffusion map with several regions of interest (ROIs) highlighted in different colors: ROI1 (green), ROI2 (purple), ROI16 (red), and ROI6 (blue).
- Graph:** A plot showing a curve of data points (red circles) with a blue fit line. The x-axis is labeled 'DIFFUSION COEFFICIENT= 0.0012981 PIXEL= 166-156' and the y-axis ranges from 0 to 2. Below the graph, it shows 'RMSE= 771.8859 R2= 0.98524'.
- Data Table:** A table with columns: ROI AREA, CUT, No IMAGE, TYPE OF IMAGE, MEAN, STD, MIN, MAX, and SUBJECT ID. It contains 6 rows of data.
- Export Options:** A text input field for the filename and two buttons: 'Export Excel' and 'Export MATLAB'.

	ROI AREA	CUT	No IMAGE	TYPE OF IMAGE	MEAN	STD	MIN	MAX	SUBJECT ID
1	1183	3	1	Mapa de difusión	6.3805e-04	1.2558e-04	1.5526e-04	0.0012	<PIG32inf01>
2	978	1	1	Mapa de difusión	6.0404e-04	1.3719e-04	2.7160e-05	0.0011	<PIG32inf01>
3	2813	2	1	Mapa de difusión	6.2204e-04	1.1624e-04	1.2542e-04	7.6065e-04	<PIG32inf01>
4	1505	4	1	Mapa de difusión	6.7590e-04	8.3287e-05	1.4056e-04	0.0014	<PIG32inf01>
5	269	3	2	Imagen potenciada en T2	1.5927e+04	2.8239e+03	5602	21039	<PIG32inf01>
6	224	2	1	Mapa de difusión	6.3712e-04	6.4206e-05	6.7871e-04	0.0010	<PIG32inf01>

Results

Image Options Types of images



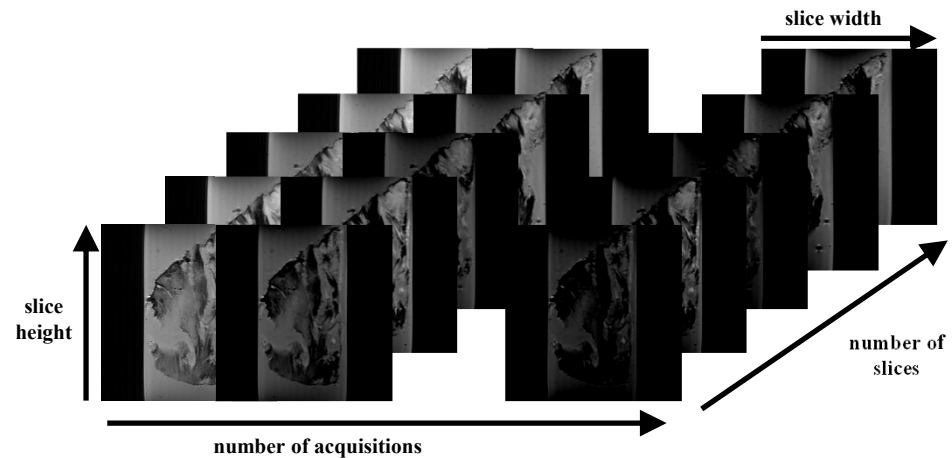
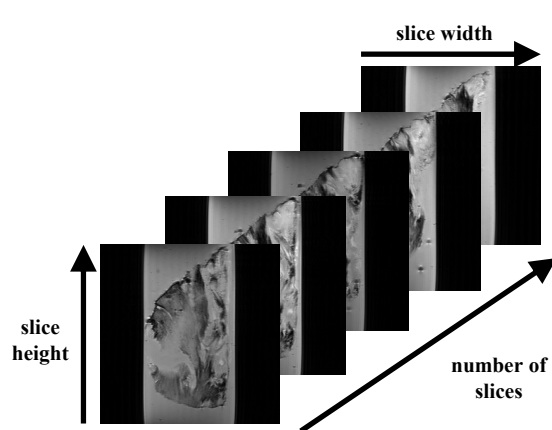
⌘ The images are classified in two groups:

➤ GROUP A: Reference images that do not need a fitting process:

- T1-weighted image
- T2-weighted image

➤ GROUP B: Images that need a fitting process in order to generate a map:

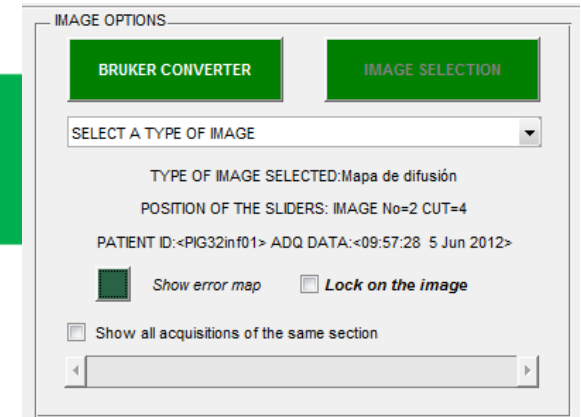
- DWI (16 acq.) → ADC map
- T2-weighted images (16 acq.) → T2 map
- T2*-weighted images (12 acq.) → T2* map



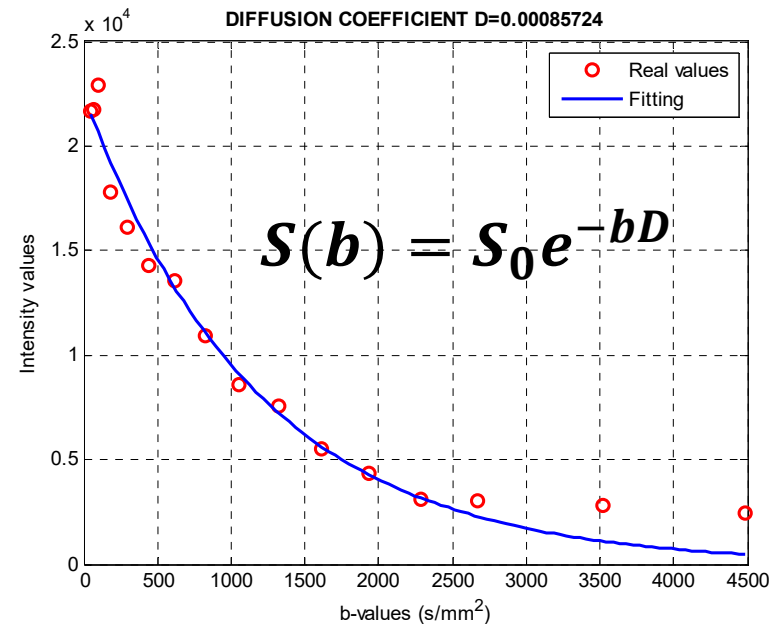
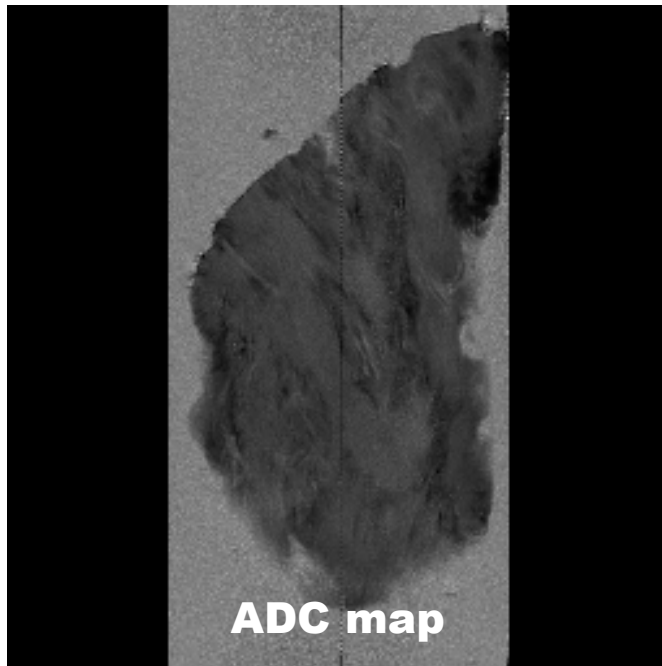
⌘ The tool implements four methods in order to fit the data.

Results

Image Options Maps

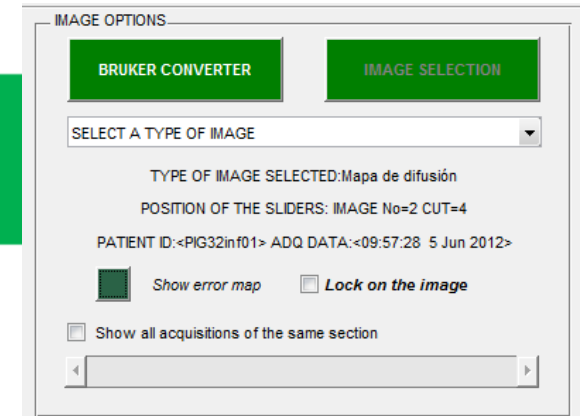


- ⌘ Method 1: **High resolution exponential.**
 - Curve fitting using nonlinear regression, with previous models
- ⌘ Good fitting and graphical results for many cases but improvable



Results

Image Options Maps

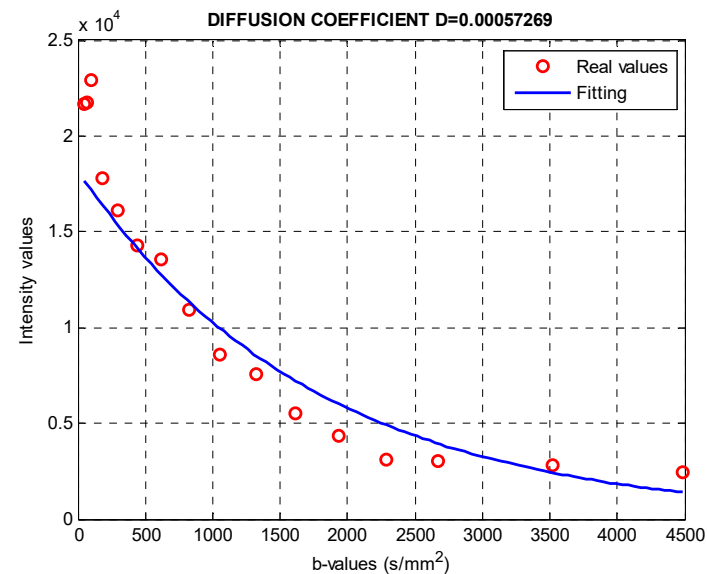
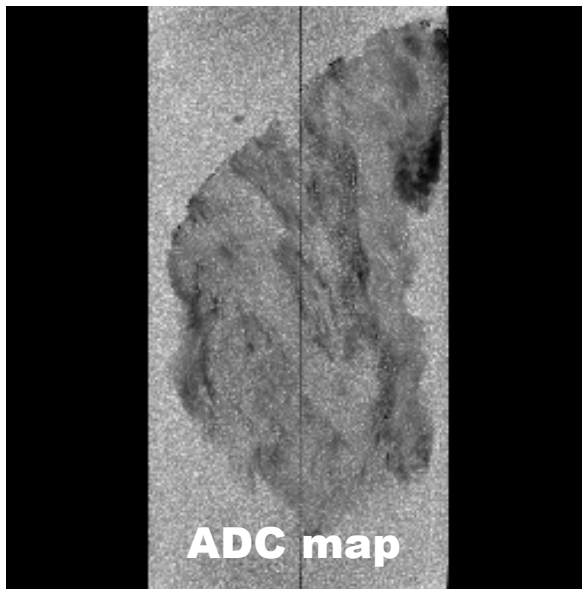


⌘ Method 2: **Low resolution exponential.**

➤ Linearization of exponential equation → Linear regression.

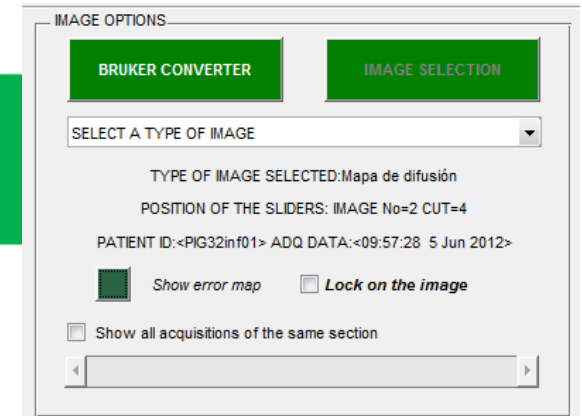
$$S' = \log S(b) = \log S_0 + (-bD) = S'_0 - bD$$

⌘ Worst fitting results but faster operations



Results

Image Options Maps

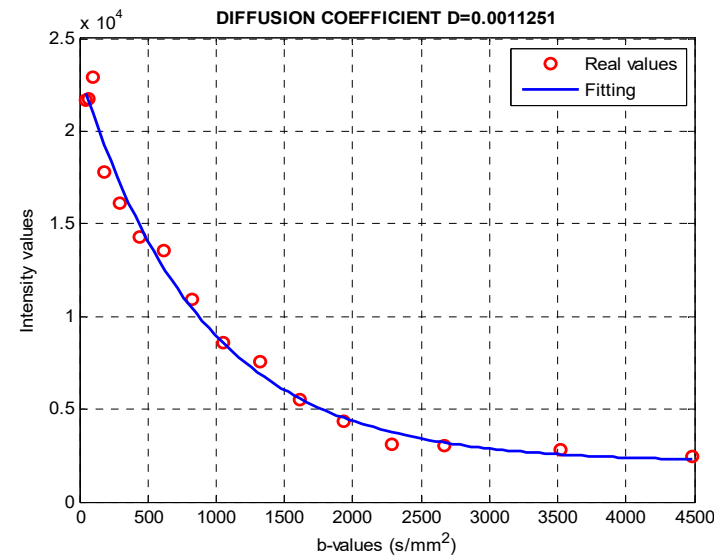
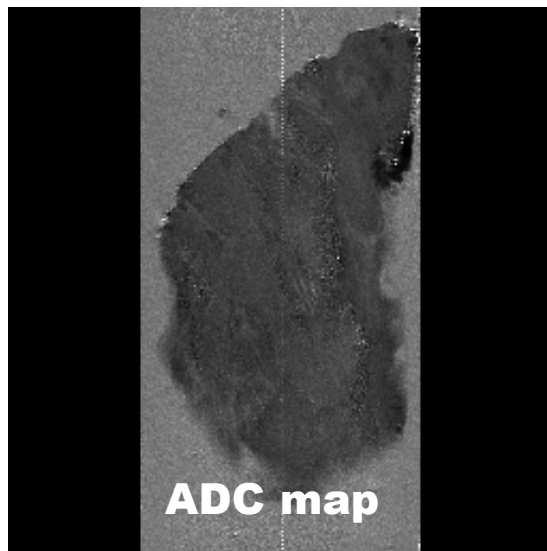


⌘ Method 3: Exponential with baseline.

- Compensation of the biexponential behavior of some curves by introducing a baseline → Nonlinear regression using customized models

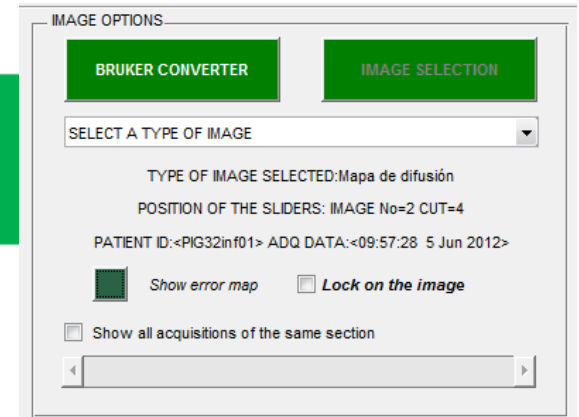
$$S(b) = S_0 [1 + \xi e^{-bD}]$$

⌘ Better approach (reliable data and image) but slower operations



Results

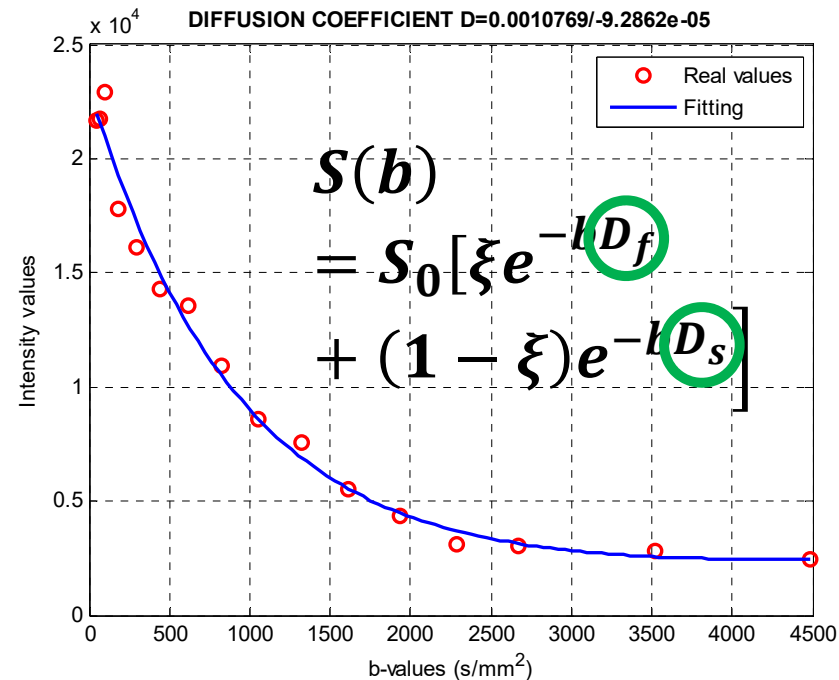
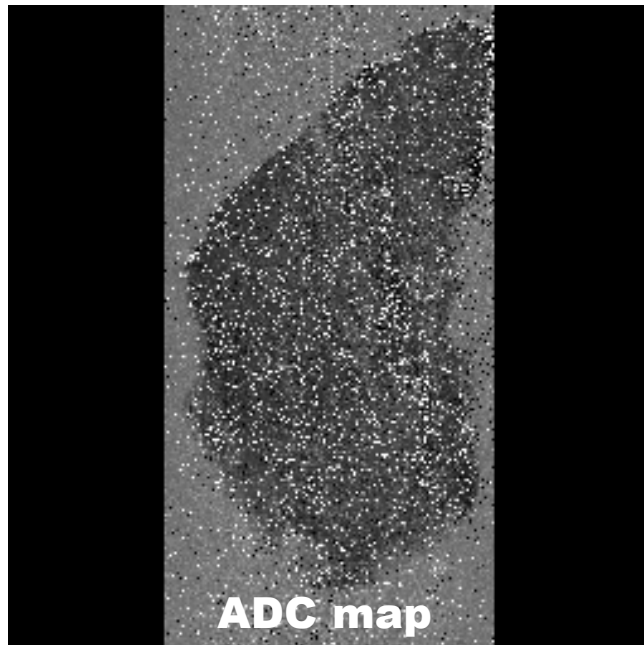
Image Options Maps



⌘ Method 4: **Biexponential.**

➤ Curve fitting using nonlinear regression, with previous models

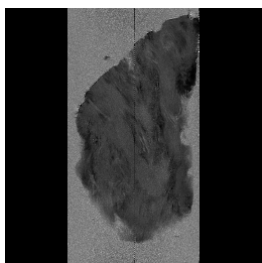
⌘ Perfect fitting results but problems with the resulting image



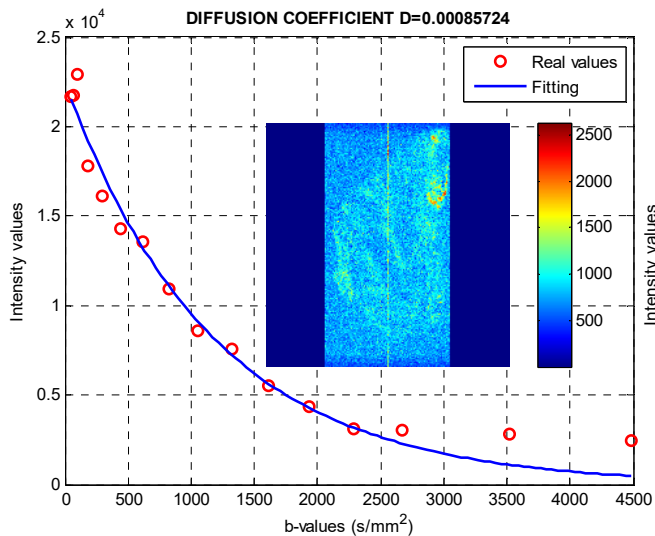
Results

Image Options Maps

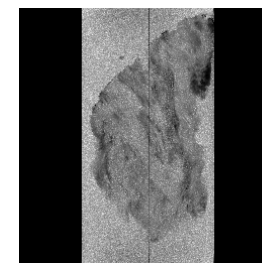
**High resolution
exponential**



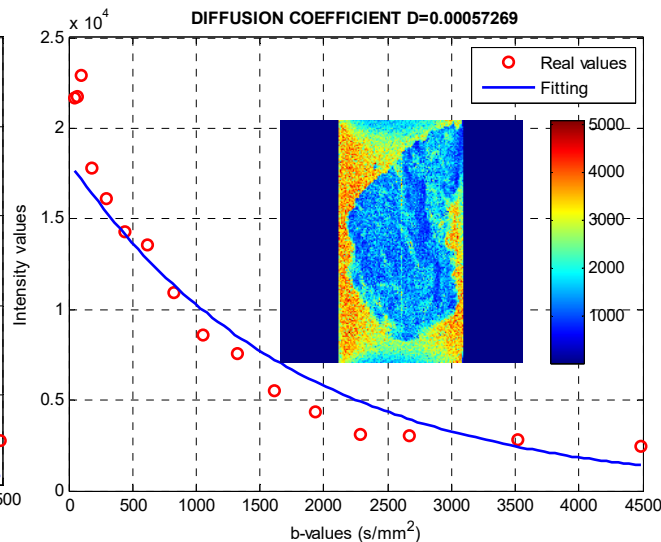
11.81 min/slice *



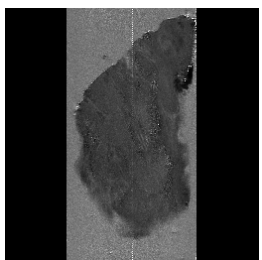
**Low resolution
exponential**



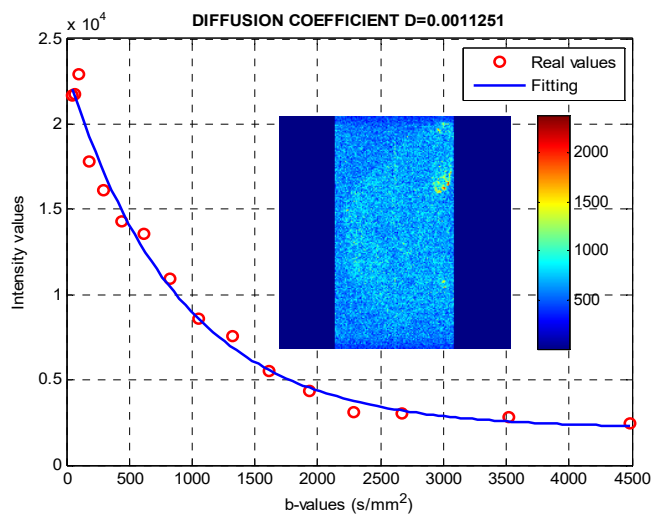
1.41 min/slice *



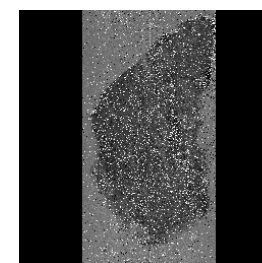
22.45 min/slice *



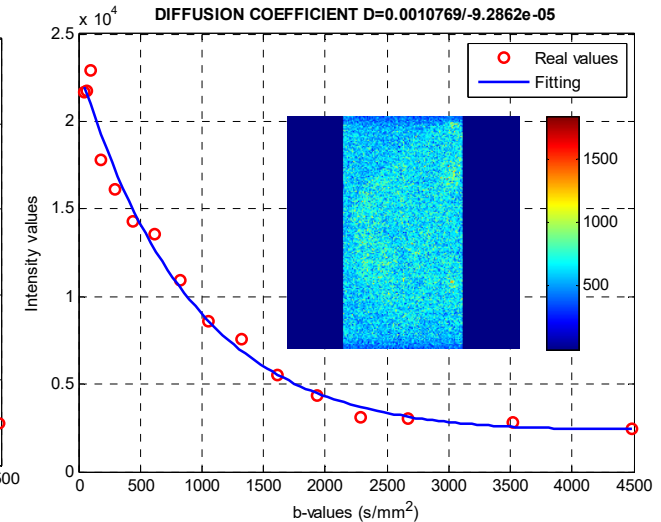
**Exponential
with baseline**



18.91 min/slice *



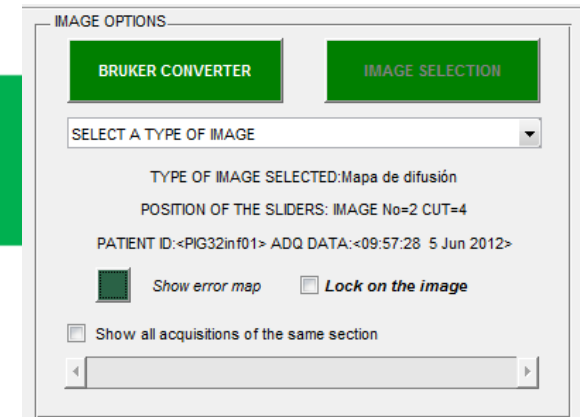
Biexponential



* Tested with a Dell Computer with Intel Core i7-4790 Processor, 16 GB of RAM and Windows 7 Professional 64 bit

Results

Image Options Maps

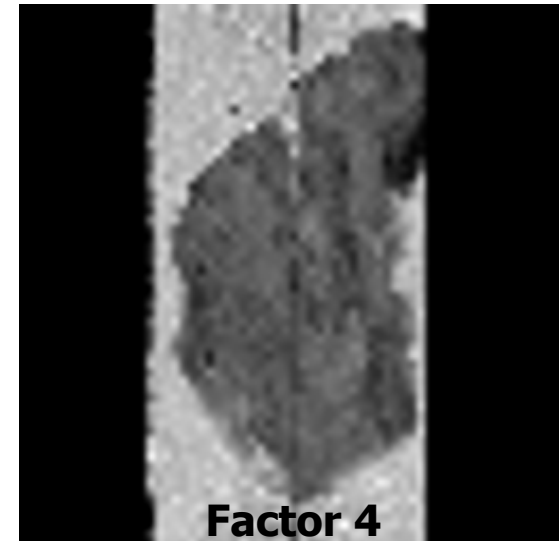
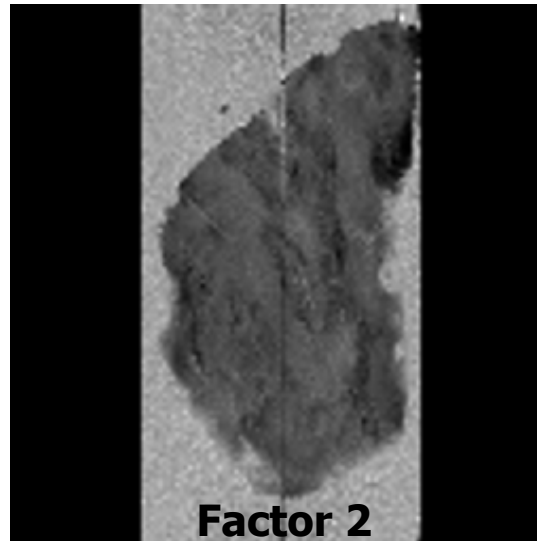
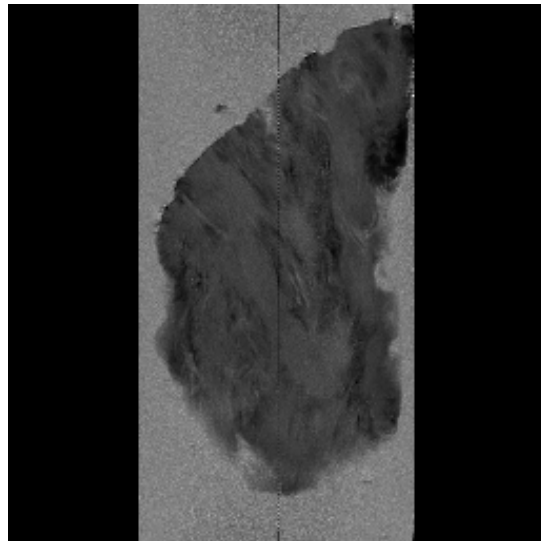


⌘ The duration of the process is very variable:

- It depends on the selected fitting method and the power of the computer.
- Generally SLOW.

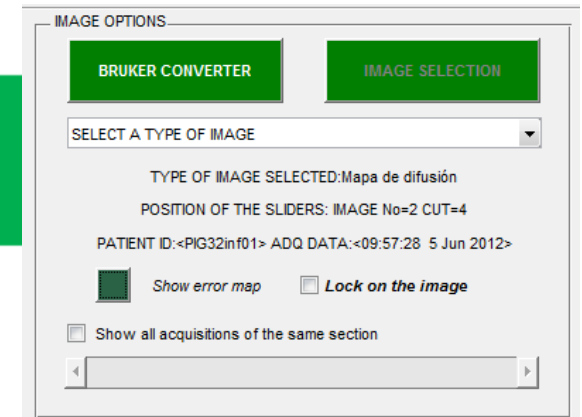
⌘ **Downsampling**

- Decimate the image: fitting method applied to a reduced number of pixels and the rest of the pixels reconstructed by interpolation.
- Decrease of the quality of the map but faster process



Results

Image Options Error Maps



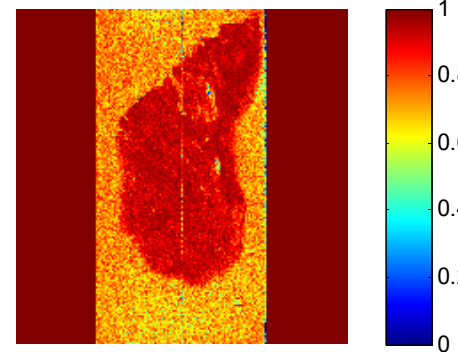
⌘ Color-based Error Maps

- Wide view of the differences between the original data and its approximated curve
- Each pixel of the Error Map represents the error caused when applying the fitting on the respective data.

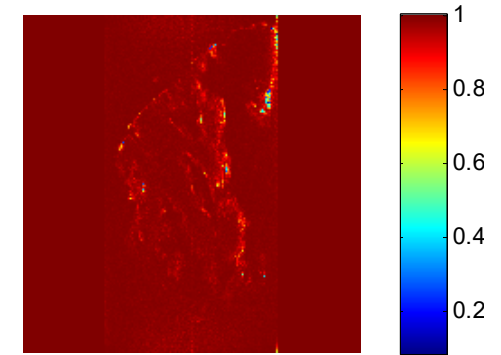
- R-squared error map:

$$SST = \sum_{i=1}^n (y_i - \bar{y})^2 \quad SSR = \sum_{i=1}^n (\hat{y}_i - \bar{y})^2 \quad R^2 = \frac{SST}{SSR}$$

Low Resolution Exponential Method

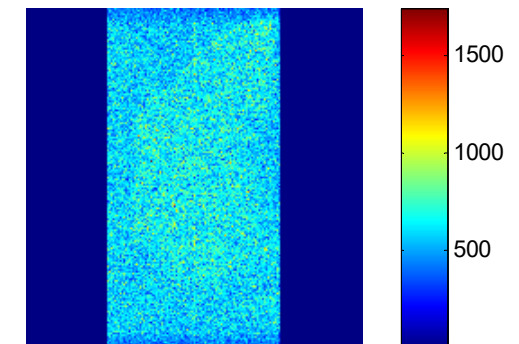
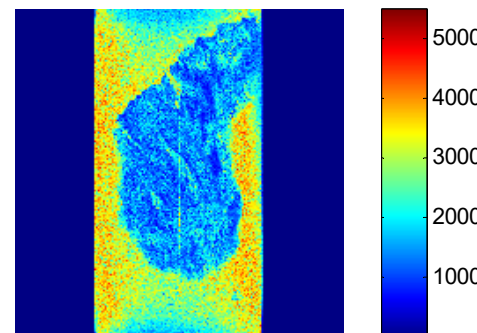


Biexponential Method



- RMSE error map:

$$RMSE = \sqrt{MSE} = \sqrt{\frac{1}{n} \sum_{i=1}^n (\hat{y}_i - y_i)^2}$$



Results

Image Options Error Maps

IMAGE OPTIONS

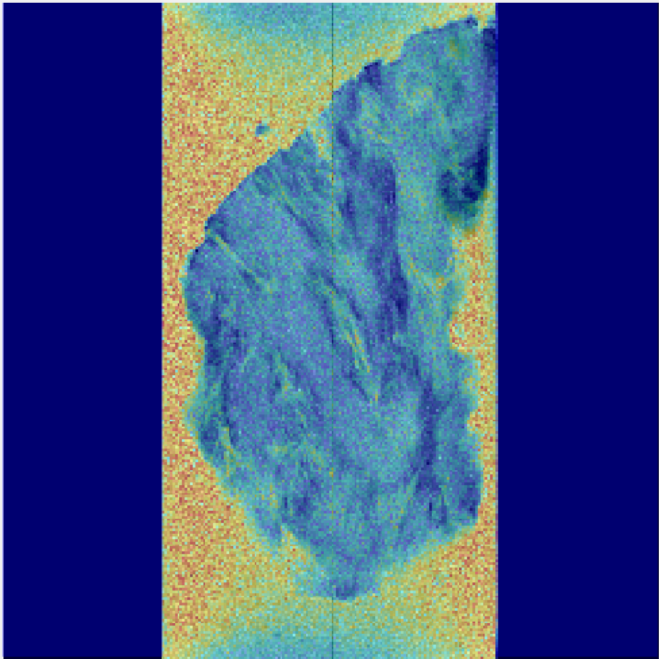
BRUKER CONVERTER **IMAGE SELECTION**

Imagen potenciada en T2

TYPE OF IMAGE SELECTED: Mapa de difusión
POSITION OF THE SLIDERS: IMAGE No=2 CUT=3
PATIENT ID: <PIG32in f01> ADQ DATA: <09:57:28 5 Jun 2012>

Show error map **Lock on the image**

Show all acquisitions of the same section



SEGMENTATION OPTIONS

NEW REGION **MERGE**

SEGMENT **CUT**

ADD REGION **DIVIDE**

LOCK AREA WINDOW

ROI OPTIONS

DRAW ROI LOCK Selected ROI: 5

TIPOS DE ROI:

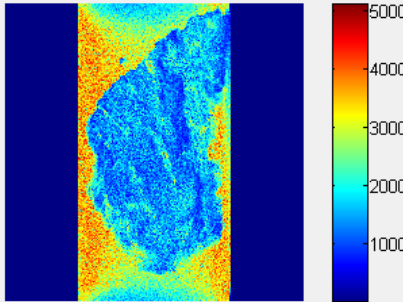
CIRCULAR ROI Copy ROI

SQUARE ROI Paste ROI

POLIGONAL ROI Delete selected ROI

HANDMADE ROI Delete all ROIs

Hide all ROIs



ERROR MAP (ROOT MEAN SQUARE ERROR)

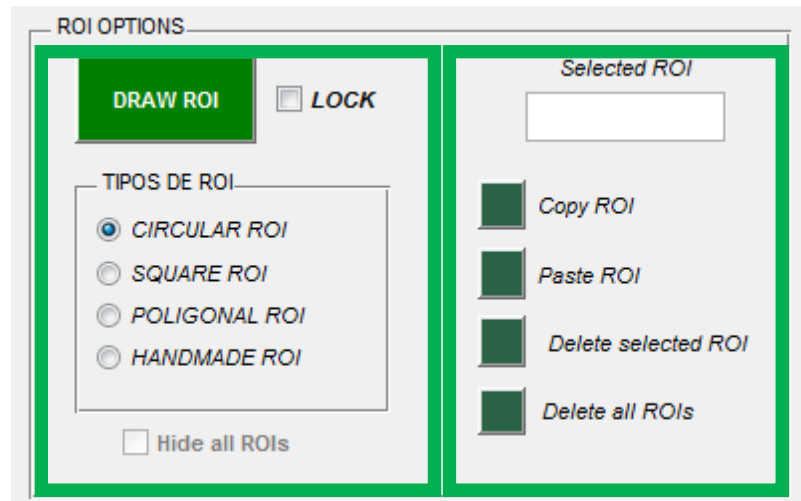
	ROI AREA	CUT	No IMAGE	TYPE OF IMAGE	MEAN	STD	MIN	MAX	SUBJECT ID
1	3384	4	1	Imagen potenciada en T2	7.8704e+03	1.4969e+03	1448	14666	<PIG32in f01>
2	441	3	1	Imagen potenciada en T2	9.8811e+03	979.1478	5003	12799	<PIG32in f01>
3	1040	1	2	Mapa de difusión	4.1812e-04	1.1243e-04	1.2665e-04	8.3129e-04	<PIG32in f01>
4	803	4	2	Mapa de difusión	5.8857e-04	1.0713e-04	1.1682e-04	9.6617e-04	<PIG32in f01>

Enter the name of the .xls file to be created

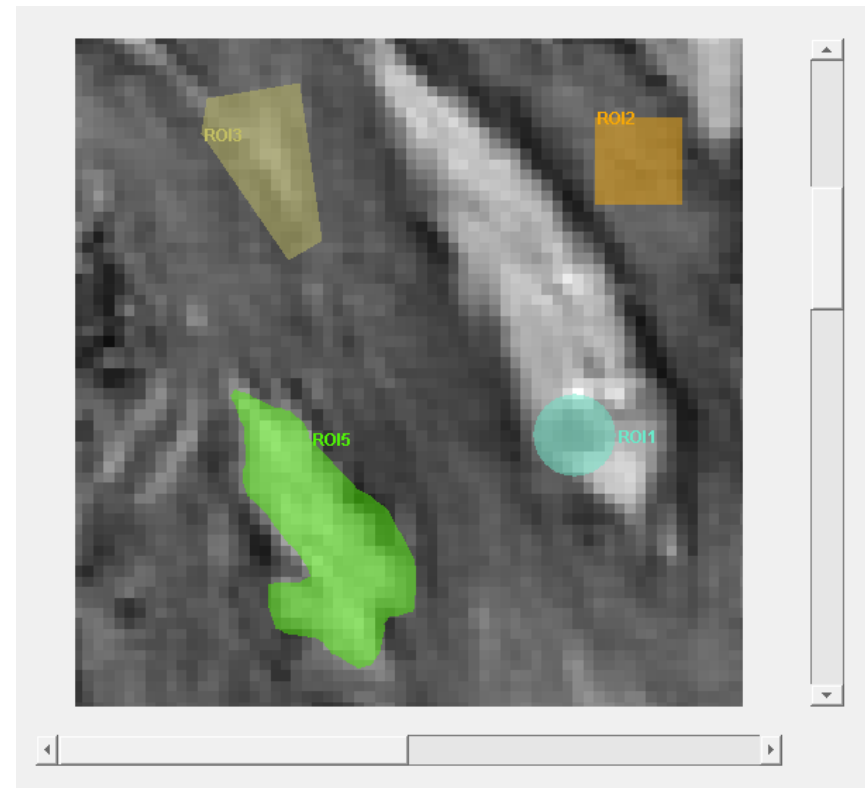
Export Excel **Export MATLAB**

Results

ROI options

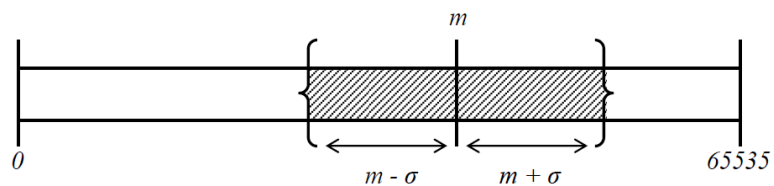
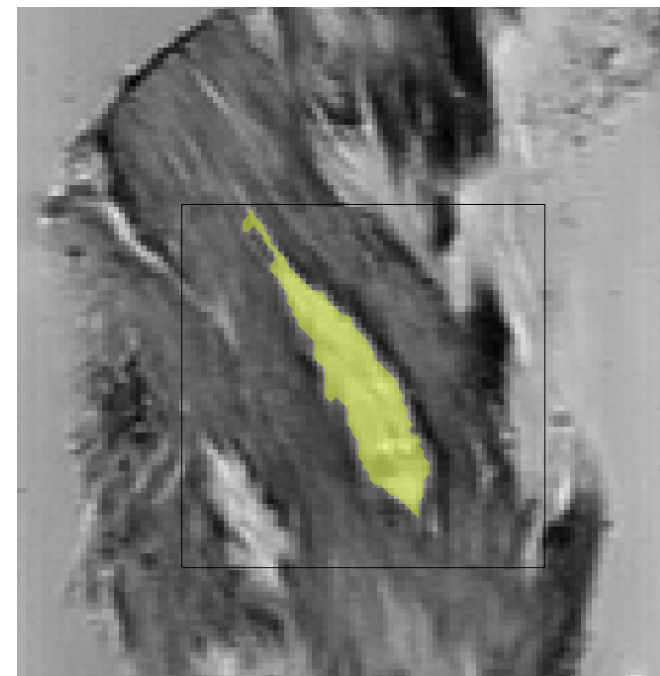
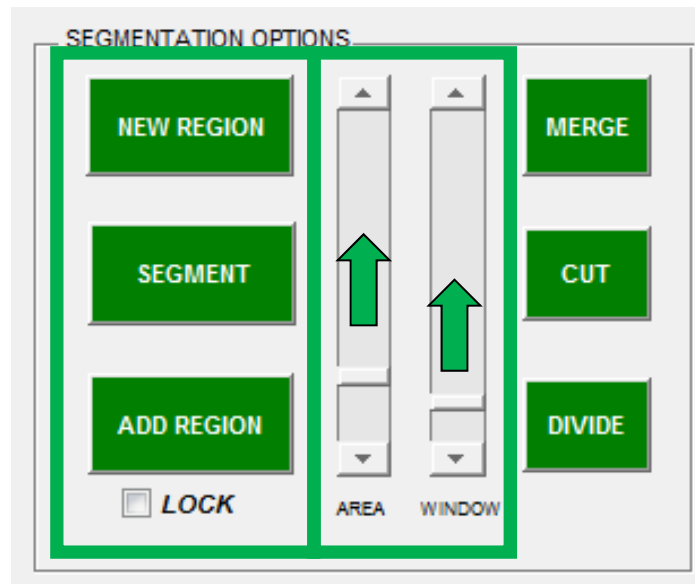


- ⌘ ROI area, in number of pixels
- ⌘ Slice number
- ⌘ MR microimage number
- ⌘ Type of image
- ⌘ Mean value of the pixels of the ROI
- ⌘ Standard deviation of the pixels of the ROI
- ⌘ Minimum of the ROI
- ⌘ Maximum of the ROI
- ⌘ Identifier of the sample
- ⌘ Acquisition date of the sample



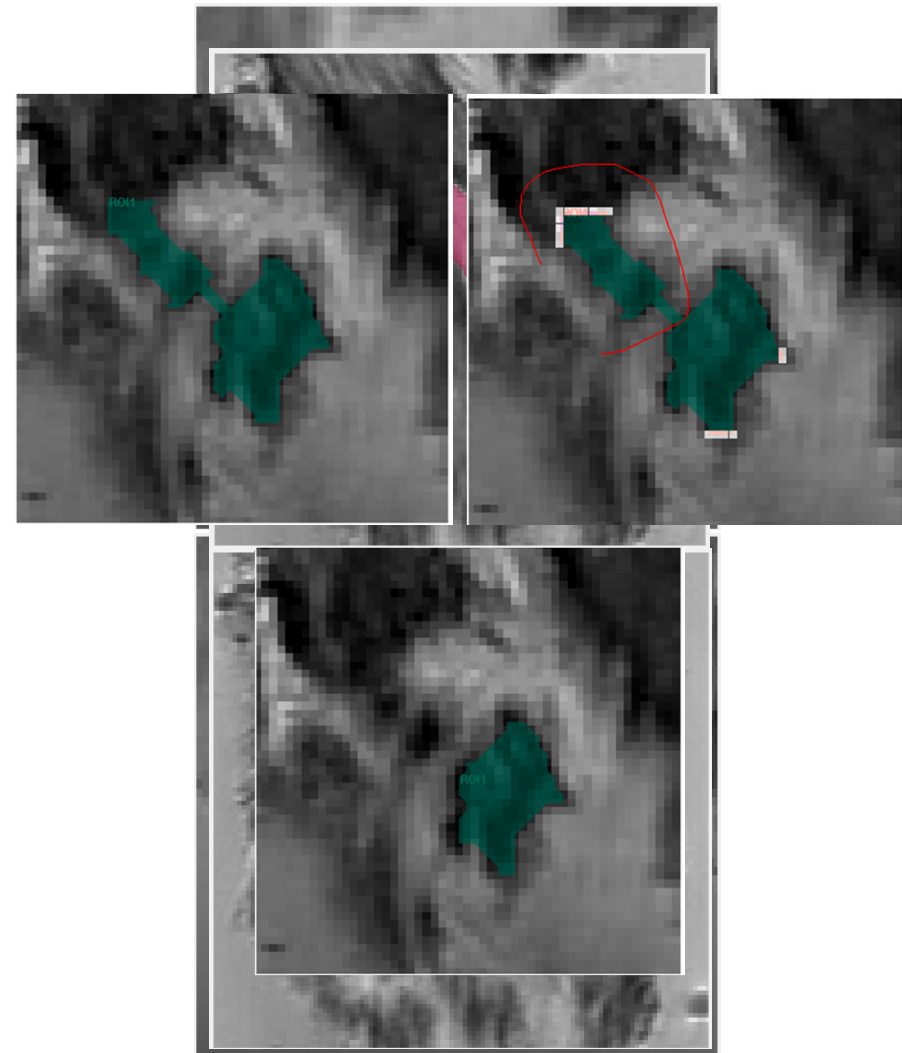
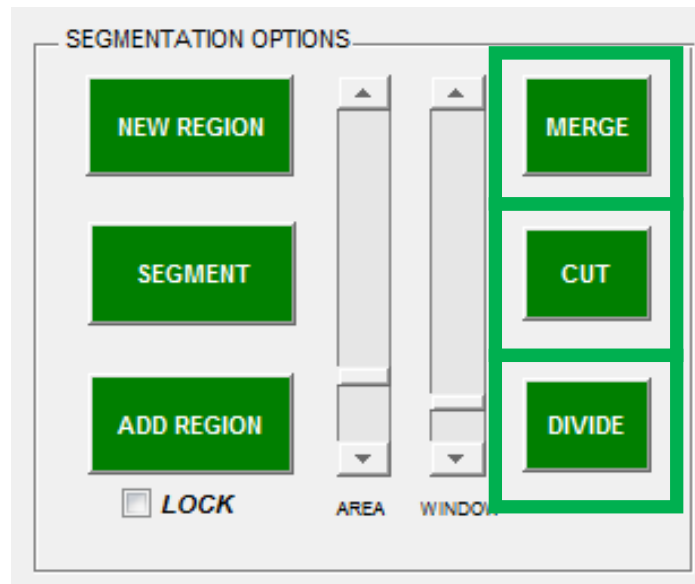
Smart and semiautomatic selection of regions

- **Region-growing method:** Region growing criterion based on an "analysis window"



Results

Segmentation Options



Conclusions

- ⌘ Development of an intuitive tool to perform virtual histologies by analyzing MR microimages of swine infarcted heart samples.
 - Processing of 5 type of MR microimages.
 - Implementation of 4 types of exponential fitting methods in order to obtain ADC, T2 and T2* maps.
 - Evaluation of the fitting results using Error maps.
 - Image analysis using ROIs.
 - Smart selection of regions using segmentation methods.

- ⌘ The results have been tested comparing them with previously validated virtual histologies analysed with *Paravision* (Bruker Biospin, Ettlingen, Germany).

- ⌘ The tool is currently being used by medical personnel of the Molecular Imaging and Metabolomics Group (UIMM) of the Fundación de Investigación of the Hospital Clínico Universitario de Valencia (Valencia, Spain).

Workshop on Reconstruction Schemes for MR Data
17th August 2016

Magnetic Resonance MicroImaging of a Swine Infarcted Heart: Performing Cardiac Virtual Histologies

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