

# MP<sup>3</sup> : Medical software for Processing multi-Parametric Images Pipelines

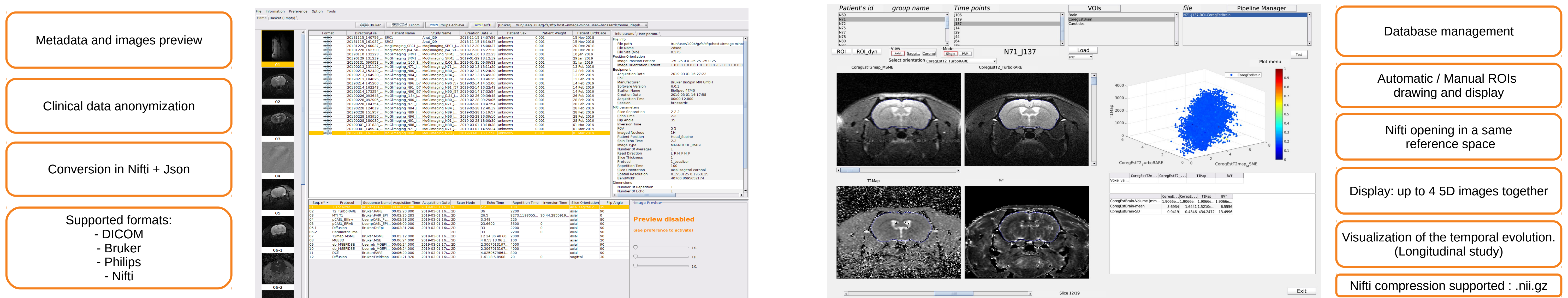


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The constant improvement of storage capacities and supercomputers allow researchers to study huge amounts of data. These studies usually imply complex processing applied to whole or parts of those data. Classical medical softwares, although efficient and useful to process a few data, are becoming obsolete when dealing with huge databases and repetitive tasks. MP<sup>3</sup> is a free, open-source software able to order, display, and wisely process medical images by any kind of pipeline, from simple to complex ones, from well known to homemade ones. Testing MP<sup>3</sup> will allow you to analyse up to 4 images together, and co-register them, or even draw regions of interest (ROIs). Our software has been tested in different studies, as clinical and preclinical MRI or clinical CT ones, and has been appreciated for its ease of use and its intuitiveness.



DICOM  
Bruker  
Philips  
Nifti

**Viewer + Converter**  
Since Java 8  
(O. Montigon)

Project  
Nifti + Json

**Viewer**  
Since MATLAB 2017b  
(B. Lemasson)

Nifti + Json  
Database

**Pipeline Manager**  
Since MATLAB 2017b  
(C. Brossard)

Figure 3 – Overview of the software architecture

## + 35 modules availables among which:

- Relaxometry
- VSI : Vessel Size Index (*Tropea L.*)
- Perfusion
- CBF : Cerebral Blood Flux (*Hirschler L.*)
- Oxygenation (*Christen T.*)
- Permeability (*Lemasson B.*)
- Arithmetic functions
- Bias correction: MICO algorithm
- Brain extraction
- Some functions from FSL
- Some functions from SPM
- Clustering (*Arnaud A.*)

## Easy creation of new modules:

- Normalized Matlab function
- Define the module's input and outputs
- Define its parameters
- Code the module's core in Matlab
- Move the file in the related folder
- Close and re-open the Pipeline Manager
- Template available!

Free, open-source software, downloadable, editable, and documented on:

<https://github.com/nifm-gin/MP3.git>

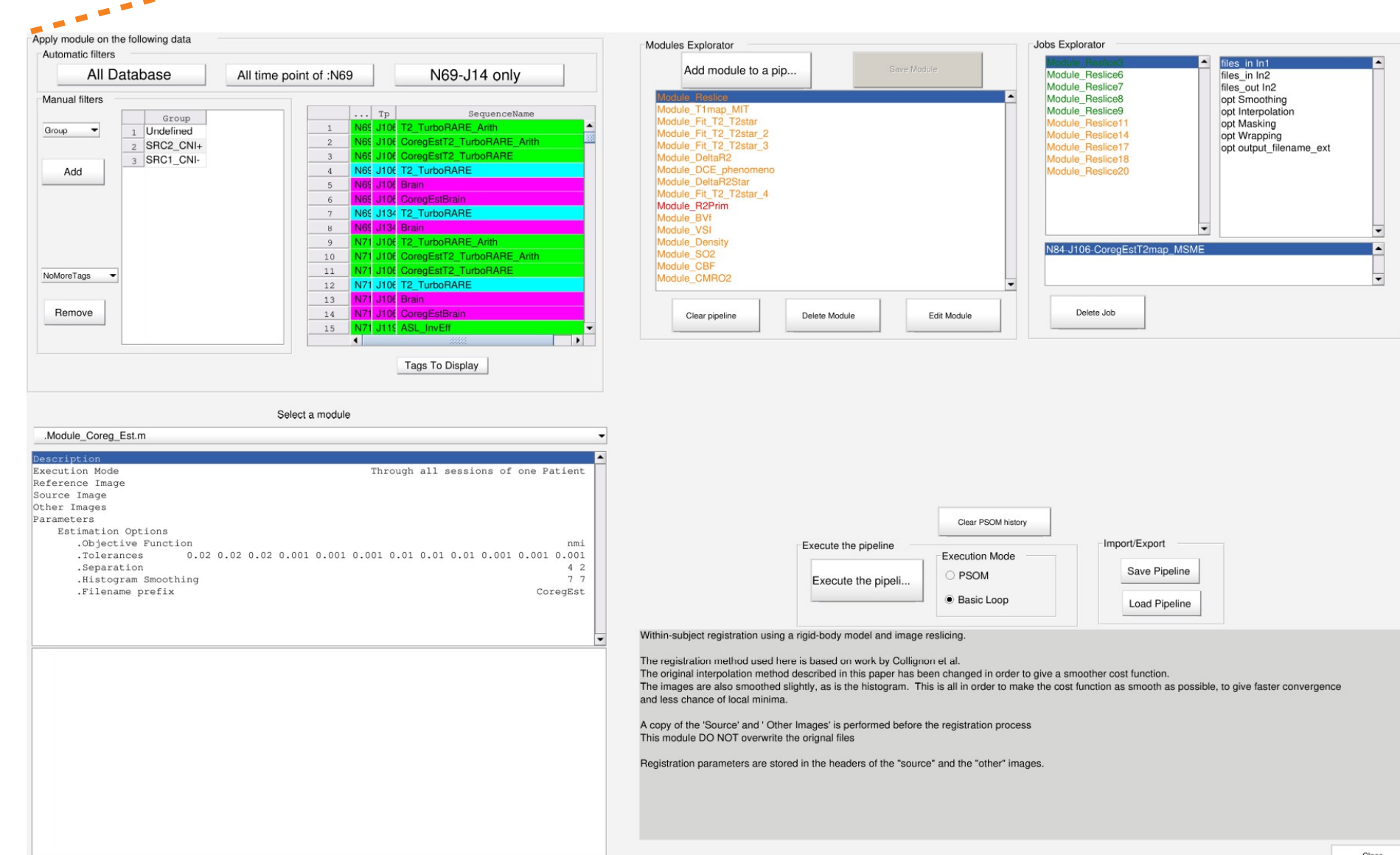
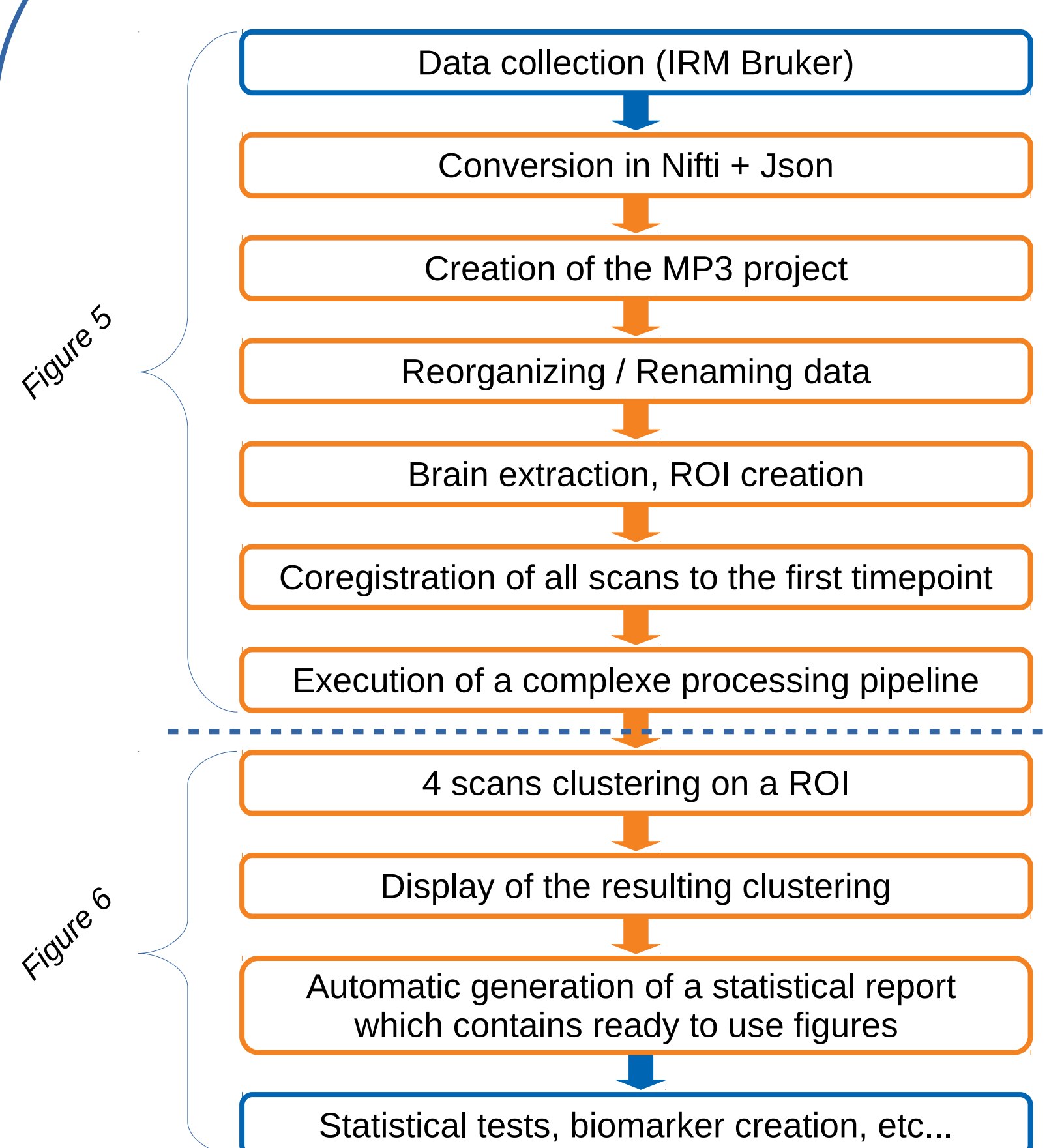


Figure 4 – Pipeline Manager screenshot:  
Creation, modification and execution of complex pipelines.

- Filtering of the data to process
- Set a module's parameters
- Automatic jobs generation from a module + the database to process
- Create, modify, save and share pipelines
- PSOM [1] integration: Wise and optimized execution on several cores or cluster
- Historic save: How was obtained an image?
- Results reproducibility

MP<sup>3</sup> was tested on several different projects. From preclinical to clinical, from IRM to scanner, and is now used within our laboratory team and by some researchers in France and abroad. An example of a study conducted thanks to MP<sup>3</sup> : **Glioblastome's heterogeneity - clinical and preclinical study**. MoGlimaging project, HTE programm.



Whole processing and analysis pipeline applied during the preclinical and/or the clinical study. In orange stand the operations computed in MP3. In blue stand the ones computed outside.

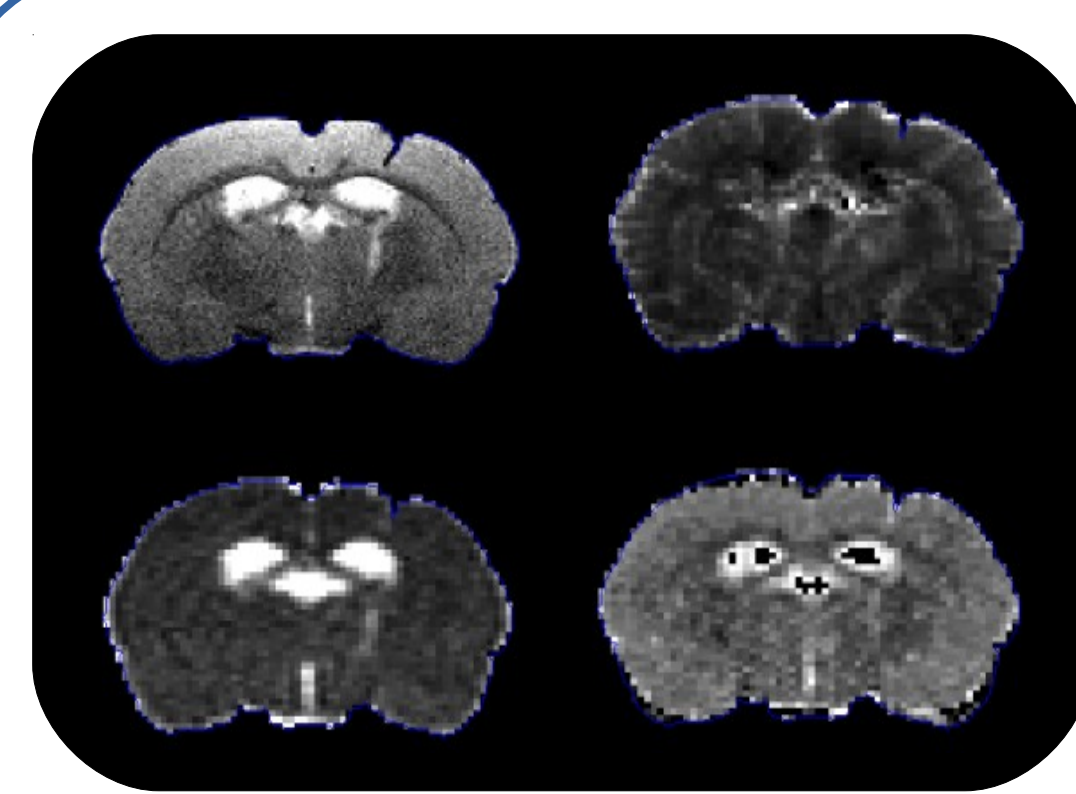


Figure 5 – On the left, 4 preclinical images [2] (T2, Bv, ADC, T1map) obtained thanks to the complex analysis pipeline displayed on the right: Brain extraction + Coregistration of the 2 subjects + analysis pipeline. Data and results non published.

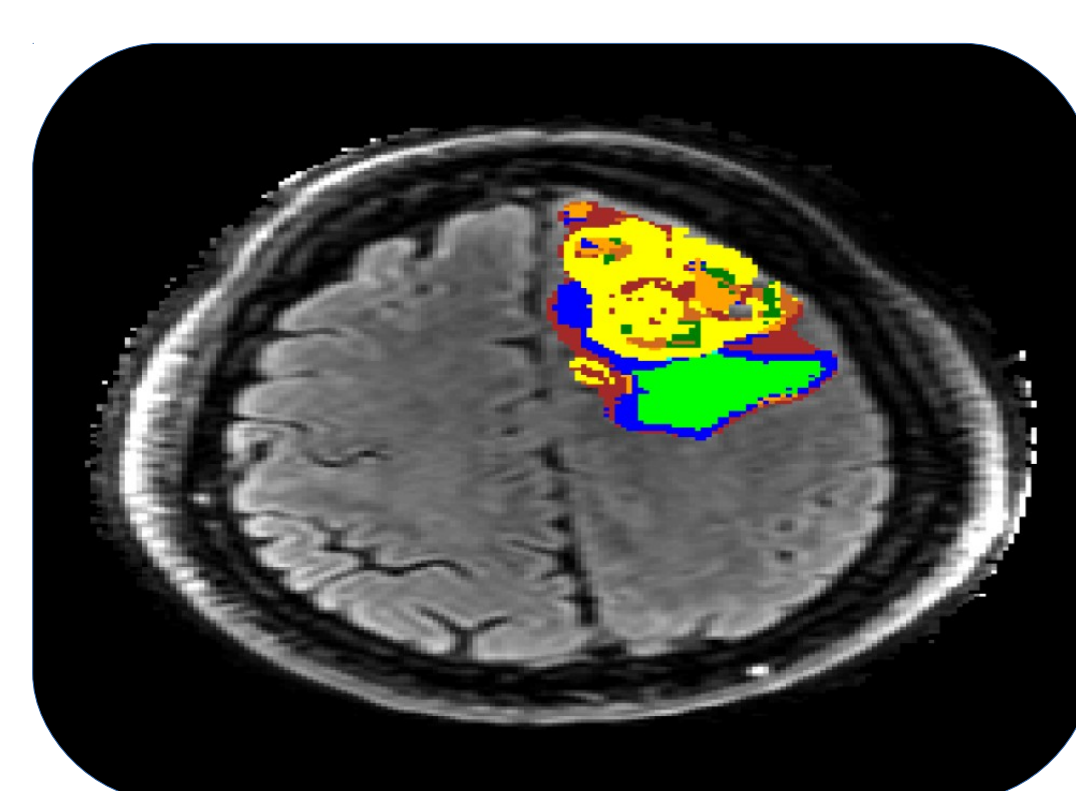
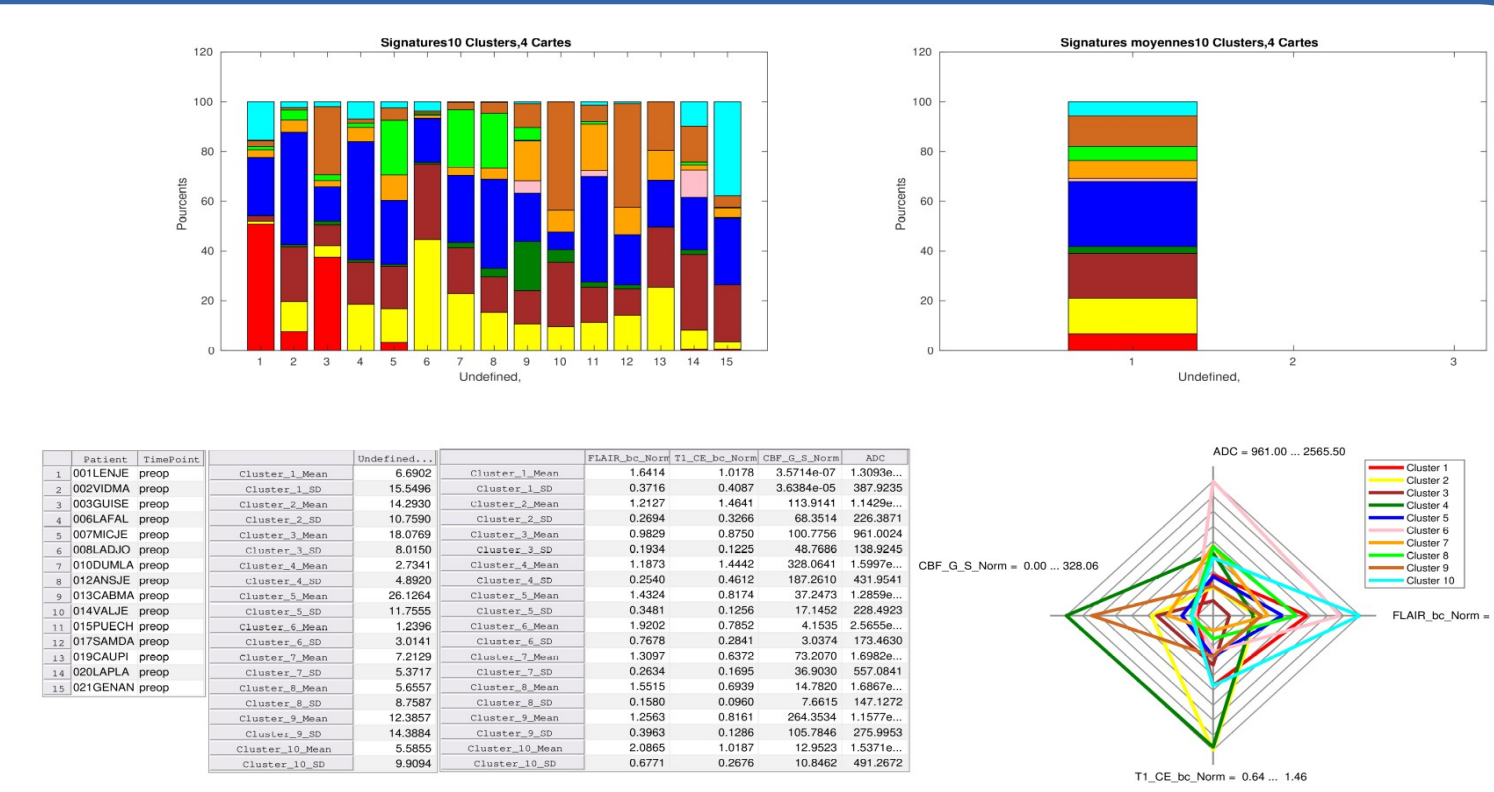


Figure 6 - Clinical FLAIR scan with a 10 classes clustering computed on 4 scans (T1, FLAIR, ADC, CBF), on 15 patients of the STEMRI cohort. The related statistical report is displayed on the right. Data and results non published.



The clinical and preclinical studies led by B. Lemasson, within the Moglimaging project, in the frame of the HTE programm, are aimed to study the glioblastome's heterogeneity and to create biomarkers able to predict the patients clinical state or the radiologic diagnostic. The MoGlimaging project also allows to study the modalisation of the post surgery cavity or the cellular nature of the several areas of a heterogeneous tumor. The whole project is led by 8 french research teams.

