

# Shanoir: Software as a Service Environment to Manage Population Imaging Research Repositories

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Bienvenue dans Shanoir

|                    |                          |
|--------------------|--------------------------|
| Nom d'utilisateur  | <input type="text"/>     |
| Mot de passe       | <input type="password"/> |
| Se souvenir de moi | <input type="checkbox"/> |

Connexion

[shanoir-contact@lists.gforge.inria.fr](mailto:shanoir-contact@lists.gforge.inria.fr)

# What is Shanoir ?

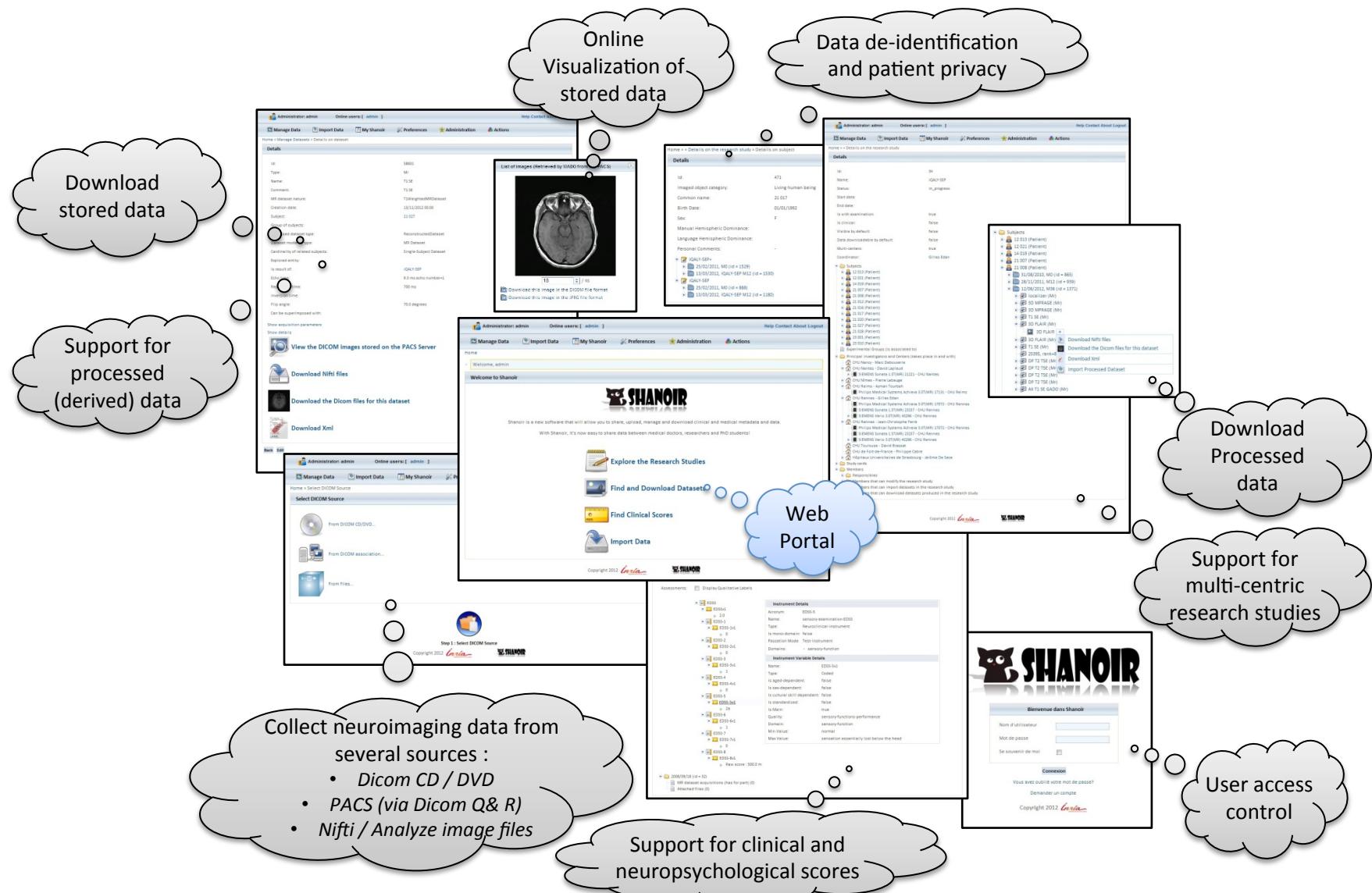
- An open source web application designed to:
  - Archive and Index
  - Search and Retrieve
  - Share
- With:
  - a user-friendly **secure** web access
  - a database model build on an **ontology**<sup>1</sup>  
(OntoNeuroLOG, from the NeuroLOG<sup>2</sup> project)
- In order to:
  - Enhance data availability and integrity
  - Structure the data / Manage data provenance
  - Facilitate collaborative research works
  - Pool acquisition resources





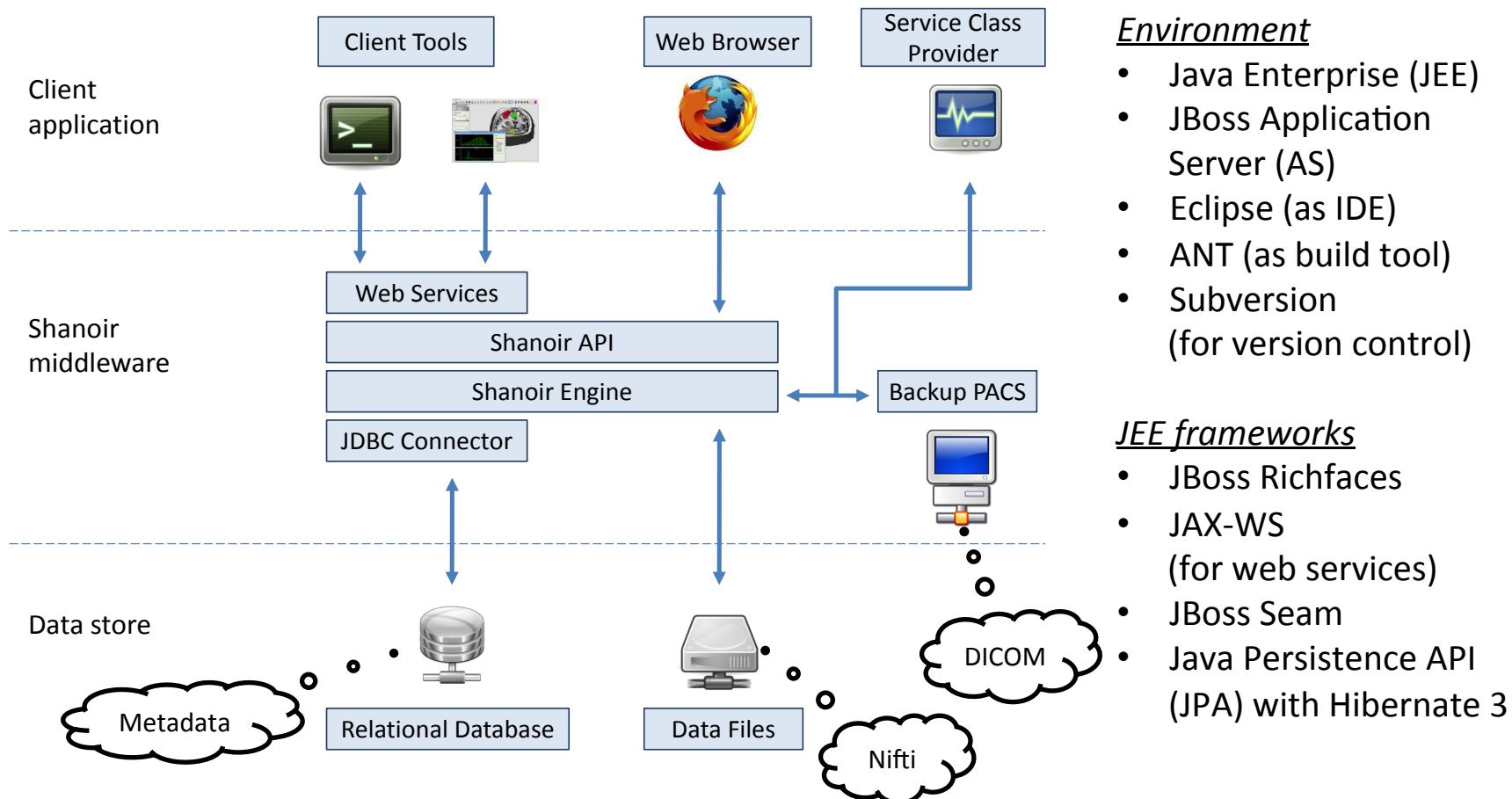
# SHAring NeurOImaging Resources

## An open source web platform for population imaging



# Software architecture

Shanoir is organized as a repository of neuroimaging files coupled with a relational database where additional metadata are stored.



## Environment

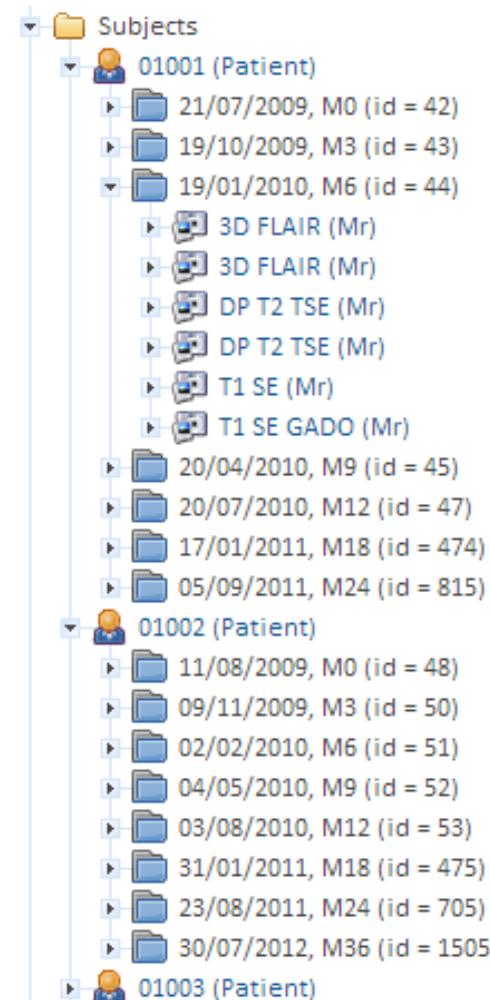
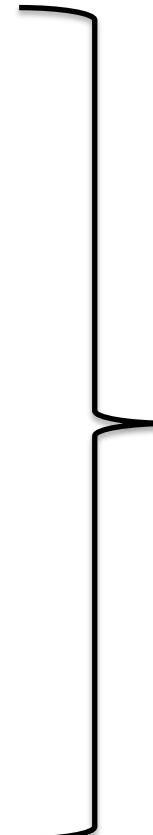
- Java Enterprise (JEE)
- JBoss Application Server (AS)
- Eclipse (as IDE)
- ANT (as build tool)
- Subversion (for version control)

## JEE frameworks

- JBoss Richfaces
- JAX-WS (for web services)
- JBoss Seam
- Java Persistence API (JPA) with Hibernate 3

# Data organization

- Study
  - Subject
    - Examination (date)
      - Dataset
      - Dataset
    - Examination (date)
      - Dataset
      - Dataset
    - Subject
      - Examination (date)
        - Dataset
        - Dataset
      - Examination (date)
    - ...





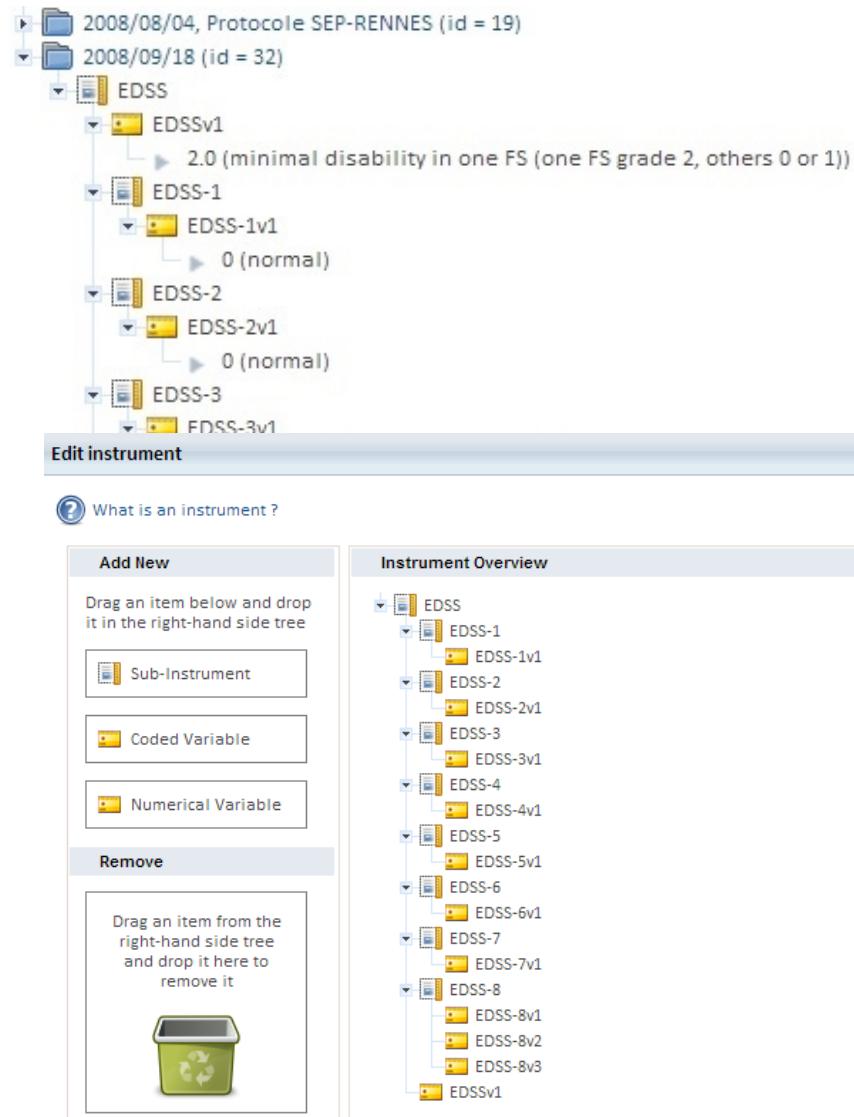
# The Study card mechanism

**Purpose: Alignment of Ontology concepts to the actual imported data**

- Objectives:
  - Assign in a unique semantics meta-data that are not natively in the DICOM format
    - e.g. Sequence MR Contrast (T1, T2, T2\*, DP, ...), physical parameters of the MR sequence, MR head coil, parallel acquisition technique, contrast agent (Gd, ...)
  - Reduce the workload to assign the meta-data for the user (defined once)
  - Allow an automatic quality control of the conformity of the data to the protocol
- How it works:
  1. The user defines a set of conditions based on DICOM tag(s) value  
(e.g. on "Serie Description", "Protocol Name", "Echo Time", ...)
  1. Each set of conditions corresponds to a set of rules
  2. If a serie fulfills a set conditions, the corresponding set of rules is applied
- Example :
  - **If « Serie Description » contains « 3D T1 Gado » then**
    - AcquisitionContrast > T1
    - MrDatasetNature > T1WeightedMRDataset
    - ContrastAgentUsed > GADOLINIUM
    - MrSequencePhysics > Magnetization prepared spoiled GRE
    - SliceOrientationAtAcquisition > sagittal
- ➔ Information you cannot find in DICOM tags, can be attached as metadata.
- Each Study card is applied during the DICOM import and depends on the study, the center and its acquisition equipment.

# Clinical Scores Management in Shanoir

- Instrument-based assessments (i.e. neuropsychological tests such as **EDSS** or **MMS**) results in Clinical Scores
  - Shanoir offers features for hosting such scores and assign them to the related stored image data
  - Export features are available for different formats (Excel, CVS, XML...)
  - The “instrument” database is extendable thanks to a user-friendly interface



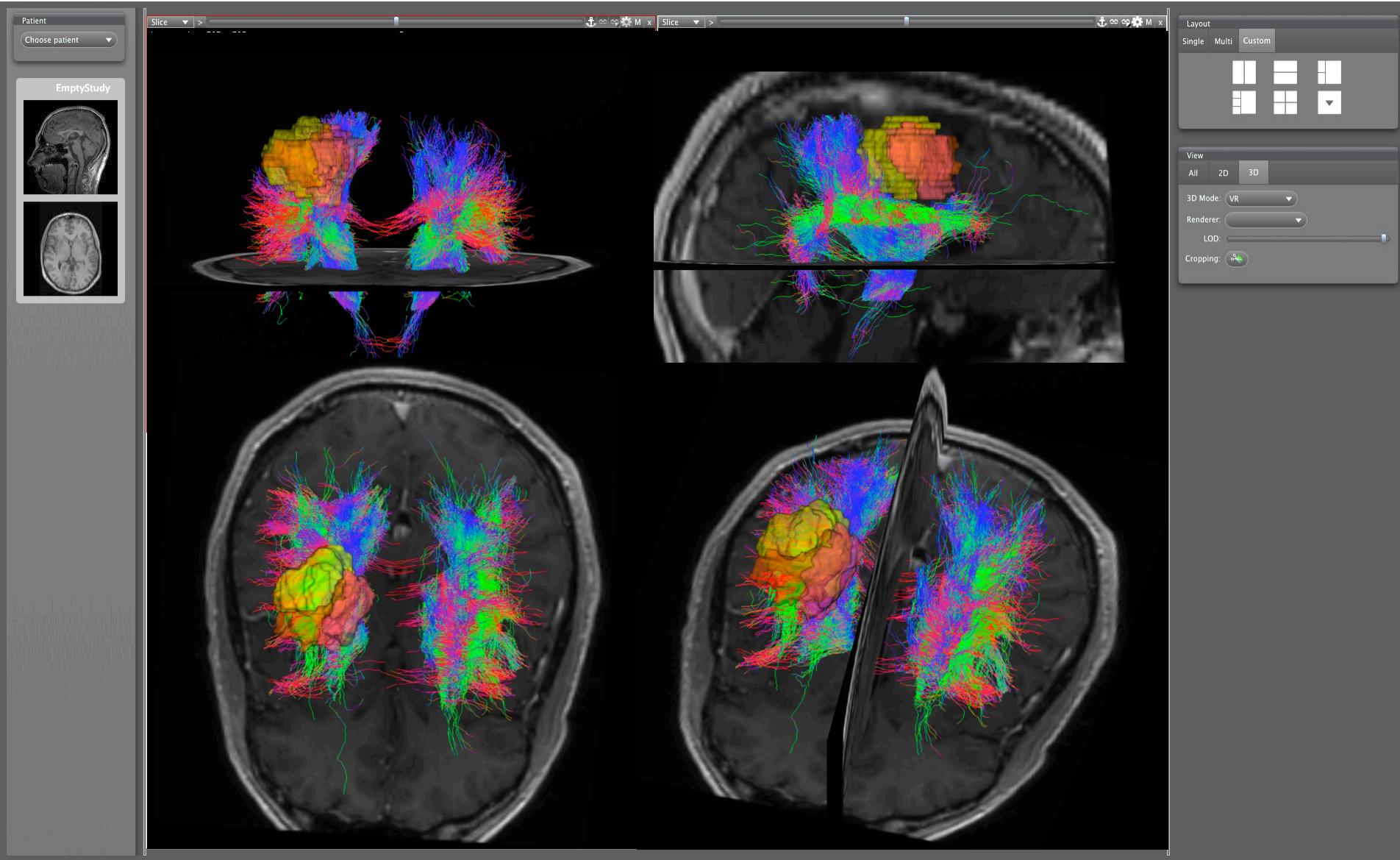


# Client applications

- Client applications can query and retrieve the data from the Shanoir server through web-services (SOAP).
- Two libraries are publically available to implement this feature:
  - **ShanoirTk** (Java toolkit)
  - **QtShanoir** (C++ client) for:
    - browsing the data inside a graphical widget
    - Import derived (processed) data with registration to the source images, with assignment of specific semantic concepts (i.e. “Processing instrument”)
    - QtShanoir has been integrated as a plug-in in MedInria<sup>3</sup>, for advanced image processing software.



# SHANOIR in MedInria





# SHANOIR: Import Derived Data

- Objective

- Import processed data sets
- Register the derived data to the source one
- Align the meta-data to the ontology
- Allow batch process import

The image displays three screenshots of the SHANOIR Import Derived Data software interface, illustrating the workflow for importing derived data.

**Screenshot 1: Step 4 - Select the list of process.**

This window shows a list of available processes:

- Segmentation
- Boundary surface Based segmentation
- Region based segmentation
- Boundary surface and region based segmentation
- Brain segmentation
- Tissues segmentation
- Subcortical segmentation
- Lesion segmentation
- Reconstruction
- Registration
- Normalization
- Registration with distortion correction
- Affine registration
- Multi modality affine non-rigid registration
- Mono modality non-affine registration
- Multi modality non-affine registration
- Resampling
- Cropping
- Re-orientation
- Datasets addition
- Datasets subtraction
- Datasets multiplication
- Datasets division

Buttons on the left include: Select files, Select input Datasets, Choose Files/Inputs, and Select process.

**Screenshot 2: Step 2 - Select the input Datasets corresponding to files early selected.**

This window shows a list of selected datasets:

| Description          | Type    |
|----------------------|---------|
| patient1             | SUBJECT |
| Protocole SEP-RENNES | EXAM    |
| T1 3D N NAV          | DATASET |
| T1 3D AX 138coupes   | DATASET |
| T1 SE                | DATASET |
| T1 SE GADO           | DATASET |
| FLAIR                | DATASET |
| DTI_16DIR            | DATASET |
| DUAL TSE 1           | DATASET |
| DUAL TSE 2           | DATASET |
| FLAIR AX             | DATASET |
| MS-patient2          | EXAM    |
| MS-patient3          | SUBJECT |

3 files selected.

**Screenshot 3: Step 5 - Match your files with the correct process and Datasets.**

This window shows a mapping table:

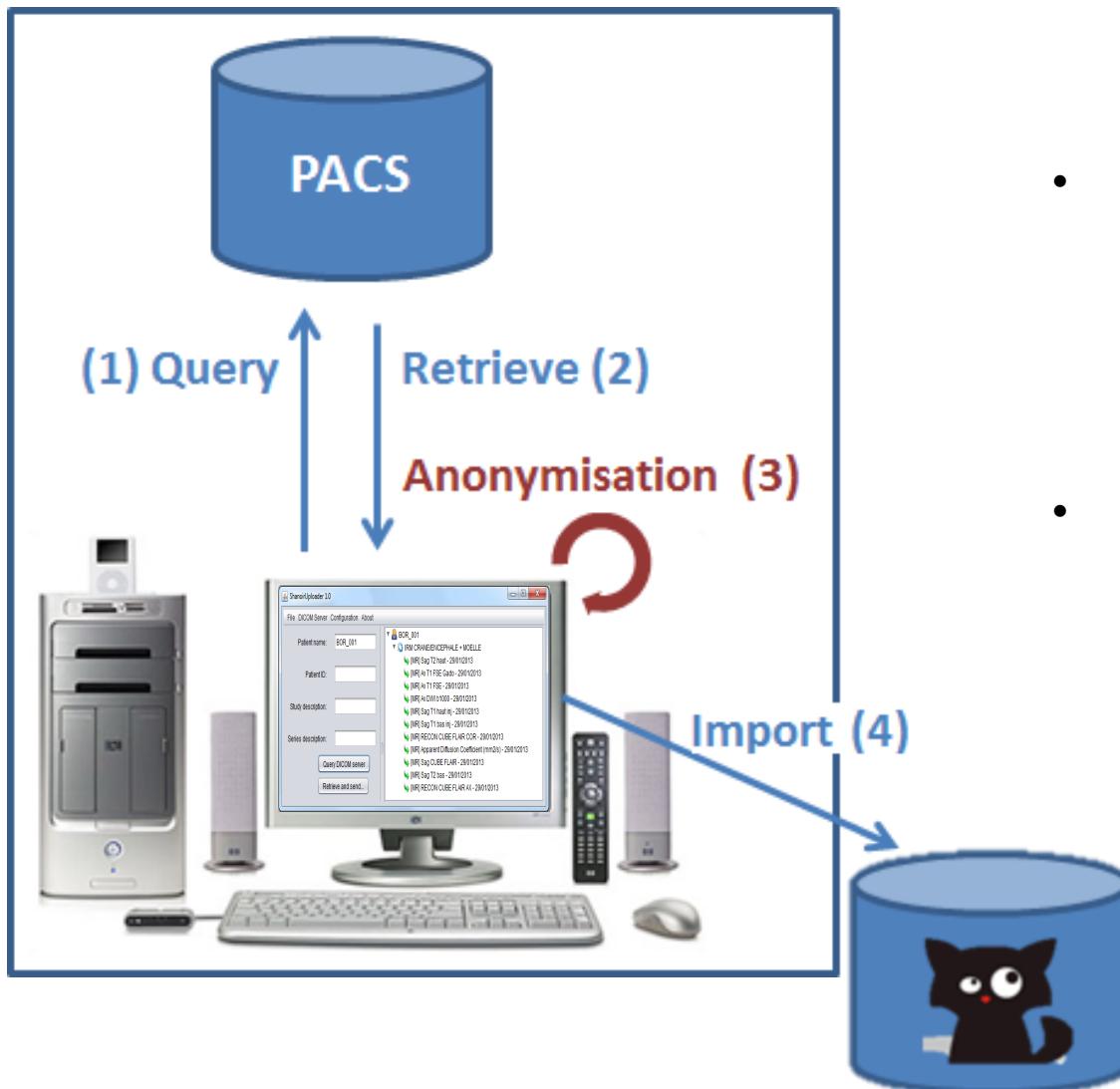
| Process                                | Segmentation                        | Resampling               | Cropping                 | MriDataset               | EegDataset               | MegDataset                          | PetDataset               | RegistrationDataset      | Spec                     |
|--|-------------------------------------|--------------------------|--------------------------|--------------------------|--------------------------|-------------------------------------|--------------------------|--------------------------|--------------------------|
| /Desktop/test/DUALTSECLEARs701a007.nii | <input checked="" type="checkbox"/> | <input type="checkbox"/>            | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| /Desktop/test/DUALTSECLEARs701a207.nii | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |



# Shanoir development Roadmap

- **ShanoirUploader** : make the import easier and safer
- **iShanoir** : iOS application for Ipad, increase the portability
- **Apache/SOLR integration**: makes query/ retrieve easier

# ShanoirUploader



## Functionalities

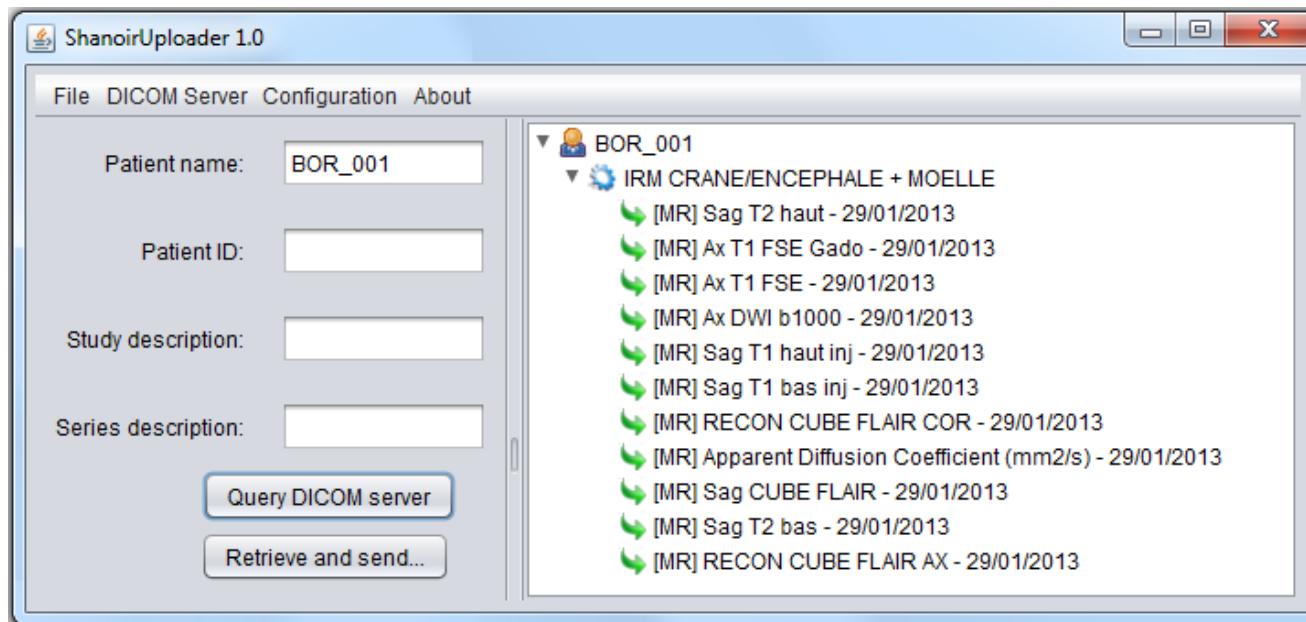
- Installed on the desktop
- Implemented with Java Web Start (JWS)
- At the MR console:
  - (1) Query & Retrieve from local PACS
  - Upload local data stored on the PACS (2)
  - On site Anonymization (3)
  - Storing the anonymized data to the Shanoir server (4)
- **Later on:** Et plus tard, connect to the Shanoir server to complete the registration of the data and resume import.

## Advantages:

- Easy and Fast
- Can be done on packs of data
- Can be performed by a technician
- Secured solution accredited by Hospitals IT managers

# ShanoirUploader

- Installed on the desktop
- Implemented with Java Web Start (JWS)
- Query & Retrieve from any PACS
- Futur functionalities:
  - Choosing local file for import
  - Drag-and-Drop of CD-ROMs
  - Local anonymization
  - Local NIfTI conversion
  - Local StudyCard changes





# Shanoir Integration

## Motivation

- Allow easy indexing and search of the data
- Allow a direct mapping between Shanoir ontology and SOLR catalogue
- Allow easy batch download
- Ease Interoperability between Shanoir database and other system (e.g. FLI-IAM interoperability project)

The screenshot shows the Shanoir web application running on localhost:8080. The top navigation bar includes links for Expert, Online users, Solr Search, Manage Data, Import Data, My Shanoir, Preferences, and Actions. The main content area features the Shanoir logo and a brief introduction: "Shanoir is a new software that will allow you to share, upload, manage and download clinical and medical metadata and data. With Shanoir, it's now easy to share data between medical doctors, researchers and PhD students!" Below this are four main buttons: "Explore the Research Studies" (with a notepad icon), "Find and Download Datasets" (with a brain scan icon), "Find Clinical Scores" (with a heart icon), and "Import Data" (with a download icon). The footer contains the Inria logo and the text "Copyright 2014".

This screenshot displays the Shanoir integration interface. It includes a sidebar for "Current Selection" showing "Viewing all documents!". The main content area is divided into several sections:

- Study Name:** Lists various MRI protocols: T1WI100 ASL DEM ASL IP AVCPOSTIM AngioIRM\_NATIVE\_QISS DEPAPATHIE DEPRESIST HEPAT\_M MS-REPAIR MS-SPI NATIVE Divers NCE MRA Perft1 SURFER Transfert USPIO-6 VP1PRO asl\_SEP asl\_tum transIRMF.
- Subject Name:** Lists subject IDs: 01001, 01002, 01003, 01004, 01005, 01006, 01007, 01009, 01010, 01011, 01012, 01014 (No CSI because protocol too long), 01015, 01017, 01019, 02002, 02003, 04007, 04008, 04012.
- Dataset Type:** Lists acquisition types: 3D FLAIR 3D MPRAGE AX DUAL\_dp T2 AX T2 CALC DP T2 TSE FIELD MAP LOCA HASTE MULTI ECHOS APNEE 32 CNX 20° MULTI ECHOS APNEE BODY 20° ERFUSION T2 Perfusion\_Weighted RELAXO T2 ELAKO T2 USPIO RELAXO T2STAR RELAXO T2STAR USPIO 2 EG 3D 1/2 T2 EG 3D 2/2 ep2d\_pcasl\_UI\_PHC REPOS localizer elCBF.
- Dataset Creation Date:** A calendar showing November 2009.
- Subjects:** A tree view showing "01001 (Patient)" with a child node "21/07/2009, M0 (id = 42)". This node has several sub-items: "RECO FLAIR CA CP (Mr)", "RECO FLAIR CA CP", "RECO FLAIR CA CP", "DP T2 TSE (Mr)", "ep2d\_diff\_mddw\_30\_2", "gre\_field\_mapping (Mr)", "loca\_t2\_tse\_AXIAL (Mr)", "MP RAGE\_iso (Mr)", and "MP RAGE\_iso\_gado (Mr)".
- Download Options:** Buttons for "Download Nifti files", "Download the Dicom files for this dataset", "Download Xml", and "Import Processed Dataset".



# Work in Progress: Shanoir Quality Control

[Home](#) » [Details on the research study](#)

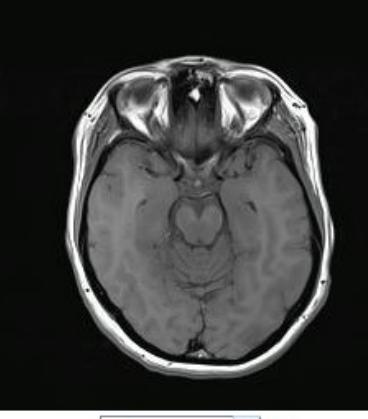
## Quality Control

Quality checkers : shannoun ; fcotton

| Automatic QC results     |              |        |       |
|--------------------------|--------------|--------|-------|
| Parameters               | Range        | Value  | Flag  |
| FOV                      | 240-260      | 250    | GREEN |
| Matrice                  | 240-260      | 250    | GREEN |
| Nombre de coupes         | 46           | 46     | GREEN |
| Epaisseur de coupes (mm) | 3            | 3      | GREEN |
| Gap (mm)                 | 0            | 0      | GREEN |
| Technique                | TSE-FE       | TSE-FE | GREEN |
| TE (ms)                  | 15-30/80-120 | 10-100 | RED   |
| TR (ms)                  | >3800        | 3500   | RED   |
| TI (ms)                  |              |        | GREEN |
| Taille voxel (mm3)       | <1x1x3       | 1x1x3  | GREEN |

Sequence

## DUAL TSE



18 / 46

Download this image in the DICOM file format  
 Download this image in the JPEG file format

| Quantitative QC results |    |  |
|-------------------------|----|--|
| SNR                     | 53 |  |
| CNR                     | 32 |  |
| Smin                    |    |  |
| Smax                    |    |  |

| Qualitative QC results    |                                  |  |                       |  |
|---------------------------|----------------------------------|--|-----------------------|--|
| Herringbone artifact      | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Moire fringes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Zebra stripes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Susceptibility / magnetic | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Herringbone artifact      | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Moire fringes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Zebra stripes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Susceptibility / magnetic | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Herringbone artifact      | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Moire fringes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Zebra stripes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Susceptibility / magnetic | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Herringbone artifact      | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Moire fringes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Zebra stripes             | <input checked="" type="radio"/> |  | <input type="radio"/> |  |
| Susceptibility / magnetic | <input checked="" type="radio"/> |  | <input type="radio"/> |  |

[Home](#) > General quality control  
**Detailed Quality Control**

Quality checkers: sharmann - Boston

**Examination**

- 20110108\_1801** (Patient)
- 20110108\_1801** (MRI Cereau)
- SABER Sagittal (MR)**
- SABER Coronal (MR)**
- SABER Axial (MR)**
- SDTI** (MR)
- SDTI** (MR)
- SDTI** (MR)
- DUAL\_TSE** (MR)
- DUAL\_TSE** (MR)
- DUAL\_TSE** 2 +
- 1x1x3** (MR)

**View**



18 57.14

[Download this image in the DICOM file format](#)  
[Download this image in the JPEG file format](#)

**Sequence**

**DUAL\_TSE**

**QC Result**



**QC Result**



---

<< Quality Control details

**Automated QC results**

| Parameters                     | Range       | Value  | Flag   |
|--------------------------------|-------------|--------|--------|
| FOV                            | 240-260     | 250    | green  |
| Matrix                         | 240-260     | 250    | green  |
| Number of images               | 40          | 40     | yellow |
| Exposure time (seconds)        | 0.000-0.005 | 0      | green  |
| Flip angle (deg)               | 0-180       | 0      | green  |
| Technique                      | TSE-FE      | TSE-FE | green  |
| TE (ms)                        | 15-3000-120 | 14-100 | yellow |
| TR (ms)                        | >3000       | 3000   | green  |
| TI (ms)                        | 0           | 0      | green  |
| Total voxel (mm <sup>3</sup> ) | <1x1x3      | 1x1x3  | green  |

**Quantitative QC results**

| Stat | 12  | Flag   |
|------|-----|--------|
| SNR  | 0.1 | green  |
| Smin | 3   | green  |
| Smax | 21  | yellow |

**Qualitative QC results**

| Hemorrhage artifact       | green |
|---------------------------|-------|
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |
| Hemorrhage artifact       | green |
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |
| Hemorrhage artifact       | green |
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |

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I Cerveau  
(MR)

r)  
(MR)  
d)

**View**



18 57.14

[Download this image in the DICOM file format](#)  
[Download this image in the JPEG file format](#)

**Sequence**

**DUAL\_TSE**

**QC Result**



**QC Result**



---

**Value** **Flag**

|        |        |
|--------|--------|
| 250    | green  |
| 250    | green  |
| 46     | green  |
| 3      | green  |
| 0      | green  |
| TSE-FE | red    |
| 14-100 | yellow |
| 3500   | red    |
| 1x1x3  | green  |

**Quantitative QC results**

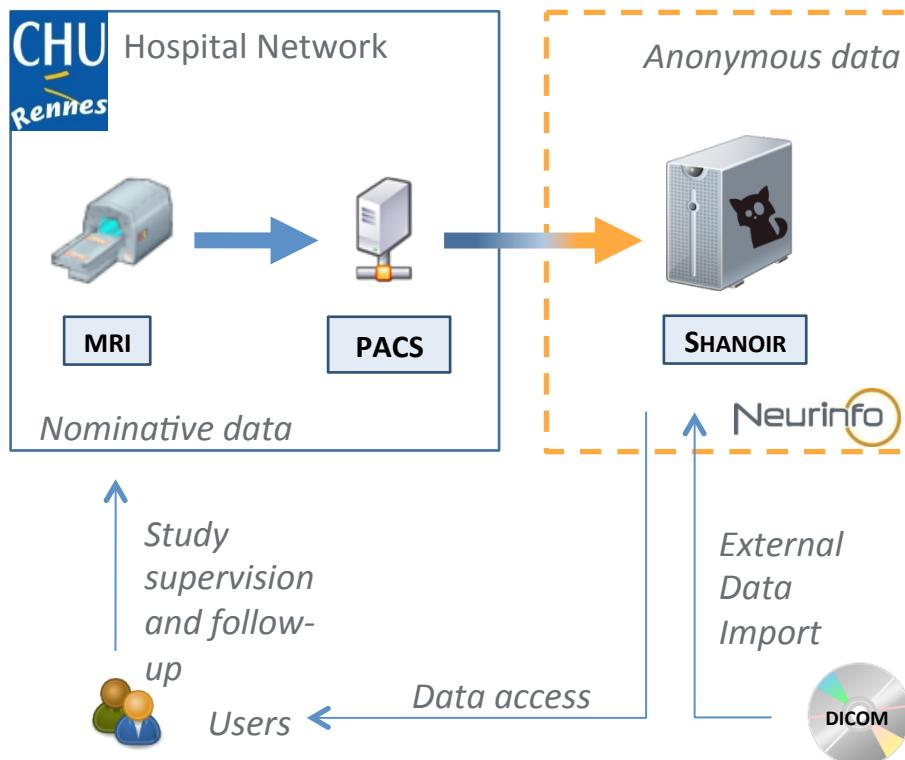
| SNR  | 12  | Flag   |
|------|-----|--------|
| CNR  | 0.1 | green  |
| Smin | 3   | green  |
| Smax | 21  | yellow |

**Qualitative QC results**

| Hemorrhage artifact       | green |
|---------------------------|-------|
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |
| Hemorrhage artifact       | green |
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |
| Hemorrhage artifact       | green |
| More fringes              | green |
| Zebra stripes             | green |
| Susceptibility / magnetic | green |

# Shanoir@Neurinfo server

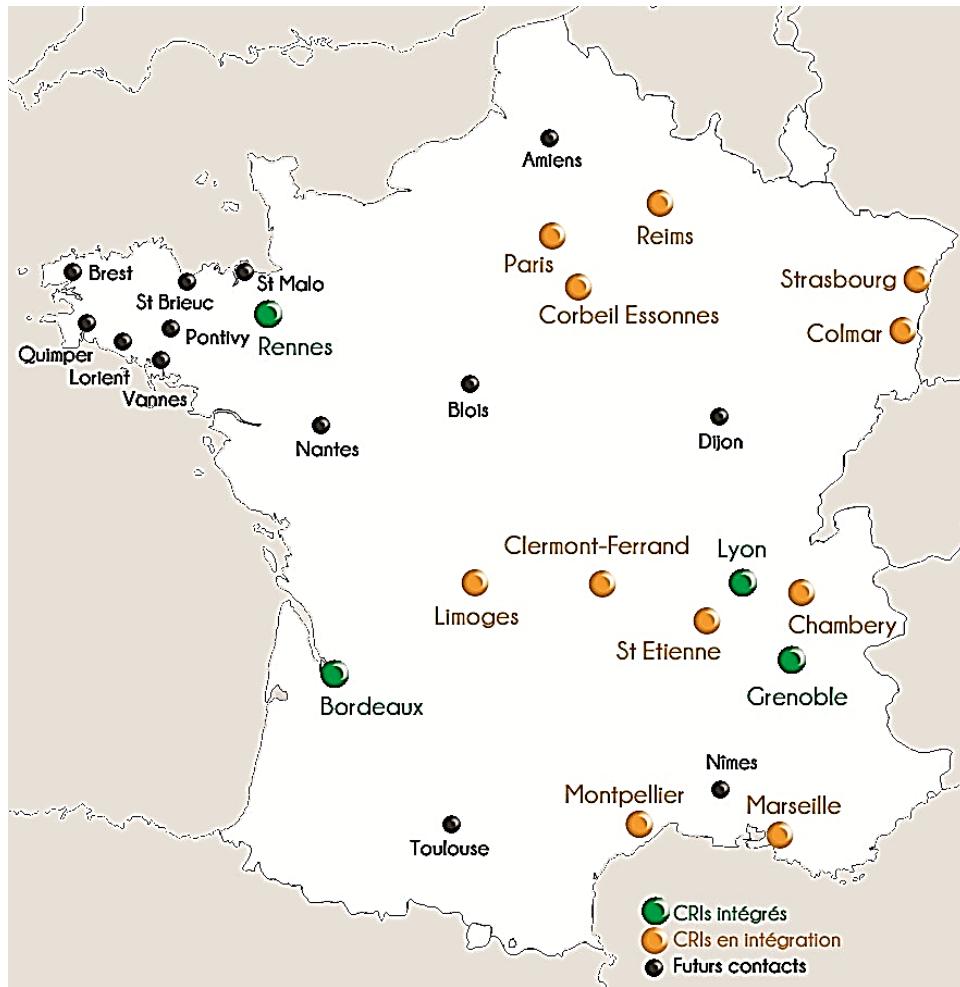
Neurinfo\* is a **research** platform, from the University of Rennes I, located at the University Hospital of Rennes. It operates a Siemens 3T Verio™ MRI and a data center (50TB, 250 cores) and uses **Shanoir** to manage and publish its data as well as data from **multicentric studies**.



|          |                      |
|----------|----------------------|
| 31 (37)  | Centers (Equipments) |
| 127 (52) | Users (active)       |
| 60       | Studies              |
| 2228     | Subjects             |
| 3157     | Examinations         |
| 114 441  | Datasets             |
| 3099 GB  | Raw & Processed Data |
| 20 GB    | Meta-Data            |

Stats Jan. 2015

# Shanoir@OFSEP server

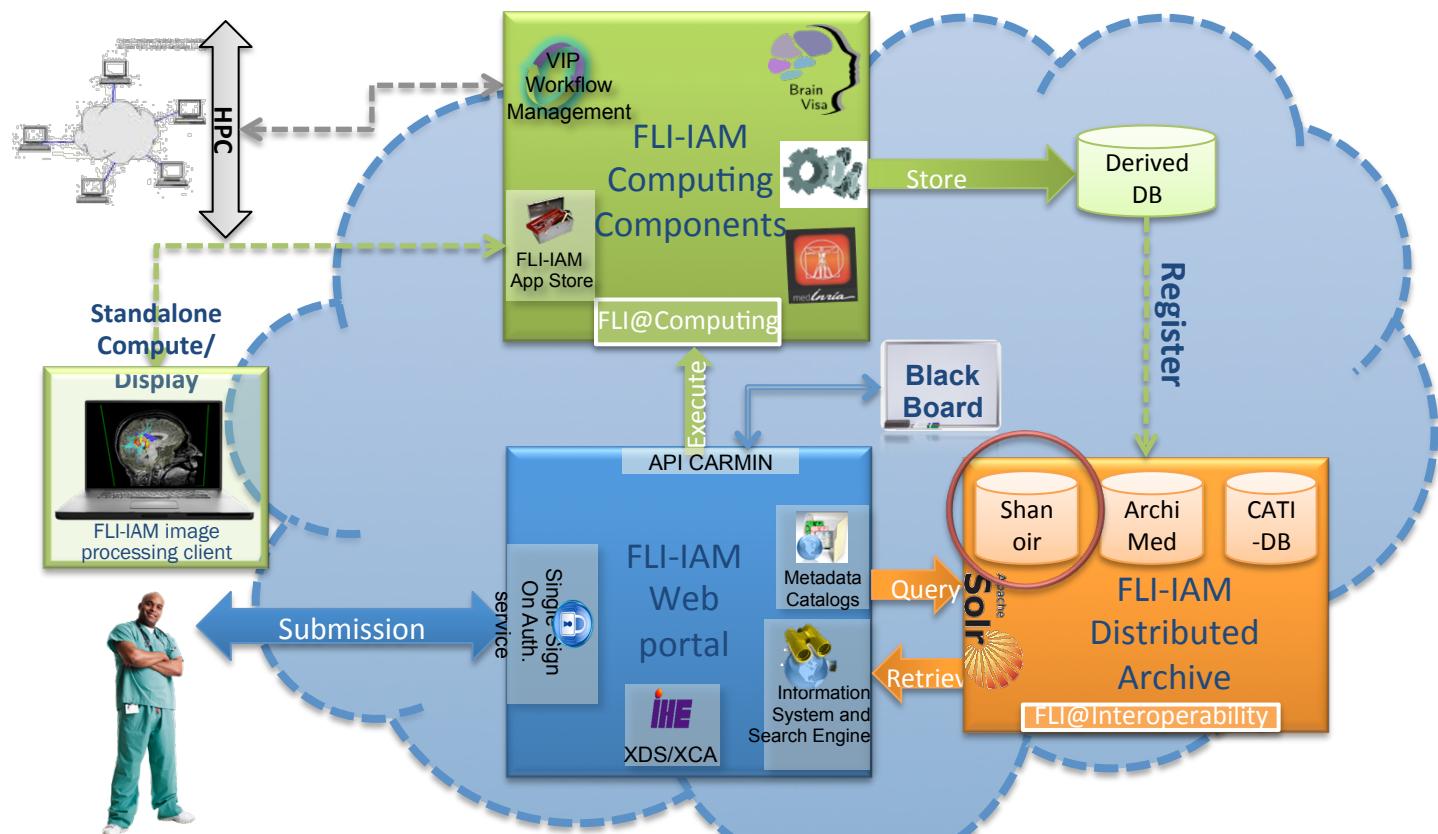


OFSEP is a nationwide, **clinical**, cohort, representing about half of the MS patients population living in France, for a **longitudinal follow-up** (clinical, biological and neuroimaging data). **Shanoir** has been chosen to be the OFSEP neuroimaging data management platform

## MR models diversity in OFSEP

|   |  |
|---|--|
| 8 | Siemens - Aera 1,5T                    |
| 7 | Philips - Achieva 3T                   |
| 2 | General Electric - DISCOVERY MR750w 3T |
| 2 | Philips - Ingenia 1,5T                 |
| 2 | Siemens - Avanto 1,5T                  |
| 2 | Siemens - Skyra 3T                     |
| 1 | General Electric - Signa HDxt 3T       |
| 1 | Philips - Achieva 1,5T                 |
| 1 | Philips - Ingenia 3T                   |
| 1 | Siemens - Espreo 1,5T                  |
| 1 | Siemens - Spectra 3T                   |
| 1 | Siemens - Symphony Tim 1,5T            |
| 1 | Siemens - Trio 3T                      |
| 1 | Siemens - Verio 3T                     |

FLI\* is research infrastructure aiming to build an organised and standardized network for in-vivo imaging in France. The IAM node is a consortium of teams that set up an infrastructure of in-vivo image storage and processing.





# Shanoir Major functionalities

- Data organization
- Study card mechanism
- Clinical scores
- Clients applications

## Undergoing large scale projects

- Neurinfo imaging platform (*31 sites connected*)
- OFSEP's cohort in MS (*35 sites connected*)
- France Life Imaging (FLI-IAM) national infrastructure for in-vivo imaging



SHAring NeurOImaging Resources  
An open source web platform for neuro-imaging

Thank you for your attention !

