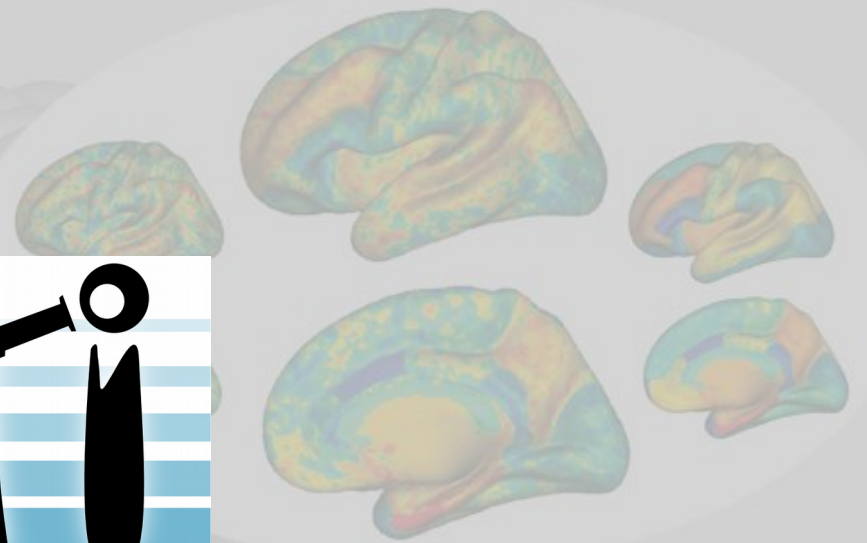


Morphometry of the cortical folds

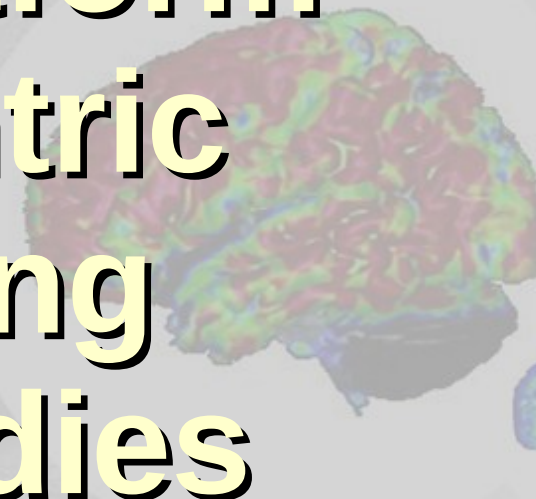


Cortical regions discriminating AD patient and healthy subjects (classifier)

a national platform for multi-centric neuroimaging research studies



Dopamine transporter SPECT imaging



Amyloid PET imaging with ^{18}F -Florbetapir in a patient with AD (top) and a healthy subject (bottom)

What is the CATI ?

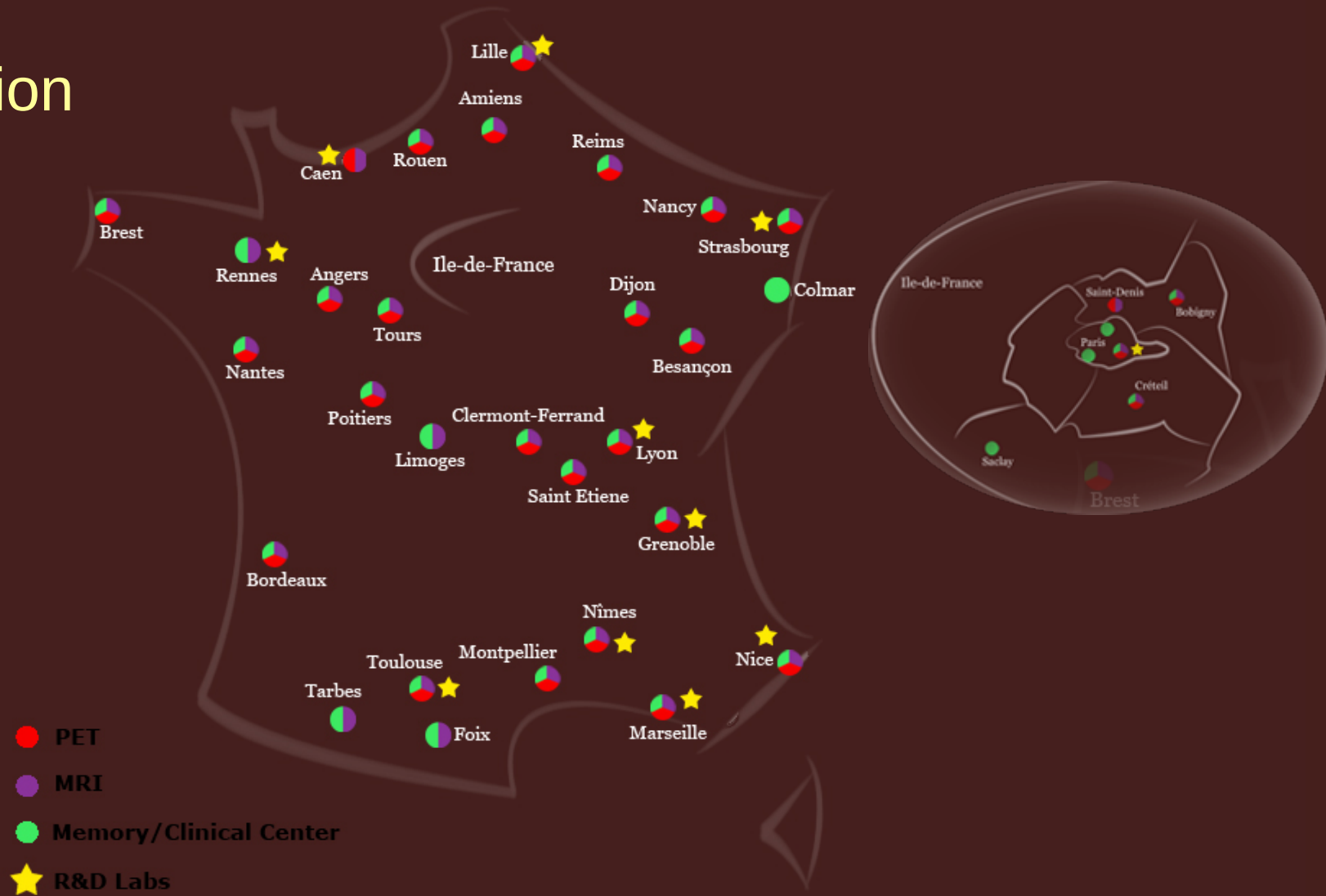
French national **platform** for research projects requiring **neuroimaging** data on **big cohorts** of subjects.

- ▶ Scientific advices (MRI, nuclear imaging)
- ▶ Data acquisition
- ▶ Data management
- ▶ Data analysis
- ▶ Quality control



Acquisition network

50 acquisition centers in France



CATI consortium

CEA Neurospin:

UNATI, Neurospin, I2BM, DSV, CEA: J.-F. Mangin, Y. Cointepas, D. Rivière, E. Duchesnay, F. Poupon

UNIRS, Neurospin, I2BM, DSV, CEA: C. Poupon, A. Vignaud

UNIACT, Neurospin, I2BM, DSV, CEA: M. Bottlander

Parietal, Neurospin, INRIA: B. Thirion, G. Varoquaux

I2BM, DSV, CEA: R. Trebossen

Pitié-Salpêtrière Hospital (GHPS):

CENIR, ICM: S. Lehéricy, E. Bardinet

ARAMIS team, CNRS, INSERM, UPMC, INRIA, ICM: M. Chupin, O. Colliot, S. Durrleman

IM2A: B. Dubois, B. Batrancourt

LIB, INSERM, UPMC: H. Benali, M.-O. Habert, M. Pellegrini-Issac, A. Kas



CATI Partners

CHU Toulouse: P. Payoux

Clinical Imaging Core faCility – CI2C, CHRU Lille: C. Delmaire, R. Lopes, J. Dumont

INSERM U1077, Caen: G. Chételat

Neurinfo platform / IRISA VisAGeS research team, Rennes, France: E. Bannier, I. Corouge, C. Barillot, J.-C. Ferré

Plateforme d'imagerie in-vivo / ICube lab, Strasbourg: P. Loureiro de Sousa

IRMaGe platform / GIN lab, Grenoble: I. Tropès, L. Lamalle, A. Krainik, J. Warnking

IR4M, UMR8081, Paris-Sud University – CNRS, Orsay: L. de Rochefort

Plateforme Ibio / INCIA, Bordeaux: B. Dilharreguy, M. Allard

CERMEP, Lyon: F. Lamberton, D. Ibarrola

MRI platform, ISCT, Toulouse: H. Gros-Dagnac, N. Vayssière

MRI platform, I2FH, CHU Gui de Chauliac, Montpellier: E. Le Bars, N. Menjot de Champfleury

Unité Imagerie et Cerveau, Tours: L. Barantin

LaBRI – UMR 5800, Bordeaux : P. Coupé

Asclepios, Sofia-Antipolis : N. Ayache, X Pennec

INSERM U897 ISPED / GMA / Bordeaux: C. Dufouil, G. Chêne, V. Bouteloup

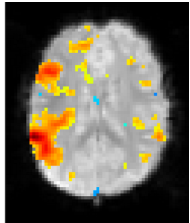
INT / CNRS UMR6168, Marseille: O. Coulon, G. Auzias, J. Lefèvre

MIRCent, Fontenay-aux-Roses: T. Delzescaux, N. Souedet

Athena, Sofia-Antipolis : R. Deriche

Distribution of skills

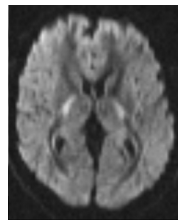
Acquisition



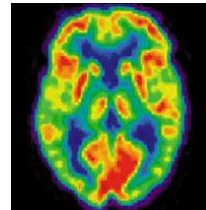
fMRI



aMRI



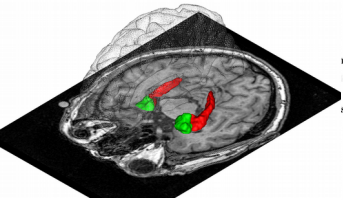
dMRI



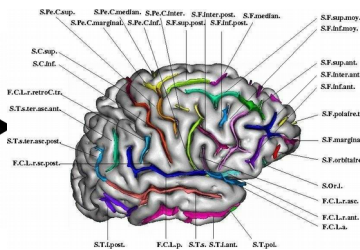
PET



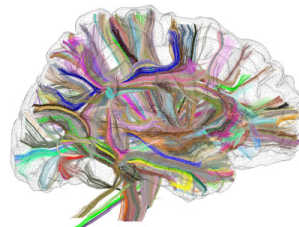
Processing



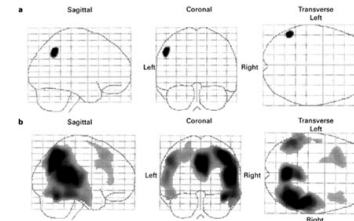
Sacha



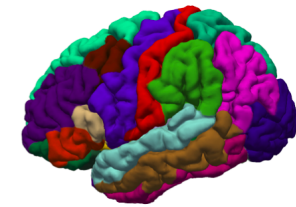
Morphologist



connectomist



SPM



freesurfer



5 research labs

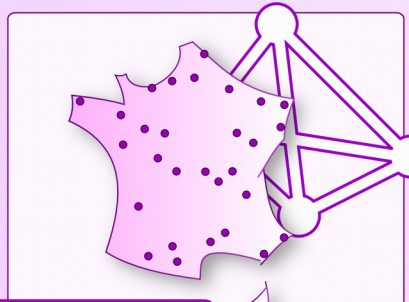


Data management

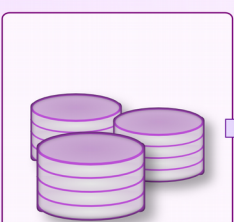


26.1 millions files

22.3 To
disk usage



harmonized network



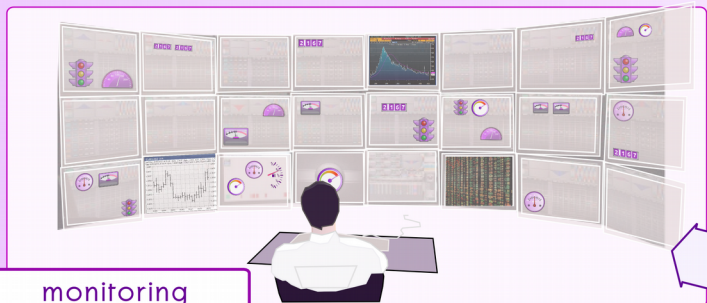
data collection



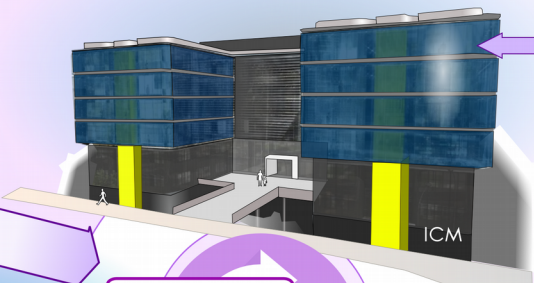
quality check



pushzone

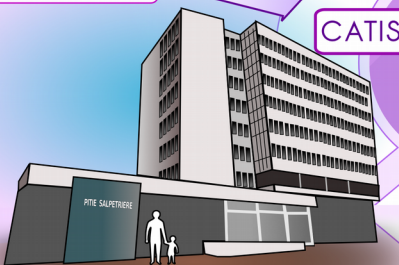


monitoring software platform

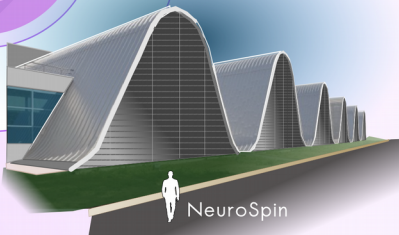


CATISHARED

CATIDB



UPMC - Pitié-Salpêtrière site



NeuroSpin

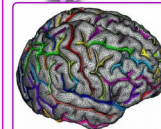
synchronization between partner labs



pushzone

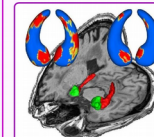
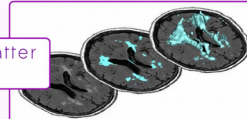


processing



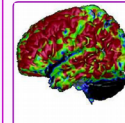
Morphometry of cortical folds

Segmentation of white matter hyperintensities



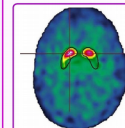
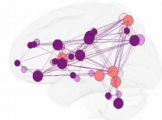
Segmentation of the hippocampus and the amygdala

White matter fiber bundles analysis



FDG and amyloid PET data analysis

Functional networks from resting-state fMRI



Dopamine transporter SPECT imaging

...

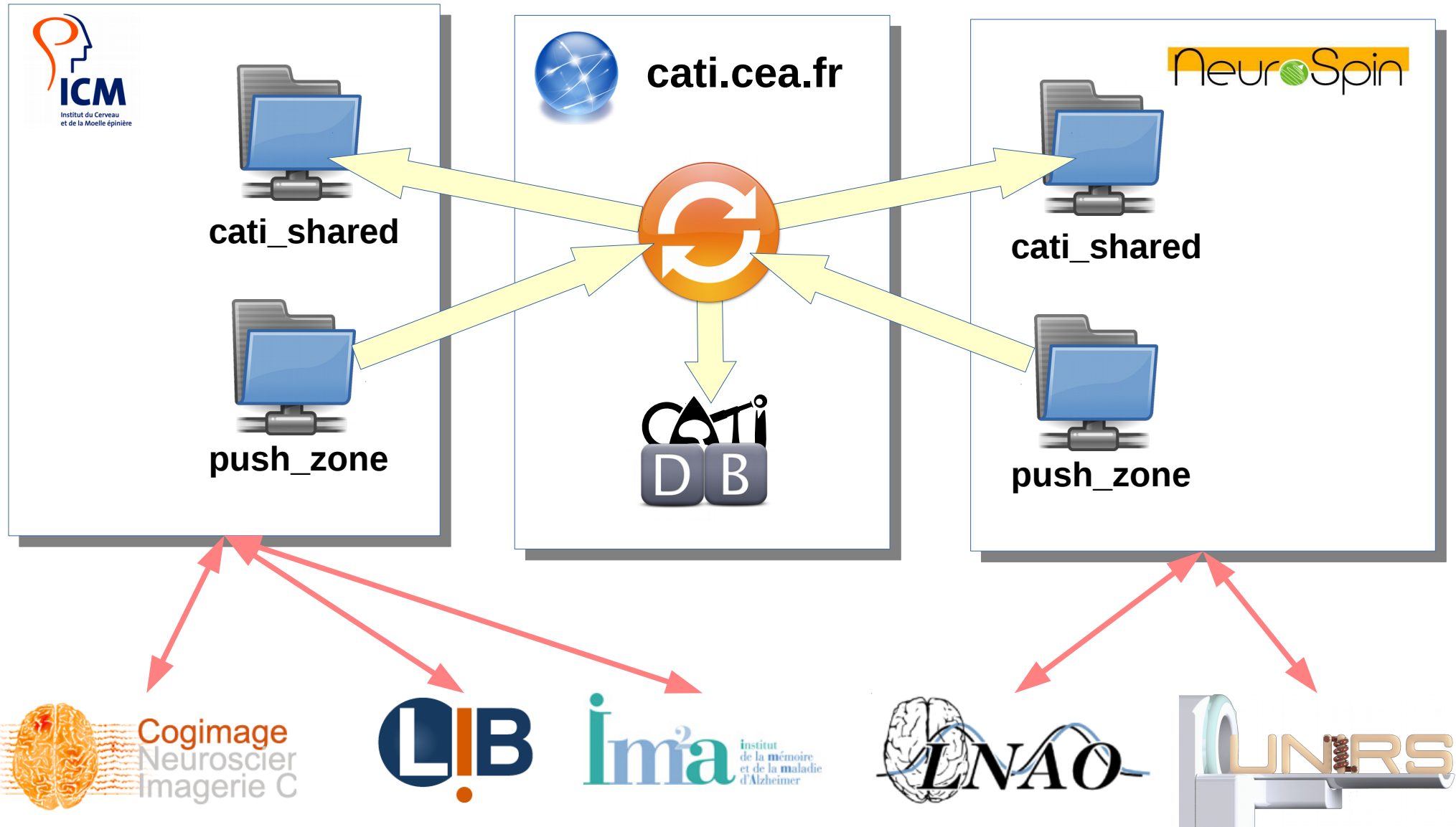
results shipping



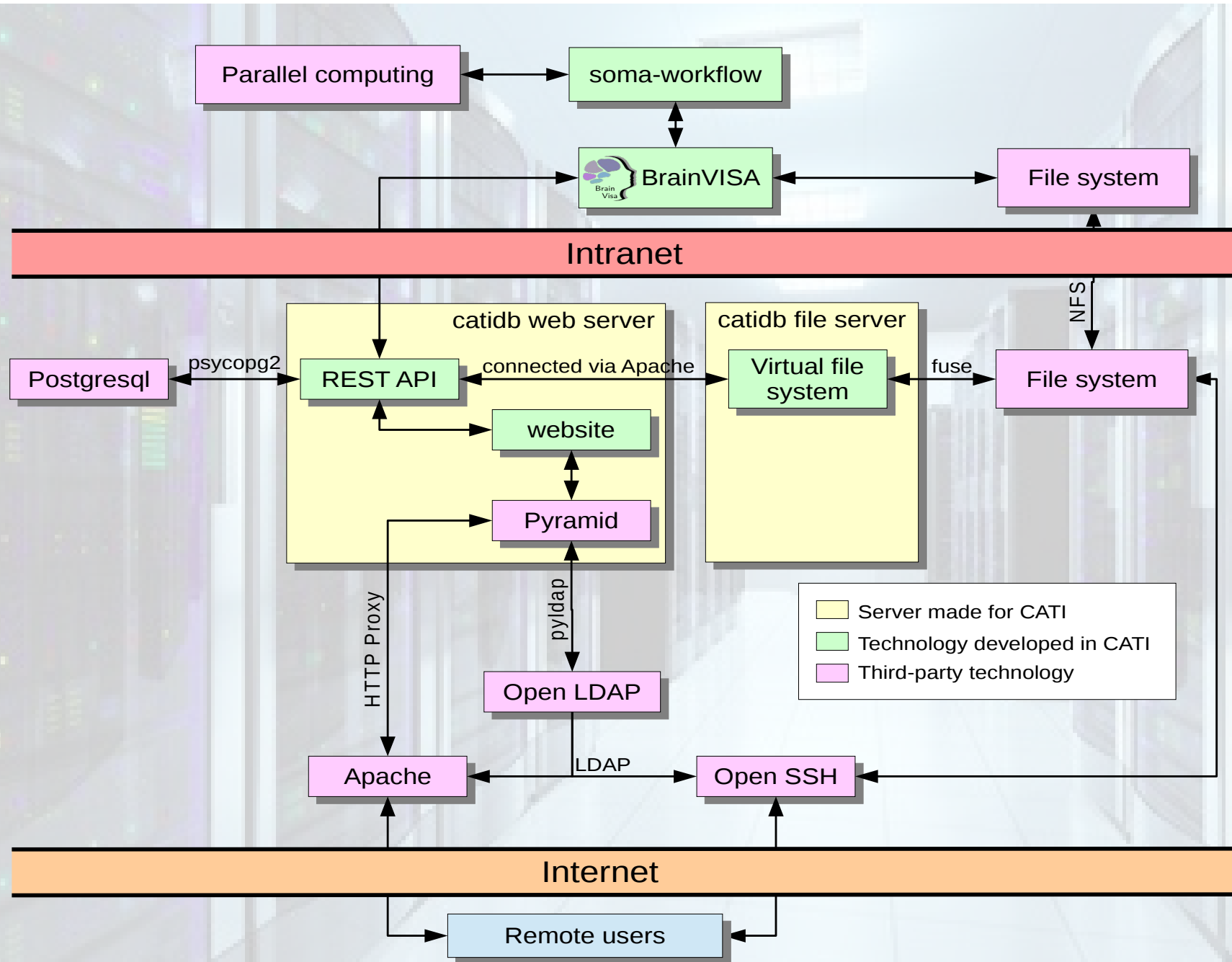
results quality control



Distributed architecture



Server infrastructure





BrainVISA platform

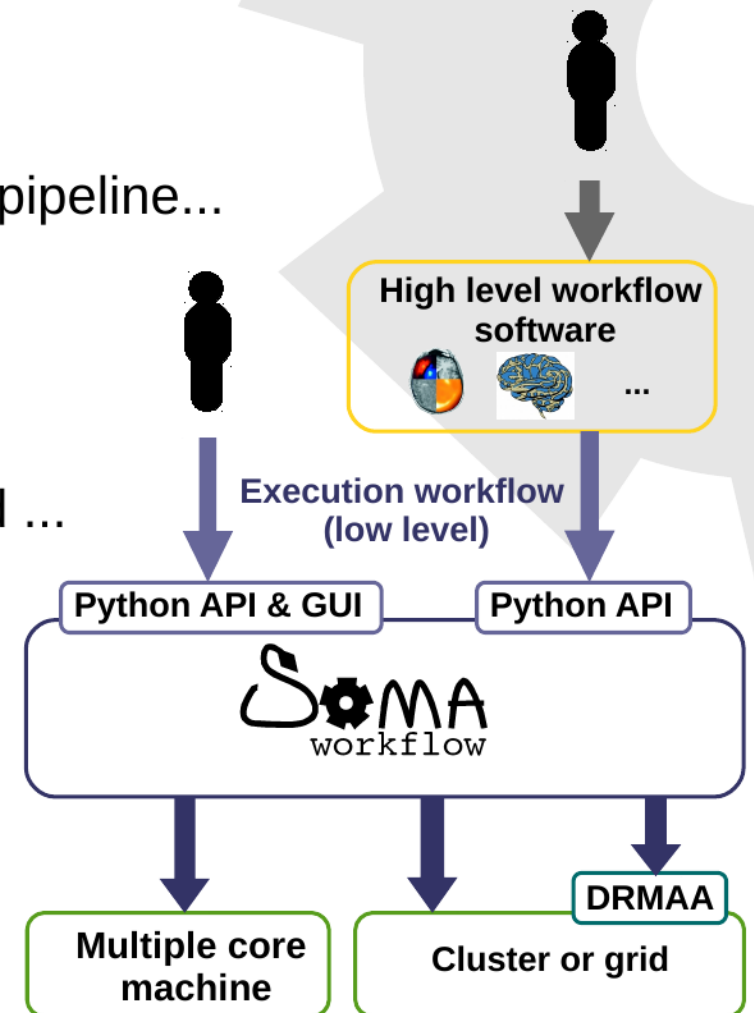
<http://brainvisa.info>

- ▶ Multi OS development environment
- ▶ Data organization framework
- ▶ Pipeline infrastructure
- ▶ User interfaces
- ▶ Interactive visualization



SOMA workflow

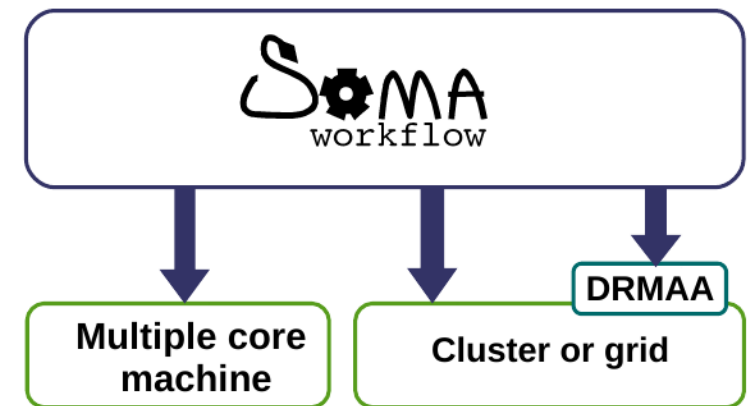
- Soma-workflow deals with execution workflows (low level)
- ≠ from high level workflow software
 - In neuroimaging: BrainVISA, NiPype, LONI pipeline...
 - Higher level description of workflow
 - Higher level features
- Bridges the gap between parallel resources and ...
 - Non expert user
 - Documentation
 - Python API made to be simple
 - GUI
 - High level workflow software



Interface with computing resources

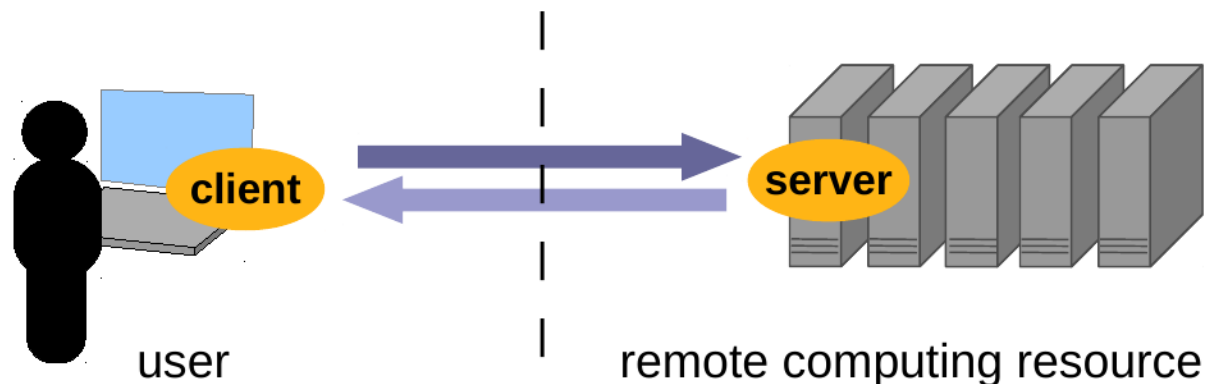
- Uses only very basic computing resource functionalities
 - Compatibility with a wide range of resources
- Creation of an interface with a new resource
 - Implementation of 4 Python methods
- Built in interfaces:
 - Ready to use on multiple core machines
 - Interface with the Distributed Resource Management Application API (DRMAA)
 - Software standard developed by the Open Grid Forum
 - S-w was used with success on clusters with the systems:
 - Oracle Grid Engine
 - Torque
 - LSF
 - Condor

- Job submission
- Job suppression
- Job status
- Job exit information



Remote access to computing resources

- Soma-workflow can be used as a client-server application :
 - Same Python API and same GUI
 - Disconnection at any time
 - The remote communication done with Pyro in a ssh tunnel
- If no shared file system between the user machine and the resource:
 - File path mapping tool
 - File and directory transfer tool
 - Soma-workflow takes into account the state of file transfer when executing a workflow.



GUI overview

List of the configured resources

Submitted workflows

Current workflow information

Current selection information (here a ended job)

The screenshot shows the 'soma-workflow - DSV_cluster' application window. It features a menu bar with 'File' and 'Workflow', and a toolbar with 'Open', 'Submit', 'Restart', 'Transfer Input Files', and 'Transfer Output Files'. The main interface is divided into several sections:

- Left Panel:** A dropdown menu shows 'DSV_cluster'. Below it, a list of 'Submitted workflows' includes 'sulci recognition 100 subjects' and 'sulci recognition 3 subjects'. A 'Delete' button is present.
- Workflow Information:** A section titled 'Workflow' shows 'name: ci recognition 100 subjects', 'status: workflow_in_progress', and 'expiration date: 9 Apr 2011 15:44:23'. A 'Change date' button is also visible.
- Status:** A box displays 'Status: running', 'jobs: 400', 'Ended jobs: 200', 'Total time (since sub.):', and 'Theoretical serial time: 5:0:44'.
- Tree View:** A hierarchical tree shows the workflow structure. The root is 'sulci recognition -- subject 9' through 'subject 36'. Under 'subject 25', there is a checked box for 'Gray/white segmentation', which contains 'Sulci recognition' (with sub-items for left and right hemispheres).
- Job Info:** A panel at the bottom shows details for a selected job: 'job name: ray/white segmentation', 'job status: done', 'Exit status: finished_regularly', 'Exit value: 0', 'Terminating signal:', 'Resource usage: submission_time=13', 'Command: python "/home/l2bm-r...', 'Time in queue: 0:0:11', 'Execution time: 0:2:2', 'Submission date: 04/04/11 15:46:54', 'Execution date: 04/04/11 15:47:05', and 'Ending date: 04/04/11 15:49:07'.
- Plot:** A 'Plot' window on the right shows 'jobs fct time' on the y-axis (0 to 300) and 'Time' on the x-axis (15:45:00 UTC to 15:54:00 UTC). The plot displays a series of horizontal bars representing the execution of individual jobs over time.

Representation of the workflow as a tree

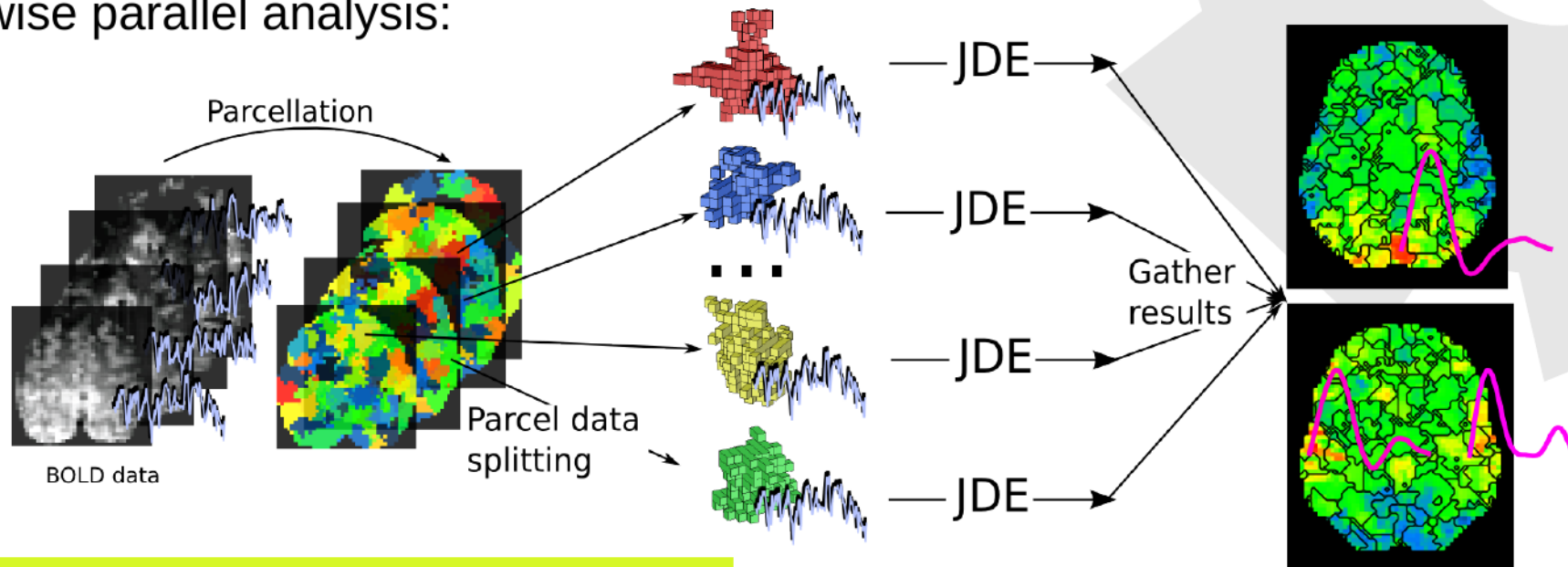
workflow execution plots

The future of CATI



Case 1: Acceleration of a single data analysis

- Functional neuroimaging application: Joint detection-estimation (JDE)^[1]
 - Detection of the parts of the brain which are involved in a given stimulus
 - Estimation of the Hemodynamic Response Function (HRF)
- Parcel-wise parallel analysis:

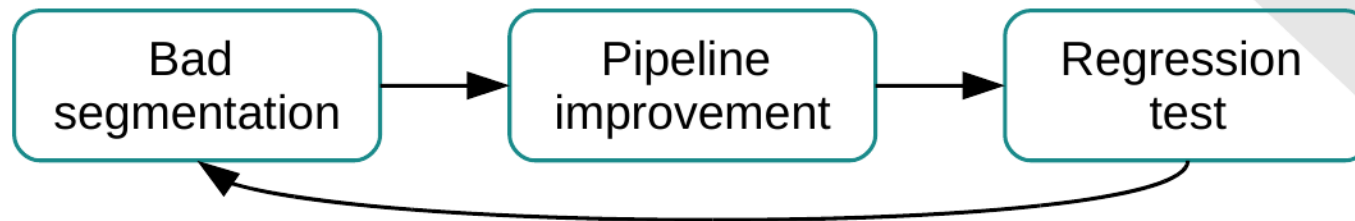


- Wrapping of existing code in a workflow
- A whole brain processing:
 - 10 hours on 1 CPU
 - 15 mins on the cluster
- A group study of 20 subjects: ~ 1 day

^[1] Vincent, T., Risser, L., Ciuciu, P. Spatially adaptive mixture modeling for analysis of within-subject fMRI time series
IEEE Trans. Med. Imag. 29, 1059–1074 (2010)

Case 2: Robustness improvement with regression tests

- Objective: to reduce the sensitivity of the Morphologist pipeline of BrainVISA ^[2]
- Morphologist: extraction of the main brain structures from T1 MRI
 - hemispheres, gray/white matter, cortical surface, cortical folds, etc.
- Step by step morphologist was tested on about 1000 T1 MR images.



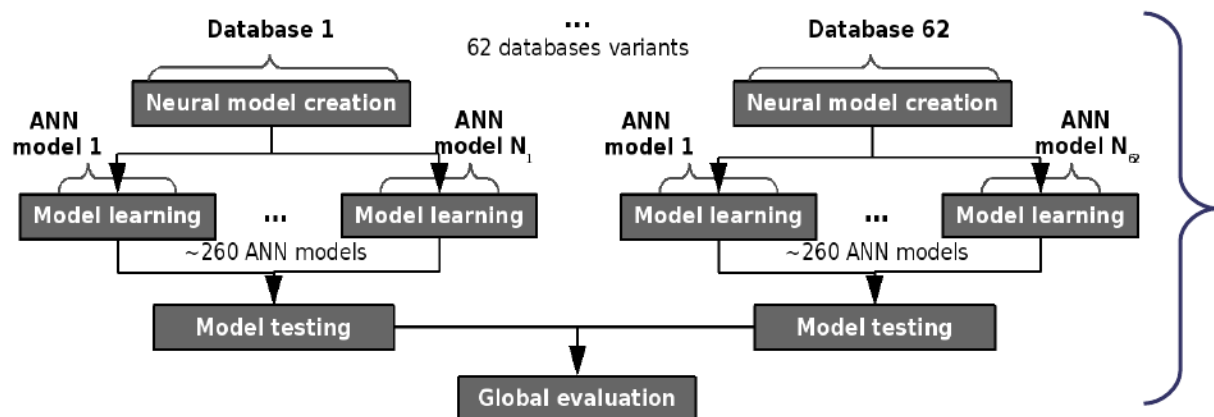
- Regression test are frequently done on a database made of 80 T1 MRI

→ workflows generated by BrainVISA
→ 23 hours on 1 CPU
→ ~ 1h on the cluster

➔ { More frequent regression tests
Tests on larger dataset

Case 3: Extensive validation

- Extensive cross-validation of cortical sulci identification models ^[3] and comparison with the newer method by Perrot ^[4]
- Each neural model is trained using a supervised learning scheme, based on a learning database of 62 manually identified brains
- Leave-one-out cross-validation of the models on the learning database



→ 70000 individual jobs
→ > 7 months on 1 CPU
→ ~ 3 days on ~ 100 CPU

^[3] Rivière, D., Mangin, J.-F., Papadopoulos-Orfanos, D., Martinez, J.-M, Frouin, V., Régis, J. Automatic recognition of cortical sulci of the Human Brain using a congregation of neural networks. Medical Image Analysis. vol. 6, no. 2, pp. 77–92 (2002)

^[4] Perrot, M., Rivière, D., Mangin, J.-F. Cortical sulci recognition and spatial normalization. In: Medical Image Analysis. In press (2011)