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## MEDILAXY

A Galaxy Platform For Medical Image Analysis

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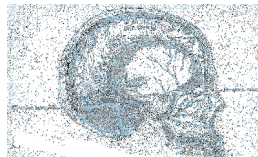
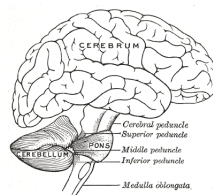
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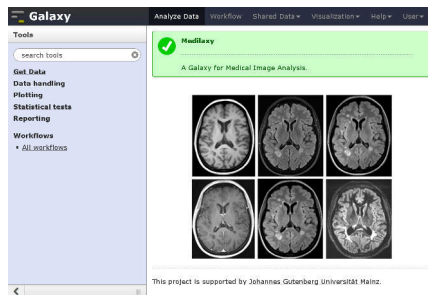
# The motivation

- Multiple sclerosis (MS)
- MRI – water diffusion in the brain
- Spatial-dependent properties
- Different regions:
  - Inferior Cerebellar Peduncle
  - Supratentorial
- Different groups:
  - Patients
  - Controls
  - NAWM



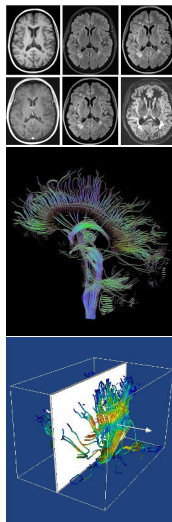
# Why Galaxy

- Integrated collection of tools:
  - Filling/querying database
  - Different plot types
  - Correlation studies
  - Statistical tests
  - L<sup>A</sup>T<sub>E</sub>X reports
  
- Online platform for sharing data
- Easy to use web interface
- Hiding the programming part to users
- Integration with genetics data (existing tools in galaxy)



# Input data

- Acquiring MRI images
- Combining images
- Noise reduction
- Estimation of diffusion tensor
- Fiber tracking
- Selection of fibers
- Selection of patients
- SPM (MATLAB tool),  
Fiberviewer, MRICron, python  
modules



# Workflow

The screenshot displays the Galaxy workflow editor interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The main workspace is titled 'Workflow Canvas | Workflow' and contains a sequence of workflow steps connected by arrows:

- Creating a list of files to add to the database**: Input is 'list\_of\_files (txt)'. Output is 'List of files'.
- Fill the database with data**: Inputs are 'List of files' and 'Input database' (database.sqlite). Output is 'database (sqlite)'. This step is expanded to show:
  - Database to be read**: internal\_database (xml)
  - Database to be read**: database (sqlite)
- Create internal XML database**: Input is 'internal\_database (xml)'. Output is 'internal\_database (xml)'.
- Create a scatter plot**: Input is 'output (py)'. Output is 'output (html)'. This step is expanded to show:
  - Database to be read**: output (py)
  - Script to be executed**: output (html)
- Run a script**: Input is 'output (html)'. Output is 'output (html)'.

The right-hand panel shows the configuration for the selected tool, 'Create a scatter plot' (Version: 0.9.6). It includes the following settings:

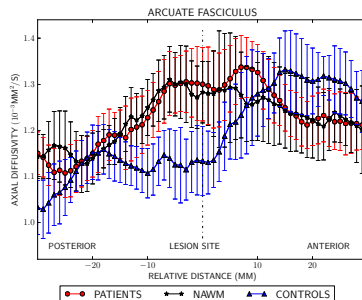
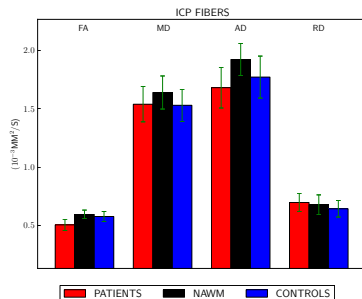
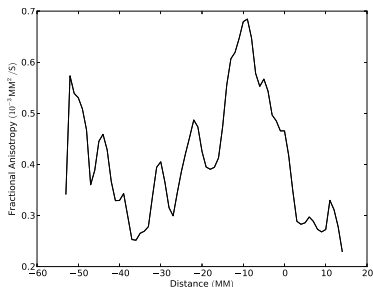
- Database to be read**: Data input 'database' (data)
- Group to be selected**: id
- Subgroup to be selected**: patients
- Second subgroup to be selected**: st
- Ascissa quantity**: position
- Ordinate quantity**: fa
- Plot format**: Pdf

A preview window at the bottom right shows a scatter plot with several data points.

- sqlite
- generateDS
- matplotlib

## Current state

- Not online
- Results for the original study:
  - MAGNIMS talk in Milano (8-9 November 2012)
  - Article in preparation



## Perspectives

- Including some preprocessing steps:
  - integrating Fiberviewer
  - studying tractography algorithms
  - segmentation images
  - denoising
- Allowing user to modify python scripts
- Add plot options
- Study MS time evolution
- Including genetic studies
- Supporting more formats

Thank you for your kind attention  
Any questions?

- Johannes Gutenberg University
  - Prof.Dr. Andreas Hildebrandt
  - Dr. Katerina Taškova
  - M.Sc. Sonika Rao
- Saarland University
  - Dr. Anna-Katharina Dehof
- Mainz Uniklinik
  - Prof.Dr.med. Frauke Zipp
  - M.Sc. Amgad Droby

