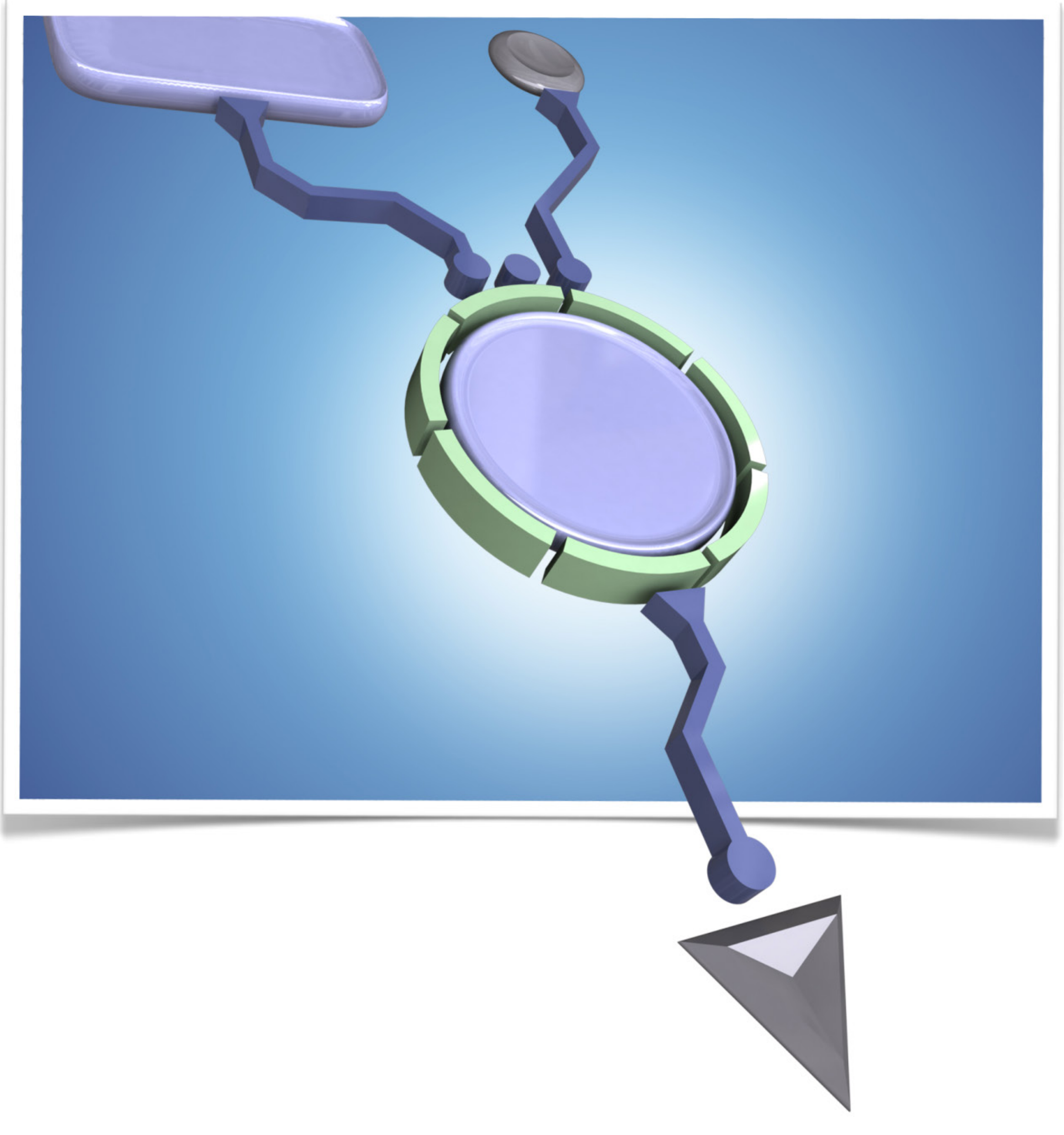
LONI Pipeline

Neuroimaging Solutions

A practical, hands-on guide to using the LONI Pipeline for neuroimaging analysis



LONI Pipeline version 7.0.1
Handbook version 1.6
http://pipeline.loni.usc.edu

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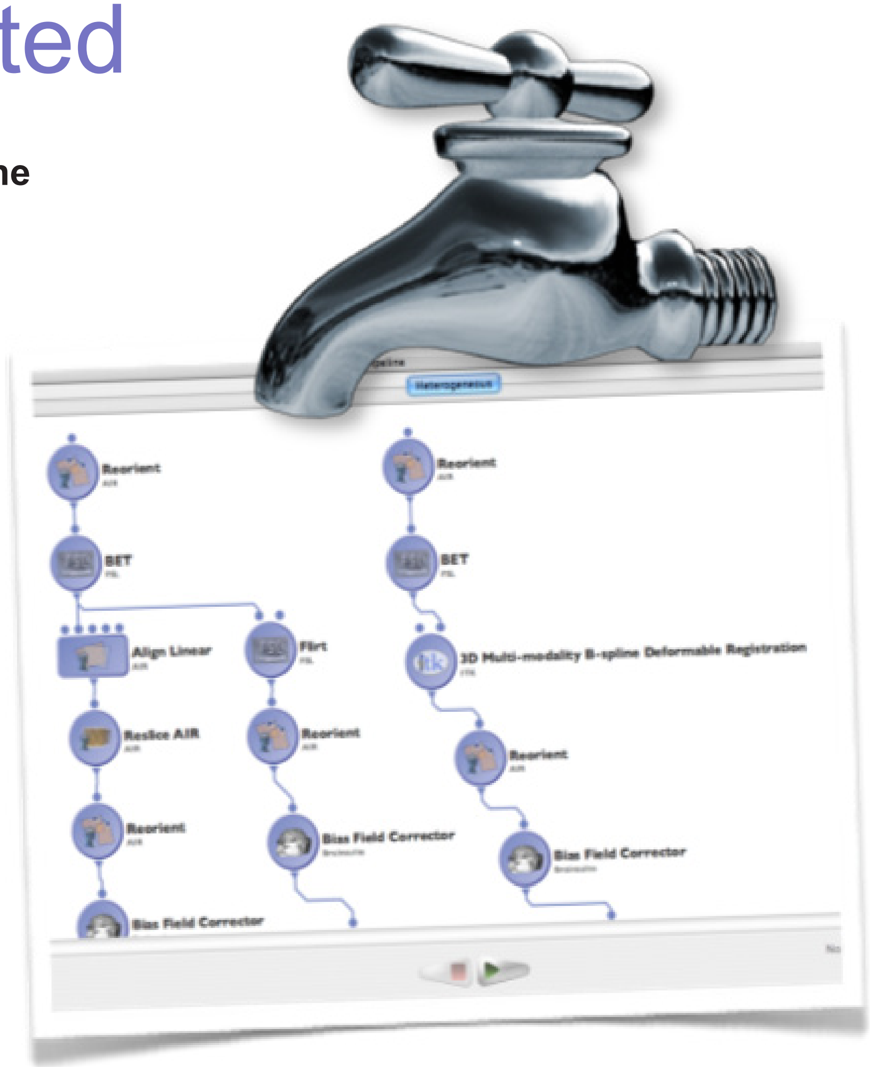


Overview: About LONI Pipeline

The LONI Pipeline is a free workflow application primarily aimed at neuroimaging researchers. With the LONI Pipeline, users can quickly create workflows that take advantage of any and all neuroimaging tools available. They can also gain access to the supercomputing cluster housed at LONI, free of charge, or install and use the LONI Pipeline entirely locally.

Benefits

The LONI Pipeline is a workflow application that allows users to easily describe executables in a graphical user interface (ie. create a module) and connect them to create complex analyses, without having to code a single line in a scripting language. Instead of manually managing intermediate data in a script, the LONI Pipeline handles the passing of data between programs and stores it in a cache directory. Once you've created a module for use in the LONI Pipeline, you can save it into your personal library and reuse it in other workflows you create by simply dragging and dropping it in. The same is also true of entire wosrkflows.

Requirements

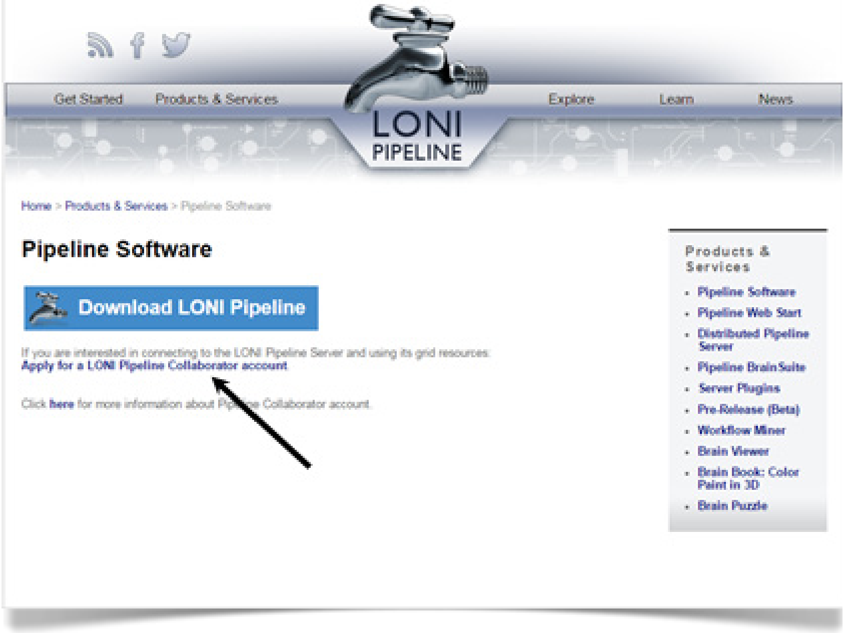
The LONI Pipeline is platform independent, thus the only computer requirement of the Pipeline client is an installation of JRE 1.5 or higher, which can be downloaded from Sun (http://www.java.com). In terms of memory consumption, it's unlikely that you'll need to worry about having sufficient RAM to run the Pipeline. However, you will need to ensure sufficient RAM is available if you choose to run the Pipeline from a virtual machine.

Installation

Software Download

To get the latest version of the LONI Pipeline, go to the Pipeline web site (http://pipeline.loni.usc.edu) and click on the download link in the menu at the top.

If you do not already have a LONI User Account, you will be asked to create an account before you download.



Home > Products & Services > Pipeline Software

Pipeline Software

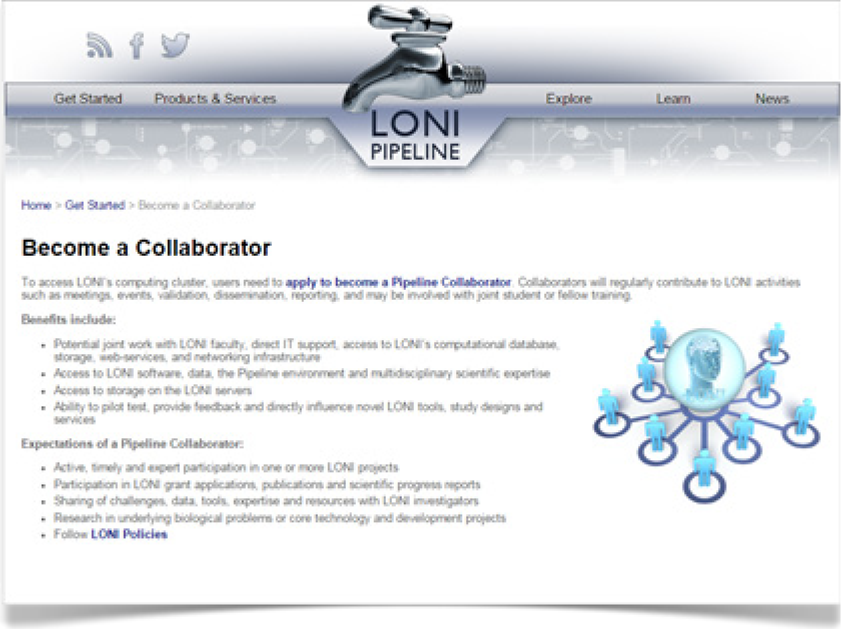
If you are interested in connecting to the LONI Pipeline Server and using its grid resources:
Apply for a LONI Pipeline Collaborator account

Click here for more information about Pipeline Collaborator account.

LONI Cluster Usage Account

When downloading the LONI Pipeline, you are given the option to connect to the server running on LONI's supercomputing resources (available free of charge). By choosing this option, you are prompted to complete an online form. This form is then reviewed and you are notified of the status of your account through email.

Please note that the approval process can take up to one working day.



Home > Get Started > Become a Collaborator

Become a Collaborator

To access LONI's computing cluster, users need to **apply to become a Pipeline Collaborator**. Collaborators will regularly contribute to LONI activities such as meetings, events, validation, dissemination, reporting, and may be involved with joint student or fellow training.

Benefits include:

- Potential joint work with LONI faculty, direct IT support, access to LONI's computational database, storage, web-services, and networking infrastructure
- Access to LONI software, data, the Pipeline environment and multidisciplinary scientific expertise
- Access to storage on the LONI servers
- Ability to pilot test, provide feedback and directly influence novel LONI tools, study designs and services

Expectations of a Pipeline Collaborator:

- Active, timely and expert participation in one or more LONI projects
- Participation in LONI grant applications, publications and scientific progress reports
- Sharing of challenges, data, tools, expertise and resources with LONI investigators
- Research in underlying biological problems or core technology and development projects
- Follow **LONI Policies**

Platform-Specific Installation

OS X

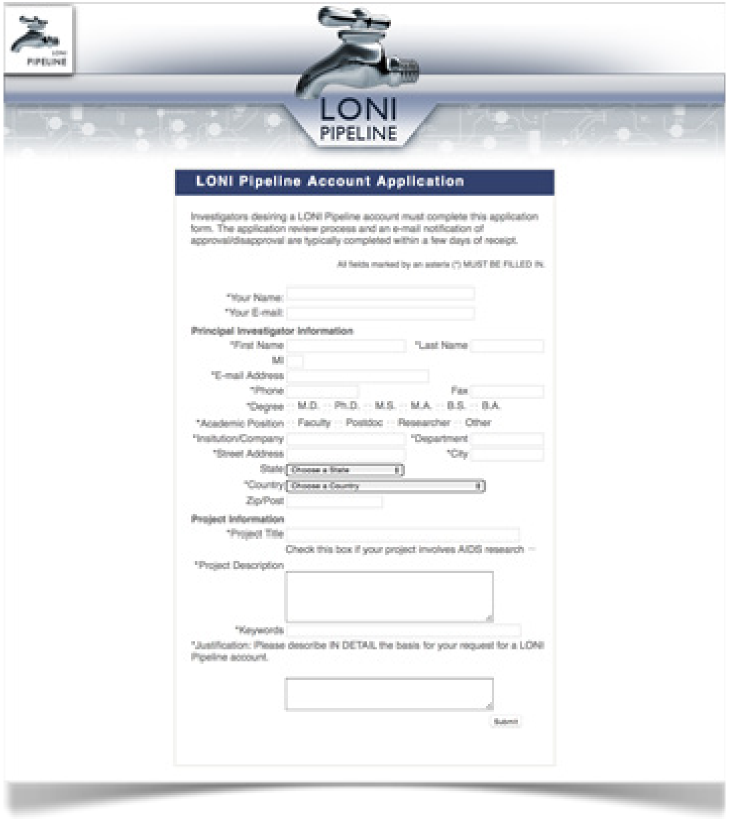
To install the program, double click the disk image file you downloaded, and drag the LONI Pipeline application into the Applications folder. Once the program is done copying you can unmount (eject) the disk image and throw it in the trash. To start the Pipeline, just go to your Applications folder and double-click on the LONI Pipeline application.

Windows

To install on Windows, double-click the installer and follow the on-screen instruction. Once it finishes installing, you can throw away the installer and launch the program by going to the Start menu->Programs->LONI Pipeline and start the program.

Linux/Unix

Extract the contents of the file to a location on disk, and execute the PipelineGUI script. Make sure you have the java binary in your path.



LONI Pipeline Account Application

Investigators desiring a LONI Pipeline account must complete this application form. The application review process and an e-mail notification of approval/disapproval are typically completed within a few days of receipt.

All fields marked by an asterisk (*) MUST BE FILLED IN.

*Your Name:
*Your E-mail:

Principal Investigator Information

*First Name   *Last Name
MI
*E-mail Address
*Phone   Fax
*Degree ○ M.D. ○ Ph.D. ○ M.S. ○ M.A. ○ B.S. ○ B.A.
*Academic Position ○ Faculty ○ Postdoc ○ Researcher ○ Other
*Institution/Company   *Department
*Street Address   *City
State Choose a State
*Country Choose a Country
Zip/Post

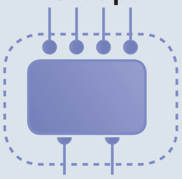
Project Information

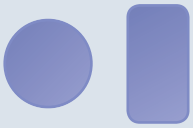
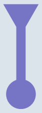
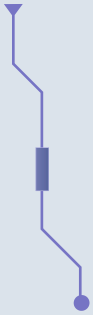
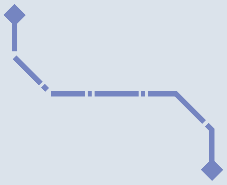
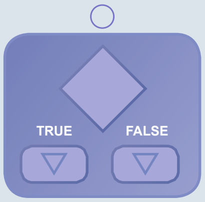
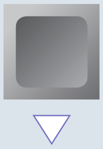
*Project Title
Check this box if your project involves AIDS research □
*Project Description
*Keywords
*Justification: Please describe IN DETAIL the basis for your request for a LONI Pipeline account.

Interface

Overview

The LONI Pipeline has an easy to use interface. Putting together workflows only requires knowledge of your tools and your goal, instead of programming languages and scripts. While your workflow is executing you can see exactly what step the Pipeline is currently on, and even see the output of a particular step when it finishes instead of waiting for the entire workflow to finish.

Data Source ●	The data to be processed is input here. Double click to set the data path.	**Software Module Group** 	Software modules can be grouped together to simplify the look of your workflow.
Play Button ▶	Clicking play will initiate processing. The workflow will connect to the computer cluster and process the workflow.	**Pause** ⏸	Clicking on Pause will temporarily pause the workflow. All running jobs/instances will be stopped and their output files will be deleted, but not the outputs of completed jobs.
Stop ■	Clicking on reset will stop the execution and reset the workflow. All temporary output files will be deleted.	**Reset** ↻	Clicking on reset will reset the workflow and all temporary output files will be deleted.
Data Sink ▼	Workflow results will output to this module's destination. Double click to set the output path.	**Empty Output Parameter** ▽	Modules also have Output Parameters, this one is empty.

Software Module 	Each module holds a unique piece of software.	**Specified Output Parameter** ▼	After an Output Parameter is specified it will appear as a darker triangle.
Empty Input Parameter ○	Modules often require Input Parameters. An empty parameter has no value specified.	**Connections** 	Lines that connect the output of one module to the input of another module.
Input Parameter ●	A darker circle donates an Input Parameter with a value specified.	**Smartlines** 	A Smartline connects two modules and will automatically perform the necessary file conversion on the output of the first module in order to ensure that the input to the second module is of the proper type.
Optional Input Parameter ■	Occasionally, Input Parameter do not require arguments but offer them optionally.		
Flow Control 	Flow Control parameter is used to ensure the sequential execution of modules. Connecting flow control parameters between two modules enforces a strict ordering on the execution of these modules.	**Conditional Module** 	Conditional Module is used when the execution path of various inputs to a workflow is dependent on some criteria. Use of Conditional Modules makes the workflow more dynamic.
Study Module 	Study Module incorporates imaging data and non-imaging meta-data, and enables queries, groupings and construction of study-designs based on user-specified criteria.	**Label** 	Software modules and module groupings have been labeled to describe the processing.

Data Sources & Sinks

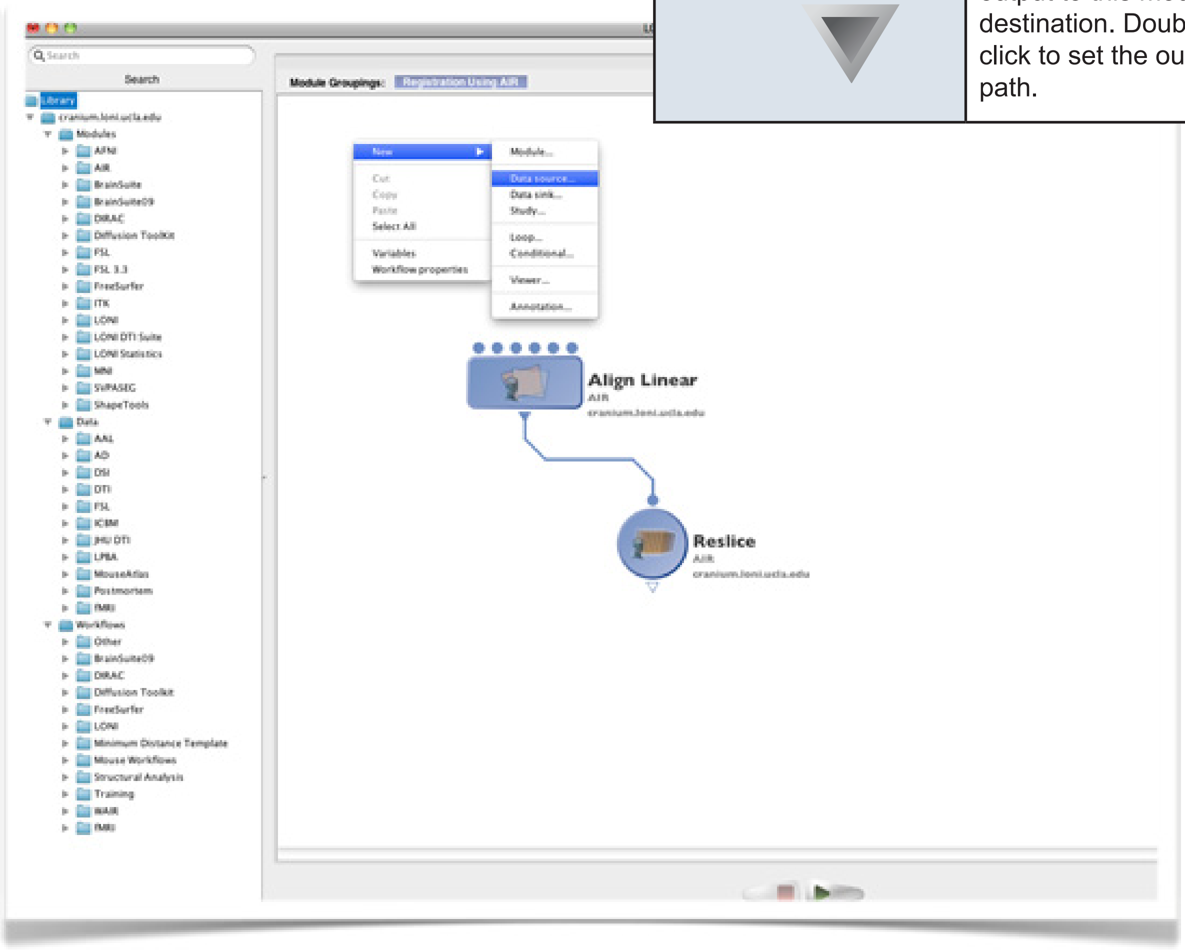
Overview

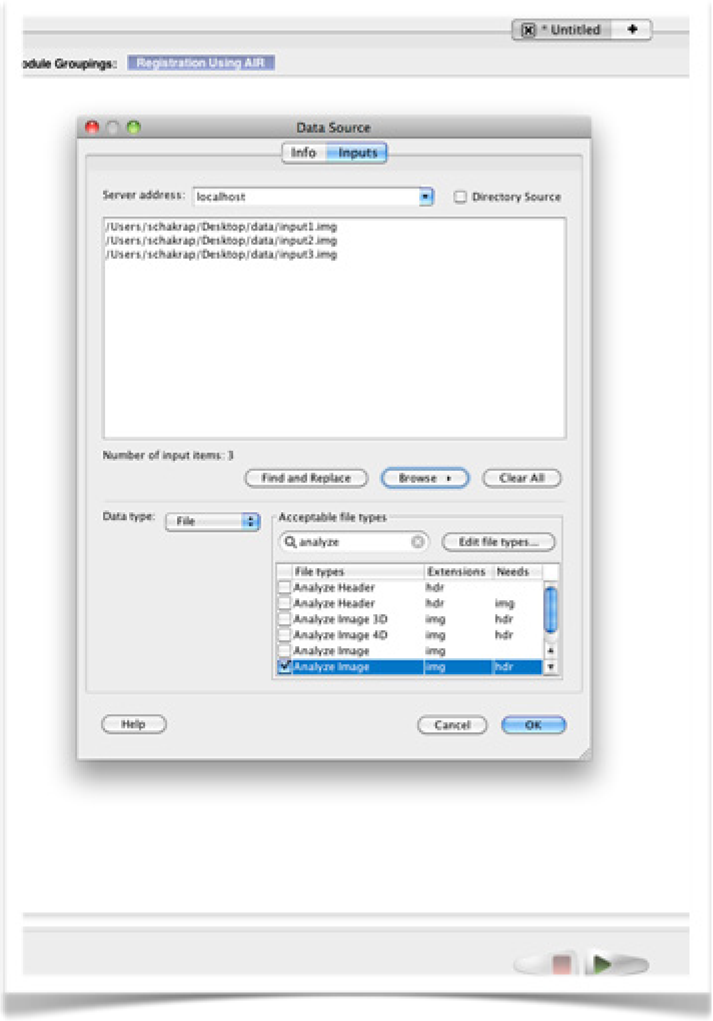
Data Sources and Sinks are a simple way to take advantage of parallelization of data processing. Users may specify all the files to be processed in much the same way one would specify all the subjects in a simple loop. What's more, the files can reside locally or remotely. Please note that in order to specify remote files, or to remotely browse for files, a Pipeline server must be running on the specified server.

How-to

Right click on the canvas
Choose new data source

Data Source ●	The data to be processed is input here. Double click to set the data path.
Data Sink ▼	Workflow results will output to this module's destination. Double click to set the output path.





Server address: localhost

□ Directory Source

```
/Users/schakrap/Desktop/data/input1.img
/Users/schakrap/Desktop/data/input2.img
/Users/schakrap/Desktop/data/input3.img
```

Number of input items: 3

Data type: File

Acceptable file types: analyze

	File types	Extensions	Needs
□	Analyze Header	hdr	
□	Analyze Header	hdr	img
□	Analyze Image 3D	img	hdr
□	Analyze Image 4D	img	hdr
□	Analyze Image	img	
☑	Analyze Image	img	hdr

All fields under the Module's tab are optional, including Name, Package, Package version, Tags, Description, website and comments
Click the Inputs tab
In the Input Data field, choose localhost (for local files) or use the drop down to specify remote server
Choose Browse
Choose Local Files to browse for local files, or Remote files to browse for remote files
Browse for file, click open
Repeat for all input files
Choose Data type (Directory, File, Number, String, Enumerated)
For File, choose File Type
Click OK
Connect to input parameter

Find & Replace

This features is particularly useful for data sinks as it allows you to cut and paste input file names, and manipulate them, thus creating explicit outputs. This feature is similar to find and replace in any text editing program.

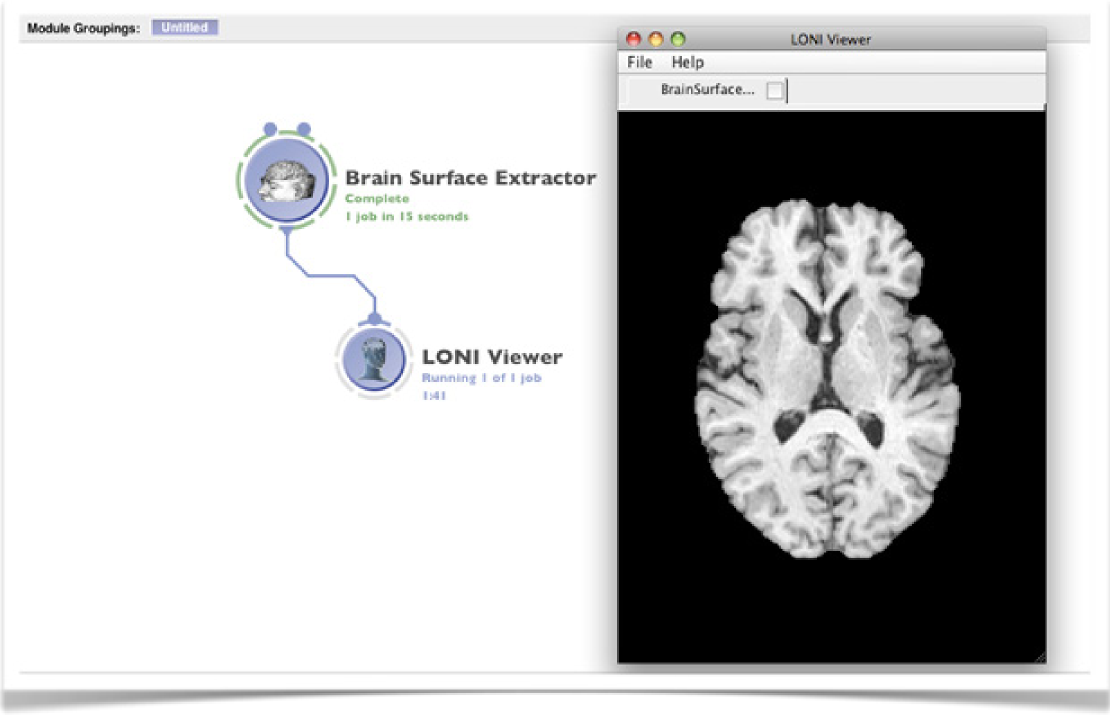
- Specify files to be processed using instructions above
- Choose Find and Replace
- In the Find field, specify string to search for (eg, .img)
- In the Replace field, specify string to replace the previous instance (eg _SkullStripped.img)
- Choose Replace All

NOTE: The above process is applicable to data sources as well as data sinks, simply right click on the canvas and specify data sink.

LONI Pipeline Viewer

Overview

The LONI Pipeline now has a built-in visualization tool (LONI Viewer) that lets you view results as soon as the execution completes. Simply choose Insert -> New Viewer on the top menu or right click on the workflow canvas and select “New Viewer…”. You can give inputs to this viewer by connecting the input parameter of the viewer to the output of other modules. When the file is ready, a separate Viewer window will pop up with the file to display. You can exit the LONI Pipeline, the Viewer will keep running until you close it.



Beginning Example Workflows

Registration Using AIR

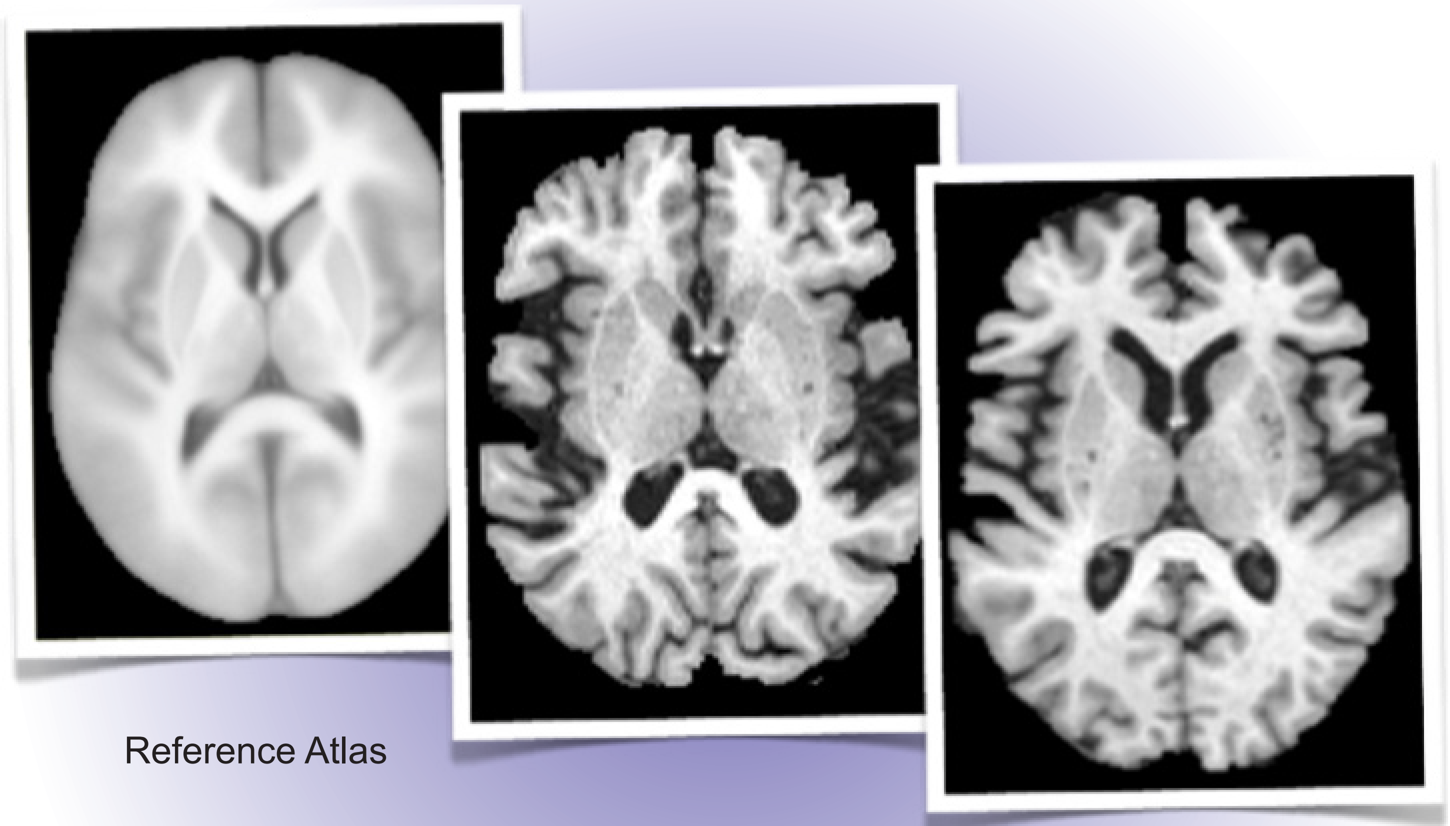
This is a simple registration workflow. The structural MRI images are aligned to a standard brain image by using AIR registration tools. To build this workflow follow the steps mentioned on the following pages.

Image Processing with the Quantitative Imaging Toolkit - Denoising

This workflow demonstrates several options for denoising with the Quantitative Imaging Toolkit (QIT).

Registration Using AIR

Automated Image Registration



Reference Atlas

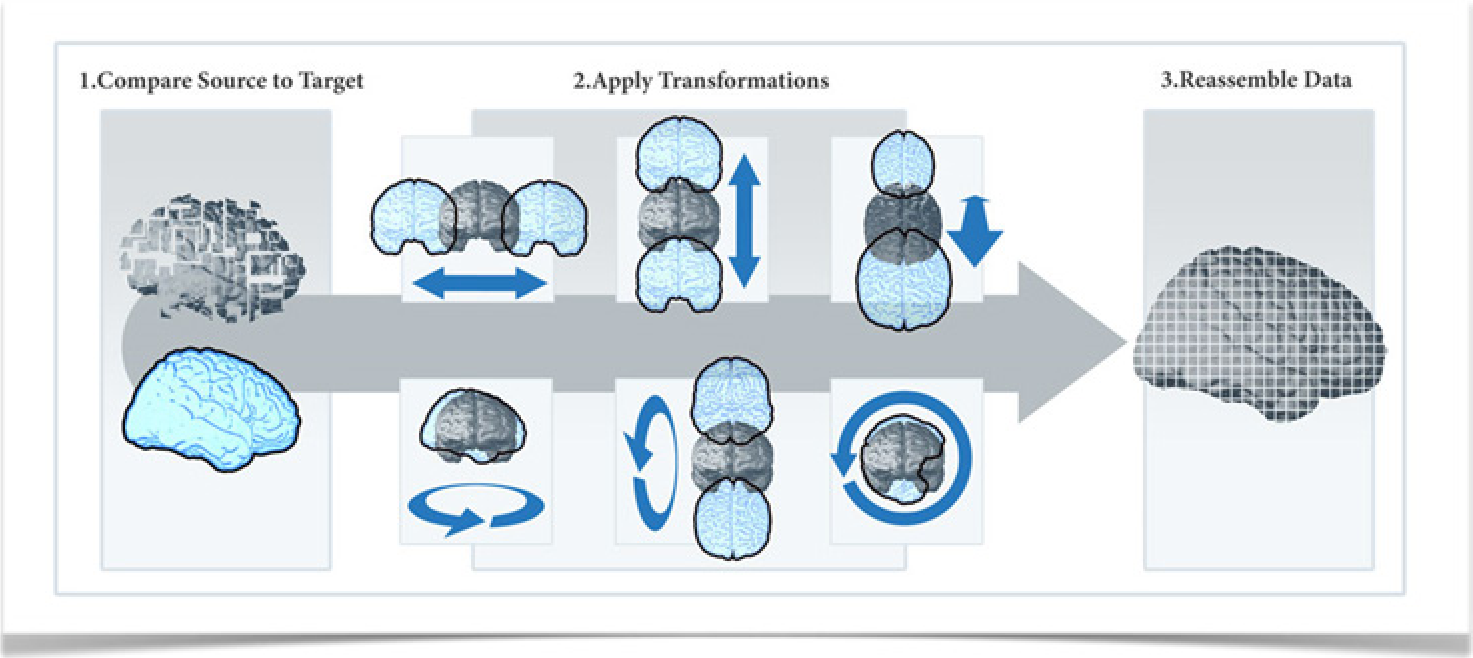
Source Volume

6 Parameter Registration

Registration Using AIR

Introduction

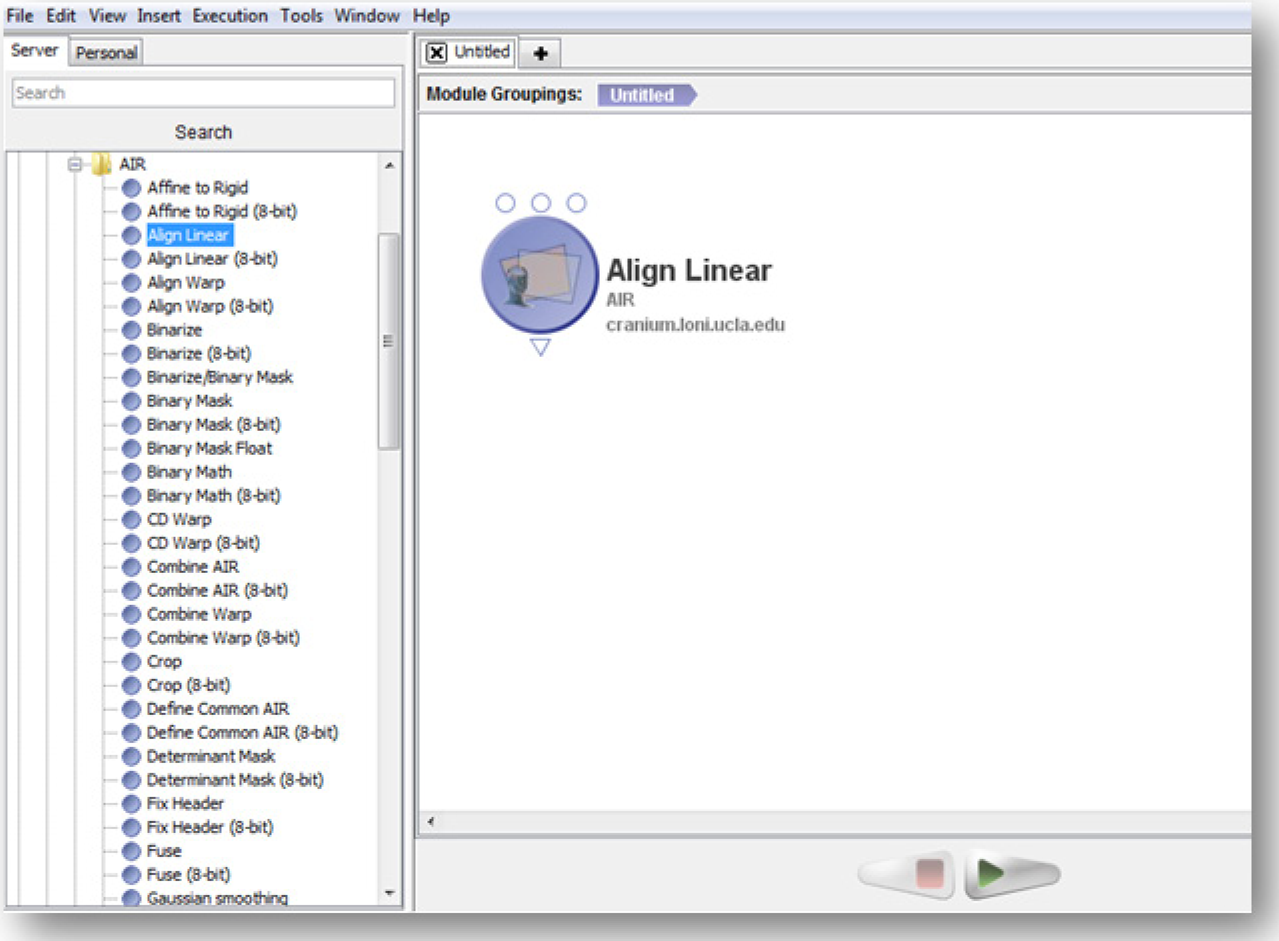
In this simple workflow, a registration algorithm generates a transformation matrix and applies it to move the source into the standard space.



Overview
This is a simple registration workflow. The structural MRI images are aligned to a standard brain image by using AIR registration tools. To build this workflow follow the steps mentioned on the following pages.

Registration Using AIR

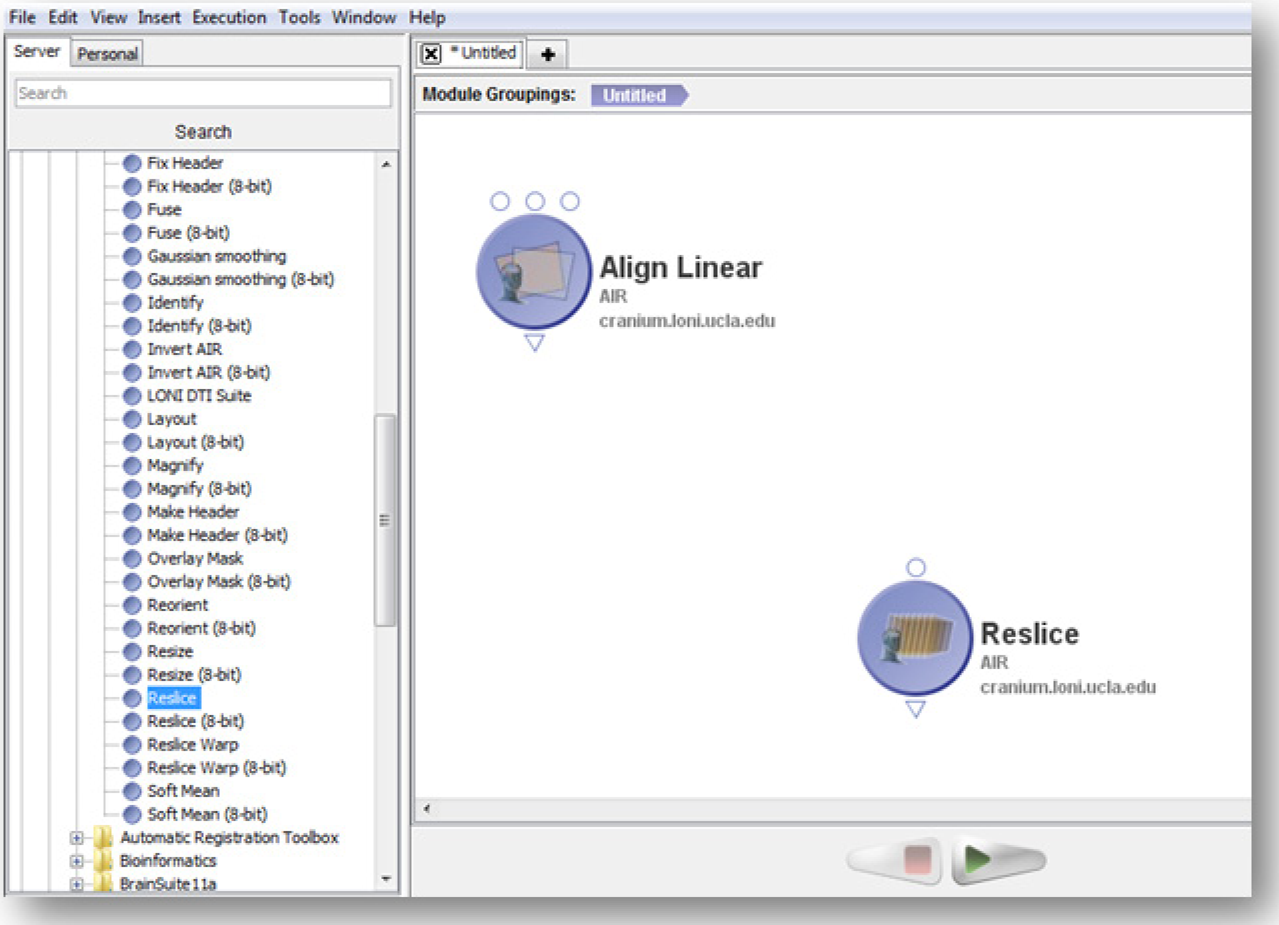
Select Align Linear



1) On the LONI Pipeline window, open the AIR package on the left side panel. Drag the module labeled Align Linear onto the canvas within the larger right panel of the Pipeline window.

Registration Using AIR

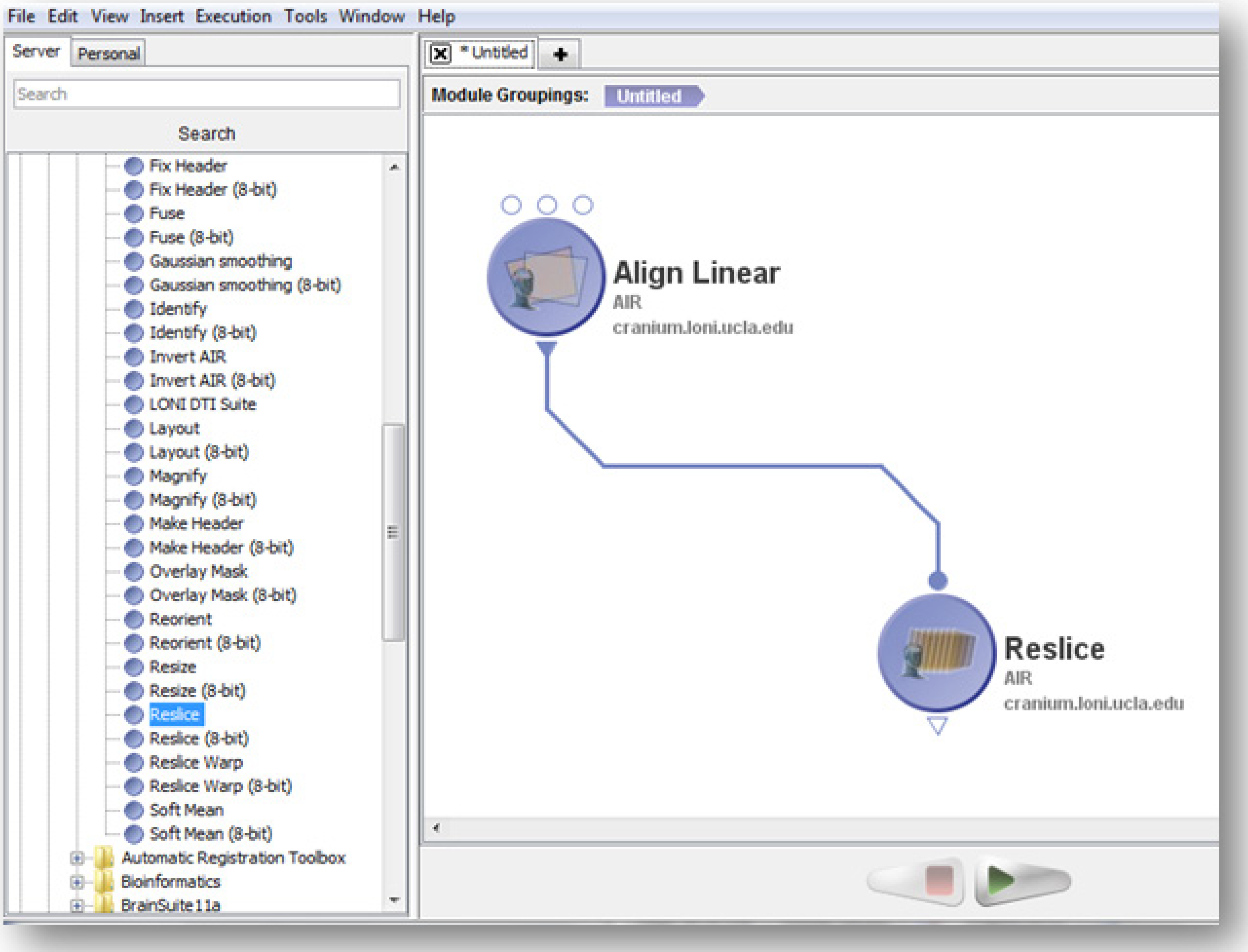
Select Reslice



2) In much the same way we added Align Linear to the canvas, drag across the Reslice module so that it is positioned below Align Linear.

Registration Using AIR

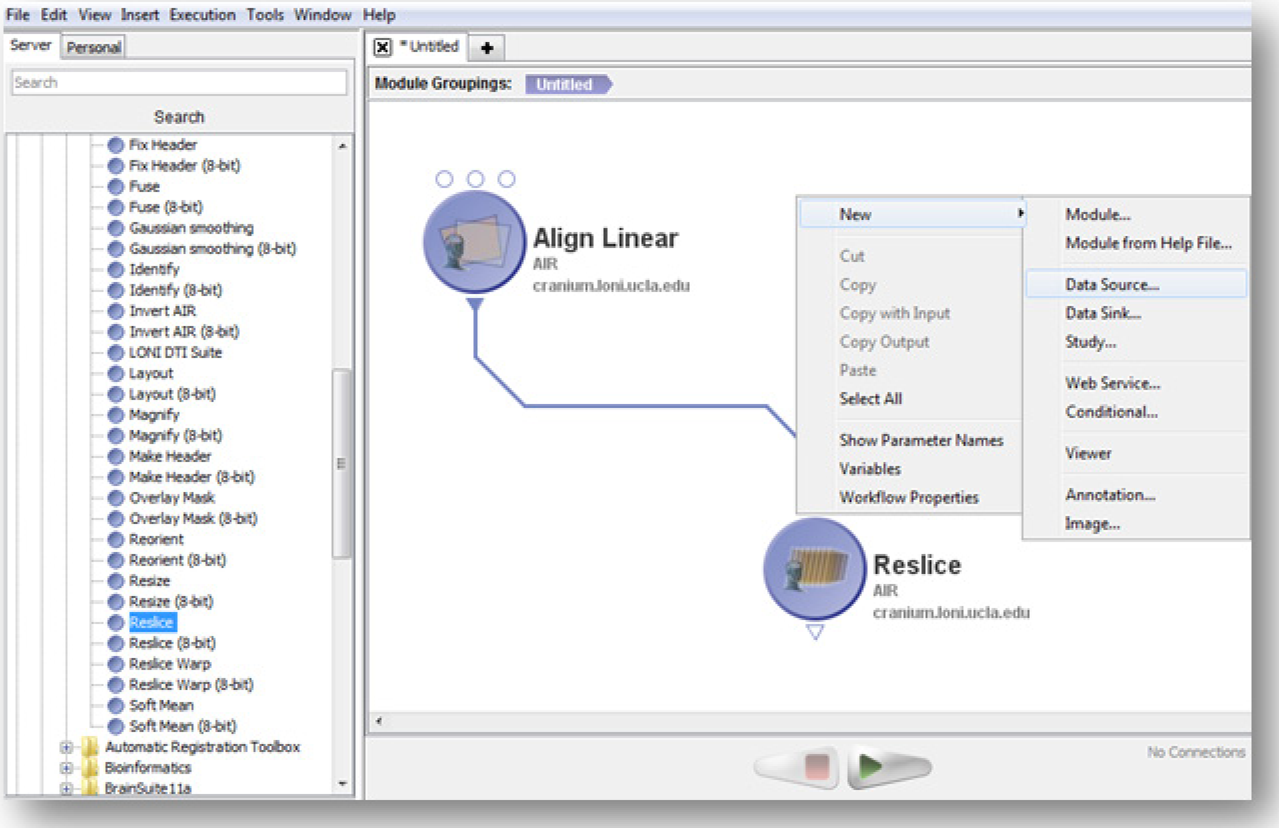
Connect Align Linear to Reslice



3) Connect the two modules by left-clicking on the output triangle of Align Linear and dragging the connecting line to the input circle of Reslice.

Registration Using AIR

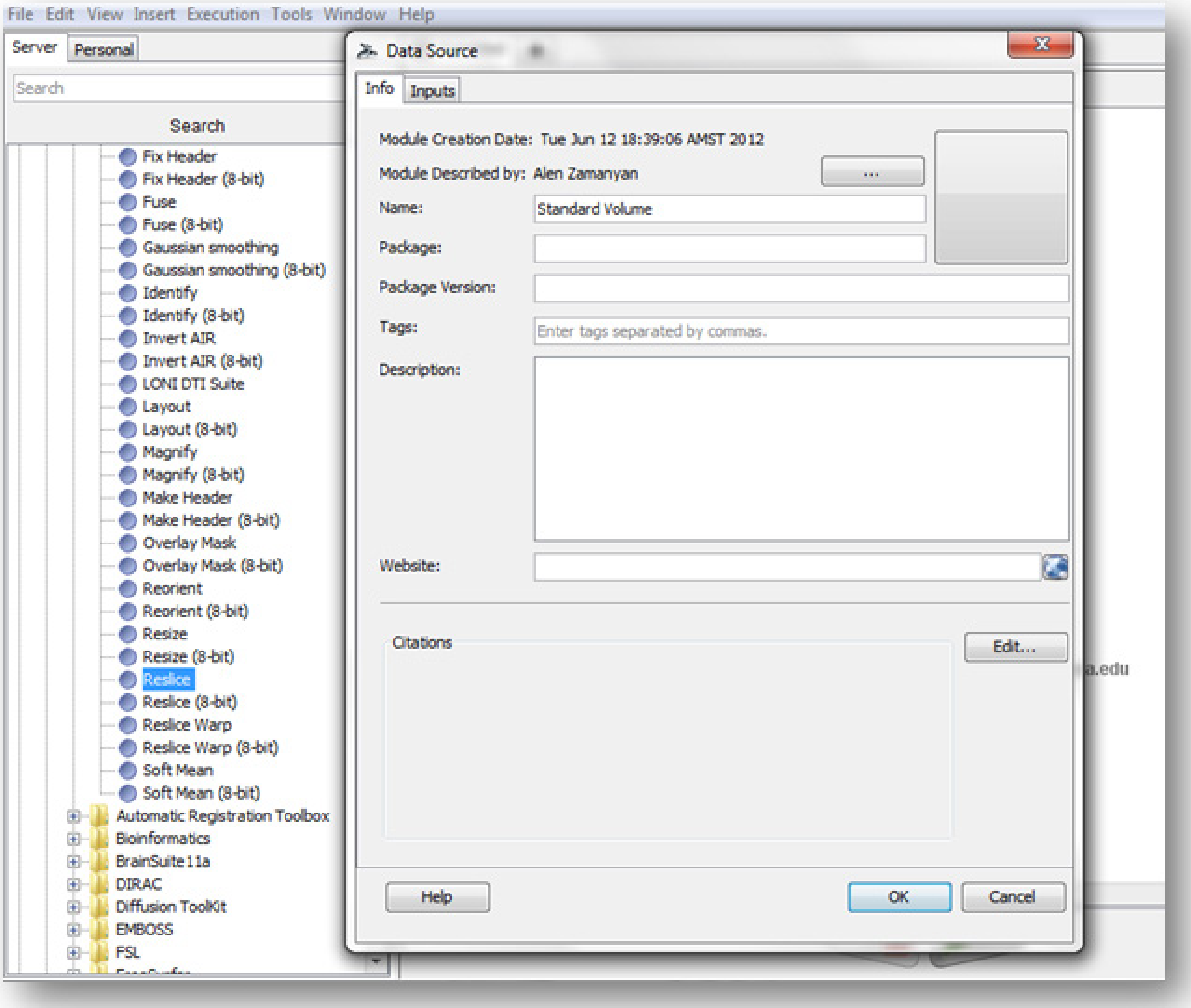
Create Data Source



4) The two modules are connected, but we have yet to specify any names of input files or destinations of output files. Let's begin with the inputs. Right clicking on the canvas will display workflow options. Select "New data source..."

Registration Using AIR

Name Data Source



Module Creation Date: Tue Jun 12 18:39:06 AMST 2012

Module Described by: Alen Zamanyan

Name: Standard Volume

Package:

Package Version:

Tags: Enter tags separated by commas.

Description:

Website:

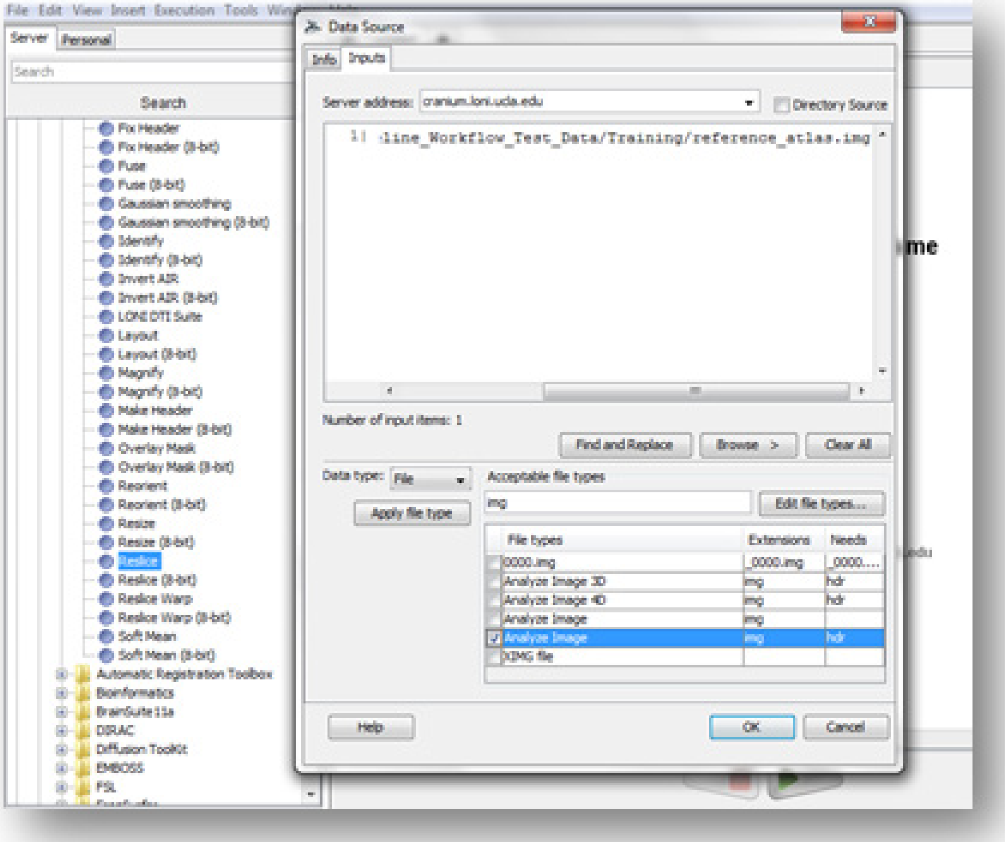
5) A dialog box "Data Source" appears on the screen, which has two tabs, namely Module and Data.

Module

In this tab, we can specify the **optional** information about the input data. In order to distinguish this source from others we will create, it is a good idea to complete the "Name:" field. Type in "Standard Volume".

Registration Using AIR

Specify Input Data



Server address: cranium.loni.ucla.edu

□ Directory Source

```
1| line_Workflow_Test_Data/Training/reference_atlas.img
```

Number of input items: 1

Data type: File

Acceptable file types: img

	File types	Extensions	Needs
□	0000.img	_0000.img	_0000....
□	Analyze Image 3D	img	hdr
□	Analyze Image 4D	img	hdr
□	Analyze Image	img	
☑	Analyze Image	img	hdr
□	XIMG file		

Data

There are three components that are **required** to be completed in this tab.

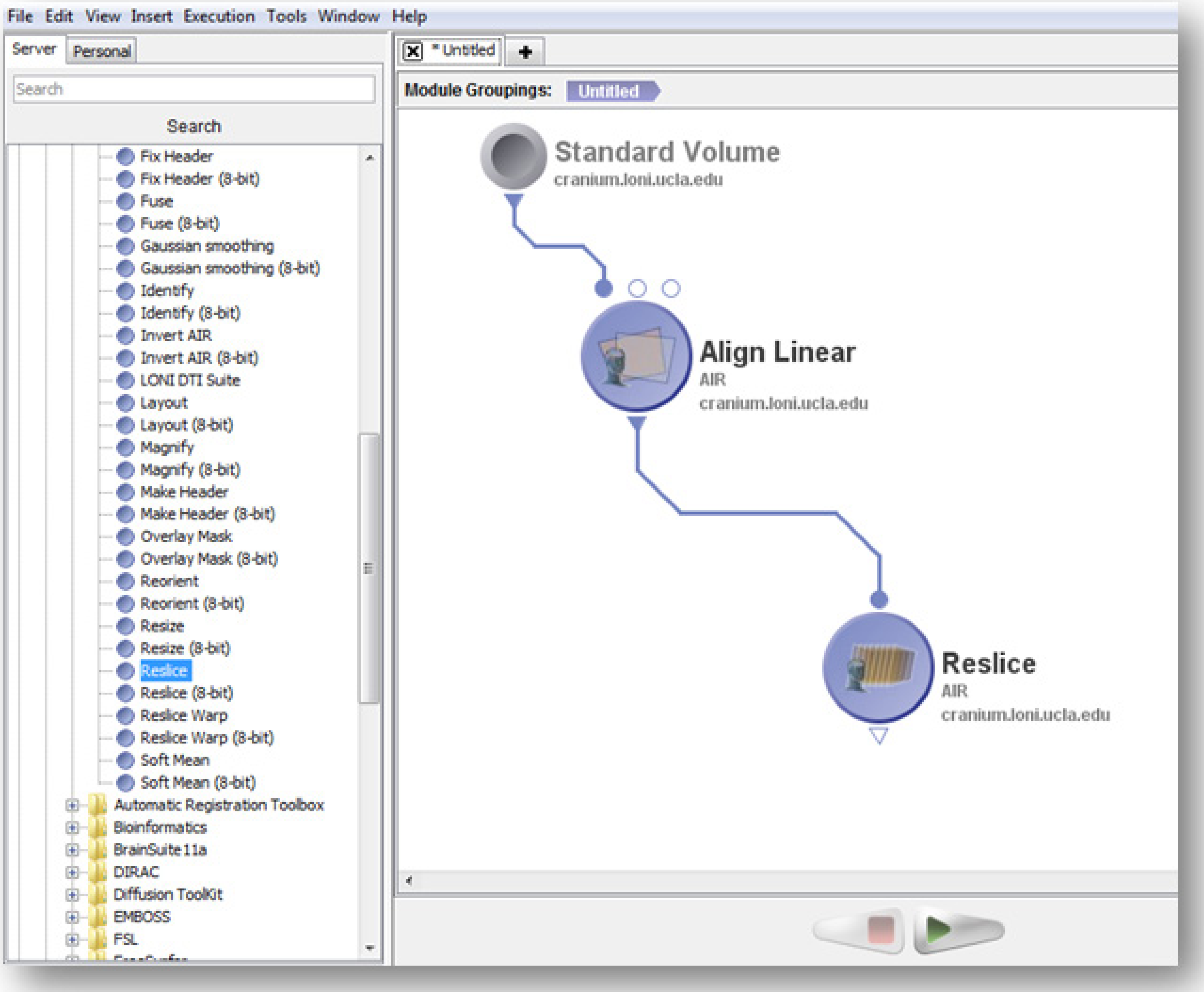
Input Data Field: First we will need to specify that the data is stored on the servers at LONI. There is a dropdown menu that appears for this field, which has two values, Local host and cranium.loni.usc.edu. **Choose cranium.loni.usc.edu**

Test Field (Below the Input Data Field): Type in the full path to the file in the text area. In this case, we will use the file stored at **/usr/local/loniData/Pipeline_Workflow_Test_Data/Training/reference_atlas.img**

Input file Type: We need to select the input file type. Select (by checking) "Analyze Image" and uncheck the file option (which is the default). Hitting the OK button will return us to the workflow canvas.

Registration Using AIR

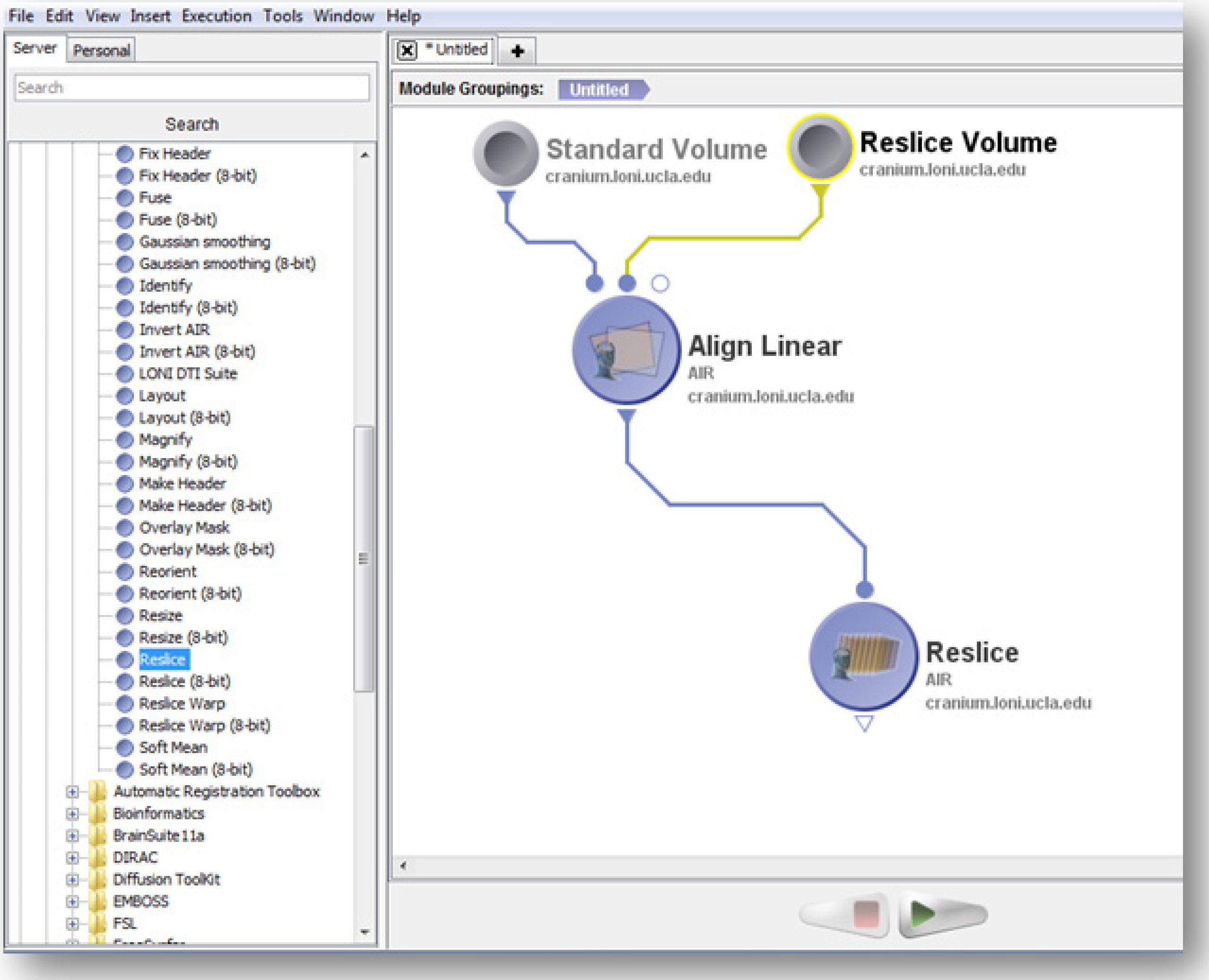
Connect Standard Volume to Align Linear



6) Connect the data source that we just created to the first input parameter of Align Linear, labeled "Standard Volume." Do this in much the same way we connected Align Linear to Reslice. Click on the empty triangle of the data source and drag into the first empty circle above the Align Linear module.

Registration Using AIR

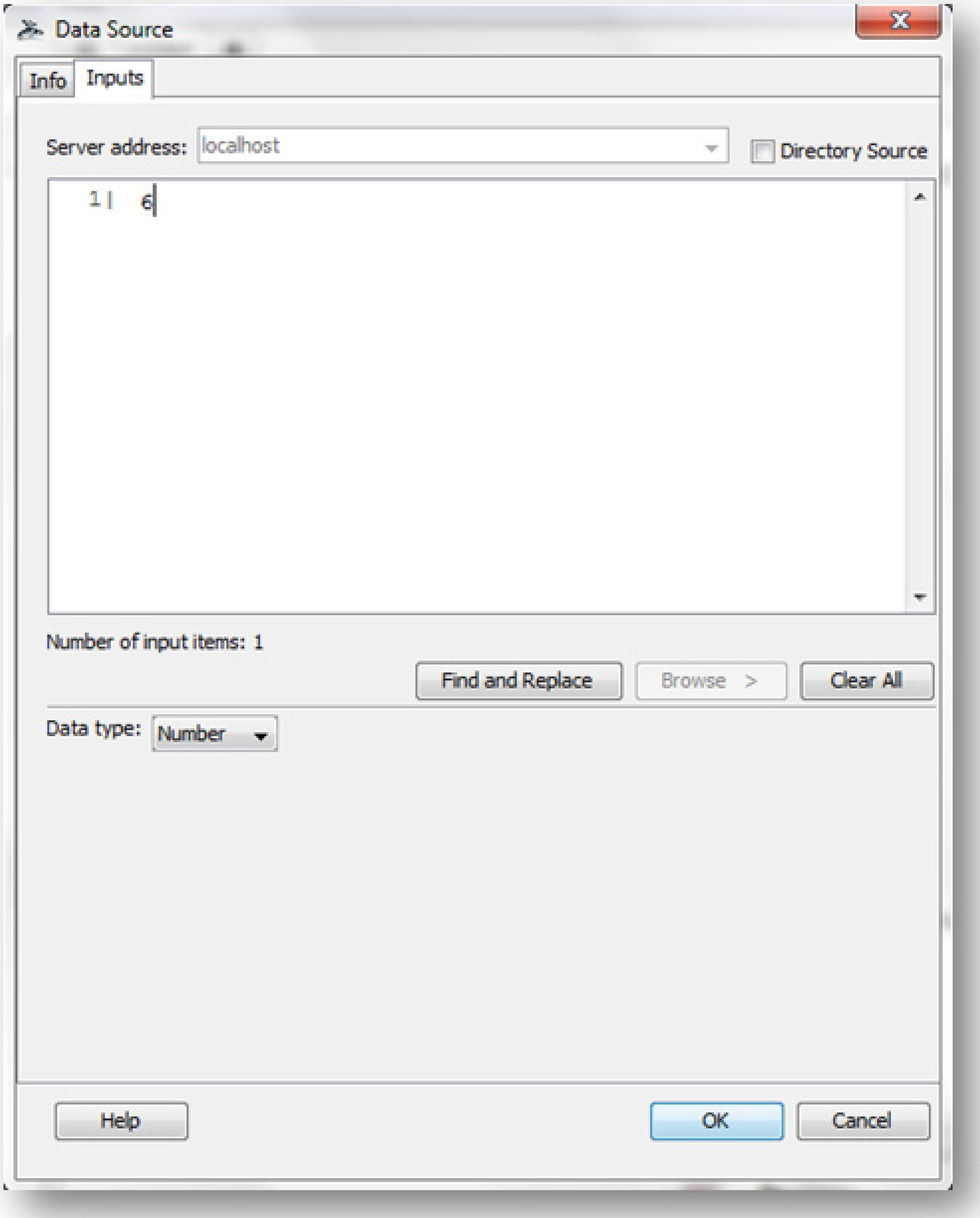
Reslice Volume Data Source



7) Repeat steps four through seven to create a data source for the file that is to be aligned to the standard. Call the data source **"Reslice Volume"** and specify the input filename as **/usr/local/loniData/Pipeline_Workflow_Test_Data/Training/source_volume.img**. Make sure to switch from **localhost to cranium.loni.usc.edu** and change the **filetype to Analyze Image**. Connect the input to the second empty circle above Align Linear (the parameter name is "Reslice Volume").

Registration Using AIR

Model Number Data Source



Server address: localhost

```
1| 6
```

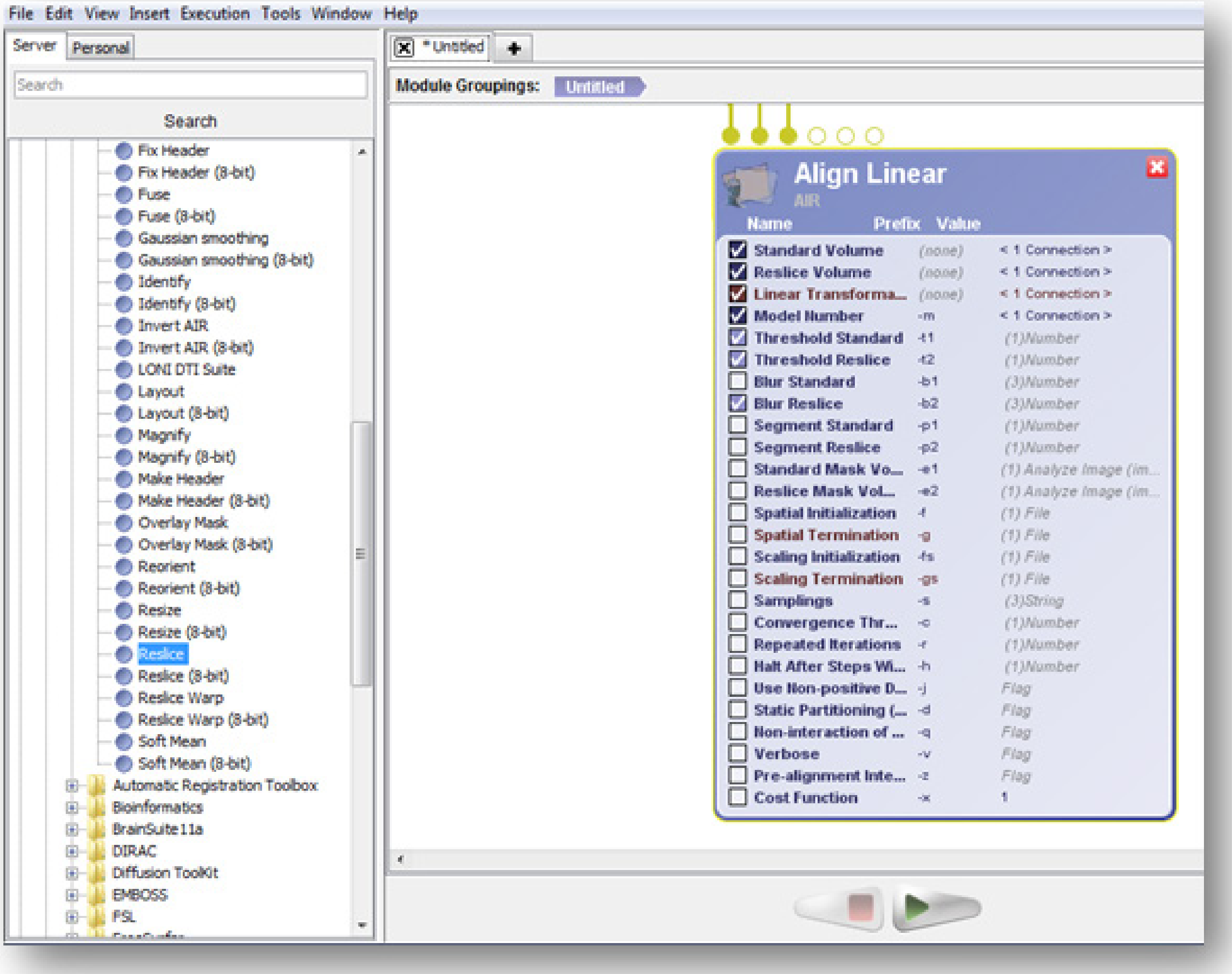
Number of input items: 1

Data type: Number

8) Create a third data source by right clicking on the canvas and selecting "New data source..." Name the data source **"Model Number"**. In the Data tab, change the **"Data type"** to **"Number"**. In the text area, enter the number 6.

Registration Using AIR

Select Optional Parameters

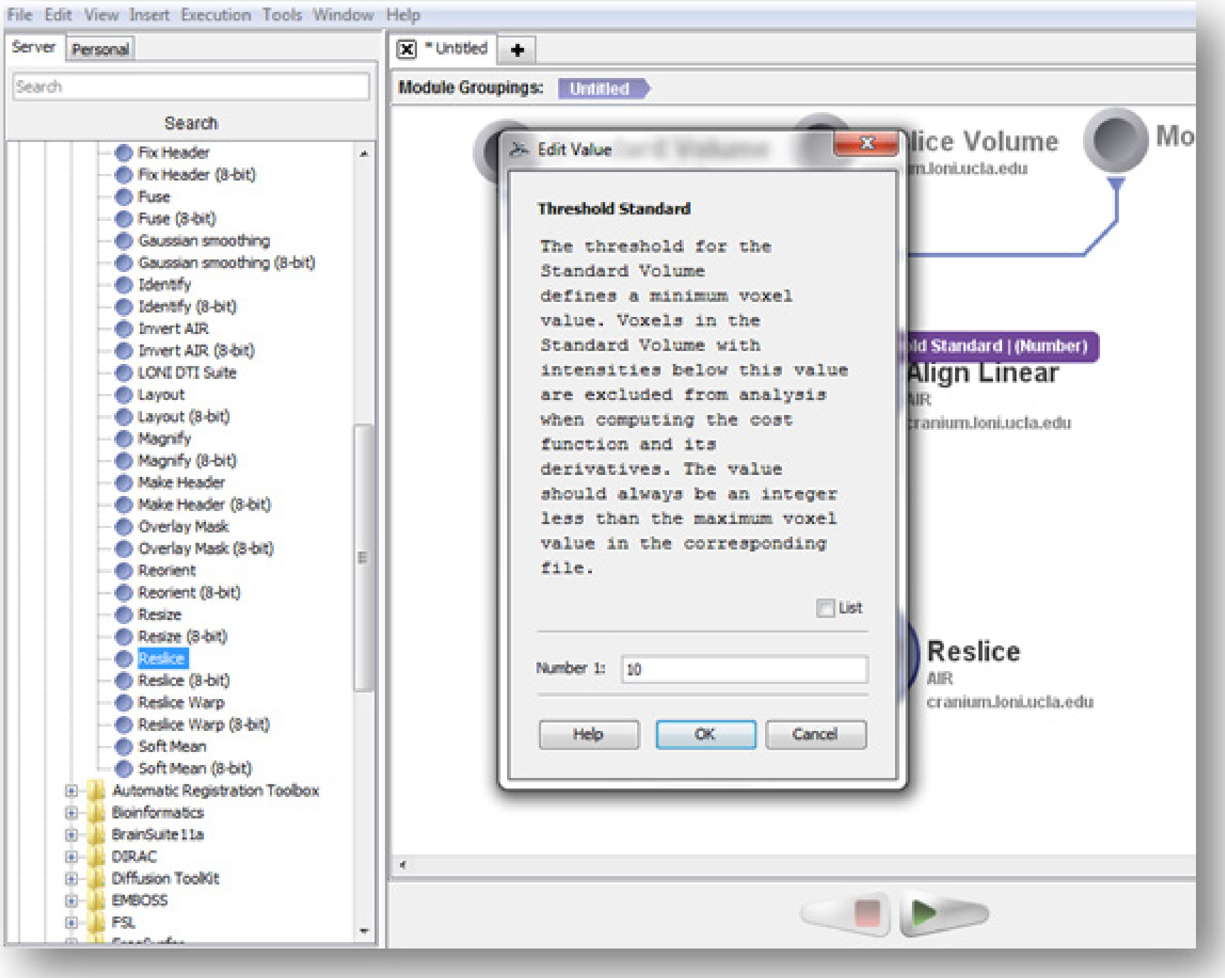


	Name	Prefix	Value
☑	Standard Volume	(none)	< 1 Connection >
☑	Reslice Volume	(none)	< 1 Connection >
☑	Linear Transforma...	(none)	< 1 Connection >
☑	Model Number	-m	< 1 Connection >
☑	Threshold Standard	-t1	(1)Number
☑	Threshold Reslice	-t2	(1)Number
☐	Blur Standard	-b1	(3)Number
☑	Blur Reslice	-b2	(3)Number
☐	Segment Standard	-p1	(1)Number
☐	Segment Reslice	-p2	(1)Number
☐	Standard Mask Vo...	-e1	(1) Analyze Image (im...
☐	Reslice Mask Vol...	-e2	(1) Analyze Image (im...
☐	Spatial Initialization	-f	(1) File
☐	Spatial Termination	-g	(1) File
☐	Scaling Initialization	-fs	(1) File
☐	Scaling Termination	-gs	(1) File
☐	Samplings	-s	(3)String
☐	Convergence Thr...	-c	(1)Number
☐	Repeated Iterations	-r	(1)Number
☐	Halt After Steps Wi...	-h	(1)Number
☐	Use Non-positive D...	-j	Flag
☐	Static Partitioning (...	-d	Flag
☐	Non-interaction of ...	-q	Flag
☐	Verbose	-v	Flag
☐	Pre-alignment Inte...	-z	Flag
☐	Cost Function	-x	1

9) For some modules, there are a number of options, which are optional, but highly recommended. In the case of Align Linear, we will threshold the standard and reslice volumes, along with blurring the reslice volume in order to achieve optimal results. To do this, double-click on the Align Linear module to bring up a panel with the complete list of parameters. In order to enable the optional parameters mentioned, click the box on the left of the Threshold Standard, Threshold Reslice, and Blur Reslice.

Registration Using AIR

Arguments to Threshold Standard/Reslice Parameters



Threshold Standard

The threshold for the Standard Volume defines a minimum voxel value. Voxels in the Standard Volume with intensities below this value are excluded from analysis when computing the cost function and its derivatives. The value should always be an integer less than the maximum voxel value in the corresponding file.

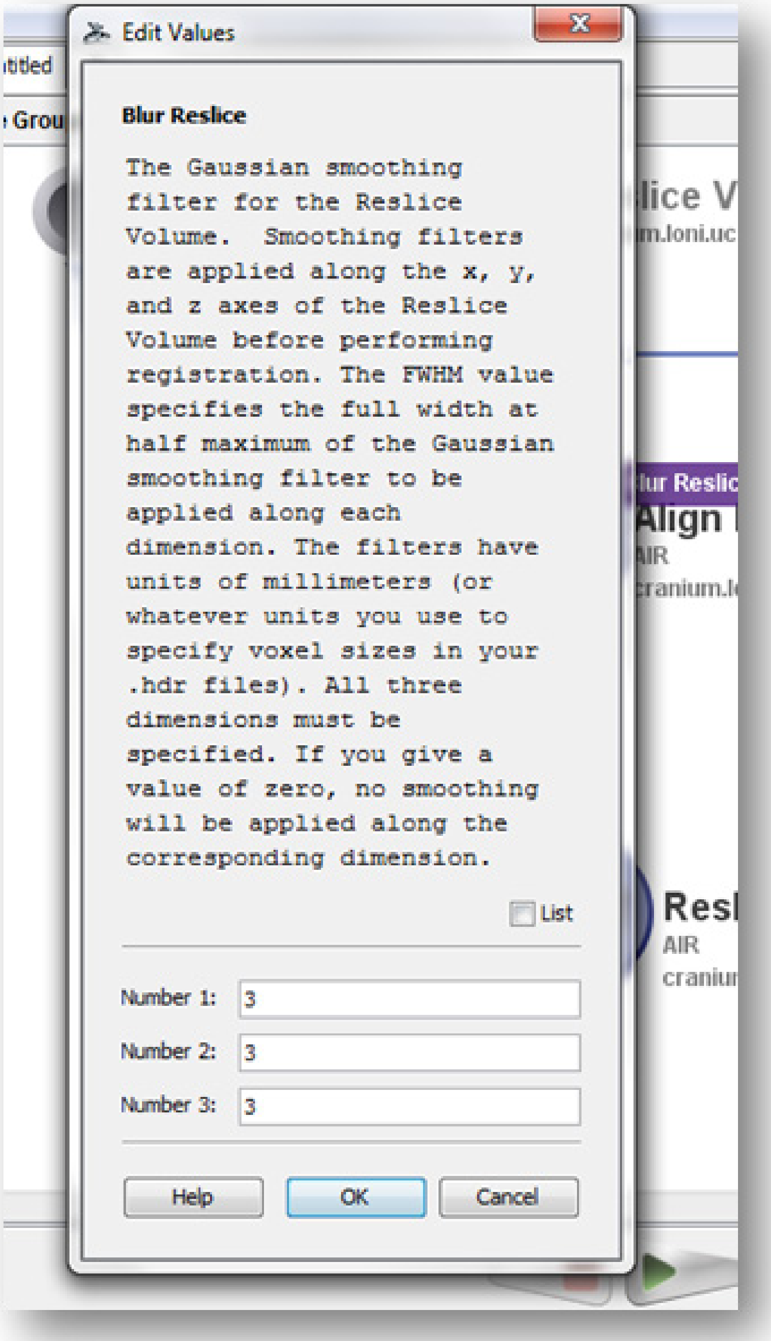
□ List

Number 1: 10

10) Three new empty circles will appear above the Align Linear rectangular module. Double clicking on these will produce dialog boxes, which we will use to specify arguments. In the threshold dialogs, the parameters are described as such: "The threshold for the Standard/ Reslice Volume defines a minimum voxel value. Voxels in the Standard/Reslice Volume with intensities below this value are excluded from analysis when computing the cost function and its derivatives. The value should always be an integer less than the maximum voxel value in the corresponding file." If we were to be meticulous about it, we could produce a histogram of the MRI data and find the threshold below which the values would be considered noise. For most MRI data, 10 is a reasonable value. Specify this value for both the standard and reslice files.

Registration Using AIR

Arguments to Blur Reslice Parameter



Blur Reslice

The Gaussian smoothing filter for the Reslice Volume. Smoothing filters are applied along the x, y, and z axes of the Reslice Volume before performing registration. The FWHM value specifies the full width at half maximum of the Gaussian smoothing filter to be applied along each dimension. The filters have units of millimeters (or whatever units you use to specify voxel sizes in your .hdr files). All three dimensions must be specified. If you give a value of zero, no smoothing will be applied along the corresponding dimension.

□ List

Number 1: 3

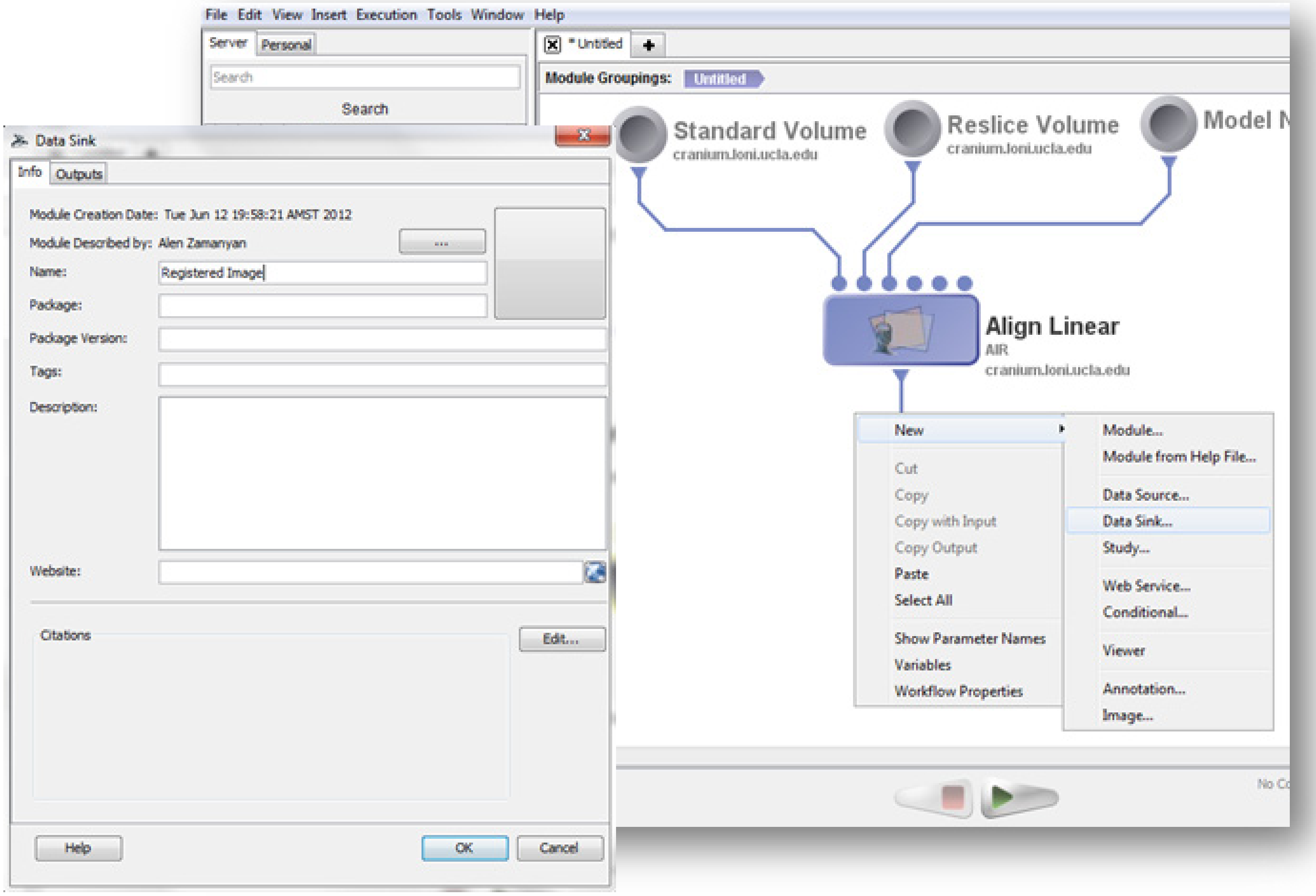
Number 2: 3

Number 3: 3

11) The description of the blurring option states: "The Gaussian smoothing filter for the Reslice Volume. Smoothing filters are applied along the x, y, and z axes of the Reslice Volume before performing registration. The FWHM value specifies the full width at half maximum of the Gaussian smoothing filter to be applied along each dimension. The filters have units of millimeters (or whatever units you use to specify voxel sizes in your .hdr files). All three dimensions must be specified. If you give a value of zero, no smoothing will be applied along the corresponding dimension." The concept is a simple one. In structural MRI, the atlas is typically an average of many subject MRIs, hence, if visualized, it looks blurry. A single subject's MRI is much crisper. In this instance, simply blurring the subject MRI may provide better registration. So for a voxel size of 1x1x1, blurring at a rate of 3x3x3 should be appropriate. Enter in the value 3 for each of the three text boxes in the edit parameter dialog box.

Registration Using AIR

Data Sink for Registered Image



Data Sink

Module Creation Date: Tue Jun 12 19:58:21 AMST 2012

Module Described by: Alen Zamanyan

Name: Registered Image

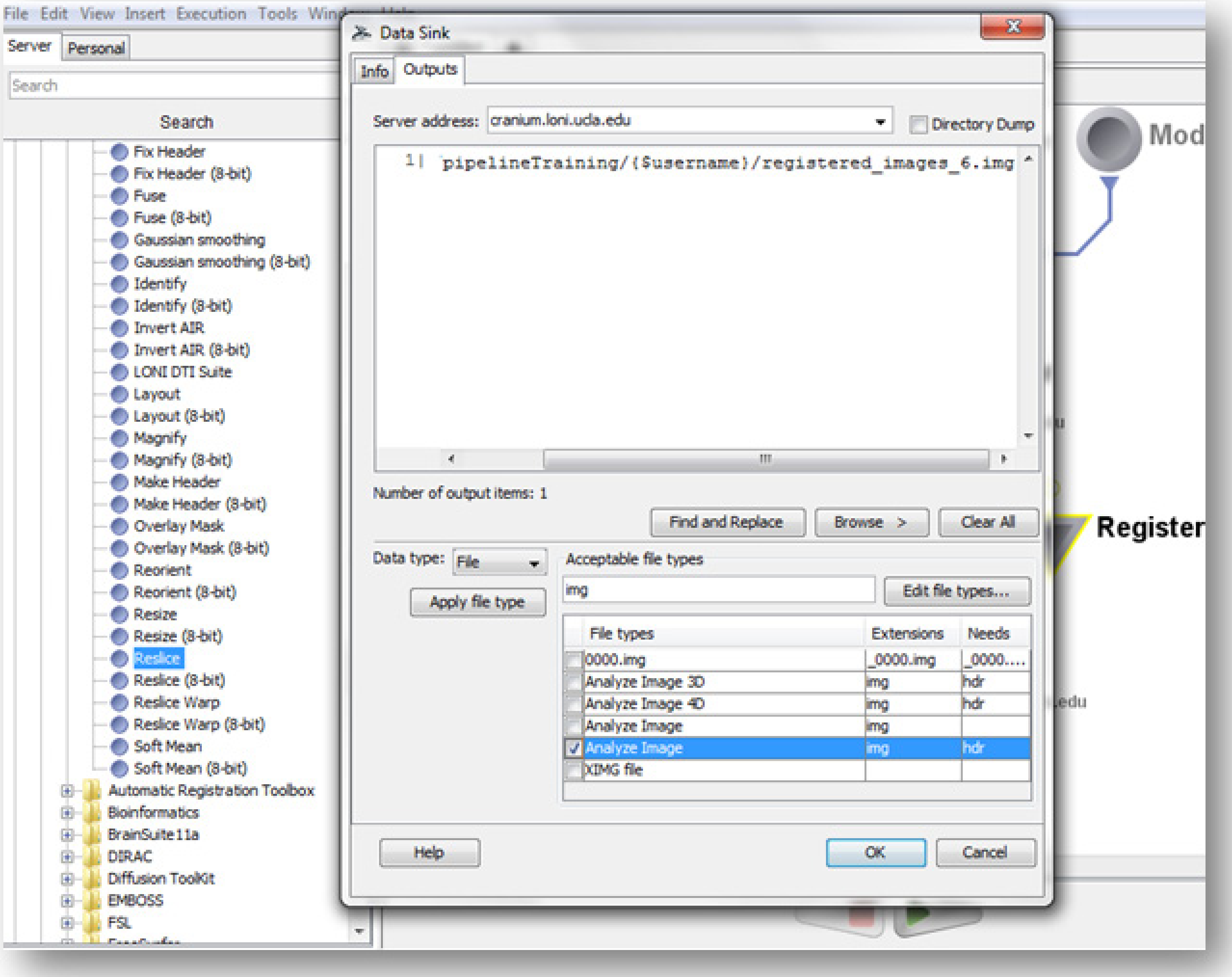
12) We can now proceed to specify the destination of the output of Reslice. Right click on the workflow canvas, and select "New data sink..."

Module tab

Fill in the name field with the value "Registered Image."

Registration Using AIR

Destination of Output File



Server address: cranium.loni.ucla.edu

□ Directory Dump

```
pipelineTraining/{$username}/registered_images_6.img
```

Number of output items: 1

Data type: File

Acceptable file types: img

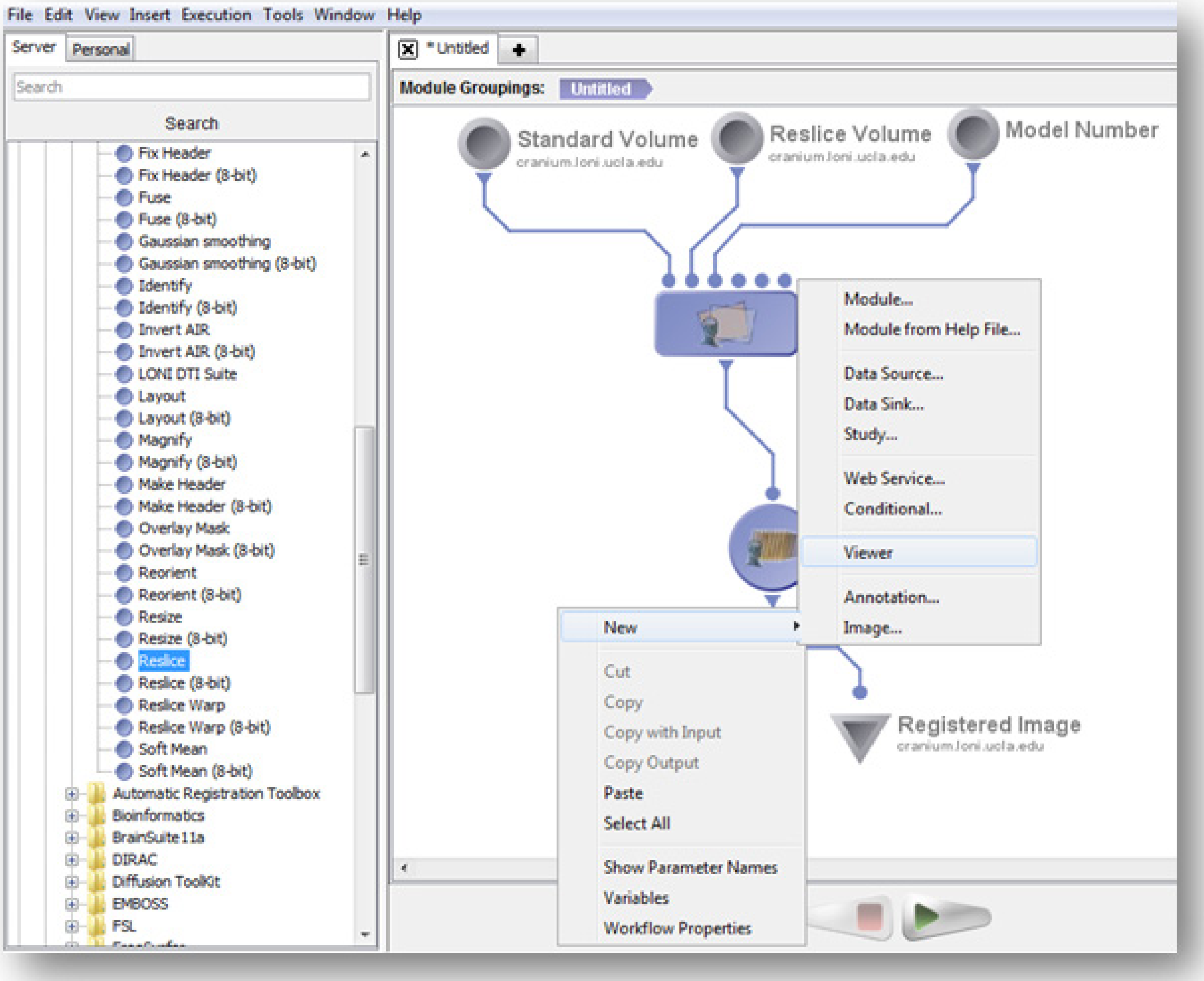
	File types	Extensions	Needs
□	0000.img	_0000.img	_0000....
□	Analyze Image 3D	img	hdr
□	Analyze Image 4D	img	hdr
□	Analyze Image	img	
☑	Analyze Image	img	hdr
□	XIMG file		

Data tab

Select cranium.loni.usc.edu from the dropdown at the top of the window. The output filetype is Analyze Image. In the text area, specify the output file as /ifs/tmp/pipelineTraining/{$username}/registered_images_6.img. Hit OK and connect the output of Reslice to the input of the data sink.

Registration Using AIR

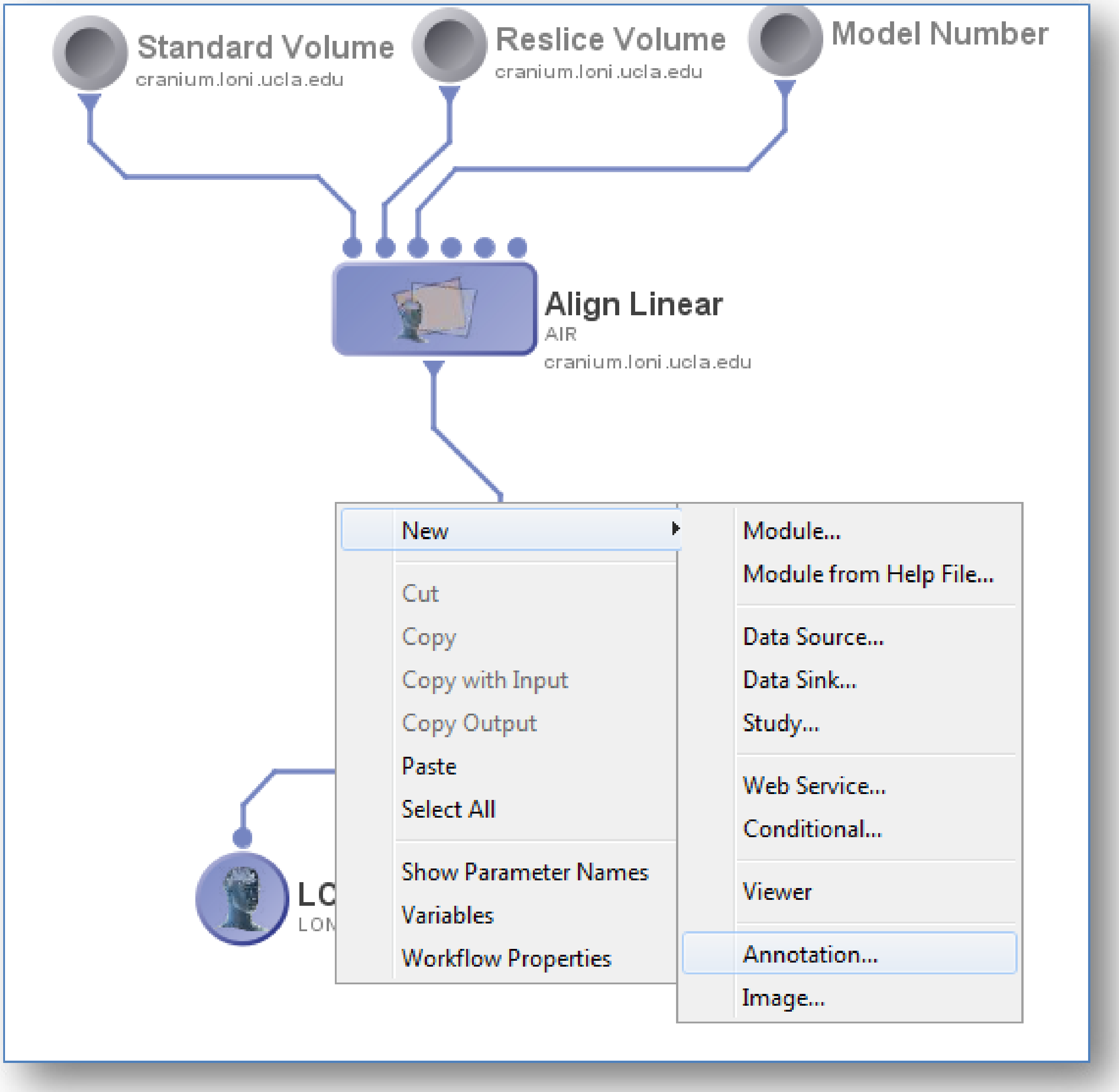
LONI Viewer



13) Finally, for visualization purposes, we will create a LONI Viewer module. Right-click on the canvas and select "LONI Viewer..." Hit the OK button and connect the output of Reslice to the input of the viewer. Optionally, we can create another viewer and connect it to the input volumes.

Registration Using AIR

Annotation Option



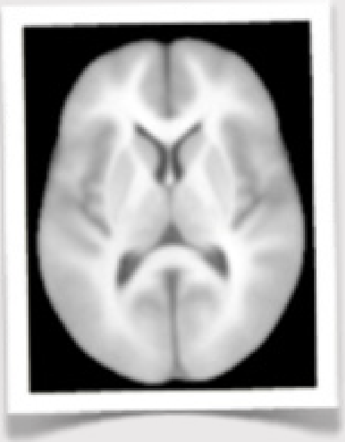
14) Optionally, you can create annotations by right-clicking on the canvas and selecting “New annotation...”

Registration Using AIR

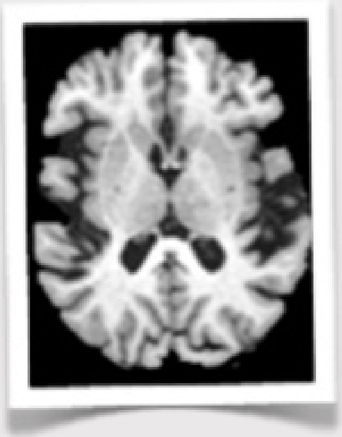
Results

The results of this Pipeline Workflow would look like the 6 Parameter Registration image. The Reference and Source Volumes are included for comparison.

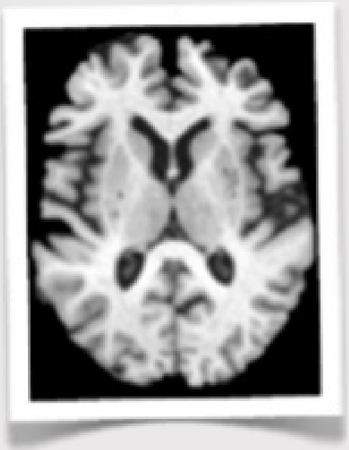
Optionally, you could also increase the degrees of freedom to fit the source volume to the reference even tighter. To get these optional results, in step 8, list the numbers 6, 7, 9, and 12, each on its own line.



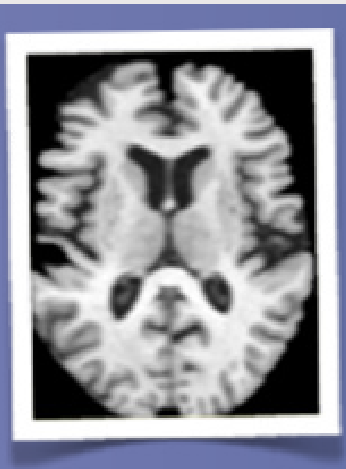
Reference Atlas



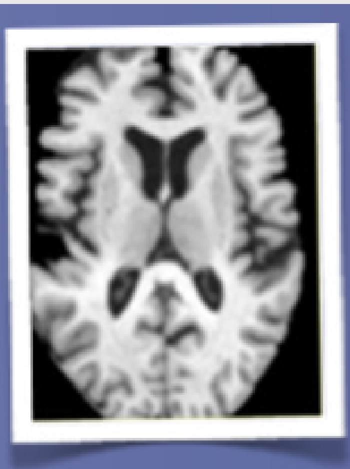
Source Volume



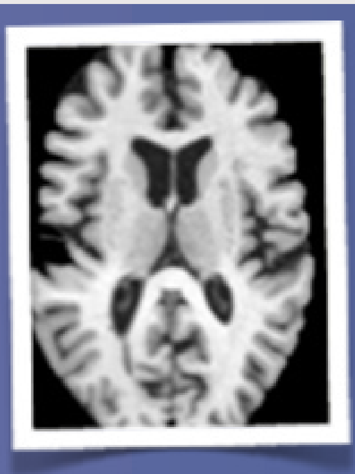
6 Parameter Registration



7 Parameter Registration



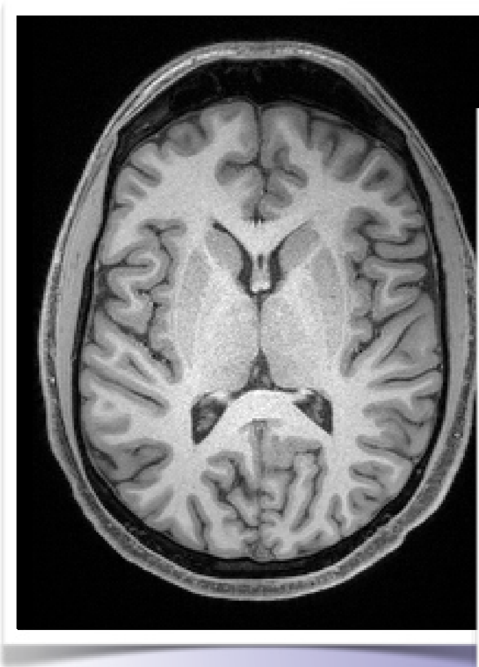
9 Parameter Registration



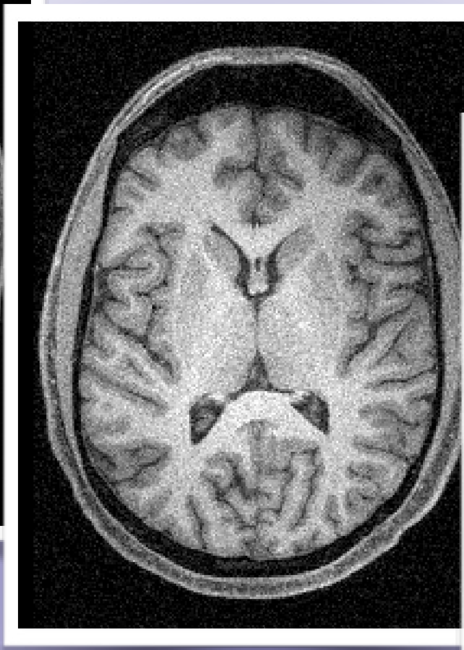
12 Parameter Registration

Other Options...

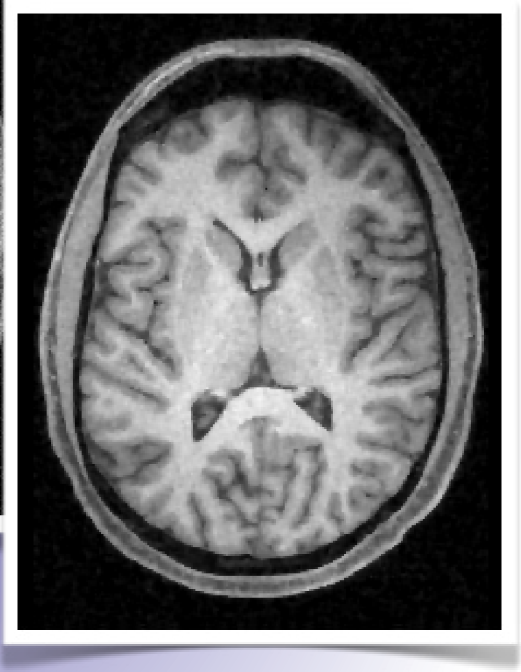
Image Processing with the Quantitative Imaging Toolkit - Denoising



Input Raw



Output Noisy



Output Denoised

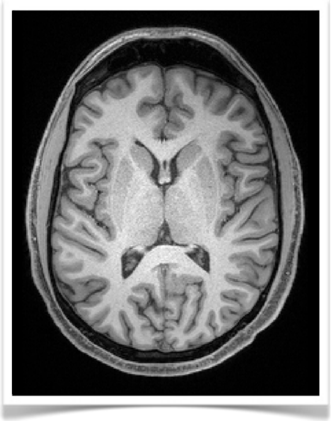
Processing with QIT - Denoising

Introduction

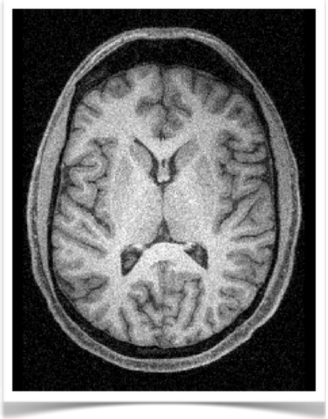
This workflow demonstrates several options for denoising with the Quantitative Imaging Toolkit (QIT).

This example demonstrates the use of different denoising algorithms on brain imaging data. Denoising is an important preprocessing step in most image analysis pipelines, since even small amounts of noise can impact the reliability and accuracy of quantitative imaging metrics. To demonstrate these algorithms, we first add noise to a brain image and then compare the results of three different types of denoising algorithms.

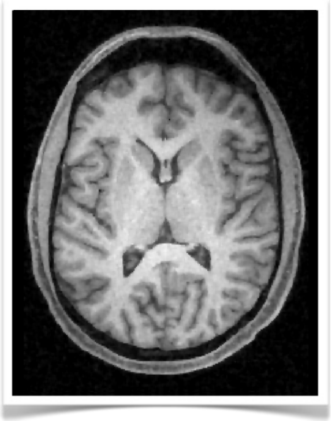
Input Raw



Output Noisy

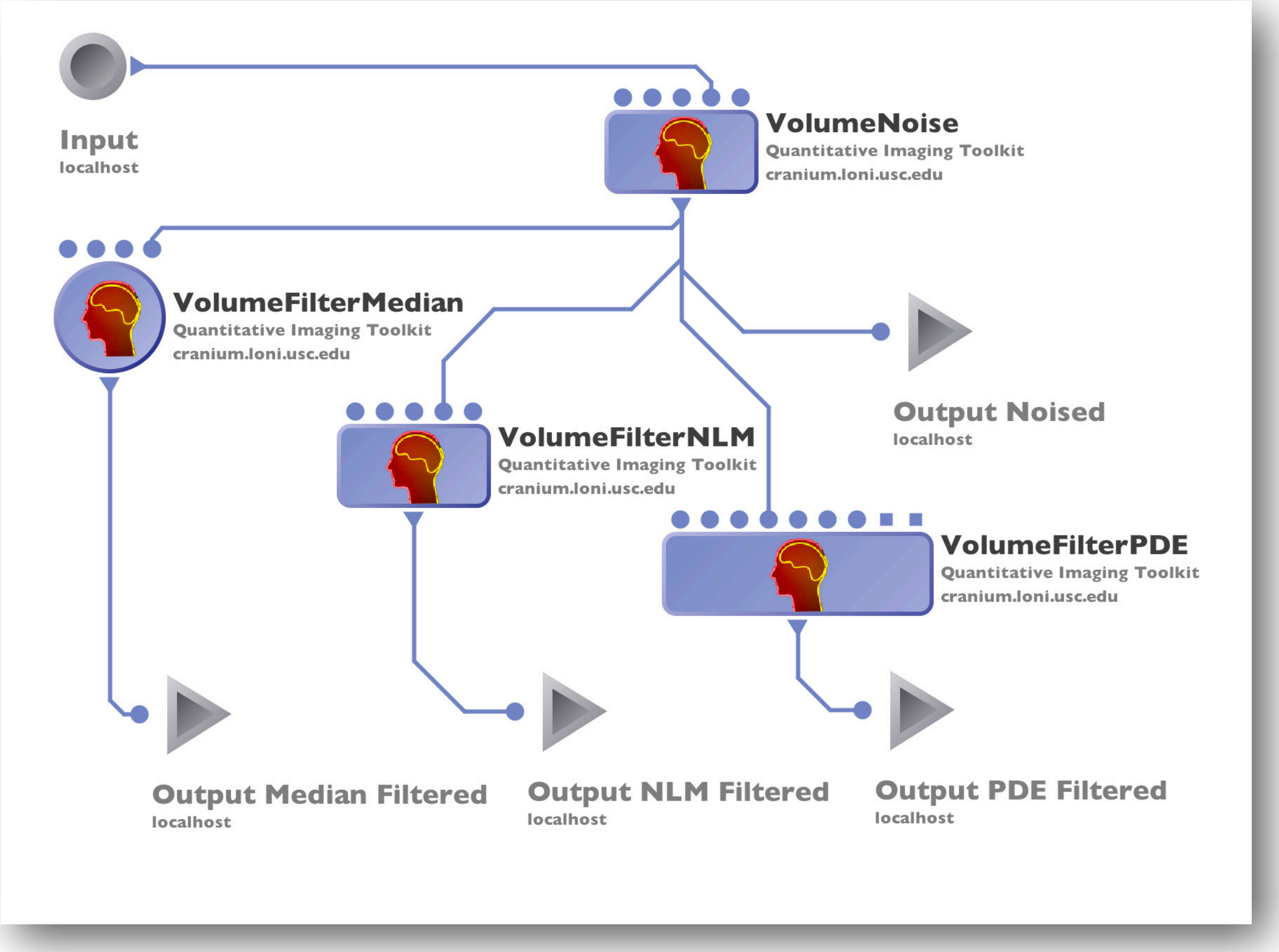


Output Denoised



Processing with QIT - Denoising

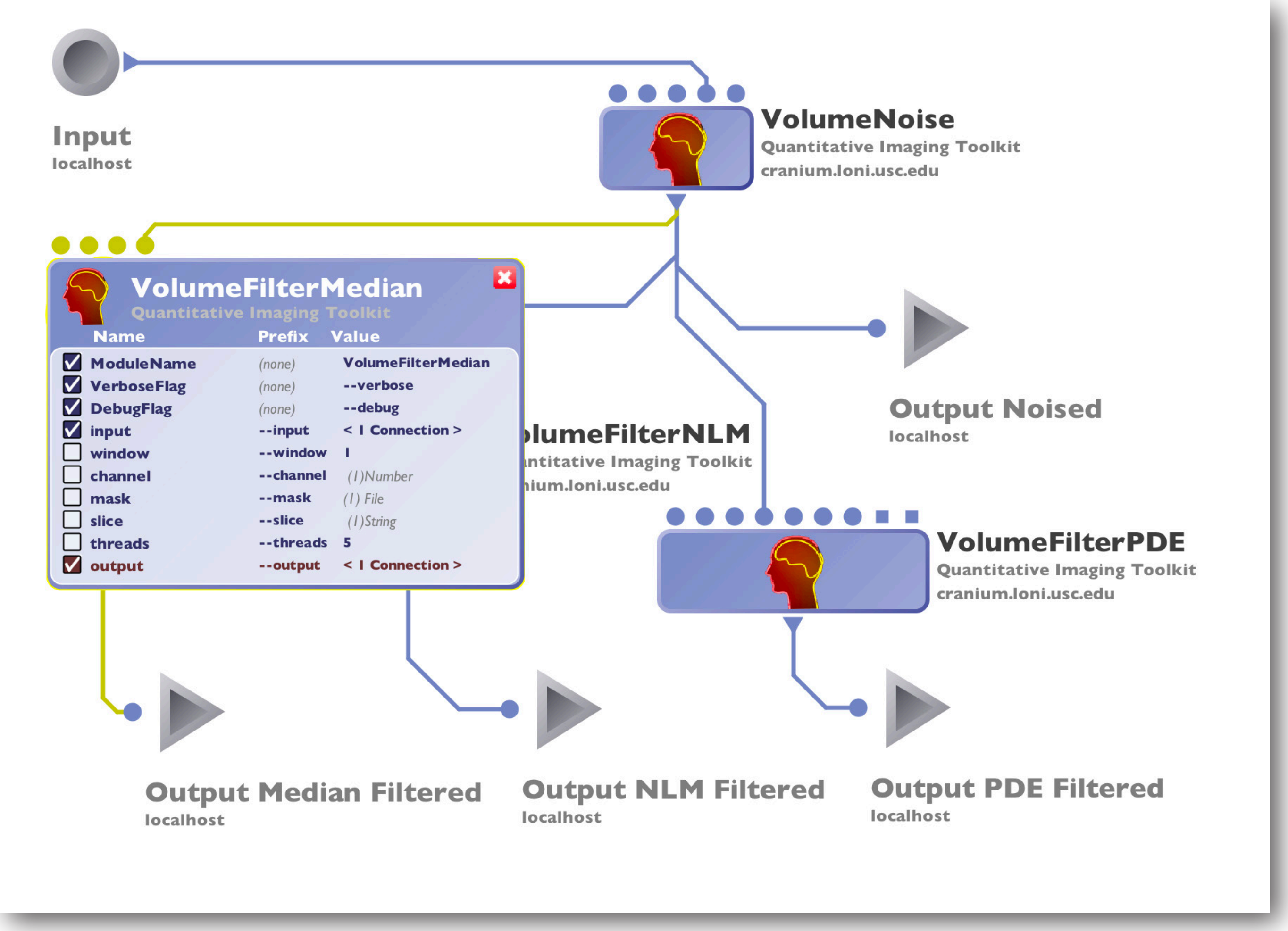
Workflow Overview



Shown above is a simple workflow for testing denoising algorithms. The input dataset is a T1-weighted MRI of a typical brain. First, synthetic noise is added to the image using the VolumeNoise module in QIT. Then, three different denoising algorithms are applied to the noisy image and the results are saved for comparison. Next, we will examine the different algorithms and the important parameters.

Processing with QIT - Denoising

Median Filtering



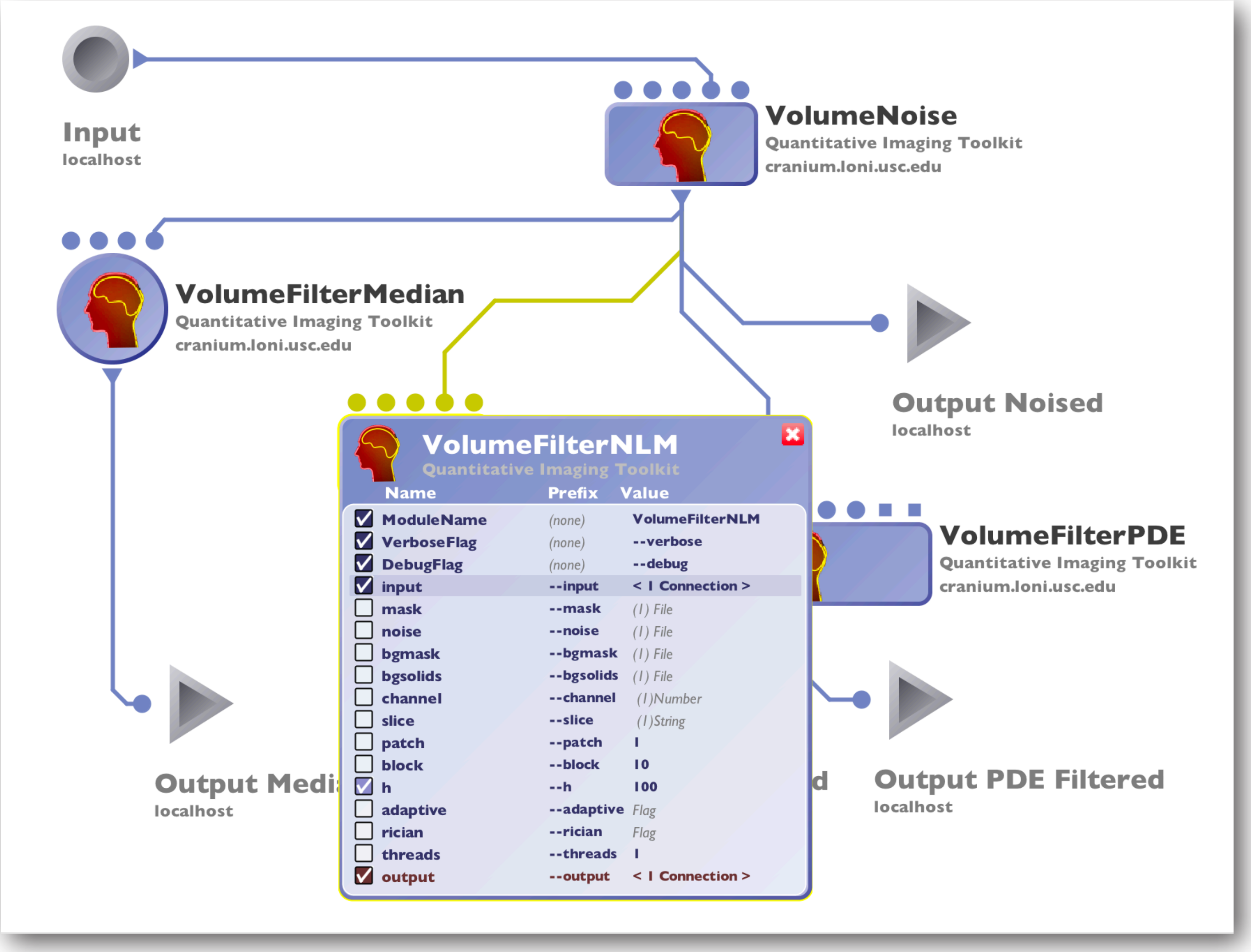
VolumeFilterMedian
Quantitative Imaging Toolkit

Name	Prefix	Value
☑ ModuleName	*(none)*	VolumeFilterMedian
☑ VerboseFlag	*(none)*	--verbose
☑ DebugFlag	*(none)*	--debug
☑ input	--input	< 1 Connection >
☐ window	--window	1
☐ channel	--channel	*(1)Number*
☐ mask	--mask	*(1) File*
☐ slice	--slice	*(1)String*
☐ threads	--threads	5
☑ output	--output	< 1 Connection >

Shown above is the VolumeFilterMedian module from QIT. This algorithm is a simple statistical procedure that denoises an image by examinging a neighborhood around each voxel and replacing the image intentensity with the median value from the intensities in the neighborhood. The window parameter specifies how far the neighborhood extends from a given voxel. We will leave this on the default value of 1 voxel. There are other advanced options, included multi-threading, slice-specific filtering, and channel specific filtering.

Processing with QIT - Denoising

Non-local Means Filtering

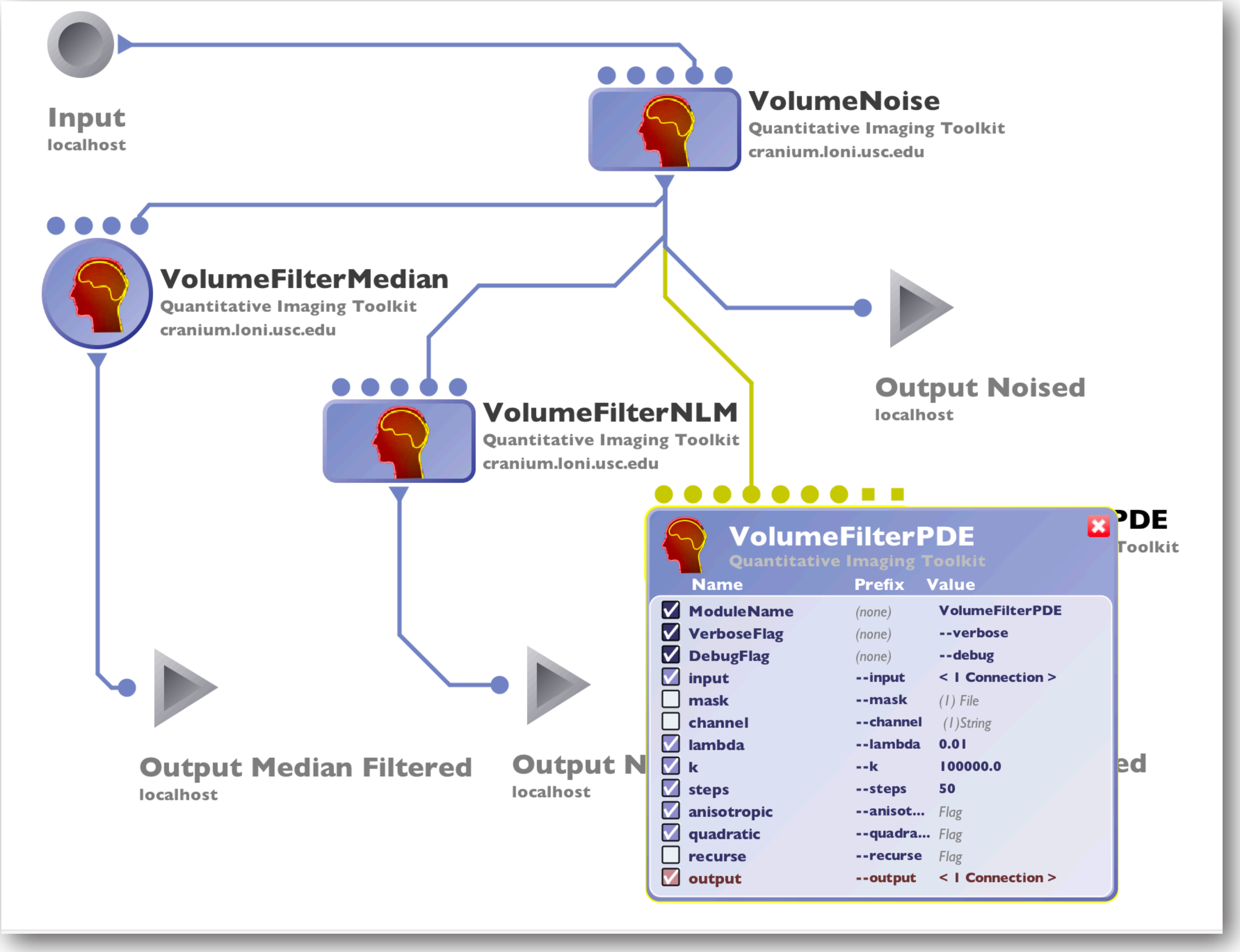


Name	Prefix	Value
☑ ModuleName	(none)	VolumeFilterNLM
☑ VerboseFlag	(none)	--verbose
☑ DebugFlag	(none)	--debug
☑ input	--input	< 1 Connection >
□ mask	--mask	(1) File
□ noise	--noise	(1) File
□ bgmask	--bgmask	(1) File
□ bgsolids	--bgsolids	(1) File
□ channel	--channel	(1)Number
□ slice	--slice	(1)String
□ patch	--patch	1
□ block	--block	10
☑ h	--h	100
□ adaptive	--adaptive	Flag
□ rician	--rician	Flag
□ threads	--threads	1
☑ output	--output	< 1 Connection >

Shown above is the VolumeFilterNLM module from QIT. This algorithm is an advanced denoising algorithm known as non-local means, which uses the similarity of image patches to denoise the dataset. Each voxel is replaced by the weighted average of voxels from patches throughout the image, where patches are weighted by their similarity to the patch around the given voxel. The weighting is controlled by a noise level parameter h, which we set to 100. There are other advanced setting for specifying the patch size, search procedure, noise model, and multi-threading.

Processing with QIT - Denoising

Anisotropic Diffusion Filtering



VolumeFilterPDE
Quantitative Imaging Toolkit

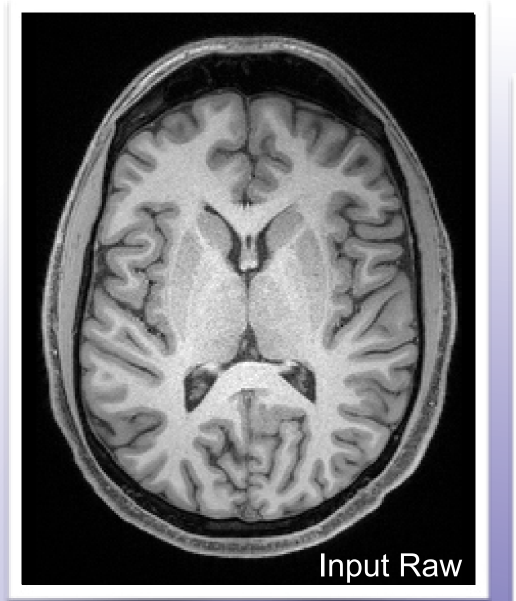
	Name	Prefix	Value
☑	ModuleName	(none)	VolumeFilterPDE
☑	VerboseFlag	(none)	--verbose
☑	DebugFlag	(none)	--debug
☑	input	--input	< 1 Connection >
☐	mask	--mask	(1) File
☐	channel	--channel	(1)String
☑	lambda	--lambda	0.01
☑	k	--k	100000.0
☑	steps	--steps	50
☑	anisotropic	--anisot...	Flag
☑	quadratic	--quadra...	Flag
☐	recurse	--recurse	Flag
☑	output	--output	< 1 Connection >

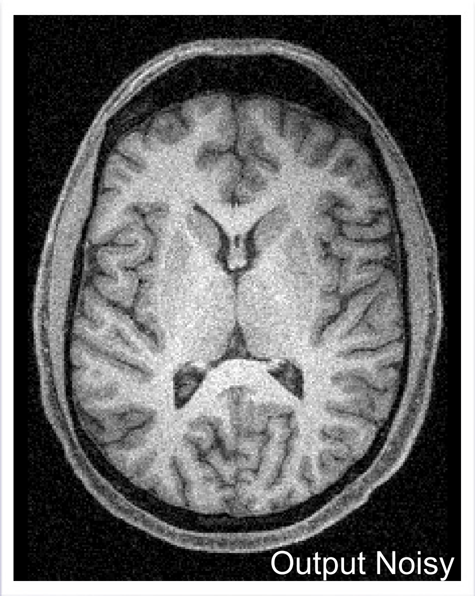
Shown above is the VolumeFilterPDE module from QIT. This algorithm is an advanced denoising algorithm based on partial differential equations that can smooth the image while preserving details. The algorithm models the image as a physical domain in which diffusion occurs anisotropically, where magnitude and direction of diffusion depends on variations in intensities throughout the image. The diffusion is controlled by parameters lambda, k, and the number of iterations, which we set to 0.01, 100000, and 50 respectively. There are also options for specifying a mask or specific channel for filtering as well.

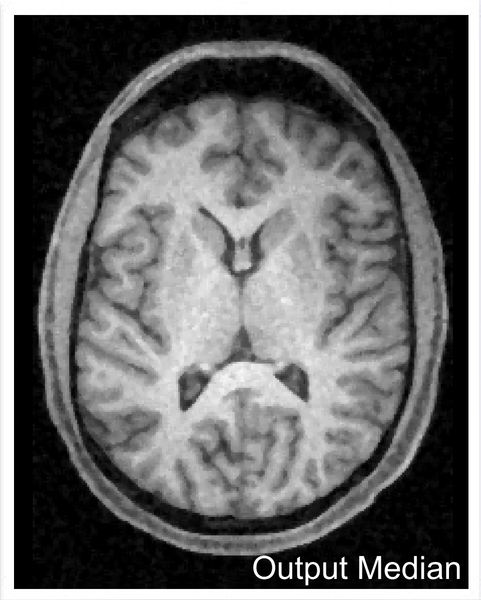
Processing with QIT - Denoising

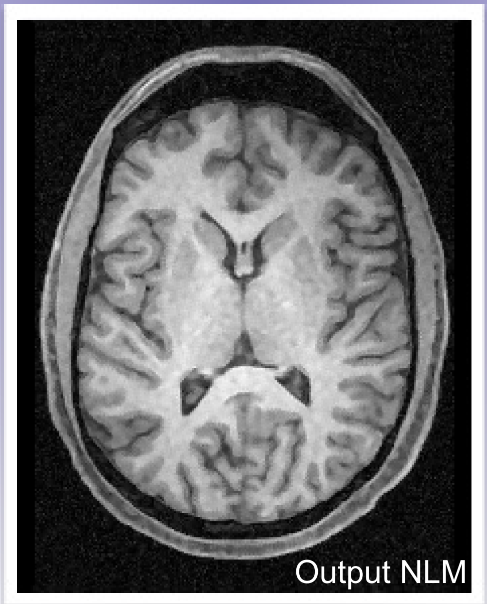
Results

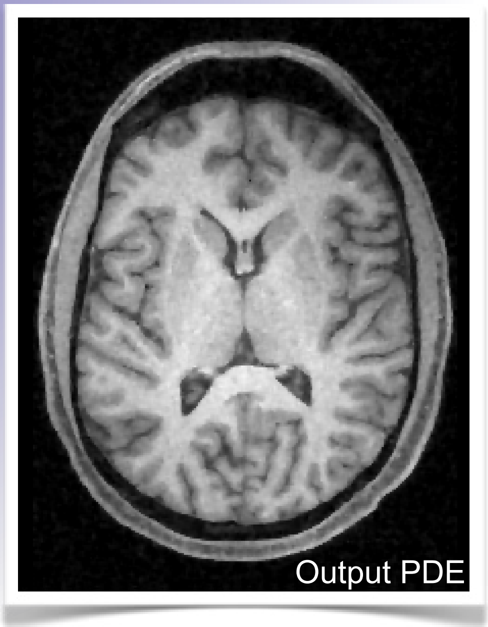
Shown below are results from running the workflow showing the relative performance of the three algorithms in removing the noise added to the image.











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Intermediate Topics

LONI Image Data Archive

The LONI Image Data Archive or IDA (https://ida.loni.usc.edu) is a user-friendly environment for archiving, searching, sharing, tracking and disseminating neuroimaging and related clinical data.

Change Server for Entire Workflow

The Server Changer option in the Pipeline allows one to reset the server associated with any workflow.

LONI Image Data Archive

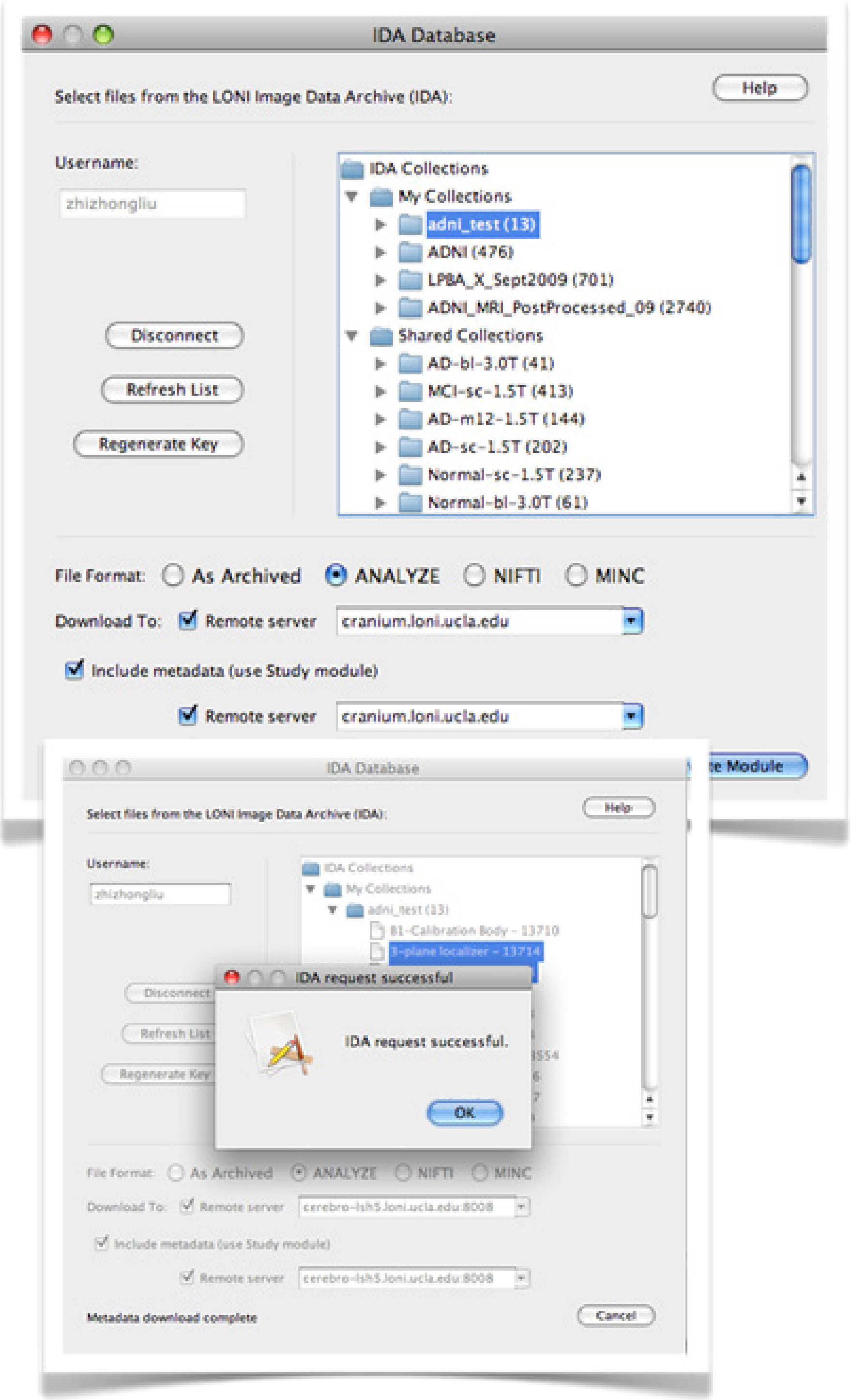
Overview

The Pipeline has the capability to utilize data from the LONI Image Data Archive or IDA (https://ida.loni.usc.edu). The Pipeline takes advantage of our cluster nodes to download files in parallel from the IDA database. This improves download time drastically, and you don't have to keep connected to the server during the download. You can also enable metadata so that metadata files will be downloaded along with data as a Study design module.

In order to establish a connection to the database, go to Tools > IDA Database. Enter in your IDA username and password and click Connect. You will see on the right hand side the data that you have access to through the IDA.

Select the files that you want to process with the Pipeline, desired file format and path for the files to be downloaded. Data can be downloaded on to remote server or locally to your machine. If destination is remote, check the Remote box and specify server name. If you want to download metadata as well, check the Include metadata option and select destination server.

Click on Create Module, a new workflow is created. This workflow will have an IDAGet module and either a data source (if metadata is not downloaded) or a study



IDA Database

Select files from the LONI Image Data Archive (IDA):

Username: zhizhongliu

IDA Collections
- My Collections
  - adni_test (13)
  - ADNI (476)
  - LPBA_X_Sept2009 (701)
  - ADNI_MRI_PostProcessed_09 (2740)
- Shared Collections
  - AD-bl-3.0T (41)
  - MCI-sc-1.5T (413)
  - AD-m12-1.5T (144)
  - AD-sc-1.5T (202)
  - Normal-sc-1.5T (237)
  - Normal-bl-3.0T (61)

File Format: ○ As Archived ● ANALYZE ○ NIFTI ○ MINC

Download To: ☑ Remote server cranium.loni.ucla.edu

☑ Include metadata (use Study module)

☑ Remote server cranium.loni.ucla.edu

IDA Database

Select files from the LONI Image Data Archive (IDA):

Username: zhizhongliu

IDA Collections
- My Collections
  - adni_test (13)
    - B1-Calibration Body - 13710
    - 3-plane localizer - 13714

IDA request successful

IDA request successful.

File Format: ○ As Archived ● ANALYZE ○ NIFTI ○ MINC

Download To: ☑ Remote server cerebro-lsh5.loni.ucla.edu:8008

☑ Include metadata (use Study module)

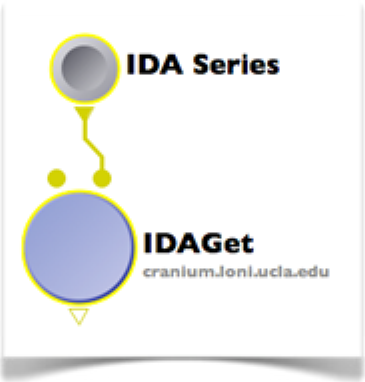
☑ Remote server cerebro-lsh5.loni.ucla.edu:8008

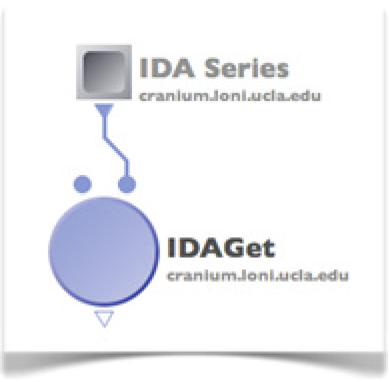
Metadata download complete

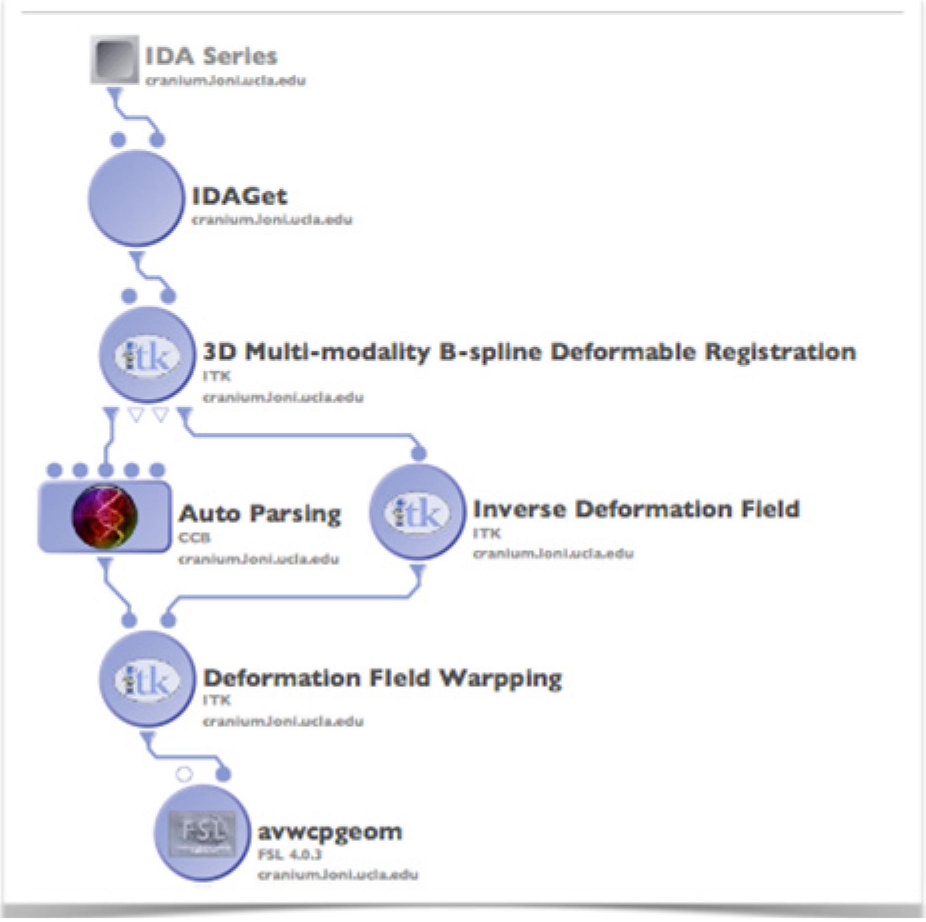
module (if metadata is also being downloaded). Once you create this workflow the metadata files alone are downloaded to a temporary location.

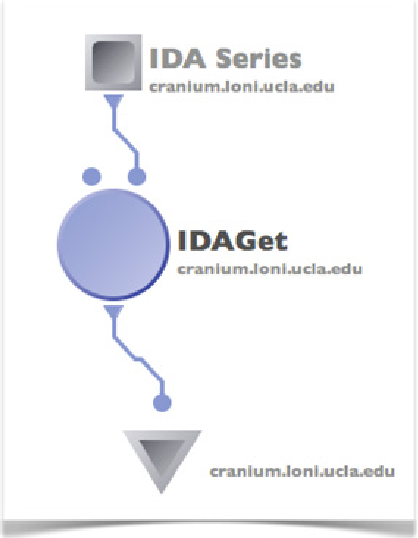
You will notice that the output of the IDAGet module has the file type you specified. You can now connect this output to the input parameters of any module in your workflow and execute the workflow. As the first module of the workflow begins to execute, the data will be downloaded and will be directly passed on to the following modules. The data and metadata files downloaded are temporarily stored and will be deleted if you reset the workflow.

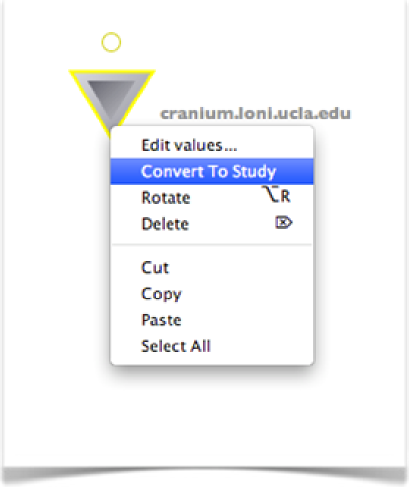
The data can also be downloaded to a permanent location from IDA database. To do this create a data sink and connect it to the output of the IDAGet module. You can either list the output items or use directory dump and specify an output directory. After successfully running the workflow, you can copy this data sink and paste it to any workflow, right click on it and choose “Convert to study” option. The data sink will be automatically converted to a study module with proper inputs. To reuse this data set, you can simply copy this study module to your workflow.











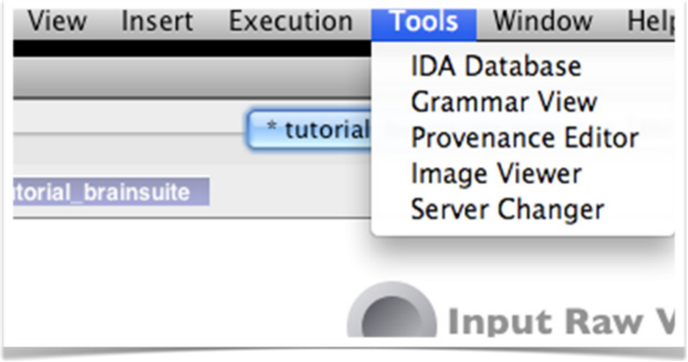
Change Server for Entire Workflow

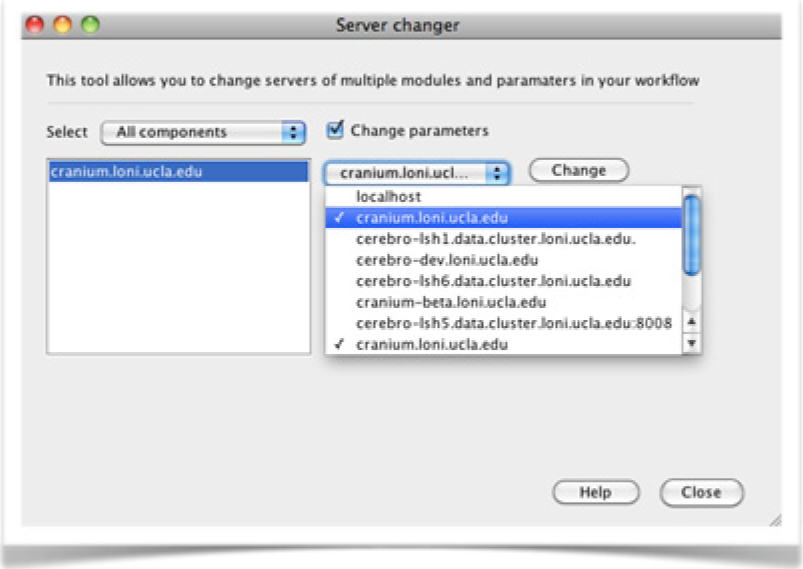
Overview

The **Server Changer** option in the Pipeline allows one to reset the server associated with any workflow. All data, binaries and workflows have servers associated with them. One of the core features of the Pipeline is the ability to have input & output files and binaries on remote servers as well as your local computer; all within a single workflow.

How-to

- Under Tools, choose Server Changer
- Under Select, choose either All Servers, Modules, Data Sources or Data Sinks to narrow which servers to reset
- In the Select window, choose the server to be replaced
- Choose whether you'd like the change to be applied to parameters as well
- Use the drop-down menu to specify the server to be changed to
- Click Change, followed by Close




Server changer

This tool allows you to change servers of multiple modules and paramaters in your workflow

Select: All components ☑ Change parameters

cranium.loni.ucla.edu

cranium.loni.ucl...

Change
localhost
✓ cranium.loni.ucla.edu
cerebro-lsh1.data.cluster.loni.ucla.edu.
cerebro-dev.loni.ucla.edu
cerebro-lsh6.data.cluster.loni.ucla.edu
cranium-beta.loni.ucla.edu
cerebro-lsh5.data.cluster.loni.ucla.edu:8008
✓ cranium.loni.ucla.edu
Help
Close

NOTE: You may change servers to and from servers you have connected to at least once.

Intermediate Example Workflows

fMRI First Level Analyses
Generate first level analyses fMRI results on a single subject.

DTI Analyses
DTI (DICOM/NIfTI) images are reconstructed and fiber tracks are generated for TrackVis Software.

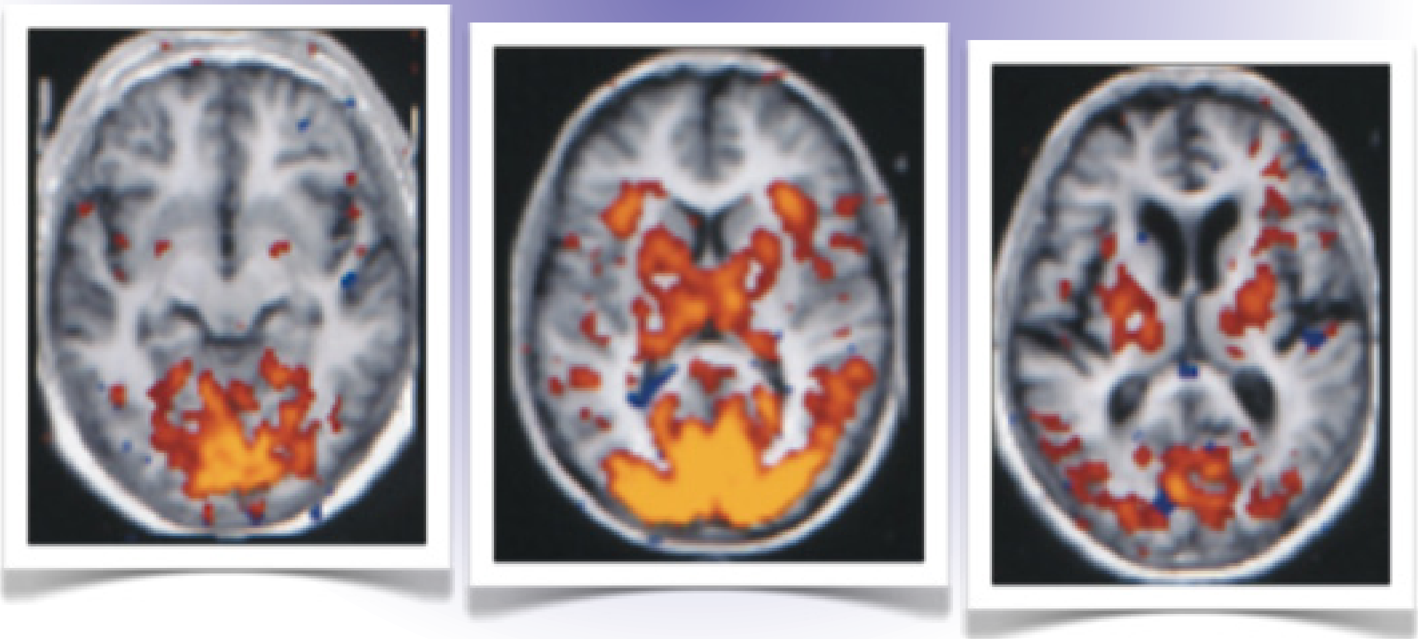
DSI Analyses
DSI (DICOM/NIfTI) images are reconstructed and fiber tracks are generated for TrackVis.

Image Processing with the Quantitative Imaging Toolkit - Tractography Metrics
This workflow demonstrates how to extract whole brain tractography metrics from a diffusion-weighted MRI dataset with the Quantitative Imaging Toolkit (QIT).

fMRI First Level Analyses

FSL FEAT

Raw Input

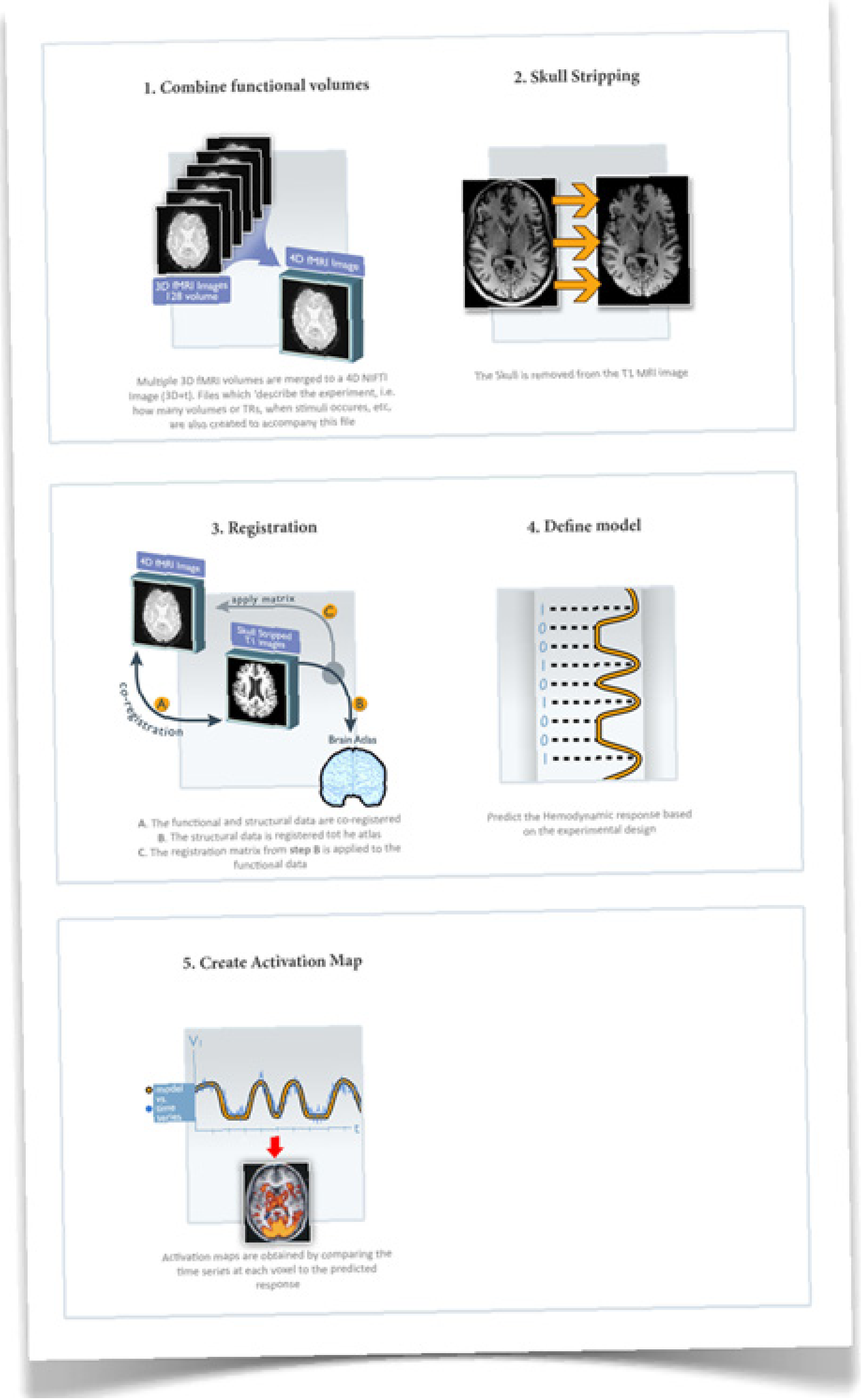


Results

fMRI First Level Analyses

Introduction

Generate first level analyses fMRI results on a single subject.



1. Combine functional volumes

Multiple 3D fMRI volumes are merged to a 4D NIFTI image (3D+t). Files which 'describe the experiment, i.e. how many volumes or TRs, when stimuli occures, etc, are also created to accompany this file

2. Skull Stripping

The Skull is removed from the T1 MRI image

3. Registration

A. The functional and structural data are co-registered
B. The structural data is registered tot he atlas
C. The registration matrix from **step B** is applied to the functional data

4. Define model

Predict the Hemodynamic response based on the experimental design

5. Create Activation Map

Activation maps are obtained by comparing the time series at each voxel to the predicted response

Overview

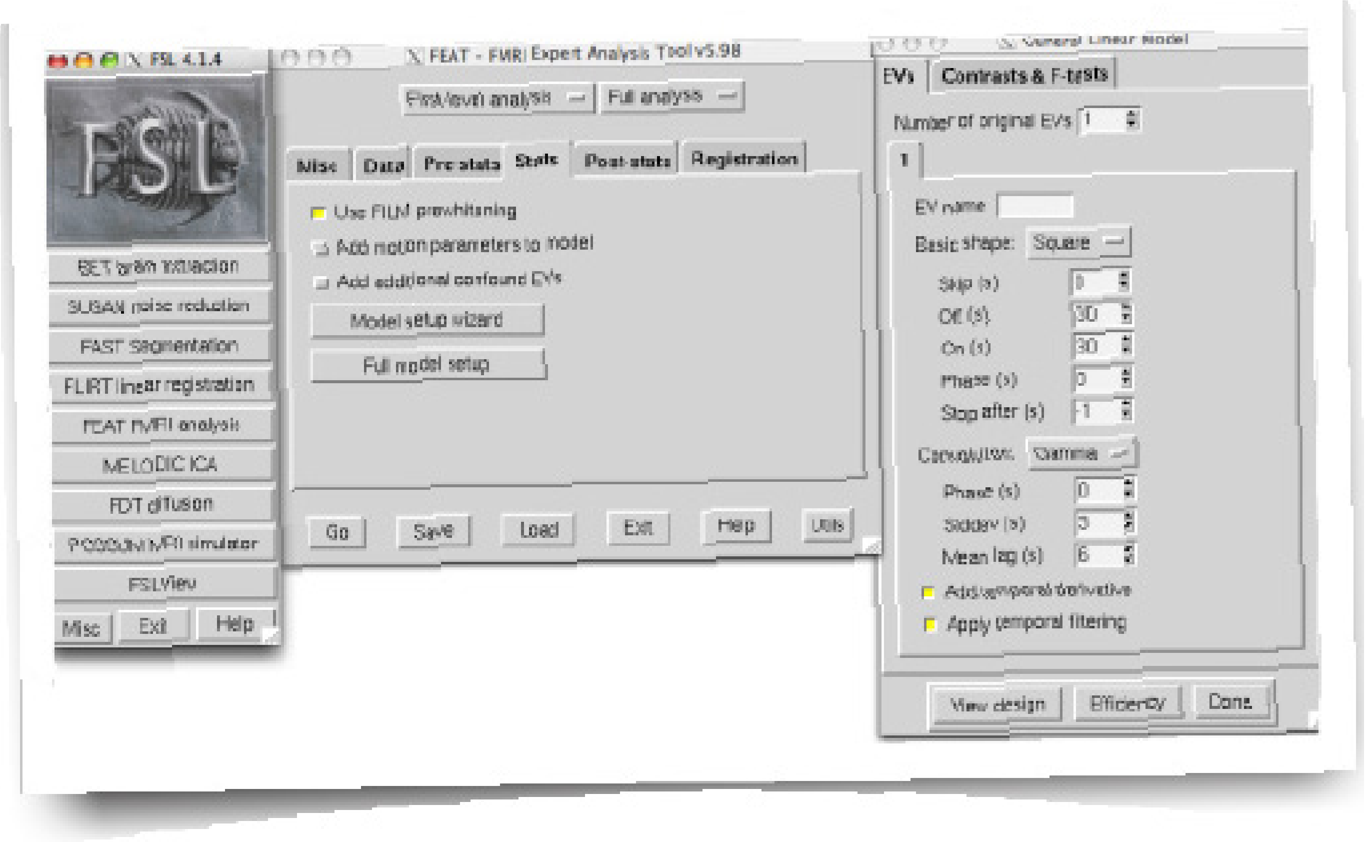
This workflow is a simple single subject, first level fMRI analysis. The workflow features FSLmerge, BET (in case the data is not already skull stripped for non-skullstripped data) and first level FEAT analysis.

Test data is available in the LONI Pipeline Library from the Buckner et al 2000 study. The experimental stimulus is a simple checkerboard flicker. For every subject there are 4 runs and in each run there are 2 conditions. In this workflow, we are using a single run from one subject.

fMRI First Level Analyses

Before you begin...

Before we begin, a design file is required (design.fsf) from FSL FEAT. You may need to launch FSL FEAT to create a design file—the LONI Pipeline can edit items in an existing file but cannot add new items, such as more experimental variables to a design file. The included, pre-made design.fsf file is a single subject with 2 experimental variables. If your experiment matches, you can just use the template included. However, if your experiment differs from this, you will have to create your own design file in FSL FEAT first.



Number of original EVs: 1

Basic shape: Square

Skip (s): 0

Off (s): 30

On (s): 30

Phase (s): 0

Stop after (s): -1

Convolution: Gamma

Phase (s): 0

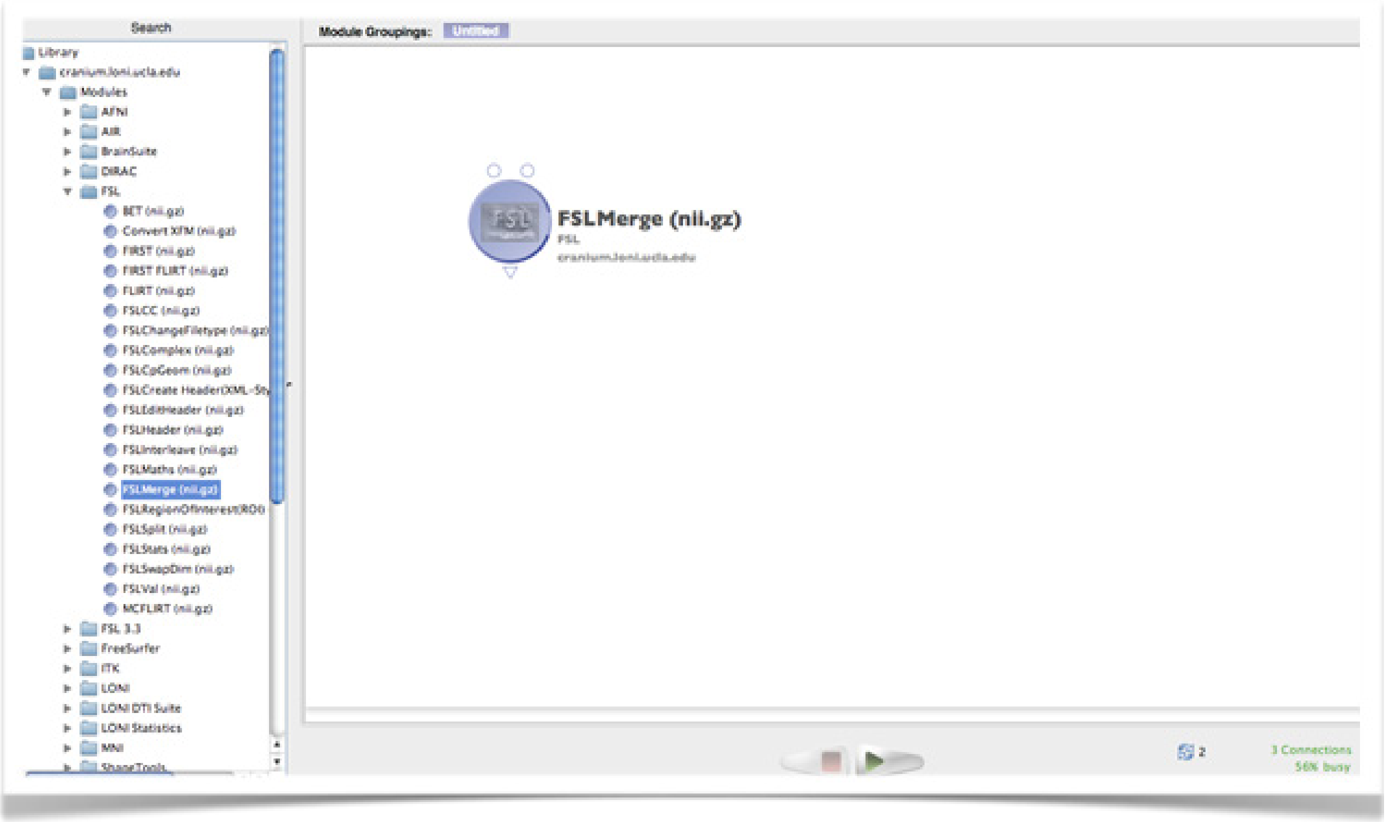
Stddev (s): 3

Mean lag (s): 6

fMRI First Level Analyses

3D to 4D FSLMerge

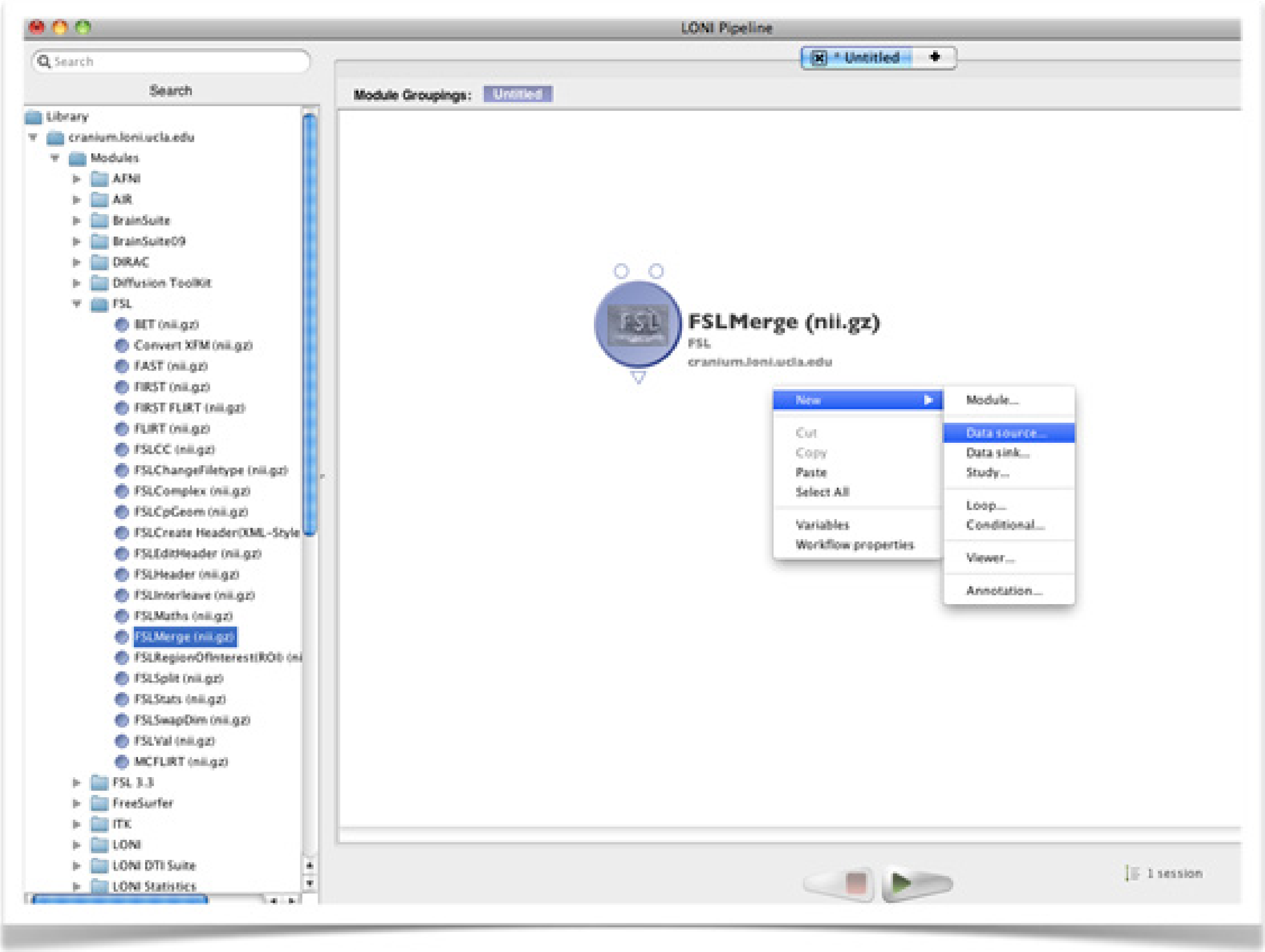
1) To begin, open the LONI Pipeline. Click on new workflow. Expand the FSL folder in the Library on the left and select FSLMerge. Drag the module to the empty canvas.



fMRI First Level Analyses

Specify 3D Files

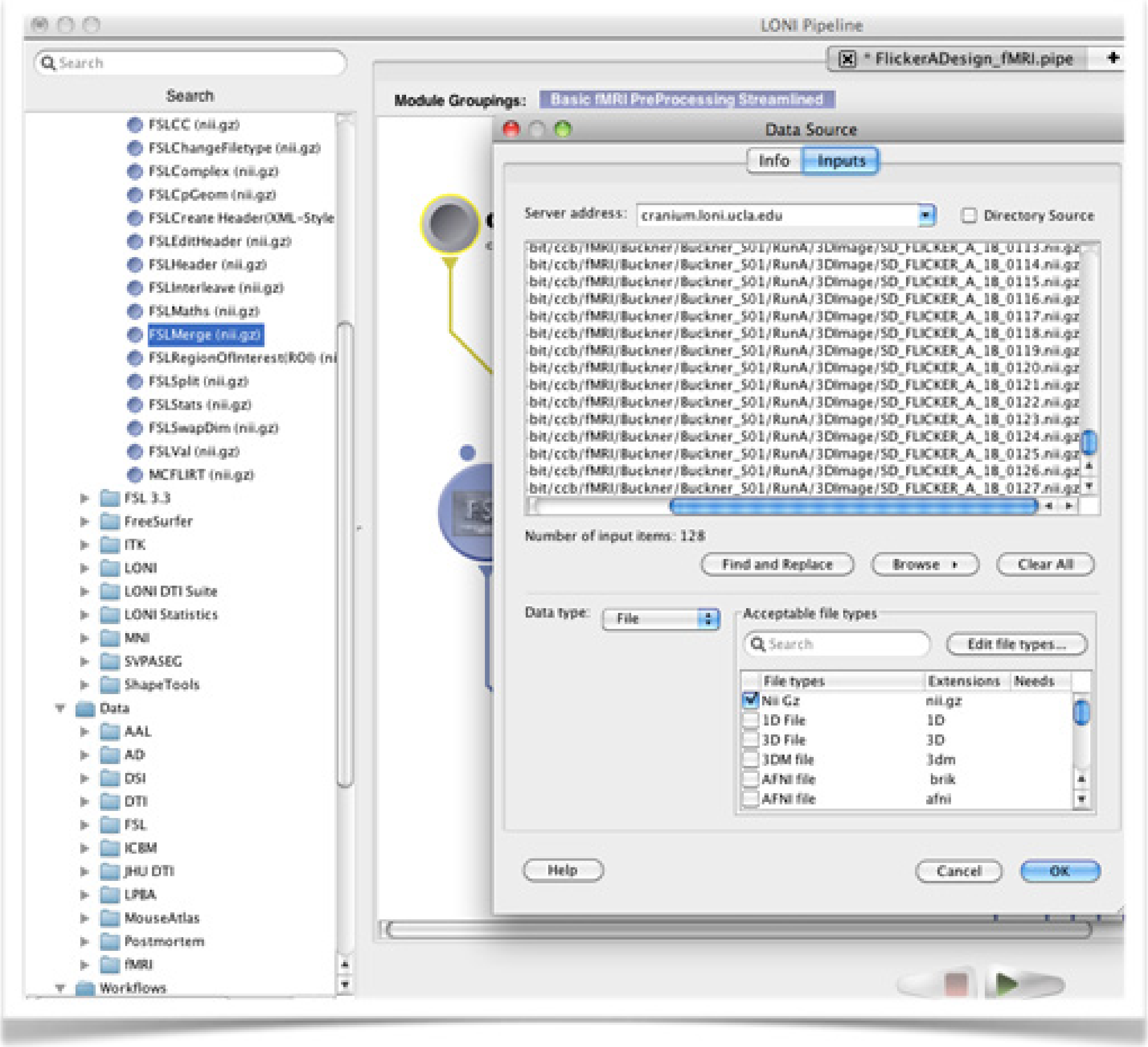
2) Right click on the canvas and select a data source from the Pipeline Library “One Functional Run”.



fMRI First Level Analyses

Specify 3D Files

3) Choose all the 3D fMRI files for the subject. Connect the output of the data source to the input of FSLMerge.



Server address: cranium.loni.ucla.edu ☐ Directory Source

```
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0113.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0114.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0115.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0116.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0117.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0118.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0119.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0120.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0121.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0122.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0123.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0124.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0125.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0126.nii.gz
bit/ccb/fMRI/Buckner/Buckner_S01/RunA/3DImage/SD_FLICKER_A_18_0127.nii.gz
```

Number of input items: 128

Data type: File

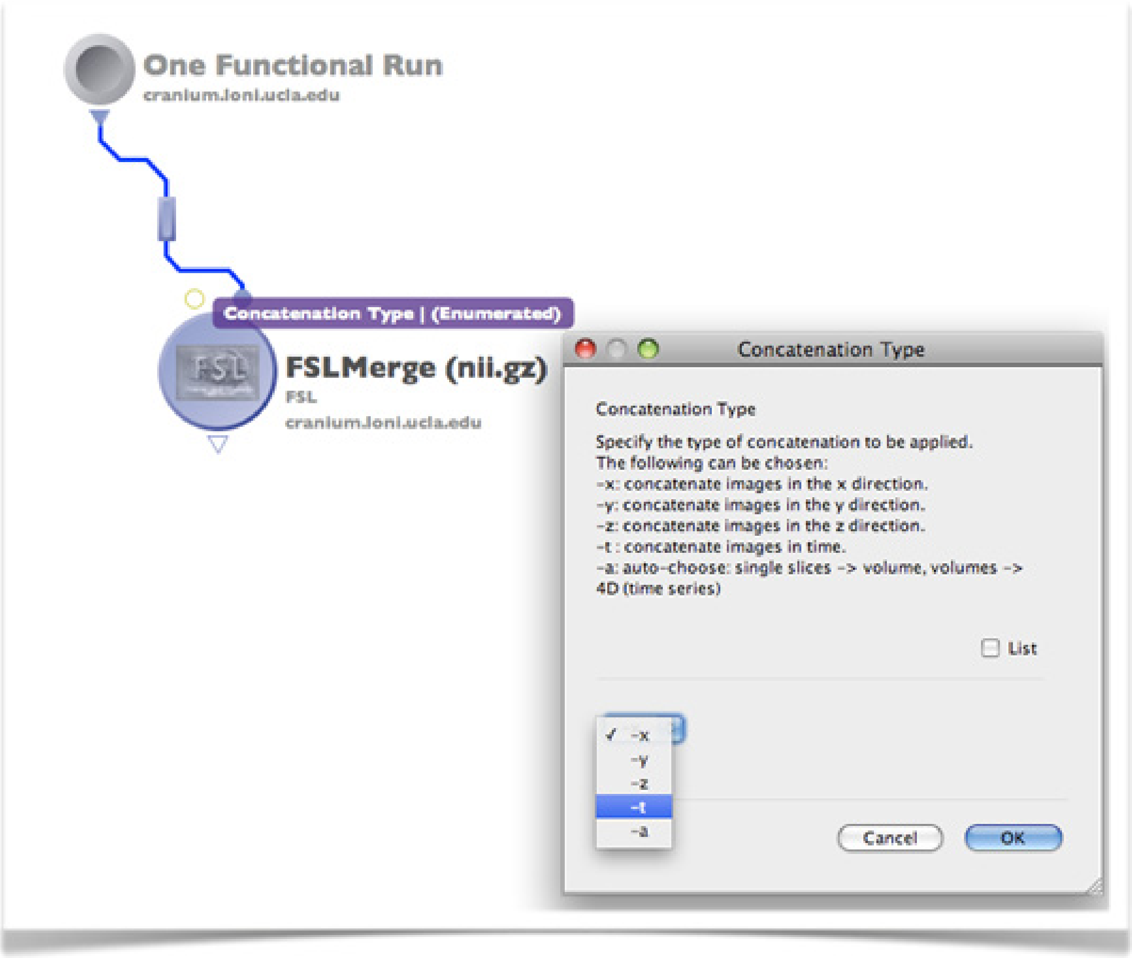
Acceptable file types

	File types	Extensions	Needs
☑	Nii Gz	nii.gz	
☐	1D File	1D	
☐	3D File	3D	
☐	3DM file	3dm	
☐	AFNI file	brik	
☐	AFNI file	afni	

fMRI First Level Analyses

Concatenate 3D Files Across Time

4) Double click on the “Concatenation Type.” Select -t in the drop down menu.



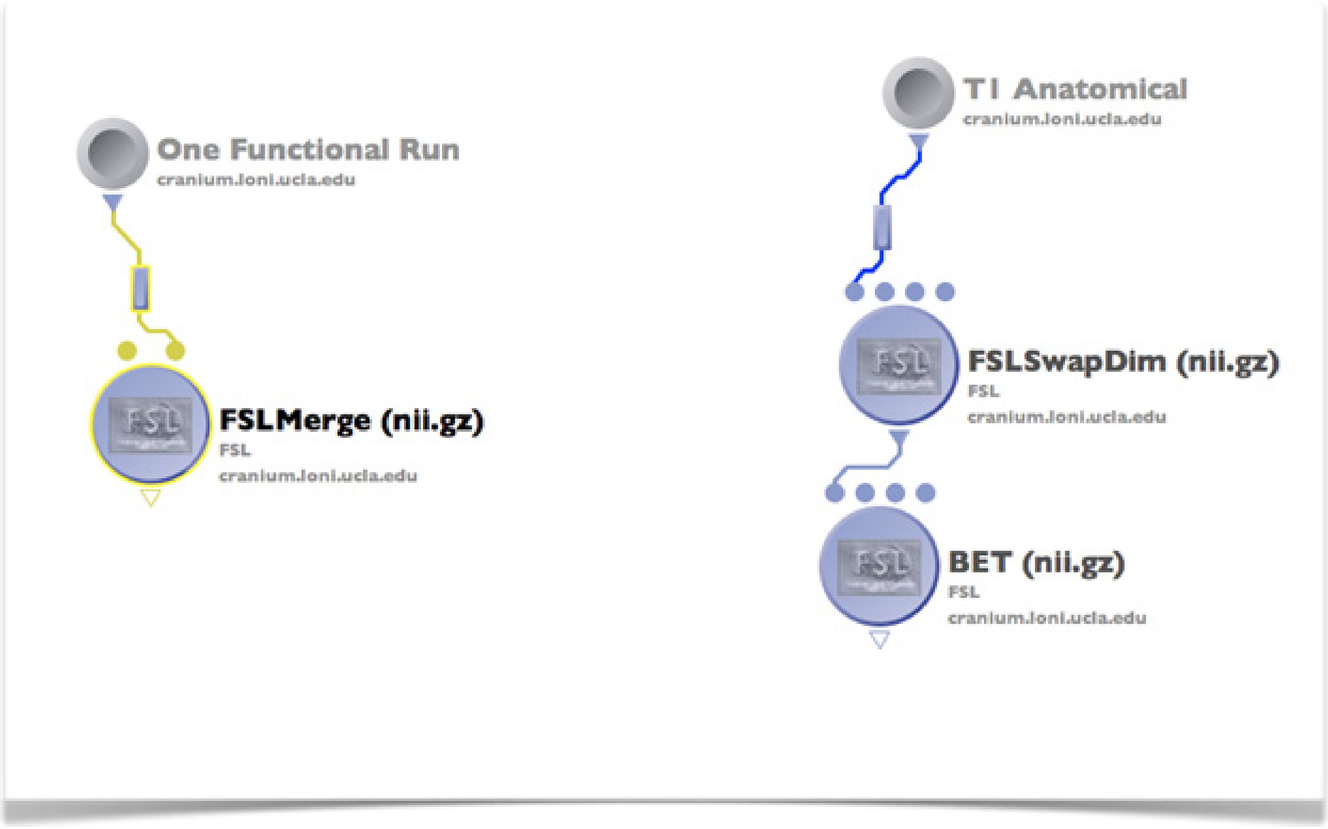
Concatenation Type

Specify the type of concatenation to be applied.
The following can be chosen:
-x: concatenate images in the x direction.
-y: concatenate images in the y direction.
-z: concatenate images in the z direction.
-t : concatenate images in time.
-a: auto-choose: single slices -> volume, volumes -> 4D (time series)

fMRI First Level Analyses

Brain Extraction

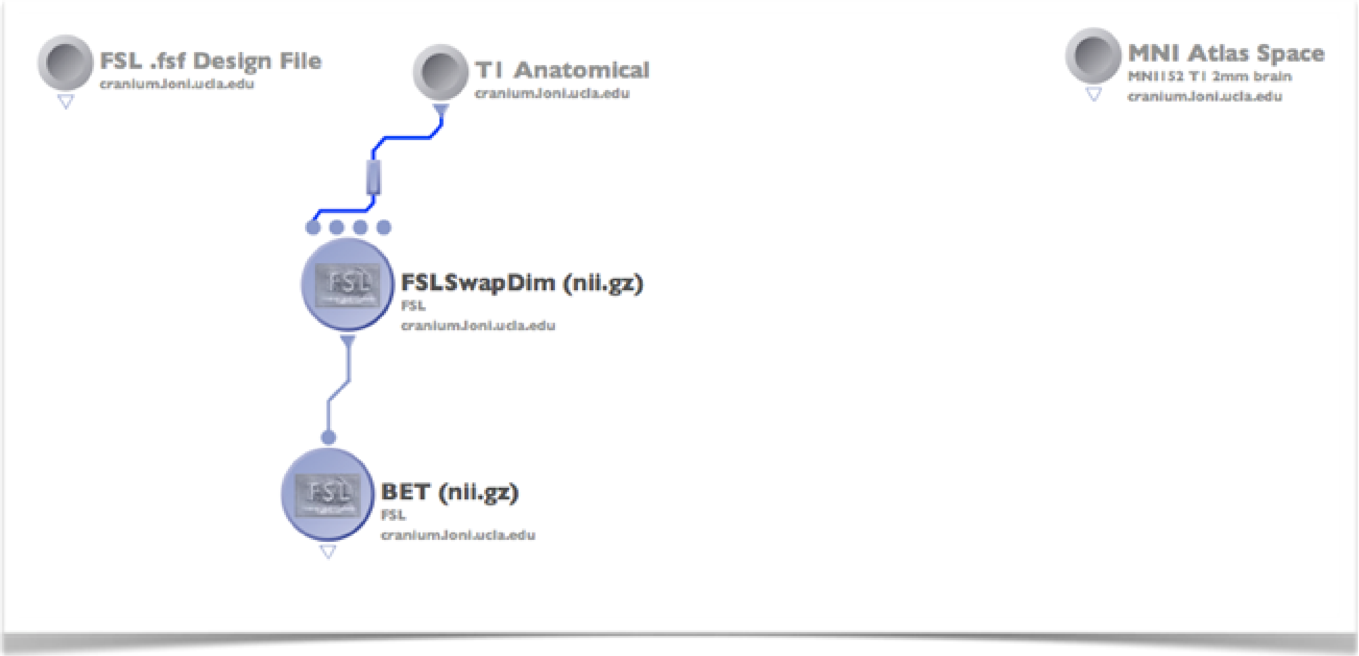
5) Choose FSLSwapDim and BET (nii.gz) modules. Drag them to the canvas. Right click and select New data source, name it “T1Anatomical”. Select the T1 Anatomical data of the corresponding subject. Connect all the 3 modules, Data source to FSLSwapDim and FSL SwapDim to BET



fMRI First Level Analyses

Specify the Atlas and the Template Design File

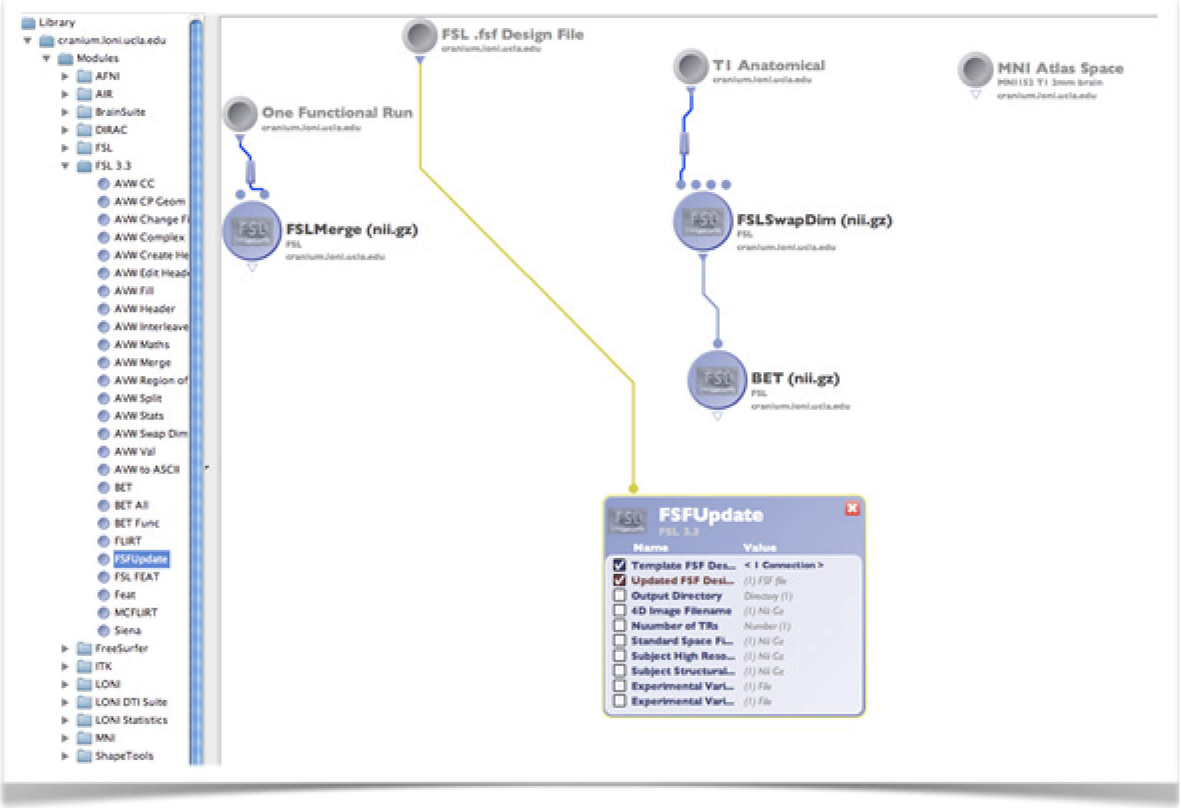
6) Right click on the canvas and create two new data sources. Name one “MNI Atlas Space”. Double click on it a Select the MNI Atlas, which will be used as a reference. Name the second source, “FSL .fsf Design file.” Select the design file created using the FSL FEAT interface.



fMRI First Level Analyses

Update Design File

7) Select the FSF Update Module under the FSL library. Drag it to the canvas. Connect the data source “FSL .fsf Design file” to the empty circle that says “Template FSF design file”. Double click on the FSF Update Module and select all the other optional parameters.



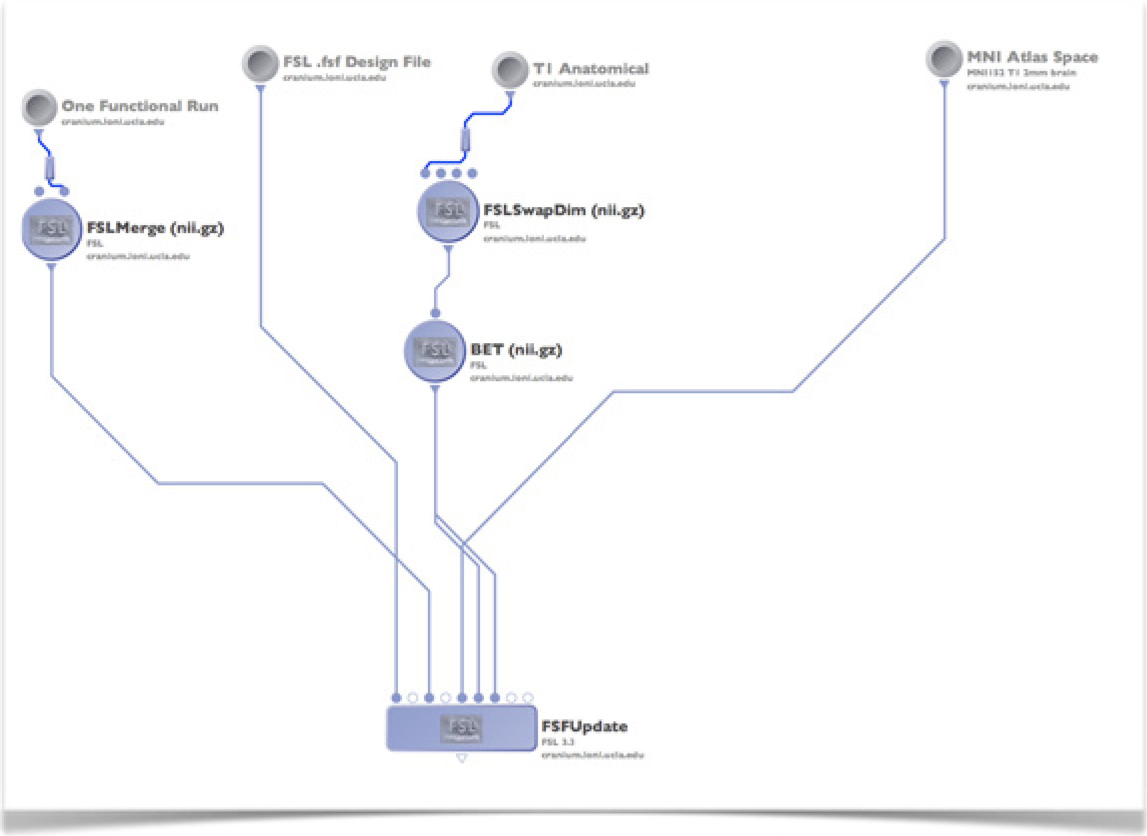
FSFUpdate
FSL 3.3

Name	Value
☑ Template FSF Des...	< 1 Connection >
☑ Updated FSF Desi...	(1) FSF file
☐ Output Directory	Directory (1)
☐ 4D Image Filename	(1) Nii Gz
☐ Nuumber of TRs	Number (1)
☐ Standard Space Fi...	(1) Nii Gz
☐ Subject High Reso...	(1) Nii Gz
☐ Subject Structural...	(1) Nii Gz
☐ Experimental Vari...	(1) File
☐ Experimental Vari...	(1) File

fMRI First Level Analyses

Update Design File

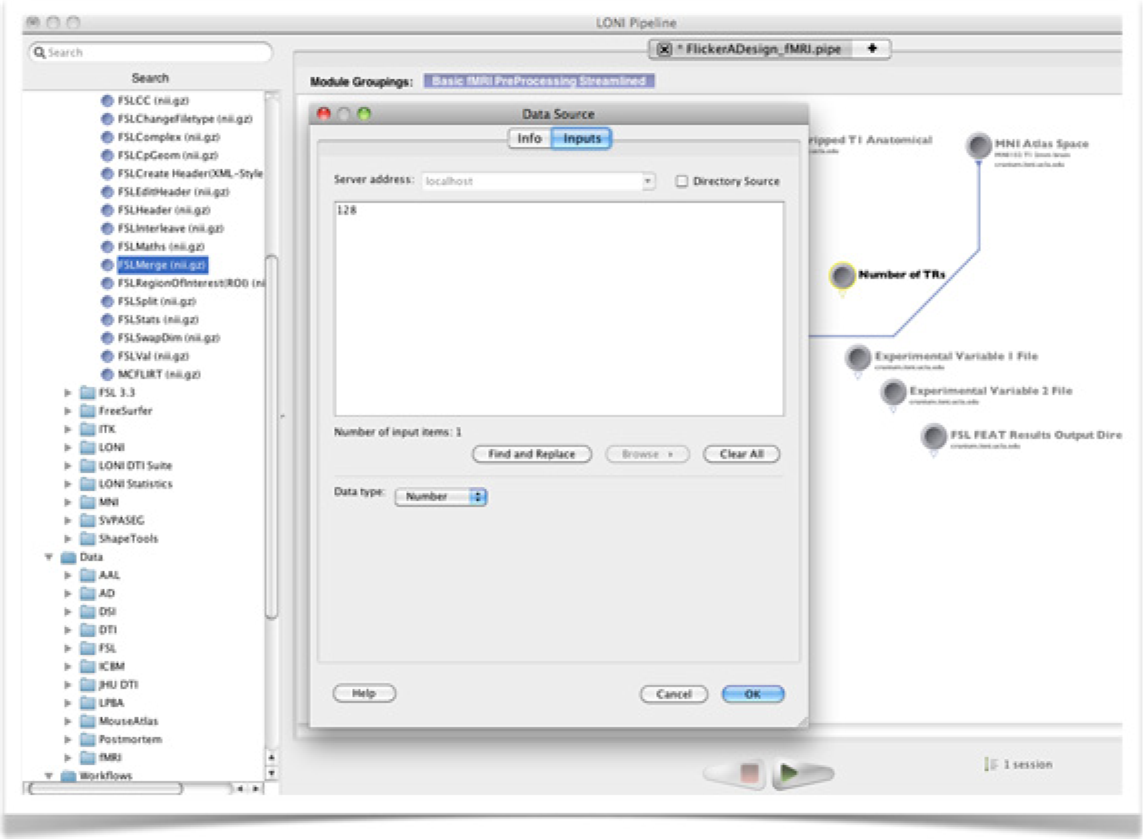
8) Connect the “MNI Atlas Space” data source to the corresponding empty circle on the FSF Update Module. Connect the output of BET to the circles labeled, Subject High Resolution Anatomical and Subject Structural Image for Analysis. Connect the output of FSLMerge to the corresponding circle.



fMRI First Level Analyses

Update Design File

9) For this analysis, we have two experimental variables. our Number of TRs is equal to 128. We will create four data sources to update the fsf design file. Name the first data source “Number of TRs.” Enter 128. Connect the Number of TRs data source to the FSF Update module’s input parameter that also reads “Number of TRs”.



Server address: localhost

128

Number of input items: 1

Data type: Number

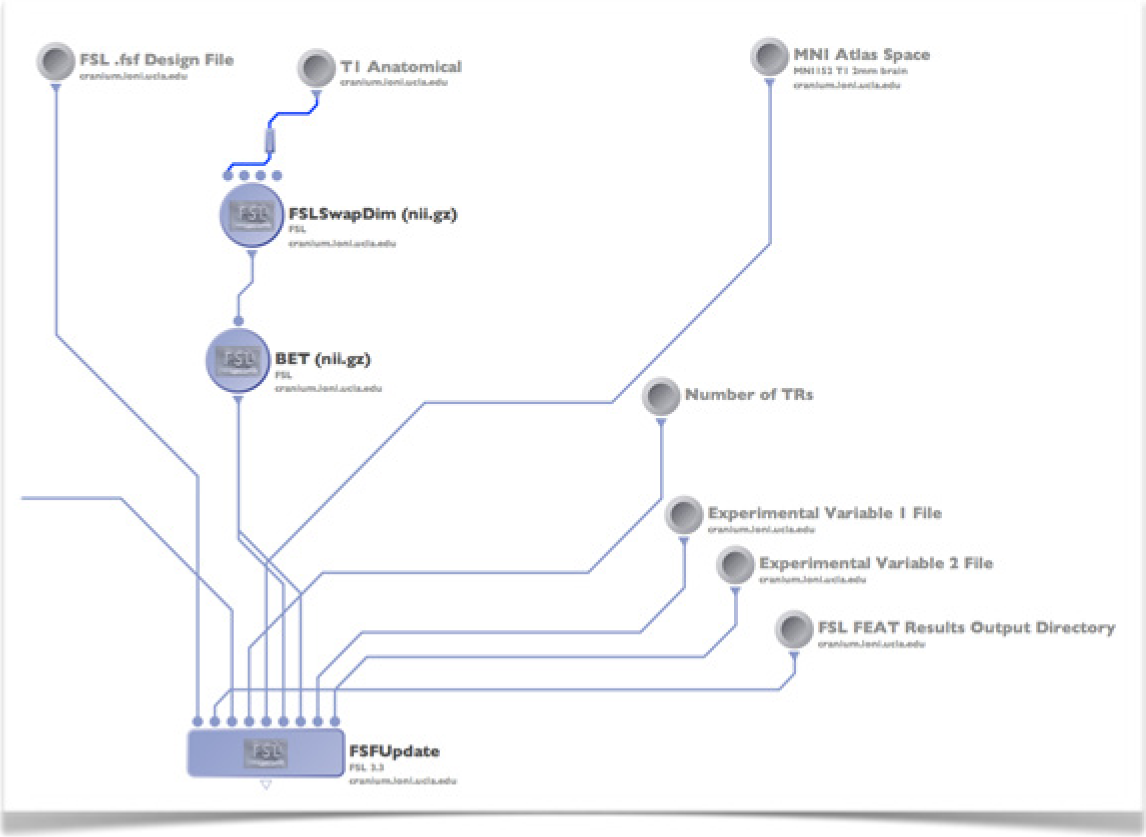
fMRI First Level Analyses

Update Design File

10) The next two data sources can be named Experimental Variable 1 and Experimental Variable 2. Double click on each of the Experimental Variables and select the corresponding timing file (a text file which has information about the onset times and duration of the stimuli).

    The third data source can be named “Output Directory”. Use this data source to set the path location to your final results directory.

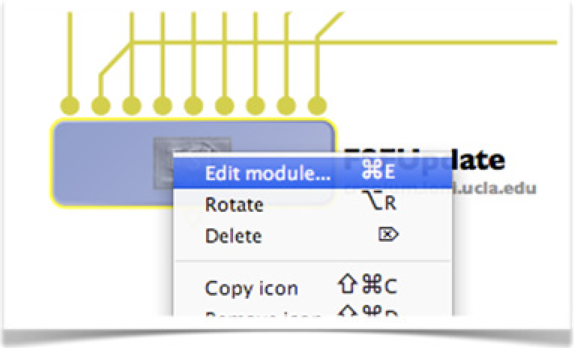
    Connect all the modules to the respective empty input parameters in the FSF Update module. To do this, drag a line connecting each of the above-mentioned data source output parameters to the corresponding input parameters on the FSF Update module.

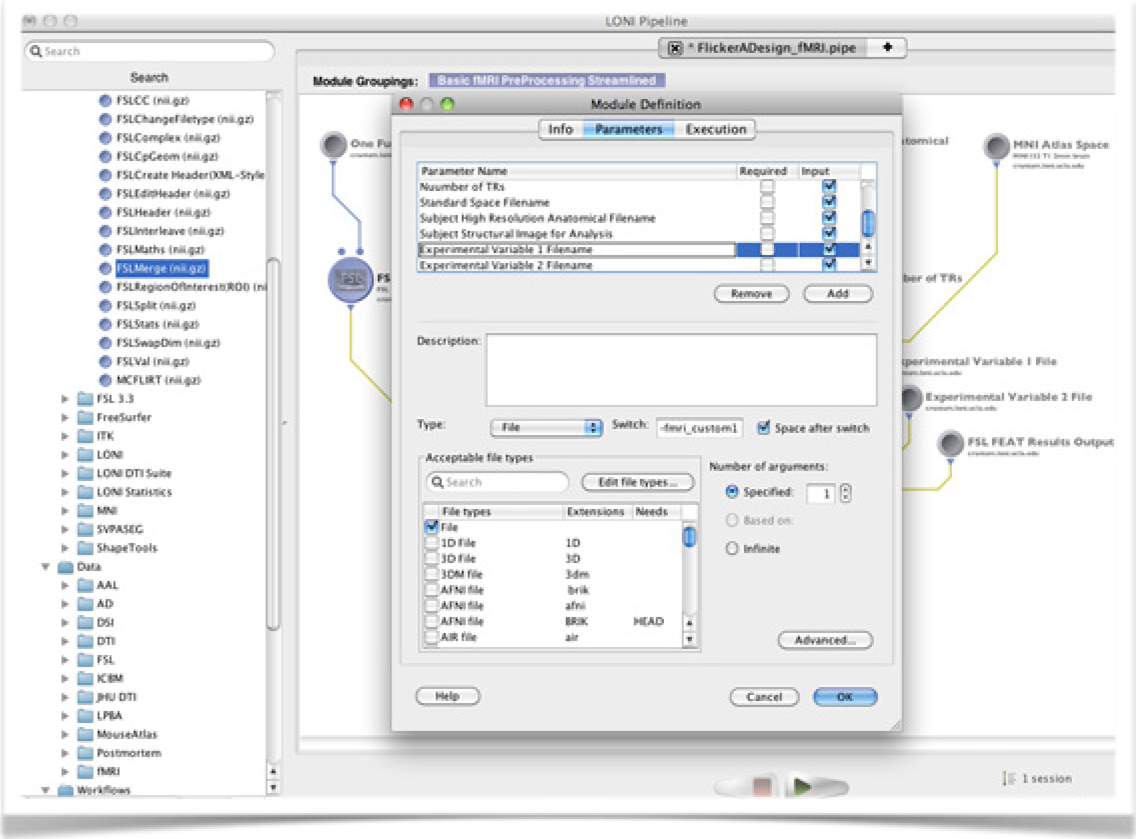


fMRI First Level Analyses

Add Optional Parameters

11) If you are using a new design file rather than the template we provided (see the section before step 1, "Before you begin…") you may now have to add a parameter to the FSF Update module. For instance, if your design file has three Experimental Variables, rather than two, you would need to right click and edit the FSLUpdate module. Under the parameters tab, add a new parameter and name it "Experimental Variable 3 File Name".





Parameter Name	Required	Input
Nuumber of TRs	☐	☑
Standard Space Filename	☐	☑
Subject High Resolution Anatomical Filename	☐	☑
Subject Structural Image for Analysis	☐	☑
Experimental Variable 1 Filename	☐	☑
Experimental Variable 2 Filename	☐	☑

Description:

Type: File   Switch: -fmri_custom1   ☑ Space after switch

Acceptable file types

	File types	Extensions	Needs
☑	File		
☐	1D File	1D	
☐	3D File	3D	
☐	3DM file	3dm	
☐	AFNI file	brik	
☐	AFNI file	afni	
☐	AFNI file	BRIK	HEAD
☐	AIR file	air	

Number of arguments:

● Specified: 1

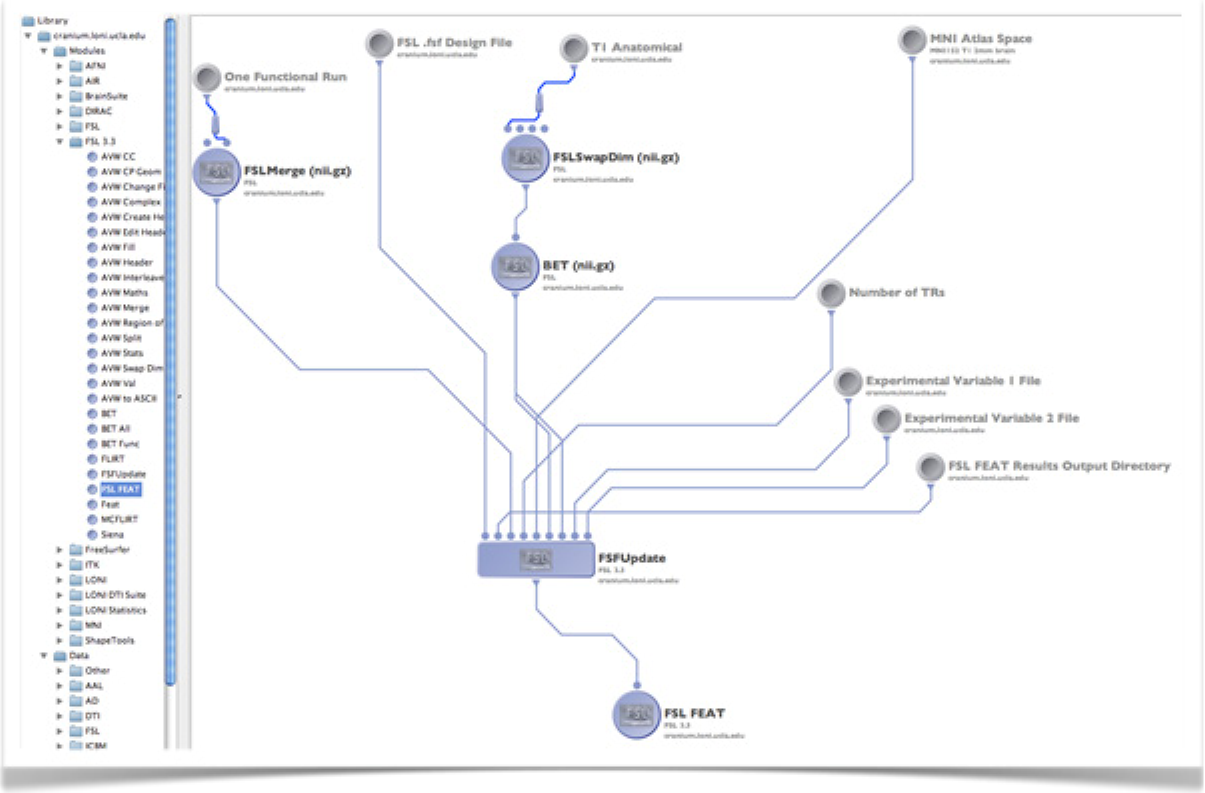
○ Based on:

○ Infinite

fMRI First Level Analyses

Setup FEAT

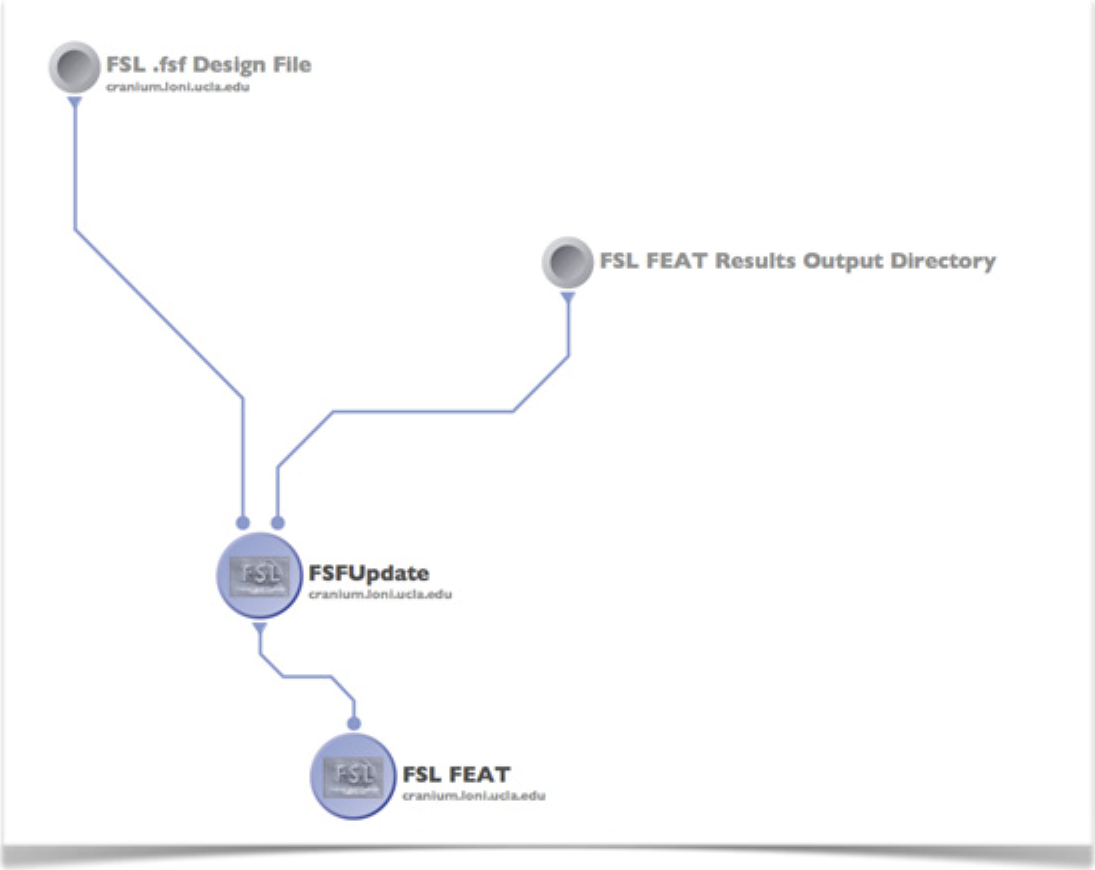
12) Select the FSL FEAT module under the FSL suit and drag it to the canvas. Connect the output of the FSFUpdate module to the FSL FEAT module.



fMRI First Level Analyses

Re-run FEAT

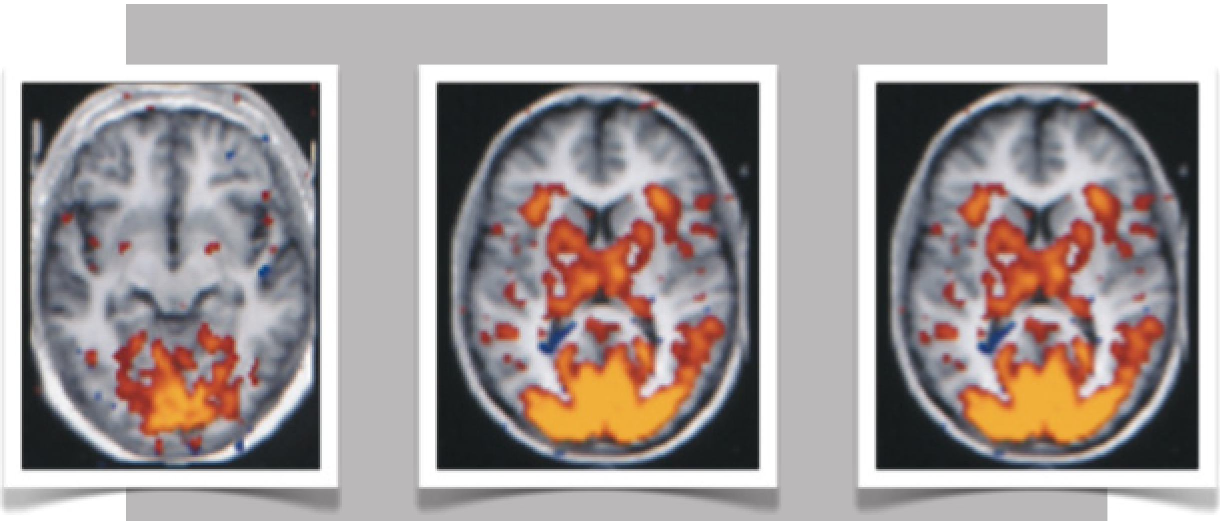
13) If you would like to re-run the analysis on the same subject with the same parameters, you can simplify the workflow as shown in the picture below and described as follows. Double click on the FSFUpdate Module and uncheck all the parameters, except Template FSF Design File, Updated FSFDesign File and Output Directory. Delete all the modules that are not connected to the FSFUpdate module. The input to the FSL Design data source will now be the updated design file created in the previous workflow (this has been saved as a separate design.fsf file in the results directory). Next specify the output directory path and run the new workflow. This simplified workflow will save you from having to run through the steps of updating the template design file again.



fMRI First Level Analyses

Results

Raw Input



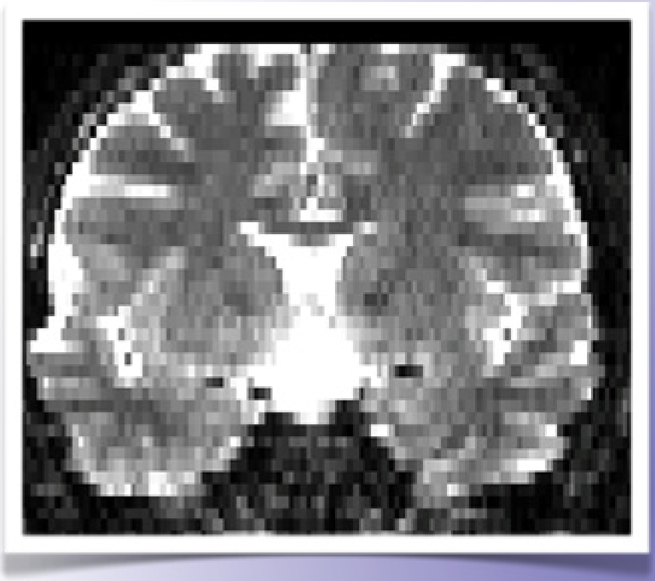
Results

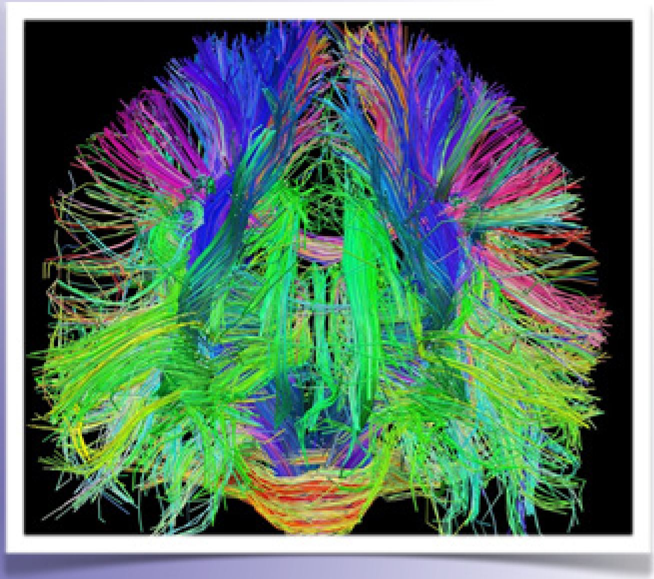
Data for this workflow was graciously provide from:
Buckner RL, Snyder AZ, Sanders AL, Raichle ME, Morris JC (2000) “Functional Brain Imaging of Young, Nondemented, and Demented Older Adults", Journal of Cognitive Neuroscience, 12 Supplement 2, pp. 24-34.

DTI Analyses

Introduction

This workflow creates white matter tracts for viewing in TrackVis from DTI files.





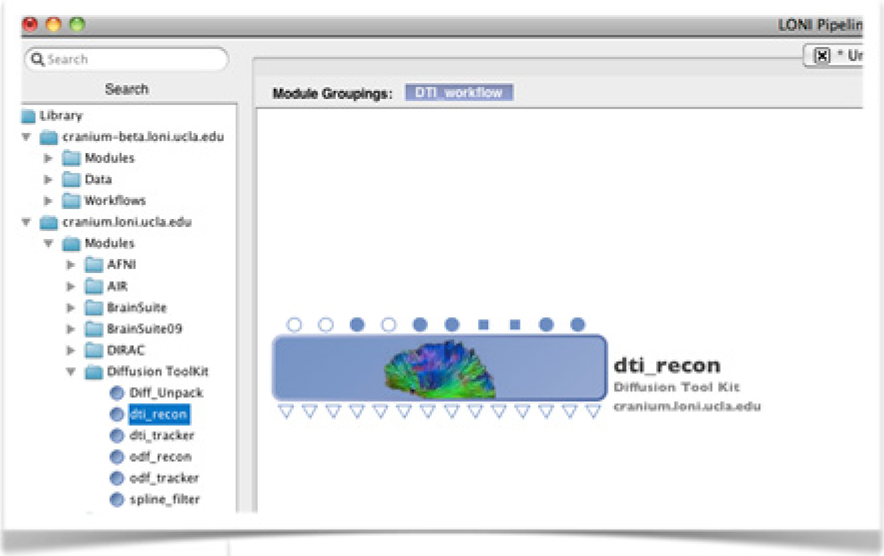
Overview

In this workflow, DTI (DICOM/NIfTI) images are reconstructed and fiber tracks are generated for TrackVis. Diffusion toolkit command-line tools are used to build the workflow. Individual command-line tools are available as modules in the pipeline library. To build this workflow follow the steps below.

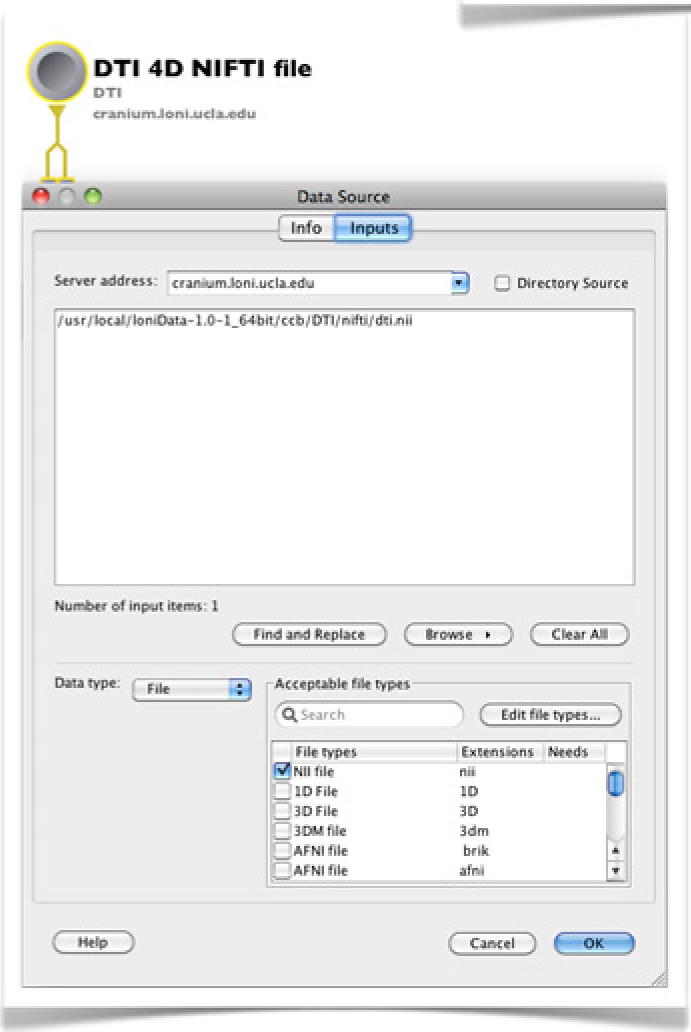
DTI Analyses

Copy DTI Recon and specify the input

1) Start by opening a new workflow. Expand the Diffusion Toolkit folder under the Library and choose dti_recon module.



Module Groupings: DTI_workflow



Server address: cranium.loni.ucla.edu

☐ Directory Source

/usr/local/loniData-1.0-1_64bit/ccb/DTI/nifti/dti.nii

Number of input items: 1

Data type: File

Acceptable file types

	File types	Extensions	Needs
☑	NII file	nii	
☐	1D File	1D	
☐	3D File	3D	
☐	3DM file	3dm	
☐	AFNI file	brik	
☐	AFNI file	afni	

Create a new data source and choose the 4Ddti.nii file.

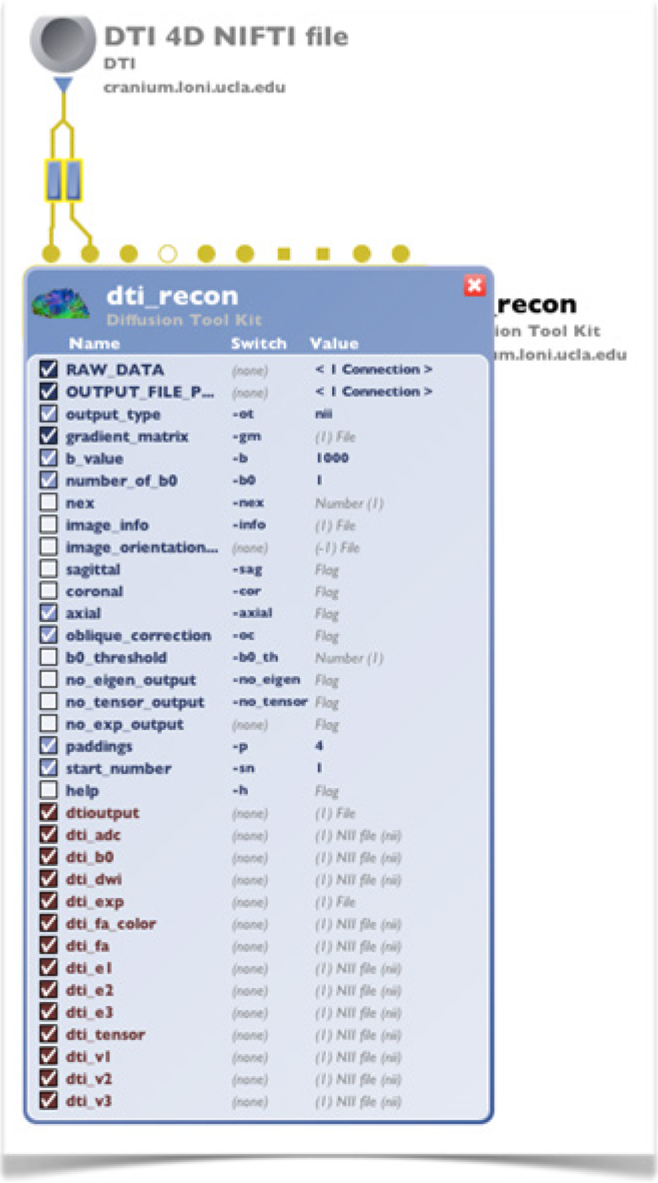
DTI Analyses

DTI Recon Optional Parameters

2) Connect the data source to the RAW_DATA and the OUTPUT_FILE_PREFIX input parameters in the dti_recon module. Double click on the module and choose the following optional parameters (Pic3).

    output type: this is always set to nii
    b-value: this is set to 1000 based on the data that is used.
    number_of_b0: 1 for this dataset
    axial: flag
    oblique_correction: flag
    padding: is set to 4
    start_number: is set to 1

NOTE: These options are for the dataset that is used in this example. It can be changed according to any dataset.



dti_recon
Diffusion Tool Kit

	Name	Switch	Value
☑	RAW_DATA	(none)	< 1 Connection >
☑	OUTPUT_FILE_P...	(none)	< 1 Connection >
☑	output_type	-ot	nii
☑	gradient_matrix	-gm	(1) File
☑	b_value	-b	1000
☑	number_of_b0	-b0	1
□	nex	-nex	Number (1)
□	image_info	-info	(1) File
□	image_orientation...	(none)	(-1) File
□	sagittal	-sag	Flag
□	coronal	-cor	Flag
☑	axial	-axial	Flag
☑	oblique_correction	-oc	Flag
□	b0_threshold	-b0_th	Number (1)
□	no_eigen_output	-no_eigen	Flag
□	no_tensor_output	-no_tensor	Flag
□	no_exp_output	(none)	Flag
☑	paddings	-p	4
☑	start_number	-sn	1
□	help	-h	Flag
☑	dtioutput	(none)	(1) File
☑	dti_adc	(none)	(1) NII file (nii)
☑	dti_b0	(none)	(1) NII file (nii)
☑	dti_dwi	(none)	(1) NII file (nii)
☑	dti_exp	(none)	(1) File
☑	dti_fa_color	(none)	(1) NII file (nii)
☑	dti_fa	(none)	(1) NII file (nii)
☑	dti_e1	(none)	(1) NII file (nii)
☑	dti_e2	(none)	(1) NII file (nii)
☑	dti_e3	(none)	(1) NII file (nii)
☑	dti_tensor	(none)	(1) NII file (nii)
☑	dti_v1	(none)	(1) NII file (nii)
☑	dti_v2	(none)	(1) NII file (nii)
☑	dti_v3	(none)	(1) NII file (nii)

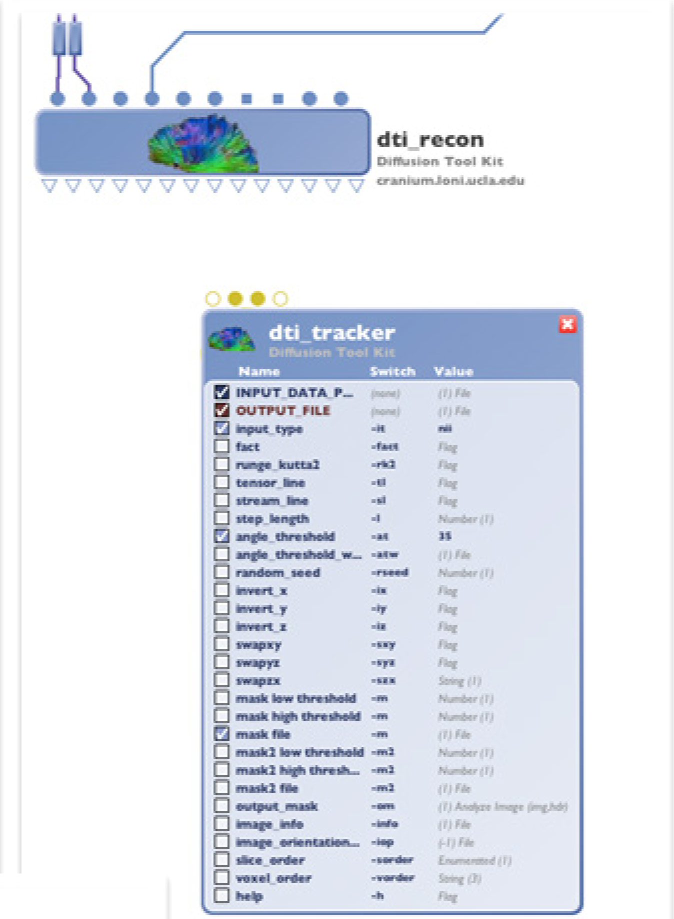
DTI Analyses

DTI Tracker

3) Click on dti_tracker module in the library and drag it to the empty canvas. Double click on the module and enable the following optional parameters (Pic5).

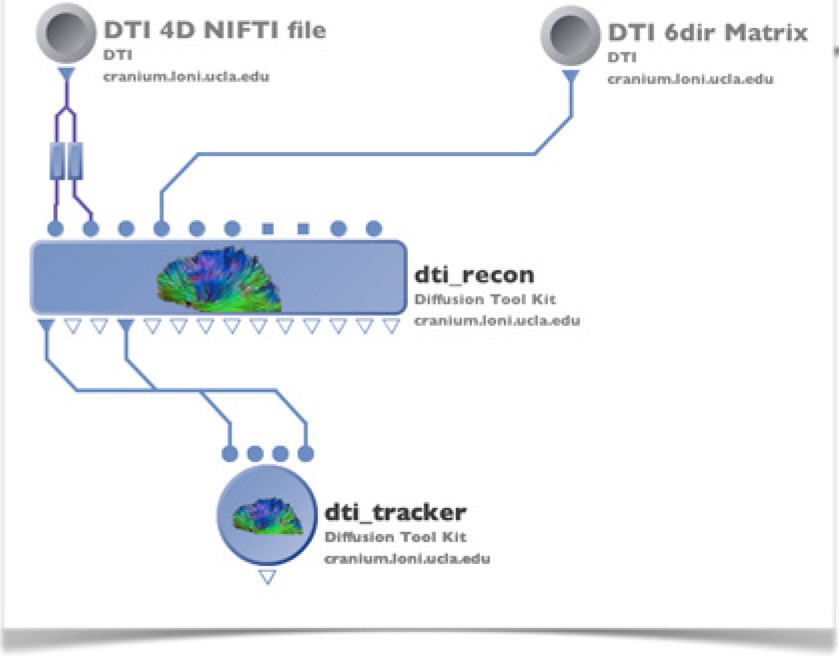
    Input_type: choose nii option only.
    angle_threshold: enter the value 35
    mask file

Connect the output parameters, dtioutput and dti_dwi in the dti_recon module to the input parameters, INPUT_DATA_PREFIX and mask file in the dti_tracker module.



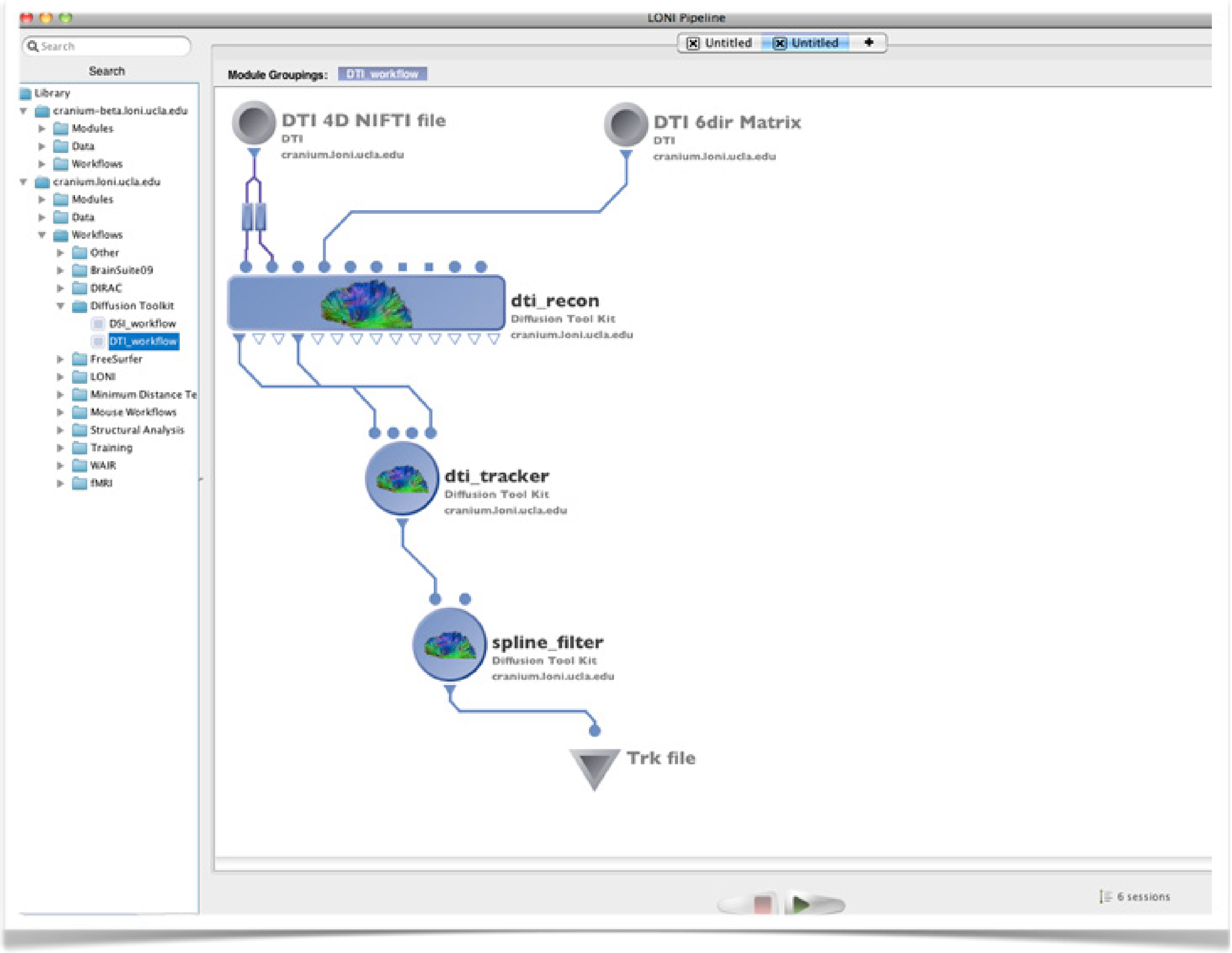
dti_tracker
Diffusion Tool Kit

	Name	Switch	Value
☑	INPUT_DATA_P...	(none)	(1) File
☑	OUTPUT_FILE	(none)	(1) File
☑	input_type	-it	nii
□	fact	-fact	Flag
□	runge_kutta2	-rk2	Flag
□	tensor_line	-tl	Flag
□	stream_line	-sl	Flag
□	step_length	-l	Number (1)
☑	angle_threshold	-at	35
□	angle_threshold_w...	-atw	(1) File
□	random_seed	-rseed	Number (1)
□	invert_x	-ix	Flag
□	invert_y	-iy	Flag
□	invert_z	-iz	Flag
□	swapxy	-sxy	Flag
□	swapyz	-syz	Flag
□	swapzx	-szx	String (1)
□	mask low threshold	-m	Number (1)
□	mask high threshold	-m	Number (1)
☑	mask file	-m	(1) File
□	mask2 low threshold	-m2	Number (1)
□	mask2 high thresh...	-m2	Number (1)
□	mask2 file	-m2	(1) File
□	output_mask	-om	(1) Analyze Image (img,hdr)
□	image_info	-info	(1) File
□	image_orientation...	-iop	(-1) File
□	slice_order	-sorder	Enumerated (1)
□	voxel_order	-vorder	String (3)
□	help	-h	Flag



DTI Analyses

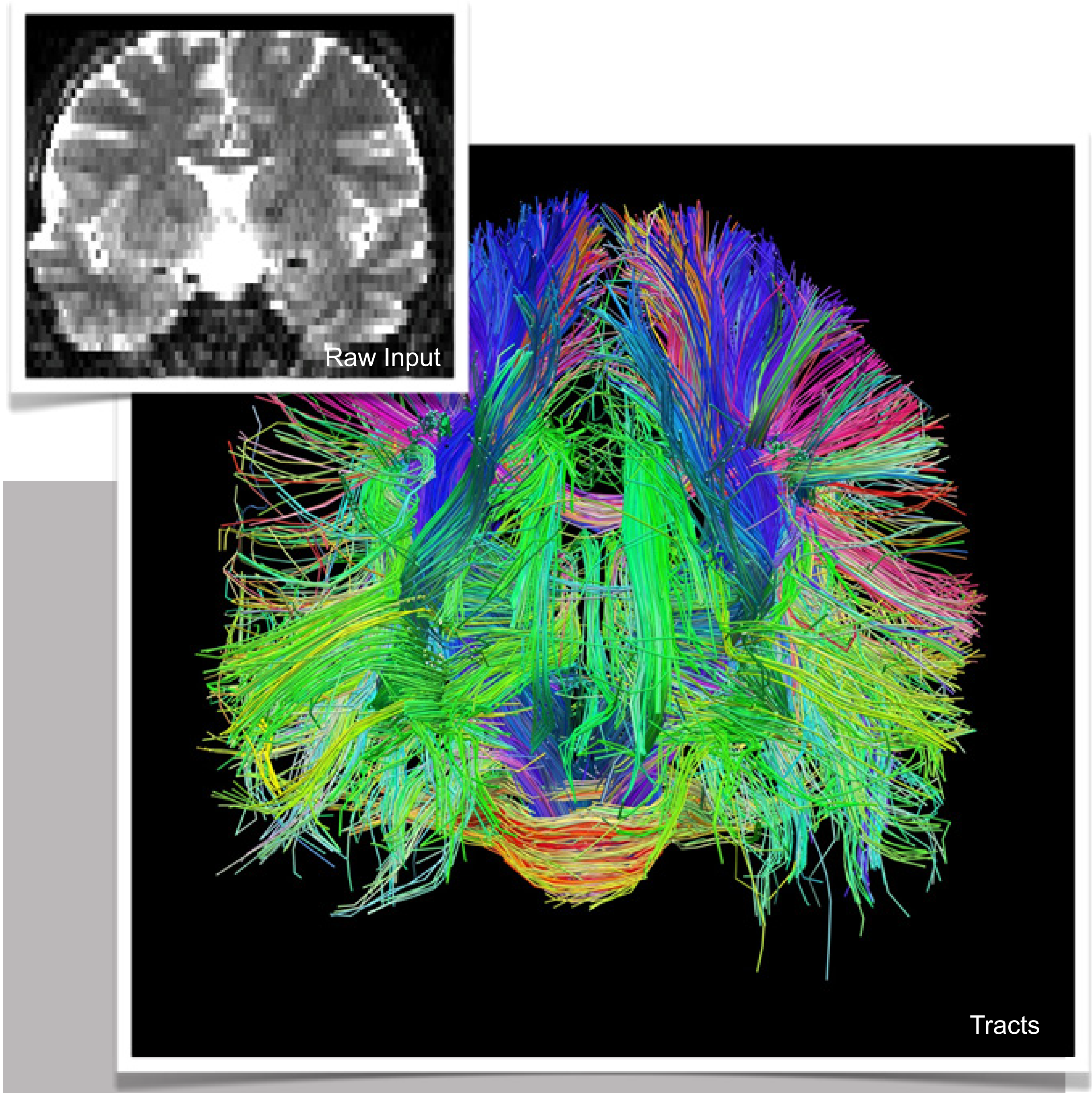
Spline Filter and Output TRK file



4) Choose and drag the spline_filter module and connect the output of the dti_tracker module to the INPUT_TRACK_FILE parameter in the spline_filter module. Choose value 1 for the STEP_LENGTH option. Save the output of the spline_filter as a data sink or simply specify the file path. To save outputs at intermediate steps you can add data sinks and specify the file path.

DTI Analyses

Results

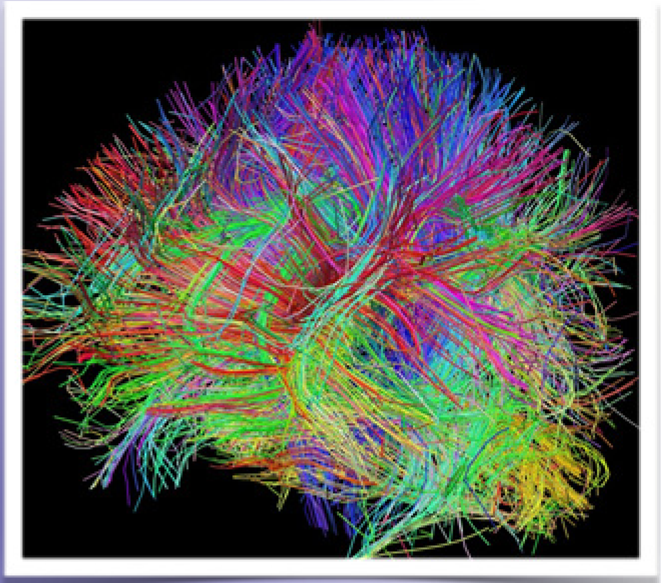


The results of this workflow is a DTI Track file that can be used in TrackVis program for further analysis.

DSI Analyses

Introduction

This workflow creates white matter tracts for viewing in TrackVis from DSI files.



Overview

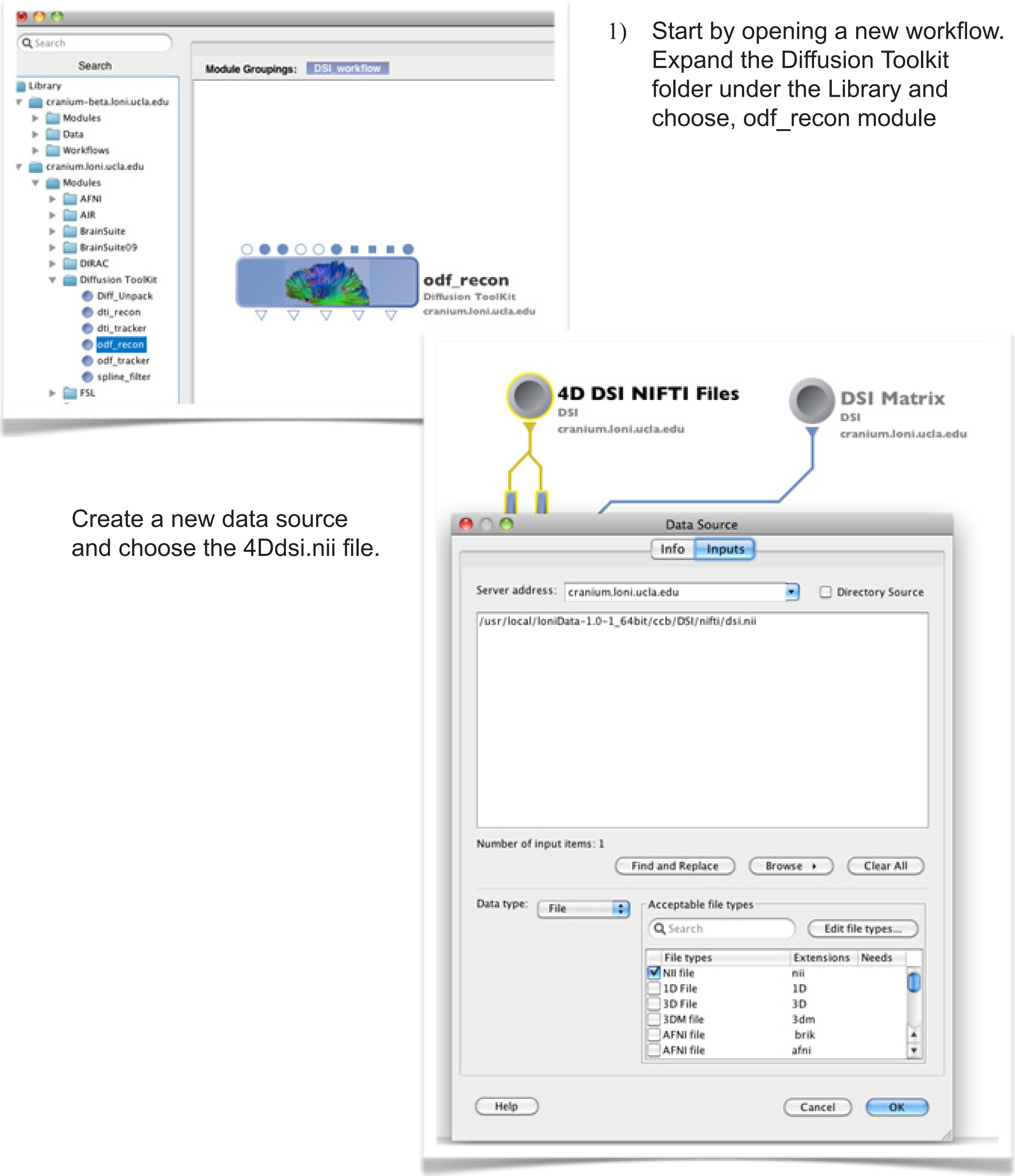
In this workflow, DSI (DICOM/NIfTI) images are reconstructed and fiber tracks are generated for TrackVis. Diffusion toolkit command-line tools are used to build the workflow. Individual command-line tools are available as modules in the Pipeline library.

DSI Analyses

Copy ODF Recon and Specify the Input

1) Start by opening a new workflow. Expand the Diffusion Toolkit folder under the Library and choose, odf_recon module

Create a new data source and choose the 4Ddsi.nii file.



Module Groupings: DSI_workflow

- Library
  - cranium-beta.loni.ucla.edu
    - Modules
    - Data
    - Workflows
  - cranium.loni.ucla.edu
    - Modules
      - AFNI
      - AIR
      - BrainSuite
      - BrainSuite09
      - DIRAC
      - Diffusion ToolKit
        - Diff_Unpack
        - dti_recon
        - dti_tracker
        - odf_recon
        - odf_tracker
        - spline_filter
      - FSL

odf_recon
Diffusion ToolKit
cranium.loni.ucla.edu

4D DSI NIFTI Files
DSI
cranium.loni.ucla.edu

DSI Matrix
DSI
cranium.loni.ucla.edu

Data Source

Server address: cranium.loni.ucla.edu □ Directory Source

/usr/local/loniData-1.0-1_64bit/ccb/DSI/nifti/dsi.nii

Number of input items: 1

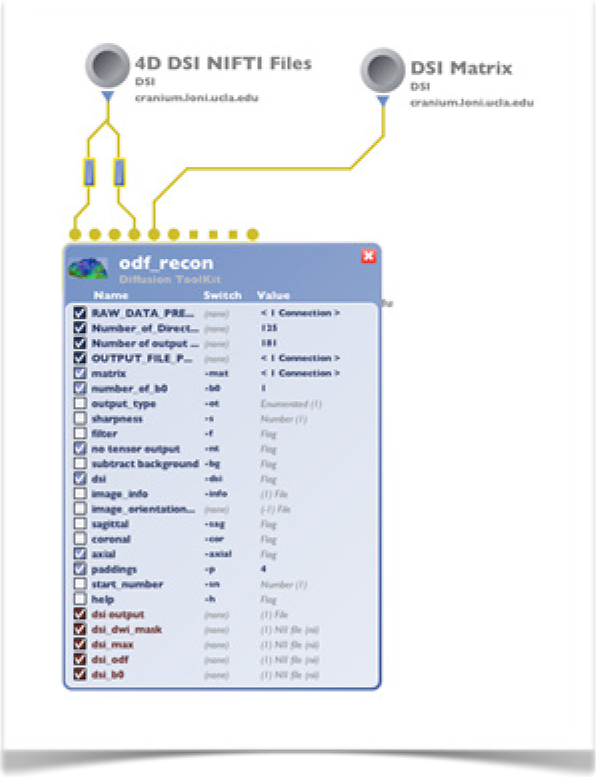
Data type: File

Acceptable file types

File types	Extensions	Needs
☑ NII file	nii	
□ 1D File	1D	
□ 3D File	3D	
□ 3DM file	3dm	
□ AFNI file	brik	
□ AFNI file	afni	

DSI Analyses

ODF Recon Optional Parameters



	Name	Switch	Value
☑	RAW_DATA_PRE...	(none)	< 1 Connection >
☑	Number_of_Direct...	(none)	125
☑	Number of output ...	(none)	181
☑	OUTPUT_FILE_P...	(none)	< 1 Connection >
☑	matrix	-mat	< 1 Connection >
☑	number_of_b0	-b0	1
☐	output_type	-ot	Enumerated (1)
☐	sharpness	-s	Number (1)
☐	filter	-f	Flag
☑	no tensor output	-nt	Flag
☐	subtract background	-bg	Flag
☑	dsi	-dsi	Flag
☐	image_info	-info	(1) File
☐	image_orientation...	(none)	(-1) File
☐	sagittal	-sag	Flag
☐	coronal	-cor	Flag
☑	axial	-axial	Flag
☑	paddings	-p	4
☐	start_number	-sn	Number (1)
☐	help	-h	Flag
☑	dsi output	(none)	(1) File
☑	dsi_dwi_mask	(none)	(1) Nll file (nii)
☑	dsi_max	(none)	(1) Nll file (nii)
☑	dsi_odf	(none)	(1) Nll file (nii)
☑	dsi_b0	(none)	(1) Nll file (nii)

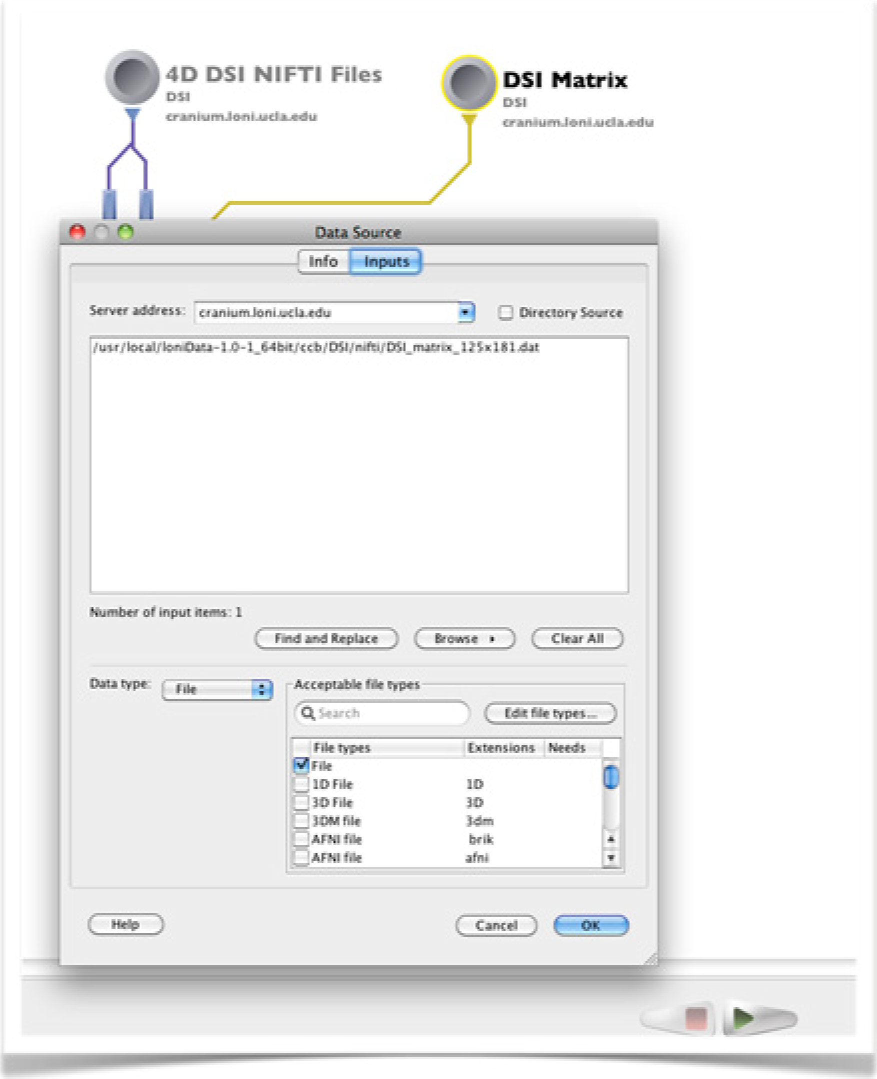
2) Connect the data source to the RAW_DATA and the OUTPUT_FILE_PREFIX input parameters in the dti_recon module. Double click on the module and choose the following optional parameters,
   Number_of_Directions: 125 (for the data set being used)
   Number of output directions: 181
3) To enable optional parameters, double click on the module and choose the following,
   matrix
   Number_of_b0: enter value 1 (this is for the data that is used here)
   No tensor output flag
   dsi: flag
   axial: flag
   padding: enter value 4

NOTE: These options are based on the dataset that is used in this example.

DSI Analyses

Specifying the Gradient Matrix

4) One of the input parameters in the odf_recon module is called the gradient_matrix. This matrix contains the directional information of the data that is used. This matrix can be saved or copied from the diffusion toolkit interface Gradient table option. For this example we use 125x181 directional matrix. Create a data source or double click on the parameter and enter the path to this file.



Server address: cranium.loni.ucla.edu ☐ Directory Source

/usr/local/loniData-1.0-1_64bit/ccb/DSI/nifti/DSI_matrix_125x181.dat

Number of input items: 1

Data type: File

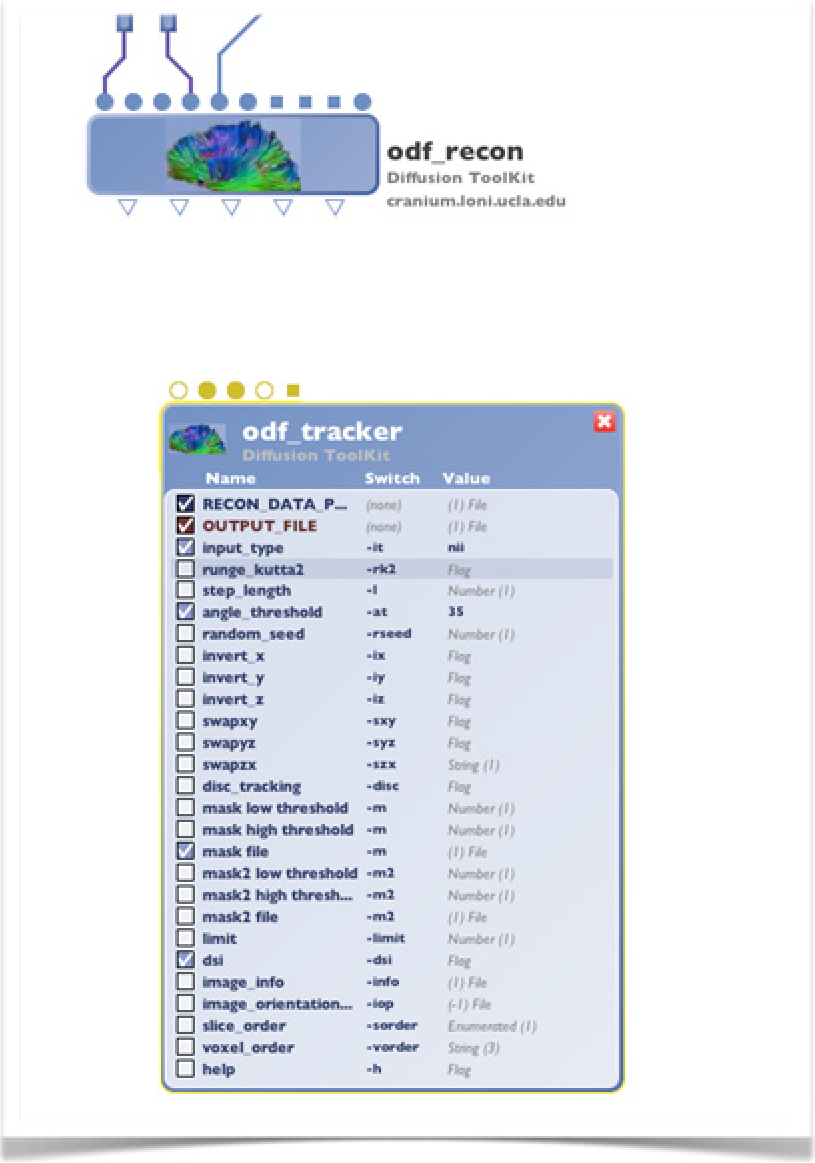
Acceptable file types

	File types	Extensions	Needs
☑	File		
☐	1D File	1D	
☐	3D File	3D	
☐	3DM file	3dm	
☐	AFNI file	brik	
☐	AFNI file	afni	

DSI Analyses

ODF Tracker Optional Parameters

5) From the library click on odf_tracker module and drag it to the empty canvas. Double click on the module and enable the following optional parameters.
   - Input_type: choose nii option only.
   - angle_threshold: enter the value 35
   - mask file
   - dsi



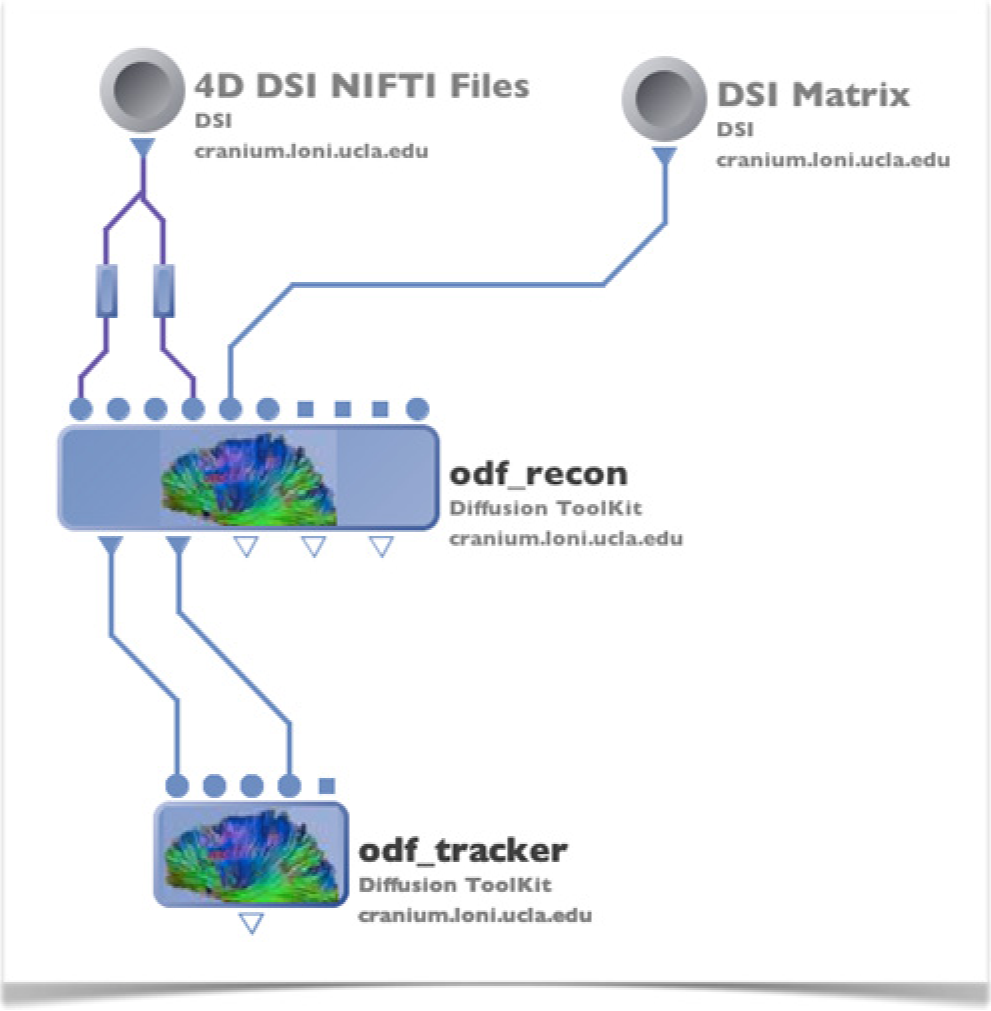
odf_tracker
Diffusion ToolKit

	Name	Switch	Value
☑	RECON_DATA_P...	(none)	(1) File
☑	OUTPUT_FILE	(none)	(1) File
☑	input_type	-it	nii
□	runge_kutta2	-rk2	Flag
□	step_length	-l	Number (1)
☑	angle_threshold	-at	35
□	random_seed	-rseed	Number (1)
□	invert_x	-ix	Flag
□	invert_y	-iy	Flag
□	invert_z	-iz	Flag
□	swapxy	-sxy	Flag
□	swapyz	-syz	Flag
□	swapzx	-szx	String (1)
□	disc_tracking	-disc	Flag
□	mask low threshold	-m	Number (1)
□	mask high threshold	-m	Number (1)
☑	mask file	-m	(1) File
□	mask2 low threshold	-m2	Number (1)
□	mask2 high thresh...	-m2	Number (1)
□	mask2 file	-m2	(1) File
□	limit	-limit	Number (1)
☑	dsi	-dsi	Flag
□	image_info	-info	(1) File
□	image_orientation...	-iop	(-1) File
□	slice_order	-sorder	Enumerated (1)
□	voxel_order	-vorder	String (3)
□	help	-h	Flag

DSI Analyses

Connect the ODF Recon to the ODF Tracker

6) Connect the output parameters, dsioutput and dsi_dwi_mask in the odf_recon module to the input parameters, RECON_DATA_PREFIX and mask file in the odf_tracker module.

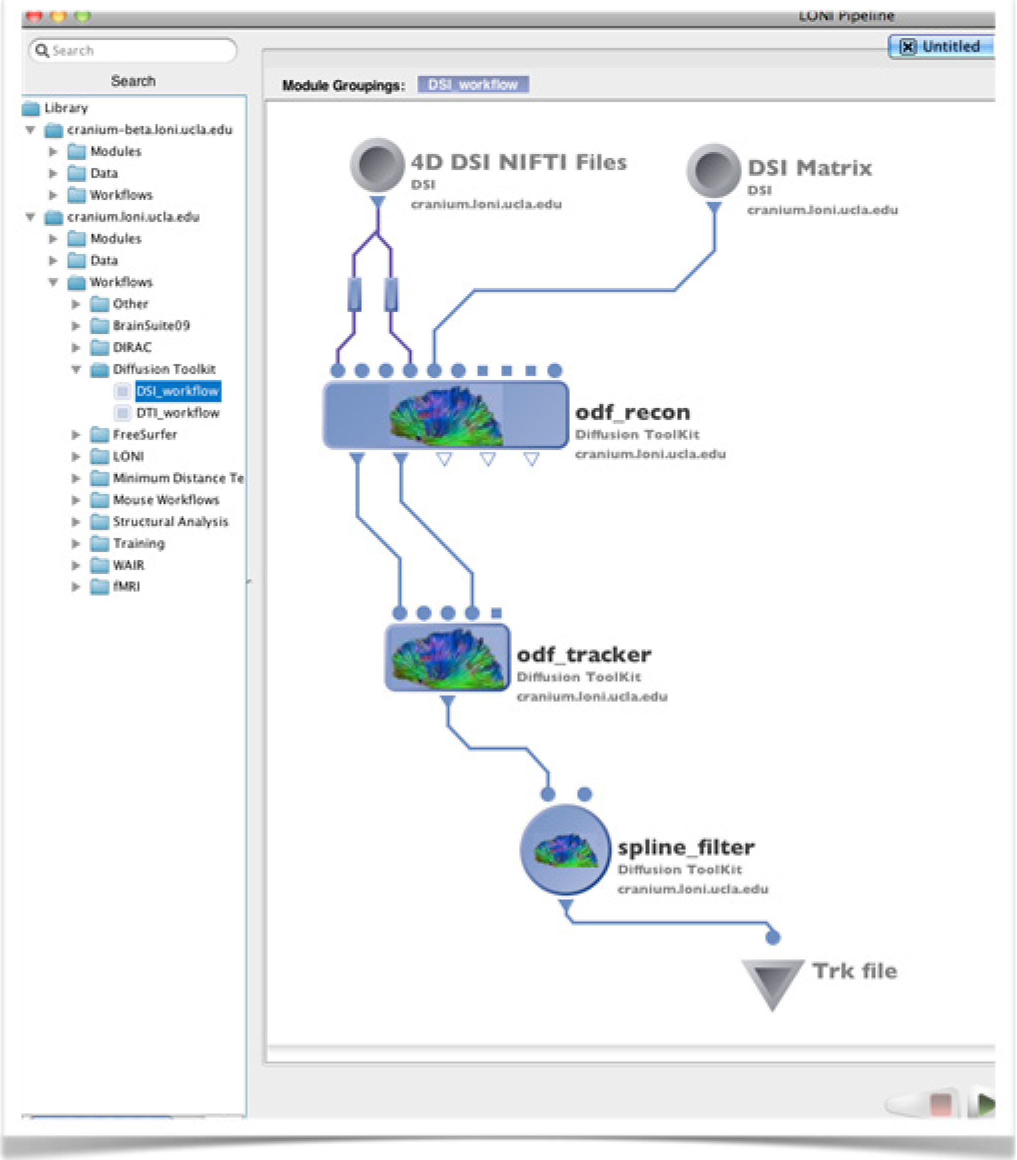


DSI Analyses

Spline Filter and Output TRK file

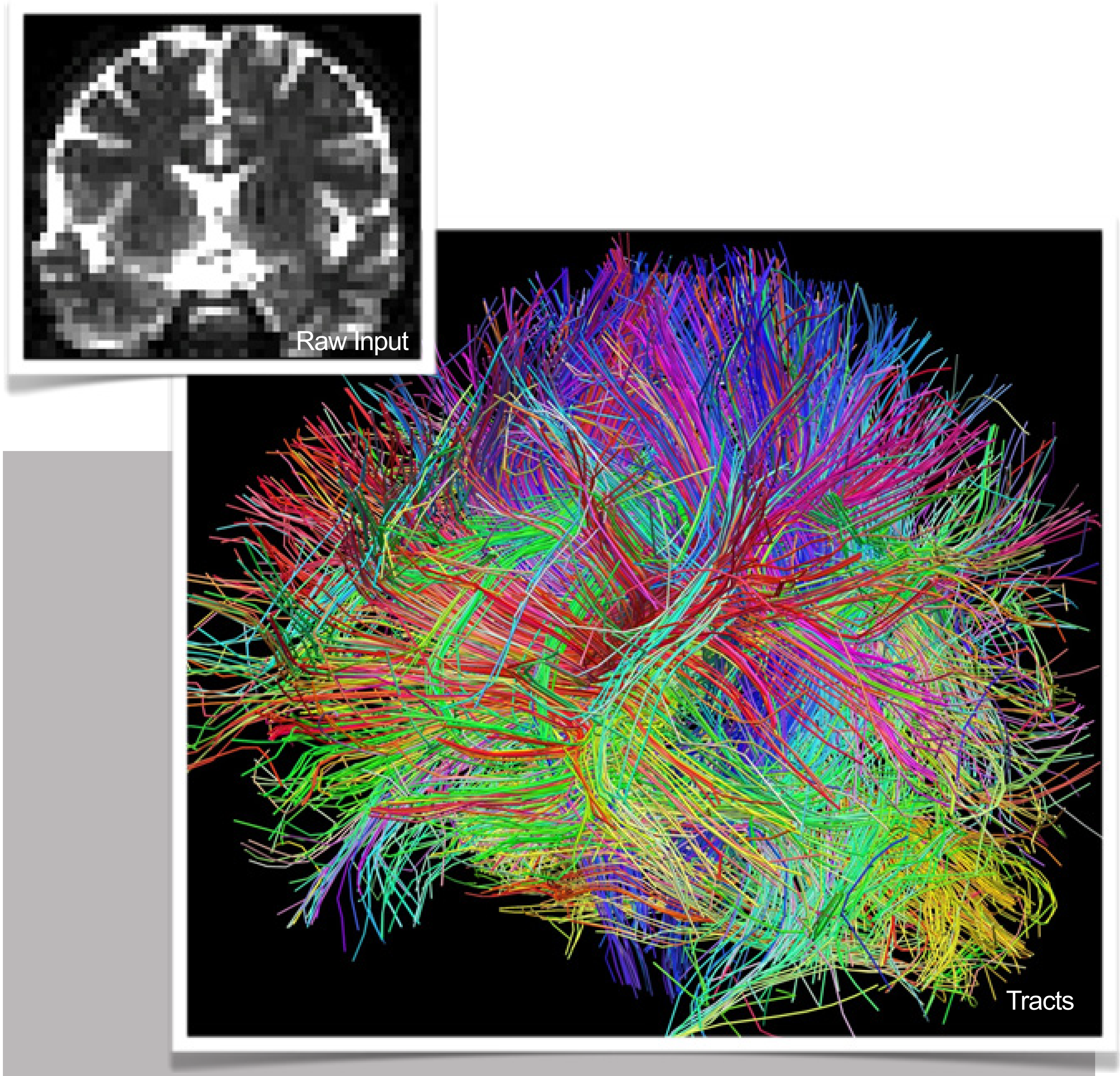
7) Choose and drag the spline_filter module and connect the output of the dti_tracker module to the INPUT_TRACK_FILE parameter in the spline_filter module. Choose value 1 for the STEP_LENGTH option.
8) Save the output of the spline_filter a data sink or simply specify the file path.

NOTE: To save outputs at intermediate steps you can add data sinks and specify the file path.



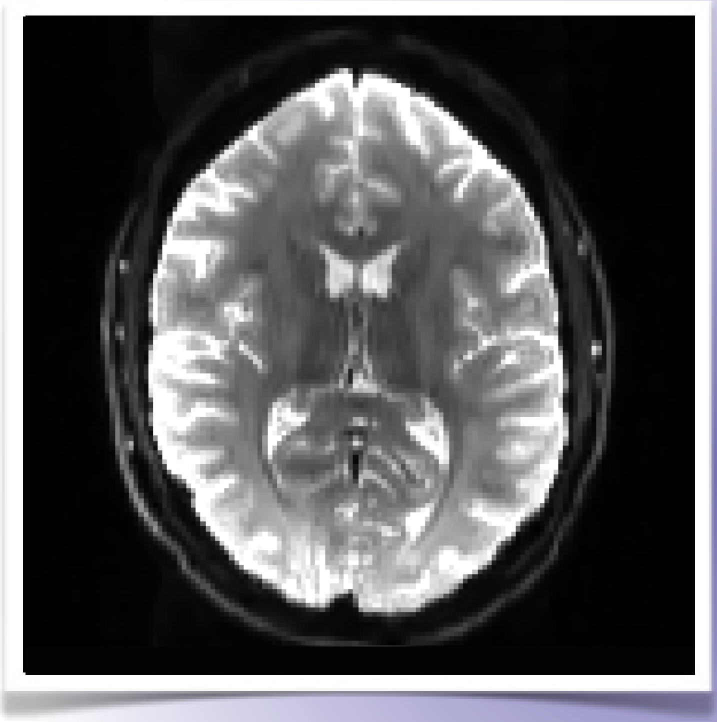
DSI Analyses

Results

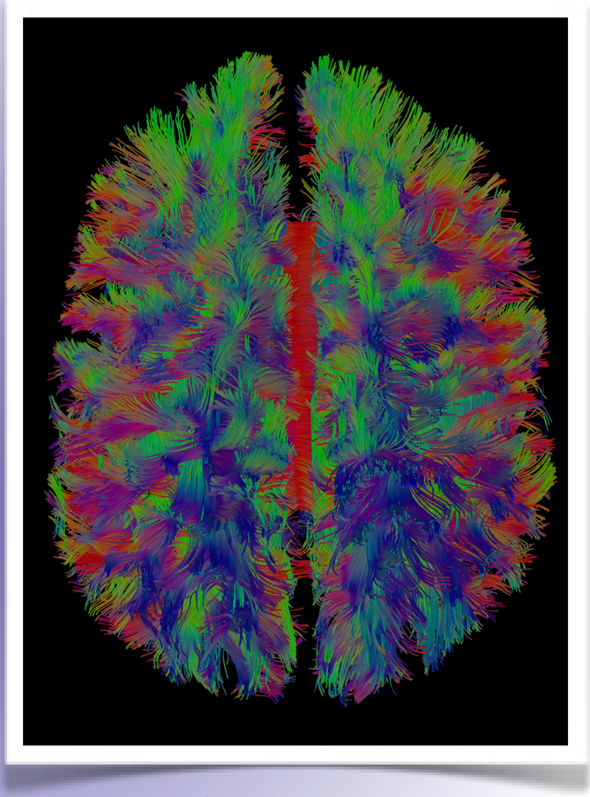


The results of this workflow is a DSI Track file that can be used in TrackVis program for further analysis.

Image Analysis with the Quantitative Imaging Toolkit - Tractography Metrics



Input DWI



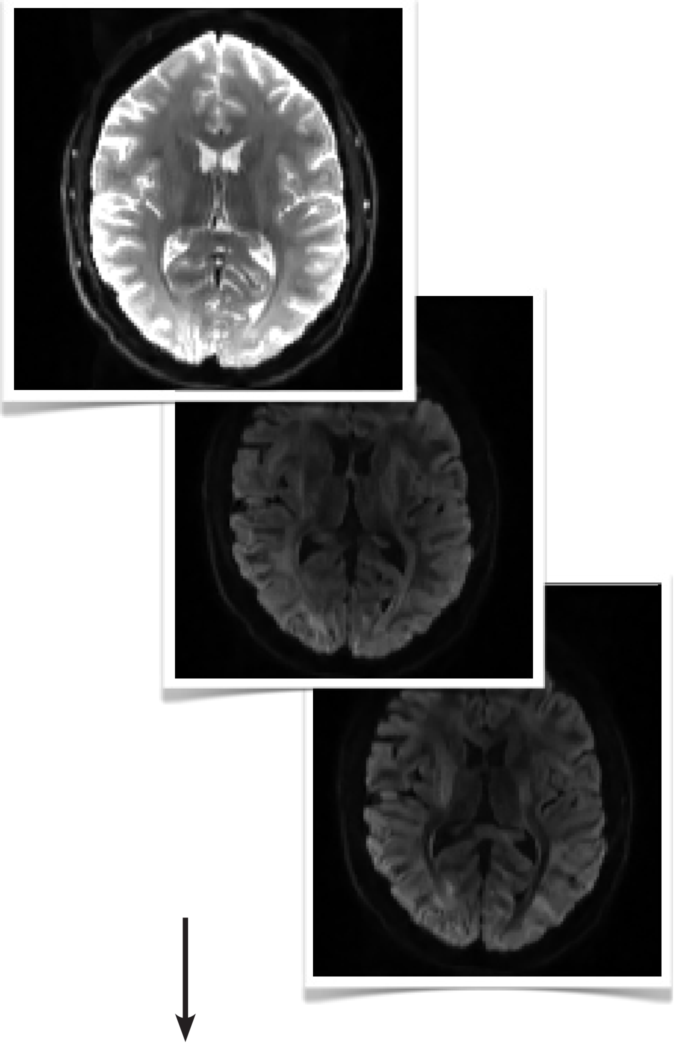
Output Tracts

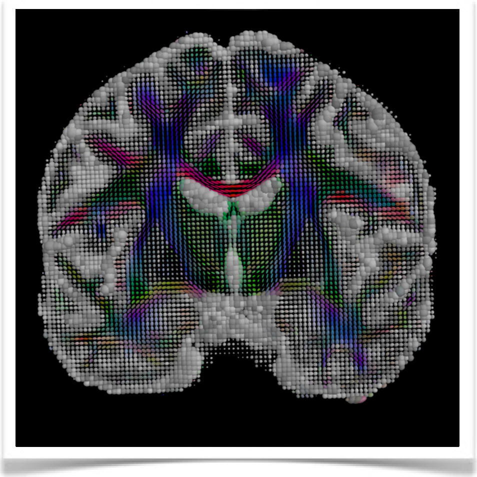
Analysis with QIT - Tractography

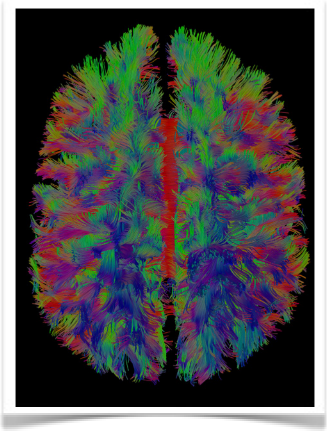
Introduction

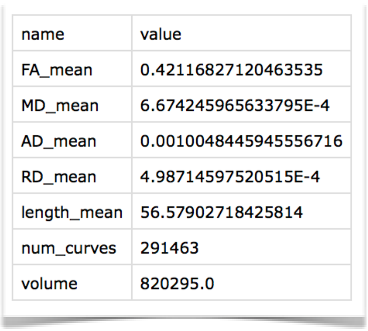
This workflow demonstrates how to extract whole brain tractography metrics from a diffusion-weighted MRI dataset with the Quantitative Imaging Toolkit (QIT).

Tractography is the process of reconstructing connections within the brain using diffusion-weighted MRI, and it has many applications in the study of the brain in health and disease. The reconstruction includes multiple steps that are demonstrated in this workflow, including image processing, modeling, and quantitative analysis. In the following pages, we discuss the various modules, describe their usage, and explain the user-defined parameters.





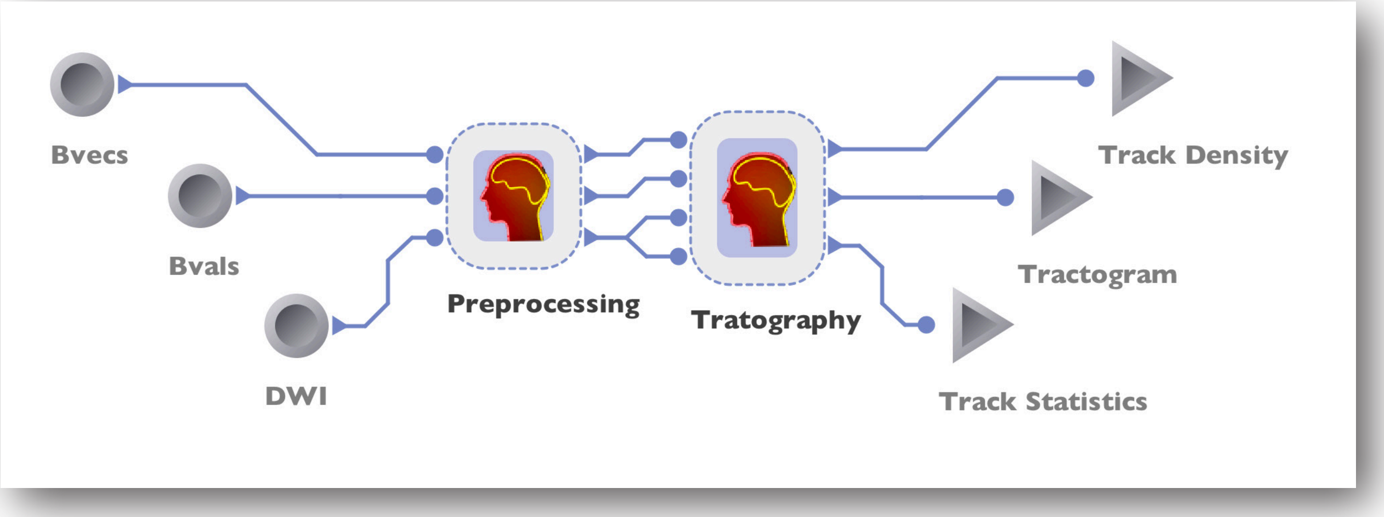




name	value
FA_mean	0.42116827120463535
MD_mean	6.674245965633795E-4
AD_mean	0.0010048445945556716
RD_mean	4.98714597520515E-4
length_mean	56.57902718425814
num_curves	291463
volume	820295.0

Analysis with QIT - Tractography

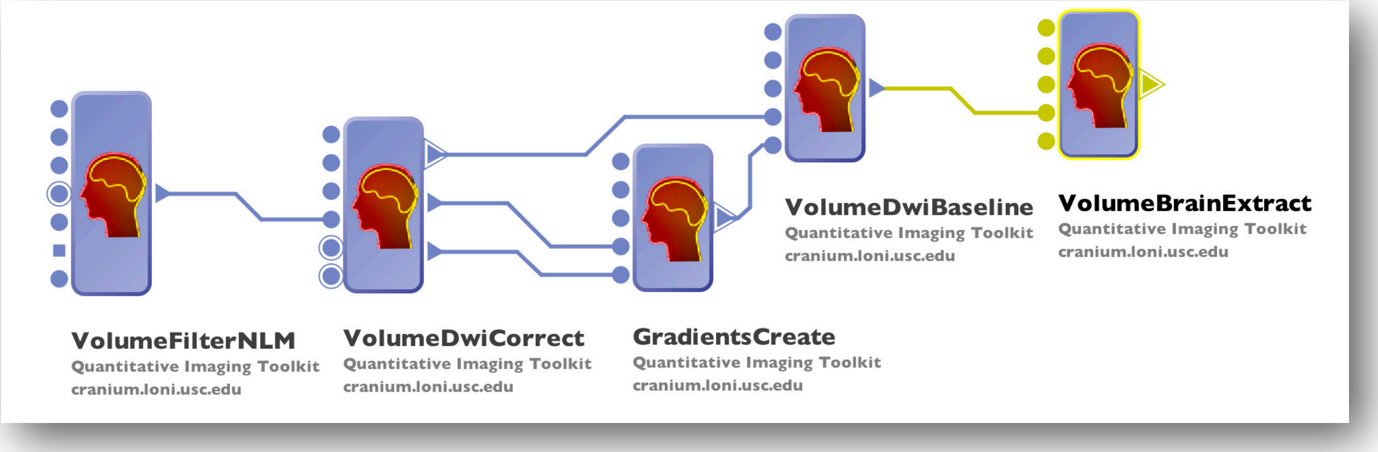
Workflow Overview



Shown above is a simplified workflow for whole brain tractography reconstruction. The input data includes a diffusion-weighed MRI and associated b-vectors and b-values. The output is a track density image, a 3D tractogram, and a statistical summary of the results. There are many modules involved, but for simplicity, they have been grouped into two subsets for image preprocessing and tractography analysis. Next, we examine each of these module groups and their constituent parts.

Analysis with QIT - Tractography

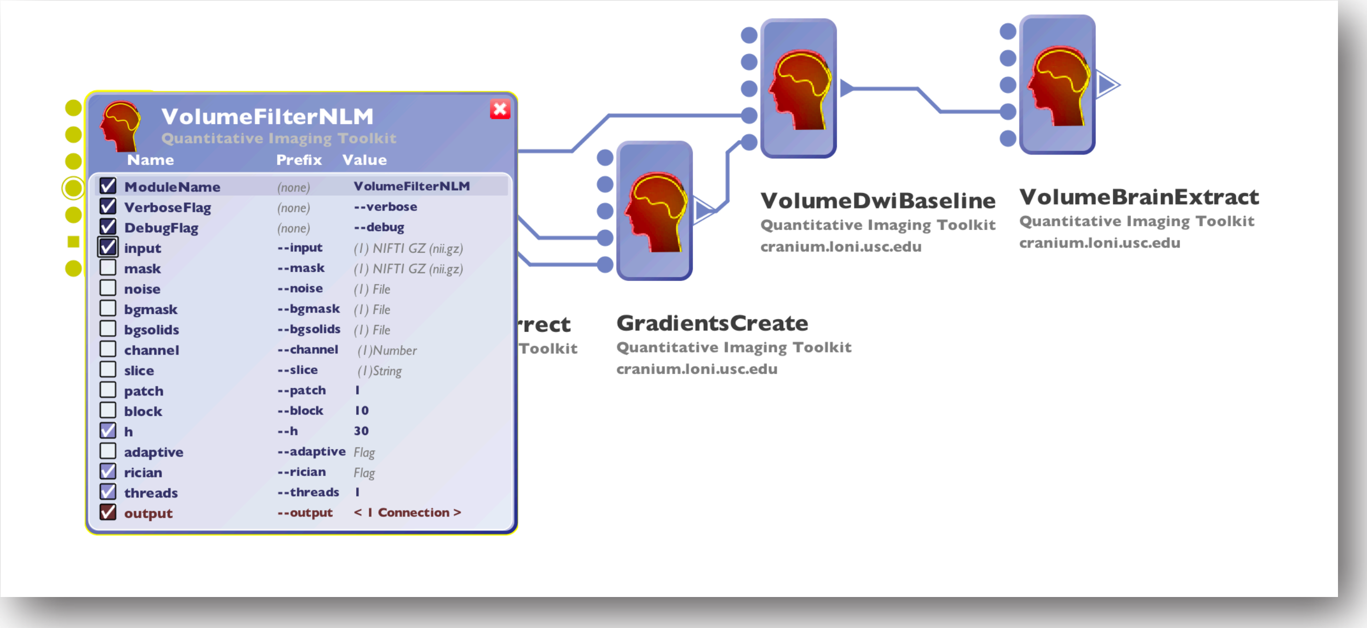
Image Preprocessing



Shown above is the module group for image preprocessing. Diffuson-weighted MRI is susceptible to a variety of types of imaging artifacts, particularly noise and motion, and this workflow is designed to help reduce the effects of these artifacts on the tractography reconstruction. The modules include steps for denoising, motion correction, and brain extraction, which are described in detail next.

Analysis with QIT - Tractography

Denoising



VolumeFilterNLM

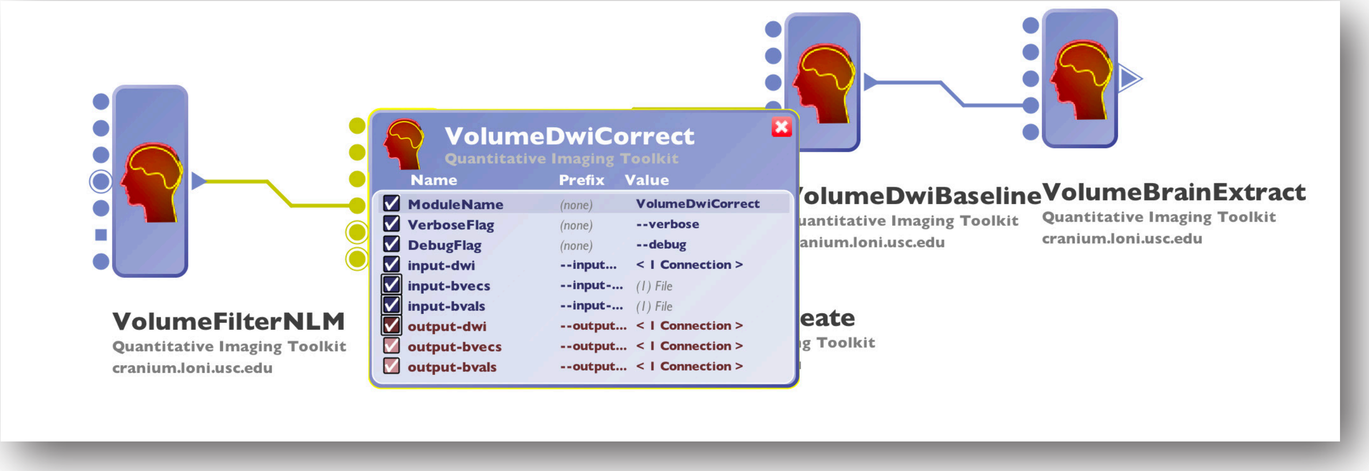
Quantitative Imaging Toolkit

	Name	Prefix	Value
☑	ModuleName	(none)	VolumeFilterNLM
☑	VerboseFlag	(none)	--verbose
☑	DebugFlag	(none)	--debug
☑	input	--input	(1) NIFTI GZ (nii.gz)
□	mask	--mask	(1) NIFTI GZ (nii.gz)
□	noise	--noise	(1) File
□	bgmask	--bgmask	(1) File
□	bgsolids	--bgsolids	(1) File
□	channel	--channel	(1)Number
□	slice	--slice	(1)String
□	patch	--patch	1
□	block	--block	10
☑	h	--h	30
□	adaptive	--adaptive	Flag
☑	rician	--rician	Flag
☑	threads	--threads	1
☑	output	--output	< 1 Connection >

Shown above is the VolumeFilterNLM module from QIT. This algorithm is an advancing denoising algorithm known as non-local means, which uses the similarity of image patches to reduce noise in the dataset. This is an important step for improving the reliability of tractography reconstructions. The amount of denoising is controlled by a noise level parameter h, which we set to 30. There are other advanced setting for specifying the patch size, search procedure, noise model, and multi-threading.

Analysis with QIT - Tractography

Motion Correction

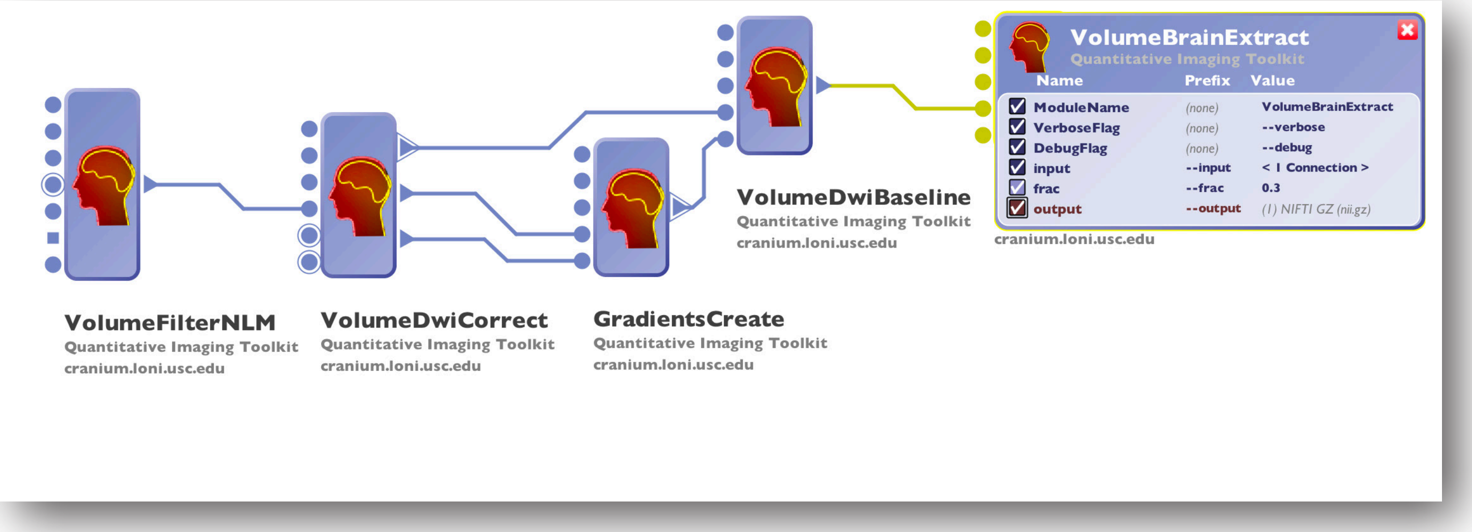


	Name	Prefix	Value
☑	ModuleName	(none)	VolumeDwiCorrect
☑	VerboseFlag	(none)	--verbose
☑	DebugFlag	(none)	--debug
☑	input-dwi	--input...	< I Connection >
☑	input-bvecs	--input-...	(I) File
☑	input-bvals	--input-...	(I) File
☑	output-dwi	--output...	< I Connection >
☑	output-bvecs	--output...	< I Connection >
☑	output-bvals	--output...	< I Connection >

Shown above is the VolumeDwiCorrect module from QIT. This procedure for correcting intra-scan motion of the subject during the imaging session. A diffusion-weighed dataset is made up of many individual scans, each with different acquisition parameters. This module corrects for motion among these scans by registering them to the first scan using FSL FLIRT. The b-vectors are also related to the orientation of the scan, so when there is a rotation between scans, the b-vectors are rotated to reflect this as well.

Analysis with QIT - Tractography

Brain Extraction

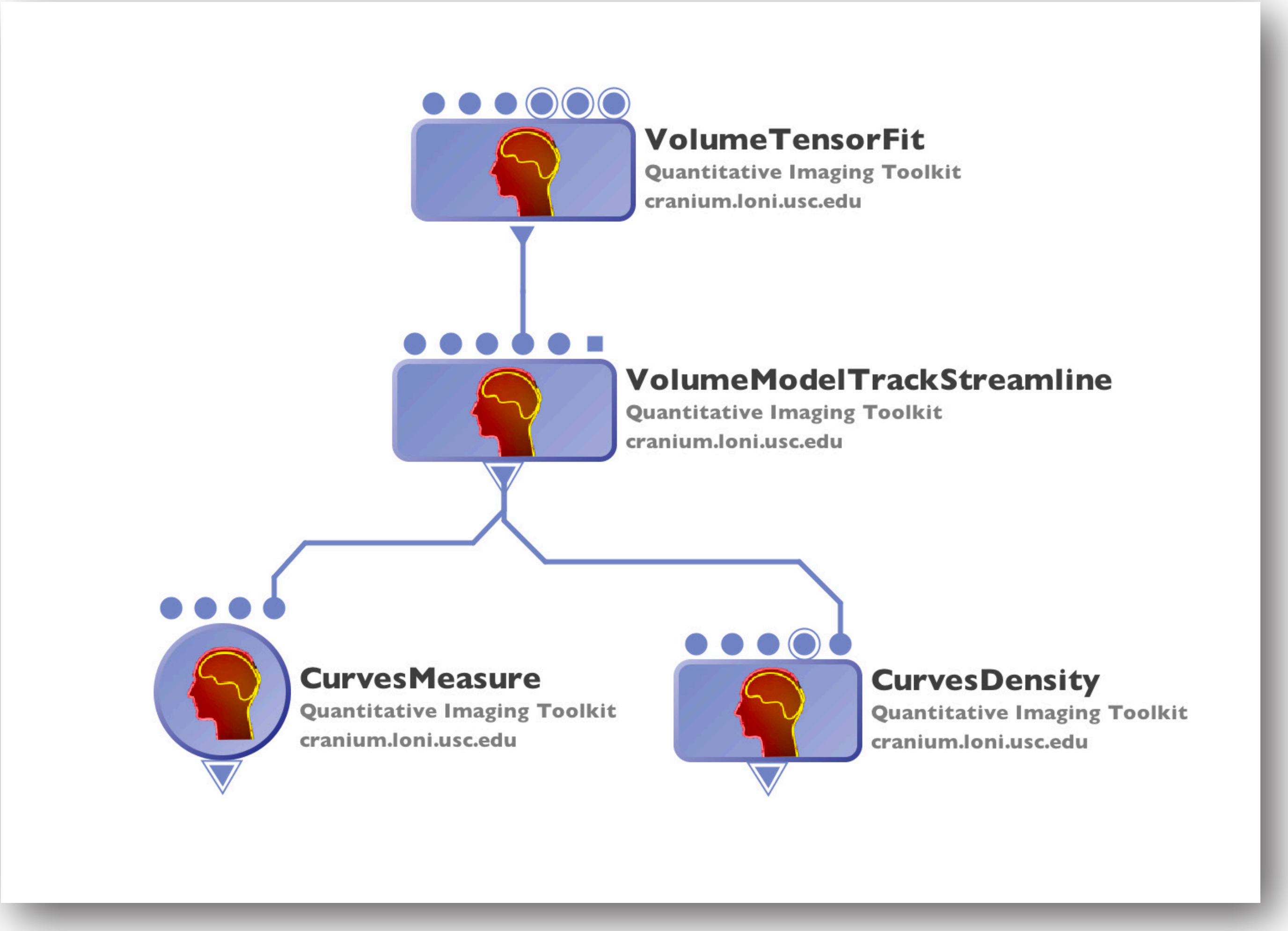


	Name	Prefix	Value
☑	ModuleName	(none)	VolumeBrainExtract
☑	VerboseFlag	(none)	--verbose
☑	DebugFlag	(none)	--debug
☑	input	--input	< 1 Connection >
☑	frac	--frac	0.3
☑	output	--output	(1) NIFTI GZ (nii.gz)

Shown above is the VolumeBrainExtract module from QIT. This procedure for extracting the brain from the MRI, which is needed because the skull and other non-brain tissue can negatively affect tractography analysis. This uses the FSL BET algorithm, which uses a deformable surface model that is automatically fitted to fit the boundary of the brain. The most relevant parameter is the fractional threshold, which we set to 0.3.

Analysis with QIT - Tractography

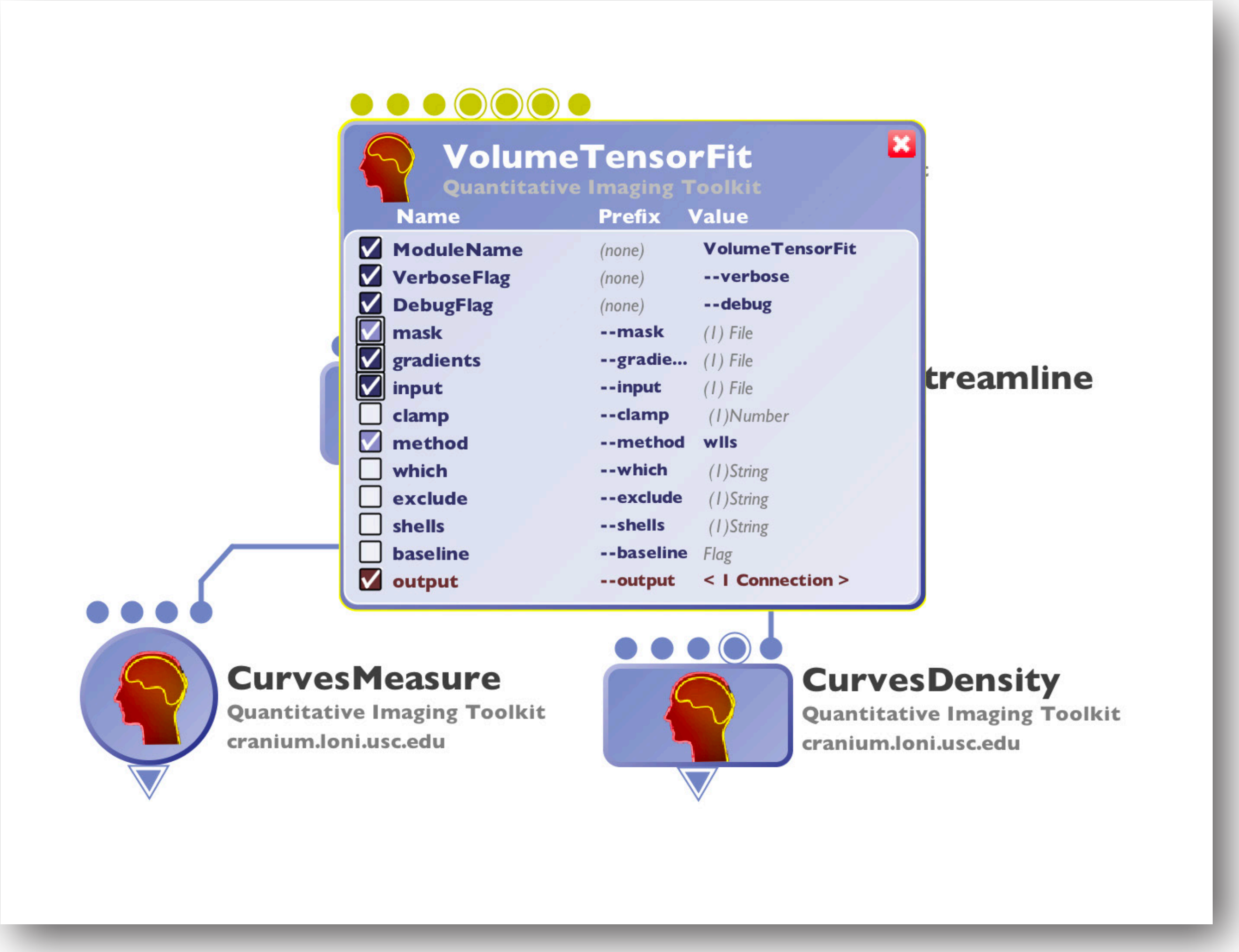
Tractography Analysis


VolumeTensorFit
Quantitative Imaging Toolkit
cranium.loni.usc.edu
VolumeModelTrackStreamline
Quantitative Imaging Toolkit
cranium.loni.usc.edu
CurvesMeasure
Quantitative Imaging Toolkit
cranium.loni.usc.edu
CurvesDensity
Quantitative Imaging Toolkit
cranium.loni.usc.edu

Shown above is the module group for the tractography analysis, which takes as input the preprocessed diffusion MRI, gradients, and brain mask. This process performs image analysis to produce geometric and statistical models of the data. The module group include steps for diffusion modeling, streamline integration, and data mapping, which are described in detail next.

Analysis with QIT - Tractography

Diffusion Modeling

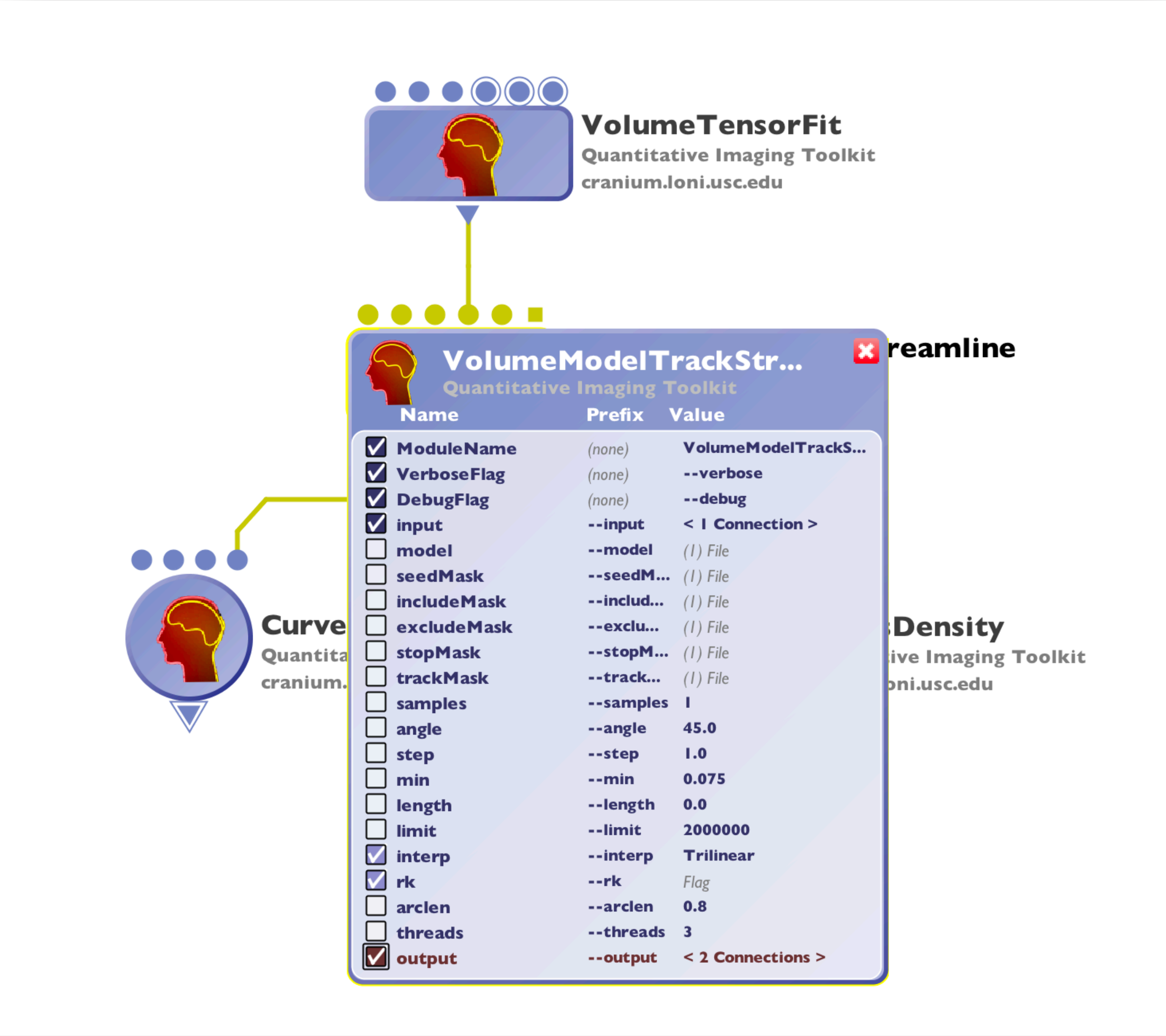


	Name	Prefix	Value
☑	ModuleName	(none)	VolumeTensorFit
☑	VerboseFlag	(none)	--verbose
☑	DebugFlag	(none)	--debug
☑	mask	--mask	(I) File
☑	gradients	--gradie...	(I) File
☑	input	--input	(I) File
☐	clamp	--clamp	(I)Number
☑	method	--method	wlls
☐	which	--which	(I)String
☐	exclude	--exclude	(I)String
☐	shells	--shells	(I)String
☐	baseline	--baseline	Flag
☑	output	--output	< I Connection >

Shown above is the VolumeTensorFit module from QIT. This algorithm fits a diffusion tensor model to the diffusion-weighted signal in each voxel of the imaging data. This model summarizes the pattern of diffusion using an ellipsoidal shape that reflects the primary orienation of white matter fibers, as well as indices of their structural integrity, such as fractional anisotropy (FA). There are many ways to fit tensors, and in this example, we specified wlls (weighted linear least squares) using the method parameter.

Analysis with QIT - Tractography

Streamline Integration



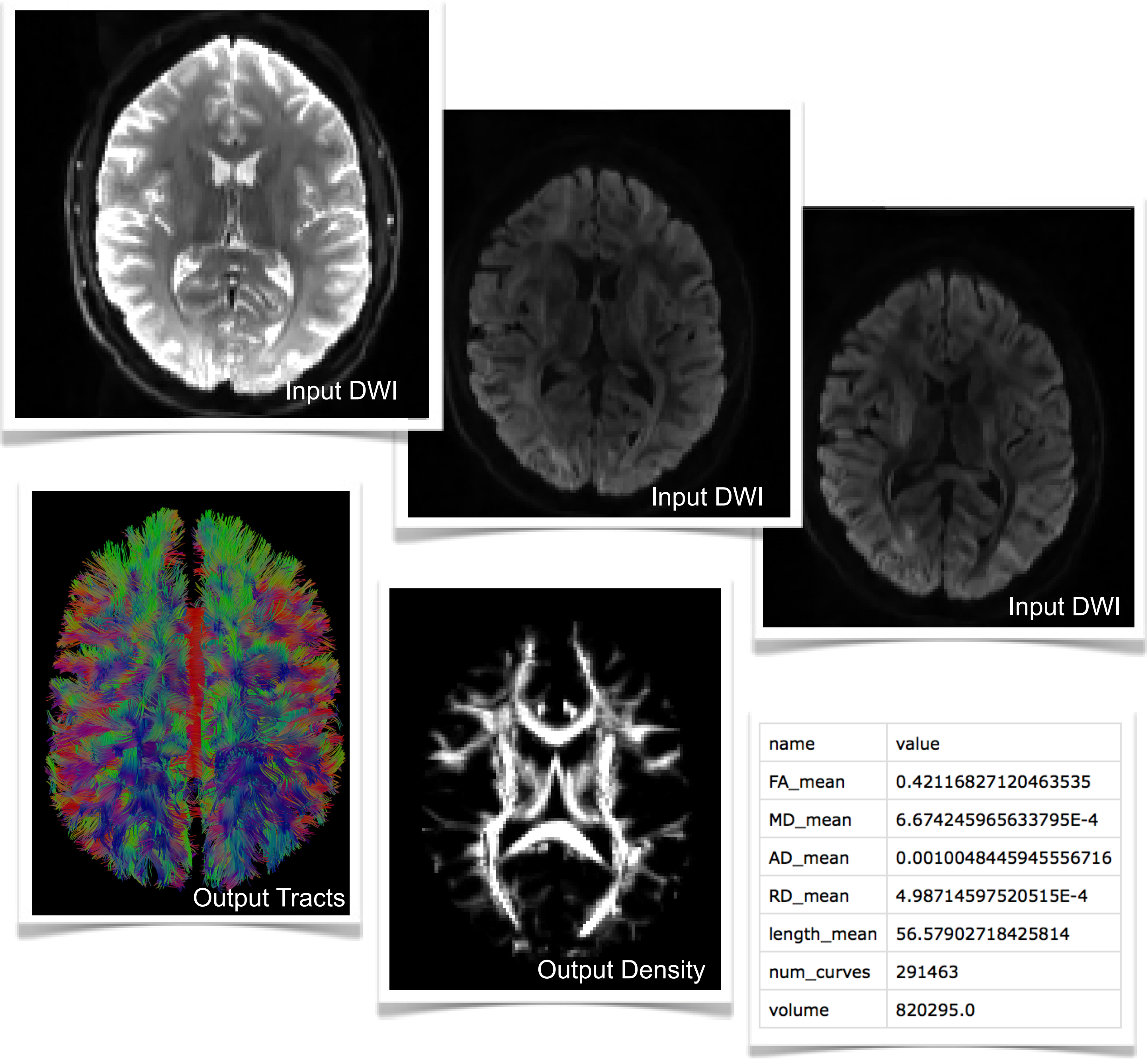
	Name	Prefix	Value
☑	ModuleName	(none)	VolumeModelTrackS...
☑	VerboseFlag	(none)	--verbose
☑	DebugFlag	(none)	--debug
☑	input	--input	< 1 Connection >
□	model	--model	(I) File
□	seedMask	--seedM...	(I) File
□	includeMask	--includ...	(I) File
□	excludeMask	--exclu...	(I) File
□	stopMask	--stopM...	(I) File
□	trackMask	--track...	(I) File
□	samples	--samples	1
□	angle	--angle	45.0
□	step	--step	1.0
□	min	--min	0.075
□	length	--length	0.0
□	limit	--limit	2000000
☑	interp	--interp	Trilinear
☑	rk	--rk	Flag
□	arclen	--arclen	0.8
□	threads	--threads	3
☑	output	--output	< 2 Connections >

Shown above is the VolumeModelTrackStreamline module from QIT. This algorithm extracts three dimensional curves (or tracks) from diffusion tensor imaging. This algorithm works by first randomly placing many seed points in the image volume and then by propagating each seed along the primary diffusion direction exracted from the tensor in each voxel. The process terminates when diffusion tensor indices indicate the track is leaving white matter or turning too sharply. There are parameters for the seed density, termination criteria, and other aspects. We mostly used the default settings, but we changed the interpolation method to Trilinear and the integration type to Fourth order Runge Kutta. Following this, the curves are discretized to produce a track density image, and statistics are collected to summarize the number of tracks, their volume, the average length, and the averages of diffusion tensor indices.

Analysis with QIT - Tractography

Results

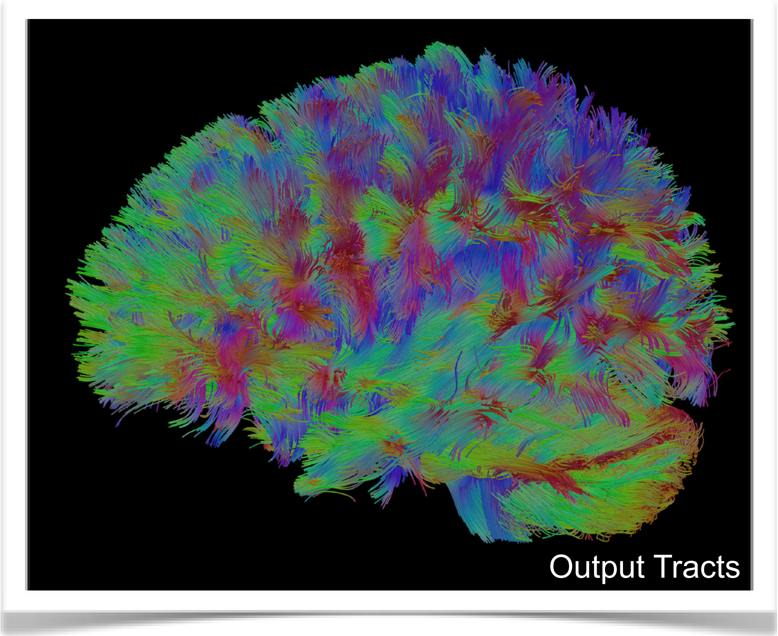
Shown below are results from running the workflow, including the input diffusion-weighted MRI and the output tractography, track density image, and statistical results. The tractography curves can be visualized using QIT, and this process can be repeated for many subjects to conduct a group analysis.

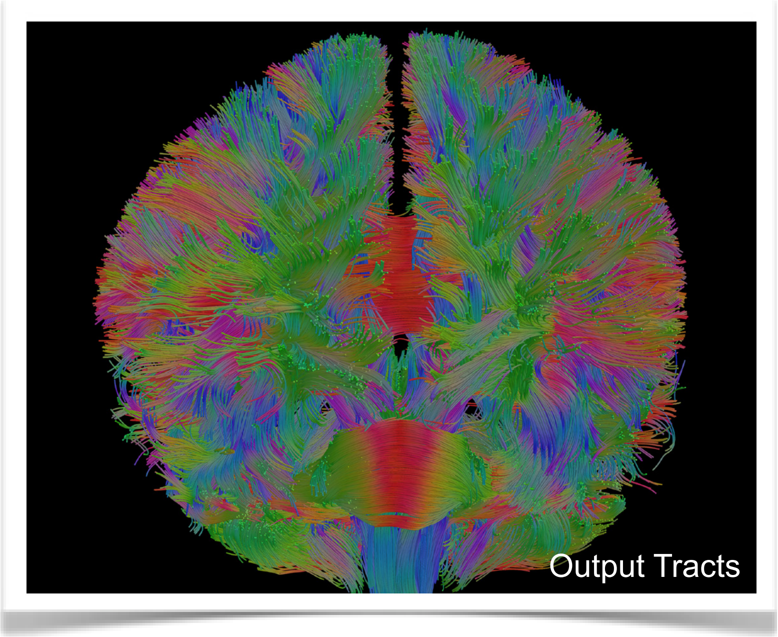


name	value
FA_mean	0.42116827120463535
MD_mean	6.674245965633795E-4
AD_mean	0.0010048445945556716
RD_mean	4.98714597520515E-4
length_mean	56.57902718425814
num_curves	291463
volume	820295.0

Output Stats

Analysis with QIT - Tractography





Advanced Topics

Building a Module

A module is a simple XML descriptor used to define a binary. When connected to LONI's computer cluster resources, the LONI Pipeline will automatically download the library of modules available on the cluster.

LONI Pipeline Provenance

Provenance in the Pipeline context equates to history. There are 3 categories of provenance in the Pipeline: Data provenance, binary provenance, and execution provenance.

Adding Metadata

The "add metadata" button is a feature inside regular data sources that extends its functionality, allowing you to incorporate imaging data and non-imaging meta-data together, enable queries groupings, and construct study-designs based on user-specified criteria.

Conditional Module

This module is used when the execution path of various inputs to a workflow is dependent on some criteria.

Building a Module

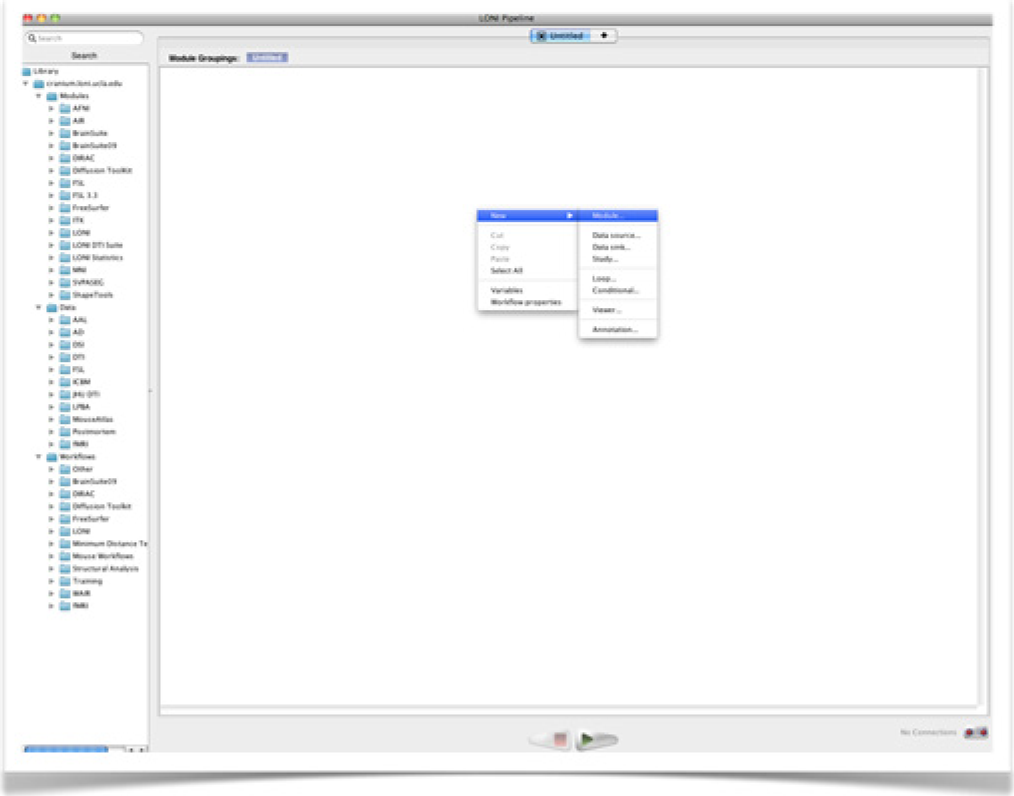
Overview

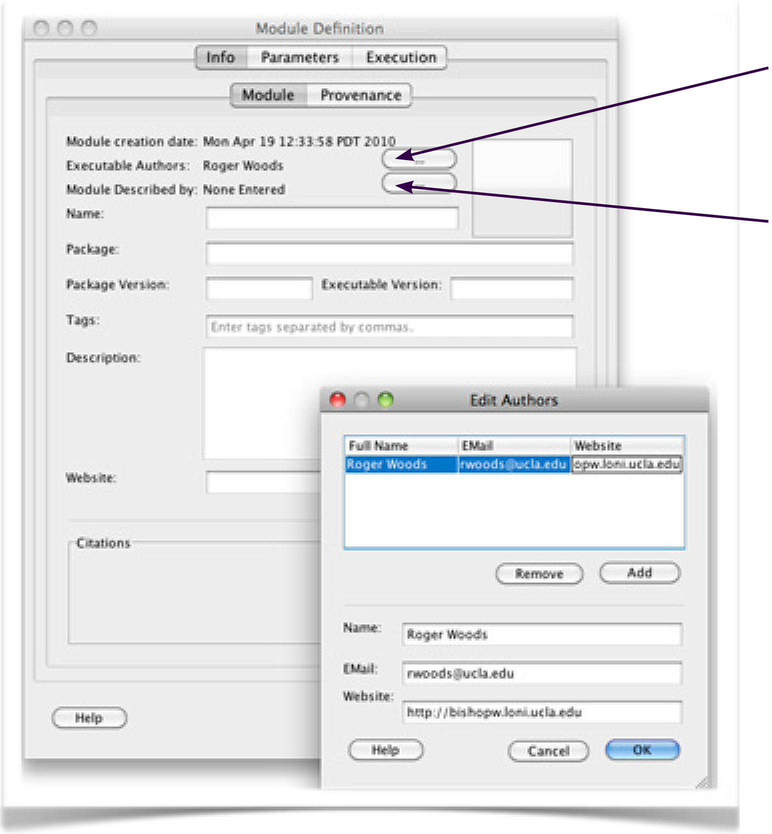
A module is a simple XML descriptor used to define a binary. When connected to LONI's computer cluster resources, the LONI Pipeline will automatically download the library of modules available on the cluster.

Although advanced users may prefer to create their own modules run their executables locally or on their own computing resources, having this list of modules is a great place to begin.

How-to

- Right click on the canvas
- Choose New Module

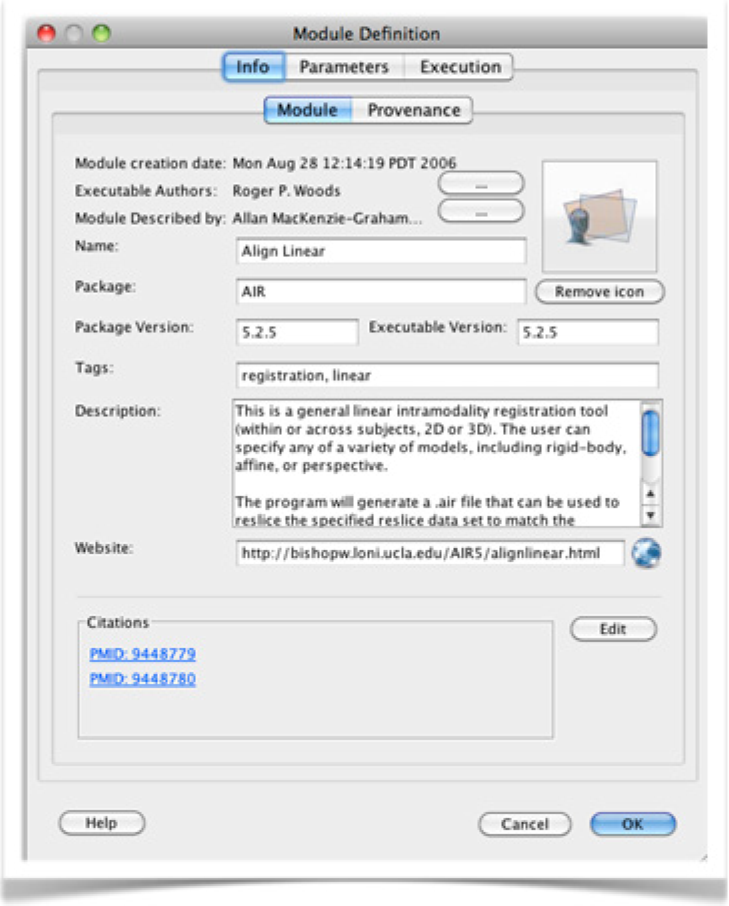




Module creation date: Mon Apr 19 12:33:58 PDT 2010
Executable Authors: Roger Woods
Module Described by: None Entered
Name:
Package:
Package Version: Executable Version:
Tags: Enter tags separated by commas.
Description:
Website:

Full Name	EMail	Website
Roger Woods	rwoods@ucla.edu	opw.loni.ucla.edu

Name: Roger Woods
EMail: rwoods@ucla.edu
Website: http://bishopw.loni.ucla.edu



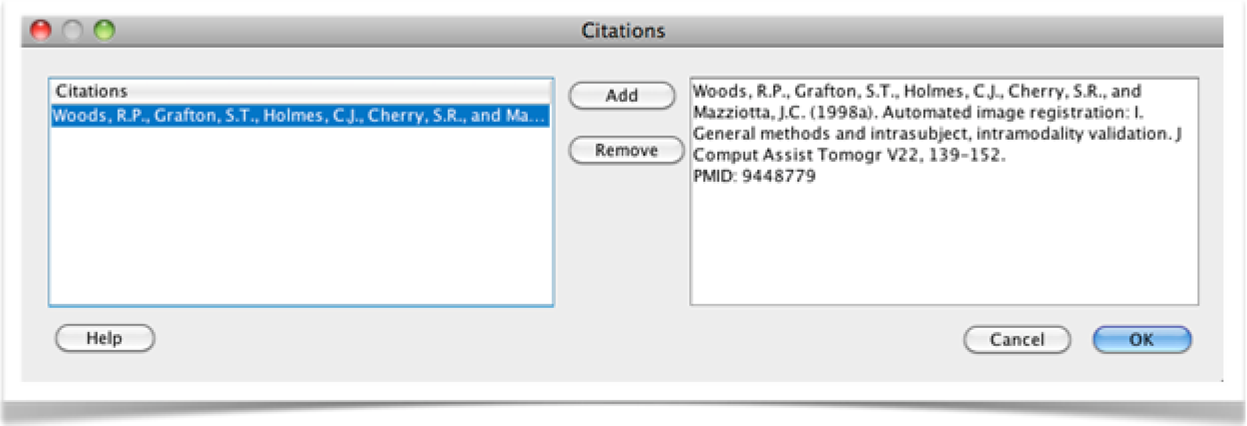
Module creation date: Mon Aug 28 12:14:19 PDT 2006
Executable Authors: Roger P. Woods
Module Described by: Allan MacKenzie-Graham...
Name: Align Linear
Package: AIR
Package Version: 5.2.5 Executable Version: 5.2.5
Tags: registration, linear
Description: This is a general linear intramodality registration tool (within or across subjects, 2D or 3D). The user can specify any of a variety of models, including rigid-body, affine, or perspective.

The program will generate a .air file that can be used to reslice the specified reslice data set to match the
Website: http://bishopw.loni.ucla.edu/AIR5/alignlinear.html

Citations
PMID: 9448779
PMID: 9448780

Optional Actions

- Click Executable Authors button
- Click Add
- Enter Name, email, and website information
- Repeat for all Authors
- Repeat for 'Module Described by' button
- Click OK
- In the Name field, enter the name of the binary
- In the Package field, enter the name of the software suite
- In the Package Version, enter the version number of the software
- In the Executable Version, enter the version number of the executable
- In the Tags field, enter keywords for the software (eg registration, skull-stripping, tissue classification)
- In the Description field, enter the description of the functionality of the binary
- In the website field, enter relevant website



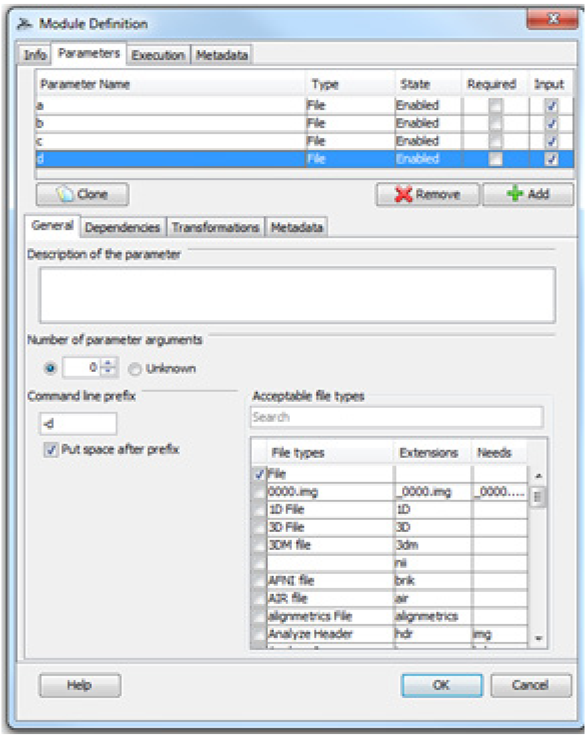
Citations
Woods, R.P., Grafton, S.T., Holmes, C.J., Cherry, S.R., and Ma...

Woods, R.P., Grafton, S.T., Holmes, C.J., Cherry, S.R., and Mazziotta, J.C. (1998a). Automated image registration: I. General methods and intrasubject, intramodality validation. J Comput Assist Tomogr V22, 139-152.
PMID: 9448779

- Click Edit in the Citations field
- Click Add
- Enter either the Digital Object Identifier or the PubMed ID
- Click OK
- Click the Executable tab
- Enter information for Binary, BinaryConfigOptions, Compiler, SystemConfig, Operating System, Library, Library Compiler, Libary System Config, Library Operating System & Library Config Options

Required Options

- Click Add under the Parameter Name field
- Double Click on New Parameter 1 and specify name of parameter (eg Standard File) Choose Required if this a required parameter, else, it is optional
- Choose Input if the parameter is of type input, else, it will be output
- In the Description field, describe the functionality of the parameter
- In the Switch field, specify the required flags (eg -m)
- Choose whether the switch required a space to follow or not
- Choose the type of parameter being described, the options are Directory, Enumerated, File, Number, and String



Parameter Name	Type	State	Required	Input
a	File	Enabled	□	☑
b	File	Enabled	□	☑
c	File	Enabled	□	☑
d	File	Enabled	□	☑

Description of the parameter

Number of parameter arguments

● 0 ○ Unknown

Command line prefix

-d

☑ Put space after prefix

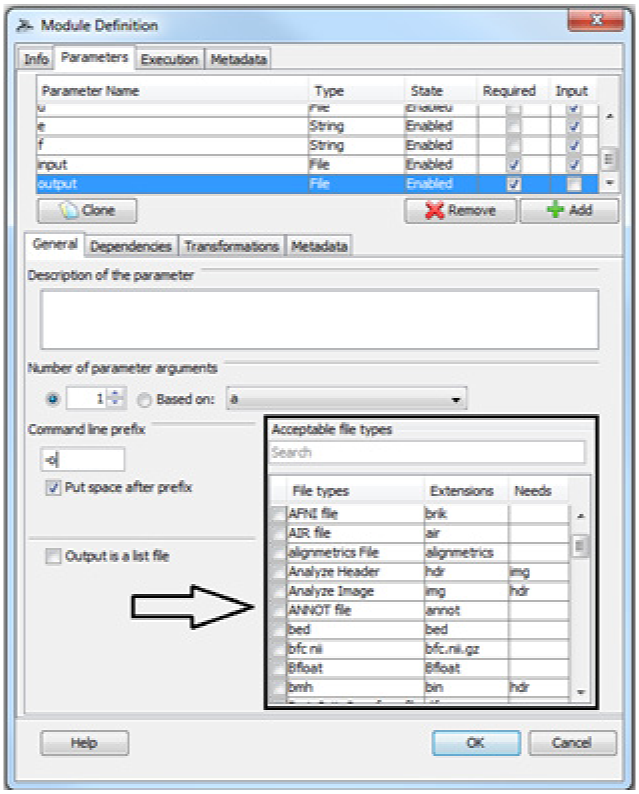
Acceptable file types

Search

	File types	Extensions	Needs
☑	File		
□	0000.img	_0000.img	_0000....
□	1D File	1D	
□	3D File	3D	
□	3DM file	3dm	
□		nii	
□	AFNI file	brik	
□	AIR file	air	
□	alignmetrics File	alignmetrics	
□	Analyze Header	hdr	img

Specify the number of Arguments the parameter expects

- For Enumerated, click Add, double click on value, specify value (NOTE character, strings, or numbers are acceptable; enumeration equates to a drop down menu when selecting the parameter with predefined values)
- For File, please choose the Acceptable file types for the parameter by using the search option (eg search analyze and choose one of the file types) NOTE: You may create your own file type.
- Choose Edit file types, click the + icon
- Type the name of file type (eg, Analyze Image)
- In the Description field, include a description
- In the Extension field, included appropriate extension (eg .img)
- In the Needs filed, include dependancies (eg .hdr)



Parameter Name	Type	State	Required	Input
d	File	Enabled	□	☑
e	String	Enabled	□	☑
f	String	Enabled	□	☑
input	File	Enabled	☑	☑
output	File	Enabled	☑	□

Description of the parameter

Number of parameter arguments

● 1 ○ Based on: a

Command line prefix

-o

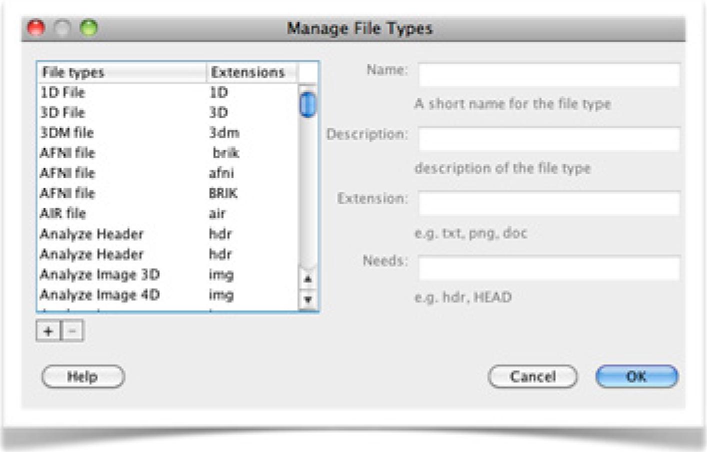
☑ Put space after prefix

□ Output is a list file

Acceptable file types

Search

File types	Extensions	Needs
AFNI file	brik	
AIR file	air	
alignmetrics File	alignmetrics	
Analyze Header	hdr	img
Analyze Image	img	hdr
ANNOT file	annot	
bed	bed	
bfc nii	bfc.nii.gz	
Bfloat	Bfloat	
bmh	bin	hdr



File types	Extensions
1D File	1D
3D File	3D
3DM file	3dm
AFNI file	brik
AFNI file	afni
AFNI file	BRIK
AIR file	air
Analyze Header	hdr
Analyze Header	hdr
Analyze Image 3D	img
Analyze Image 4D	img

Name:

A short name for the file type

Description:

description of the file type

Extension:

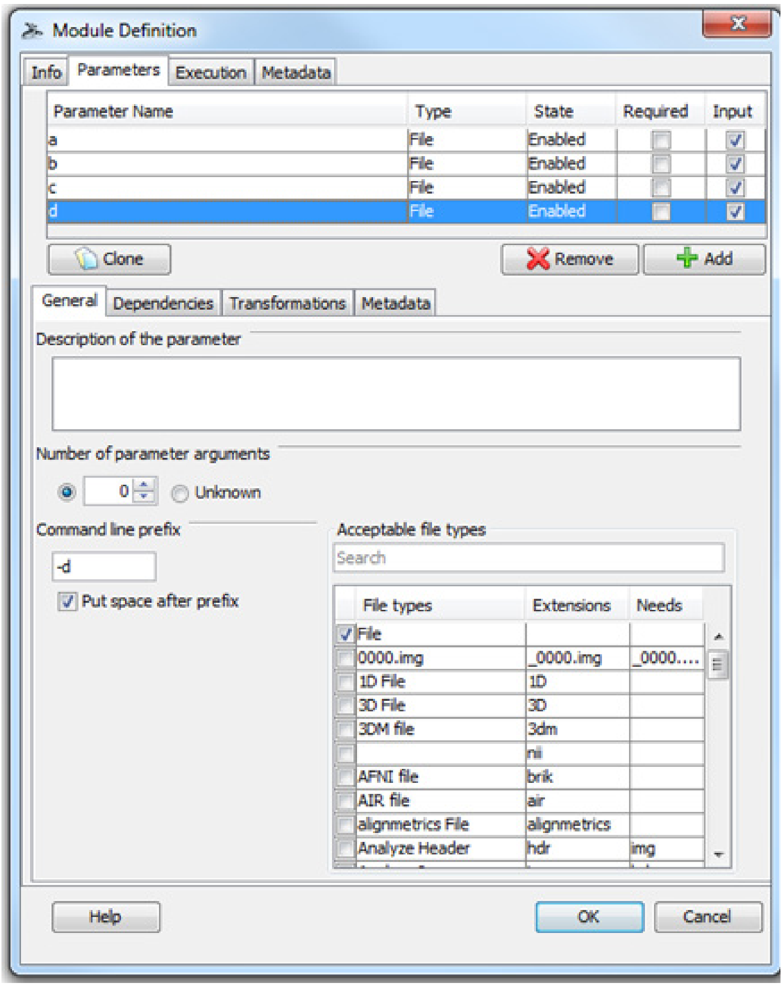
e.g. txt, png, doc

Needs:

e.g. hdr, HEAD

Adding additional parameters

Choose **Add** in the Parameter Name box. If the file is required for the binary to execute, choose **Required**, else, it's considered optional, and users may elect to use the parameter. If the parameter is an input, choose **input**, else, the parameter is considered an output. As with each parameter, one must specify the type of the parameter. The acceptable types are **File**, **Directory**, **String**, **Character** or **Enumerated**. With type File, please specify the expected file type; for example, analyze image, as the dependancy of an analyze file with a header (.hdr) is the preserved. This is required when moving files from and to various directories for execution.



Parameter Name	Type	State	Required	Input
a	File	Enabled	☐	☑
b	File	Enabled	☐	☑
c	File	Enabled	☐	☑
d	File	Enabled	☐	☑

Description of the parameter

Number of parameter arguments

● 0 ○ Unknown

Command line prefix

-d

☑ Put space after prefix

Acceptable file types

Search

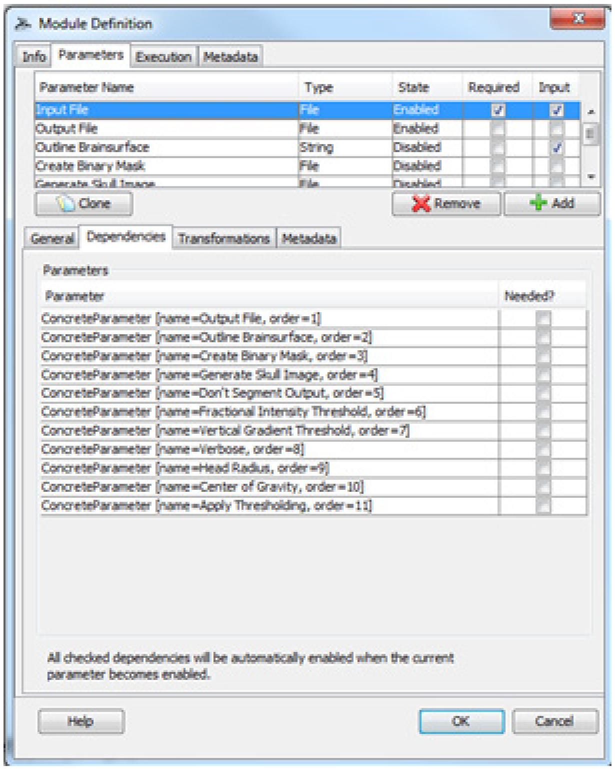
File types	Extensions	Needs
☑ File		
☐ 0000.img	_0000.img	_0000....
☐ 1D File	1D	
☐ 3D File	3D	
☐ 3DM file	3dm	
☐	nii	
☐ AFNI file	brik	
☐ AIR file	air	
☐ alignmetrics File	alignmetrics	
☐ Analyze Header	hdr	img

Specify dependencies and manipulate file names

The LONI Pipeline allows you to specify dependancies between parameters. For example, if using MNI's **-segment** (part of mincmath) one must also specify **-const2** to specify a min and max range to extract. Select the parameter, then click **Advanced**, the in the **Select Dependencies** window, choose **Needed** for the required parameter, click **OK.**

Additionally, the Pipeline allows for file name manipulations. For example, using -m (provide skull stripped mask) which is a part of FSL BET will result in <root_name>_mask.img & <root_name>_mask.hdr files being generated in the same directory. If one were then to connect the output to another module, and execution error would occur. In this instance, choose the parameter, click Advanced, provide the Base (this is the parameter name whose base you'd like to manipulate, choose the Transformation (**append**, **prepend**, **replace**, **subtract**), choose the text to **Find**, and the text to **Replace** the text with, and hit **OK**. This will result in the type of transformation specified.

- In the Program Location field enter the full path and binary name (eg /usr/local/air/bin/alignlinear)

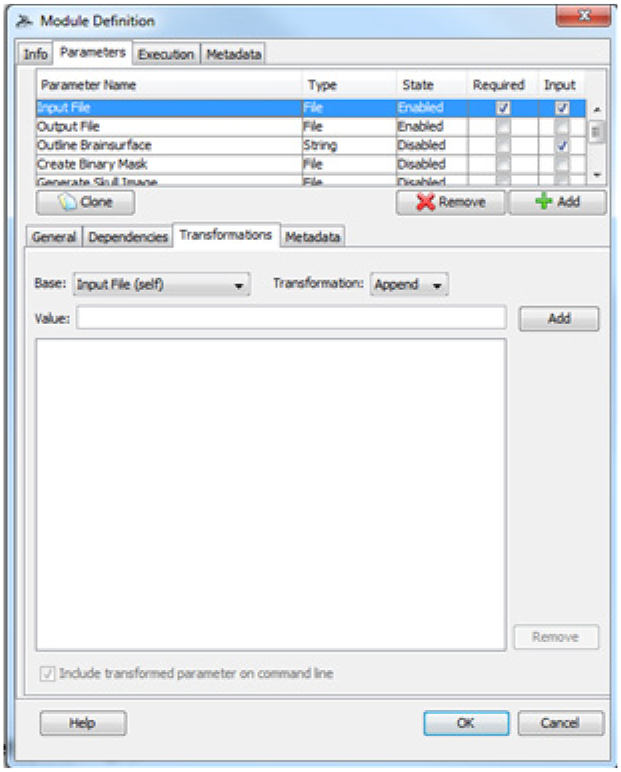


Parameter Name	Type	State	Required	Input
Input File	File	Enabled	☑	☑
Output File	File	Enabled	□	□
Outline Brainsurface	String	Disabled	□	☑
Create Binary Mask	File	Disabled	□	□
Generate Skull Image	File	Disabled	□	□

Parameters

Parameter	Needed?
ConcreteParameter [name=Output File, order=1]	□
ConcreteParameter [name=Outline Brainsurface, order=2]	□
ConcreteParameter [name=Create Binary Mask, order=3]	□
ConcreteParameter [name=Generate Skull Image, order=4]	□
ConcreteParameter [name=Don't Segment Output, order=5]	□
ConcreteParameter [name=Fractional Intensity Threshold, order=6]	□
ConcreteParameter [name=Vertical Gradient Threshold, order=7]	□
ConcreteParameter [name=Verbose, order=8]	□
ConcreteParameter [name=Head Radius, order=9]	□
ConcreteParameter [name=Center of Gravity, order=10]	□
ConcreteParameter [name=Apply Thresholding, order=11]	□

All checked dependencies will be automatically enabled when the current parameter becomes enabled.



Parameter Name	Type	State	Required	Input
Input File	File	Enabled	☑	☑
Output File	File	Enabled	□	□
Outline Brainsurface	String	Disabled	□	☑
Create Binary Mask	File	Disabled	□	□
Generate Skull Image	File	Disabled	□	□

Base: Input File (self)

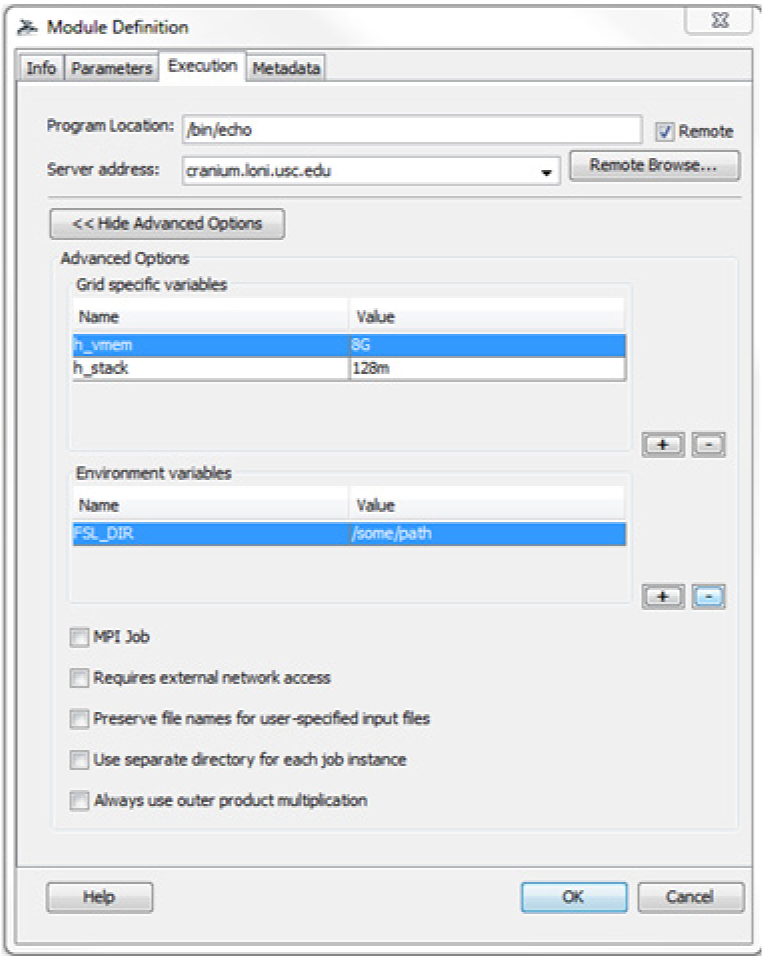
Transformation: Append

Value:

☑ Include transformed parameter on command line

- Choose remote and specify server if binary resides on a remote server

NOTE: A Pipeline server must be running on the specified server in order for the client to connect Choose the Show Advanced Options to change the memory limit or the stack size limit.



Program Location: /bin/echo

☑ Remote

Server address: cranium.loni.usc.edu

Advanced Options

Grid specific variables

Name	Value
h_vmem	8G
h_stack	128m

Environment variables

Name	Value
FSL_DIR	/some/path

□ MPI Job

□ Requires external network access

□ Preserve file names for user-specified input files

□ Use separate directory for each job instance

□ Always use outer product multiplication

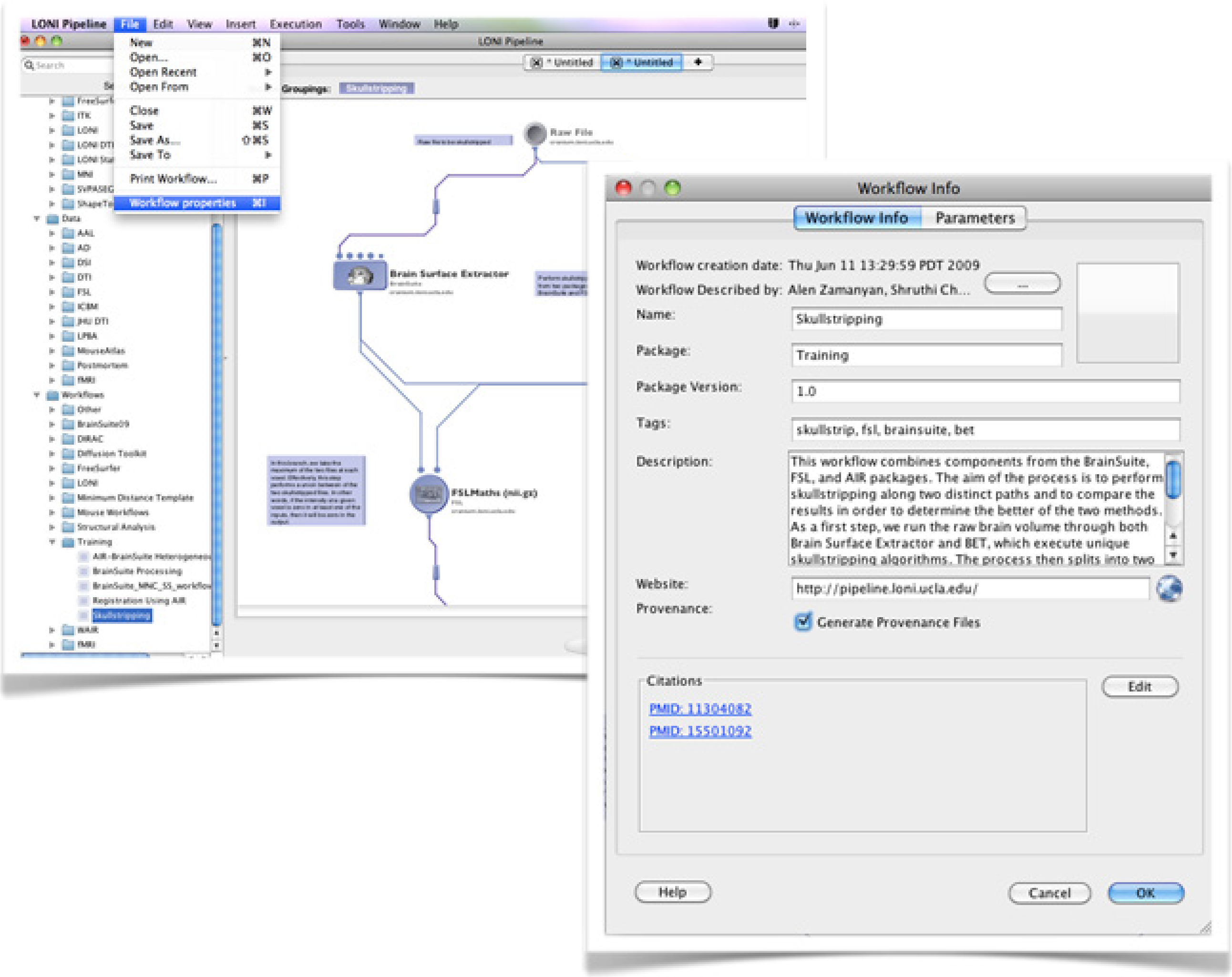
LONI Pipeline Provenance

Overview

Provenance in the Pipeline context equates to history. There are 3 categories of provenance in the Pipeline: Data provenance, binary provenance, and execution provenance. Data provenance is a snapshot of the state of the data pre & post manipulation by a binary. Binary provenance is a record of all the factors influencing the creation of the binary, examples of which include the OS, the compiler used, the library dependencies, and the optimization flags. The execution provenance is a record of the list of executables the data has gone through.

How-to

- To generate a provenance file, go to File, choose Workflow Properties
- Under Provenance, choose Generate Provenance Files



Workflow Info

Workflow Info | Parameters

Workflow creation date: Thu Jun 11 13:29:59 PDT 2009

Workflow Described by: Alen Zamanyan, Shruthi Ch...

Name: Skullstripping

Package: Training

Package Version: 1.0

Tags: skullstrip, fsl, brainsuite, bet

Description: This workflow combines components from the BrainSuite, FSL, and AIR packages. The aim of the process is to perform skullstripping along two distinct paths and to compare the results in order to determine the better of the two methods. As a first step, we run the raw brain volume through both Brain Surface Extractor and BET, which execute unique skullstripping algorithms. The process then splits into two

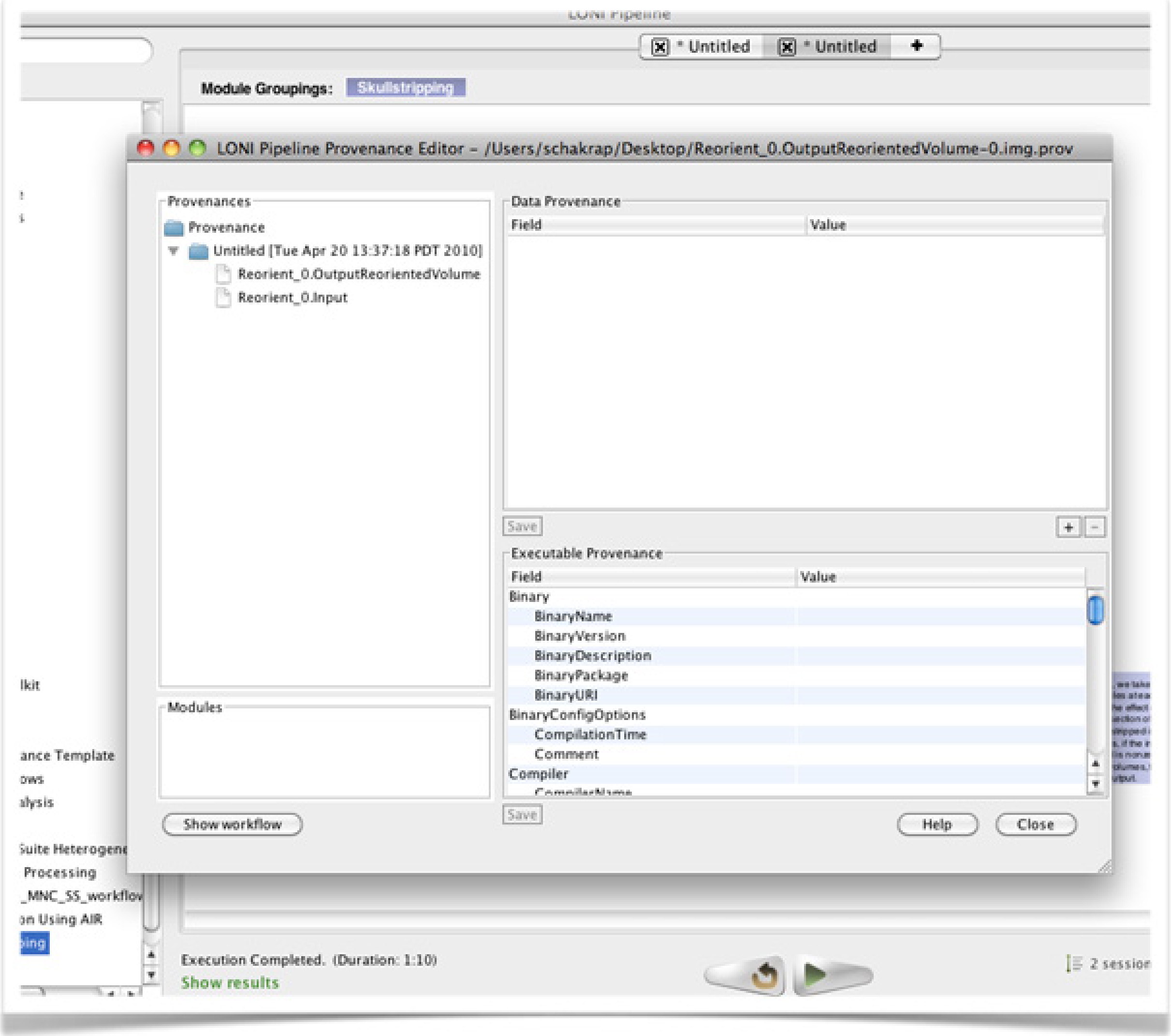
Website: http://pipeline.loni.ucla.edu/

Provenance: ☑ Generate Provenance Files

Citations

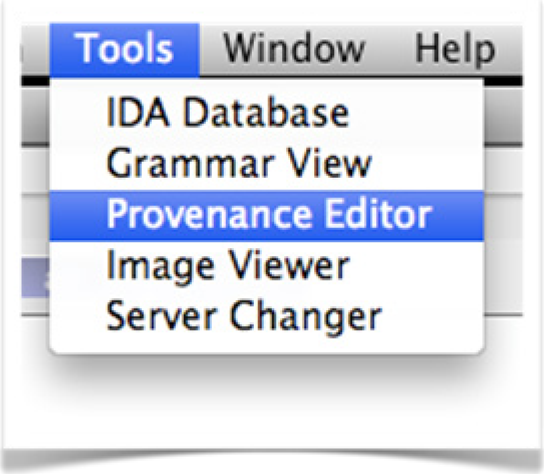
PMID: 11304082

PMID: 15501092

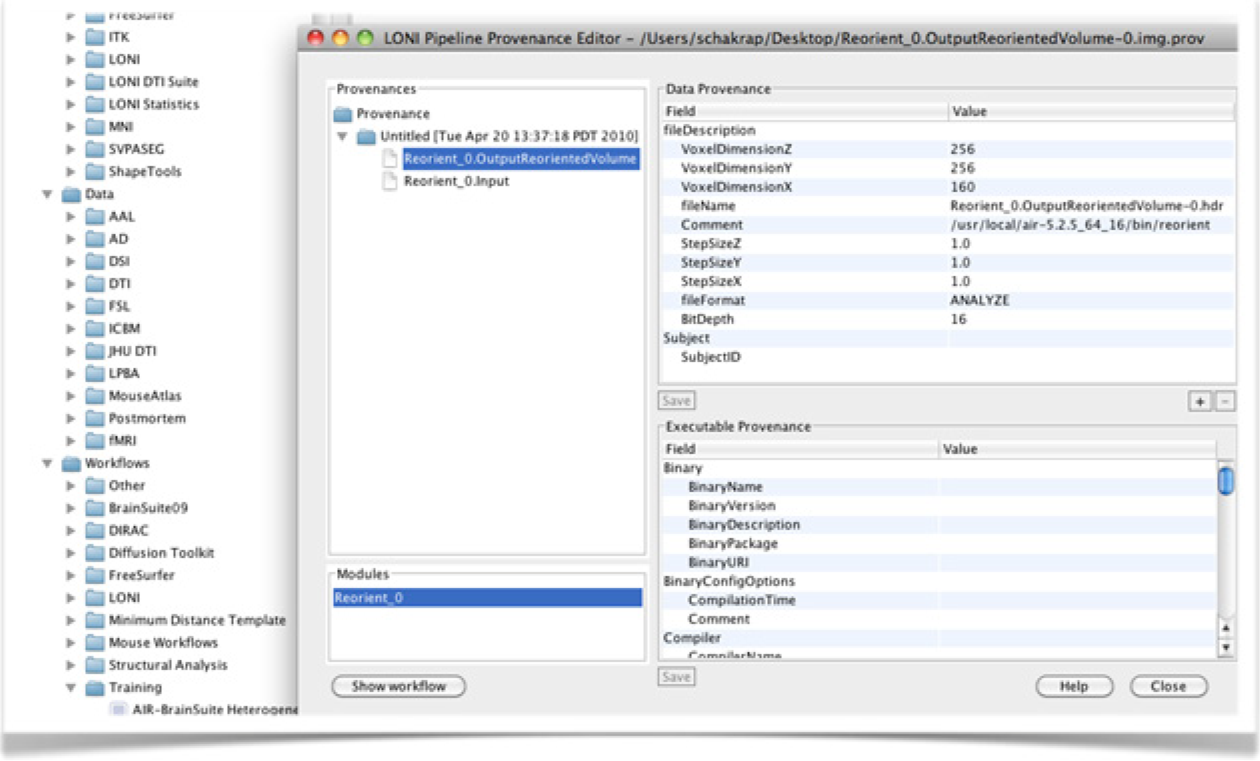


Execution Completed. (Duration: 1:10)

- Execute workflow
- The Pipeline now generates a .prov file for each file generated by a binary
- Download this file
- Under Tools, choose Provenance Editor



- Under provenance, expand the directory
- Under Data provenance, you will find all metadata stored in the header
- To edit or add any additional field, choose the + icon
- Choose Category or field, edit accordingly
- Under Executable Provenance, you'll find all binary provenance
- Click on Show workflow, this will generate the Pipeline used for processing the data



Data Provenance

Field	Value
fileDescription	
VoxelDimensionZ	256
VoxelDimensionY	256
VoxelDimensionX	160
fileName	Reorient_0.OutputReorientedVolume-0.hdr
Comment	/usr/local/air-5.2.5_64_16/bin/reorient
StepSizeZ	1.0
StepSizeY	1.0
StepSizeX	1.0
fileFormat	ANALYZE
BitDepth	16
Subject	
SubjectID	

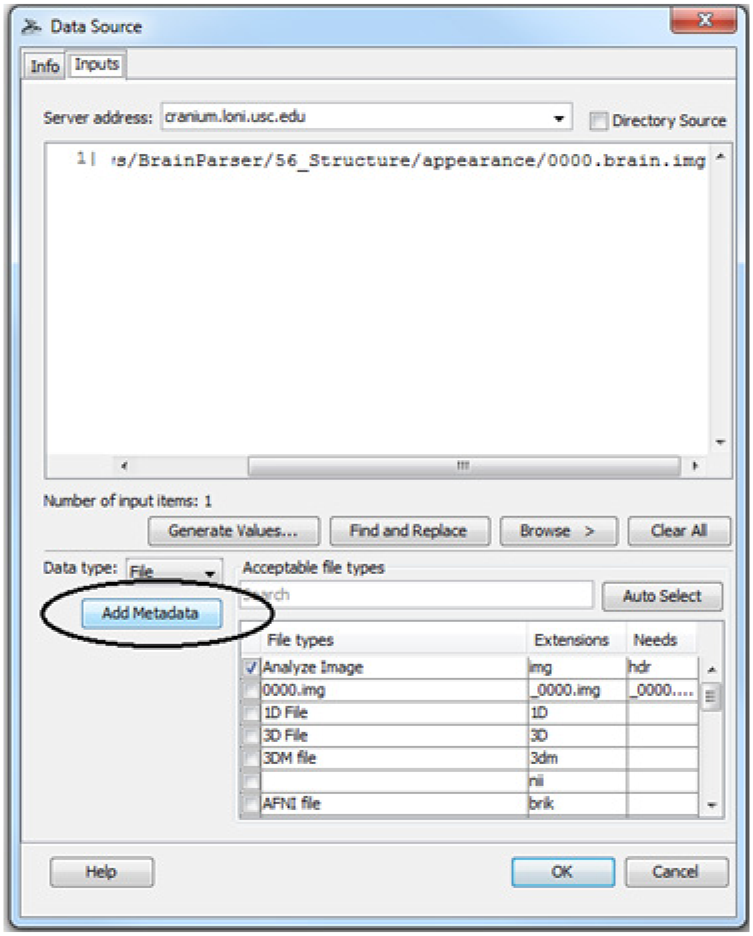
Executable Provenance

Field	Value
Binary	
BinaryName	
BinaryVersion	
BinaryDescription	
BinaryPackage	
BinaryURI	
BinaryConfigOptions	
CompilationTime	
Comment	
Compiler	
CompilerName	

Adding Metadata

Overview

The “add metadata” button is a feature inside regular data sources that extends its functionality, allowing you to incorporate imaging data and non-imaging meta-data together, enable queries groupings, and construct study-designs based on user-specified criteria. Both the imaging data and the metadata information are passed to subsequent modules throughout the pipeline workflow in data-metadata pairs generated by the Pipeline. You can inspect the metadata for any module’s output under the module output files panel. The metadata can be read and fed to any module (Data Extraction), and values produced by any module can be added back to the metadata (Metadata Augmentation). The metadata may be used for setting up various conditional criteria in Conditional modules. The metadata information may be represented as an XML file, as long as it’s schema is valid (well-formed) and consistent (uniform for every subject in the study), or as a tabular spreadsheet (CVS).



Server address: cranium.loni.usc.edu

□ Directory Source

```
1| s/BrainParser/56_Structure/appearance/0000.brain.img
```

Number of input items: 1

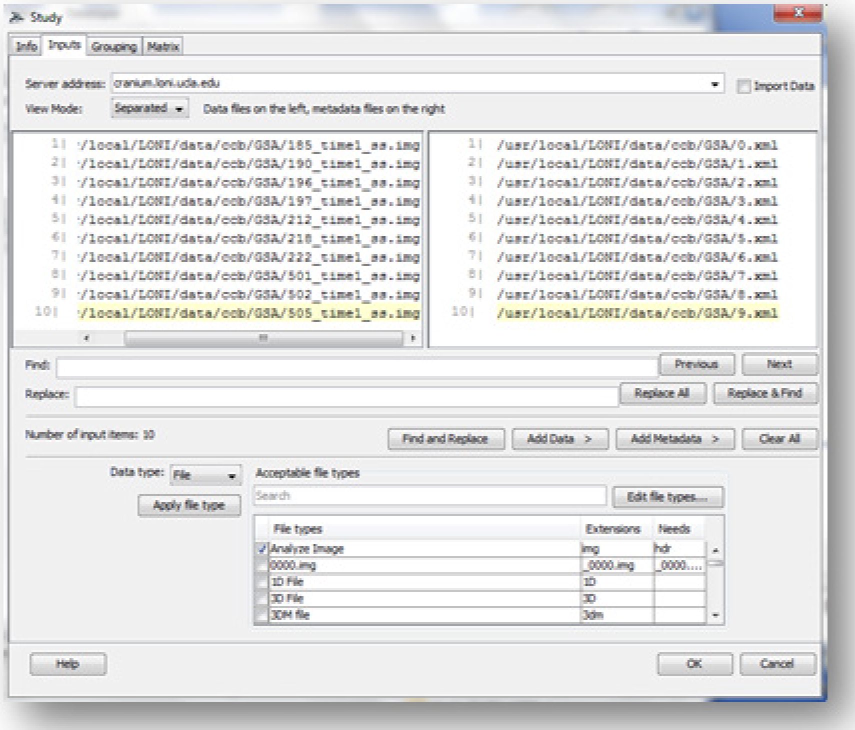
Data type: File

Acceptable file types

	File types	Extensions	Needs
☑	Analyze Image	img	hdr
□	0000.img	_0000.img	_0000....
□	1D File	1D	
□	3D File	3D	
□	3DM file	3dm	
□		nii	
□	AFNI file	brik	

How-to

Under the Input tab, data, metadata file and file formats are specified.



Server address: cranium.loni.ucla.edu

View Mode: Separated — Data files on the left, metadata files on the right

```
/local/LONI/data/ccb/GSA/185_time1_ss.img    /usr/local/LONI/data/ccb/GSA/0.xml
/local/LONI/data/ccb/GSA/190_time1_ss.img    /usr/local/LONI/data/ccb/GSA/1.xml
/local/LONI/data/ccb/GSA/196_time1_ss.img    /usr/local/LONI/data/ccb/GSA/2.xml
/local/LONI/data/ccb/GSA/197_time1_ss.img    /usr/local/LONI/data/ccb/GSA/3.xml
/local/LONI/data/ccb/GSA/212_time1_ss.img    /usr/local/LONI/data/ccb/GSA/4.xml
/local/LONI/data/ccb/GSA/218_time1_ss.img    /usr/local/LONI/data/ccb/GSA/5.xml
/local/LONI/data/ccb/GSA/222_time1_ss.img    /usr/local/LONI/data/ccb/GSA/6.xml
/local/LONI/data/ccb/GSA/501_time1_ss.img    /usr/local/LONI/data/ccb/GSA/7.xml
/local/LONI/data/ccb/GSA/502_time1_ss.img    /usr/local/LONI/data/ccb/GSA/8.xml
/local/LONI/data/ccb/GSA/505_time1_ss.img    /usr/local/LONI/data/ccb/GSA/9.xml
```

Find:

Replace:

Number of input items: 10

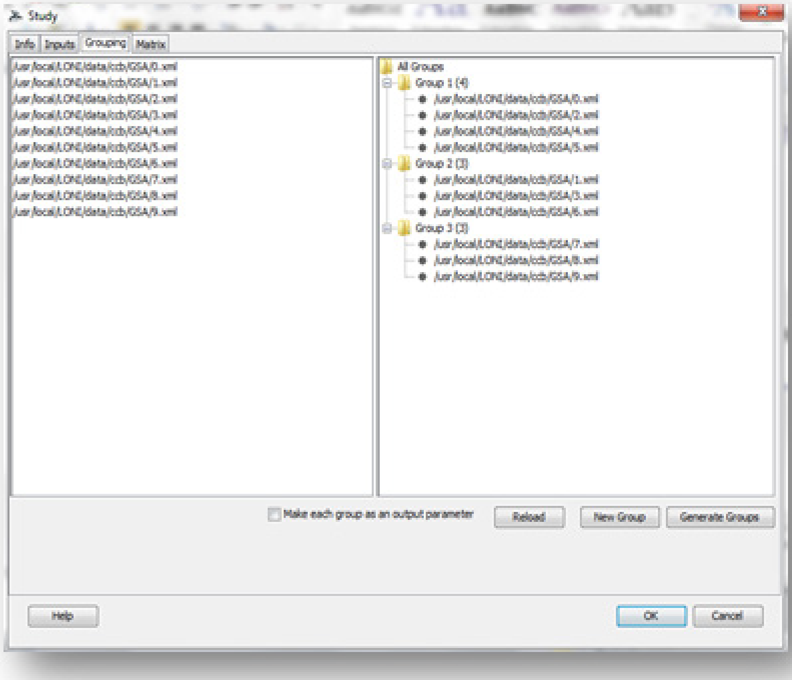
Data type: File

Acceptable file types

Search

	File types	Extensions	Needs
☑	Analyze Image	img	hdr
□	0000.img	_0000.img	_0000....
□	1D File	1D	
□	3D File	3D	
□	3DM file	3dm	

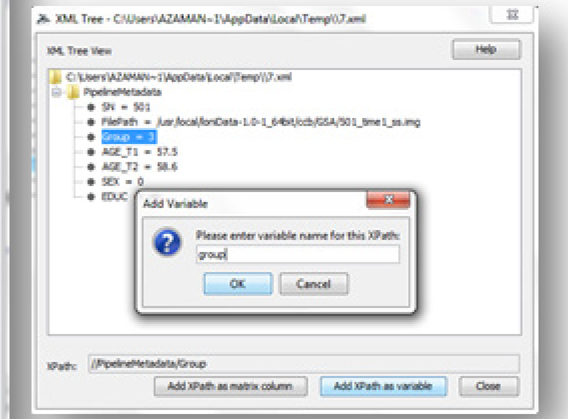
Under the Grouping tab, different groups can be created based on some criteria (conditional expressions) on the metadata.



```
/usr/local/LONI/data/ccb/GSA/0.xml
/usr/local/LONI/data/ccb/GSA/1.xml
/usr/local/LONI/data/ccb/GSA/2.xml
/usr/local/LONI/data/ccb/GSA/3.xml
/usr/local/LONI/data/ccb/GSA/4.xml
/usr/local/LONI/data/ccb/GSA/5.xml
/usr/local/LONI/data/ccb/GSA/6.xml
/usr/local/LONI/data/ccb/GSA/7.xml
/usr/local/LONI/data/ccb/GSA/8.xml
/usr/local/LONI/data/ccb/GSA/9.xml
```

```
All Groups
  Group 1 (4)
    /usr/local/LONI/data/ccb/GSA/0.xml
    /usr/local/LONI/data/ccb/GSA/2.xml
    /usr/local/LONI/data/ccb/GSA/4.xml
    /usr/local/LONI/data/ccb/GSA/5.xml
  Group 2 (3)
    /usr/local/LONI/data/ccb/GSA/1.xml
    /usr/local/LONI/data/ccb/GSA/3.xml
    /usr/local/LONI/data/ccb/GSA/6.xml
  Group 3 (3)
    /usr/local/LONI/data/ccb/GSA/7.xml
    /usr/local/LONI/data/ccb/GSA/8.xml
    /usr/local/LONI/data/ccb/GSA/9.xml
```

□ Make each group as an output parameter



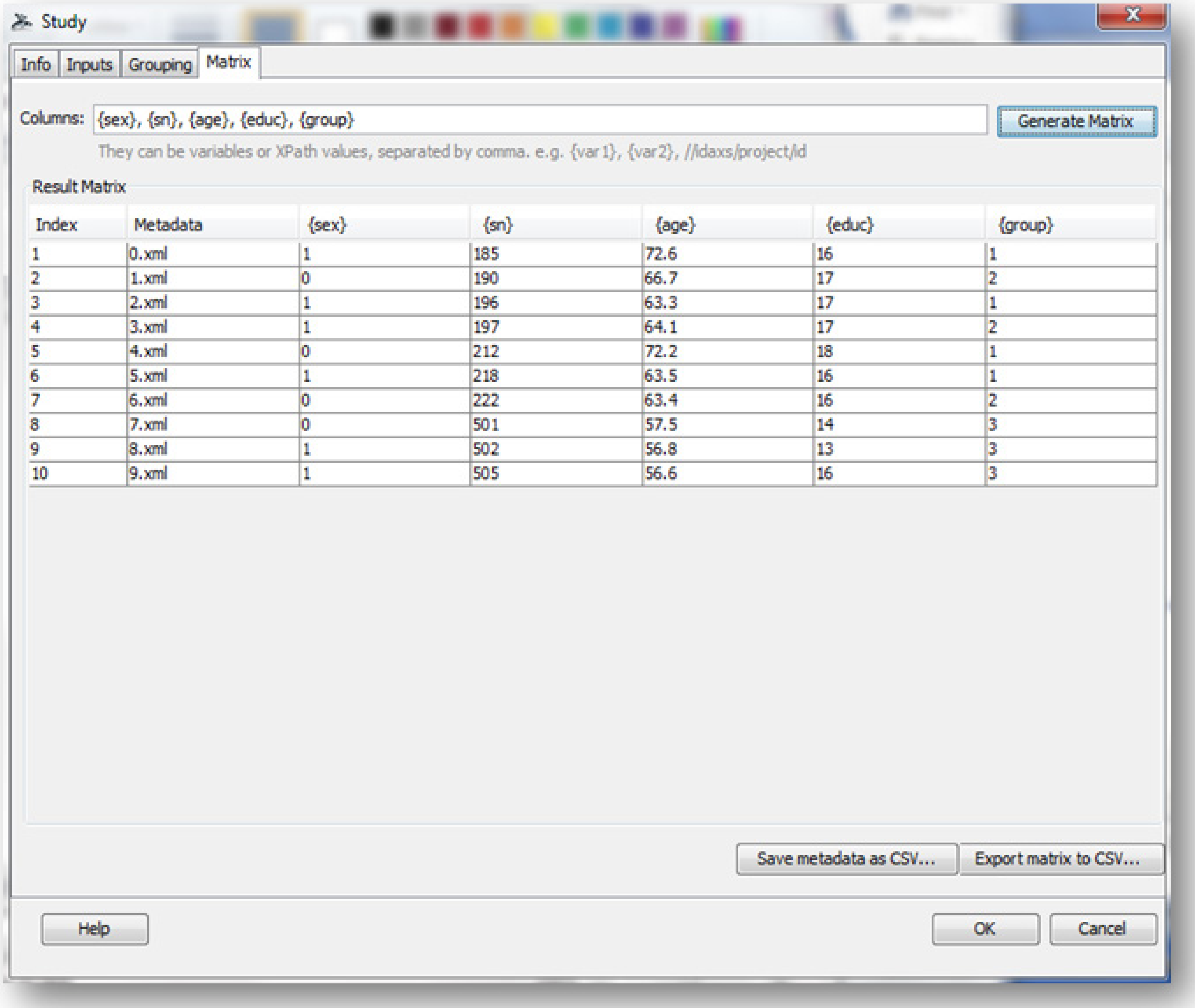
XML Tree - C:\Users\AZAMAN~1\AppData\Local\Temp\\7.xml

```
C:\Users\AZAMAN~1\AppData\Local\Temp\\7.xml
  PipelineMetadata
    SN = 501
    FilePath = /usr/local/loniData-1.0-1_64bit/ccb/GSA/501_time1_ss.img
    Group = 3
    AGE_T1 = 57.5
    AGE_T2 = 58.6
    SEX = 0
    EDUC
```

Please enter variable name for this XPath: group

XPath: //PipelineMetadata/Group

Under the Matrix tab, a table displays the associated meta-data. The columns relate to your specifications. The rows represent values for each subject.



Columns: {sex}, {sn}, {age}, {educ}, {group}

They can be variables or XPath values, separated by comma. e.g. {var1}, {var2}, //idaxs/project/id

Result Matrix

Index	Metadata	{sex}	{sn}	{age}	{educ}	{group}
1	0.xml	1	185	72.6	16	1
2	1.xml	0	190	66.7	17	2
3	2.xml	1	196	63.3	17	1
4	3.xml	1	197	64.1	17	2
5	4.xml	0	212	72.2	18	1
6	5.xml	1	218	63.5	16	1
7	6.xml	0	222	63.4	16	2
8	7.xml	0	501	57.5	14	3
9	8.xml	1	502	56.8	13	3
10	9.xml	1	505	56.6	16	3

NOTE: For more detailed information about the Study Module, please see the Pipeline website: http://pipeline.loni.usc.edu/learn/user-guide/building-a-workflow/#Study

Conditional Module

Overview

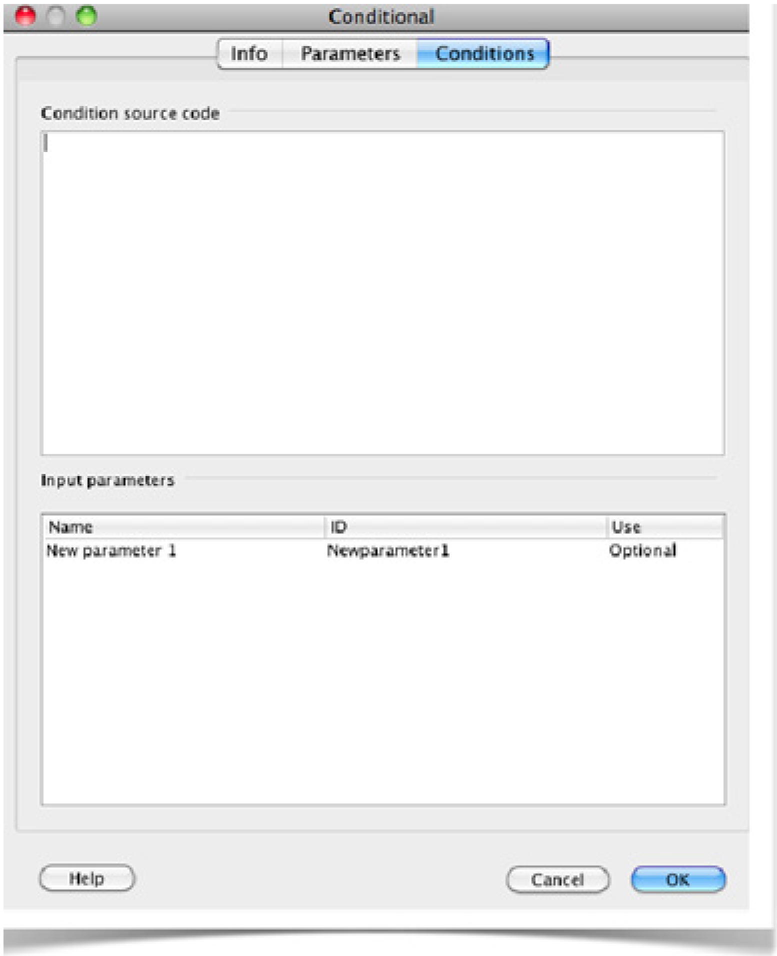
Pipeline 5.0 introduces a new feature called the “Conditional Module”. This module is used when the execution path of various inputs to a workflow is dependent on some criteria. Use of Conditional Modules makes the workflow more dynamic.

This module can be created by right clicking on the empty area in any workflow and choosing “Conditional” under the “New” option.

A new dialog will appear that has three tabs. The first and second tab is similar to what is seen in other type of modules. The third tab is different and is called "Conditions". Under this tab there is a “Condition source code” section where the conditional criteria should be entered. The syntax of the code entered is the same as the Pipeline Programming Language (PPL), which is similar to Java/C. Pipeline programming language is very simple and easy to learn.

How-to

The following examples will help better understand the functionality of the Conditional module.



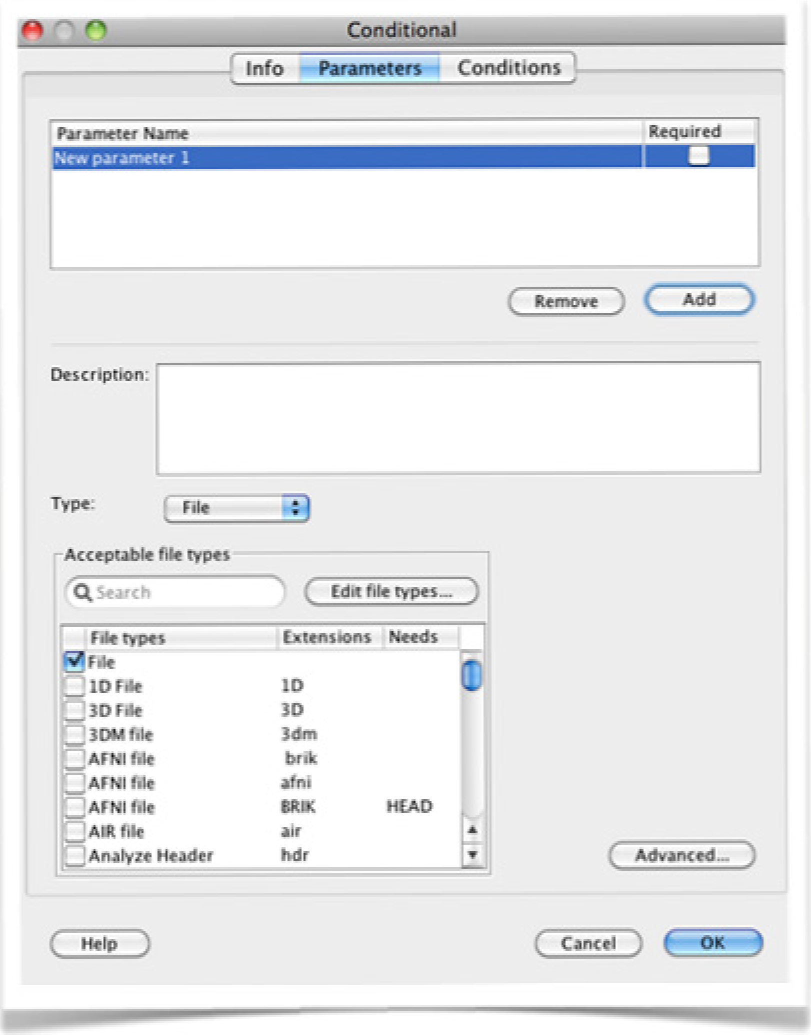
Name	ID	Use
New parameter 1	Newparameter1	Optional

File Conditions

This example will help understand how to set up a conditional module that chooses the execution path based on weather a file exists at a specific module output.

To create this conditional module follow the steps below:

1) Right click on the empty area in any workflow and select "New->Conditional"
2) Click on the "Parameters" tab and click on "Add" button to create a new parameter. Name the parameter, for example as "inputFile". Choose the file type if needed and click "OK".
3) Go to the "Conditions" tab and click on the "Condition source code" area and press the F1 Key to see a list of available parameters (NOTE: If there are no parameters declared, then there will be no parameters displayed when F1 key is pressed. New parameters have to be defined for the current conditional module before the conditional source code is specified). Choose the "inputFile" parameter by double clicking on this option.



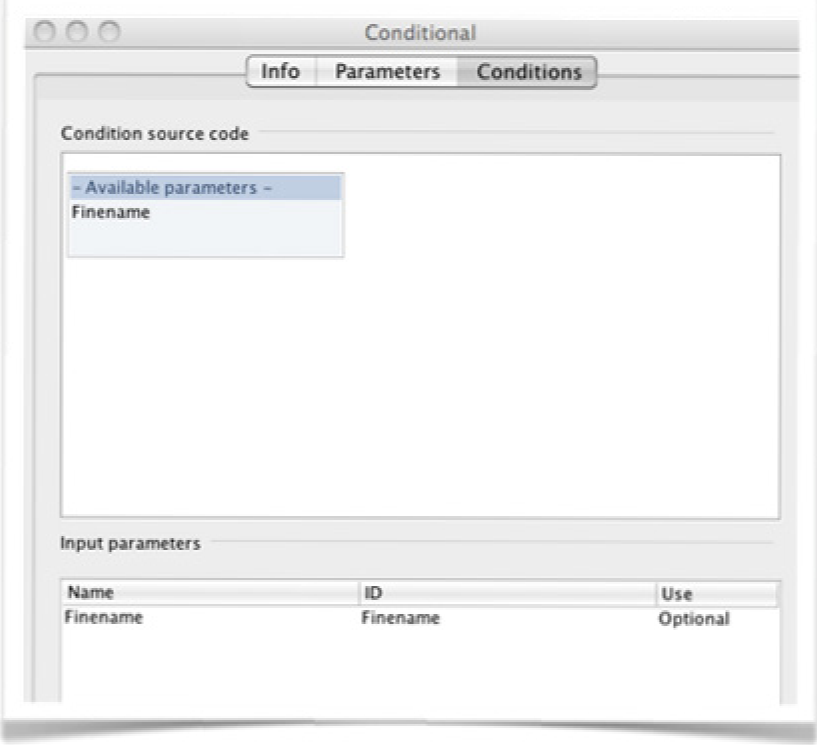
Parameter Name	Required
New parameter 1	□

Description:

Type: File

Acceptable file types

	File types	Extensions	Needs
☑	File		
□	1D File	1D	
□	3D File	3D	
□	3DM file	3dm	
□	AFNI file	brik	
□	AFNI file	afni	
□	AFNI file	BRIK	HEAD
□	AIR file	air	
□	Analyze Header	hdr	



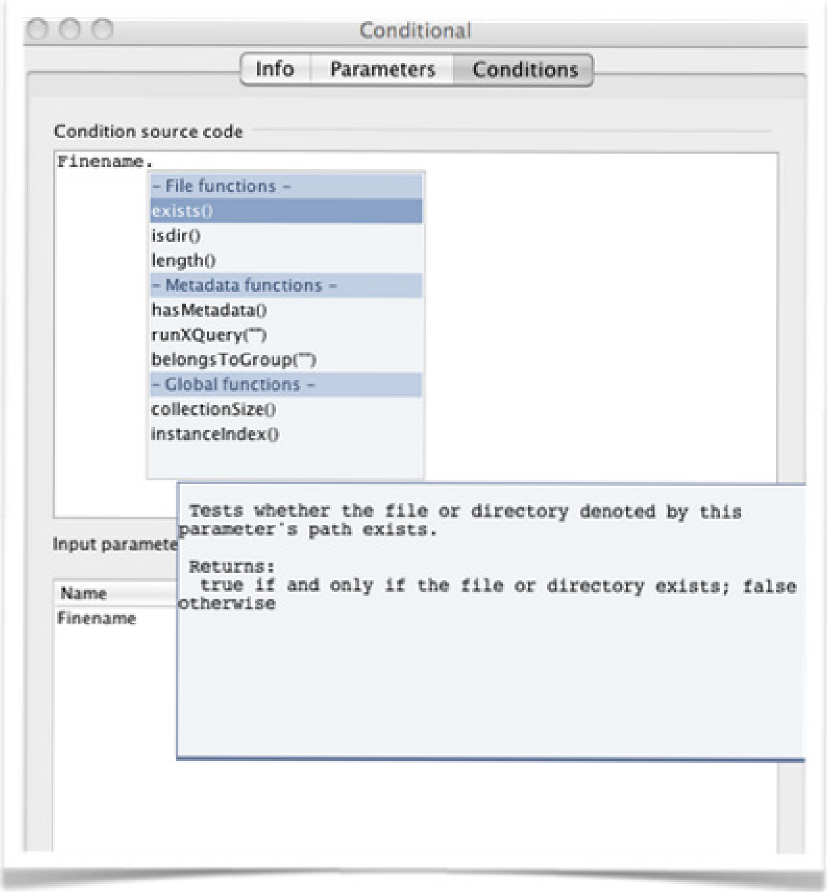
Condition source code

- Available parameters -
Finename

Input parameters

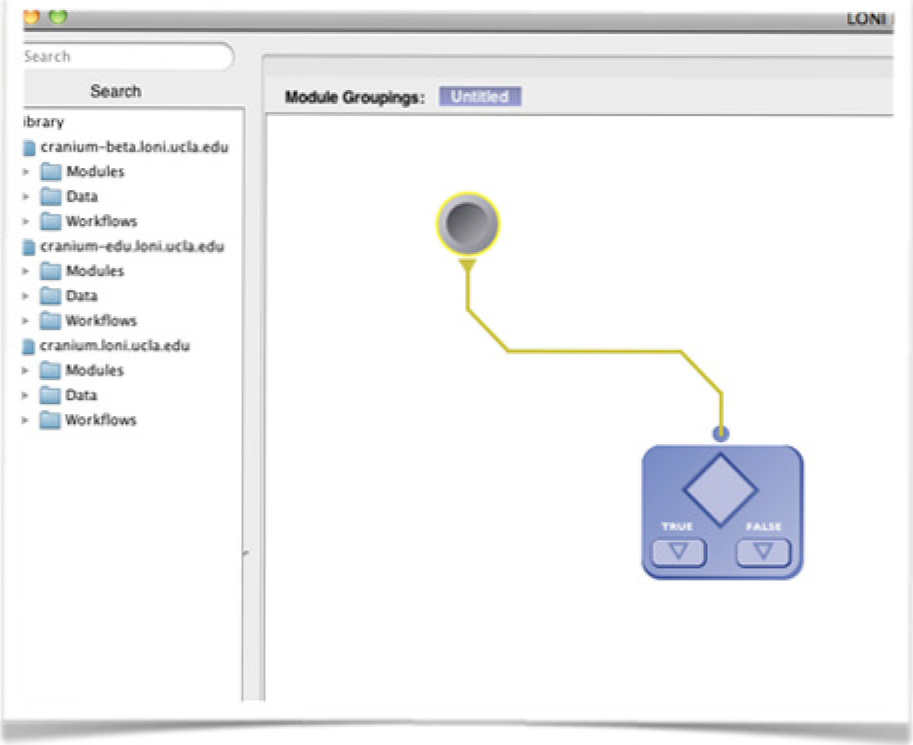
Name	ID	Use
Finename	Finename	Optional

4) Enter a "." after the inputFile (inputFile.) to access the various functions. Choose "exists()" under the "File functions" option by double clicking on it (inputFile.exists()). This condition checks if the parameter "inputFile" exists.
5) Click OK and a new conditional module is created with one input and two outputs, "TRUE" and "FALSE". If the parameter "inputFile" exists then the conditional will feed the inputFile to the "TRUE" output Parameter else to the "FALSE" output parameter.
6) Other functional modules can be connected to the outputs of TRUE/FALSE accordingly. If one output is always used, the other output could be disabled like any other module output.



```
Finename.
```

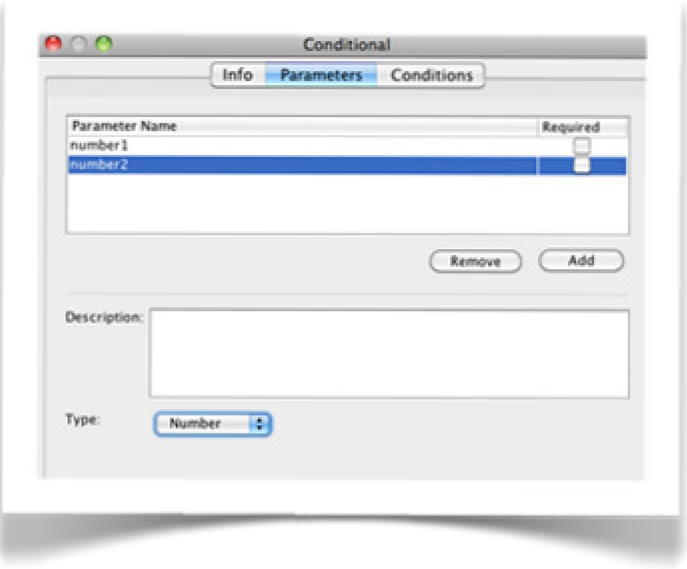
```
Tests whether the file or directory denoted by this
parameter's path exists.

Returns:
  true if and only if the file or directory exists; false
otherwise
```



Arithmetical/Comparison and Metadata Conditions

This example will demonstrate how to check the value of a parameter and determine if it has positive value (this number could be output of a previous module or information in the metadata).

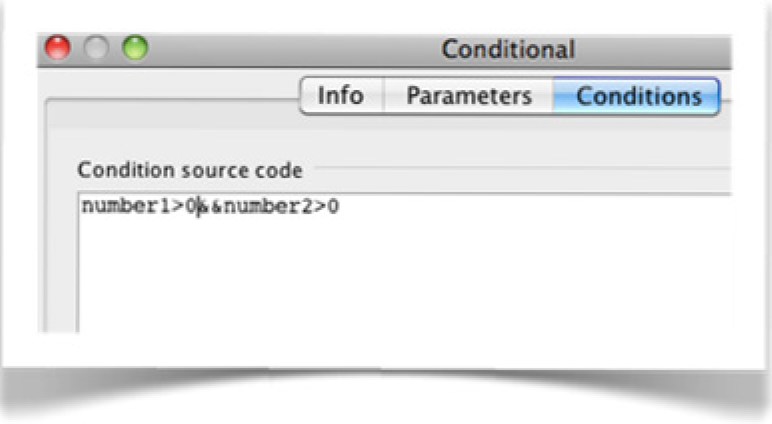
1) Follow the previous example until the step where the parameters are defined. Click on edit and create 2 input parameters, number1, number2 and both are of type "Number”. Click “OK”.
2) In the “Condition source code” area type the following "Number1 > 0 && Number2 > 0". This condition will check if both the inputs, Number1 and Number2 are greater than zero i.e. positive values. The conditional module created thus will have two inputs (Number1 and Number2) and four outputs (2 True and 2 False).



Parameter Name	Required
number1	□
number2	□

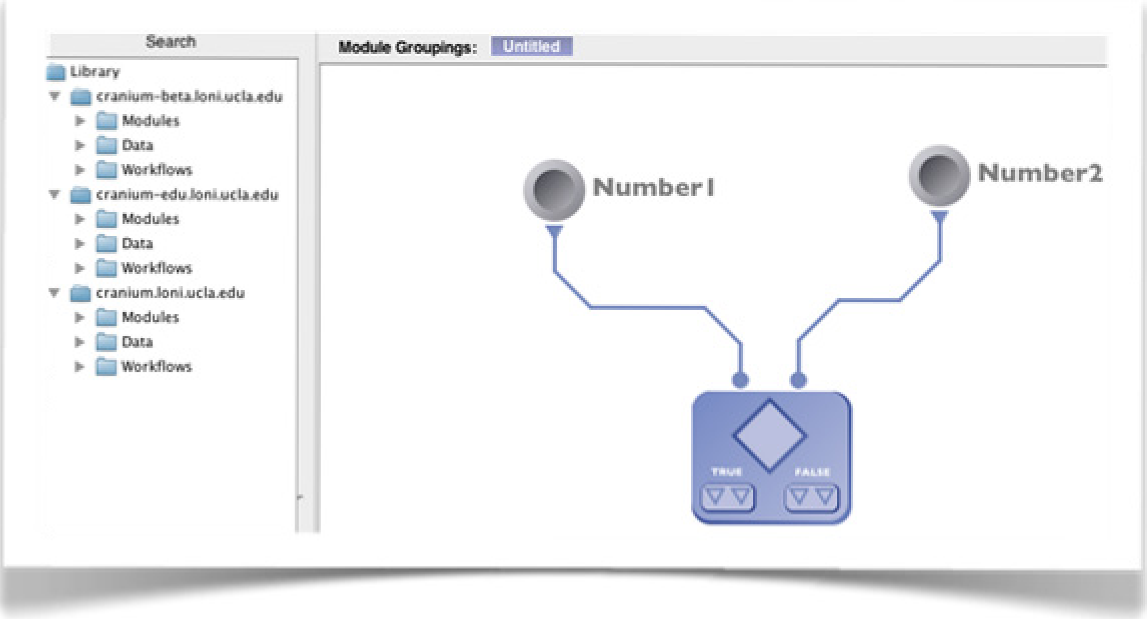
Description:

Type: Number



Condition source code

```
number1>0&&number2>0
```



Distributed Pipeline Server Installation

Introduction

Setting up your own Pipeline server is a great way to remotely take advantage of the power of a cluster or a just a dedicated computer with many helpful programs installed on it. More importantly, you can enable many people to take advantage of all this power all through the easy to use interface of the Pipeline client.

GUI Installation

The Distributed Pipeline Server Installer is a GUI installer that allows you to install and configure 3 types of resources – backend grid management resources (Oracle Grid Engine), the Pipeline server, and a number of computational imaging and informatics software tools. After successfully running the installer, you will have a running Pipeline server with Oracle Grid Engine managing jobs on your machine(s), imaging and informatics software tools installed, as well as a set of predefined workflows and modules in your server library.

Requirements

The requirements for the Pipeline server installation:
One or more machines running CentOS Linux operating system version 5.4 or above
OpenJDK or Sun/Oracle JDK 1.5 or above (If Sun/Oracle JDK is not installed, our installer will guide you to install it)
NFS V.3 server and network connected nodes with a shared partition
At least 30 GB available space for full installation (including tools and data)
Remote Root Access (with SSH credentials) to all hosts (to install Grid Engine)
A user that will run the Pipeline server process (a dedicated user is recommended)
Static IP Addresses for all the hosts, and their hostnames properly configured on DNS
Internet connection is needed during the installation.

Warning: if any of the requirements is not met, there may be unexepcted behavior (e.g. hanging, crashing of the installer). If you have any questions, please contact pipeline@loni.usc.edu

A complete installation (including Grid Engine, the Pipeline server, and download and install all the tools) takes approximately 6-7 hours. Some of the tools take a long time to download (e.g. FSL takes 6 hours to download). If you skip the tools or have all the tools downloaded, the total installation time is less than 30 minutes.

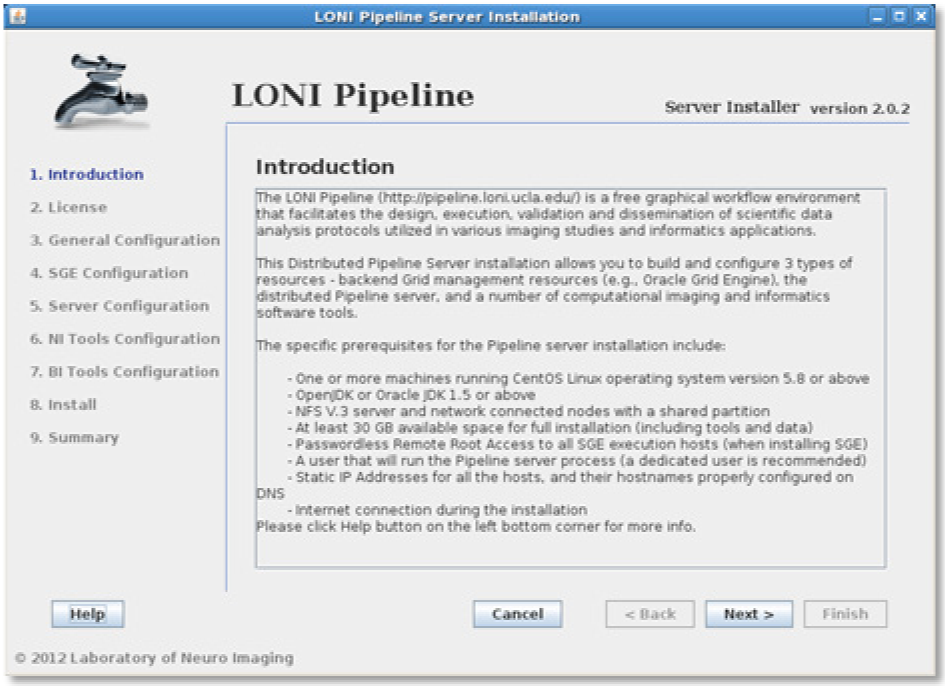
Downloading

Download the installer from the Pipeline website, under Downloads > Distributed Pipeline Server Installer.

Start the Installer

To start the installer, open a Terminal, sudo as root, go to the directory where the installer file is located, and type

```
tar -zxvf pipelineServerInstaller.tar.gz
cd pipelineServerInstaller
./launchInstaller.sh
```



Introduction

The LONI Pipeline (http://pipeline.loni.ucla.edu/) is a free graphical workflow environment that facilitates the design, execution, validation and dissemination of scientific data analysis protocols utilized in various imaging studies and informatics applications.

This Distributed Pipeline Server installation allows you to build and configure 3 types of resources - backend Grid management resources (e.g., Oracle Grid Engine), the distributed Pipeline server, and a number of computational imaging and informatics software tools.

The specific prerequisites for the Pipeline server installation include:

- One or more machines running CentOS Linux operating system version 5.8 or above
- OpenJDK or Oracle JDK 1.5 or above
- NFS V.3 server and network connected nodes with a shared partition
- At least 30 GB available space for full installation (including tools and data)
- Passwordless Remote Root Access to all SGE execution hosts (when installing SGE)
- A user that will run the Pipeline server process (a dedicated user is recommended)
- Static IP Addresses for all the hosts, and their hostnames properly configured on DNS
- Internet connection during the installation

Please click Help button on the left bottom corner for more info.

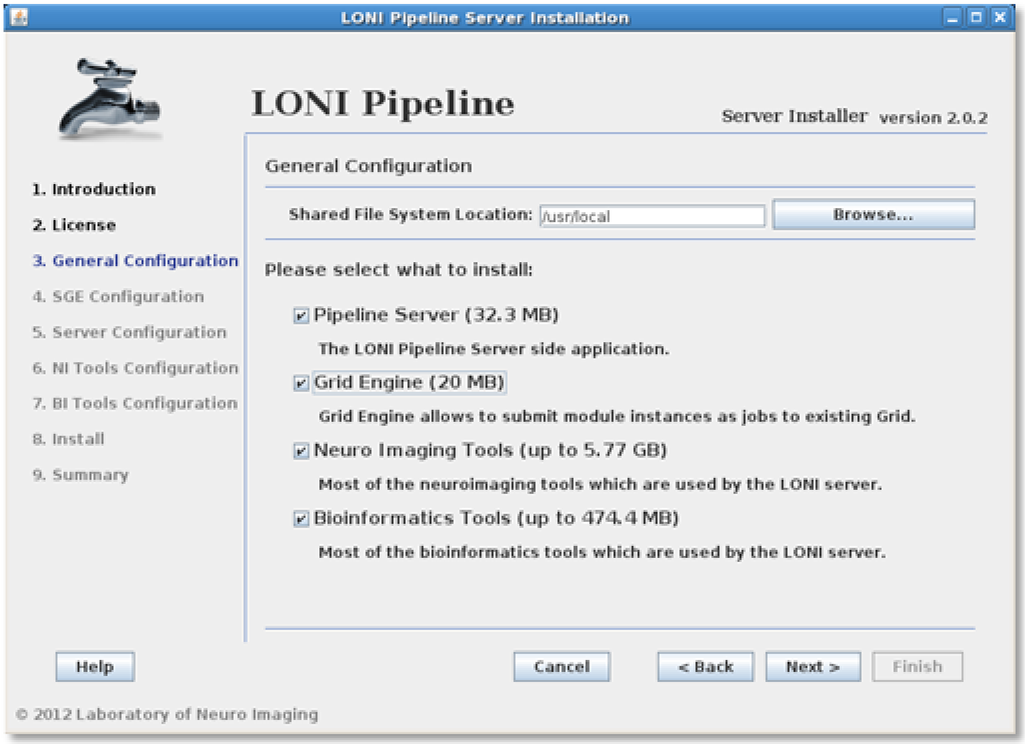
Select Components

After you read and agree the license, it asks you the installation location and what components you want to install:

You can select **any*** or all of the components. It will guide you through all the steps needed for the installation.

* For example, if you have already installed SGE before launching this installer, then deselect the Sun Grid Engine component. Likewise, if you only want to install the latest tools, you can select the Neuro Imaging Tools component and uncheck the rest.

The installer will verify the Shared File System Location given. It is required to have it on NFS if the server is set to use a grid. The shared file system is used for the Pipeline server to store intermediate files of workflows and to install Grid Engine and Neuro Imaging Tools.



General Configuration

Shared File System Location: /usr/local

Please select what to install:

☑ Pipeline Server (32.3 MB)

The LONI Pipeline Server side application.

☑ Grid Engine (20 MB)

Grid Engine allows to submit module instances as jobs to existing Grid.

☑ Neuro Imaging Tools (up to 5.77 GB)

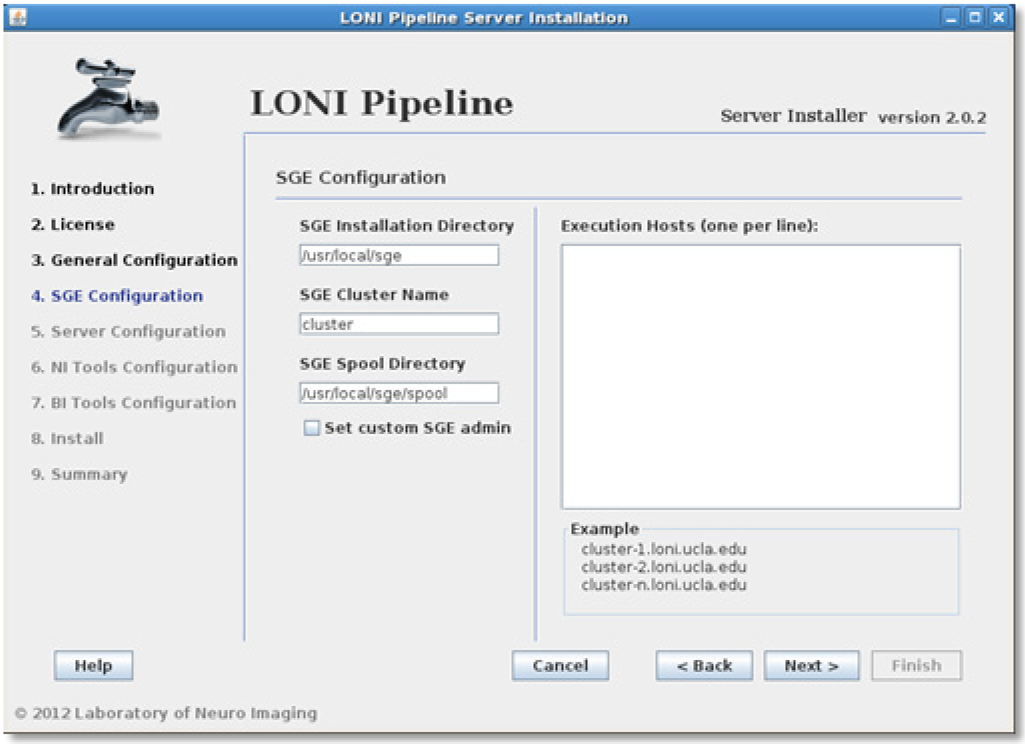
Most of the neuroimaging tools which are used by the LONI server.

☑ Bioinformatics Tools (up to 474.4 MB)

Most of the bioinformatics tools which are used by the LONI server.

Install Grid Engine

In this section you can configure Grid Engine installation. You can specify installation location, cluster name, spool directory, and execution hosts. You can leave installation location, cluster name and spool directory as they are, but you must provide a list of hostnames. You must provide fully qualified domain names, so something like “host1”, “localhost” or “127.0.0.1” is not allowed.



SGE Configuration

SGE Installation Directory: /usr/local/sge

SGE Cluster Name: cluster

SGE Spool Directory: /usr/local/sge/spool

□ Set custom SGE admin

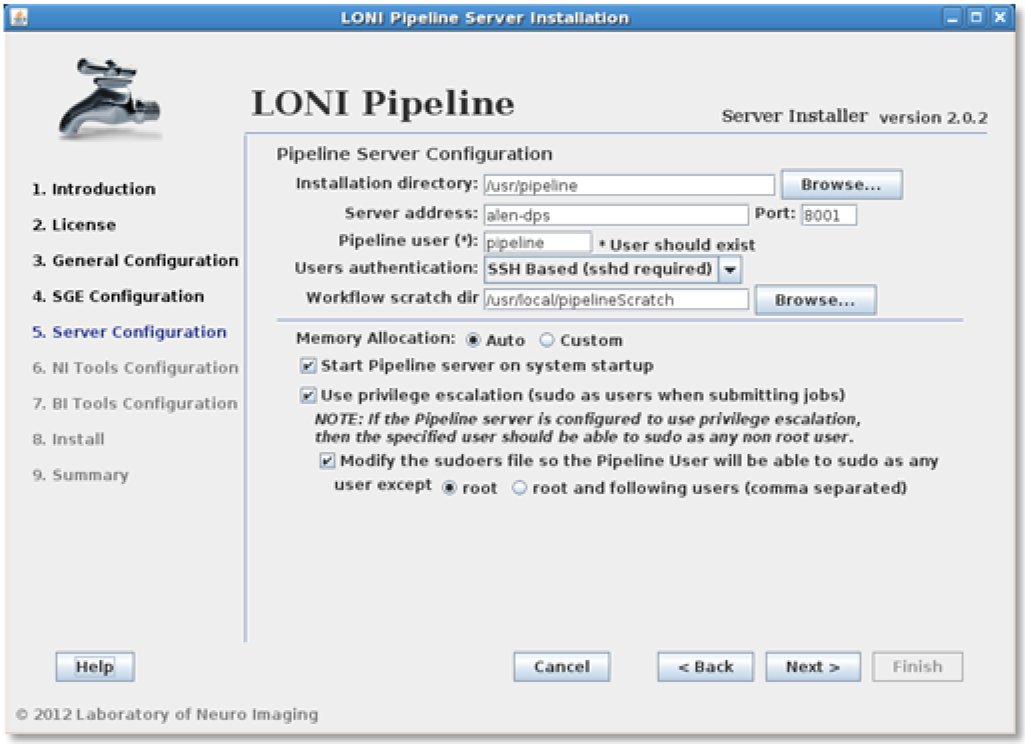
Execution Hosts (one per line):

Example
cluster-1.loni.ucla.edu
cluster-2.loni.ucla.edu
cluster-n.loni.ucla.edu

Install Pipeline

In this section you can configure the Pipeline server. You can specify installation directory, Pipeline server address, port and user to run the Pipeline server process. The user has to be created and you can have the option to have its sudo file modified to accommodate privilege escalation.

If modify sudo option is selected, the installer will modify operating system's sudoers file so that the Pipeline server user will be able to sudo as any user, except root and a list of users provided. For example, if you have some user that can sudo as root, then this user should be listed in the exception list, so that the Pipeline user will not be able to sudo to and ultimately gain root access.



Pipeline Server Configuration

Installation directory: /usr/pipeline Browse...

Server address: alen-dps Port: 8001

Pipeline user (*): pipeline * User should exist

Users authentication: SSH Based (sshd required)

Workflow scratch dir /usr/local/pipelineScratch Browse...

Memory Allocation: ● Auto ○ Custom

☑ Start Pipeline server on system startup

☑ Use privilege escalation (sudo as users when submitting jobs)

NOTE: If the Pipeline server is configured to use privilege escalation, then the specified user should be able to sudo as any non root user.

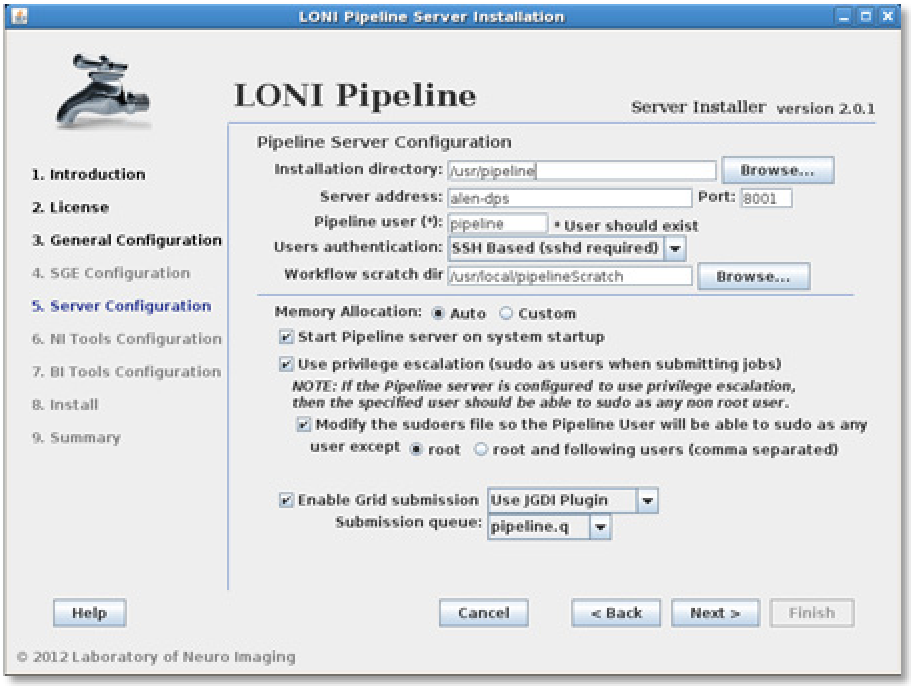
☑ Modify the sudoers file so the Pipeline User will be able to sudo as any user except ● root ○ root and following users (comma separated)

Install Pipeline with already installed SGE

If you have deselected the Sun Grid Engine checkbox from step 3 (General Configuration), then the Pipleine configuration window will have slightly different look. There should be a checkbox "Enable Grid Submission" which needs to be checked if you want to use Pipeline with your pre-installed SGE.

Upon checking the "Enable Grid Submission" checkbox, a combox with two options should appear. In order to communicate with SGE, Pipeline uses Grid Plugins. LONI Provides two plugins for SGE and those are JGDI Plugin and DRMAA Plugin. If you are using SGE we highly recommend to use JGDI Plugin as it supports more Pipeline features and is more reliable. You can choose DRMAA Plugin if you have other DRMAA supported Grid Manager installed and want to integrate Pipeline with it.

And the last step is to choose the submission queue. The installer will list all the queues you have and you have to pick one for the Pipeline. If you don’t have a special queue for Pipeline then you can use the default queue of SGE (SGE’s default queue is all.q). If you do not have any queue defined in SGE, you have to create one yourself and run the installer again.



LONI Pipeline Server Installation

LONI Pipeline

Server Installer version 2.0.1

1. Introduction
2. License
3. General Configuration
4. SGE Configuration
5. Server Configuration
6. NI Tools Configuration
7. BI Tools Configuration
8. Install
9. Summary

Pipeline Server Configuration

Installation directory: /usr/pipeline [Browse...]
Server address: alen-dps Port: 8001
Pipeline user (*): pipeline * User should exist
Users authentication: SSH Based (sshd required)
Workflow scratch dir /usr/local/pipelineScratch [Browse...]

Memory Allocation: ● Auto ○ Custom

☑ Start Pipeline server on system startup

☑ Use privilege escalation (sudo as users when submitting jobs)

NOTE: If the Pipeline server is configured to use privilege escalation, then the specified user should be able to sudo as any non root user.

☑ Modify the sudoers file so the Pipeline User will be able to sudo as any user except ● root ○ root and following users (comma separated)

☑ Enable Grid submission Use JGDI Plugin
Submission queue: pipeline.q

[Help] [Cancel] [< Back] [Next >] [Finish]

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Install Pipeline without SGE

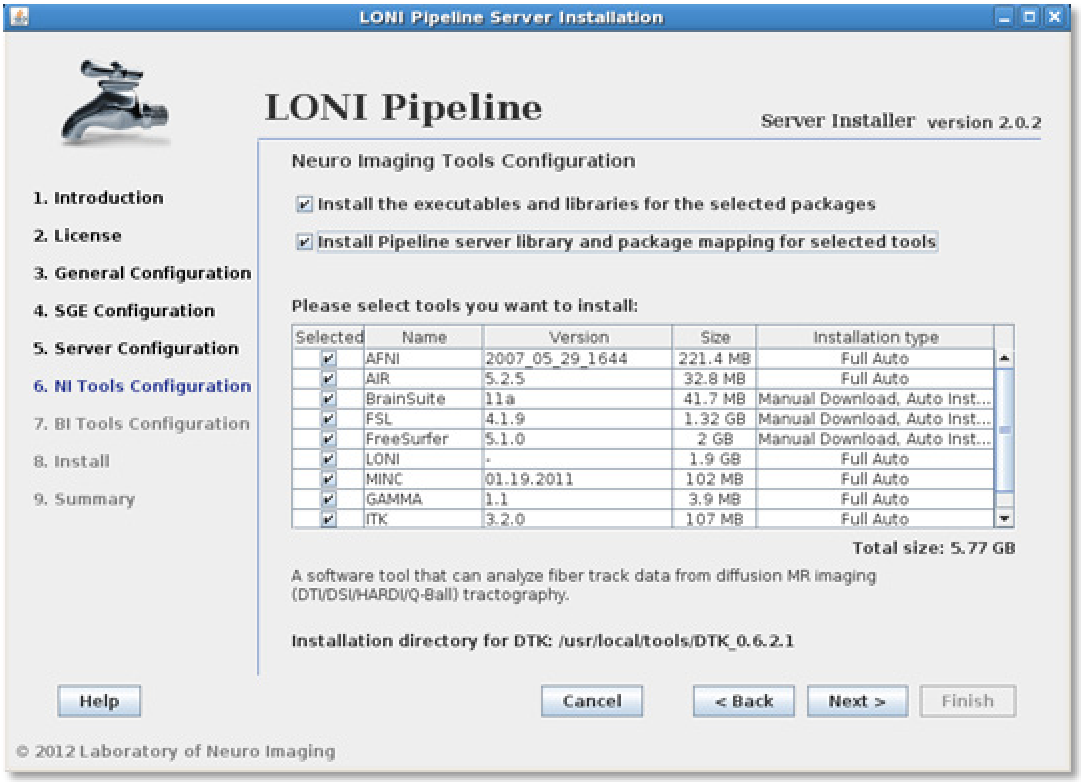
It is also possible to configure Pipeline to not use any queue. In this case all the jobs will be executed locally on the server and you have to be careful with number of jobs submitted to the server as high number of jobs will affect on server’s performance. Please see “Maximum Number of threads for active jobs” if you want to set limits to number of parallel running jobs.

Install Neuro Imaging Tools

In this section you have can select the imaging and informatics software tools and server library files for these tools.

If the installation type for a tool is “Full Auto”, it will be installed automatically. For some tools, it is marked as “Manual Download”, this means you will be asked to go to a website to download (e.g. FSL, FreeSurfer). This is because the licensing restriction imposed on the software.

Click on Open download page to open the browser, the page will be loaded for you, follow the instructions on the dialog and download the tool to your computer. After it is done, click “I have the archive” to locate the file. If you already downloaded the file, you can also click on “I have the archive” to provide the path of the file. Click on Skip for now will go to the next tool. If some other tool needs manual download, it will show instructions for that tool as well, so that you can download all the tools in parallel. All the message dialogs will cycle through if you click “Skip for now”, until your download is complete and you provide the file by clicking “I have the archive.”



Neuro Imaging Tools Configuration

☑ Install the executables and libraries for the selected packages

☑ Install Pipeline server library and package mapping for selected tools

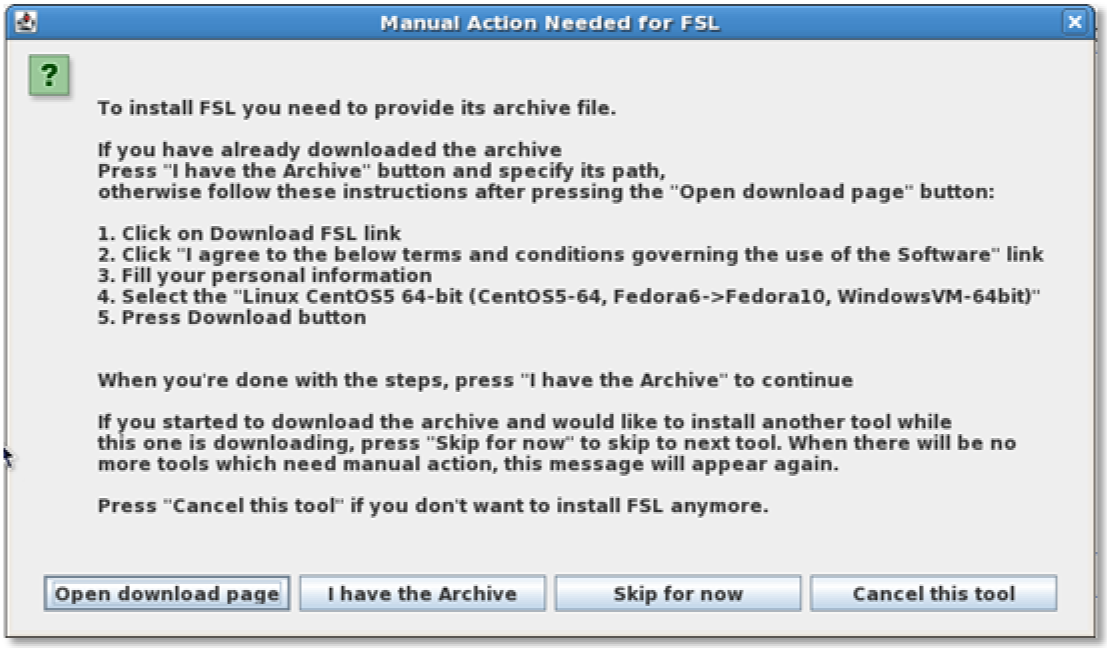
Please select tools you want to install:

Selected	Name	Version	Size	Installation type
☑	AFNI	2007_05_29_1644	221.4 MB	Full Auto
☑	AIR	5.2.5	32.8 MB	Full Auto
☑	BrainSuite	11a	41.7 MB	Manual Download, Auto Inst...
☑	FSL	4.1.9	1.32 GB	Manual Download, Auto Inst...
☑	FreeSurfer	5.1.0	2 GB	Manual Download, Auto Inst...
☑	LONI	-	1.9 GB	Full Auto
☑	MINC	01.19.2011	102 MB	Full Auto
☑	GAMMA	1.1	3.9 MB	Full Auto
☑	ITK	3.2.0	107 MB	Full Auto

Total size: 5.77 GB

A software tool that can analyze fiber track data from diffusion MR imaging (DTI/DSI/HARDI/Q-Ball) tractography.

Installation directory for DTK: /usr/local/tools/DTK_0.6.2.1



To install FSL you need to provide its archive file.

If you have already downloaded the archive
Press "I have the Archive" button and specify its path,
otherwise follow these instructions after pressing the "Open download page" button:

1. Click on Download FSL link
2. Click "I agree to the below terms and conditions governing the use of the Software" link
3. Fill your personal information
4. Select the "Linux CentOS5 64-bit (CentOS5-64, Fedora6->Fedora10, WindowsVM-64bit)"
5. Press Download button

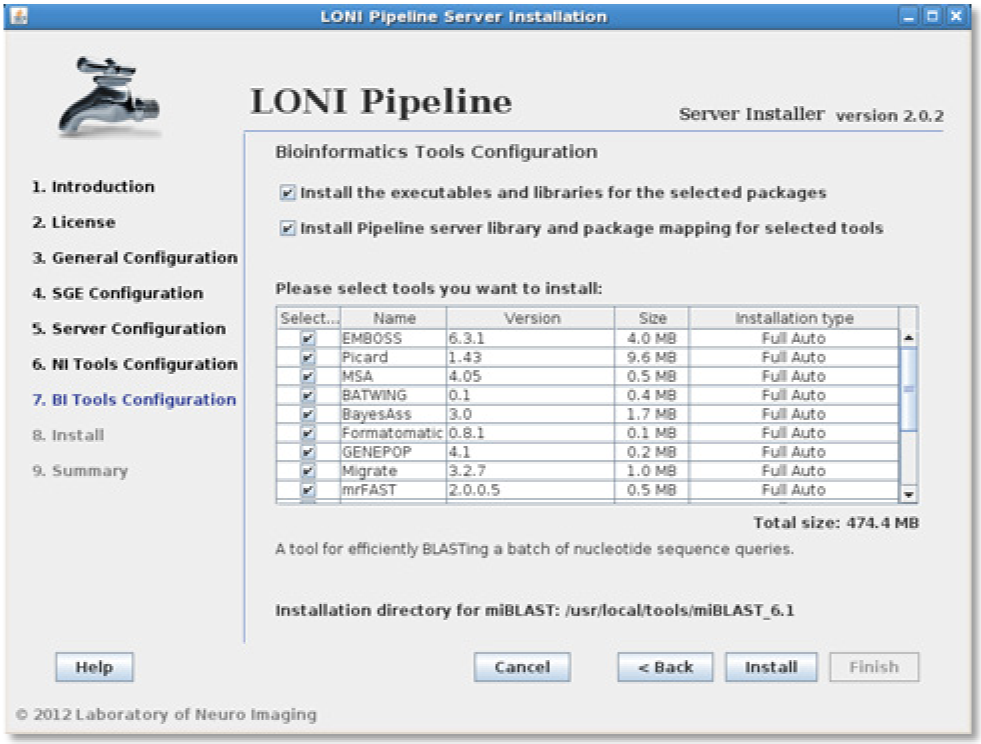
When you're done with the steps, press "I have the Archive" to continue

If you started to download the archive and would like to install another tool while this one is downloading, press "Skip for now" to skip to next tool. When there will be no more tools which need manual action, this message will appear again.

Press "Cancel this tool" if you don't want to install FSL anymore.

Install Bioinformatics Tools

Follow the same instructions given above for neuro imaging tools. In particular, select the packages that you would like to install. Also, you can choose to only install the executables, the Pipeline server library files, or both. After selecting the packages that you need, press the Next button to proceed with the installation. Note that this is the final step before the Pipeline installation utility takes over and starts to download/install files.



Bioinformatics Tools Configuration

☑ Install the executables and libraries for the selected packages

☑ Install Pipeline server library and package mapping for selected tools

Please select tools you want to install:

Select...	Name	Version	Size	Installation type
☑	EMBOSS	6.3.1	4.0 MB	Full Auto
☑	Picard	1.43	9.6 MB	Full Auto
☑	MSA	4.05	0.5 MB	Full Auto
☑	BATWING	0.1	0.4 MB	Full Auto
☑	BayesAss	3.0	1.7 MB	Full Auto
☑	Formatomatic	0.8.1	0.1 MB	Full Auto
☑	GENEPOP	4.1	0.2 MB	Full Auto
☑	Migrate	3.2.7	1.0 MB	Full Auto
☑	mrFAST	2.0.0.5	0.5 MB	Full Auto

Total size: 474.4 MB

A tool for efficiently BLASTing a batch of nucleotide sequence queries.

Installation directory for miBLAST: /usr/local/tools/miBLAST_6.1

Install the tools without installing Pipeline or SGE

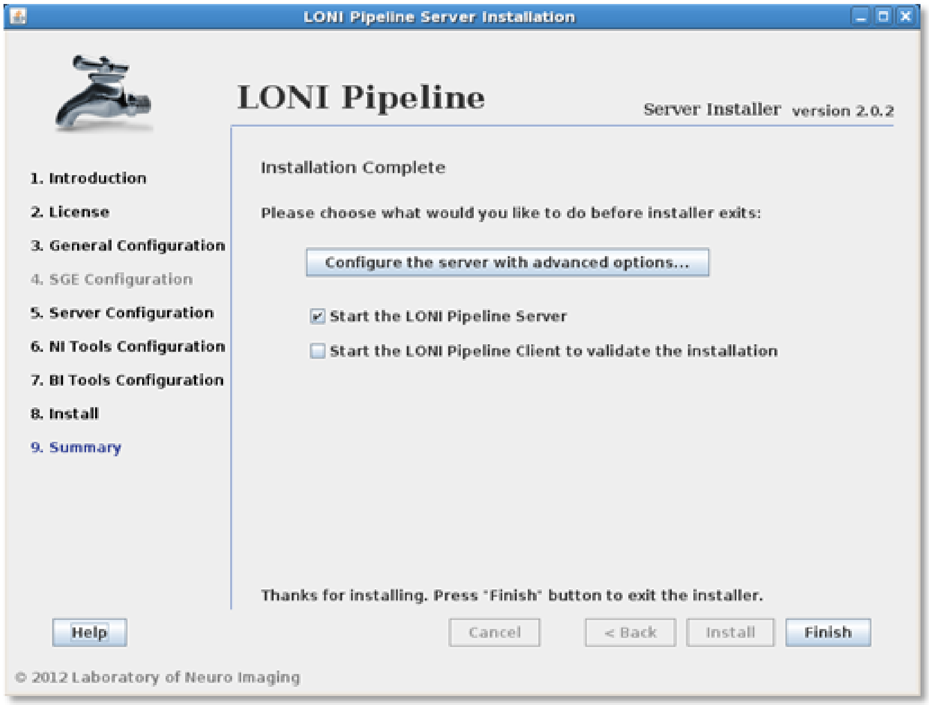
If at a later time, you want to install updated version of some tool, you can have it installed without installing the Pipeline and SGE. Simply check only the Neuro Imaging Tools in the general configuration section of the installer, then click Next, it will skip the Pipeline and SGE installation steps and go directly to the tools installation step.

Finish Install

After the installation is successfully done, it will show a summary screen. Click Finish with Start Server checked will exit the installer and launch the Pipeline server. You can also check Start client option to launch the client to validate installation.

You can also configure advanced server preferences using the server configuration tool by clicking on “Configure the server with advanced option…”.

If you have any questions, please contact pipeline@loni.usc.edu


LONI Pipeline Server Installation
LONI Pipeline
Server Installer version 2.0.2
1. Introduction
2. License
3. General Configuration
4. SGE Configuration
5. Server Configuration
6. NI Tools Configuration
7. BI Tools Configuration
8. Install
9. Summary
Configure the server with advanced options...
Help
Cancel
< Back
Install
Finish

Installation Complete

Please choose what would you like to do before installer exits:

☑ Start the LONI Pipeline Server

□ Start the LONI Pipeline Client to validate the installation

Thanks for installing. Press 'Finish' button to exit the installer.

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Start the Server

If you checked “Start the LONI Pipeline Server” option on the summary page of the installation, the Pipeline server process should be started. To check the logs of the Pipeline server, go to the Pipeline server’s directory (/usr/pipeline by default), specified in the “Install Pipeline” step. You will find files called outputStream.log and errorStream.log, which stores output stream and error stream. You can verify if the server started successfully by checking the contents of the outputStream.log file, it should look something like this:

```
[ 1/6 ] Connecting to Persistence Database.........DONE [117ms]
[ 2/6 ] Starting server on port 8008...............DONE [1152ms]
[ 3/6 ] Loading server library.....................DONE [31ms]
[ 4/6 ] Loading server packages info...............DONE [7ms]
[ 5/6 ] Checking to resume backlogged workflows....DONE [0ms]
[ 6/6 ] Checking to resume active workflows........DONE [0ms]
[ SUCCESS ] Server started.
```

You can stop and start the Pipeline server by calling (root access required)

```
/etc/init.d/pipeline stop
/etc/init.d/pipeline start
```

If you don’t have root access, you can stop and start the Pipeline server by going to the Pipeline server’s directory and type

```
./killServer.sh./launchServer.sh
```

Always check if the server has started successfully by viewing the outputStream.log file. If it shows error on persistence database, you can stop and start the persistence database process by typing:

```
./db/stopDB.sh./db/startDB.sh
```

Troubleshoot

The following is a list of error messages and explanation:

- **The provided directory seems not to be a network file shared (NFS) directory.**

The installer will verify the Shared File System Location given. It is required to have it on NFS if the server is set to use a grid. The shared file system is used for the Pipeline server to store intermediate files of workflows and to install Grid Engine and Neuro Imaging Tools.

- **It is not supported for a Grid Engine installation that the local hostname is "localhost" and/or the IP address is like 127.0.*.***

You must provide fully qualified domain names as hostnames, so something like "host1″, "localhost" or "127.0.0.1″ is not allowed.

- **Cannot enable Grid submission as SGE doesn't have any queue.**

If you do not have any queue defined in SGE, you have to create one yourself and recheck "Enable Grid submission" checkbox and select the queue.

Command Line Installation

Alternative to DPS installer, you can also install the Pipeline server using an automated method that relies on a preference file. All of the fields that would otherwise have to be entered via the GUI can be specified within a hierarchical XML file. First of all, you need to download the same archive that contains the graphical version of the installer (you can get it here). A default configuration file is included in the distribution (in the dist/install_files directory). You can run the installation in automatic mode by typing the following into your shell:

```
tar -zxvf pipelineServerInstaller.tar.gz
cd pipelineServerInstaller
./launchInstaller.sh -auto dist/install_files/DefaultInstallationPreferencesFile.xml
```

A complete template for the XML file can be found here. If you use this template as a starting point, note that it has a lot of placeholders and is not set up to run "as is", so you would have to make many modifications. For reference, each of the tags is documented below:

- DistributedPipelineServerInstaller: root tag, contains all other tags
- SharedFileSystemPath: path to a directory that is shared (via NFS) between the host running the Pipeline server and qmaster, admin, and execution hosts of SGE
- JDKLocation: only include this tag if you don't already have Oracle JDK running on the host where you're installing the Pipeline server; the value should be the path to the JDK RPM, which you can install from the Oracle page
- PipelineServer: use attribute enabled="true" to indicate that you would like to install the Pipeline server; the children of this element will specify information about the server installation
    - InstallLocation: specifies location where Pipeline server is to be installed
    - Hostname: specifies the hostname of the host where Pipeline server is being installed
    - Port: specifies port on which the Pipeline server will be accepting connections from clients
    - Username: specifies user that will be running the Pipeline server
    - TempDir: specifies a directory where Pipeline modules will write intermediate files
    - ScratchDir: specifies a scratch directory where sample workflows will write their outputs;

this value then becomes available to users through the pre-defined ${tempdir} variable, documented here

  - GridSubmission: use attribute enabled=”true” to indicate that you would like the Pipeline to submit jobs via grid engine to execution hosts; otherwise, the jobs will be run locally on the host running the Pipeline server
    - GridPlugin: options are JGDI or DRMAA
    - GridSubmissionQueue: the SGE queue where Pipeline should submit its jobs
    - UsePrivilegeEscalation: options are true or false; privilege escalation is documented here
  - DBInstallLocation: path to a directory where you would like to install the Pipeline database; if it doesn’t exist, it will be created by the installer
  - StartPipelilneOnSystemStartup: set value to true if you would like to configure the system to start the Pipeline server on startup; false, otherwise
  - AuthenticationModule: options are SSH, NIS, and NoAuth; these are documented here
  - ModifySudoers: use attribute enabled=”true” to indicate that you want to add the Pipeline user to the sudoers list
    - SuperUsers: comma-separated list of users that you don’t want the Pipeline server to sudo as (default: root)
  - MemoryAllocation: specify the amount of memory you would like to allocate to the Pipeline server/database, in megabytes
- SGE: use attribute enabled=”true” to indicate that you would like to install Son of Grid Engine; the tags that follow will describe some of the preferences for the installation; you can find documentation on SGE here
  - SGERoot: path to directory where you would like to install SGE (default: /usr/local/sge)
  - SGECluster: name of cluster that you would like to install (default: cluster)
  - SubmitHosts: specify hostnames of machines which will be configured to handle job submission and control; you can do this using one hostname per Host element, as children of the SubmitHosts element
  - ExecHosts: specify hostnames of machines which will be execution hosts; use same format as for SubmitHosts
  - AdminHosts: specify hostnames of machines that will be used for SGE administration purposes; use same format as for SubmitHosts
  - AdminUsername: user that will serve as SGE administrator
  - SpoolDir: path to a directory that will be used for spooling during installation
  - Queue: use attribute configure=”true” to indicate that you would like to configure a queue at the end of SGE installation; this is documented here
    - Name: the name of the new queue that you would like to configure
    - Hosts: the hosts that you would like to add to the queue
    - Slots: the slots that you would like to add to the queue (the difference between hosts and slots is documented here)
- Tools: use the attribute enabled=”true” to indicate that you would like to install some tools; also use the path attribute to specify the directory where you would like to install the tools (note that this should be in an NFS-shared directory)
  - NeuroImagingTools: use the attribute enabled=”true” to indicate that you would like to install one or more neuro imaging tools; true/false values for the executables/serverLib attributes indicate whether you need only the executables, the .pipe files, or both for the

  neuro imaging tools
  - Available neuroimaging tools: AFNI, AIR, BrainSuite, FSL, FreeSurfer, LONI, MINC, ITK, DTK, GAMMA; for each of these, the enabled=”true” attribute is used to activate the tool installation; note that BrainSuite, FSL, FreeSurfer, and DTK require that the user specify a sub element, namely ArchivePath, whose value is the path to the archive file, downloaded manually from the software website; FreeSurfer additionally requires a LicensePath element with the path to the FreeSurfer license
- BioinformaticsTools: same attributes as NeuroImagingTools tag
  - Available bioinformatics tools: EMBOSS, Picard, MSA, BATWING, BayesAss, Formatomatic, GENEPOP, Migrate, GWASS, MrFAST, Bowtie, SamTools, PLINK, MAQ, miBLAST; again, the enabled attribute can be used to indicate activation or deactivation of installation for each of these elements

Requirements

The Pipeline server can run on any system that is supported by JRE 1.5 or higher, so the first thing to do is head over to the official Java website to download the latest JRE/JDK. If you run the server on Windows, you will not be able to use privilege escalation (you might not even need/want it). Also the Failover feature is only supported by Unix/Linux systems. All other features are available for all platforms.

The amount of memory required varies based on the load you will expect on the server, but for a reference point, the Pipeline server running on cranium.loni.usc.edu has been set to accept a max load of 620 jobs, and its memory footprint hovers between 50-300MB depending on the load and garbage collection scheme.

Downloading

Head over to the Pipeline download page (http://pipeline.loni.usc.edu/downloads/) and download the latest version of the program for Linux/Unix. The server and the client are both in the same jar file, so you only need to change the Main entry point when starting up the server. Extract the contents of the download to the location you want to install the server at.

Starting the Server

Now let’s start the server for the first time. Get to a prompt and switch to the directory where you copied the Pipeline.jar and lib directory and type:

```
$ java -classpath Pipeline.jar server.Main
```

Assuming you have java in your path, you should have received the following message back in your terminal window:

```
[ 1/6 ] Connecting to Persistence Database..........DONE [61ms]
[ 2/6 ] Starting server on port 8001................DONE [747ms]
[ 3/6 ] Loading server library......................DONE [336ms]
[ 4/6 ] Loading server packages info................DONE [2ms]
[ 5/6 ] Checking to resume backlogged workflows.....DONE [46ms]
[ 6/6 ] Checking to resume active workflows.........DONE [0ms]
[ SUCCESS ] Server started.
```

That’s not enough to have a fully functional server yet, but we’re a step closer, so go ahead and break out of the process by hitting Ctrl-C.

Glossary

AFNI - (Analysis of Functional NeuroImages) is a Neuroimaging tool that is used for processing and viewing of structural and functional MRI images. There are many tools that are available within this program, like; file conversion tools (AFNI to Analyze, MINC, NIfTI etc), Statistical analysis tools (3D ANOVA, 3D ANOVA2 etc), Surface Tools (Surface clustering, Surface Measures etc) and so on. For more information about the tools and its application please visit the website, http://afni.nimh.nih.gov/afni

AIR - Automated Image Registration is an automated Image registration tool (3D or 2D images) that is used to register images of different modalities either between or across subjects. There are many AIR programs that can be used to manipulate the images. A list of tools can be found at, http://bishopw.loni.usc.edu/AIR5/programsabc.html

AlignLinear - This is an intramodality registration tool (within or across subjects). Users can specify the models that includes, rigid-body, affine or perspective. For more information on usage and examples follow the link, http://bishopw.loni.usc.edu/AIR5/alignlinear.html

Reslice - This program takes a . air file and uses the information that it contains to load the corresponding image file and generate a new, realigned file.The link below has more information on the usage of this program. http://bishopw.loni.usc.edu/AIR5/reslice.html

AVW Maths - Simple but powerful FSL program to allow mathematical (add, subtract, divide, multiply, square) manipulation of images.

BET - FSL's Brain Extraction Tool Deletes non-brain tissue from an image of the whole head. It can also estimate the external skull surface.

Bias Field Corrector - Computes local estimates of gain variation in the image using an adaptive partial volume tissue model. Uses the estimates to compute a tri-cubic B-spline. Corrects the extracted brain image using values of the spline.

BrainSuite - An Image analysis tool that is used for MR Images. This tool is used for identifying the tissue type and surfaces in the MR images. BrainSuite was specifically designed for surface extraction.

Brain Surface Extraction - Removes non-brain tissue from the MRI using a combination of anisotropic diffusion filtering, MArr-Hildreth edge detection, and mathematical morphology. http://brainsuite.usc.edu/

Cache - A directory in which the application creates intermediate output files, streams, and log files.

Command String - The exact command that was submitted by the Pipeline to the underlying operating system for execution.

Connection Manager - The dialog box which holds connections that you have created to Pipeline servers.

Data Sink - A special module that takes one or more output values and can be used as the output destination of one or more modules.

Data Source - A special module that takes one or more input values and can be used as the input source of one or more modules.

DRMAA - Distributor Resource Management Applications API. A library, or specifications, which allow applications to interact, or submit control to jobs on one or more DRM systems.

Executable - A file whose contents are meant to be interpreted as a program by a computer.

FSL - FMRIB Software Library is a set of tools, which can be used for analyzing the MRI, fMRI and DTI brain imaging data. The various tools that are available through the FMRIB library are categorized based on the type of analyses that needs to be performed (e.g. functional MRI analyses, Structural analyses, DTI analyses and other miscellaneous tools). http://www.fmrib.ox.ac.uk/fsl/index.html

FSF Update - A special module used to update the design.fsf setup file. It is a very flexible module that is used to add/update information to the design file (adding experimental variables and/or updating the T1 image, 3D images etc).

FSL Design.fsf - This is a setup file that has information about various options and design specified using the FSL FEAT interface.

FSL FEAT - FEAT is part of FSL (FMRIB's Software Library). It is a software tool for high quality model-based FMRI data analysis, with an easy-to-use graphical user interface (GUI). FEAT automates as many of the analysis decisions as possible, and allows easy (though still robust, efficient and valid) analysis of simple experiments whilst giving enough flexibility to also allow sophisticated analysis of the most complex experiments.**FreeSurfer -** This is a group of software programs that are used to process the MRI images in two ways, one volumetric analyses and the other surface analyses. The freesurfer pipeline is completely automated which is very helpful for large sets of data.

FSL Merge - FSL’s miscellaneous utility that is used to concatenate files into a single file. Concatenation can be along time or X, Y r Z-axis. All image dimensions (except for the one being concatenated over) must be the same in all input images. For example, this can be used to take multiple 3D files (eg as output by SPM) and create a single 4D image file.

FSLSwapDim - This program re-orders the data storage to permit changes between axial, sagittal and coronal slicing. When used in this mode no warning should be printed and the output files will maintain the same left-right order.

Image Data Archive (IDA) - An acronym that stands for Image Database Archive. Along with being one of the protocol which the LONI Pipeline support, IDA offers the following benefits:

- **De-identification -** Addresses government regulations for protection of human subject privacy
- **Data Transmission -** Data is transmitted over the internet using Hyper-Text Transfer Protocol with SSL encryption (HTTPS)
- **Storage -** Data is archived on a fault-tolerant storage area network (SAN), providing near 24/7 availability
- **Execution Dialog -** A dialog which shows important messages printed by the different times during its execution.

ITK - Insight Segmentation and registration toolkit is a set of programs that employs leading edge algorithms for segmentation and registration of images. There are 3 main programs that are used in the ITK toolkit, 3D Deformable Model Segmentation, 3D Deformable Registration, 3D Multi-modality B-spine Deformable Registration

LONI - Laboratory of Neuro Imaging offers a set of tools that are used for structural, functional and DT Image data manipulation. This tool kit is available through the LONI Pipeline library.

LONI Viewer - An Image Viewer that allows viewing of shape, surface, volume and geometric image data.

MiND - Metadata in NIfTI for DWI is a set of extensions to NIfTI header, which serve as a mechanism for preserving the metadata in direct association with the Diffusion Weighted datasets.

Module - The smallest unit of a Pipeline workflow. Specifically, it is a chunk of XML that describes an executable and its inputs and outputs. It can be created by a user and placed directly into a workflow, or a user can drag and drop predefined modules from the library of any server to which they are connected.

Module Definition - The collection of information including the executable author, name, package, version, description and parameter names that must be specified for each executable to create a module that can be used in the Pipeline. Once a module definition has been created for an executable, it can be saved in the library and reused by other users.

Module Group - A collection of modules. The Pipeline can abstract a Module Group to be represented as a single module in a workflow.

MNI - MINC toolkit was developed at the Brain Imaging Centre at Montreal. They are a set of applications and tools that are used for medical image processing and data management. There are five categories of software programs available, Visualization Tools, Basic Tools, Pipelining Tools and Statistical Analysis Tools.

Output Log - A collection of messages which are printed out to the output stream of the application.

Package - A suite of module definitions which are interrelated.

Parameter - An input or output to a module.

Partial Volume Classifier - Each voxel is classified according to the tissue type (WM, GM, CSF, and partial volume mixture) by combining the partial volume tissue model with a Gibbs spatial prior to produce a classifier that encourages contiguous region of similar tissue type.

Personal Library - A place to store or save workflows and modules for easy access through the Pipeline.

Play Button - This is used to validate and execute the workflows by connecting to the computer cluster.

Pipeline - An environment to develop workflows for data processing, independent of data location, program location, and platform.

Provenance - LONI Pipeline includes a new feature that enables tracking data, workflow and execution history of all processes. This functionality improves the communication, reproducibility and validation of newly proposed experimental designs, scientific analysis protocols and research findings.

ShapeTools - Shape Tool programs are a set of portable tools that support the modeling, analysis and display of interesting geometric shapes. Nearly all Shape Tools applications are written in the Java programming language.

Smartlines - A connection between two modules, which will automatically convert the output file type of the first module to be compatible with the input file type of the second module.

Validation - Occurs automatically when the user requests that a workflow be executed. Validation entails:

- Verifying the existence of inputs, outputs and executables
- Cycle detection
- File cardinality checks
- File type checking

Depending on workflow content, connection status and other variables, the validation may be more or less complex. Please refer to Pipeline documentation on validation for more information.

Workflow - A set of connected modules that performs analysis or simply processes input data.

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