



## Overview

The LONI Pipeline is a free workflow client-server application facilitating the high-throughput research of computational scientists. Using the LONI Pipeline, researchers may quickly create, execute, monitor and share processing workflows that take advantage of diverse arrays of available imaging and genomics computing tools.



**Pipeline**  
<http://pipeline.loni.usc.edu>

## Features

### Cross Platform Compatible

Work in the operating system that suits you best. Connect from your client to execute processing and analysis remotely on other operating systems.



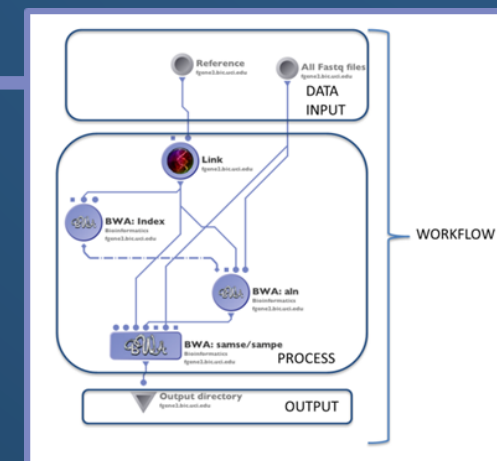
### Grid Support

Take advantage of a supercomputing environment by automatically parallelizing data-independent programs in a given analysis.



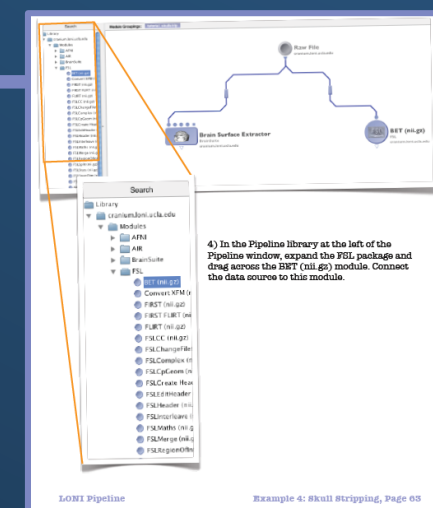
### Simple User Interface

Free yourself from the hassle of being bogged down by system administration and focus energy on current research problems.



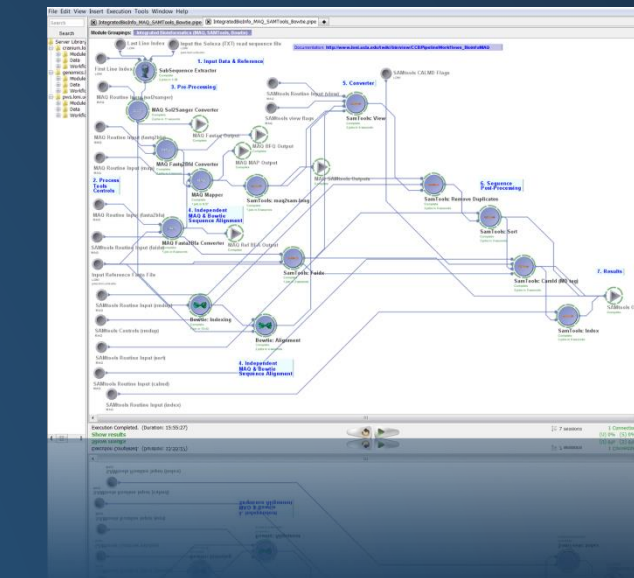
### Computational Library

Access hundreds of predefined imaging, genomics and end-to-end processing solutions, including data, modules and workflows that are automatically updated.



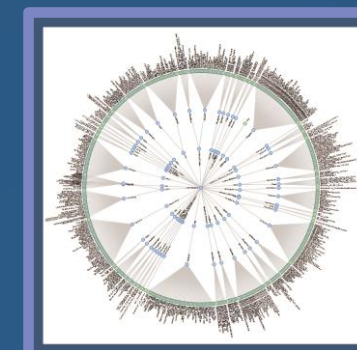
## Neuroimaging Genetics Studies

Genomics data analysis protocol processing large number of sequence data outputted by the Illumina sequencing pipeline. This protocol includes the following types of computational resources: Mapping and Assembly with Qualities (MAQ); Sequence Alignment and Mapping tools (SAMtools), Bowtie, etc.



Illumina NGS Sequence Analysis Pipeline

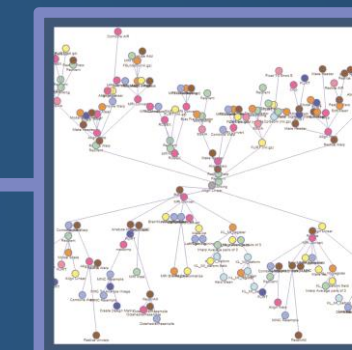
## Workflow Navigator



Flower

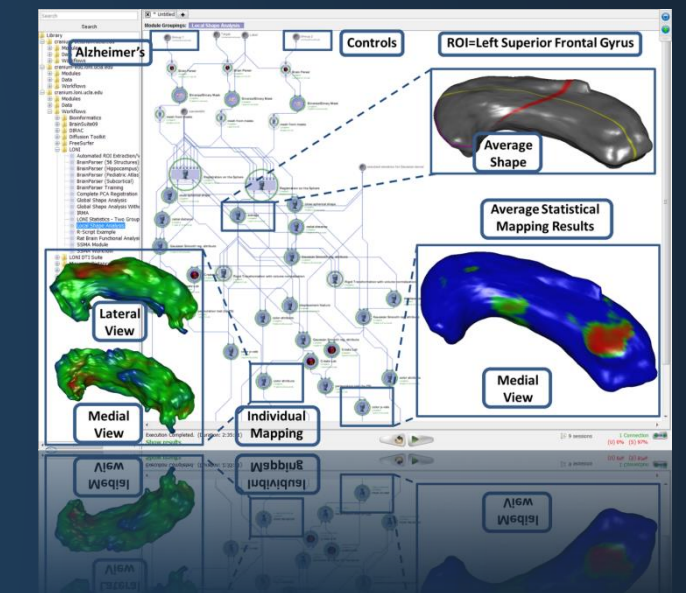


Tree



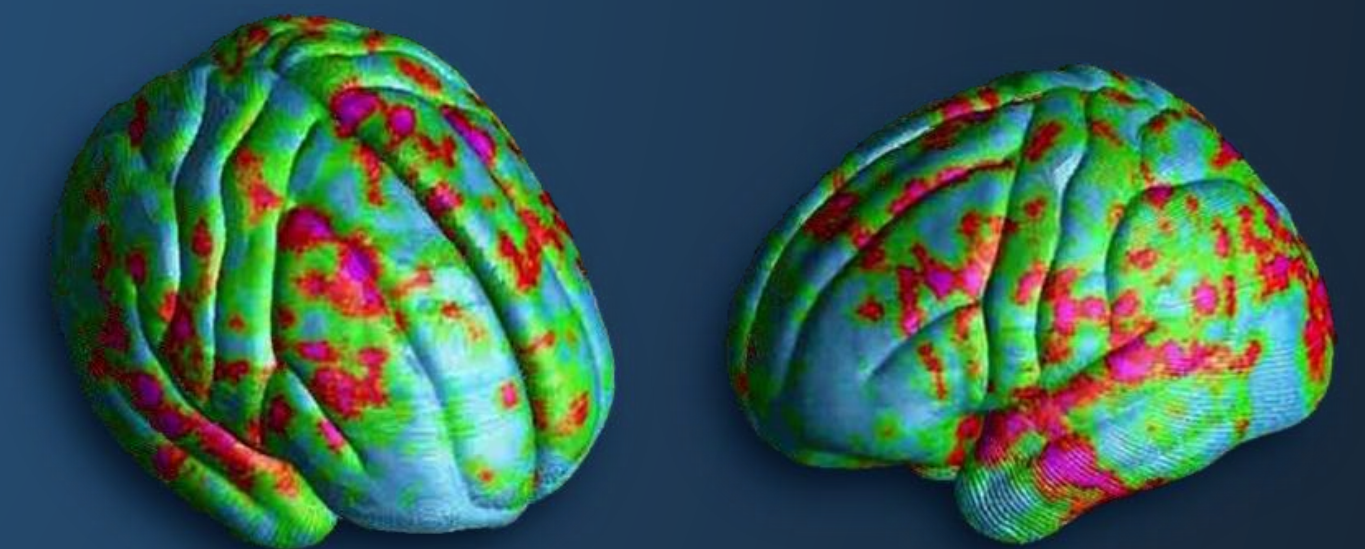
Sketcher

Local and Global Shape Analysis Pipeline Workflows



## Translational Studies

Cortical thickness decreases in first episode schizophrenia. Reductions in first-episode (FE) schizophrenia vs. healthy controls covarying for sex. Note patchy tertiary cortical distribution of significant thickness deficits would never be detected using conventional ROI-based morphometry.



## External Users

