



BIRN Pipelines for Visual Informatics and Computational Genomics

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<http://pipeline.loni.ucla.edu>

<http://wiki.birncommunity.org/x/wIBWAQ>

The Challenges

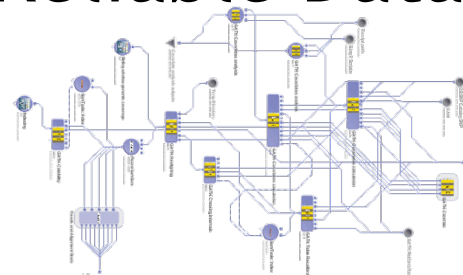
- **Massive Data** (single subject > 2GB)
- **Heterogeneous Software Tools** (platform, interface)
- **Distributed Hardware** (many clients, many servers)
- **Cross-Disciplinary Interactions** (biomed, math, eng, CS)
- **Detailed Data & Processing Protocol Provenance**
- **Design, Optimization, Execution, Validation & Distribution of Portable & Reliable Data Analyses**



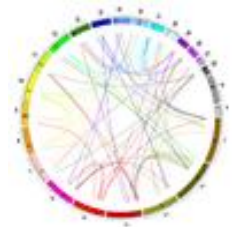
Data



Software & Hardware



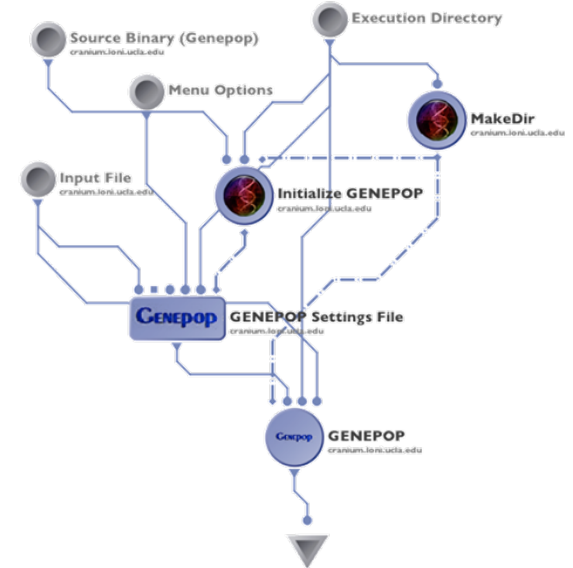
Pipeline Workflow Solutions



Results

User Community

- Non-Human Primate Research Centers (NHPRC)
 - Population genetics workflows
- James Knowles, USC
 - Imaging, genetics and pheno analysis in Schizo
- David Gutman, Emory
 - Geno-Phenotypic associations in brain trauma
- Scott K. Holland, CCHMC, Cincinnati
 - Pediatric Neuroimaging workflows
- www.MyExperiment.org users
 - Diverse arrays of imaging and genetics workflows
- A large number of anonymous users via Web-Start Interface (<http://pipeline.loni.ucla.edu/PWS>)

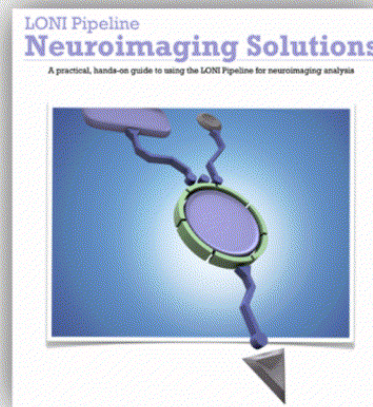


BIRN Approach

- Provide a distributed graphical interface for advanced sequence data processing, integration of diverse datasets, computational tools and web-services
- Promote community-based protocol validation, and open sharing of knowledge, tools and resources
- Utilize the LONI Pipeline, a Distributed graphical workflow environment, to provide:
 - a mechanism for interoperability of heterogeneous informatics and genomics tools
 - a complete study design, execution and validation infrastructure, supporting community result replication

Use-Cases

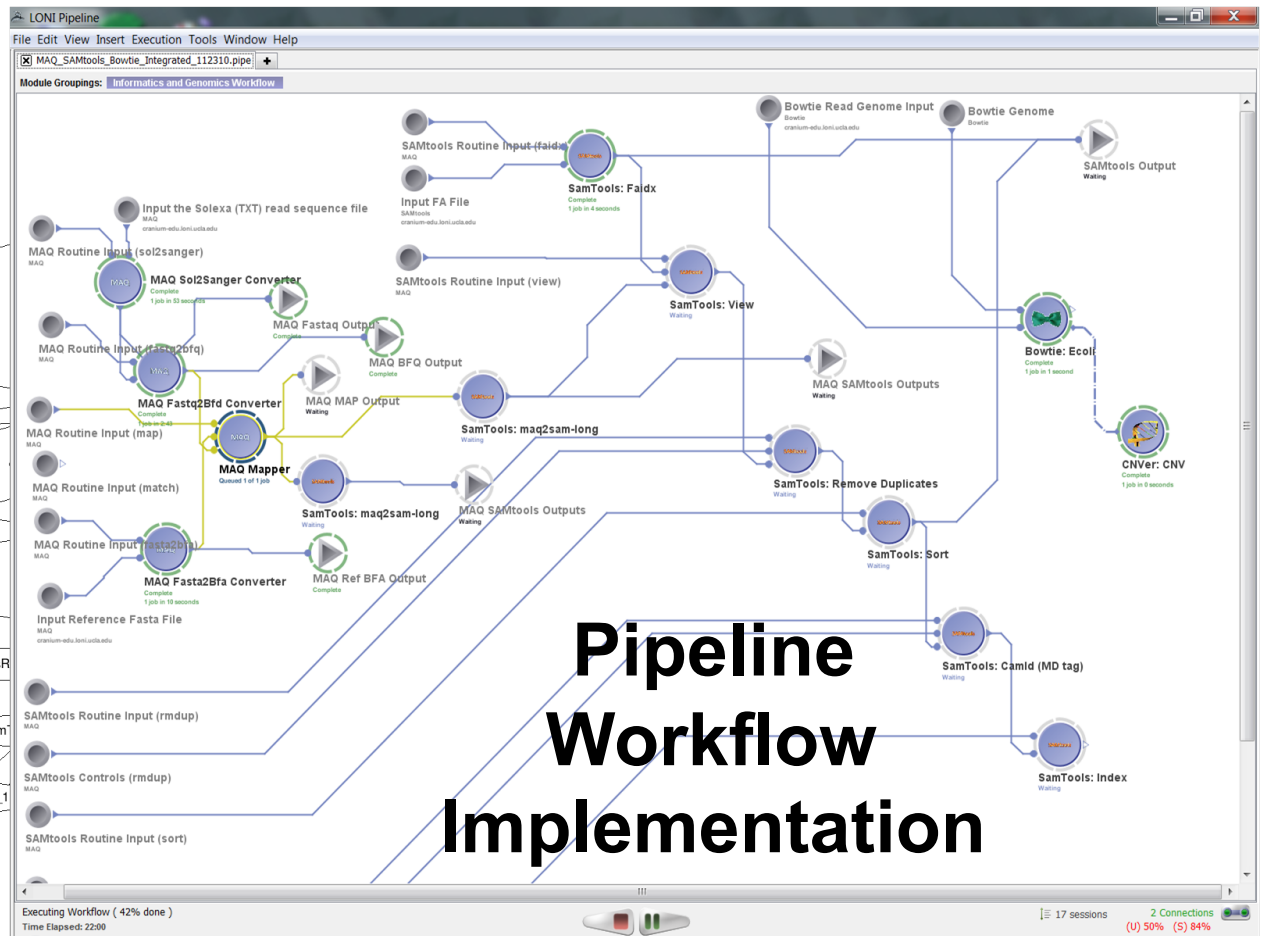
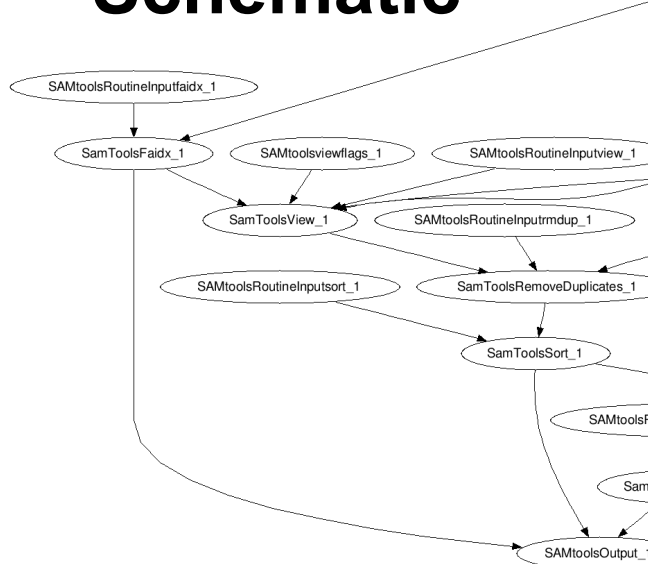
- Next Generation Sequence (NGS) analysis
- Neuroimaging Data Analysis
- Statistical Analysis of Biological Shape and Form
- Try these online: <http://pipeline.loni.ucla.edu/services/library-navigator/>



Next Generation Sequence (NGS) Analysis

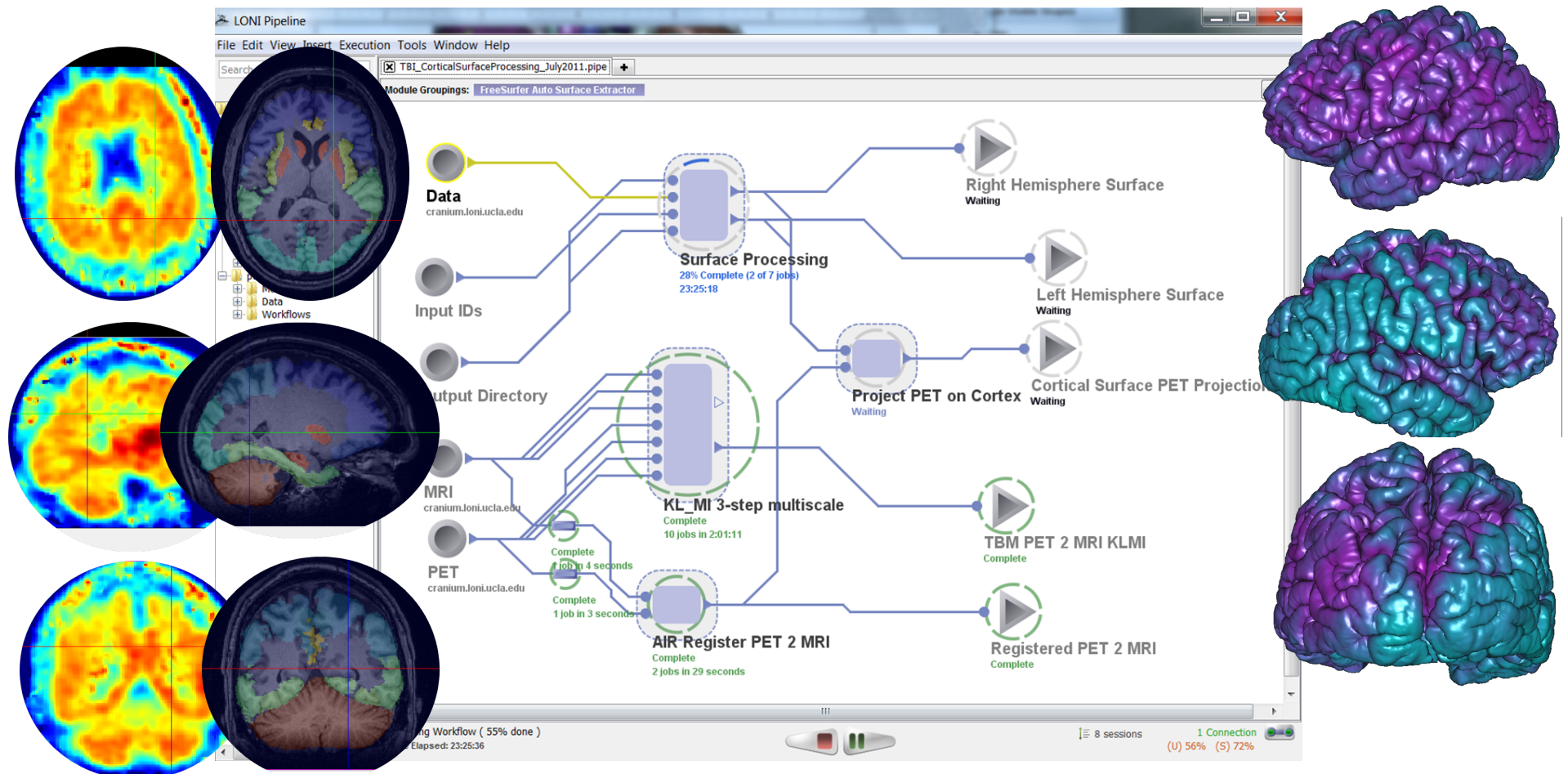
- Step I Analysis: Mapping and Assembly with Qualities (MAQ), SAMtools, Bowtie, CNVer

Workflow Schematic



Neuroimaging Data Analysis

- Cortical Mapping & Volumetric Analysis Pipeline



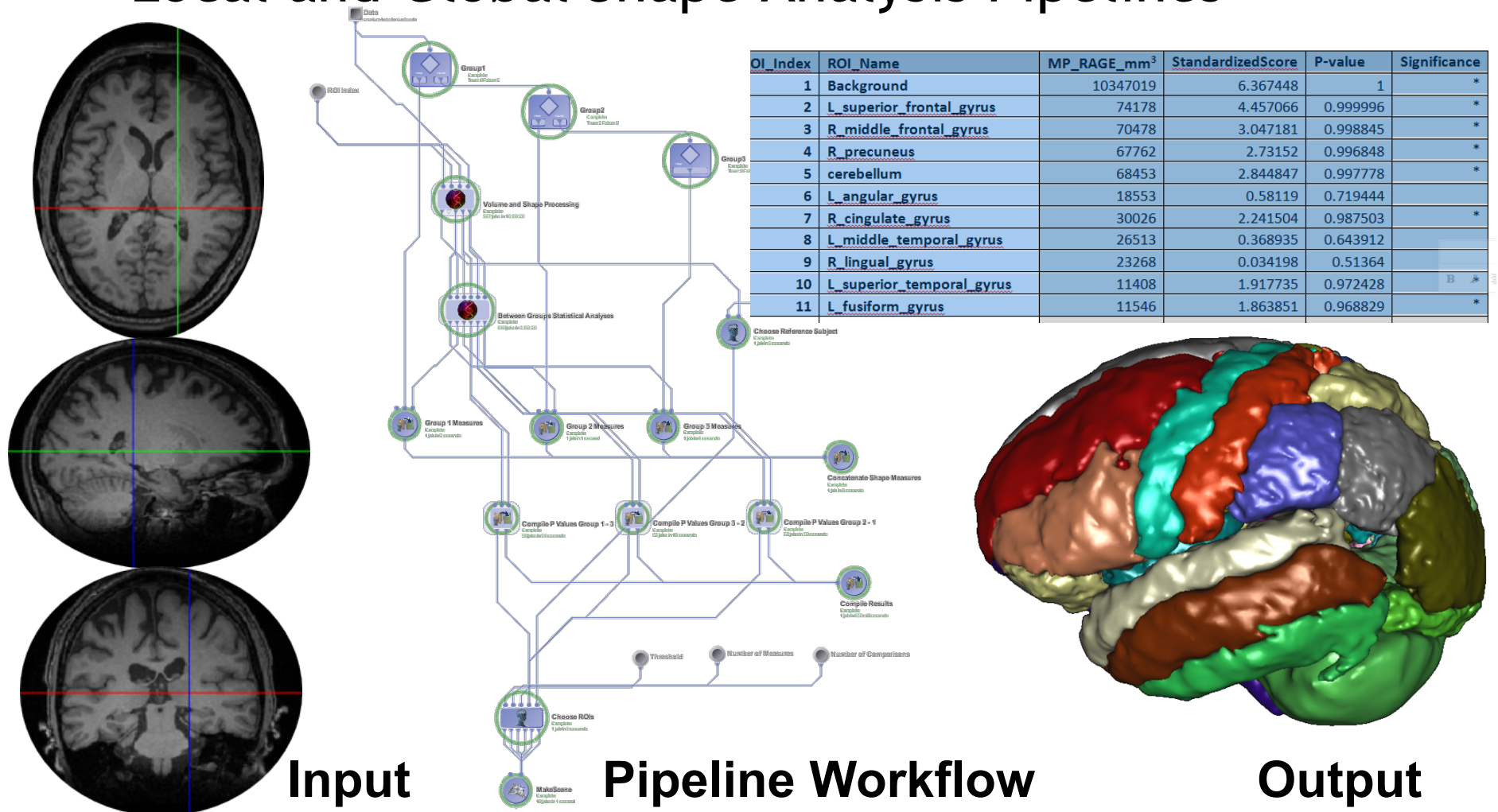
Input

Pipeline Workflow

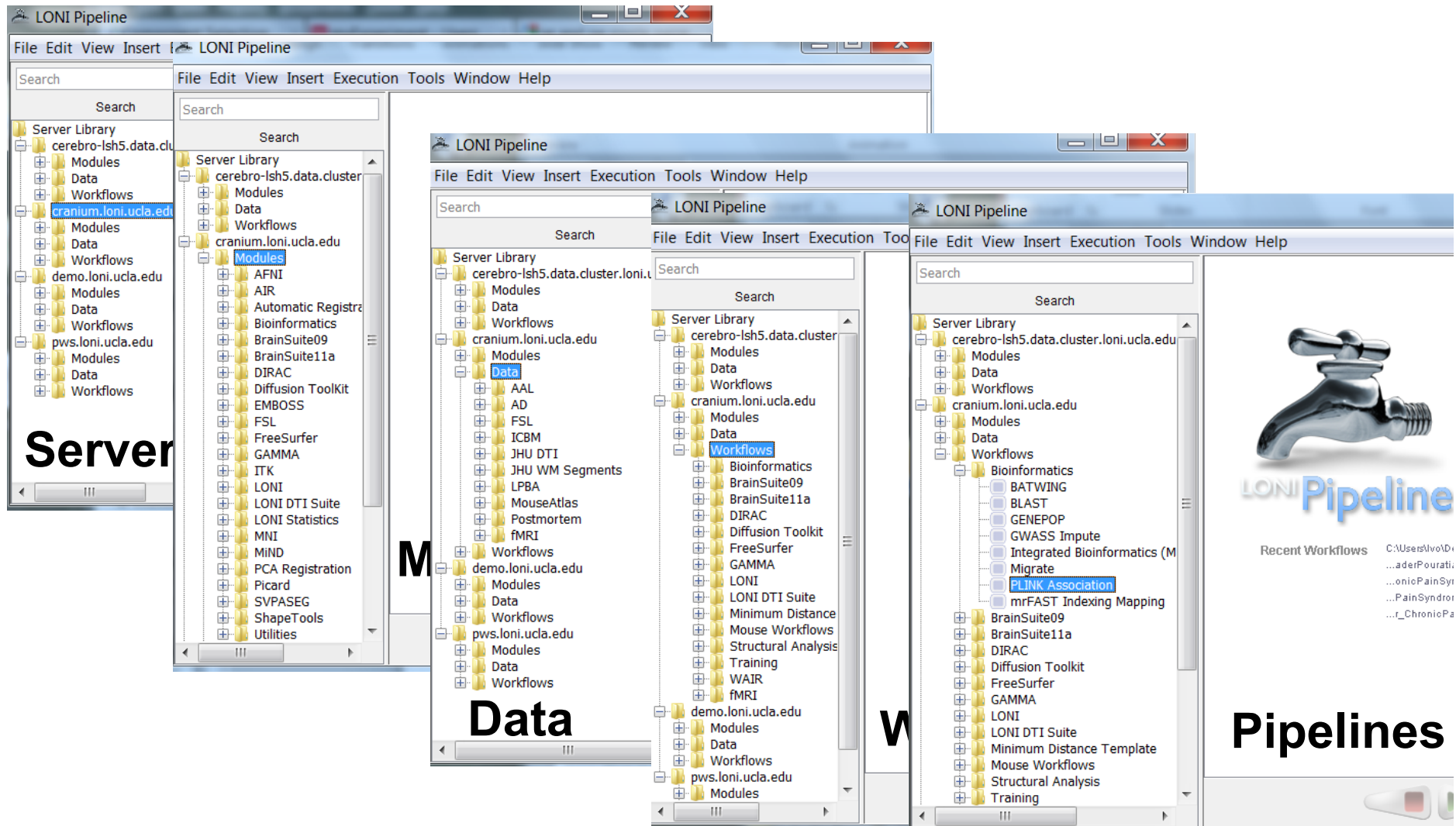
Output

Statistical Analysis of Biological Shape

- Local and Global Shape Analysis Pipelines

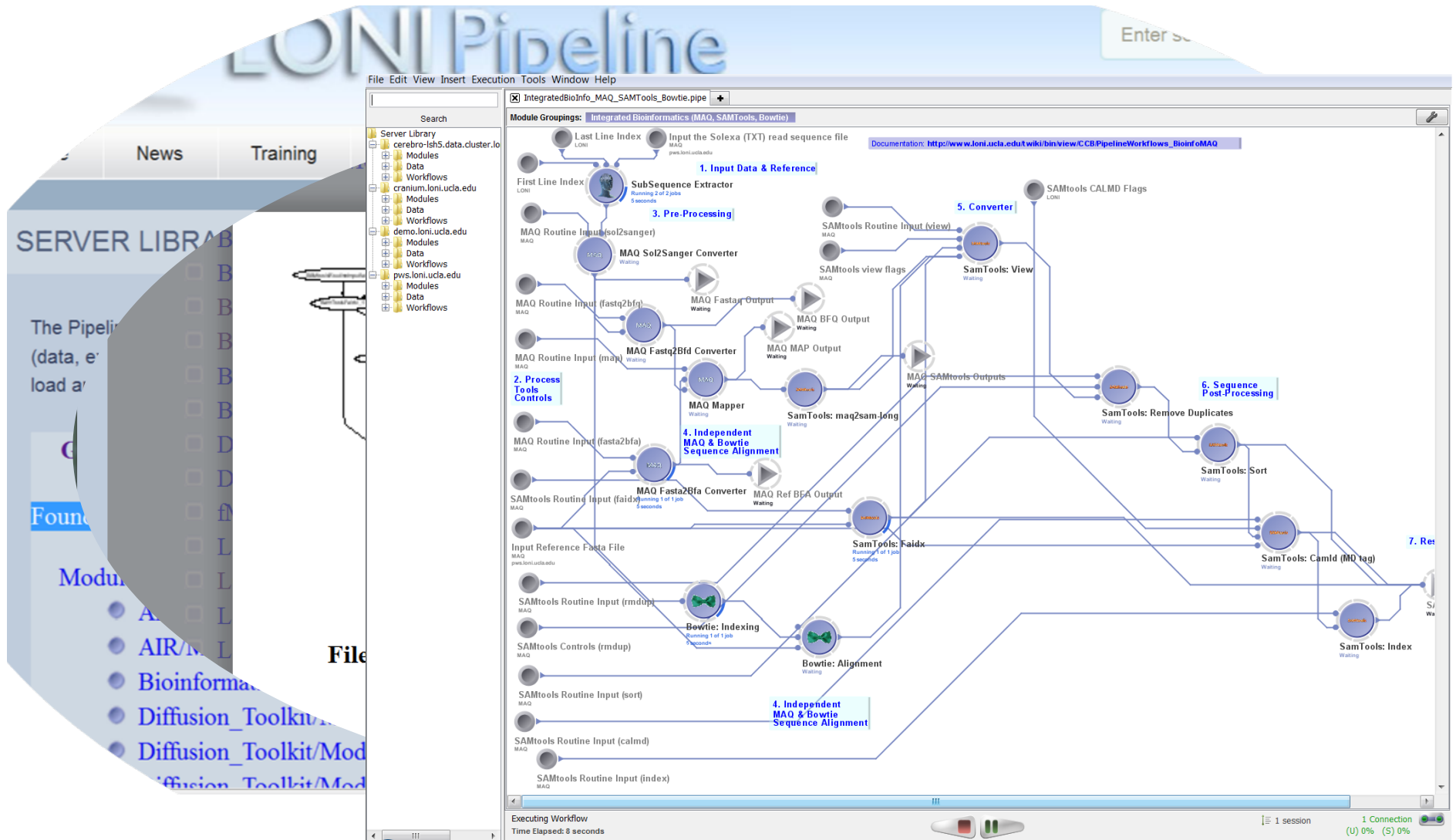


Pipeline Library of Solutions



Pipeline Web-Start (PWS)

<http://pipeline.loni.ucla.edu/PWS>



Community Pipeline Workflows

<http://www.MyExperiment.org/workflows>



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LONI Pipeline



EMBOSS-Matcher Pipeline Workflow (v1)

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Credits: Pipeline

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This page contains a number of bioinformatics workflows based on the advanced EMBOSS informatics package. This page describes as Pipeline modules several bioinformatics tools from the EMBOSS suite and demonstrates the

Acknowledgments

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 - CVRG
 - CIDR
 - Mouse Genome Informatics
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