



UCLA Brain Mapping Center

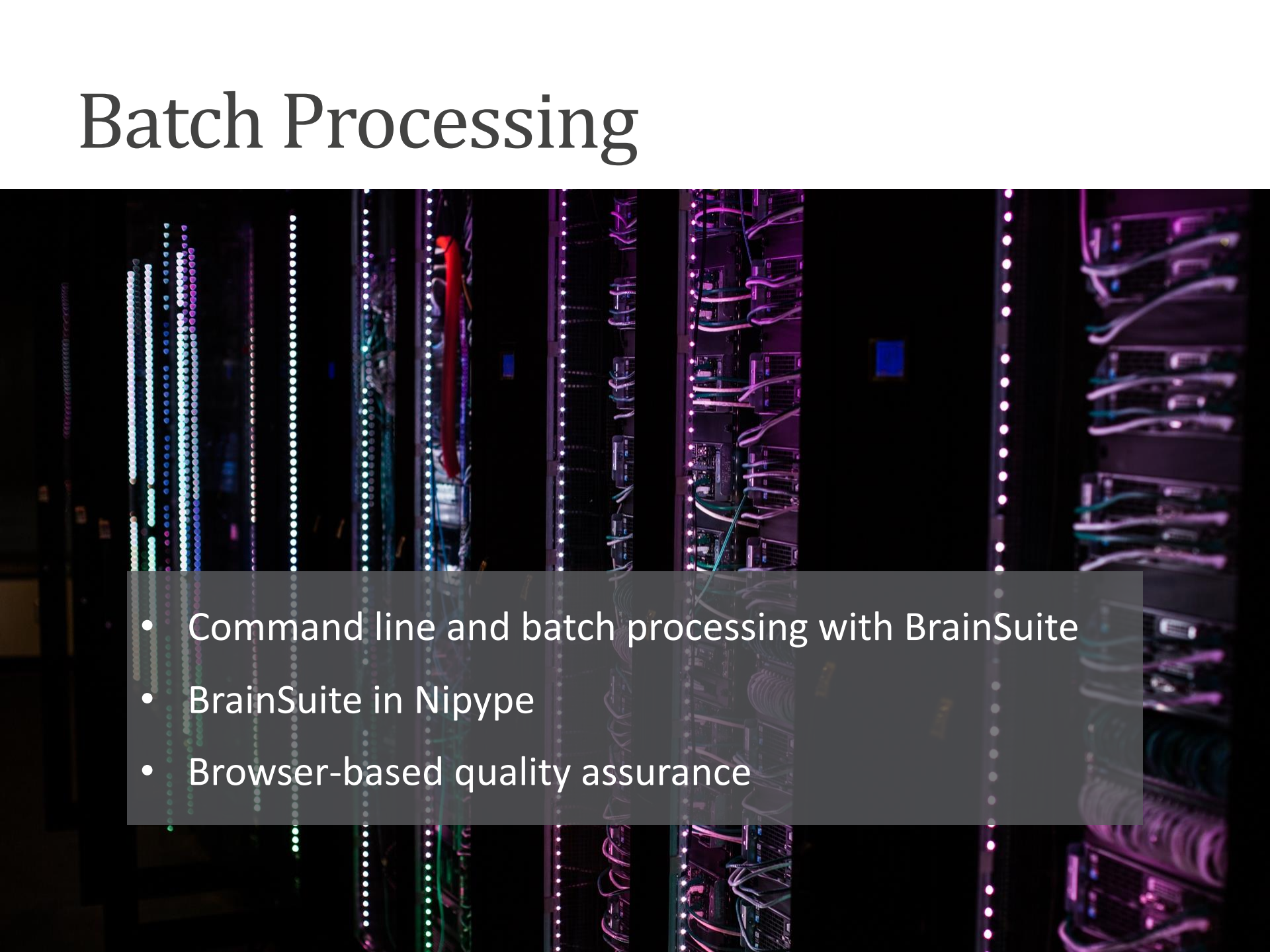
BrainSuite Batch Processing

Presented at the **2017 BrainSuite Training Workshop, Vancouver**

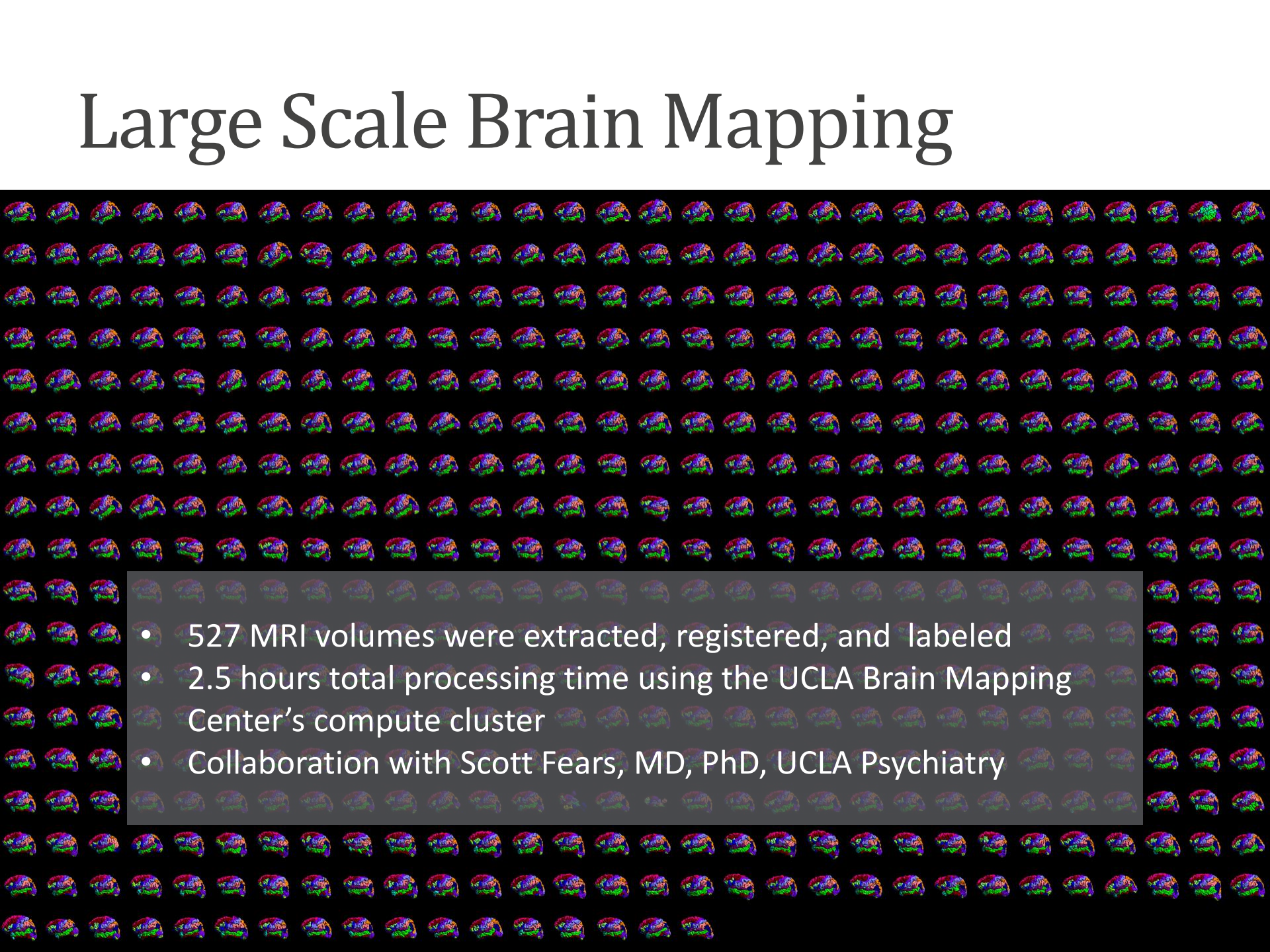
24 June 2017

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Batch Processing

- 
- Command line and batch processing with BrainSuite
 - BrainSuite in Nipype
 - Browser-based quality assurance

Large Scale Brain Mapping

- 
- 527 MRI volumes were extracted, registered, and labeled
 - 2.5 hours total processing time using the UCLA Brain Mapping Center's compute cluster
 - Collaboration with Scott Fears, MD, PhD, UCLA Psychiatry

Command Line Extraction

Cortical Surface Extraction can also be run from the command line

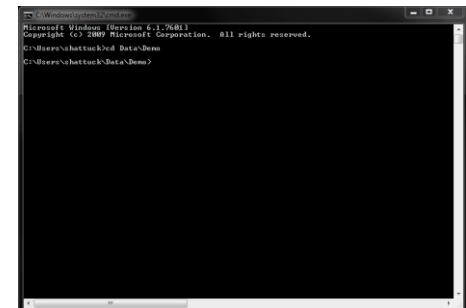
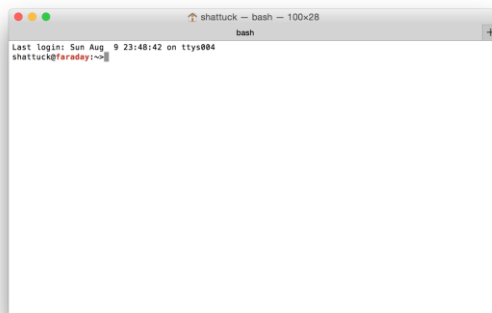
Mac (similar for Linux):

```
/Applications/BrainSuite17a/bin/cortical_extraction.sh 2523412.nii.gz
```

Windows:

```
"C:\Program Files\BrainSuite15cb10\bin\cortical_extraction.cmd" 2523412.nii.gz
```

- The scripts will automatically read a file named **BrainSuiteOptions** if it exists in the current directory.
- These commands are included as demo scripts in the extraction folder.
- Approximate run time on a 3.5GHz i7-3770k is **6 minutes**.



cortical_extraction.cmd

Part of the script:

```
@rem A few example variables that can be set. These settings match the ones in the GUI.
@rem use the VERBOSE flag to change the output option for all of the programs
@rem set VERBOSE=-v 1 --timer
@rem These values are set to match the defaults used in the GUI version of BrainSuite15b
set BSEOPTIONS=-n 3 -d 25 -s 0.64 -p --trim --auto
set BFCOPTIONS=-L 0.5 -U 1.5
@rem set PVCOPTIONS="-l 0.1"
set ATLAS=%BrainSuitePath%\atlas\brainsuite.icbm452.lpi.v08a.img
set ATLASLABELS=%BrainSuitePath%\atlas\brainsuite.icbm452.v15a.label.img
set ATLASSES=--atlas "%ATLAS%" --atlaslabels "%ATLASLABELS%"
@rem set CEREBROOPTIONS="--centroids"

@rem you can specify an options file in the directory from which you launch the script
@rem Read from the BrainSuiteOptions file if it exists: strip out any double quotes and set variables accordingly
if exist BrainSuiteOptions (
echo Reading BrainSuite extraction settings from BrainSuiteOptions file
for /f "tokens=*" %%a in (BrainSuiteOptions) do (
    set z=%%a
    set z=!z:"=!
    echo !z!
    set !z!
)
)
echo ---- Running BrainSuite Cortical Surface Extraction Sequence ----
%BrainSuiteBinDir%bse %VERBOSE% -i %1 -o %basename%.bse.%EXT% --mask %basename%.mask.%EXT% %BSEOPTIONS%
if %ERRORLEVEL% NEQ 0 ( echo cortical extraction halted because BSE failed to run. && exit /b 1 )
%BrainSuiteBinDir%bfc %VERBOSE% -i %basename%.bse.%EXT% -o %basename%.bfc.%EXT% %BFCOPTIONS% %BFCFILES%
if %ERRORLEVEL% NEQ 0 ( echo cortical extraction halted because BSE failed to run. && exit /b 1 )
%BrainSuiteBinDir%pvc %VERBOSE% -i %basename%.bfc.%EXT% -o %basename%.pvc.label.%EXT% -f %basename%.pvc.frac.%EXT% %PVCOPTIONS%
if %ERRORLEVEL% NEQ 0 ( echo cortical extraction halted because bse failed to run. && exit /b 1 )
```

cortical_extraction.sh

Part of the script:

```
# use the VERBOSE flag to change the output option for all of the programs
# VERBOSE="-v 1 --timer"
# These values are set to match the defaults used in the GUI version of BrainSuite17a
BSEOPTIONS="-n 3 -d 25 -s 0.64 -p --trim --auto"
BFCOPTIONS="-L 0.5 -U 1.5"
# PVCOPTIONS="-I 0.1"
ATLAS="{BrainSuiteDir}/atlas/brainsuite.icbm452.lpi.v08a.img"
ATLASLABELS="{BrainSuiteDir}/atlas/brainsuite.icbm452.v15a.label.img"
ATLASES="--atlas ${ATLAS} --atlaslabels ${ATLASLABELS}"
# using the centroids option can improve the initial alignment during the cerebrum labeling step
# CEREBROPTIONS="--centroids"

# you can specify an options file in the directory from which you launch the script
if [ -f BrainSuiteOptions ]; then source BrainSuiteOptions; fi;

echo ---- Running BrainSuite Cortical Surface Extraction Sequence ----
${BrainSuiteBin}bse $VERBOSE -i ${filename} -o ${basename}.bse.$EXT --mask ${basename}.mask.$EXT $BSEOPTIONS
if [ $? -ne 0 ]; then echo "cortical extraction halted because bse failed to run or return an error."; exit 1; fi;
${BrainSuiteBin}bfc $VERBOSE -i ${basename}.bse.$EXT -o ${basename}.bfc.$EXT $BFCOPTIONS $BFCFILES
if [ $? -ne 0 ]; then echo "cortical extraction halted because bfc failed to run or return an error."; exit 1; fi;
${BrainSuiteBin}pvc $VERBOSE -i ${basename}.bfc.$EXT -o ${basename}.pvc.label.$EXT -f ${basename}.pvc.frac.$EXT $PVCOPTIONS
if [ $? -ne 0 ]; then echo "cortical extraction halted because pvc failed to run or return an error."; exit 1; fi;
```

Command Line SVReg

Surface/Volume Registration can be run from the command line:

Mac (similar for Linux):

```
/Applications/BrainSuite17a/svreg/bin/svreg.sh 2523412 \  
    /Applications/BrainSuite17a/svreg/BCI-DNI_brain_atlas/BCI-DNI_brain
```

Windows:

```
"C:\Program Files\BrainSuite17a\svreg\bin\svreg.exe" 2523412.nii.gz ^  
    "C:\Program Files\BrainSuite17a\svreg\BCI-DNI_brain_atlas\BCI-DNI_brain"
```

n.b.: \ and ^ are line continuation characters for Mac/Linux and Windows, respectively.

- These commands are included as demo scripts in the extraction folder.
- Approximate run time on a 3.5GHz i7-3770k is **120 minutes**.

For additional usage flags, please see: <http://brainsuite.org/processing/svreg/usage/>

Command Line BDP

The BrainSuite Diffusion Pipeline is run from the command line:

Mac (similar for Linux):

```
/Applications/BrainSuite17a/bdp/bdp.sh 2523412.bfc.nii.gz -nii 2523412.dwi.nii.gz \  
--bvec 2523412.dwi.bvec --bal 2523412.dwi.bval --tensors --FRT --FRACT
```

Windows:

```
"C:\Program Files\BrainSuite17a\bdp\bdp.exe" 2523412.bfc.nii.gz -nii 2523412.dwi.nii.gz ^  
--bvec 2523412.dwi.bvec --bval 2523412.dwi.bval --tensors --FRT --FRACT
```

n.b.: \ and ^ are line continuation characters for Mac/Linux and Windows, respectively.

- These commands are included as demo scripts in the DWI folder.
- Approximate run time on a 3.5GHz i7-3770k is **22 minutes**.

For additional command line options, please see:

<http://brainsuite.org/processing/diffusion/flags/>

Command Line Thickness

Cortical Surface Thickness is run from the command line:

Mac (similar for Linux):

```
/Applications/BrainSuite17a/svreg/bin/thicknessPVC.sh 2523412
```

Windows:

```
"C:\Program Files\BrainSuite17a\svreg\bin\thicknessPVC.exe" 2523412
```

- These commands are included as demo scripts in the extraction folder.
- Approximate run time on an i7-3770k is **20 minutes**.

Running on a Grid Engine

```
#!/bin/bash
#$ -S /bin/bash
#$ -o logs -j y
#$ -N CSE17a
#$ -V
#$ -cwd

export TMPDIR=/ifs/tmp/
export TMP=/ifs/tmp/
export LC_ALL="C"

if [ -z "$SGE_TASK_ID" ] || [ "$SGE_TASK_ID" == "undefined" ]; then
  SubjID=$1
  echo SubjID="$SubjID"
else
  SubjID=`sed "${SGE_TASK_ID}p;d" $1`
fi;

Extract=/opt/BrainSuite17a/bin/cortical_extraction.sh
cd ${SubjID}
$Extract ${SubjID}
```

Submit subjects individually or put inside of a for loop

```
qsub extraction.sh SubjID
```

or use a task array

```
qsub -t1:100 extraction.sh SubjIDList.txt
```

Running on a Grid Engine

```
#!/bin/bash
#$ -S /bin/bash
#$ -o logs -j y
#$ -N SVReg17a
#$ -V
#$ -cwd
#$ -l h_vmem=23G

export TMPDIR=/ifs/tmp/
export TMP=/ifs/tmp/
export LC_ALL="C"

if [ -z "$SGE_TASK_ID" ] || [ "$SGE_TASK_ID" == "undefined" ]; then
SubjID=$1
echo SubjID="$SubjID"
else
SubjID=`sed "${SGE_TASK_ID}p;d" $1`
fi;

SVREG=/opt/BrainSuite17a/svreg/bin/svreg.sh
ATLAS=/opt/BrainSuite17a/svreg/BrainSuiteAtlas1/mri

cd ${SubjID}
$SVREG ${SubjID} -k
```

- May need to add special settings to enable more memory
- May need to add flags for tmp space
- May need to add other flags to deal with Matlab requirements

Running on a Grid Engine

```
#!/bin/bash
#$ -S /bin/bash
#$ -o logs -j y
#$ -N Thickness17a
#$ -V
#$ -cwd
#$ -l h_vmem=23G

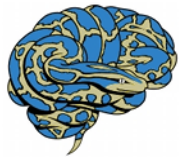
export TMPDIR=/ifs/tmp/
export TMP=/ifs/tmp/
export LC_ALL="C"

if [ -z "$SGE_TASK_ID" ] || [ "$SGE_TASK_ID" == "undefined" ]; then
  SubjID=$1
  echo SubjID="$SubjID"
else
  SubjID=`sed "${SGE_TASK_ID}p;d" $1`
fi;

THICK=/opt/BrainSuite17a/svreg/bin/thicknessPVC.sh
ATLAS=/opt/BrainSuite17a/svreg/BrainSuiteAtlas1/mri

cd ${SubjID}
$THICK ${SubjID} -k
```

BrainSuite & Nipype



Nipype:
Neuroimaging in Python
Pipelines and Interfaces

<http://brainsuite.org/nipype>

- Interfaces for BrainSuite are included in Nipype.
 - Cortical extraction
 - SVReg
 - BDP
 - Cortical thickness
- We have also developed workflows for the BrainSuite processing streams that can be performed with Nipype.
 - Can be run on a local machine, grid engine, or Amazon Web Services
 - Workflows can be run in parallel
- Provides interoperability for to connect to other software packages.

Nipype / BrainSuite Tutorial

- Online tutorial using Jupyter notebook
 - <http://brainsuite.org/nipype-interactive-tutorial/>
 - <http://nbviewer.jupyter.org/url/brainsuite.org/code/BrainSuiteNipypeParallel.ipynb>
- With full installation, can run BrainSuite workflow through the web-browser



JUPYTER

FAQ



Nipype Tutorial: Cortical Surface Extraction, BDP, SVReg in Parallel

Welcome to our interactive Nipype tutorial. Below you will find a mix of code and explanatory text. If you are viewing this from an active Jupyter Notebook server, you can execute our code as you read through our tutorial. If you are unfamiliar with Jupyter Notebook, you can learn the basics [here](#).

Or, from the toolbar, go to `Help | User | Interface Tour`.

Here are some essentials:

- The current cell is surrounded by a colored border
- Runnable code is contained in a greyed box, denoted by `In [ # ] :` next to the cell
 - To execute the code in the current cell, use `Shift+Enter`
 - `!` denotes a bash command that will be executed. All bash commands have been commented out, so you may choose whether or not to execute them. We advise that you read each bash command before choosing to execute them. To execute the commands, uncomment the command, then use `Shift+Enter` to run the bash command.
- Pressing `Shift+Enter` on a text cell simply moves you to the cell below

Nipype / BrainSuite Tutorial

Checking your installation

First, we'll check that all of BrainSuite's executables have been added to your system's path variable.

If you have not done so already, first install BrainSuite, by following the instructions on our [installation page](#). Be sure to follow the instructions for installing the required MATLAB Compiler Runtime, which is required for SVReg, BDP and ThicknessPVC.

The following python code will ensure that your system's path variable has been set up properly. In particular, the following paths must be added (replace `your_path` with the path to your BrainSuite directory):

- `/your_path/BrainSuite16a1/bin/`
- `/your_path/BrainSuite16a1svreg/bin/`
- `/your_path/BrainSuite16a1/bdp/`

Run the cell below and follow the instructions printed out.

(Note that bse is just one of many steps in CSE. Since the rest of CSE is contained in the same folder as bse, it is sufficient to ensure that bse can be called properly)

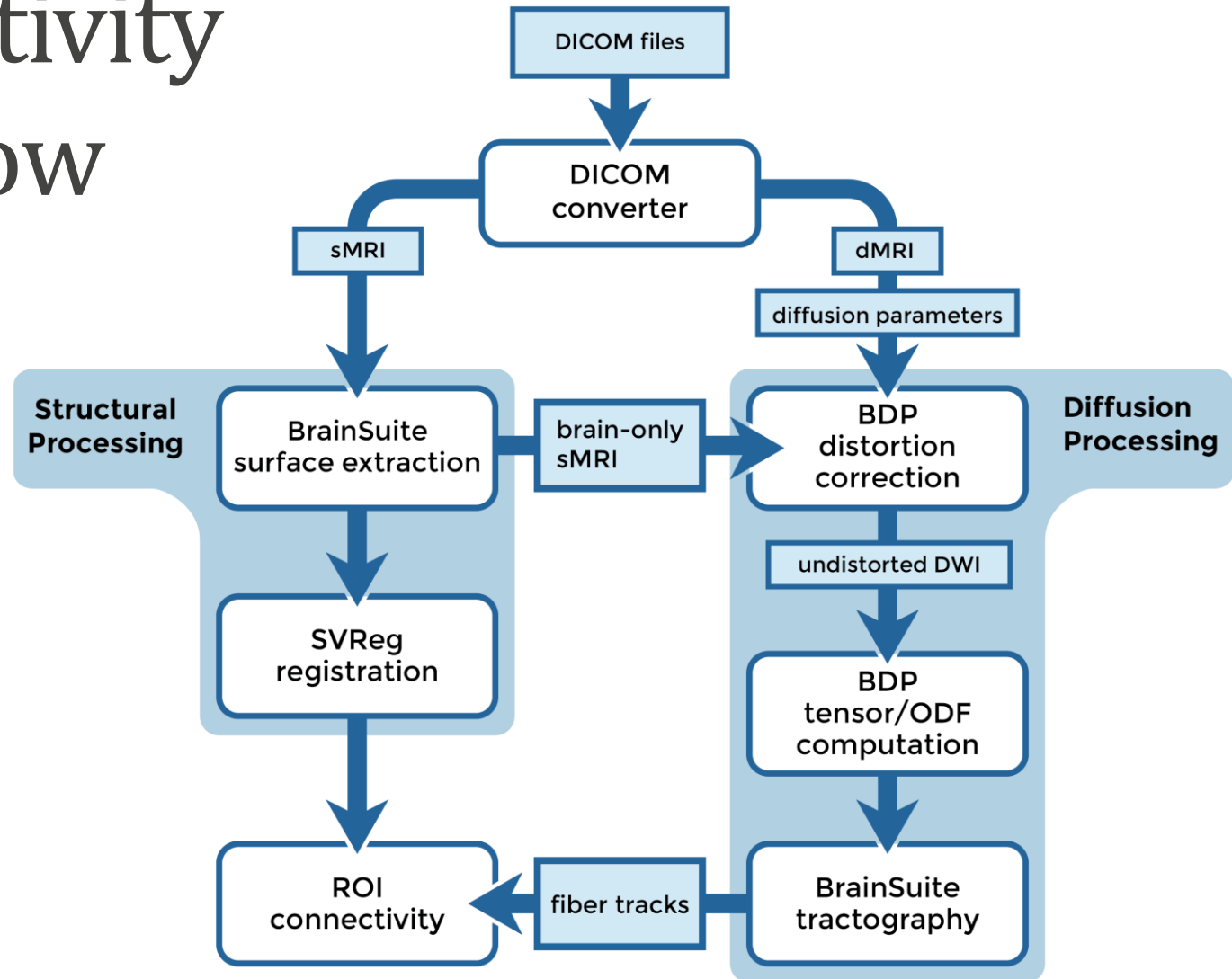
```
In [1]: from __future__ import unicode_literals, print_function
        from builtins import str

        from distutils.spawn import find_executable
        print('Message to user:')
        if(find_executable('bse') and find_executable('svreg.sh') and find_executable('bdp.sh')):
            print('Your system path has been set up correctly. Continue on with the tutorial.')
        else:
            print('Your system path has not been set up correctly.')
            print('Please add the above paths to your system path variable and restart the kernel for this tutorial.')
            print('Edit your ~/.bashrc file, and add the following line, replacing your_path with the path to BrainSuite16a1:\n')
            print('export PATH=$PATH:/your_path/BrainSuite16a1/svreg/bin:/your_path/BrainSuite16a1/bdp:/your_path/BrainSuite16a1/b
```

You must also have Nipype and its dependencies installed. See [Nipype's installation page](#) for more information. Another good resource for Nipype installation is the [Nipype Beginner's Guide](#).

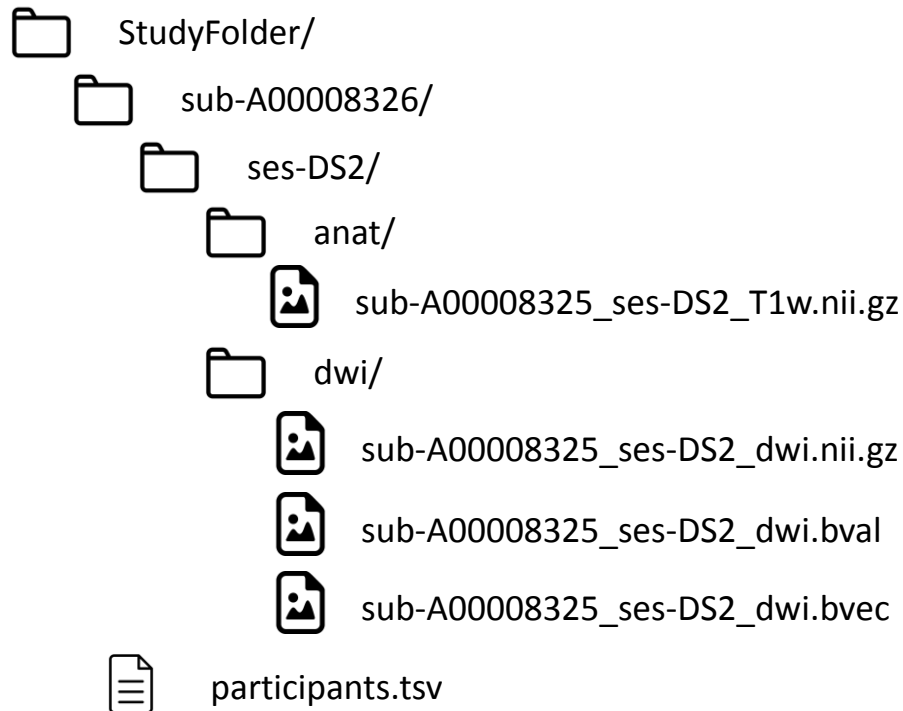
<http://nbviewer.jupyter.org/url/brainsuite.org/code/BrainSuiteNipypeParallel.ipynb>

BrainSuite Connectivity Workflow



Brain Imaging Data Structure (BIDS)

- We are currently developing support for BIDS, a standardized way of organizing and describing MRI datasets
- Example input data structure for BrainSuite:



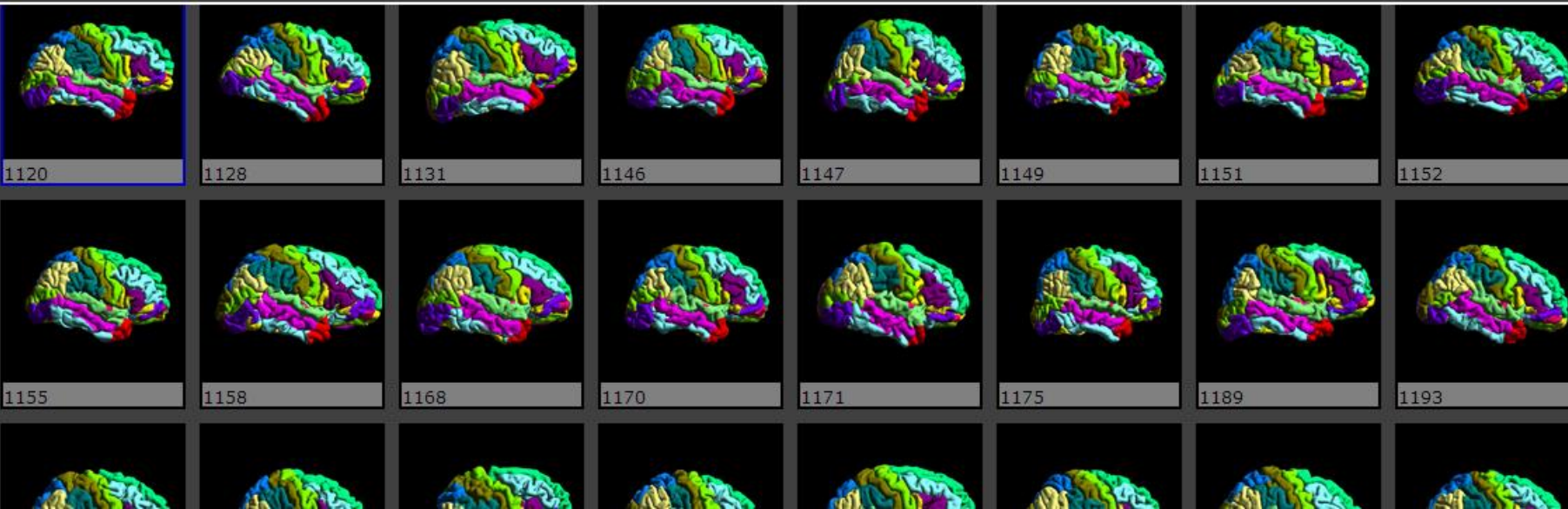
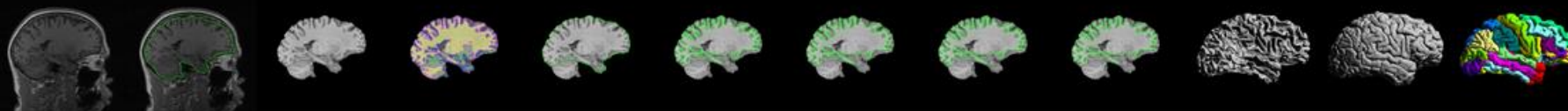
Quality Control

loaded subject list

showing subjects 1-100 of 100 subjects after surface labeling at size 128

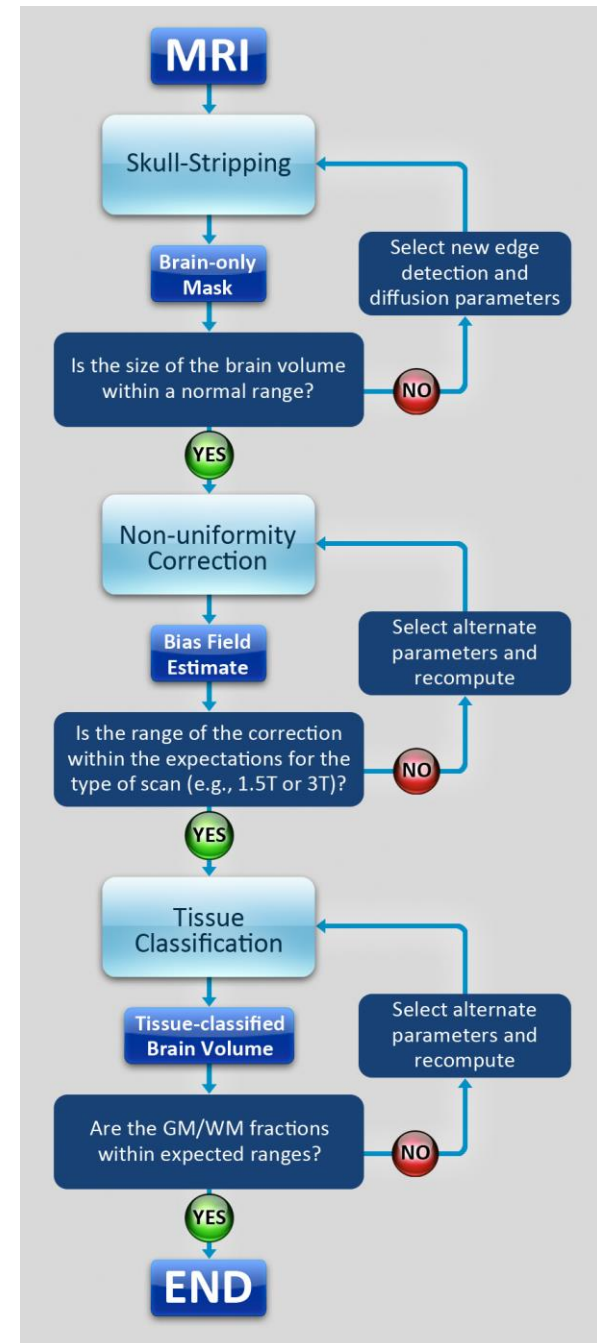
thumbnail size
first subject
number of subjects
show stage

showing subject 33 (1120)

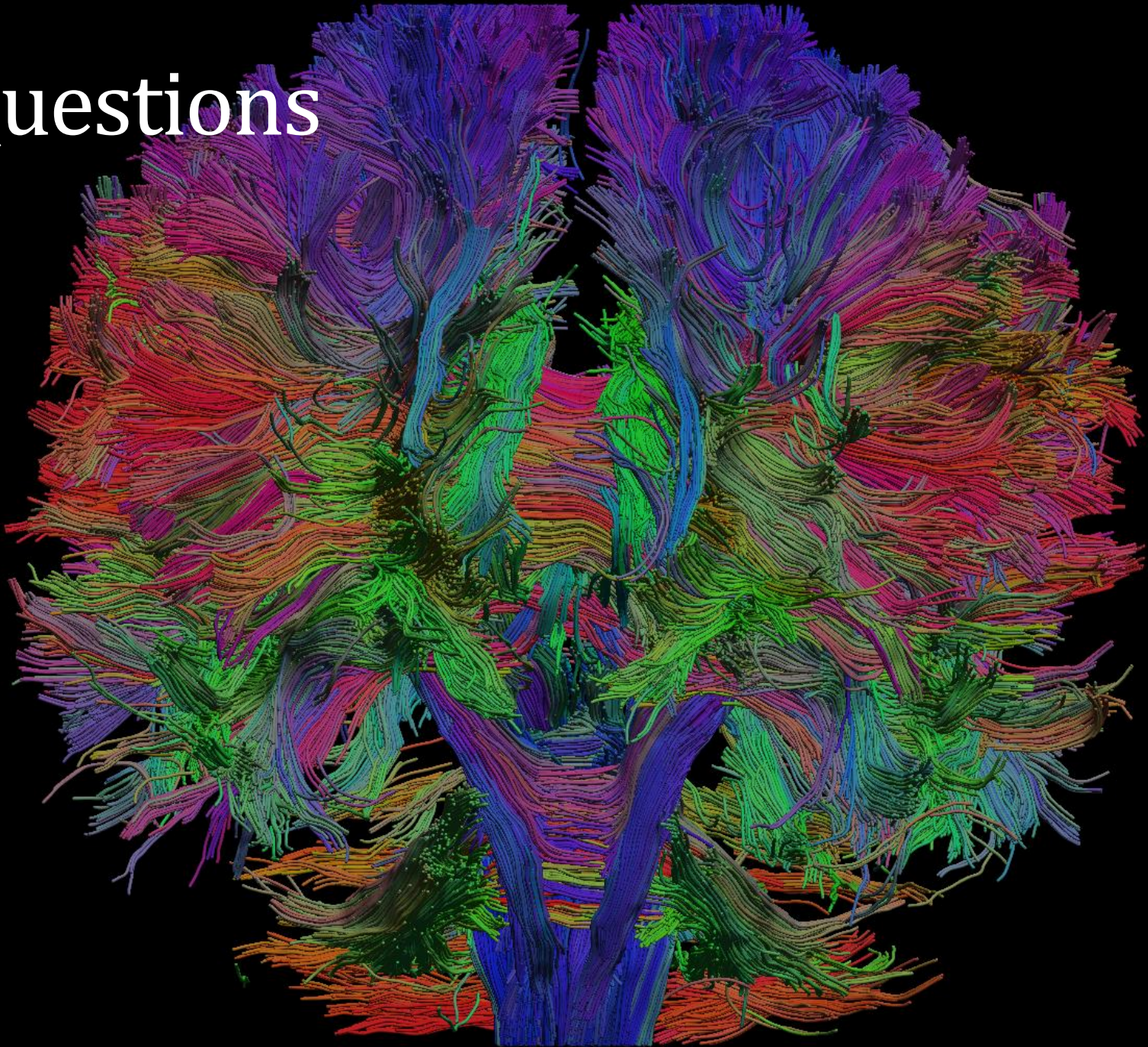


Error Detection

- We are developing interfaces that facilitate identification of errors in the processing chain.
 - Web-based reports
 - Software interfaces that allow errors to be corrected and the processing continued
- Quality assurance
 - Automatically identify potential failures based on measures.
 - For example, is the total brain volume within a normal range?

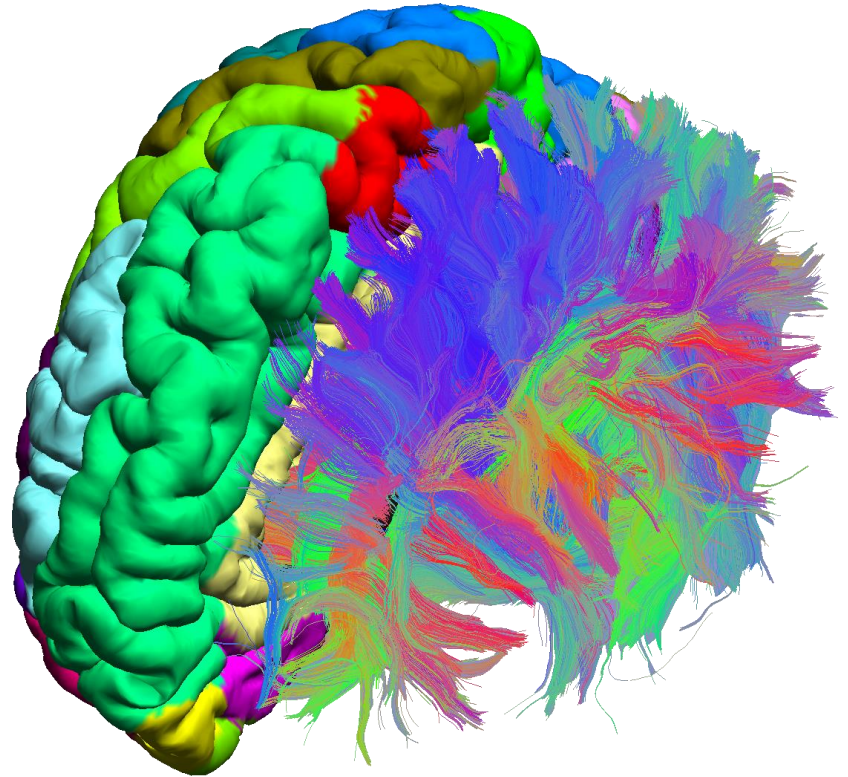


Questions



For More Information

- <http://brainsuite.org>
 - Tutorials
 - Videos
 - Slides
 - Downloads
 - Additional tools & utilities
- Questions:
 - email us:
support@brainsuite.org
 - Ask on forums:
<http://forums.brainsuite.org/>



Visit us at OHBM

#	Title	Poster Time
1650	<u>BCI-DNI^f Brain Atlas: A Volumetric and Surface Atlas Delineated by Anatomical and Functional MRI (Joshi, et al.)</u>	Mon, June 26 12:45pm - 2:45pm
1272	<u>The Anemic Brain: Hemoglobin Level Predicts Brain Volume in Watershed areas and Cognitive function (Choi, et al.)</u>	Mon, June 26 12:45pm - 2:45pm
1594	<u>The Joint Effect of Aging and HIV Infection on Integrity of the Corpus Callosum (Kuhn, et al.)</u>	Mon, June 26 12:45pm - 2:45pm
1868	<u>Global PDF-Based Non-Local Means Filtering of Resting fMRI Data (Li, et al.)</u>	Mon, June 26 12:45pm - 2:45pm
3966	<u>Synchronization of fMRI Data Across Subjects and Scans by Orthogonal Transformation (Joshi, et al.)</u> Oral Session: Connectivity Methods and Analysis Wednesday, June 28, 2017: 10:55 AM - 11:08 AM	Wed, June 28, 2017 12:45pm - 2:45pm
4102	<u>Reproducible TBM and ROI Analyses Using the BrainSuite Statistics Toolbox (BSS) (Joshi, et al.)</u>	Wed, June 28, 2017 12:45pm - 2:45pm