DIPA:
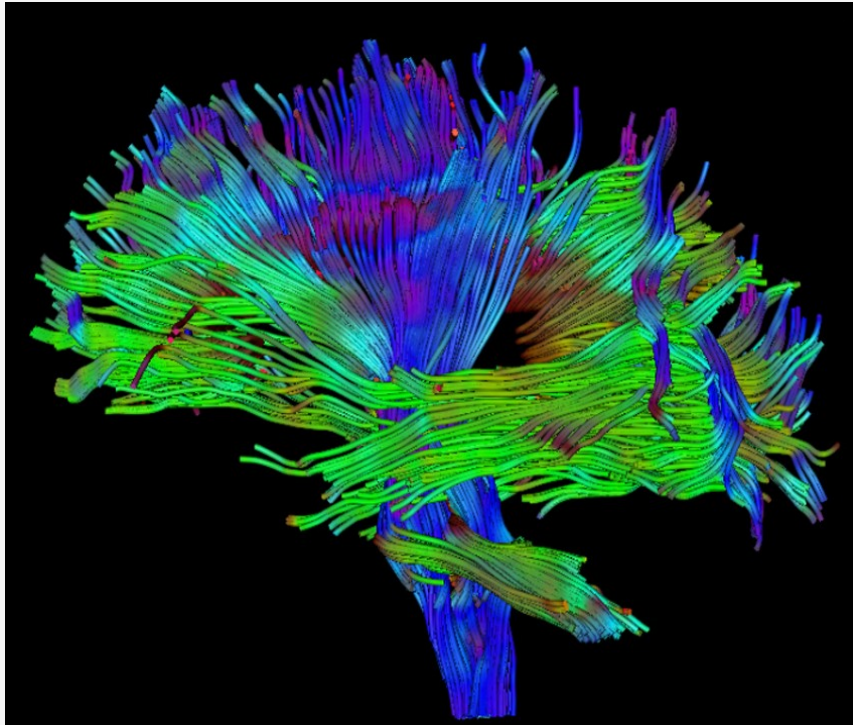# Diffusion Image Processing and Analysis

Andrew Schoen

Center for Healthy Minds at the Waisman Center

University of Wisconsin - Madison
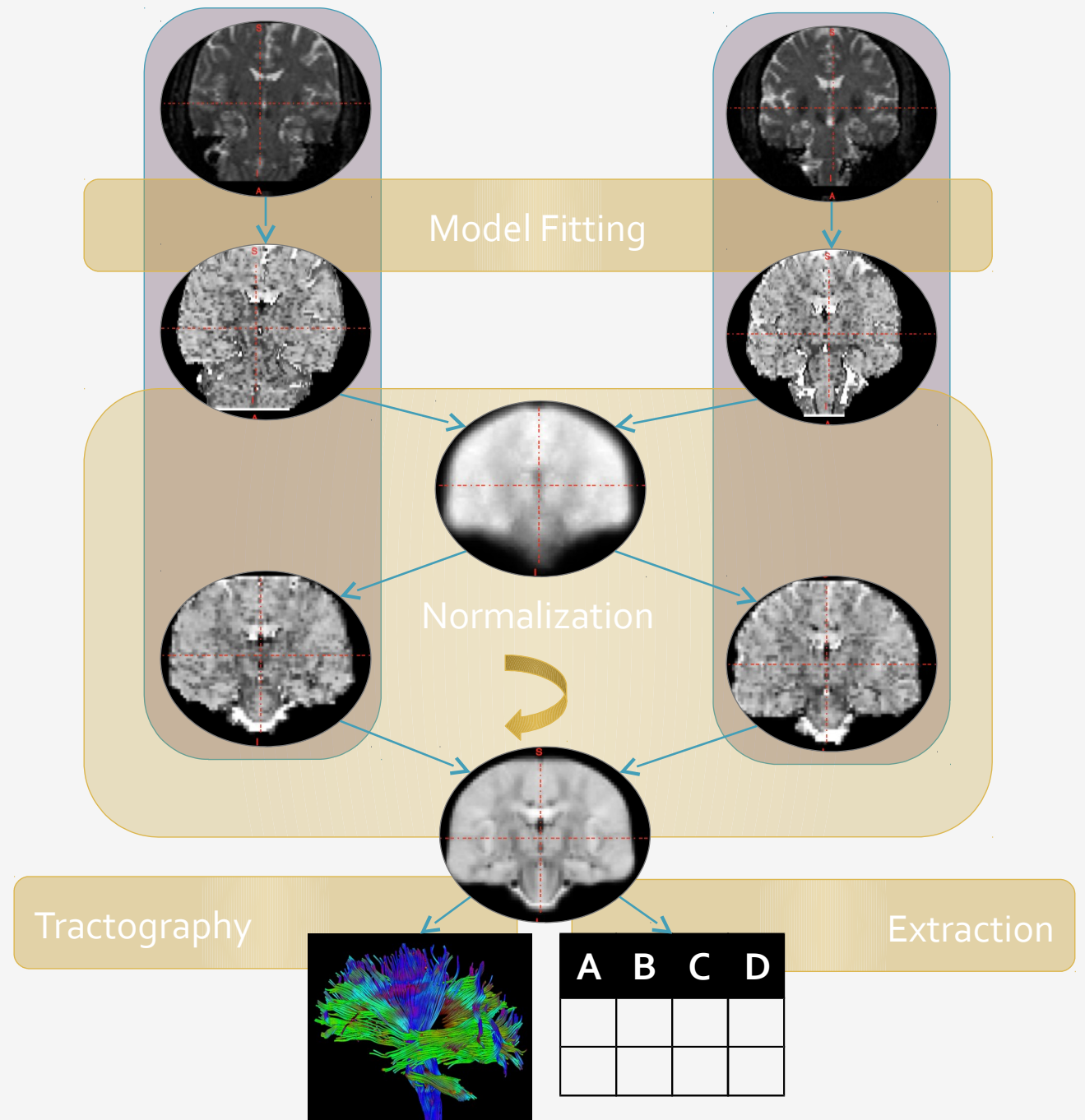
What do we do,
What this looks like:

- Waisman Center
- Center for Healthy Minds / MIDUS Study
- Wide variety of assessments

- dMRI
  - Diffusion of water molecules in the brain
  - Used to model pathways throughout the brain
  - Difficulties
- Highly susceptible to noise, artifact, motion
- Multiple levels of processing, many options
- Poorly streamlined, poorly standardized processing

Workflow

An extreme simplification of our workflow, with two participants' data.

Model Fitting

Normalization

Tractography

Extraction

A B C D

Gotchas with moving to HTCondor

- Sometimes slow rates of data collection

- Nature of individual studies determines workflow.

- Exchangeability of different processing steps

- Complicated code distributions

- Iterative processing

- Data Quality

- Accessibility

The Start of DIPA

- DTITK -> SetupCondorDTITK

- Very simple condorization of a linear, iterative processing step

- I tore apart an existing package.

- Generated a DAG.

- Only worked on shared file systems

- DIPA

  – Let's get it working with transfers

  – Rinse and repeat:

- Hey, this works pretty well. Let's add things before and after.

- Wait, this is getting a bit too complicated. Improve code base to make it easier.

```
Diffusion Image Processing and Analysis, Version 0.3 BETA.

Usage:
 DIPA <command>... [options] (--input_file=<path> | -i=<path>) (--project_dir=<path> | -p=<path>)
 DIPA <command>... [options] (--config=<path> | -c=<path>)
 DIPA <command> (-a | --additionalinfo)

Commands:
 OrientCheck  Output PNG images of the tensor orientations.
 Correct      Corrects an image for eddy currents.
 Fit          Fits a model from a DWI image.
 Normalize    Normalizes a set of images to an unbiased estimate of the mean image, or a given template.
 ROI          Extracts atlas/tractography-driven values from each subject, and assembles into a spreadsheet.
 GLM          Run a General Linear Model on the sample.

Arguments:
 <command>             The command(s) you want to run.
                       Run DIPA <command> --additionalinfo for more information about a specific command

Options:
 -h --help                        Show this screen.
 -v --version                     Show the current version.
 -a --additionalinfo              Get information on a given command.
 --credits                        Show credits.
 --verbosity                      Verbosity of logging. Show anything equal or greater than that
                                  specified in list (Log, Alert, Warning, Error). [default: Log]
 -k --keep                        Keep all intermediate files. [default: False]
 -e --execute                     Automatically execute when preparations complete. [default: False]
 -l --linear                      Do not use HTCondor, and instead run everything linearly. Not Advised
                                  (NOT IMPLEMENTED). [default: False]
 -r --remote                      Run processing remotely, by transferring gzips of the required files
```

DIPA -h

DIPA Correct -a

```
More Information: Correct

Description: Corrects an image for eddy currents.

Dependencies: OrientCheck

Options:
 --correcttype=<type>  The type of correction to be performed. [default: EDDY]

Input Specification:
                                        DESCRIPTION ISFILE ISREQUIRED  \
COLUMN
ID                                         Scan ID  False       True
DWI                    DWI File (--imain in eddy_openmp)   True       True
MASK                   Image Mask (--mask in eddy_openmp)  True       True
INDEX                  Index File (--index in eddy_openmp) True       True
ACQPARAMS  Acq Params File (--acqp in eddy_openmp)         True       True
BVEC                   BVEC File (--bvec in eddy_openmp)   True       True
BVAL                   BVAL File (--bval in eddy_openmp)   True       True


                       REMOVEIF
COLUMN
ID                         ☐
DWI        [OrientCheck]
MASK                       ☐
INDEX                      ☐
ACQPARAMS                  ☐
BVEC       [OrientCheck]
BVAL       [OrientCheck]


Additional Information:
EDDY: Utilizes FSL's eddy_openmp to correct for eddy currents.
No other eddy current correction types available at this time.
```

DIPA Structure

You provide the "Component", add it to a json file, and DIPA handles the rest.

- Subclass "Component", and overwrite necessary methods.
  - setComponentConfiguration(self, inputs, PreviousConfig, config)
  - setComponentInputSpecFile(self, config)
  - setComponentMatrices(self, config)
  - setComponentDirectories(self, config)
  - setComponentSourceFileManifest(self, config)
  - setComponentFiles(self, config)
  - setComponentScripts(self, config)
  - performComponentSetup(self, config)

DIPA in the Future

0.4.0 BETA

- Simplified developer interface
- Better handling of files, variables
- Smarter handling of input files, intermediates, and skipped processing steps
- More informative help pages
- Pegasus
  – Improved restarting/expansion of previously run workflows
  – Improved multi-site implementation
  – Granular monitoring

Credits

- Nagesh Adluru : dMRI specialist, theory consultant.

- Nate Vack : General programming consultant

- Michael Stoneman : Undergrad assistant

- Stacey Schaefer : MIDUS lead scientist

- David Thompson : Waisman Sys-Admin

- Andy Pohl : HTCondor Waisman contact

- Karan Vahi : Pegasus

- The whole HTCondor Team

QUESTIONS, SUGGESTIONS, COMMENTS