



Report from 2015 OHBM Hackathon (HI)

Human Connectome Project Minimal Preprocessing Pipelines to Nipype

Project URL: <https://github.com/ericearl/hcp2nipype-hack2015/>

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1 Introduction

The goal was to convert the Human Connectome Project (HCP) Minimal Preprocessing Pipelines into Nipype code.

The HCP minimal preprocessing pipelines [1] represent a significant advance in image processing pipelines in our time. They provide preprocessed volume and surface data in native and atlas space, for both functional and structural data. Nipype is an open source neuroimaging project for designing imaging pipelines which has been around since 2011 and provides many excellent features for provenance and reliability of processing pipelines [2]. Together, these two pieces of software would allow for a more robust, more flexible synergy of pipeline design and operability.

2 Approach

The first goal was to train the would-be Nipype developers on the Nipype python standards for writing and running interfaces. Once trained, the plan was to implement the HCP scripts into Nipype interfaces from the top-level inward to the sub-level scripts. The secondary goal was to make these sub-level scripts more flexible and require less specific scans to run the pipelines. The collection of nine ultimate pipelines to implement were with or without T1s or T2s and with or without Fieldmap or Reverse-Phase-Encode EPIs as seen in Table 1.

3 Results

Conceptually these goals sounded reasonable enough to do all HCP scripts at once during the hackathon, but the learning and additional setup time was not accounted for, so the scope of the project was too big for two days of on and off coding, even among our eleven developers. Distributing Nipype knowledge from two experts to nine novices over two days was not an easy beginning task, but most of the novices had gained knowledge of Nipype usage by the end of the hackathon. Some work began during the hackathon converting HCP scripts into Nipype pipelines, however not much progress was made due to the unanticipated large scope of work. The second day, an epiphany came about that the original goal, as stated, would have only involved making five top-level wrappers for the five HCP top-level scripts. This also slowed some progress. The secondary goal of generalizing the HCP scripts was discussed, but not thoroughly explored or documented. There has only been some progress in generalization I am aware of in the Damien Fair, PA-C, PhD, Neuroimaging Lab at OHSU. This turnout of developers during an open hackathon is encouraging and demonstrates the importance of trying to fuse these two systems (Nipype and the HCP scripts) to work together. Work on the repository halted after the hackathon, but the team is still available.

4 Conclusions

More work is needed to truly contribute back to the HCP Pipelines[1]. The greatest achievement of the hackathon project was forming a collaborative team

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[1]<https://github.com/Washington-University/Pipelines>

Table 1 Nine pipelines to be implemented.

EPI	T1	T2	Diffusion	Field Map	Reverse Phase Encode EPI
N	N	N	1		0
N	N	0	1		0
N	0	N	1		0
N	N	N	0		N
N	N	0	0		N
N	0	N	0		N
N	N	N	0		0
N	N	0	0		0
N	0	N	0		0

of interested Nipype developers who were trained and are ready to continue collaborating across seven institutions. Future work will continue trying to achieve the original goals as stated, but may need an organizer to hold the team accountable to deadlines. To get involved with this project, please contact Eric Earl, earl@ohsu.edu.

Availability of Supporting Data

More information about this project can be found at:

<https://github.com/ericearl/hcp2nipype-hack2015/>. Further data and files supporting this project are hosted in the *GigaScience* repository [doi:10.5524/100223](https://doi.org/10.5524/100223).

Competing interests

None

Author's contributions

EE wrote the report, EE and all other authors wrote the software.

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