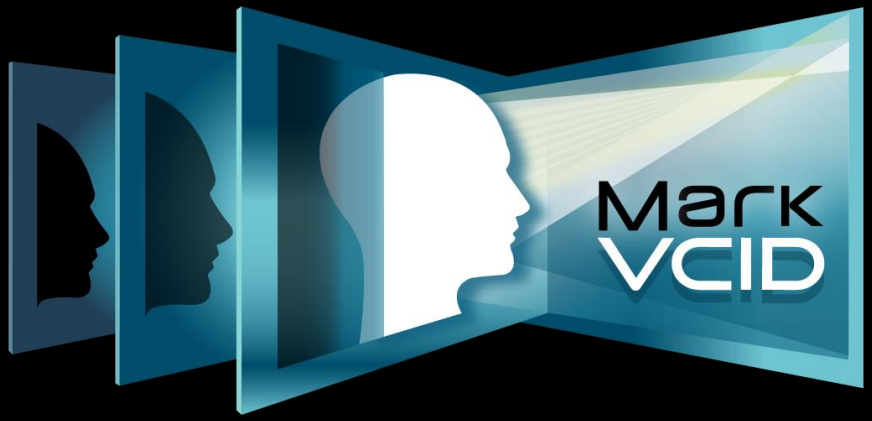


NIH Biomarkers Consortium for
Vascular Contributions to Cognitive Impairment and Dementia

MRI WMH Volume Algorithm

MarkVCID Kit Operations

Charles DeCarli | Feb 12, 2020

NIH National Institute of Neurological Disorders and Stroke

IDeA Lab
Imaging of Dementia & Aging

MGH 1811 MASSACHUSETTS GENERAL HOSPITAL

Agenda

1. Introduction of method
2. Download process
3. Operation review and discussion
4. Review of output and visualization

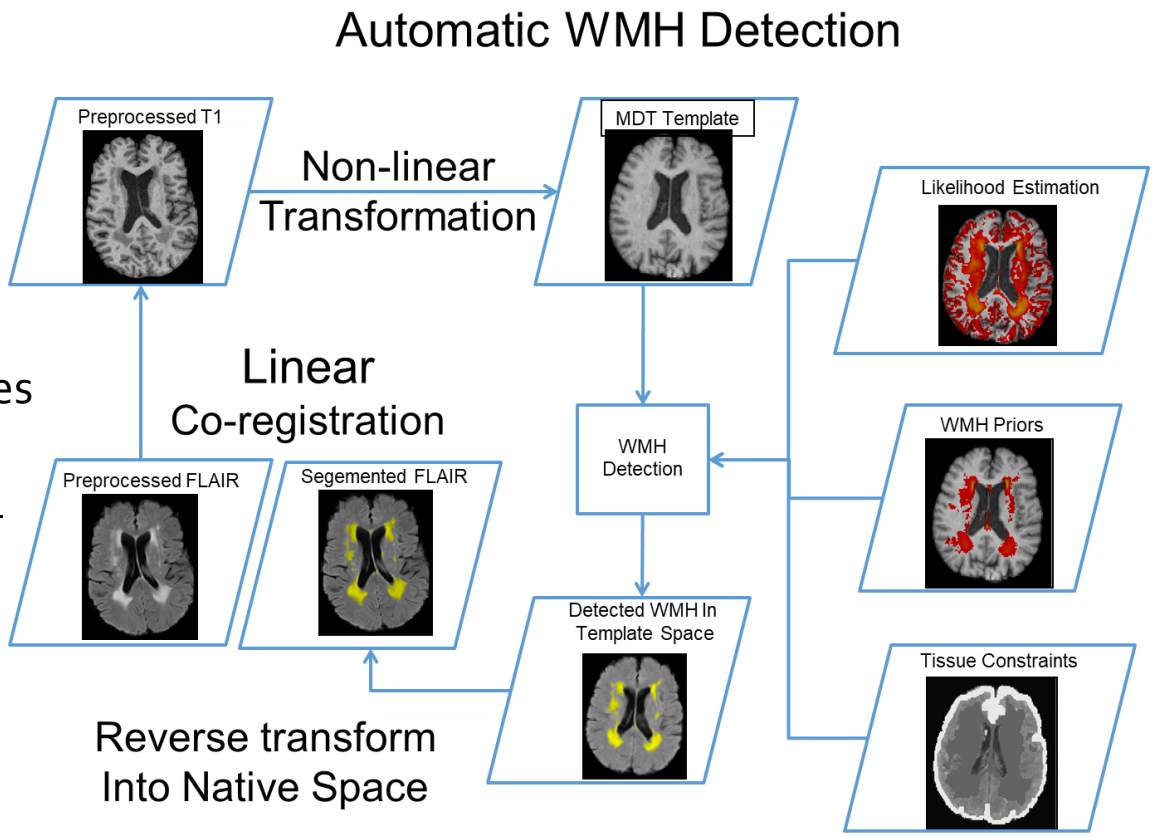
Questions/discussion

MarkVCID Biomarker:
WMH—Imaging Biomarker

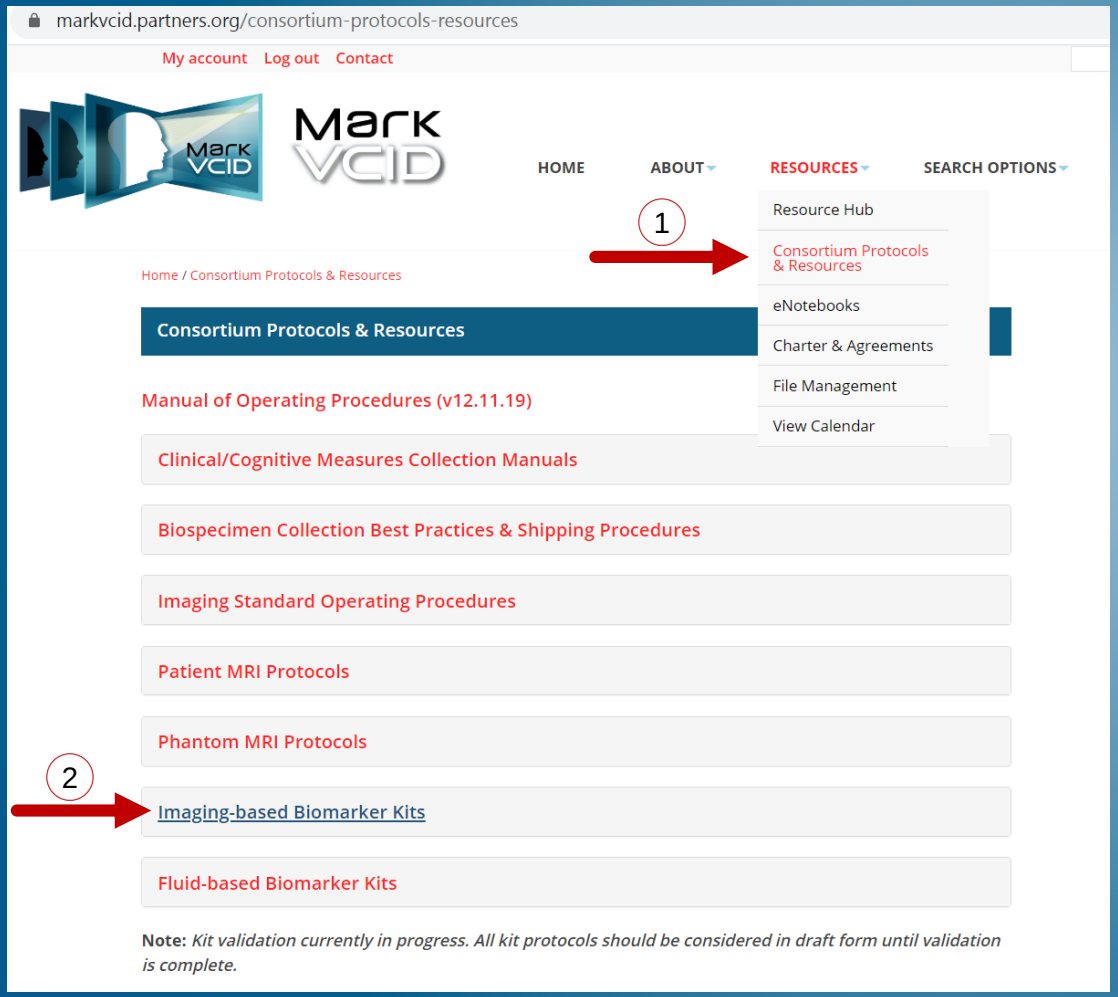
Bayesian algorithm based on quantitative prior segmentations, Gaussian likelihood and posterior probability constraints

May be used on single FLAIR images or combined with tissue segmentation of high resolution T1 weighted imaging

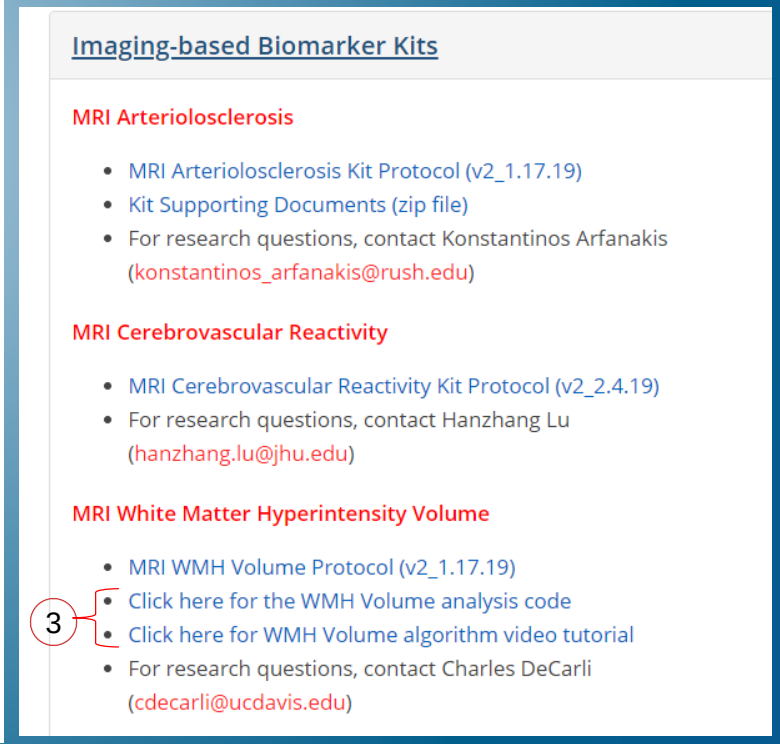
Executables can be downloaded from: http://idealab.ucdavis.edu/software/index.php



2. Download process

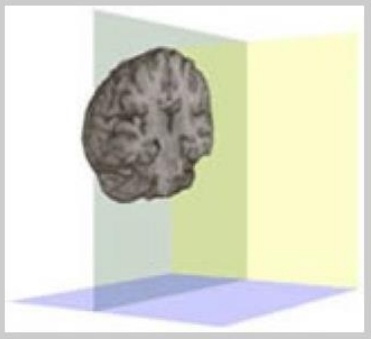


- Video tutorial available on the MarkVCID website



IDeA Webpage

IDeA Lab - Software - Download



IDeA Lab

Imaging of Dementia & Aging

- people
- software
- data management
- case studies
- publications
- current projects

Software - Download

Please let us know who you are:

Name:	blah
Institution:	blah
Email address:	bb@bb.edu
Confirm email address:	bb@bb.edu

Package Selection

Select the package(s) you are interested in downloading: (Date of the most current version is displayed after each package).

- ☐ Image File Management Utilities
- ☐ Stroke Viewer (32 bit)
- ☐ Stroke Viewer (64 bit)
- ☐ Segmenter (Tissue Classifier 32 bit)
- ☐ Segmenter (Tissue Classifier 64 bit)
- ☑ UCD WMH Segmentation (Python3 version)
- ☐ UCD WMH Segmentation (Python2 version)

Download Link

Software - Download

Thanks for your submission.

Please use the following link to download your software:

http://idealab.ucdavis.edu/software/files/ucdwmhsegmentation_linuxinstaller.run

UCD WMH Segmentation (Python3 version)

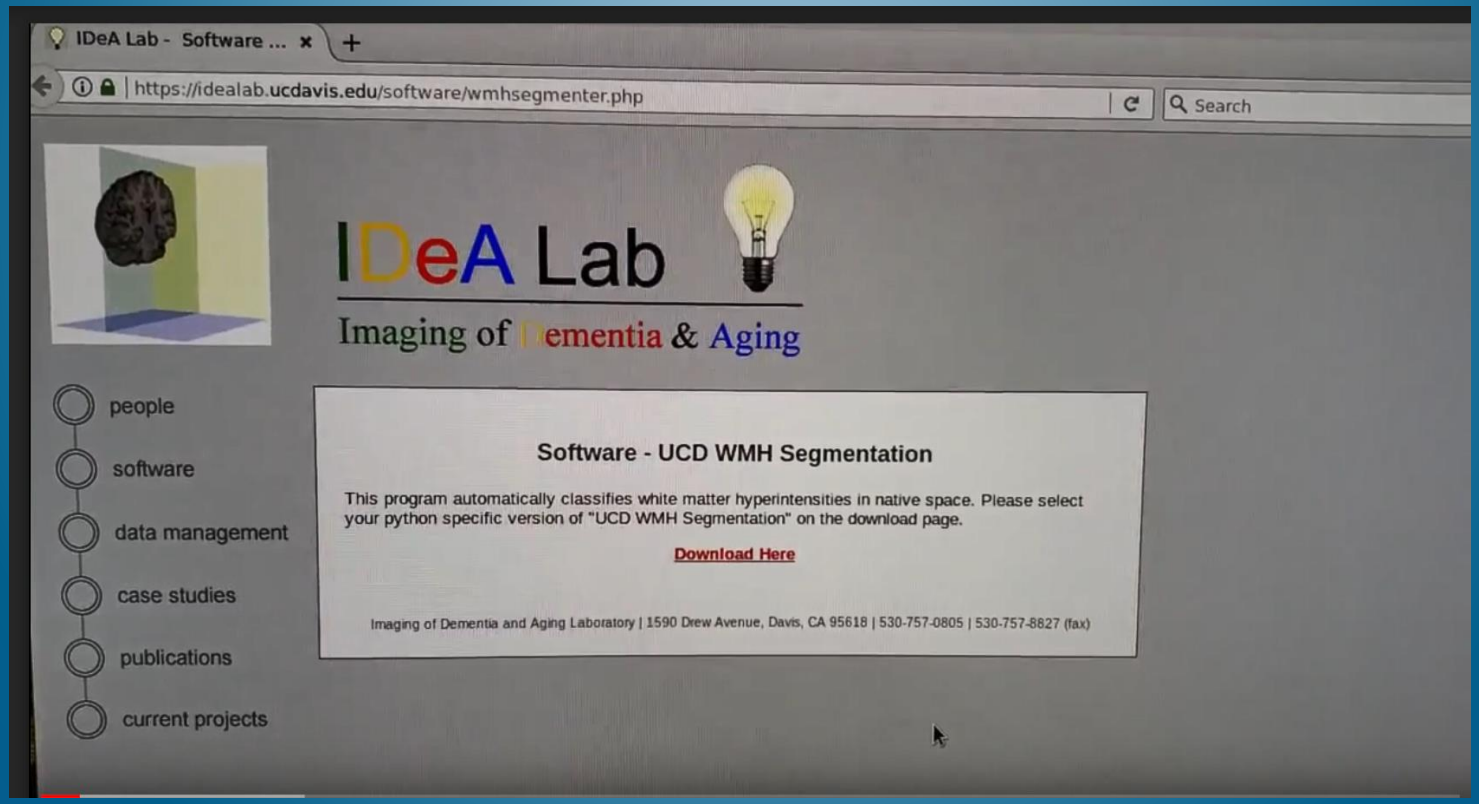
Please consult the README file(s) for directions on installing and running each individual package. If you need further support, please contact Evan Fletcher (emfletcher@ucdavis.edu).

Back to Software

Imaging of Dementia and Aging Laboratory | 1590 Drew Avenue, Davis, CA 95618 | 530-757-0805 | 530-757-8827 (fax)

2. Download process

Click WMH Volume algorithm video tutorial link:



3. Operation review & discussion

- 3 inputs
  - Brain Mask
  - 3DT1
  - FLAIR
- 6 outputs
  - WMH threshold Mask
  - WMH Z-score mask
  - Brain Mask
  - Stripped Brain
  - 4 tissue segmented image
  - CSV file containing specified segmentation results
- Working subdirectory
  - Stripped Brain
  - Bias Field
  - Co-registered FLAIR
  - Stripped FLAIR

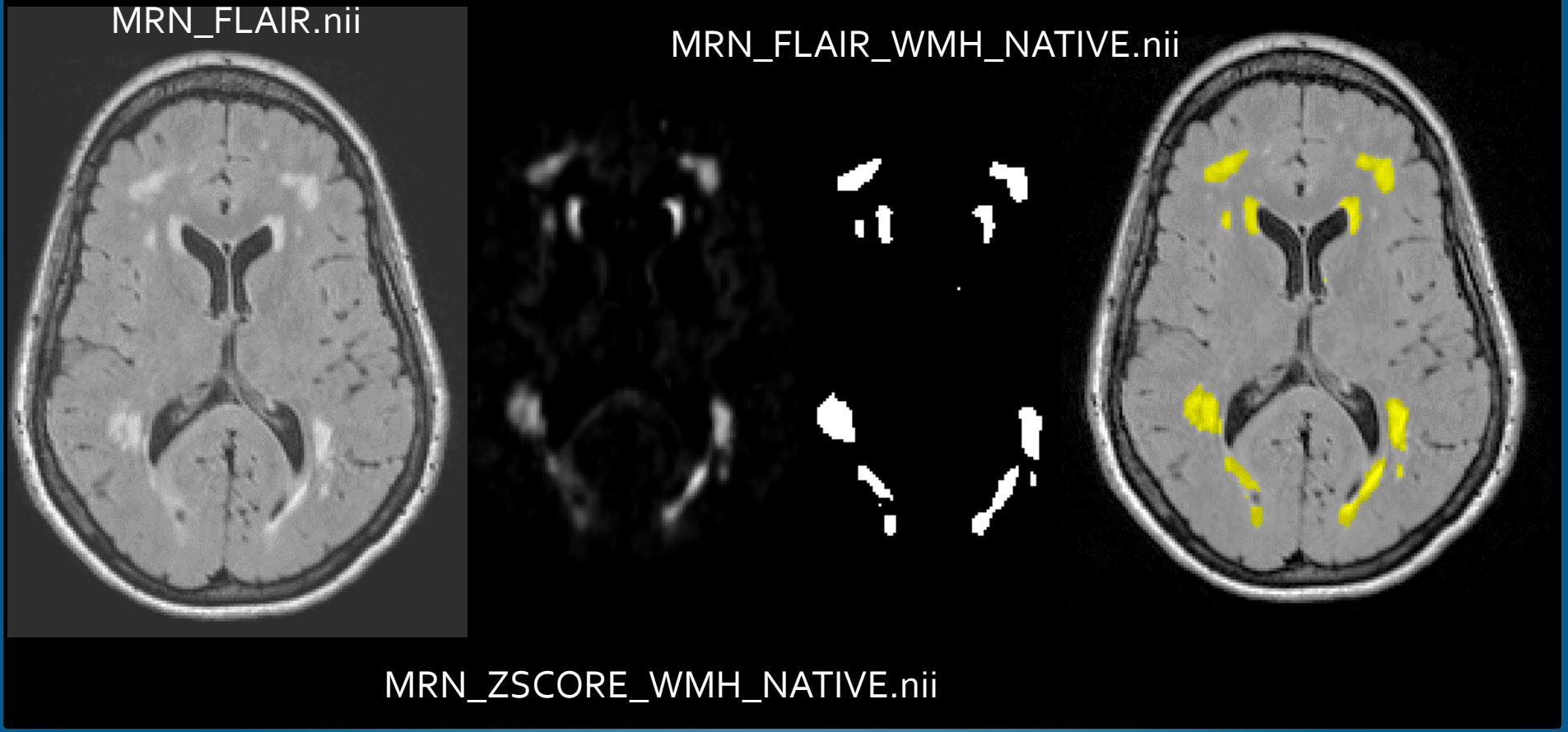
4. Review of output & visualization

```
[charliebrain@ideagate:~/wmhtest]$ ls
MRN_flair.nii.gz
MRN_flair_WMH_Native.nii.gz
MRN_flair_ZScore_Native.nii.gz
MRN_t1_data.csv
MRN_t1_mask.nii.gz
MRN_t1.nii.gz
MRN_t1_Stripped_corrSmTP_segmentedWMT-Z4T.nii.gz
MRN_t1_WMHProcess
```

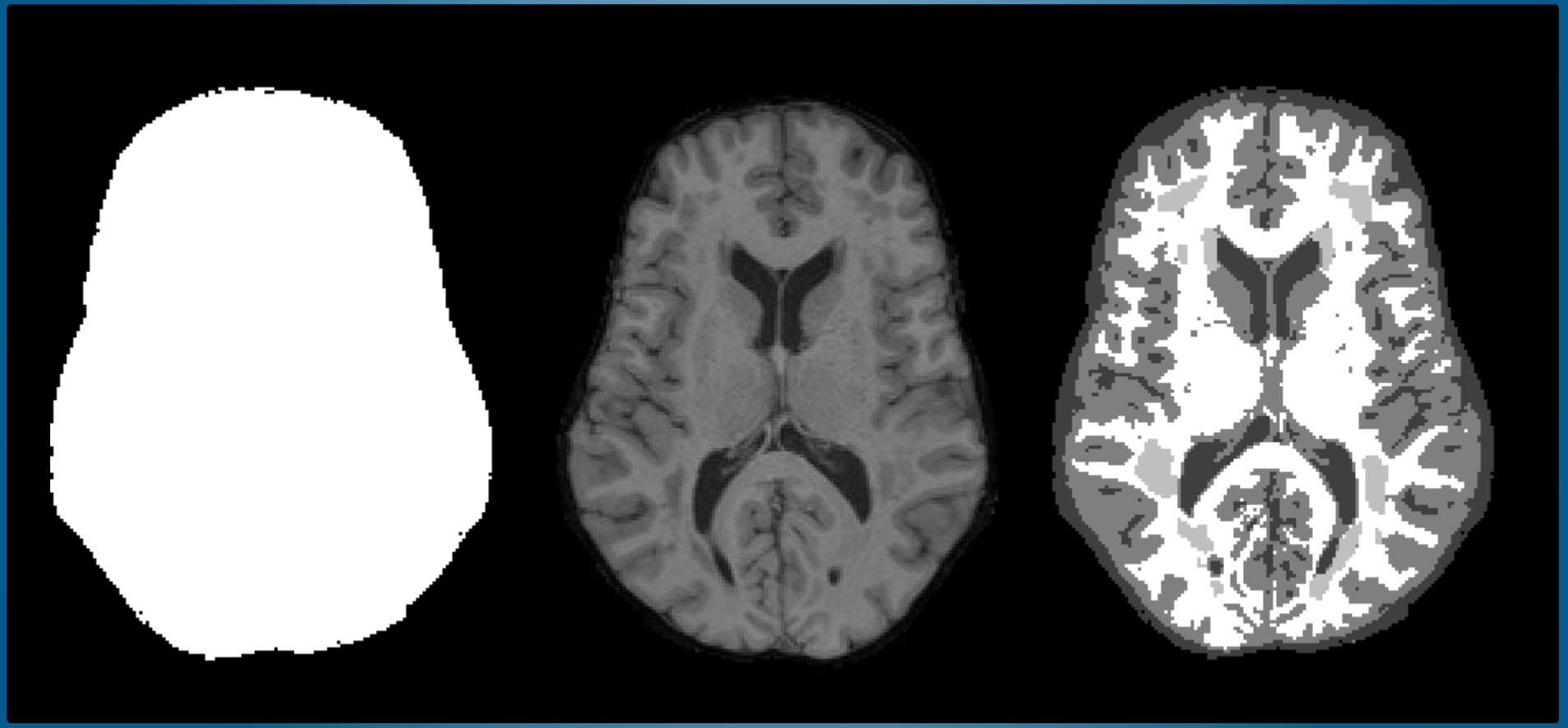
ICV	CSF	GRAY	WHITE	WMH
1541.29	366.96	645.91	487.60	40.82

MRN_t1_data.csv:
ICV, CSF, GRAY,WHITE,WMH
1541.29,366.959,645.914,487.595,40.822

Output files



Output files (Cont'd)



Input Mask

Masked Brain

4 Tissue segmentation

Questions/discussion

- Questions?

For support, please contact
Charlie DeCarli (cdecarli@ucdavis.edu) and
Baljeet Singh (bjsingh@ucdavis.edu)