Data Preparation for WHIMS MRI Data Sets
January 2022

1. Introduction

This release includes re-reads of the MRI 1 and MRI 2 data from the WHIMS Magnetic Resonance Imaging (WHIMS-MRI) study. The data provided include a subset of WHIMS participants who underwent one or two brain scans, one between 2004 and 2006 and the second between 2009 and 2010.

Timing of Data Collection

Phase	Beginning and end dates
MRI-1	2004-2006
MRI-2	2009-2010

2. Description of WHIMS MRI

The WHIMS-MRI study entitled Effects of Hormone Therapy on Subclinical Neurological Pathology was a magnetic resonance imaging substudy in women from the WHIMS Post-Trial Extension.

The data consist of total brain volume data and ischemic lesion volume data presented by brain region. These data are re-reading of the MRI scans (not the original baseline MRI readings). The re-readings were highly correlated, but not identical, to the original baseline readings and were not done on a handful of women. About half the women did not undergo follow-up MRIs (MRI-2).

For analyses involving estimates of longitudinal change, a refined image processing approach is used that accounts for both time points to improve accuracy at each step in the analysis. A fully automated pipeline was applied for processing structural MRIs. T1-weighted scan of each subject was first corrected for intensity inhomogeneities [1]. A multi-atlas skull stripping algorithm was applied for the removal of extra-cranial material [2]. Anatomical regions of interest (ROIs) were identified using an extensively validated multi-atlas segmentation method, MUSE [3]. The MUSE algorithm follows the multi-atlas image registration and label fusion framework. In this framework, multiple atlases with reference labels are independently registered to the target scan using deformable registration. Candidate labels from multiple registrations are fused together to calculate a consensus segmentation. This process has important advantages, the most notably the robustness against scanner differences and individual registration errors by the virtue of the ensemble label fusion process. Use of this refined image analysis approach yields somewhat different numerical values than the original or longitudinal image reports alone. However, when all MRI time points are reanalyzed in this framework, the resulting numerical values are internally consistent

Approximate ICV (brain+cerebellum) is included in the MRI1_totvol_pub_jan2022_final and MRI2_totvol_pub_jan2022_final datasets.

3. Included Data Sets

Data sets for each component are described below.

- MRI1_totvol_pub_jan2022_final (Total volume by region)
- MRI1_abnorvol_pub_jan2022_final (Abnormal volume by region)
- MRI2_totvol_pub_jan2022_final (Total volume by region)
- MRI2_abnorvol_pub_jan2022_final (Abnormal volume by region)

4. Data Conventions

Each SAS data set is created in version 9.4. The identifying variables in each file are Participant ID, 'ID' (referred to as the "common ID" in the WHI documentation).

Dates

No actual dates are included in the data files. All dates have been converted to the number of days since WHI randomization (mri_dy). A negative number of days indicate the date occurred before randomization. Likewise, a positive number indicates occurrence after randomization.

5. Appending and Merging Data Files

If you wish to expand your data analyses to include WHI Clinical Trial data, you can use the ID variable in the WHIMS MRI data set and the ID variable in the WHI Clinical Trial data set to merge data sets. The WHIMS MRI and WHI Clinical Trial data releases use the same participant ID.

The MRI data should not be appended to the previously released MRI data. This is a re-reading of the MRI-1 and MRI-2 scans released in June of 2017. These files should replace any previously used WHIMS MRI data.

For further information about this data release, please contact Katelyn Garcia at kgarcia@wakehealth.edu or Julia Spell at jurobert@wakehealth.edu.

Citations:

[1] Tustison NJ, Avants BB, Cook PA, et al. N4ITK: Improved N3 Bias Correction. IEEE Trans Med Imaging. 2010;29(6):1310-1320. doi:10.1109/TMI.2010.2046908.

[2] Doshi J, Erus G, Ou Y, Gaonkar B, Davatzikos C. Multi-Atlas Skull-Stripping. Acad Radiol. 2013;20(12):1566-1576. doi:10.1016/j.acra.2013.09.010.

[3] J. Doshi et. al., MUSE: MUlti-atlas region Segmentation utilizing Ensembles of registration algorithms and parameters, and locally optimal atlas selection, NeuroImage, Volume 127, Pages 186-195