README: Data and code supplement for

“Pointwise influence matrices for functional-response regression”

by Reiss, Huang, Wu, Chen and Colcombe

Three files are provided:

1. pwhat.R is an R script to runs the analyses on the corpus callosum data presented in the paper.
2. vsm\_0.1.tar.gz is a compressed archive containing the R package *vsm*, implementing the OLS, GLS and post-smoothing methods described in the paper.
3. CCFA.RData is an R data file consisting of
   * age ages of 145 participants
   * vc coordinates of 107 voxels in mid-sagittal plane
   * arclength positions of these voxels along an arc
   * cc 145 x 107 matrix of corpus callosum fractional anisotropy values
   * anat 218 x 182 anatomical image used in Figure 5

All three files should be saved to the same directory, which should be set as the working directory for running pwhat.R. The first line of the script installs the vsm package, and the second loads the data file. The R packages *mgcv*, *fda* and *vows*, all available on CRAN, should be installed as well.

By far the most time-consuming part of the analyses is the repeated five-fold cross-validation required to produce the lower subfigures of Figure 4. Running the entire script took approximately 54 minutes on the first author’s laptop.

The current version of the *vsm* package is available at <https://github.com/philreiss/vsm> and can be installed using the following two lines of code:

library(devtools)

install\_github("philreiss/vsm")