**Free-water correction**

Prior studies of anorexia nervosa indicate that some differences in DTI metrics may arise from loss of grey matter and consequent partial volume effects (voxel contamination by cerebrospinal fluid). As a sensitivity analysis we will repeat the main analyses after applying freewater correction to the diffusion images. If you have already corrected your images (using any method), then please re-run the main analysis steps (from Calculating Tensor Metrics to Running the R script) with the free-water corrected data. Otherwise, please follow the instructions below to acquire the corrected data.

The correction method we are using was developed by Parker and colleagues, and is described here: https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0233645

To perform the correction, you will need to install a docker container, using the instructions here: <https://github.com/CaitlinLloyd/FW_correction>

This container should also work for singularity systems, but if you are experiencing issues, you may wish to download the fernet repository directly from here (https://github.com/DiCIPHR-Lab/Fernet), and run the following command:

./main.sh $path\_to\_processed\_dwi\_image $path\_to\_bvec\_file $path\_to\_bval\_file $path\_to\_corrected\_image\_b0mask $output\_file\_name

Note, you will need to download the main.sh script along with the necessary fernet python files (from here: <https://github.com/CaitlinLloyd/FW_correction>), and you will need to run main.sh from the directory that contains the python files.

You can run the commands in a loop, to perform correction on all participant data.

Once you have the corrected images, you can proceed to rerunning the pipeline, completing the steps from Calculating Tensor Metrics to Running the R script.