**Details of the MRI sequence and diffusion data analyzed:**

-MRI is carried out on a 3 Tesla MR scanner (Tim-TRIO, Siemens Medical Systems, Erlangen, Germany)

-DTI (30 directions) EPI, TR = 7.8 s, TE = 83 ms, 4 b0-images (interleaved), 30 images with b = 1000 s/mm 2 , voxel resolution = 2 × 2 × 2 mm 3

**Running the PSMD pipeline:**

-Tensor fitting was done using dtifit on preprocessed 30 directions dwi data described above.

-Symbolic links were created to the MD, FA, AD, RD native maps in order for them to be compatible inputs to the supplied PSMD scripts.

-An in house parallelization script was used to parallelize the execution of MAIN\_script\_PSMD.sh over the subject pool.

**QC of PSMD pipeline results:**

-Checked if all subjects have masked images with FA skeleton.

-Checked if the dimensions of the TOTAL\_METRICS\_Skel\_header.csv file match the number of subjects and all parameters computed.

-QC of FA maps produced by tbss\_preproc1

-QC of FA maps after non-linear registration to standard space

-Randomly assessed skeleton superpositions on spatially normalized DTI metric maps with MD maps as example

-Identified outlier subjects by plotting linear regression lines of metrics against age.

-Based on the above QC methods, subjects with defective images were removed from the final result list.

**Calculation of ICV:**

-Was performed using fslstats (FSL 5.0.9)

-please see psmd\_seg\_vols.csv for age, sex, grey matter volume, white matter voume, csf and ICV data.