**1.1. Manual Segmentation Procedures**

We used Multitracer 2.0, a free online tool (<http://air.bmap.ucla.edu/MultiTracer2/MultiTracer.html>) for all manual segmentations of the amygdala. All brain scans were loaded onto the software in NIFTI format. Tracings were done on a Mac mini macOS Sierra equipped with a touchscreen (Cintiq 22HD Creative Pen Display) and pressure-sensitive pen. Total amygdala volumes were measured following recommended segmentation method from Entis and colleagues (Entis *et al.* 2012). Human tracer (TP) was trained in this protocol, largely using the methods and supplemental data portions from the publication. An atlas of the human brain was consulted to assist in correct segmentation (Mai *et al.* 2004).

**1.2. Quality control procedure for image processing**

**A three-step quality control procedure** was performed with the automated amygdala segmentations: 1) all measurements below/above two standard deviations from the mean were uploaded and re-inspected in the sagittal plane; 2) all measurements with hemispherical asymmetry between left and right amygdala measurements of 300mm3 were inspected in the coronal plane; 3) a portion of the amygdala measurements from FS6.0 subfield-specific workflow were visually compared with the results from manual segmentation of the amygdala. Any detected cases of mislabeling from the automated segmentation were eliminated from the analysis. These quality control procedures for segmentation outputs from FS6.0 workflow are in consonance with published protocols from the ENIGMA-MDD working group (Schmaal *et al.* 2016).

**1.3. Correlating amygdala segmentations between automated and manual methods**

Thirty five brain scans were randomly selected for between-methods correlations. Total amygdala measurements from manual segmentations FS6.0 subfield-specific workflow were correlated for left (Chronbach’s Alpha = .76 , Pearson *r*=0.63, p=0.000) and right amygdala (Chronbach’s Alpha =.76 , Pearson *r*=0.62, p=0.000) separately.

**References:**

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