An extended Human Connectome Project multimodal parcellation atlas of the human cortex and subcortical areas

Supplementary Material

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Validation of the thalamic parcellation provided in the extended Human Connectome Project atlas (HCPex)

The thalamic parcellation provided by Iglesias et al (2018) enabled inclusion of 21 thalamic nuclei in each hemisphere in the HCPex atlas, and was accordingly used in preference to an atlas by Tian et al (2020) which provides only 8 thalamic nuclei. The thalamic parcellation adopted from Iglesias et al was validated using the Krauth et al (2010) atlas which is based on histological analysis of the human brain, and as shown in Fig. S1 the HCPex parcels corresponded well. For a further validation, the human thalamic nuclei from the Thalamus Optimized Multi Atlas Segmentation (THOMAS) atlas which uses white matter-nulled MP-RAGE imaging that segments the thalamus into 12 nuclei (Su et al. 2019) is also shown in Fig. S1.

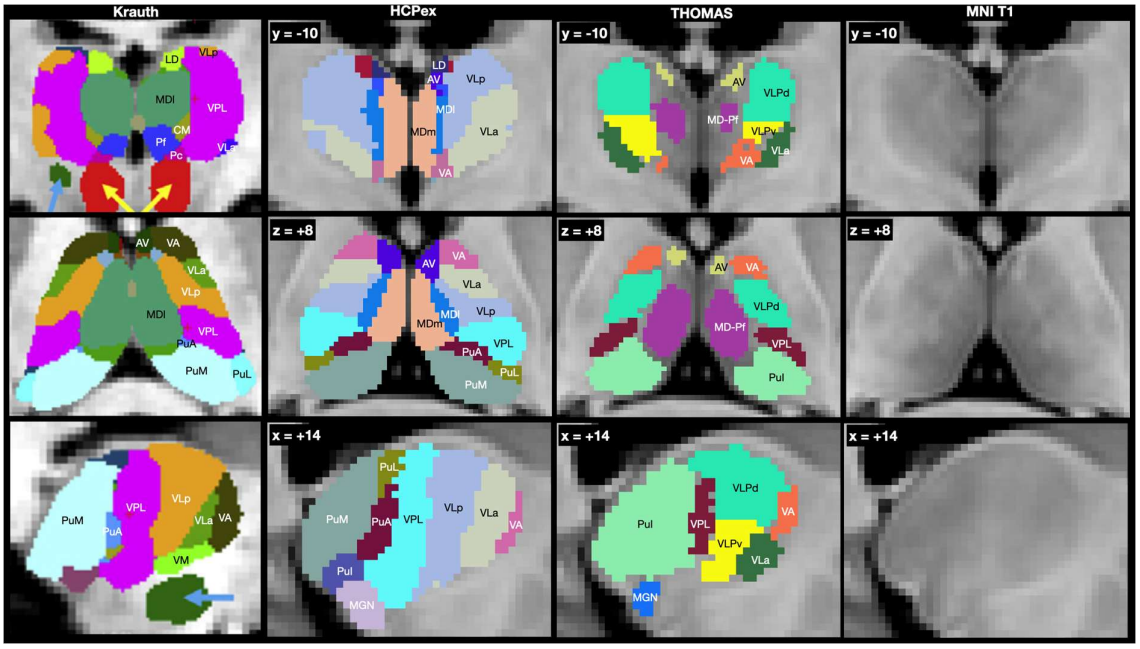

Fig. S1. Validation of the thalamic parcellation in the HCPex atlas with that in the histologically based human thalamic atlas by Krauth et al. (2010). For comparison the human thalamic nuclei from the Thalamus Optimized Multi Atlas Segmentation (THOMAS) atlas which uses white matter-nulled MP-RAGE imaging that segments the thalamus into 12 nuclei is also shown (Su et al. 2019). On the right is a T1 image of the thalamus. The top row shows coronal views; the middle row horizontal; and the bottom row parasagittal views, with the y, z and x MNI coordinates indicated. The Krauth et al (2010) atlas was histological, and did not have MNI coordinates. The abbreviations are shown in Table 1.

Validation of the cortical areas in volumetric space in HCPex

The procedure used to produce the cortical areas of the HCP-MMP atlas (Glasser et al. 2016) in volumetric space for HCPex (see Methods in the main paper) was usefully validated against a procedure used by Coalson et al (2018) to produce a volumetric version of the HCP-MMP atlas (Glasser et al. 2016), as shown in Fig. S2. The volumetric version of the Glasser et al atlas (2016) produced by Coalson et al (2018) was downloaded with grateful acknowledgement from the publicly released version of the parcellation (https://balsa.wustl.edu/file/show/nvrZ). The cortical areas in the HCPex paper correspond reasonably well to those using the procedure adopted by Coalson et al (2018). The main difference between the two procedures is that Coalson et al (2018) used T1 images from 210 HCP participants each mapped into MNI volumetric space with a group average in volumetric space then made; whereas the HCPex started with the group average in surface-based space provided from 210 HCP participants (Glasser et al 2016), and then mapped this into MNI volumetric space as described in the Methods (Mills 2016; Beauchamp 2021) (see also https://wiki.humanconnectome.org/display/PublicData/HCP+Users+FAQ) and as made available at the AFNI website (https://afni.nimh.nih.gov/pub/dist/atlases/MNI_HCP/).

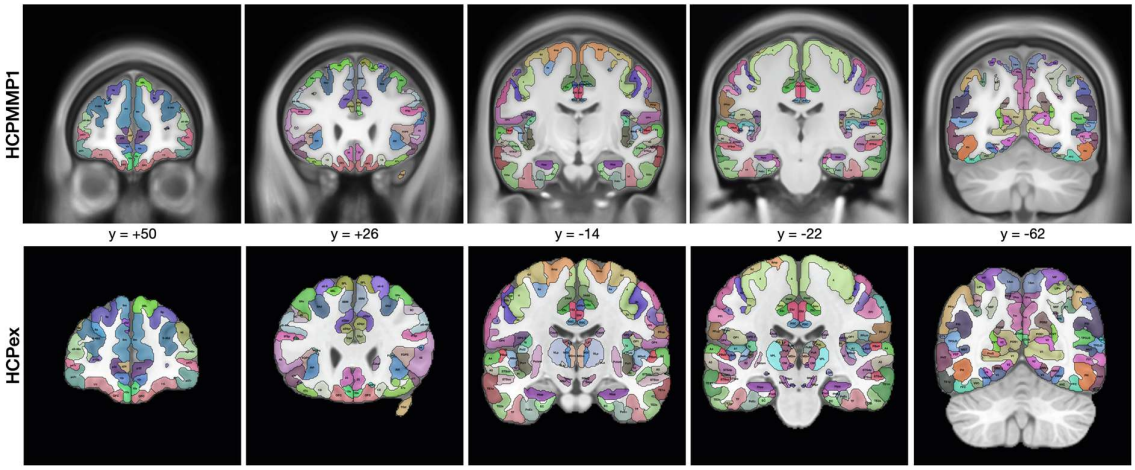

Fig. S2. Validation of the cortical areas in volumetric space in HCPex by comparing with the corresponding parcellation produced by Coalson et al (2018) labelled HCPMMP1. In both cases, the 180 cortical areas per hemisphere were from the surface-based HCP-MMP1 atlas (Glasser et al. 2016). The abbreviations are listed in Table 1, and the colors are the same for the two atlases. The y values shown are in MNI coordinates. The two versions of the atlas generally correspond, with small differences due in part to the fact that the HCPMMP1 atlas used a T1 template from the HCP, whereas the HCPex atlas utilises the widely used template from MNI ICBM 2009c which is an asymmetric T1 template based on 152 participants (Fonov et al. 2009; Fonov et al. 2011).

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