

A high-definition anatomical brain template of one individual healthy subject

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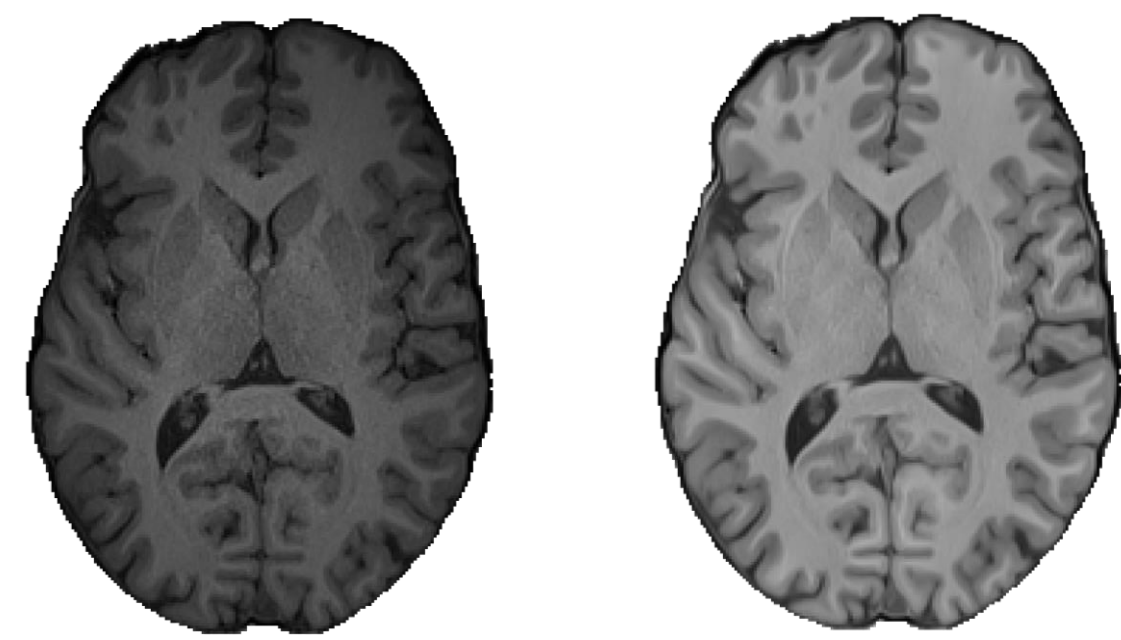
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PROCESSING

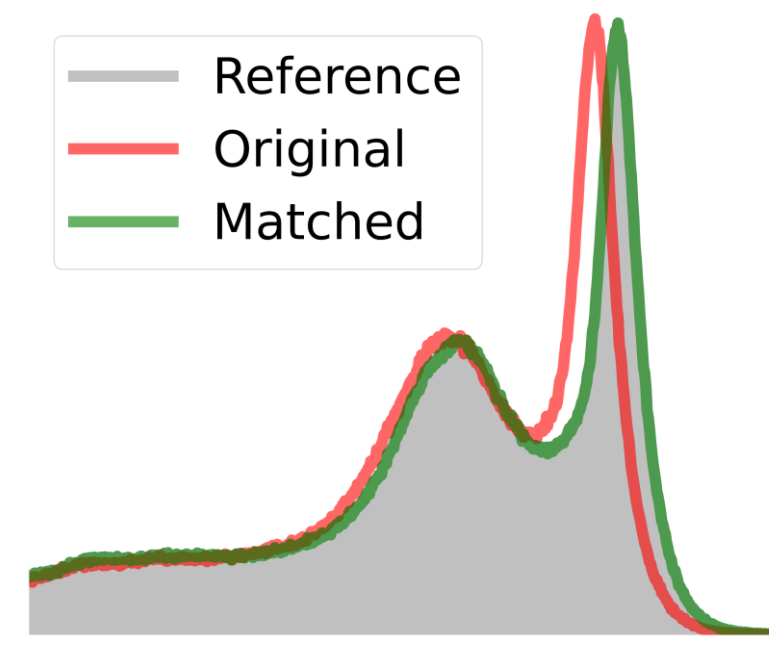
35 T1w & 35 T2w images of a single healthy male (age: 40) acquired at 3T (voxel size: 0.8 mm³) in a dense sampling protocol: the Human Connectome Phantom (HCPH) [1].

1. **Skull-stripping** (FreeSurfer [2])
mri_synstrip



2. **INU & denoising** (ANTs [3])
N4BiasFieldCorrection
DenoiseImage

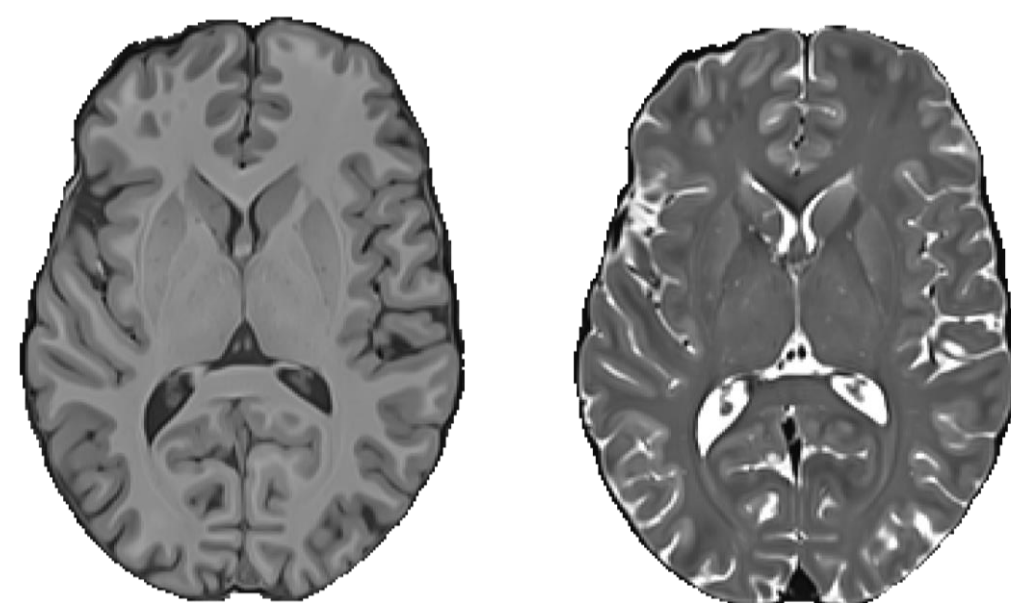
3. **Intensity normalization** (scikit-image [4])
skimage.exposure.match_histograms



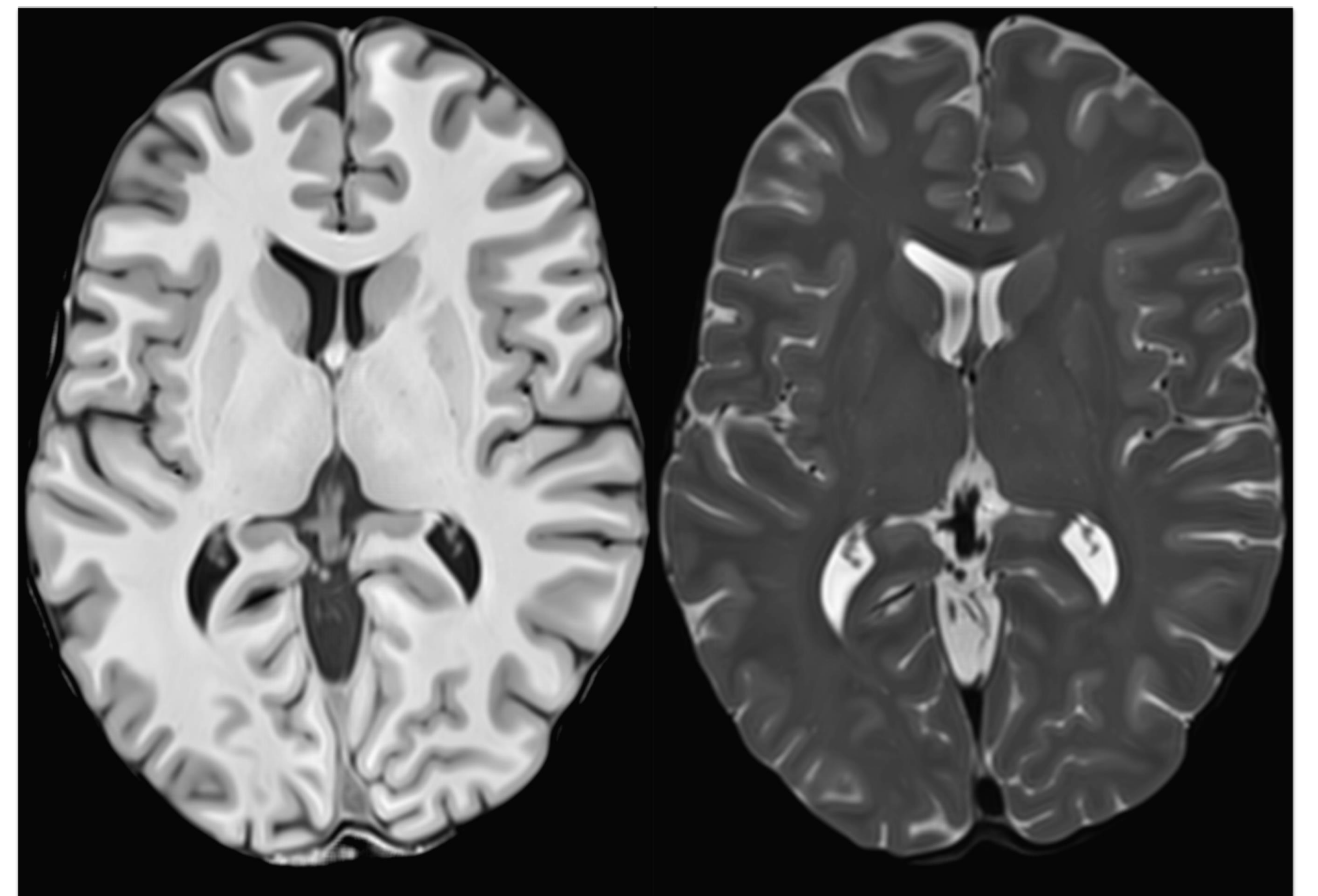
4. **Align T2w to T1w** (ANTs)
antsRegistration

5. **Build template in subject space** (ANTs)
Estimation of transform from template to subject
antsMultivariateTemplateConstruction2

6. **Interpolation** (Python script)
Using precomputed transforms

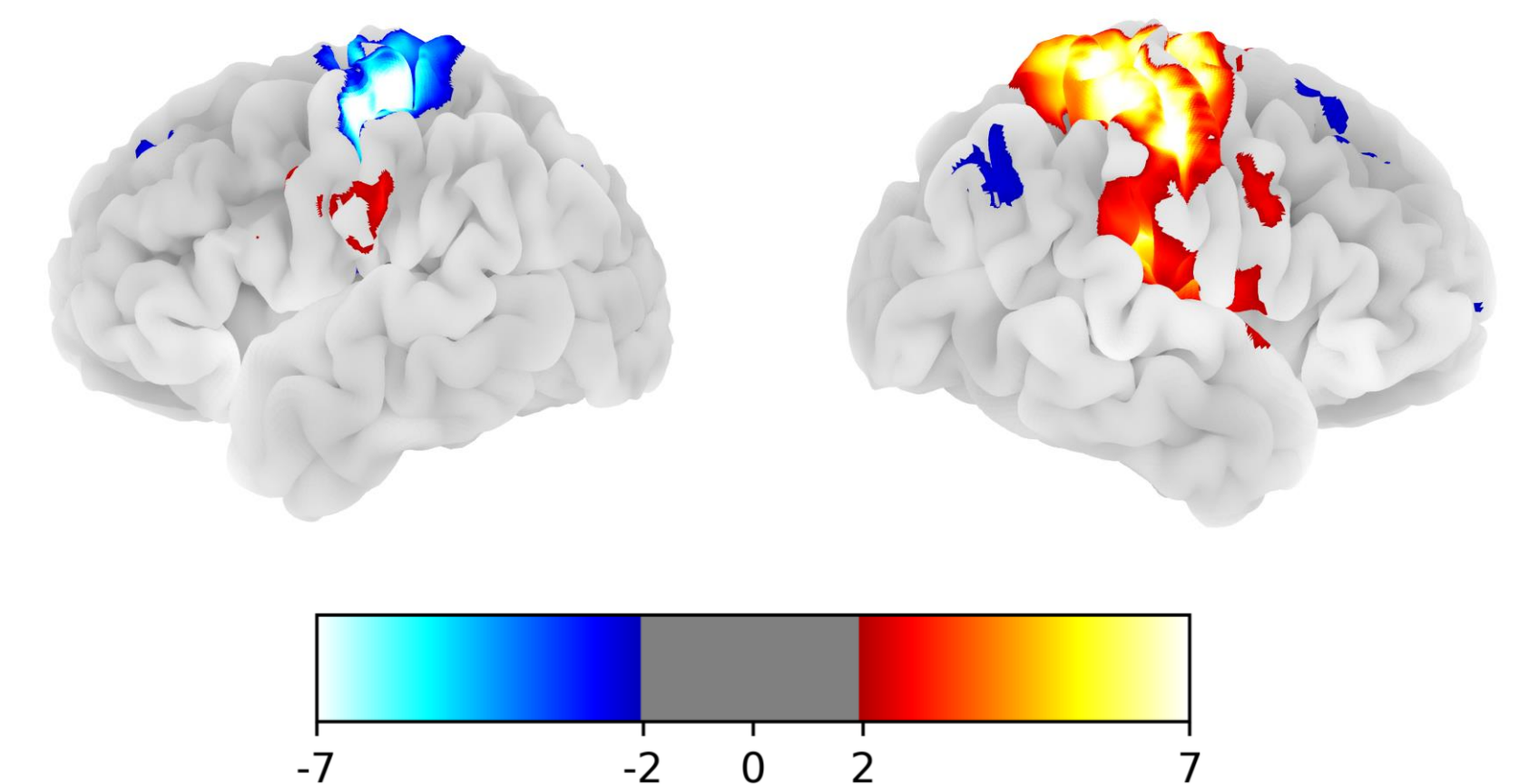


T1w & T2w TEMPLATE

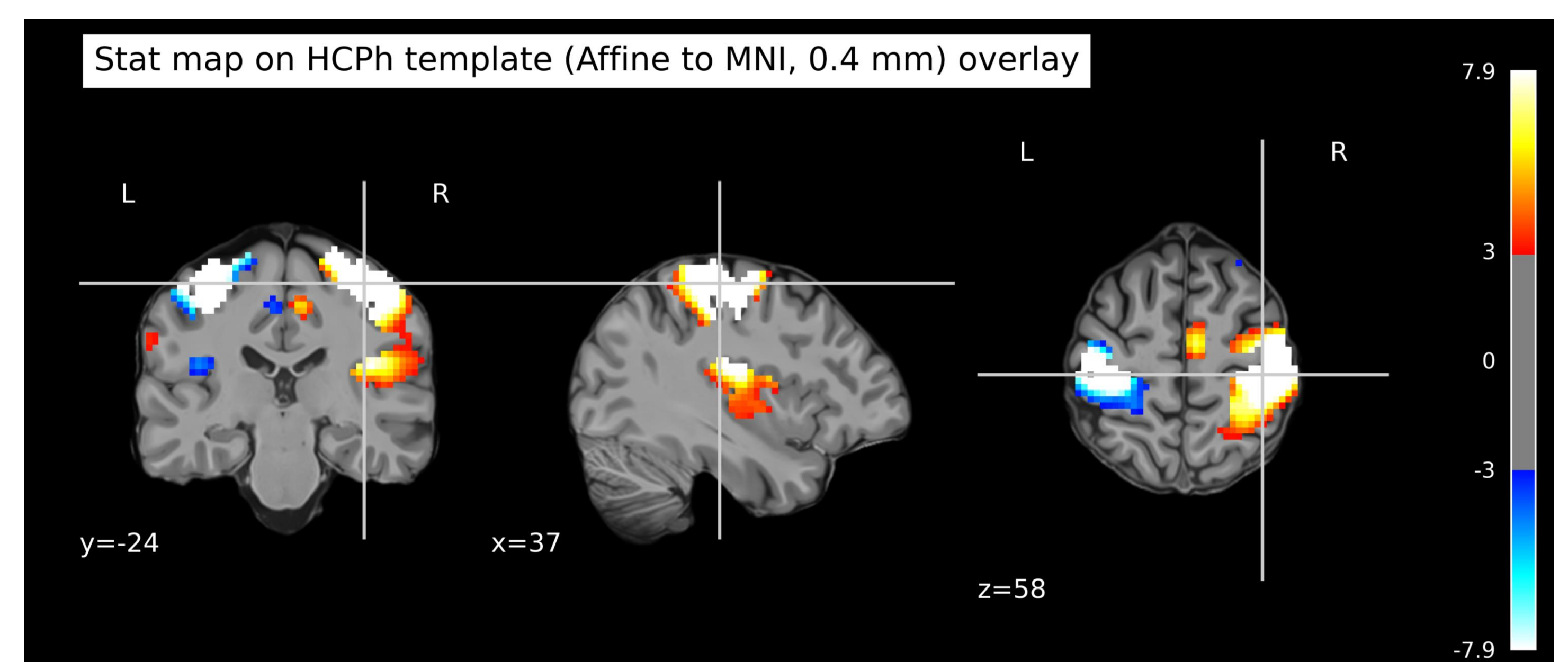


USE THE TEMPLATE

For surface plots:



As background for statistical maps:



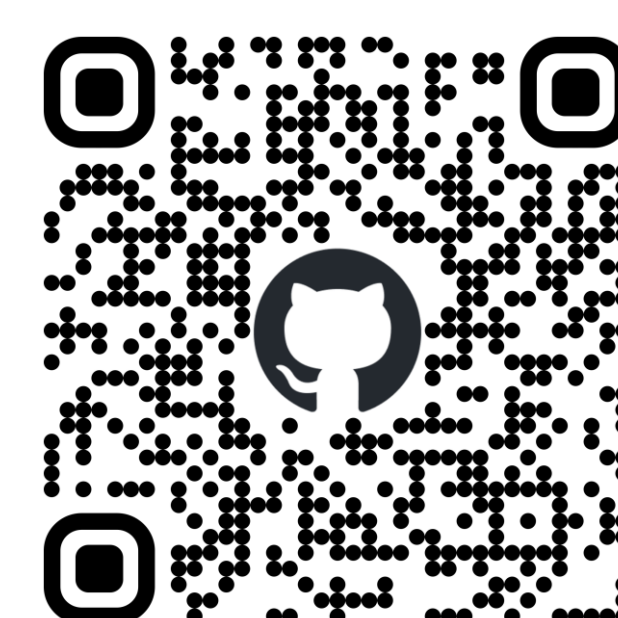
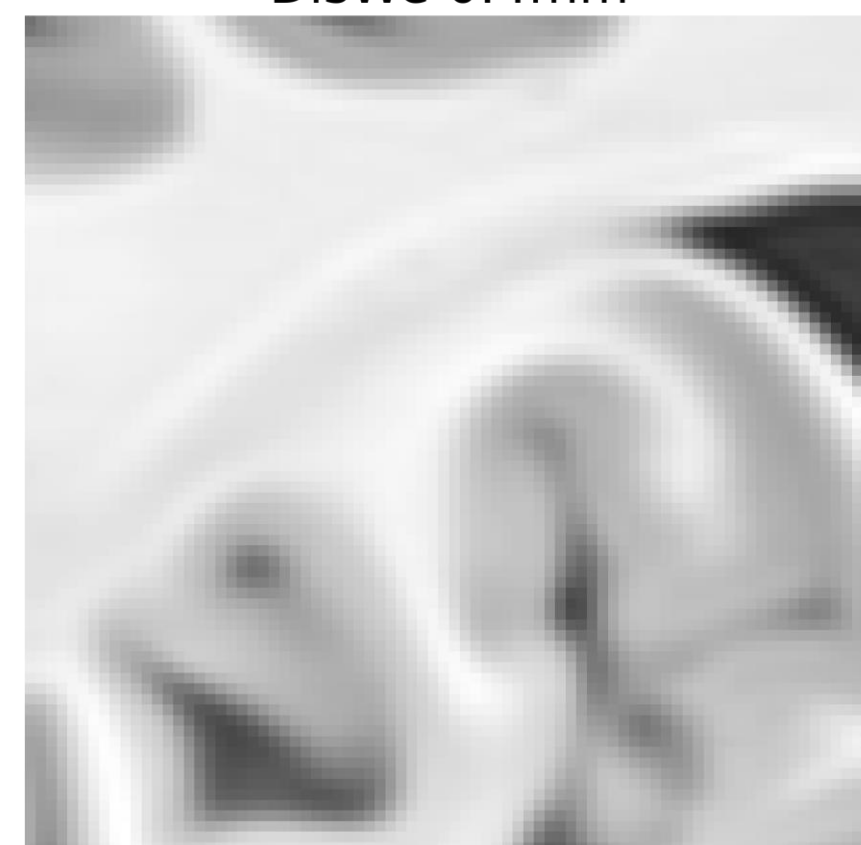
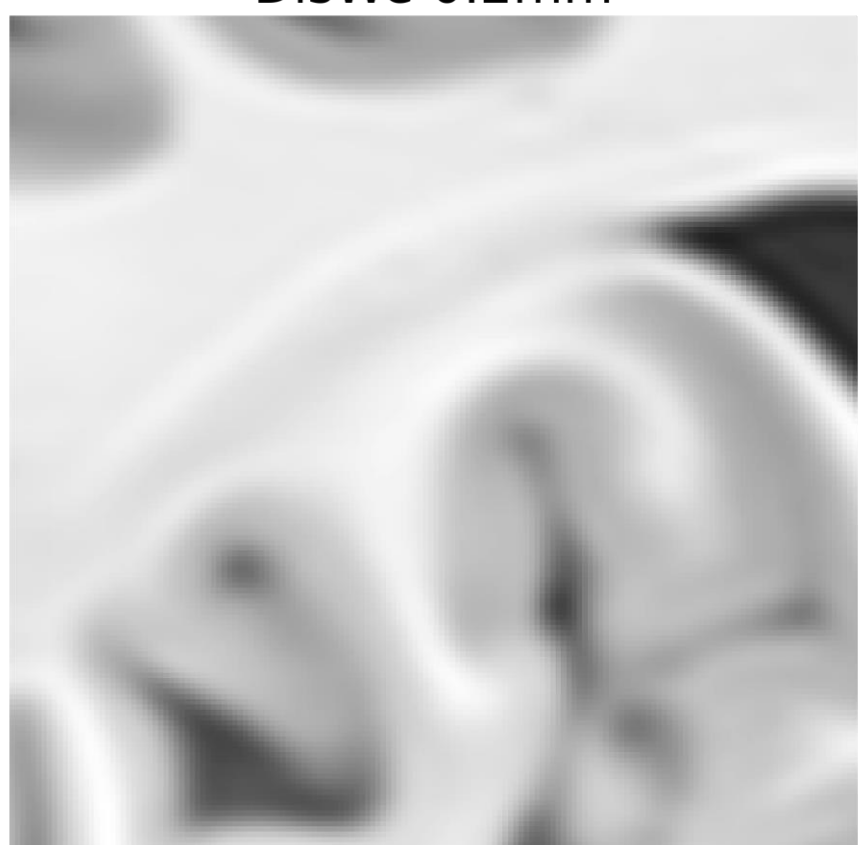
DISTANCE WEIGHTED INTERPOLATION (DisWe)

The templates are up-sampled using an interpolation based on the accuracy of registration. The center of voxels from a high-definition grid are projected onto each individual image. The distance between the projection and the center of the closest voxel (in the image space) is used as interpolation weight (the smaller the distance, the higher the weight).

DisWe 0.2mm

DisWe 0.4mm

ANTs 0.8mm



Scroll through the code

&

Get the template images

