Supplementary material

Large-Scale Automated Identification of Mouse Brain Cells in Confocal Light Sheet Microscopy Images

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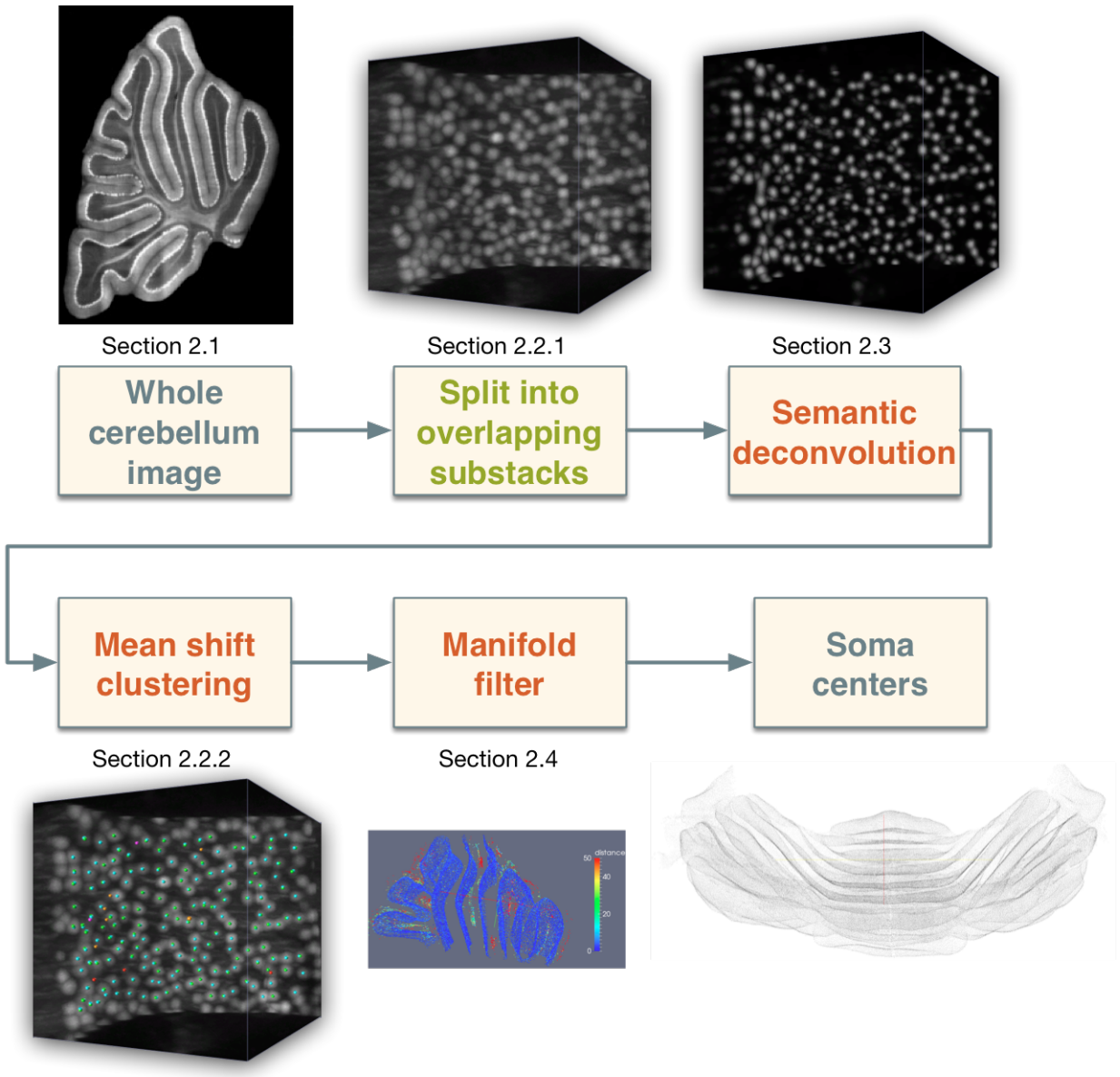
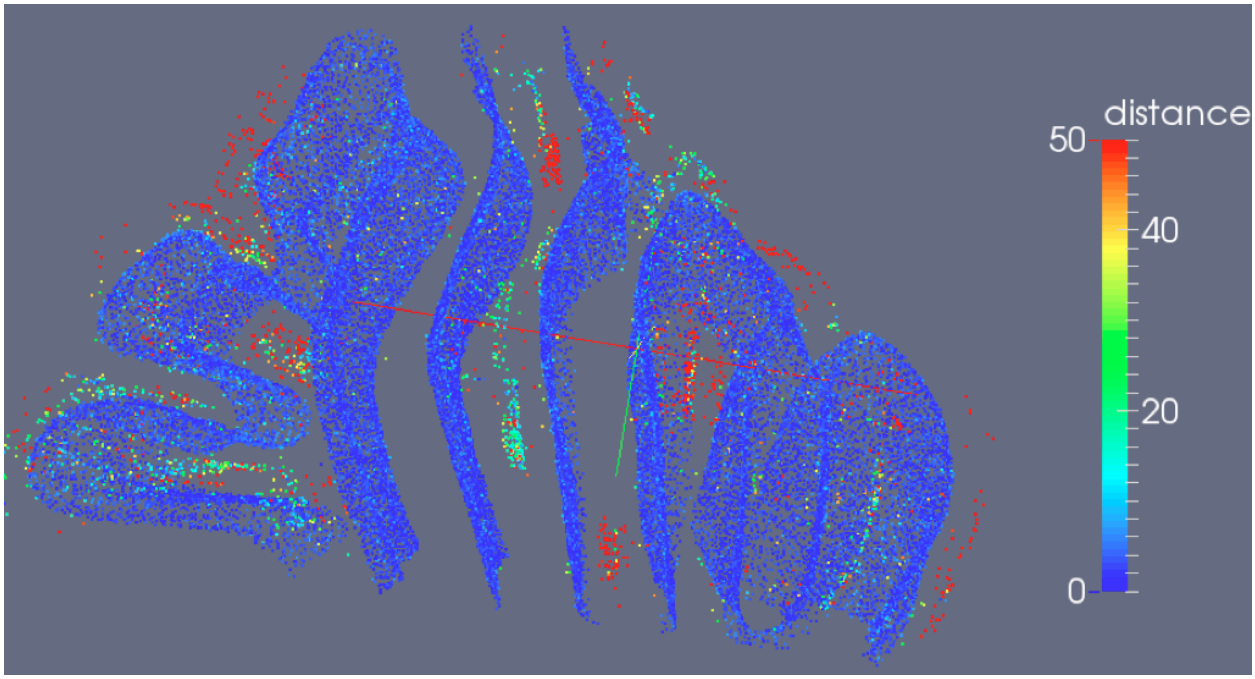
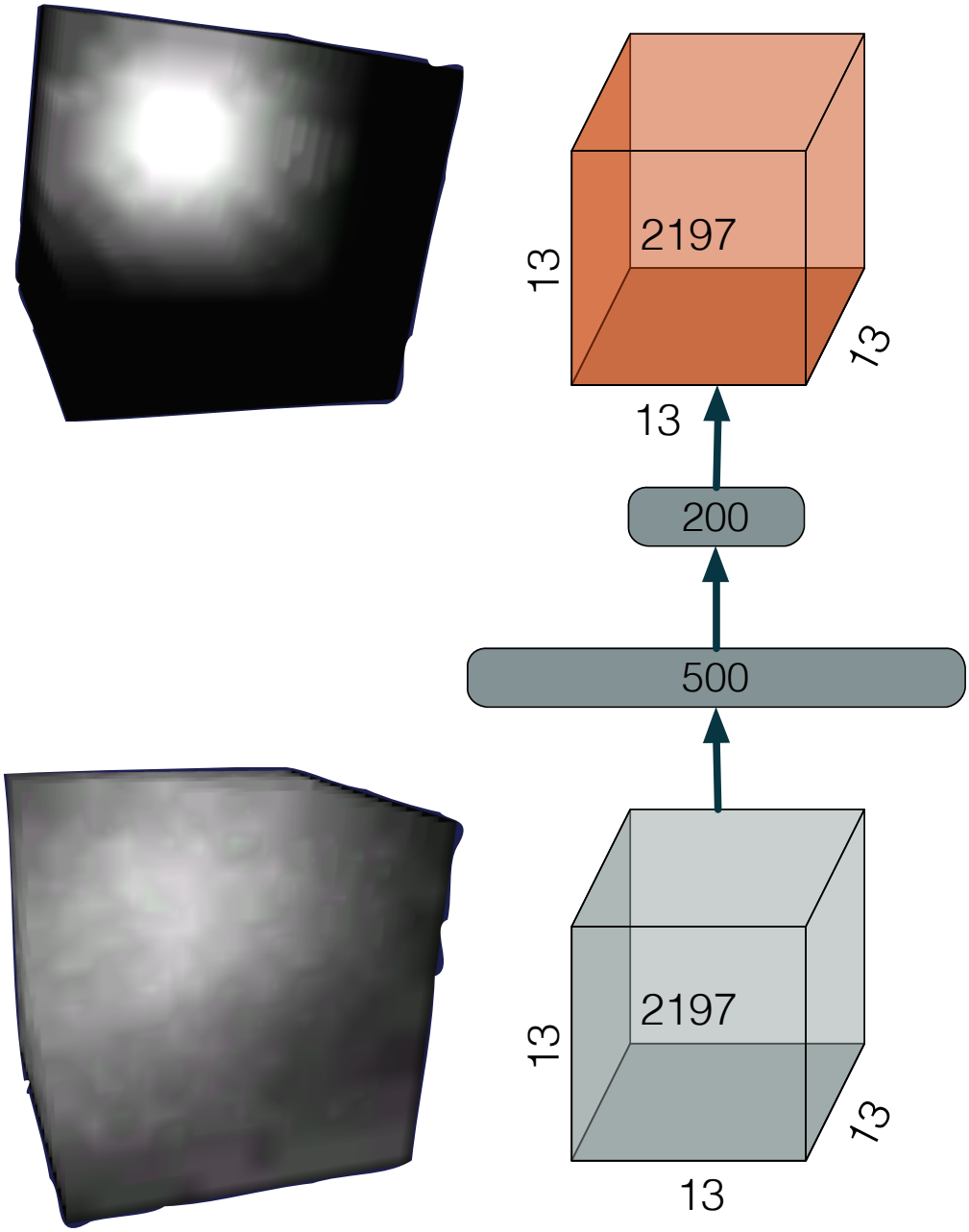
Supplementary Figure S1. Pipeline of the overall cell identification method



Supplementary Figure S2. Illustration of manifold filtering. The figure shows a portion of the Purkinje centers point cloud, with colors denoting the estimated manifold distance

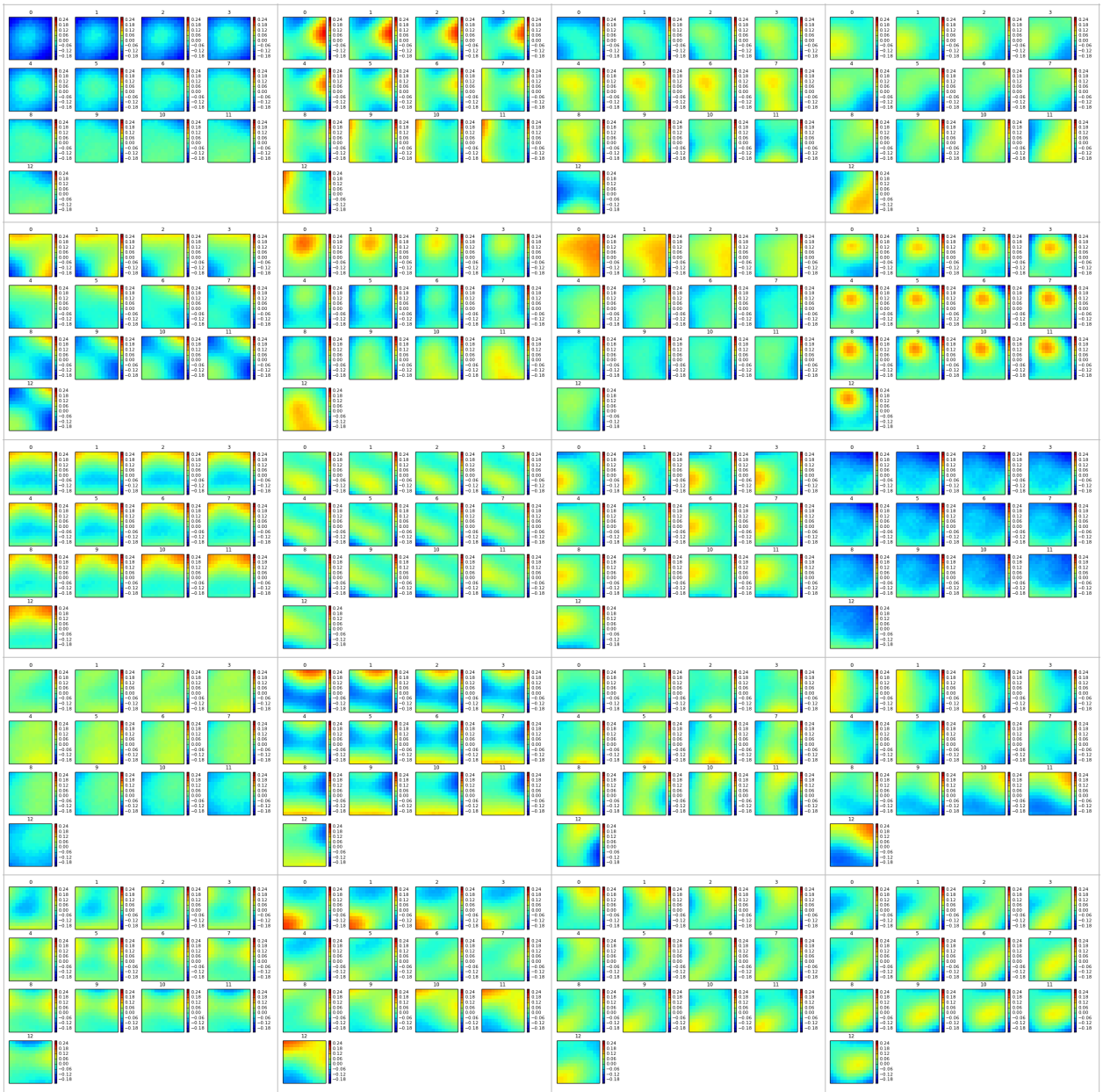


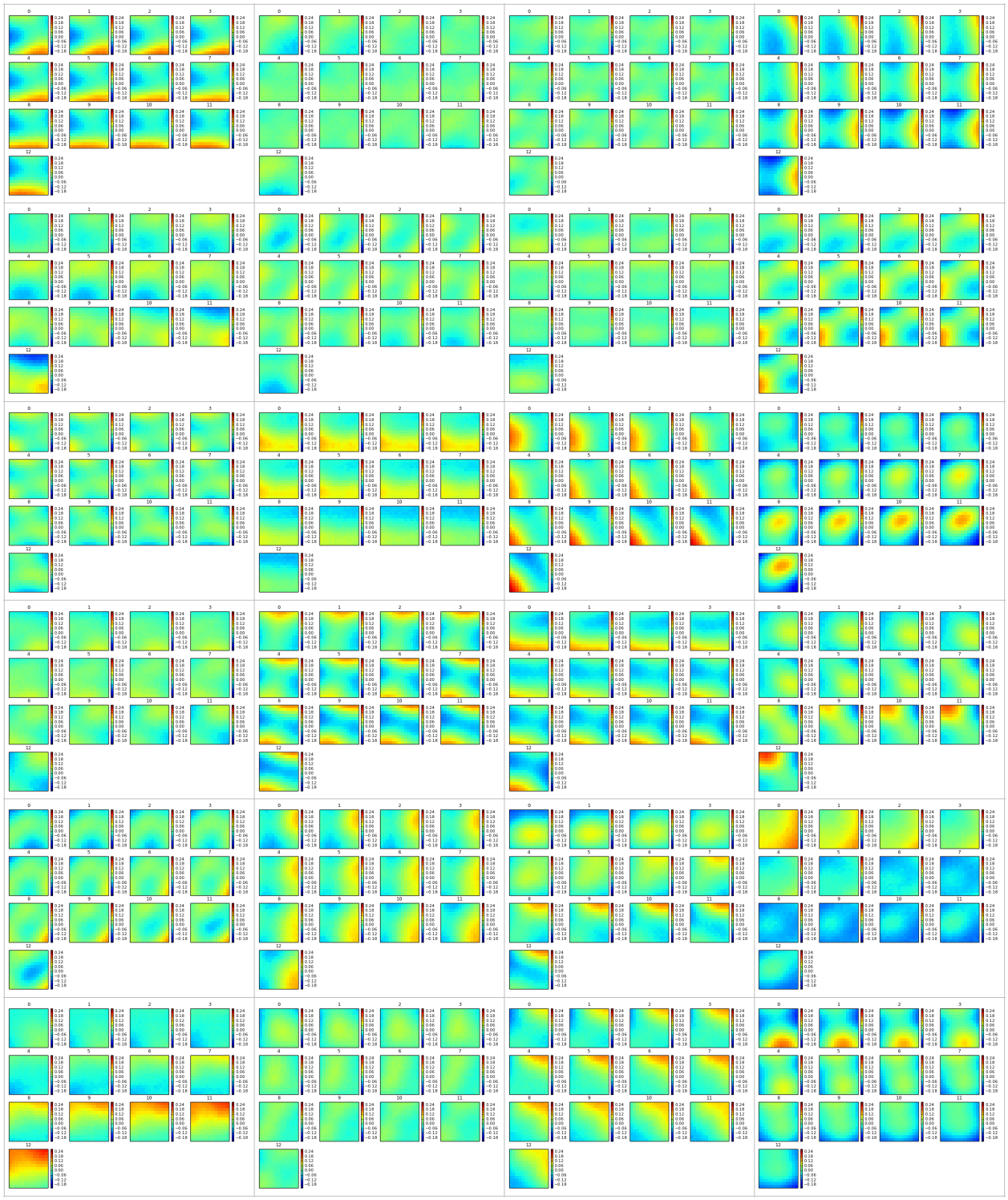
Supplementary Figure S3. Neural network used for semantic deconvolution



Supplementary Figure S4. Some of the filters learned in the first layer of the semantic deconvolution neural network

Each cell in the figure shows one 13x13x13 filter (i.e. the 2197 weights of one of the hidden units in the first layer) as a sequence of 13 2D images (one for each z coordinate). Color indicates the weight strength (blue is low intensity, red is high intensity)





The final set of predicted Purkinje soma centers

The file Cloud-xyz-d-sid.vtk.bz2 (available as supplementary data) contains a VTK file with 3D coordinates of the whole set of predicted Purkinje soma centers. Besides XYZ coordinates, it contains two scalars: distance is the estimated manifold distance, SID is the substack ID.
The file can be visualized with the help of programs such as Cloud Compare (http://www.danielgm.net/cc/) or Paraview (http://www.paraview.org/), both available for Linux, Mac or Windows.