Reproducing a meta-analysis of neuroimaging studies

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We can see that figures I reproduced are very similar to the original ones from the paper. The biggest difference is how some of them were plotted, i.e. I didn't find the correct brain atlas to plot them on so they might look a bit wrong. For the distribution of maximum proportion (fig 2) the plot on the left is the same one as provided in the paper. To do this perfectly I probably should run this with my own functions but doing that I couldn't utilize any of the provided plotting function which would make everything a lot harder to visualize.

To run this you need to run the file `runMetaRHH.m`. There are some commands you have to manually type in but I've provided the values they should be set to. The data is in the file `meta061106.mat`. I've also provided 2 of the toolboxes needed to run this. They are `densityUtility` and `SCN_Core_Support`. I recommend using the versions I have provided since they have been debugged and should work. The third package needed is `spm8`. I deemed it too big to upload here but it can be downloaded from `http://www.fil.ion.ucl.ac.uk/spm/software/spm8/`. I did have few issues with debugging SPM8 but all the errors where the same and involved the functions `flipud` and `fliplr`. If you run into the same issue the quick fix is to change the spm code by clicking on the error in matlab and changing `flipud(variable)` to `flipdim(variable,1)` and changing `fliplr(variable)` to `flipdim(variable,2)`. Good luck

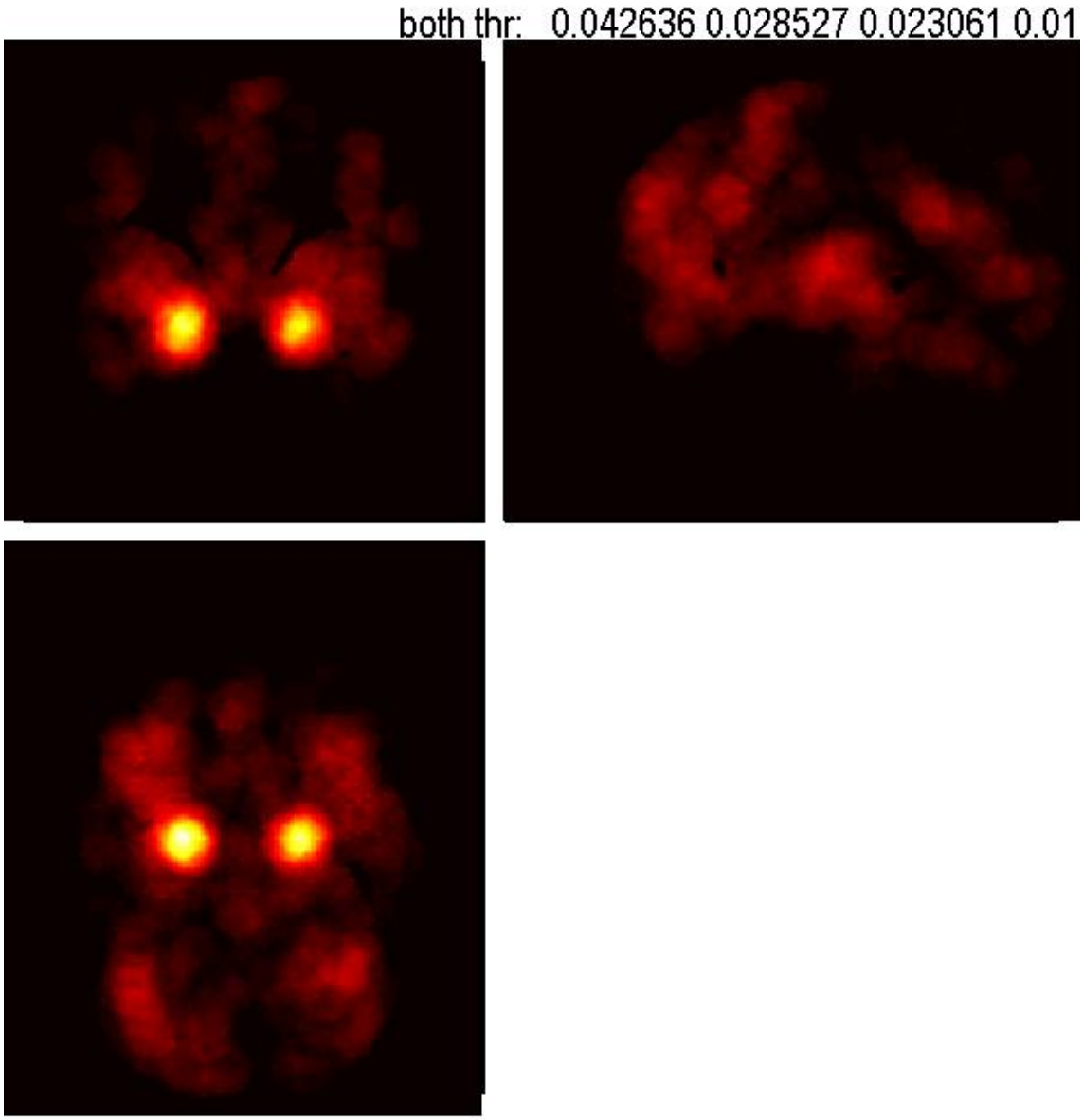

Figure 1: Density map for slice at Z=-16mm

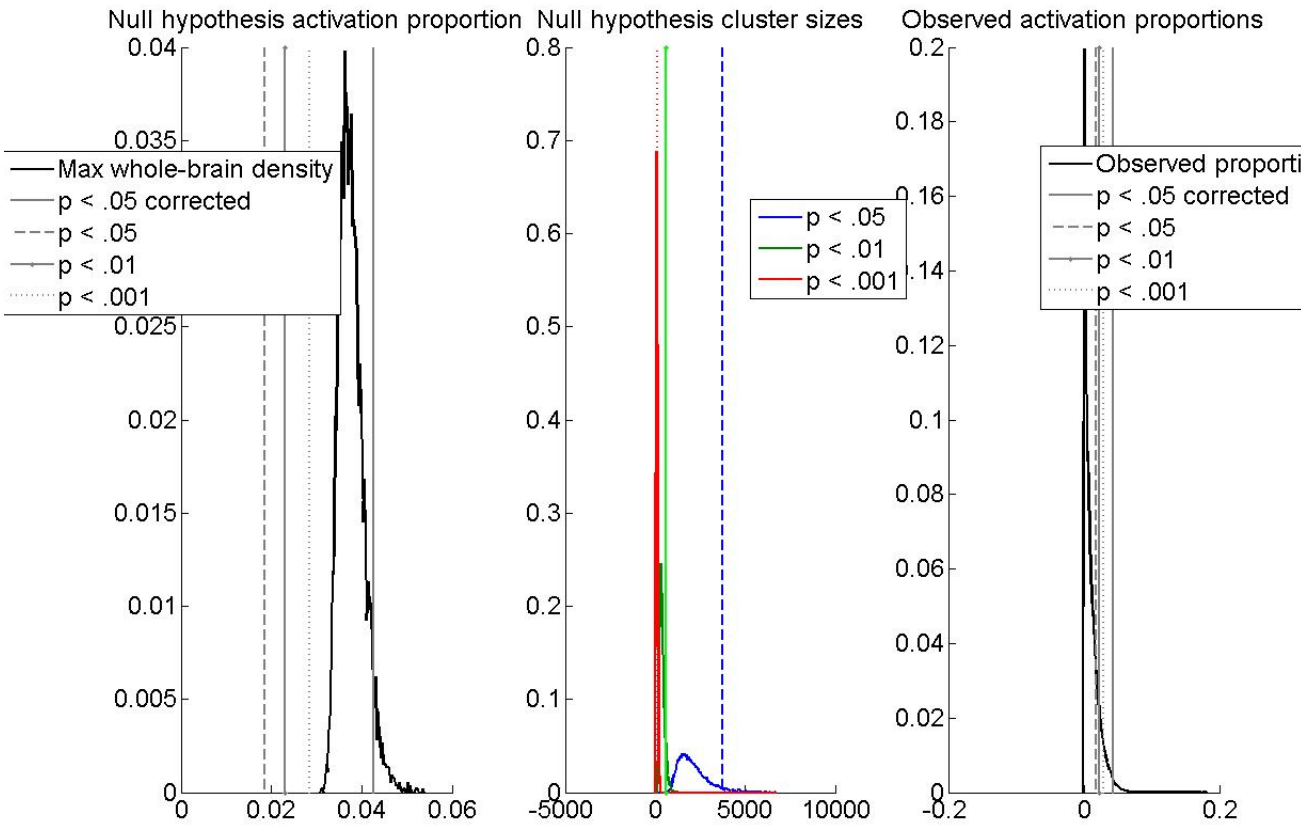

Figure 2: Expected maximum proportion under the null hypothesis.

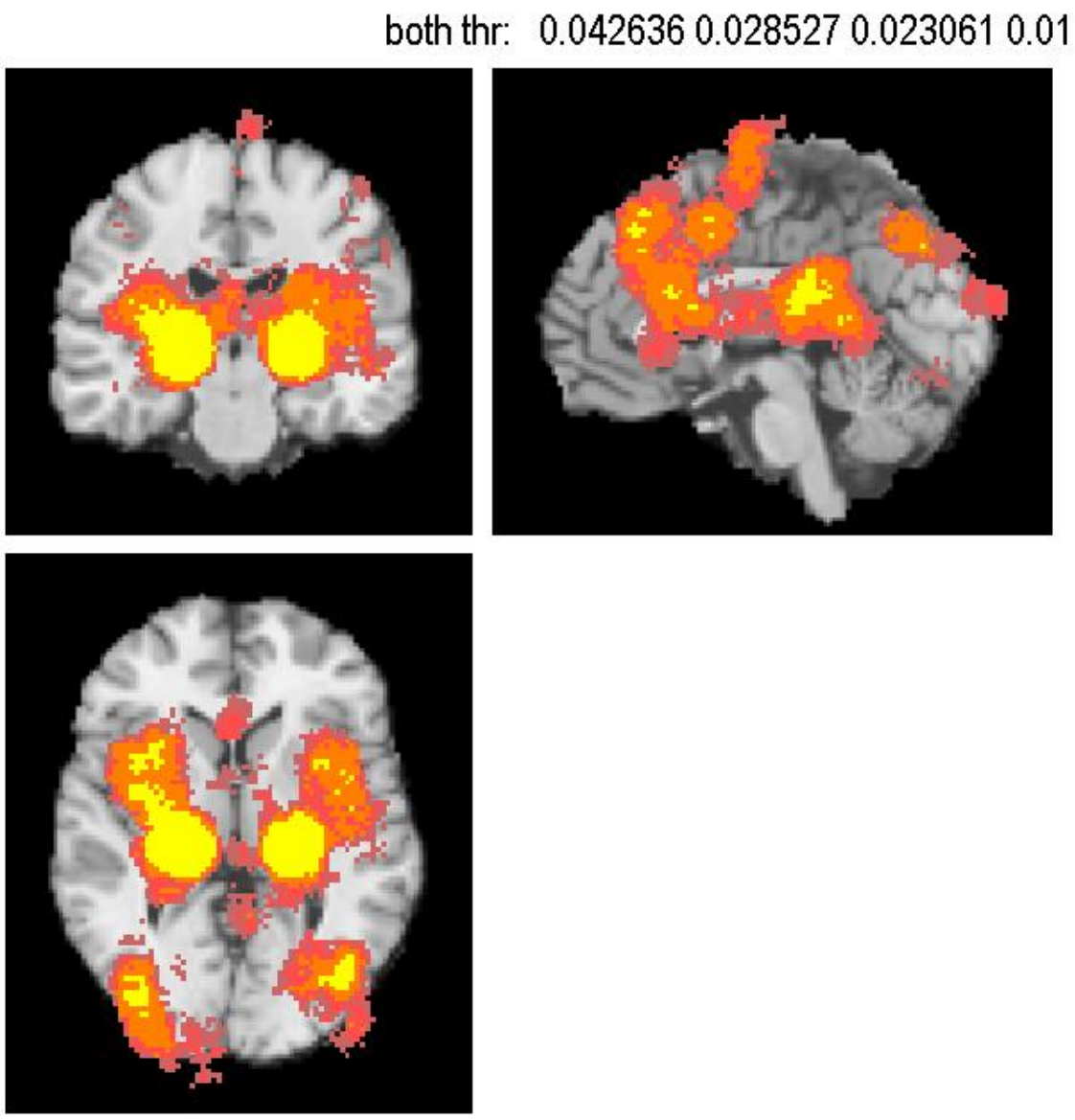

Figure 3: Significant regions at Z=-16mm