

Team Meta Practice Paper Reading

The point of this exercise is to have you go through all the steps of getting the relevant data from an fMRI neuroimaging paper of social interaction. You will not be doing all of these steps as we start getting into the flow of this, but I want to have you go through the entire process just so you know. Before going on, I need define social interaction in the context of fMRI studies.

Social interactions are the reciprocal exchanges between socially engaged individuals. This definition includes two main parts:

1) Social engagement – the participant is socially engaged with a live human partner who is engaging with the participant in real time.

- Can simply be through being told that they are engaging with a real person
- Person can be outside the scan room or in a distant location connected digitally
- The participant has to believe it, and feel as if they are engaged with the partner

2) Interaction – the participant has to be involved in a reciprocal exchange with the interaction partner, or at least be ready to reciprocate with the interaction partner.

- Exchange can be through eye-gaze, hand gestures, digital chat, game play, etc.
- Participant or partner has to make at least one response to something the other does; the response doesn't have to be immediate, but contingent on the other's action

Alright, now here is your mission!

1) Read the accompanying paper from the lab by Diana, titled "Social interaction recruits mentalizing and reward systems in middle childhood". Pay special attention to the Methods and Results sections.

2) Does this study count as a study of social interaction? Are the participants socially engaged? Do the participants reciprocate with their partner? If so, briefly describe how social engagement and reciprocation were accomplished in this experiment.

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3) Please identify and list the contrasts that target social interaction. Briefly explain how they target/isolate social interaction.

4) For each social interaction contrasts identified above, please fill in the attached spreadsheet with the contrast, coordinates, cluster size, and peak t value for each of the reported clusters. Is there anything weird about any one of these contrasts in terms of how it is reported in the coordinate table? If so, briefly describe below.

5) Pick one of these contrasts, and instead of filling in the region column with the label that is provided in the paper, please use the MRICron software to label each cluster using the **HarvardOxford** and **AAL atlases** (instructions and demo on next page). Do you notice differences between the labels provided by each atlas? Can you give any explanation about the differences between the labels provided?

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MRlcron

1) Install: To install MRlcron, go to this page, and select the download appropriate for your computer from the drop down menu in the middle of the page. For Mac, you download the .dmg file, open it, and move the MRlcron app into your application folder (that easy!). I'm not as familiar installing this on Windows, but I'm happy to help troubleshoot if you have issues: <https://www.nitrc.org/projects/mrlcron>

The screenshot shows the MRlcron project page on the nitrc.org website. The page layout includes a header with the project name and a 'Visit Website' link. The main content area describes MRlcron as a cross-platform NIFTI format image viewer, highlighting its capabilities in loading multiple layers, generating volume renderings, and drawing volumes of interest. It also mentions the inclusion of dcm2nii for converting DICOM images to NIFTI format and NPM for statistics. A small image of a brain scan is shown next to the text. Below the description is a 'Download Now' button, which has a dropdown menu open showing several download links for different operating systems and versions. The dropdown menu lists: '2-September-2019 (v1.0.20190902): MRlcron_linux.zip (17730 K)', '2-September-2019 (v1.0.20190902): MRlcron_windows.zip (19178 K)', '2-September-2019 (v1.0.20190902): mrlcron_macOS.dmg (19993 K)', 'MRlcron/NPM/dcm2nii 2MAY2016: MRlcron_macOS.dmg (29095 K)', and 'MRlcron/NPM/dcm2nii 2MAY2016: win.zip (20812 K)'. A 'Show all files' link is also present. To the right of the main content is a 'Statistics' sidebar with a dropdown arrow and an information icon. The sidebar lists: 'Home Page', 'Funding: NIH-NIDCI', 'Documents: 1', 'Forums: 284 messages', 'News Items: 3', 'Total Downloads: 6', 'Registered: Aug 19, 2016', 'Organization: University of California, San Diego', and 'Center: McCausland Center for Brain Research'. At the bottom of the page, there is a 'Specifications' section and a 'Participate' button.

MRlcron Visit Website

MRlcron is a cross-platform NIFTI format image viewer. It can load multiple layers of images, generate volume renderings and draw volumes of interest. It also provides dcm2nii for converting DICOM images to NIFTI format and NPM for statistics. MRlcron is a mature and useful tool, however you may want to consider the more recent MRicroGL as an alternative.

Download Now

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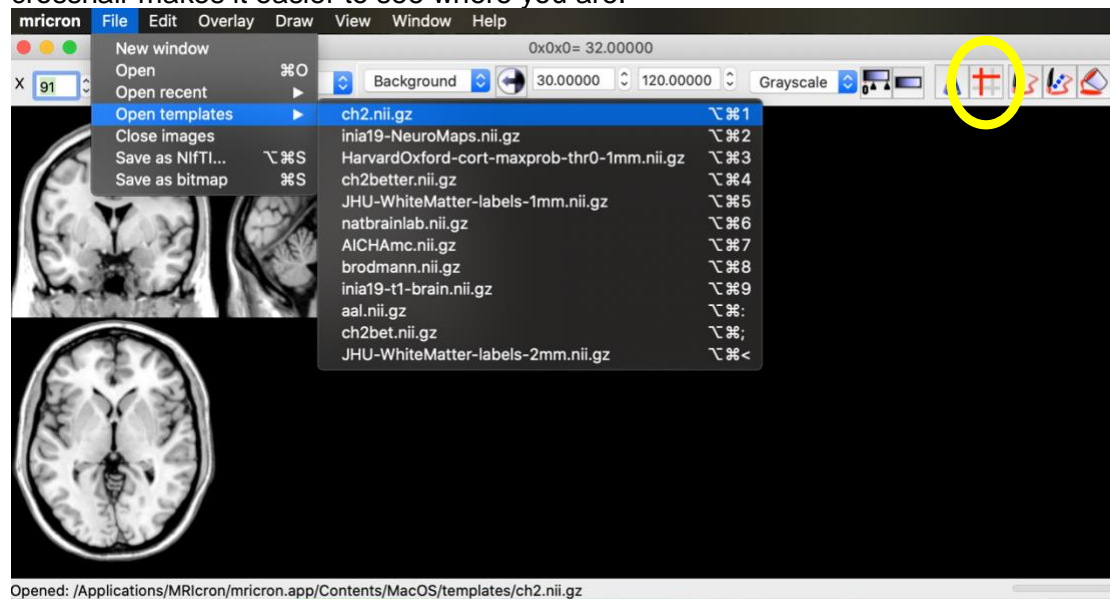
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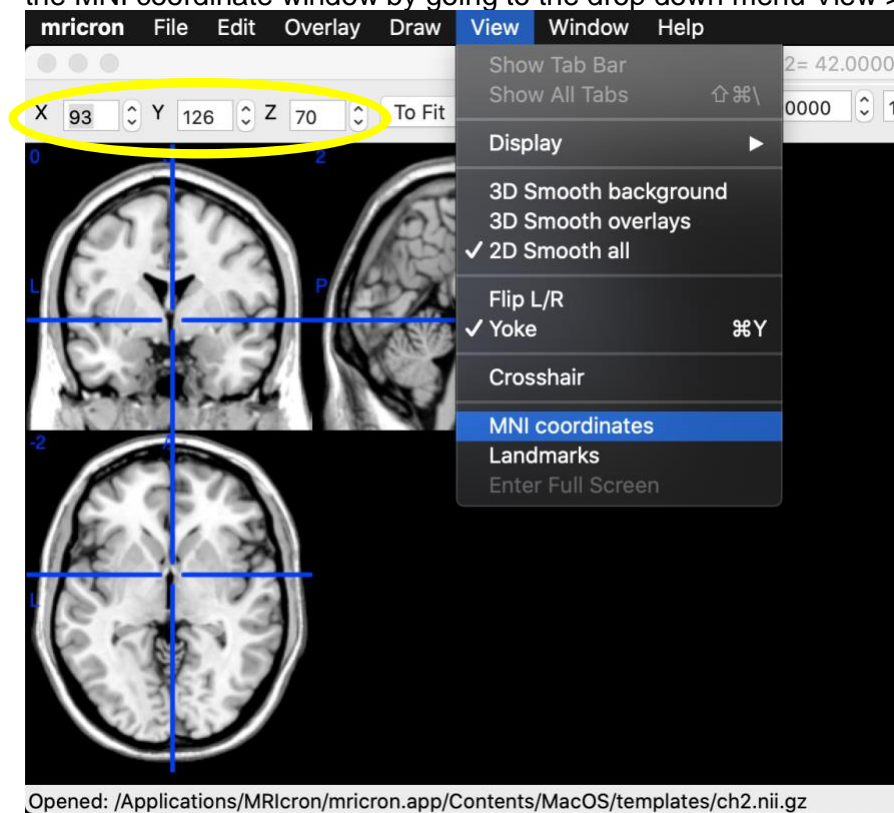
Specifications Participate

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2) Load Brain: When you launch MRIcron, it should automatically have the 'ch2' brain loaded, but if not, load it using: File > Open templates > ch2.nii.gz . This is an MNI normalized brain that you can use as a reference to see where you are in the brain. You can turn the crosshairs on and off using the circled in yellow in the screenshot below, or by going to View > Crosshair . The crosshair makes it easier to see where you are.

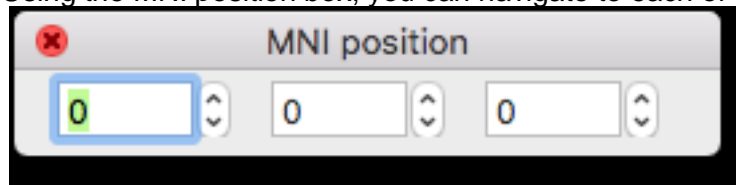


3) Go to coordinate: To examine the label from an atlas for a given coordinate, you can open the MNI coordinate window by going to the drop down menu View > MNI

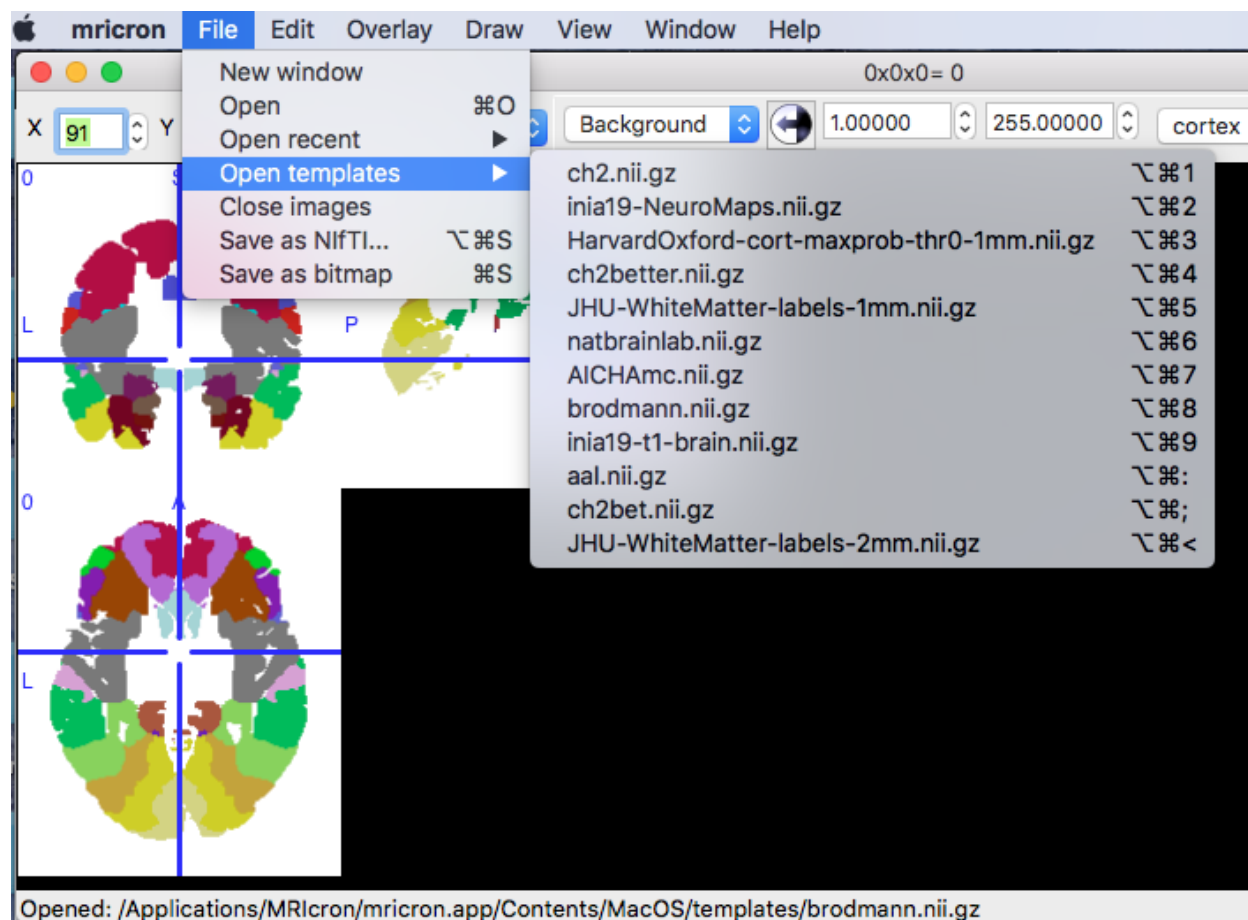


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This will open the following window. There, you can enter the x y z coordinates in millimeter space as is in the coordinates table. Notice how the values you enter in the MNI position box do not correspond with the xyz in the toolbar circled in yellow in the above screenshot. The toolbar values are in voxel space and are positioned differently (e.g., x=0 is the furthest left you can go). Using the MNI position box, you can navigate to each of the coordinates:



4) Load Atlases: You can load each of the desired atlases (i.e. **HarvardOxford** *and* **aal**) using the same drop-down menu: File > Open templates



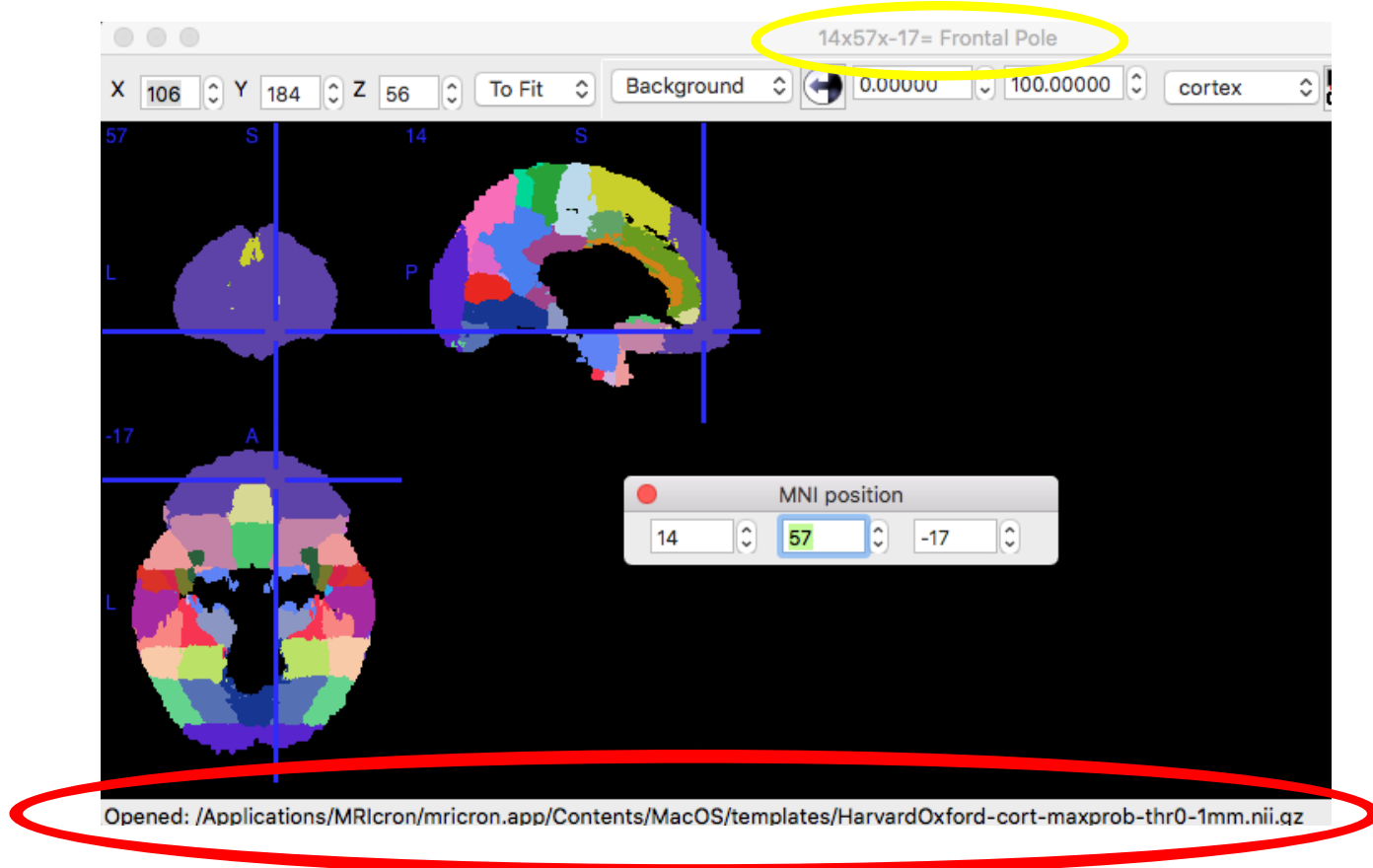
I think it would be easiest to start with one atlas, work through all the coordinates, then move to the next. That way you won't have to keep loading different atlases, but it's up to you!

Once you have the atlas loaded, you can go to the different coordinates (using the MNI coordinate approach in item 3 above) to get labels for each brain region for which you have coordinates.

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Note, when entering the coordinates, pay attention because sometimes it will not register a negative '-' sign. It's free software, so can be a bit glitchy. Also, you'll have to round to the nearest digit.

5) To determine the label is not so obvious. When you have entered the coordinate for a region, the atlas label will appear on the top bar (circled in yellow). The bottom bar will let you know what atlas is loaded (circled in red). For example, in the image below, I have the HarvardOxford atlas loaded, I went to x=14, y=57, z=-17, and the label is Frontal Pole:



Feel free to go back and forth between the atlas and ch2 brain to get an idea of what gyrus/sulcus/location you are in. You can open up two windows by going to File > New window and have the atlas loaded in one window and the ch2 brain loaded in the other. However, sometimes the two windows will not be synced (or yoked) to each other, so if you navigate somewhere on one brain the other brain may not also go to the same place. To make them "yoked" to each other, you can go to the drop-down menu: View > Yoke

PLEASE EMAIL ME WITH ANY QUESTIONS! If you spend more than 15 minutes to figure something out, and it is not working, shoot me a message! I'll appreciate your tenacity, but I do not expect you to figure this out so easily.