

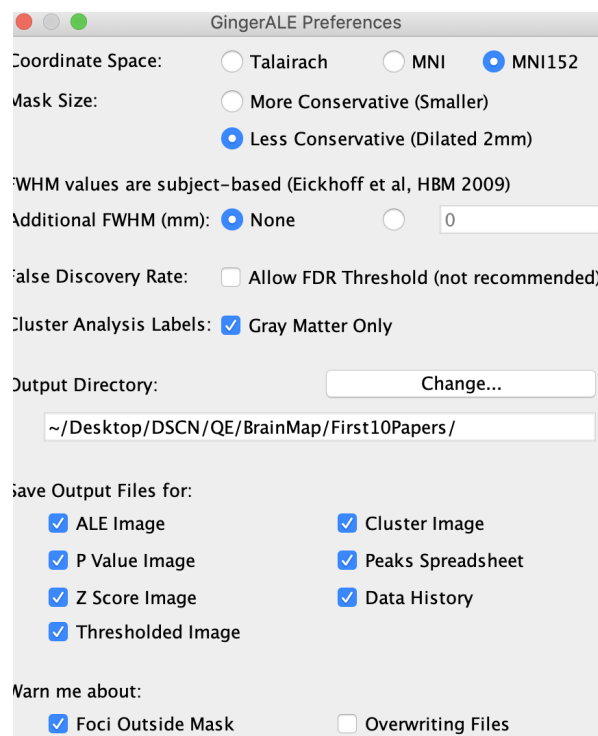
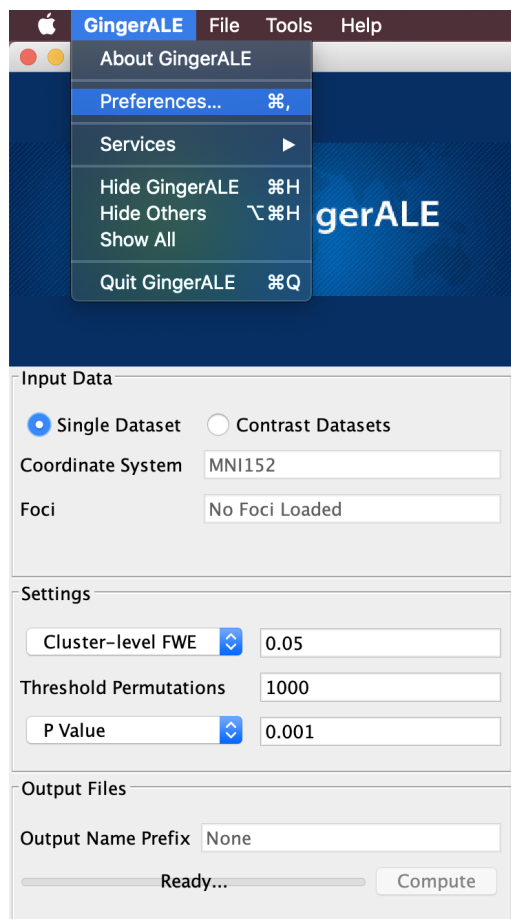
1) Software installation:

1. To install Ginger ALE, follow this link for installer and instructions:
<http://www.brainmap.org/ale/>
2. You'll probably want to download a text editor that allows you to create/edit simple text files because Mac's TextEdit and Window's Notepad automatically create rich formatted text that doesn't work with code and applications like Ginger ALE. I recommend Sublime, which is really easy to install and use: <https://www.sublimetext.com/>
3. Finally, I know I led you astray with MRlcron to view images, but Mango is a little easier, and what the Ginger ALE people recommend: <http://rii.uthscsa.edu/mango//mango.html>

2) Launching/Starting Ginger ALE

After you install Ginger ALE, please refer to the manual for full instructions, but I'll summarize how we'll use it below. Here's the manual: <https://www.brainmap.org/ale/manual.pdf>

1. When you launch Ginger ALE, the first thing you want to do is specify the Output Directory. I did not realize this before (and it was really confusing). To do this, under the Ginger ALE drop down menu, select Preferences, and Change the Output Directory to somewhere you'll be able to find out images. You can also change the Mask Size to Less Conservative. Leave all the other preference options as you see it below:



3) Creating a Foci text file

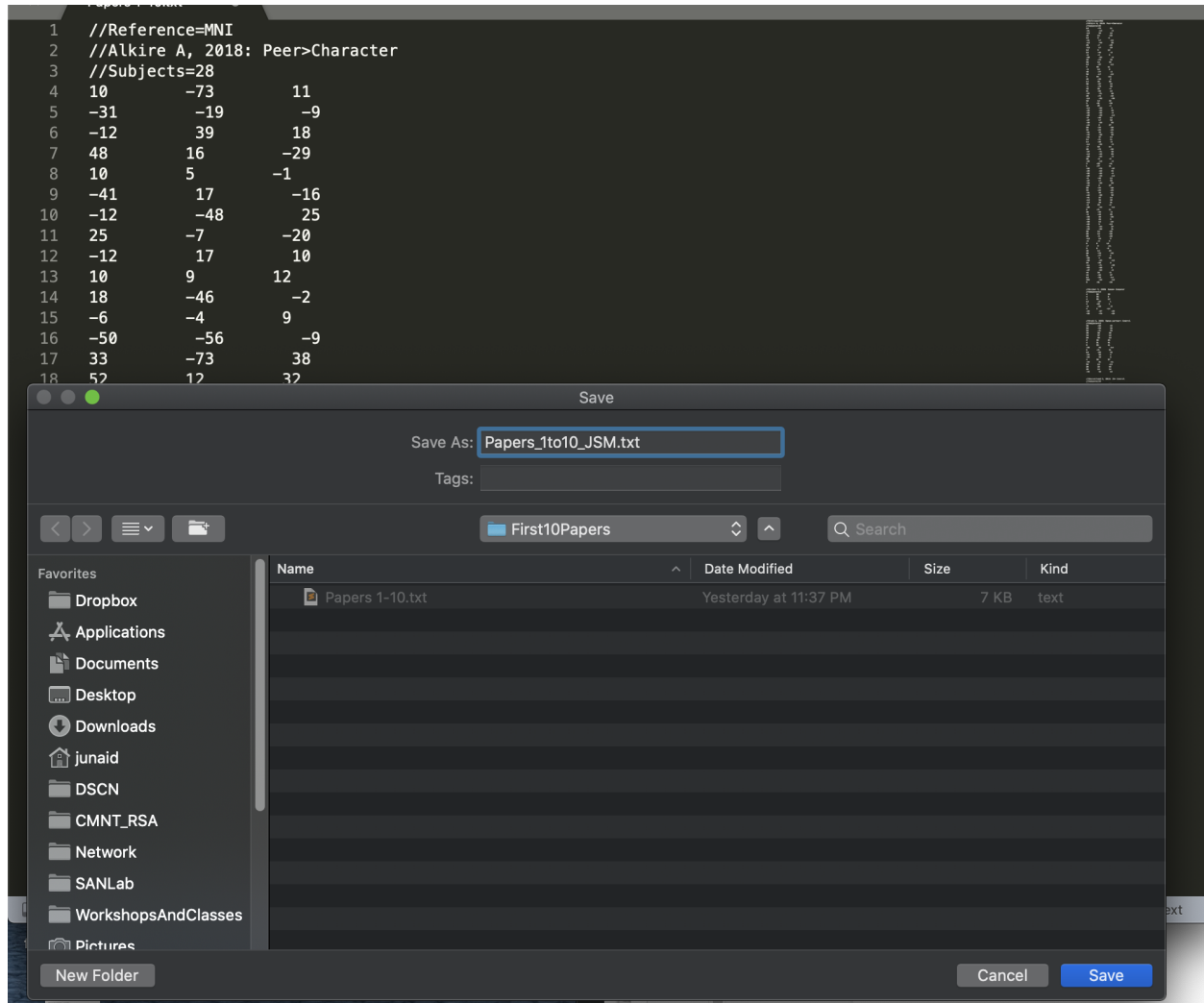
Now you want to launch the Sublime Text editor to create your Foci file that you will use as input for the Ginger ALE meta-analyses.

1. When you start Sublime, it should automatically have a new, blank document. Following the instructions in [section 2.1 of the Ginger ALE manual](#) (page 3), you want to start creating a file that contains all the foci from all the papers you've extracted coordinates from! For each paper, you start with the following lines as follows. Each of these lines has to start with 2 forward slashes, otherwise the software will not recognize it.
 - a. First line is the reference space, which will usually be MNI (but double check) as follows: 'Reference=MNI' (see below)
 - b. Second line is last name of first author, followed by the year separated by a comma, then a colon followed by the contrast name (see below).
 - c. Third line is the number of subjects as follows, for example: 'Subjects=28'
 - d. Then you can copy and paste the coordinates for that paper below.
 - e. **IMPORTANT:** Even though we separated multiple contrasts from each paper in our spreadsheets, we will not do that here. Every time we separate coordinates from different contrasts (even from the same paper), it treats it as a separate study. So here, we'll copy and paste the Peer>Character coordinates, and then without skipping a line, the next set of coordinates from this paper etc.

```
//Reference=MNI
//Alkire A, 2018: Peer>Character
//Subjects=28
10      -73      11
-31      -19      -9
-12      39      18
48      16      -29
10      5      -1
-41      17      -16
-12      -48      25
25      -7      -20
-12      17      10
10      9      12
18      -46      -2
-6      -4      9
-50      -56      -9
33      -73      38
52      12      32
18      -37      -13
4      45      11
-5      10      0
40      -77      -3
```

```
96      46      14      23
97      20      -75      -32
98      31      -77      9
99      -29      4      45
100      -58      -23      -16
101      54      -38      2
102      -11      -71      -30
103      -63      -50      2
104      -47      -53      -8
105      44      24      -2
106      44      -56      27
107      18      -38      -14
108      335      -38      -18
109      8      -51      -39
110
111      //Kircher T, 2009: Human> Computer
112      //Subjects=12
113      4      52      38
114      4      35      2
115      4      55      12
116      12      -27      1
117      4      -23      1
118      -8      -20      -6
119      4      3      -14
120      -24      -87      -23
121      -36      -79      -23
122
123      //Krach S, 2008: Human partner> Control
124      //Subjects=12
125      36      -58      43
126      53      -52      39
127      53      -41      35
```

- f. Once you have all the data entered, save it as a text file with a name that makes sense. Whatever you name this file is what Ginger ALE will label the outputted data. This example text file that I created, [you can find here](#) if you want to use it as a reference.

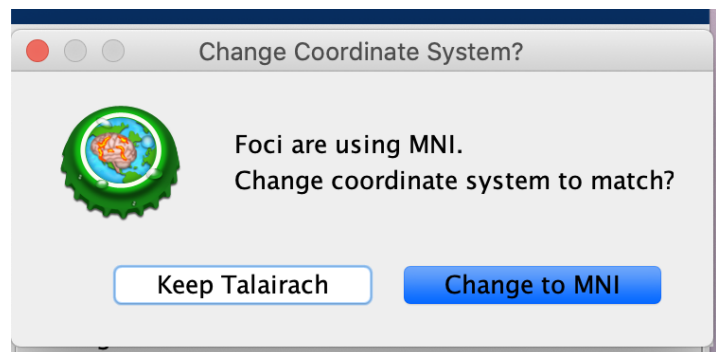
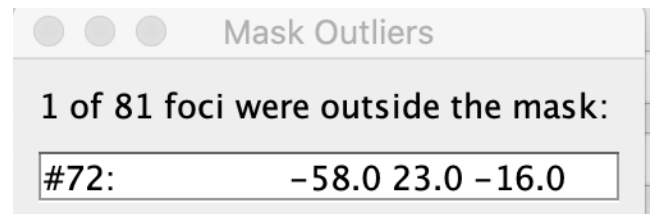
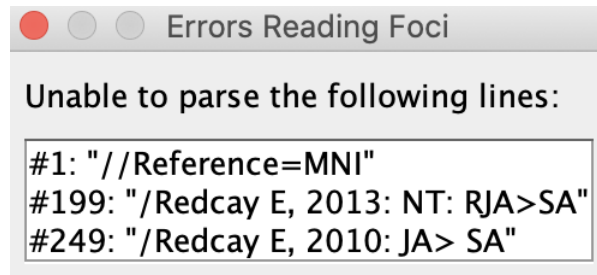
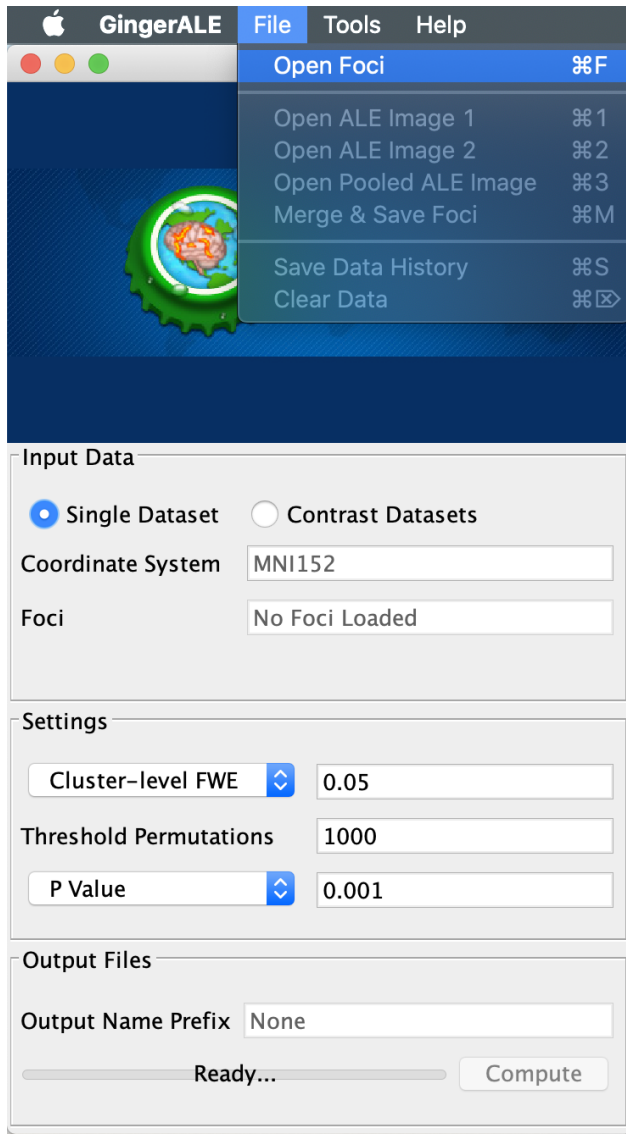


4) Running the meta-analysis

Now we are going to run the meta-analysis using Ginger ALE.


1. You'll first launch the application, and open the text file you just created. To do this, go to File > Open Foci . You'll want to make sure that you have selected Single Dataset as the input data. You might get an error message if you didn't format something right in your text file (for example using one forward slash instead of two; like the first error message below). If you get a message about a foci being outside of the mask (like the second error message below) that is totally OK. You don't have to worry about that and you can

simply close that error dialogue box. Finally, if you are asked to change to MNI, the select to do so (third box below).



- After loading your text file, it should give you some info about the text file you uploaded. Of note, even though I uploaded the text file for the first 10 papers, the Redcay E, 2010 paper had two different subject samples that I separated using different lines, and that's why Ginger ALE is saying 11 experiments!

GingerALE: Papers_1to10_JSM



GingerALE

Input Data

☒ Single Dataset ☐ Contrast Datasets

Coordinate System

Foci

271 Foci, 11 Experiments

Settings

Cluster-level FWE

Threshold Permutations

P Value

Output Files

Output Name Prefix

Ready...

```

222
223 //Redcay E, 2010: Live> Recorded
224 //Subjects=16
225 6      14      36
226 2      36      14
227 8      6       62
228 -40    14      4
229 38     16      0
230 54     -48     12
231 60     -46     24
232 38     -64     8
233 48     12     -30
234 38     -70     20
235 -48    -44     22
236 -46    16     -16
237 -48    -60     4
238 10     -74    -12
239 -42    -56    -28
240 20     -2    -18
241 26     -16    -14
242 -18    18     4
243 -12    12     -4
244 22     8     -10
245 -14    -8     6
246
247 //Redcay E, 2010: JA> SA
248 //Subjects=13
249 48     -40     6
250 54     -58     14
251 50     -70     0
252 -48    -56     14
253 -48    -68     6
254 -10    -106    14
255 2      -88     -2
256 46     30     -6
257 6       50     44
258 58     2     -24
259

```

- Now, leaving the default parameters as above, you can hit the compute button to run the meta-analysis. This is computationally heavy duty and will heat up your laptop, so if your laptop cannot handle running something this, don't worry about actually running it. Honestly, unless you have a newer laptop and/or a cooling pad, maybe don't worry about running it on your computer, unless you're running a meta-analysis with only 2-4 studies. If you do run it, it will take a little while to finish. Once it does, you'll find all the result files in the directory you specified in Part 2 of this manual! I've included the [results from this tutorial here if you want to see what the output files](#) look like. Feel free to download this folder and open up any files using the Mango app I mentioned in Part 1 of this manual. Section 2.5 of the Ginger ALE manual describes the output images, but here are brief descriptions:

- a. *Papers_1to10_JSM_ALE.nii* - This is the un-thresholded Activation Likelihood Estimation (ALE) map, which basically has all the coordinates we entered, and gives a likelihood estimate for each voxel of the brain. This gives the raw probability of getting an activation in a brain area for social interaction.
- b. *Papers_1to10_JSM_C05_1k_ALE.nii* - This is the thresholded ALE map, which gives a likelihood estimate for each voxel of the brain after statistically adjusting. This gives the probability of getting an activation in a brain area for social interaction after selecting only the statistically significant areas of overlap. See the image below—this is the meta-analytic map for the first 10 papers showing significant overlap in reward regions of the brain (ventral striatum; top image, middle of the brain next to the ventricle) and posterior superior temporal regions which are important for social cognition!!
- c. *Papers_1to10_JSM_C05_1k_clust.nii* - Same as above, except the clusters are labeled with the numbers you find in the .xls file below
- d. *Papers_1to10_JSM_C05_1k_clust.txt* - Text file that gives details about each of the resulting clusters that are statistically significant.
- e. *Papers_1to10_JSM_C05_1k_peaks.xls* - Coordinate spreadsheet that has all the clusters that are statistically significant. In this case, statistically significant means that across the coordinates we entered into this meta-analysis, these are the regions that have statistically significant amount of overlap across our studies.
- f. *Papers_1to10_JSM_P.nii* - Unthresholded p-values (stats) for each voxel of the meta-analytic map
- g. *Papers_1to10_JSM_Z.nii* - Unthresholded z-values (stats; number of standard errors) for each voxel of the meta-analytic map

