There are a lot of notes and comments in the medacoder script to myself (and some of them are from the postdoc who wrote the original script), but they're worth reading. Some main points to keep in mind:

- The attached code is specific to one version of metacoder (v1.3), and the link to download is the first line in the script.
- The shape of the tree (node rotations) is determined by set.seed() just prior to the heat_tree() command. For each of my trees, I tried out different values (see line 119 for my notes) to see which tree shape looked the best. The node identities will not be affected by this number. There is a loop at the end of the script that you can use to write a bunch of PDFs using different seed values so you can scroll through and pick an aesthetically nice tree. The loop doesn't work for some reason (I was even more of a novice when I wrote it), but you can highlight it and run it manually.
- The color of the tree is set by the node_color setting in the heat_tree() command. Unfortunately, to get custom colors on different branches, I had to export each tree as an SVG file and import it into Inkscape to edit the node and branch colors. I then exported that shape and manually annotated the nodes in PowerPoint. Illustrator is probably better for these steps if you're familiar with it, but I'm not super experienced with Illustrator. Before you put a ton of time into editing, I would recommending double-checking the labels on the nodes that you're interested in against the list of GO terms you were expecting to see in the figure.
- One last aesthetic decision I made was to prune some of the internal nodes of the tree. Because each tree represents terms from only 1 of the 3 GO domains (BP, MF, or CC), all terminal nodes can be traced back to the central node, which corresponds to the GO domain. If anyone reading the figure wanted to know the identity of the internal nodes, they could trace the relationships from the terminal node to the central node using the GO hierarchy. If I had wanted to highlight any internal nodes (i.e., if those nodes corresponded to significantly overrepresented GO terms), I would have kept them and labeled them.

I've attached an example data file and the metacoder script. You should be able to run the script through with the example file and get back a PDF that looks like the one I attached here. If that doesn't work for some reason or if you have any other questions, please let me know!