





Problems

1. The process is manual, not great for large volumes of subjects.
2. Requires access to fsaverage with HCP space in order to get HCP in patient space. Also needs access to label map for proper ordering of HCP regions. FS regions might be discarded/replaced in the future.
3. Way too many versions available (and publicly not available) will need to account for possibly several versions of the segmentations. Also comes as a full label map with its own values that will need to be overwritten.
4. None at the moment
5. None at the moment
6. See 2
7. Need to find a method to collect all volumes and combine in a way that can be understood before and after calculation, as well as a conversion to be understood by MRtrix (increment by 1, no spaces). Constantly changing regions and subdivisions will also but something that needs to be dealt with, especially when old regions are replaced. Also, we will need to be careful about the order of things being added. We don't want too much overlap, but when it happens, we want to make sure the most important ones are added last.
8. There are many permutations of parameters to generate the connectome matrix, and it might require running multiple versions.

Possible Solutions/Thoughts

- Regions will most likely be added/removed/recalculated very often. We will need a lookup table to keep track of all of the regions. We will want to keep a lot of space between groupings. Or we don't need to keep them separated but just tack new ones onto the end. Dealing with old/redundant ones will be tricky. I think we either have to remove them manually whenever we introduce a replacement, or we keep it in and designate it as 0 in the label map. This way might be better as we can keep track of what used to be in the map. We would probably need to keep track of the original labels (such as THOMAS' 2-18) so that we can reference them while combining volumes.