FIRST PRIORITIES

* + Make the software flexible, so it can easily load & work with other functional connectivity data sets
* Some kind of setup script file seems like the easiest approach, where the user can set how the data are parsed (e.g., are there two groups of subjects? Multiple scans or days for each subject? Which categorical and continuous variables should be included in the Settings panel?)
* Add behavioral metrics to the Settings tab (e.g., for the current data, a measure of memory performance).  
  **We have developed a flexible software this time e.g., you can add any attributes of subjects.**  
  + Make it easier to install the software  
     **We made installation much easier as described in the user manual.**  
     **We are still trying to find the easiest way.**
* Use the tool to test data that there is some known truth for   
  (e.g., data from Haxby, 2001: <http://www.pymvpa.org/datadb/haxby2001.html> )  
  **If I understand the data correctly, we think we need to know how to process fMRI images to obtain correlation matrices (i.e. we want the software, programs, and procedures you used). We think we could also try this data. http://www.humanconnectome.org/data/**

OTHER SUGGESTIONS

* Make it possible to restrict ROIs in the correlation matrix view in a meaningful way (e.g., MTL only, etc.).
* Questions: What is the order of the ROIs in the correlation matrix view? How is the order of ROIs set, and can it be re-ordered (after the data are loaded)?  
  **In current version, you can see the order by selecting “Order of Matrix” from a drop-down list. Also, you can change the order manually in the information view or automatically by applying clustering algorithm in the matrix view.**
* Questions: How were modules determined? Why 3 modules? Is the number of modules specific to this dataset? **In the current system, you can set the number of modules when you apply the hierarchical clustering in the matrix view. Or, with “Arrange with Modularity” in the matrix view, the system automatically find the best number of modules to optimize the modularity with the Louvain method (So sometimes 3, sometimes 5. This is based on the data).**
* Would be useful to be able to tell more easily what the different nodes are, & to flexibly select sets of nodes/ROIs
* It would be nice to select subsets of ROIs in the “Show nodes in 3D list”, because now you can only select a subset of ROIs in the “correlation matrix view” (where it is difficult to know which nodes/ROIs are selected).  
  **We added this functionality.**
* Would also be nice to select a non-contiguous subset of ROIs (as now you can only select contiguous ROIs)
  + If it’s possible to select a subset of non-contiguous ROIs, we would want a list of the select ROIs.  
    **We added this functionality too. We changed the selection method in the matrix view.**
* Seed-based analysis.
* Select a region in the list of ROIs, & it would highlight that row in the Correlation Matrix View
* Select 5 or 6 ROIs, show where they are in the correlation matrix, then regenerate the correlation matrix for only the selected subset of ROIs.  
  **In the current system, multiple ROIs can be selected from the information view. By using this functionality, the analysis above can be done.**
* Export correlation values (and distance metrics) into a .csv file so you could do stats  
  **We added this functionality. You can save it from “File” menu or a dialog appeared in the matrix view by right-clicking.**
* It would be nice to specify correlation threshold values in setup script (because it takes so long to adjust).
* Would be great to do two-tailed correlation thresholding (e.g., display correlations less than -.5 and greater than .5)  
  **We added these. By right-clicking on the threshold sliders, you can show a dialog to setup these.**
* Would be nice to hover over a point in MDS view and have it tell you what the data point is (i.e., which subject/scan).  
   **We added this functionality.**
* Implement a dendrogram — would be useful to look at similarity relationships amongst all brain regions in a hierarchical cluster format. And would help you choose subsets of nodes to examine.  
  **This will be done later. In the current version, you can set the number of clusters.**
* Make edge bundling faster  
  **This will be done later. Please, try to use this function after reducing the displayed edges. (e.g., change the thresholds, then apply edge bundling.)**
* Documentation on MDS scaling method
* Question: We still don’t fully understand why the group average points don’t fall in the middle of the control / stressed “clouds” of individuals’ points (in MDS view).  
  **A brief description about MDS is in the supplemental material. We will add a detailed description.**
* Additional information about the MDS method to help you interpret the MDS “space” you see
* Tutorial data to help a user understand how MDS plot displays relationships (e.g., dogs breeds and common / distinct features… this dog is more or less similar to this other dog).
* This might exist for the Haxby data, in which subjects viewed “categories” of objects (see URL above)
  + Would be nice to have at least 2 categories in the tutorial data. Within each category, how similar are things? Across the categories, how similar / different are they?  
    **We will add examples with the detailed description.**
* Flexibly change colors of points in MDS view
* Would allow you to easily match the colors in MDS view to other figures you have for the data
* Maybe use a color scheme that is more friendly to the color-blind  
  **We updated the colors. Additionally, in the current system, you can set your own color files.**
* Options for other types of data that the software may be able to handle (with some modification):
* RSA (Representational Similarity Analysis): This type of data involves correlating observed similarity between regions, or between “similar” trials
  + First-level similarity: vectorizing and then correlating the similarity of the “similarity structure” across brain regions
    - Doesn’t tell you anything about how the trials are organized. Instead, this is telling you about how brains are representing the different trials (or trial types).
    - Could possibly create modules of trial clusters (instead of modules of ROIs).
    - Not sure how to display this kind of data in the glass brain view, because you’re limiting the visualization to trials (or types of trials) that meet a threshold of similarity in brain activity (instead of limiting it to ROIs that meet a certain threshold of similarity).
  + NaN out the RS matrix so it only includes values for trials that share a certain feature
* Give the program pattern information instead of the trial-by-trial correlation matrices
  + Create header file listing attributes you care about and filter relationships
  + Would make it more of an analysis tool than a visualization tool

**These will be done later. Probably, we need to discuss about this to understand in more detail.**