Notes on using the Fly Protocol Designer software so far:

SETTING UP YOUR MATLAB PATH

* When you download from the G4\_Display\_Tools repository you now get all the data analysis files and designer/conductor files. Make sure the folders G4\_Protocol\_Designer and G4\_Data\_Analysis and all their subfolders are on your path.
* Please note that if a folder called PControl\_Matlab is in the repository, you must REMOVE this from your matlab path for the data processing steps to work. Also please remove ‘C:\matlabroot\PControl\_G4\_V01\TDMSReaderv2p5’ and all its subfolders and files from your path, but make sure the rest of PControl\_G4\_V01 is on the path.

START-UP

- Before running, open the G4\_Protocol\_Designer\_Settings.m file and check the path to your panel configuration file. If this path is incorrect, you'll get an error.

- To run the designer, open the "G4\_Experiment\_Designer.m" file and run in matlab. To run the conductor separately, run the file called " G4\_Experiment\_Conductor.m".

- Note: If you get an error regarding "findjobj" when you run the script file, check to make sure findjobj, a folder inside G4\_Designer\_Protocol with everything else, is on your matlab path.

THE CONDUCTOR

- Please note when running the conductor there is no button to clear out your data. However if one experiment is loaded in the conductor and you'd like to run a different one, simply open the new experiment and it will replace the old.

- I have made it so you cannot edit the experiment name in the conductor, only in the designer.

- There are two ways you can open the conductor - separately from the designer, by running “G4\_Experiment\_Conductor.m," or as a child of the designer by hitting the "Run" button on the designer. There IS a difference between these two modes, though slight.

- If you have opened the conductor by way of the run trials button, then the conductor and the designer are sharing the same underlying data. If you then change any parameters in the designer, it will also change those parameters for the conductor. If you change the experiment name in the designer, it will now also update the experiment name on the conductor so you can easily see which experiment the conductor is running.

- If you have opened the conductor by way of the " G4\_Experiment\_Conductor.m" file, then the conductor and designer are separate and what you do on one will not affect the other.

- When you open an experiment in the conductor, it will automatically update the config file to match the settings for that experiment, but you still must make sure the path in G4\_Protocol\_Designer\_Settings.m is correct!

IMPORTING:

- Please make sure to select the appropriate screen size BEFORE importing. If you import pattern files which do not match the selected screen size, you will get an error and the patterns will not import. However, any position or AO functions in the folder will import as normal. Once a folder has been imported, the screen size option will become uneditable, meaning if you need to change screen size, you will need to exit the application and restart it.

- You can import any combination of files and folders. It attempts to find the associated .pat/pfn/afn file when you import a file, but if it can't find one, it will let you know, and you'll need to move that file manually.

- Autofill will create one block trial for each pattern, as well as put pattern 1 (or the pattern with the smallest ID) in the pre, inter, and post trials. It will automatically add the corresponding position functions and AO functions to the AO 1 channel if they have been imported. If position function spaces are left blank even though position functions have been imported, it means that position function did not match the dimensions of the pattern it was paired with.

- .pat files, it turns out, are much easier to work with on this end when they follow the naming convention pat0001.pat. The program can open either convention, but I have set it up to save them as pat#.pat when you save an experiment.

- Right now, if you have already opened another .g4p file or autopopulated an imported folder, you cannot open another .g4p file. Use the "clear all" button to clear out the current data first, then open or create your next experiment.

- Opening a previously saved .g4p file will automatically import the Experiment folder in which it is located.

ENTERING DATA:

- If you erase the "Mode" cell of a trial, it will clear the entire trial and treat it as though it

does not exist (if for example you don't have a pre or post trial in this particular experiment).

- Cells 2-7 (Pattern Name, Position Function, AO 1-4) take a filename, minus the extension, as a string. To make this easier, once you have imported, clicking one of these cells while empty will provide you a list of imported files to choose from.

- Note that if you use the "Set To" method in the File menu to fill out the values of a trial, you will not have a list of files to choose from. When using "Set To" it may be easiest to fill out all numbers, leaving filenames blank, and then add the filenames after you have finished with the "Set To" window by clicking the empty cells.

- If you check a trial in the main block and then hit "Add Trial," the trial added to the bottom will be a copy of the selected trial. If no trial is selected, then a copy of the last trial in the block will be added.

- If you note that the "Select all" checkbox stays selected even after you have unchecked some items, don't worry. It is a bug to be fixed but will not affect functionality.

- Selecting a cell with a Pattern name will immediately display a preview of that pattern library in the preview panel. You can move forward and backward through the library one frame at a time, or hit play which will play through the library in sequential order.

- Position functions are simply graphed, and a red vertical line marks the duration you currently have set for that trial. If the red vertical line does not line up with the end of the position graph, note that your graph's x-axis time and the duration you have entered do not match.

- AO functions are displayed as static graphs.

- To view a cohesive preview of a selected trial, check the trial’s box and hit the "Preview" button toward the bottom right.

- When you change the mode of a trial, fields that are changeable in this mode will fill with default values, and those that are not used in this mode will clear out. You should get an error if you try to edit a field that's not appropriate for the mode.

SAVING:

- Note that you only have a “Save as” option, no “Save” option. This is to avoid the possibility of saving over another experiment of the same name. When you save, an updated timestamp will automatically be added to the end of the folder name. You can erase this when you save if you’d like, but beware of saving over something!

- When naming a file, please do not use any "-" characters. Use underscores instead. This is because the program must remove any old time stamp from the name and add an updated one, and uses dashes as the delimiter to find the time stamp. If you have any dashes in your filename, you'll lose the text after the first dash.

NOTES ON RUNNING AN EXPERIMENT

- The dry run button will display the currently checked trial. It does not activate any AO channels.

- The "Run Trials" button opens up a smaller GUI with a large "Run" button among other things. Please make sure you fill out all the metadata before running. If the plotting and processing boxes are checked, you must provide the path to files to perform the processing and plotting. You also must provide the path to the run protocol you want to use – right now there is only one, “G4\_default\_run\_protocol” in the “run\_protocols” folder. Right now the test protocol button doesn’t do anything but this feature is forthcoming!

-The intertrial does not play before the first block trial or after the last.

- Each should run for the duration specified in the trial. In the pretrial, you can set the duration for “0” if you would like it to play indefinitely until you hit a key.