Bead Image Analysis Pipeline v1:

1. Run CellProfiler:
   1. Open up CellProfiler.
   2. Go to file->open project and open “Bead\_sorting\_v1.cpproj” in the Bead\_pipeline\_v1 folder on the desktop.
   3. Drag and drop the folder(s) with your images into the images module. There should be 3 types of images.
      1. Blue (d0.TIF)
      2. Grenn (d1.TIF)
      3. Red (d2.TIF)
   4. Go to the “NamesAndTypes” module and click “Update” to verify that your images are properly recognized by the program.
   5. Got the “ExportToSpreadsheet” module. Name your experiment and database file. Set the save destination.
   6. Click “Analyze Images" to run the pipeline.
2. Put a copy of the output onto the lab google drive (lab resources->experiment tracking->quantification->*your experiment name*).