All of the Scripts Associated with Metrics and Including Metrics MAP

*Updated: 5/30/2024*

*Example data in burns: \\burns.rcc.mcw.edu\AOIP\1-Software\Script Test Data\Metricks Scripts*

1. Metrics MAP (Coordinate\_Mosaic\_Metrics\_MAP.m)
   1. The input is the original ROI TIF and the cone coords for each subject.
   2. You will also need an LUT for running the script. Save as a .csv.
      1. Column A will be a common identifier of the ROI and the coords such as JC\_XXXXX\_YYYYMMDD\_OX.
      2. Column B will be the axial length of each subject at the visit date.
      3. Column C will be the ppd scale of the AO montage.
   3. To change the window size, change the “upper bound” in line 96.
      1. If it gives you an error right after you start running it, change the {} to () on line 153.
   4. Make an input folder within the main folder containing the script. Place the ROIs and their coords in this folder.
   5. Copy/paste the LUT file into the main folder containing the script.
   6. When you run this script, you can specify microns, degrees, or arcminutes.
   7. The purpose of this script is to output density topography of an ROI, min and max density and their coordinates.
   8. Outputs will populate in a folder within the Input folder.
      1. For this script, the results are:
         1. Bound density matrix .csv
         2. Bound density matrix matfile
         3. Bound density map figure with min/max and location (.png)
         4. Bound density figure marked with PCD (.tif)
         5. Bound density map (.tif)
         6. Window results matfile
2. PCD & CDC Analysis (PCD\_CDC\_Analysis.m) (MAP Analysis >PCD CDC)
   1. Input is the bound density matrix .csv files from the metrics output. You will also need to input the same LUT table from metrics for this script.
      1. Data can be in any input folder.
   2. When you run this script, you can specify the isodensity contour that you want to report. Do 80% unless you have a reason not to.
   3. Select the units (microns or degrees).
   4. The purpose of this script is to report the PCD, CDC, their locations, and 80% isodensity contour area for each ROI in your dataset.
   5. The outputs will include individual files for each subject, an analysis summary, and a file containing all of the PCD points.
      1. All outputs should populate in the input folder.
   6. Outputs:
      1. A .csv with the coordinates of whatever isodensity contour you chose when you ran the script.
      2. A figure with the PCD and CDC marked
      3. A figure with the 80% contour only
      4. A figure with the contour, best fit ellipse, PCD, and CDC
3. Ellipse Contour (Plot\_Isodensity\_Contour\_Overlay.m) (MAP Analysis > Isodensity Contours)
   1. Input is the bound density matrix .csv files from the metrics output. You will also need to input the same LUT table from metrics.
   2. I only ran this code for the subjects I needed for figures. This will create all contours for the data and combine them. You can choose which contour percentage(s) you want to run.
   3. This script gives you a .tif that you can use for figures
   4. Outputs will populate in the input folder
   5. Outputs are:
      1. Combined contours .tif
      2. A .csv with the center coordinates for each ellipse for each subject
4. Compare Windows (PCD\_CDC\_Location\_Comparison\_95\_CI.m) (MAP Analysis > PCD CDC)
   1. Input files are a PCD and CDC excel docs. Place them in the main folder containing the script. Within my input folder there are instructions for making the input files as well as instructions for running the script. You do not need an LUT for running this script.
   2. The purpose of running this script is to see the 95% confidence ellipse when you are comparing multiple methods for one metric
      1. Niamh used this for comparing all five graders’ PCD and CDC metrics
      2. Emma used this for comparing all 10 window sizes and their PCD and CDC metrics
   3. Outputs:
      1. A matlab figure and a tif of the following
         1. Combined PCD and CDC 95% confidence ellipses with each individual point marked
         2. PCD only ellipse
         3. CDC only ellipse
5. Cells within radius from PCD (Cells\_Within\_Radius\_From\_PCD.m) (MAP Analysis PCD CDC)
   1. Input: bound density matrix .csv, coords .csv, and the LUT file used for metrics
      1. Place all of these inputs into the same folder to run the script (LUT needs “LUT” in the name of the file.
   2. When you run the script, you type the radius in microns from the PCD where you want to know the cell count
   3. The purpose to see how many cells are within a chosen radius of the PCD
   4. Outputs:
      1. .csv that tells you how many cells are within a certain radius of the PCD
6. Density at a distance from the PCD (Density\_at\_Distance\_from\_PCD.m) (MAP Analysis PCD CDC)
   1. Input: density matrix .csv and LUT
      1. The density matrix .csv can be in any input folder, the LUT file can also be in any folder.
   2. The user enters the x and y distance in um from the PCD
      1. Negative distances are to the left and up
   3. The purpose of this script is to find density at a specific distance from the PCD in a density matrix
   4. Results: a .csv containing the density at the distance you specified from the PCD
7. Density Matrix Subtraction (Density\_Matrix\_Subraction.m) (MAP Analysis folder)
   1. Before running this script, you need to scale all the ROIs and their coordinates to the same scale (see scaling ROIs word doc).
   2. Input: **two** density matrices.csv, analysis summary output from PCD & CDC analysis script as the LUT (with ONLY the information from the two matrices you are using in order of smaller then larger)
      1. You can either run the PCD CDC analysis script with just the two subjects you want to use individually, or you can run all the subjects through it at once and then make copies of the resulting analysis summary and remove the subjects you don’t need for each subtraction.
   3. When you run the script, the first matrix you select needs to be the first one listed in the analysis summary
      1. If you have different sized ROIs, select the smaller of the two ROIs as the first matrix.
      2. It is critical that the ROIs in the LUT file are in the same order as how they are selected (i.e., smaller one listed first).
   4. The purpose of this script is to compare density maps from different time points
   5. Results:
      1. .csv with the results of the subtraction in matrix form
      2. .svg of the plotted result
         1. Can input into illustrator and use it like a .tif
         2. The svg is flipped across the y-axis which you know because it still has the axis on it when it saves
         3. So you need to flip it in illustrator to have the correct orientation
      3. 2 .tifs of the plotted result – the color scale is not great on these; it looks very binary and is hard to tell what’s going on (this is why the .svg was made)
8. Stand alone map creator (Stand\_Alone\_Map\_Creator.m) (MAP Analysis folder)
   1. Input: the windows results matfile from metrics map
   2. You can select what kind of map you want to output
      1. Bound area
      2. Unbound area
      3. Bound number of cells
      4. Unbound number of cells
      5. Bound density in degrees
      6. Bound density in microns
   3. To change the clims its on line 20
   4. The purpose of this script is to make new maps from your existing data that you got from metrics map so you don’t have to rerun metrics just to get a new map
      1. This can be useful if you need to change the clims of the map but don’t want to rerun metrics just to get new maps
   5. Outputs:
      1. The new map
      2. \*If you say you want to do the bound density degrees map, it will save the results that you’re supposed to get from metrics map but this avoids having to rerun metrics in degrees and that takes too long
9. Standard Deviation Maps (Stdev\_Maps.m) (MAP Analysis folder)
   1. . This also creates average and CoV maps.
   2. Input: directory containing bound density matrix matfiles (with MATFILE listed in all caps in the file name) and directory containing PCD\_CDC analysis files.
      1. Separate matfiles and PCD\_CDC analysis files within additional folders (window size, timepoints, etc.) within the directories
      2. PCD\_CDC analysis files must only contain information from the matrices you are running
   3. The script identifies by subject ID so it will do the standard deviation for all matfiles from that ID
   4. Data needs to be the same size and scale across subjects
   5. To adjust clims for color scale see line 28
   6. Outputs: a tif of the stdev map, a tif of the stdev map with the master cdc marked, a csv for the stdev map, average map, and CoV map.
10. Window Analysis (Window\_Analysis.m) (MAP\_Analysis folder)
    1. Input: the window results matfile from metrics
       1. You don’t need a LUT
       2. matfiles can be in any input folder
    2. Select the input folder when prompted to select the directory for the window results matfiles
    3. You can choose which metric you want to check
       1. Bound area (um2 units)
       2. Unbound area (um2 units)
       3. Bound number of cones
       4. Unbound number of cones
    4. The purpose is to check the min, max, average, and range of the selected metric. This is more of a sanity check script. Originally used to double check the number of cones included in each window.
    5. Outputs: whatever you selected to output shows up on a .csv
11. Row and Column Extraction (Row\_Column\_Extraction.m) (MAP\_Analysis folder)
    1. Purpose of this is to extract the horizontal and vertical rows through the master CDC location to be able to visualize the topography of the map. The data gets averaged based on the binning spacing the user specifies. Data across subjects is also compiled into bins of overlapping data.
    2. Input:
       1. Matrices in .csv format (could be from stdev\_maps, matrix\_subtraction, etc).
       2. You will also need to enter a unique identifier for the files you are wanting the script to analyze (MINUS, coeffvar, etc).
       3. Master cdc list (result from stdev\_Maps.m) (could also make your own without running that script by averaging the
       4. PCD\_CDC analysis summary file
       5. You will also need to enter spacing and window size in microns (required for binning/averaging data)
    3. Outputs: Horizontal and vertical bin analysis .csvs for each subject, all horizontal and vertical raw data for all subjects as a matfile (can be opened in matlab and used to copy data into excel later for graphs), horizontal and vertical graphs as svgs for data between subjects, .csv with information needed to make horizontal and vertical graphs for data between subjects.