#\*#\*#\*\* all files before 10/08/18 need to be certain I have correct surf-surf-contact information.

Separate data processing from visualization:

Raw data to curated data.

* Keep all your raw data the same
* What are all the new variables I need calculate.
* Process scripts from raw data – add to curate dataset.

Keep curated dataset in full format.

Downselect at stage of visualization.

Metrics I want to calculate:

|  |  |  |  |
| --- | --- | --- | --- |
| **Metric** |  | From raw data |  |
| Average mitochondria length | .mean(length) | Length of mito- best so far may be bounding box OO measurement | df\_len |
| Average mitochondria volume | .mean(Volume) | Volume of mito | df\_vol |
| Mito distance from Nucleus | .mean(distance) | Distance measurement | df\_dist |
| Cd68 dist from Nucleus | .mean(Nucleus) | Distance measurement | df\_dist |
| Cd68 %volume | Cd68 vol/mg volume \*100 | Cd68 volume, mg volume | df\_pcnt |
| Number of mito surfaces |  | Can calculate from len/vol data |  |
| Surface contact mito-cd68 | Total SA contact / SA of mito | “Contact surface area, um^2”, SA mito, SA cd68 | df\_sa |
| Sholl filament intersections | Number of intersections vs distance from starting point. | Filament number intersections | df\_sh:  take median value of all cells |
| Size of mito in relation to distance from nucleus? |  |  |  |
| Correlation between mito and activity measurements? |  |  |  |
|  |  |  |  |

Plotting:

By sex; by mouse; by condition; by retinal layer; by cell.

Notes: Distances may need to be normalized to overall ‘sphericity of the cell’