SynAnalyzer User Guide

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Requirements for Data Organization

SynAnalyzer is setup to run in either batch or single image mode, but in both cases requires that files are organized in a specific structure (see screenshots below).

1. Top level: “YourBatchID” – All files associated with the “batch” analysis are expected to be organized within one main folder that can have any name assigned by the user.
2. Second level: user setup folders – The files in question should be organized as such
   1. ImarisStatsFiles - .xls files output by Imaris using the following naming convention
      1. Original image name
      2. “.XYZ.”
      3. “Pre” or “Post” depending on whether these surfaces were generated from the pre- or post-synaptic marker
      4. “Syn.xls”
   2. Metadata – Information about the images such as tonotopic location, animal ID, genotype, treatment, exposure status, age, etc; organized as one original image name per row, then the associated metadata in columns (see example file in repository <- coming soon).
   3. RawImages – The original Z-stack files. As of the last update the code is specifically made to work with .czi files. It can easily be adjusted to work with any type of Z-stack and future versions of the code will be ambivalent to file type.
   4. XYZCSVs – This folder needs to be setup by the user, but then the files it will contain are automatically generated by the Conversion Pyton notebook. Since this notebook is setup to run as a Google Collab notebook it is up to the user to drag and drop the automatically generated files into this folder.

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| A screenshot of a computer  Description automatically generated |
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| Figure 1. Representative images of file organization required by SynAnalyzer. |