

Code Manual

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2:33 PM

Setting up folders and paths:

- The main code should be located in an "LivemRNA\MS2Code" folder. We'll run everything from this folder. In there you should also find the "ComputerFolders.xlsx" files defining the folders related to the other parts of the code.
- The FISH code has three folders: Exec, Analysis and Data.
 - Exec folder: can be anywhere, but should be in the Matlab path.
 - Analysis folder: I'd put it in the same folder as "MS2Code", for example "FISHAnalysisData\Analysis".
 - Data folder: I'd put it in the same folder as "MS2Code", for example "FISHAnalysisData\Data".
- Raw data should be located in a folder such as "RawData", which will be indicated in "ComputerFolders.xlsx". The naming should be as follows:
 - Create a folder within the data folder with the date in format yyyy-mm-dd
 - Inside this folder you need to provide the flatfield files.
 - 2-photon: They need to be named: FFzx001.tif, where "x" is the zoom factor used.
 - Inside this folder provide create a new folder with the name of the data set. For example, "MCP(2)-X1".
 - Within this folder each image should be saved as "NameNNN.tif", where "Name" is, for example "MCP(2)-X1" and "NNN" is the image number.
 - Inside this folder create a "FullEmbryo" folder. Here, we store images of the full embryo to find the AP axis and such.
 - Here, first take an image at the location where the high-magnification ones were taken but in 1x. This should be at the surface such that nuclei are observable. Depending on where you were in the embryo you can call this "LeftSurf001.tif", "CenterSurf001.tif", or "RightSurf001.tif".
 - Go to the mid-sagittal plane and take a picture in the same position and name it according to the position along the AP axis (Left001, Right001 or Center001).
 - Take pictures of the remaining parts of the embryo so that all the images can be stitched together. Name them accordingly (Left001, Right001 or Center001).
- Nuclear segmentation and tracking code. This should be in a folder such as "tracking code". It can be anywhere as long as it's in the Matlab Path.
- The Dropbox folder is meant to store all the analysis outputs. We call it like that because it allows quick collaboration with multiple people interested in the datasets. I just have a folder within my Dropbox called "LivemRNADData".
 - In this folder you will need "HGMovieDatabase.xlsx" which has information about the movie folders (probably obsolete by now) and an estimate of the frames corresponding to the start of each nc.
 - In this folder you will need "DataStatus.xlsx". This is useful to keep track of the analysis flow between multiple people. Also, later parts of the code need this.