# LC3B\_Tandem\_Puncta\_QuantificationV2

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Code requires bioformats MATLAB Toolbox and MATLAB version R2021a or later.

#### Creator

```
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```

LC3B\_Tandem\_Puncta\_QuantificationV2 is a batch processing function used to identify LC3B vacuoles labeled with eGFP and mCherry signals and is designed for researchers investigating autophagy. Code expects the users data to be grayscale 16-bit volume data either in the form of multidimensional tiff stacks or ND2 files with three channels corresponding to the eGFP, mCherry and nuclear marker for mammalian cells. Data used to test this function was acquired using a confocal microscope as out-of-focus light will introduce issues with segmentation and other modes of image acquisition that do not minimize out-of-focus light will not produce quality results.

The file calls the functions:

userInputs imreadVolume Watershed2 FindVaculoes TabularCountVacuoles

Data for single cell analysis is reported as the number of eGFP and mCherry vacuoles counted for each cell and is printed to the command window along with the fileName the data was extracted from and the cellindex corresponding to which cell the vacuoles were found in with respect to the image used. This data is returned as a table to the command window and can also be viewed by calling or opening the structure Results\_Table.

NOTE: Each cell line is different and each optical system is as well. Users should experimentally determine the parameters to use for their data. A helper function is provided with the code to help users access and identify parameters for their data called VolumeThresholdhelper.

NOTE: Users can use MATLABs publishing option to capture all the outputs (recommended) for all figures created by the subfunctions above or place a waitfor() call after each figure to observe the results of each figure created as the processing is occuring. See MATLABs documentation for publishing options and using waitfor(). See github account for an example of the published output.

```
%clear the command window, users workspace and close all figures
clc;
clear;
close all;
```

## Ask for userInputs

```
[Input] = userInput();
```

### Create image data store

```
imds = imageDatastore(Input.Indir,...
'IncludeSubfolders',true,'FileExtensions',
{'.tif','.ND2'},'LabelSource',...
    'foldernames');
imds_NumerOfFiles = size(imds.Files(),1);
```

### Initialize data storage

```
dat = struct ;
dat.FileName = [];
dat.SingleCell = [];
```

### Start processing images

```
for ii = 1:imds_NumerOfFiles
%pull images from data store one at a time by indexing
img = bfopen(imds.Files{ii,:});
%get file name
[pathstr,name] = fileparts(imds.Files{ii,:});

**

**

**let the user know which image is being processed. Print the name to command
%window
disp("Begin processing image: ")
disp(name)
```

```
%unpack user inputs for passing to functions
Nuclear channel = Input.Nuclear channel;
eGFP_channel = Input.eGFP_channel;
mCherry channel = Input.mCherry channel;
eGFP_threshold = Input.threshG;
mCherry_threshold = Input.threshR;
MinvacVoxeGFP = Input.minGFPvacVolume;
MinvacVoxmCherry = Input.minRFPvacVolume;
MinNucVox = Input.minNucleusVolume;
Solidity = Input.Solidity;
Begin processing image:
High numbers of eGFP and mCherry
Begin processing image:
Low numbers of eGFP puncta and high mCherry Puncta (2)
Begin processing image:
Low numbers of eGFP puncta and high mCherry Puncta
Begin processing image:
Low numbers of eGFP puncta and low numbers of mCherry Puncta (Noisy
```

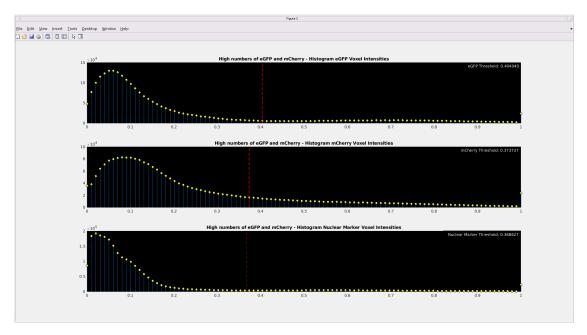
### Create subvolumes for each channel

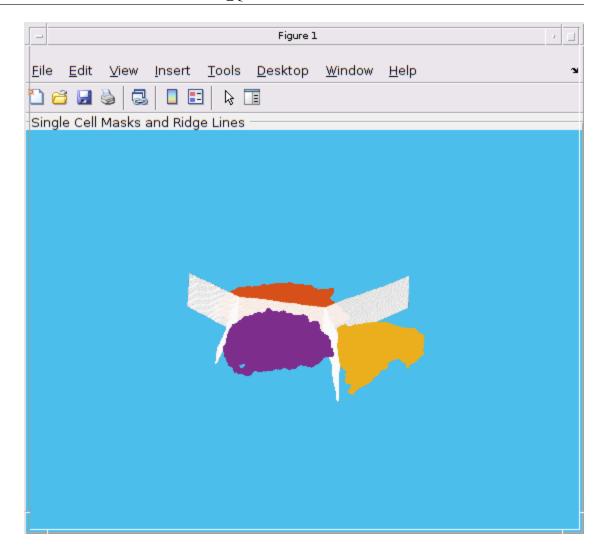
[r,g,b] =
 imreadVolume(img,Nuclear\_channel,eGFP\_channel,mCherry\_channel);

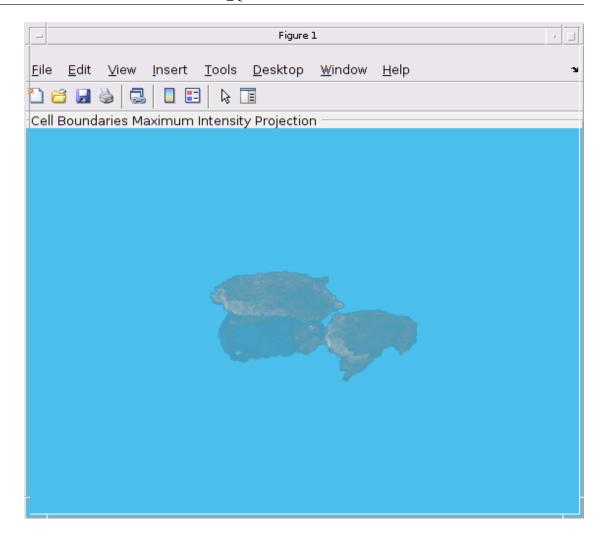
#### 3D controlled watershed

[bw\_stats] = Watershed2(r,g,b,name,MinNucVox,true);

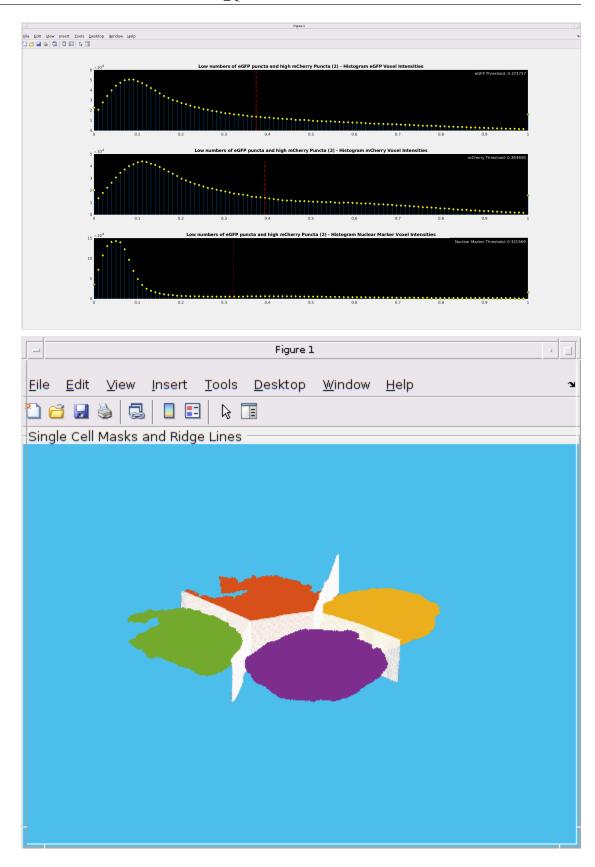
Data for plots generated from - High numbers of eGFP and mCherry

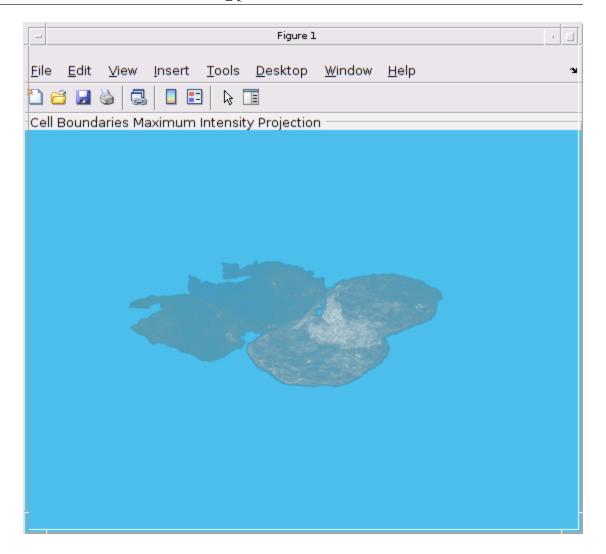




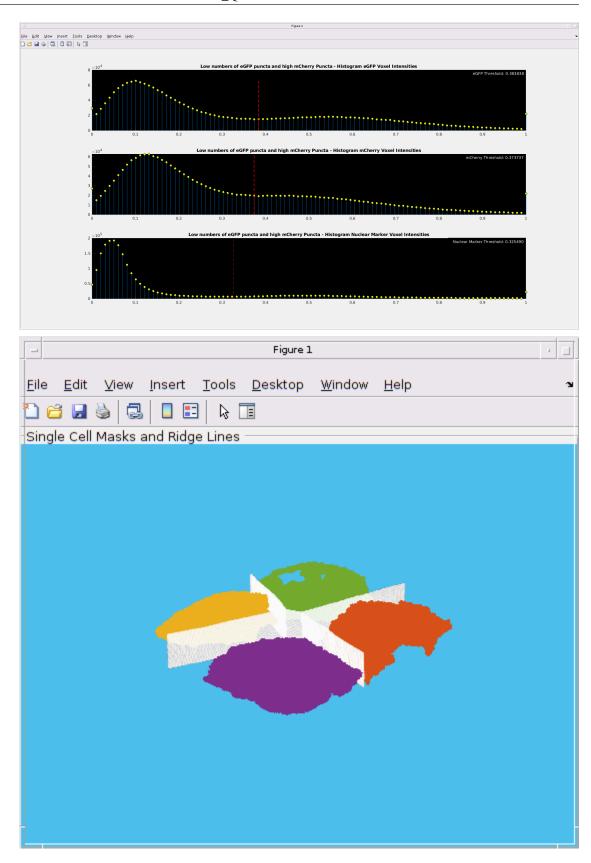


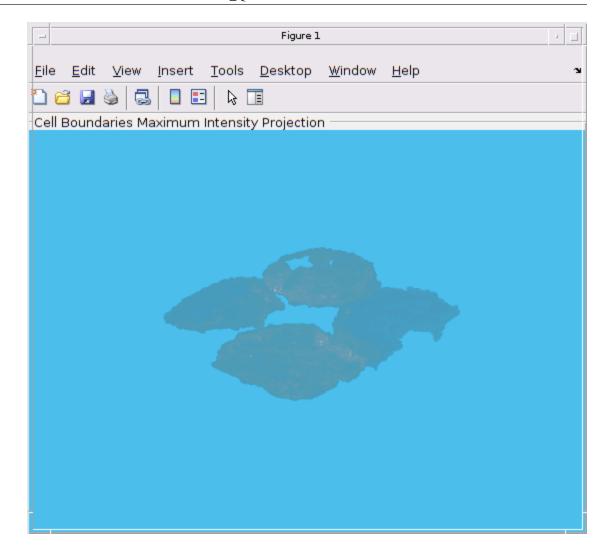
Data for plots generated from - Low numbers of eGFP puncta and high  $mCherry\ Puncta\ (2)$ 



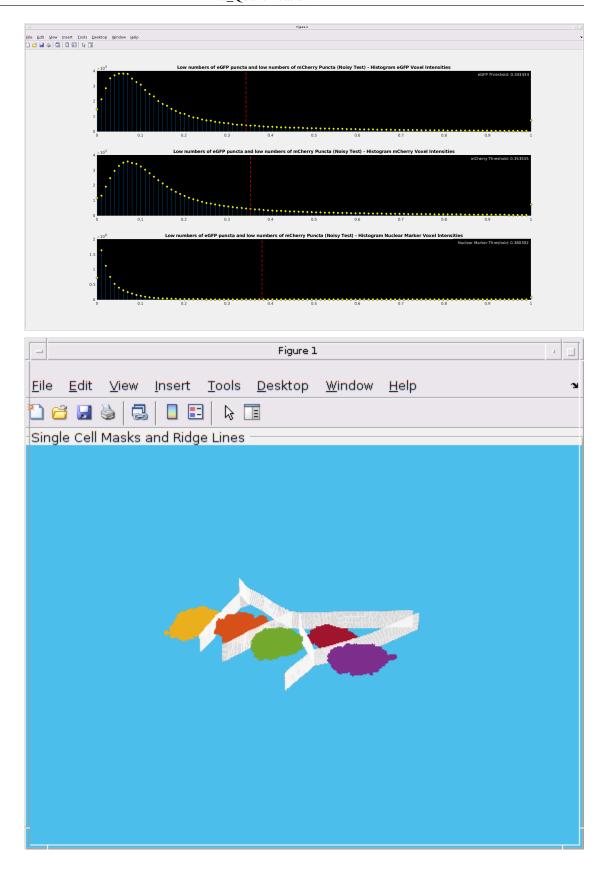


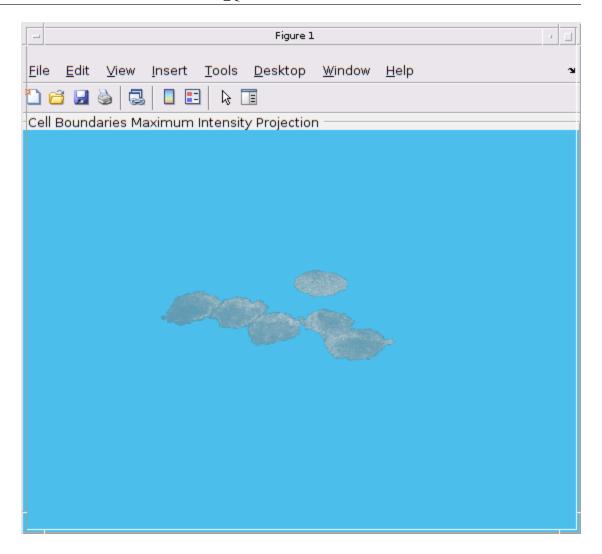
Data for plots generated from - Low numbers of eGFP puncta and high mCherry Puncta





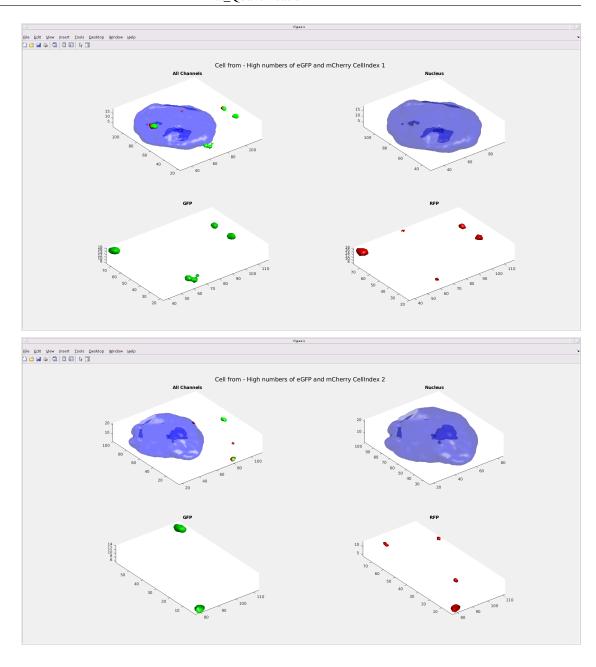
Data for plots generated from - Low numbers of eGFP puncta and low numbers of mCherry Puncta (Noisy Test)

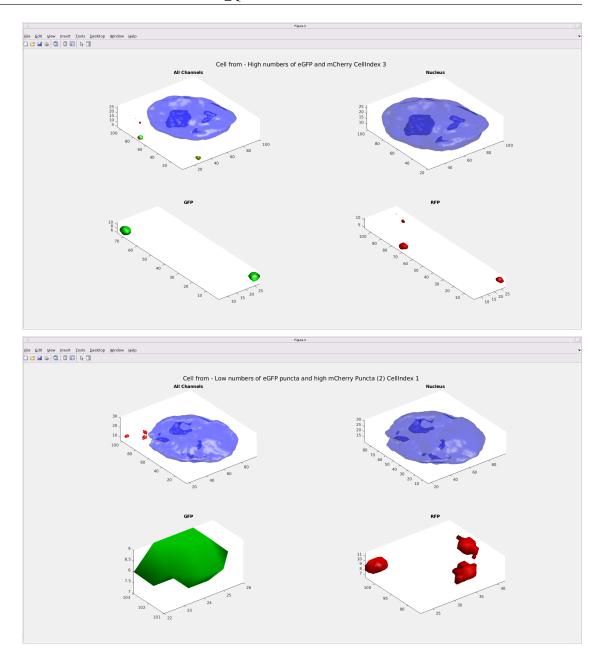


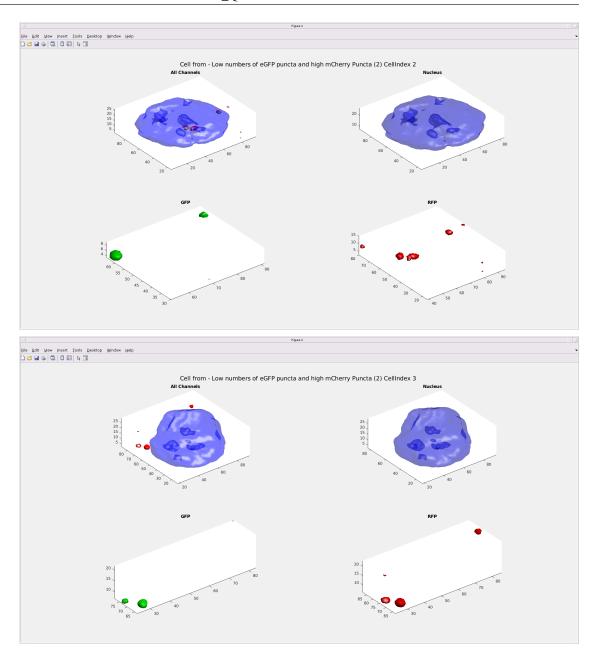


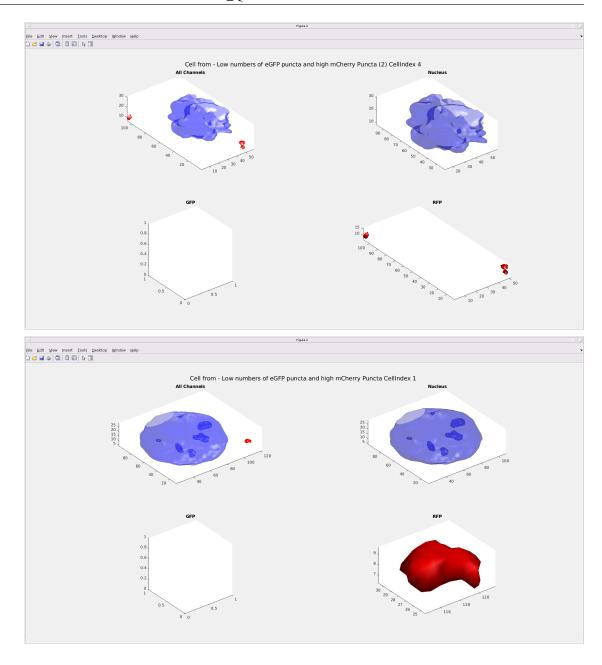
# Find the vacuoles for each cell identified

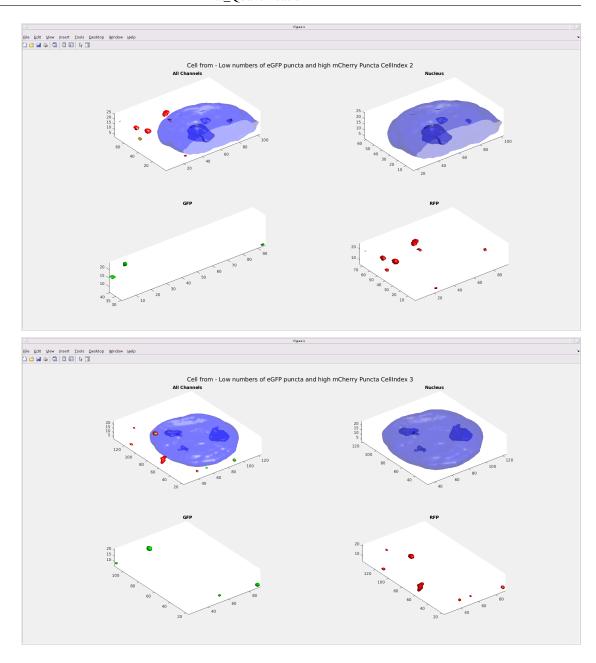
```
[SingleCellStructure] =
FindVaculoes(r,g,b,bw_stats,name,eGFP_threshold,...
mCherry_threshold,MinvacVoxeGFP,MinvacVoxmCherry,MinNucVox,Solidity);
```

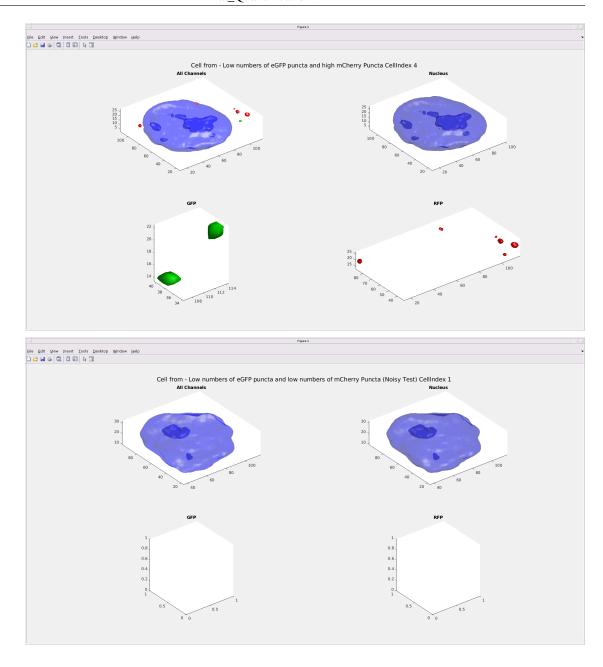


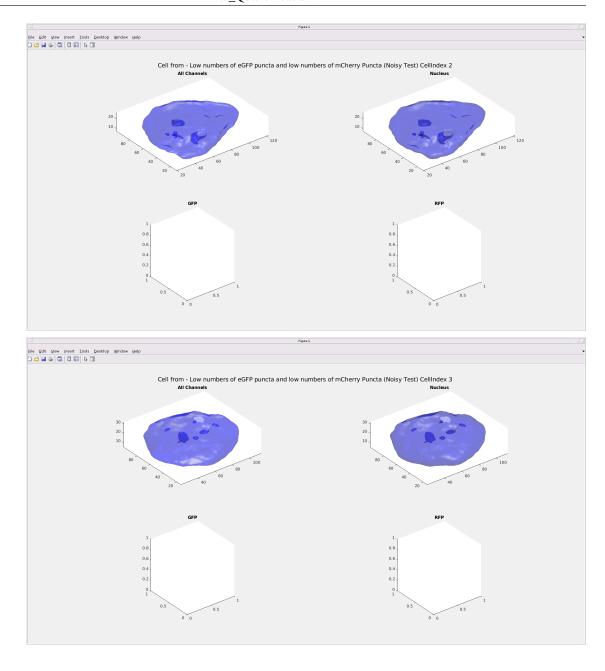


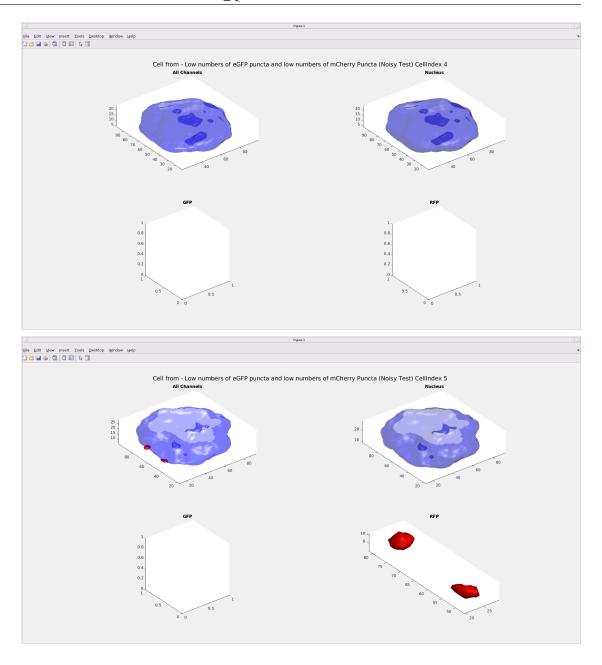


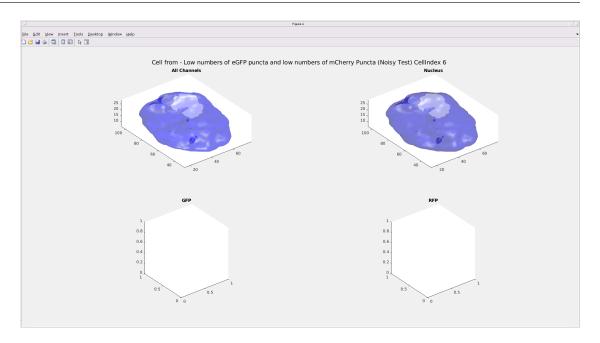












### **Accumulate results**

```
dat(ii).FileName = name;
dat(ii).SingleCell = SingleCellStructure;
end
```

### Return counts for vacuoles as table

```
{'High numbers of eGFP and mCherry'
} 1 4 5

{'High numbers of eGFP and mCherry'
} 2 2 4

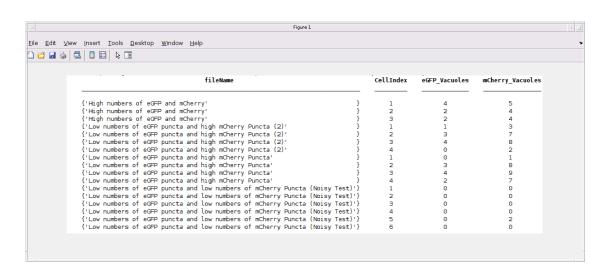
{'High numbers of eGFP and mCherry'
} 3 2 4

{'Low numbers of eGFP puncta and high mCherry Puncta (2)'
} 1 1 3

{'Low numbers of eGFP puncta and high mCherry Puncta (2)'
} 2 3 7
```

# LC3B\_Tandem\_Puncta\_QuantificationV2

```
{'Low numbers of eGFP puncta and high mCherry Puncta (2)'
   {'Low numbers of eGFP puncta and high mCherry Puncta (2)'
   {'Low numbers of eGFP puncta and high mCherry Puncta'
   {'Low numbers of eGFP puncta and high mCherry Puncta'
   {'Low numbers of eGFP puncta and high mCherry Puncta'
   {'Low numbers of eGFP puncta and high mCherry Puncta'
   {'Low numbers of eGFP puncta and low numbers of mCherry Puncta
(Noisy Test)'}
                      7
   {'Low numbers of eGFP puncta and low numbers of mCherry Puncta
(Noisy Test)'}
   {'Low numbers of eGFP puncta and low numbers of mCherry Puncta
(Noisy Test)'}
                      3
   {'Low numbers of eGFP puncta and low numbers of mCherry Puncta
(Noisy Test)' }
   {'Low numbers of eGFP puncta and low numbers of mCherry Puncta
(Noisy Test)'}
                      5
                                     0
   {'Low numbers of eGFP puncta and low numbers of mCherry Puncta
(Noisy Test)'}
```



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