**Bacterial cluster identification pipeline**

The bacterial cluster identification pipeline uses as input an aligned to ISS images Auramine image. The Auramine image needs to be of 20% original size (original data, no-compressed, no-converted) and subtracted (Cy3-FITC) if needed for avoiding background noise (ImageSubstraction.m).

Save pipelines in same folder as 20% images.

Use the BacterialClusters\_wGradientOutput\_20210112\_WITH\_AREAS\_2.m

Image: path of subtracted image

Output\_prefix: path of folder in which you want to save data, after last folder you give the prefix how you want to call the files

Blob file: QT\_details.csv from decoding folder (the localization of blobs)