Instructions

There should be included the following files:

Matlab Scripts:
segmentation.mlx
K_means.mlx
RX_cat.mlx
RX_Reflection.mlx
RX_Transmission.mlx
RX_Scattering.mlx

Matlab workspaces:
sample_Modele.mat
Reflect_cyto2_segment.mat

Load sample_Modele.mat and Reflect_cyto2_segment.mat before running the scripts.
The RX scripts require the Hyperspectral Imaging Library for Image Processing Toolbox addon.

Description:

The objective of my experiments is to try unsupervised methods to find cells with anomalous spectra that could be candidates to being infected.

The tested methods were K-means and the spectral anomaly detector algorithm Reed Xiaoli (RX).
The tests were conducted on the spectra of Reflection, Transmission and Scattering of a blood sample that is believed to have a few infected cells.

The segmentation script includes a way to reproduce my cell segmentation, though it's not the focus of the experiments, a good cell segmentation was needed to classify anomalous cells so using the model cellpose was the most efficient way to get it done (only available in Matlab 2023b and onwards).

The K_means script includes the experiments of running the K_means on all the spectra with the latest result, as the goal was to increment the amount of clusters until either a small cluster of cells appears or multiple incomprehensible small clusters appear.

The RX scripts include the experiments of running the RX algorithm on the different spectra. In the script RX_cat Reflection,Transmission and Scattering were all concatenated to see if running the algorithm on all the bands at once would reveal additional information than separately.

The RX experiments have two phases, in the first one the algorithm runs through all the pixels and in the second one we discard the background while picking only the pixels from the cells. For both, it was attempted to find a threshold for the anomaly scores to automate the anomalous cells candidate selection.
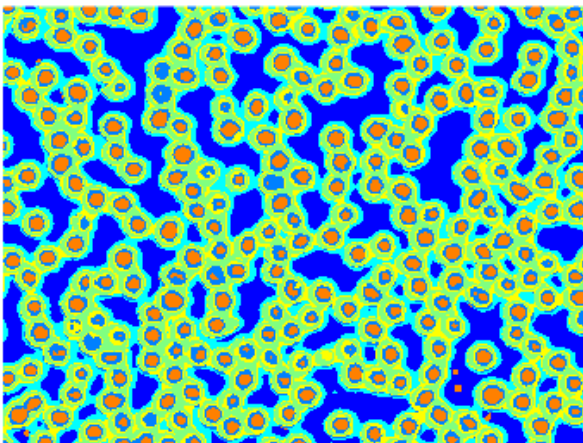
Results

K-means: For the K-means algorithm the interesting results are more about the cells that the clusters couldn't "find" them or paint their centers like the others, otherwise there is not much information we can extract from it just by the clustering, since increasing the amount of clusters would only make more clusters with no apparent relationship. Interestingly some of these cells seem to later be pointed out by the RX algorithm in some of the experiments.
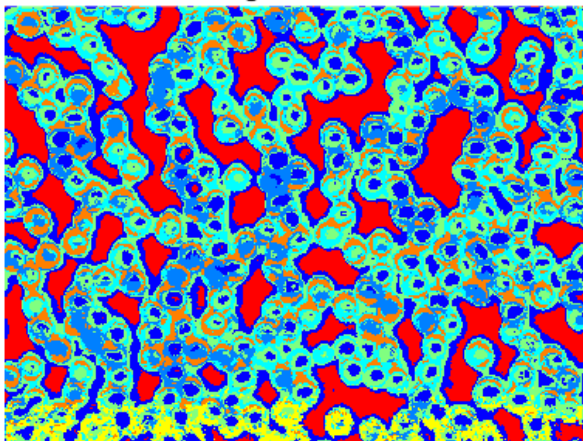

Reflection: K-means Result
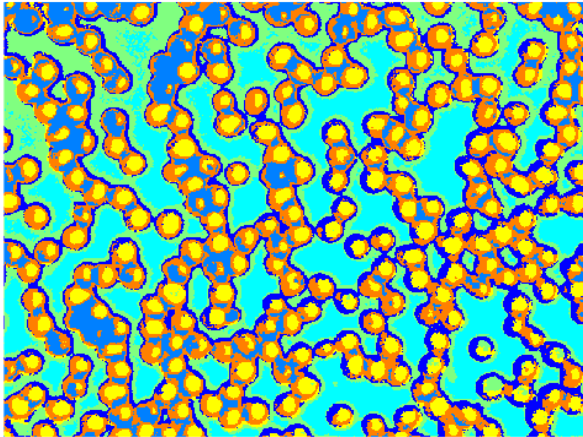

Transmission: K-means Result


Scattering: K-means Result

RX:

Results for the RX experiments seem to have a preference to pick candidate cells at the edges and also cells within noisy areas, although it also seems to consistently find some other few cells in the image, the other preferred cells make it hard to find a good threshold to automate candidate selection.
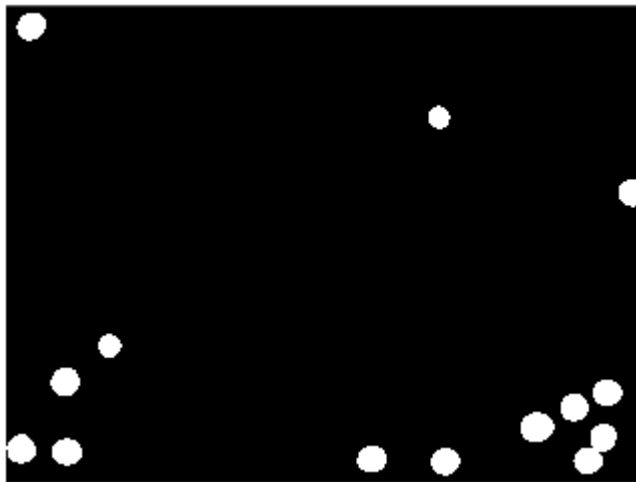
Reflection whole image results:
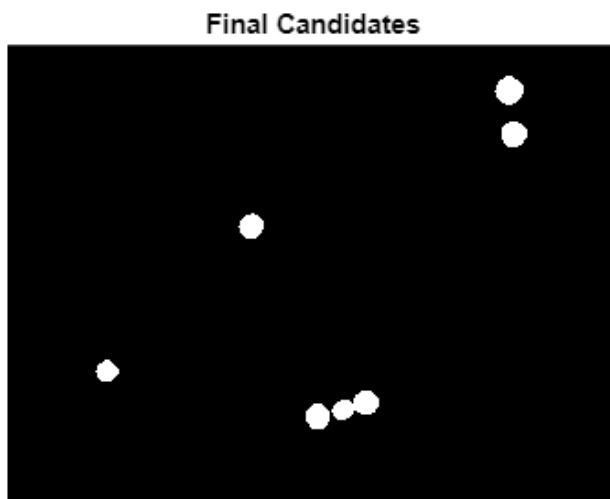
Reflection no BG results:
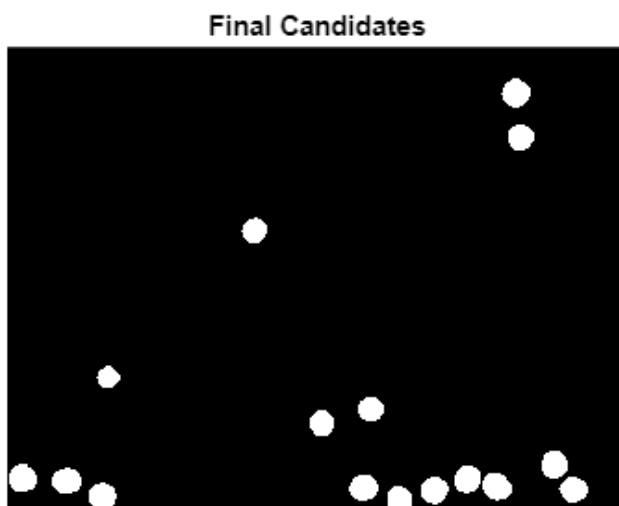
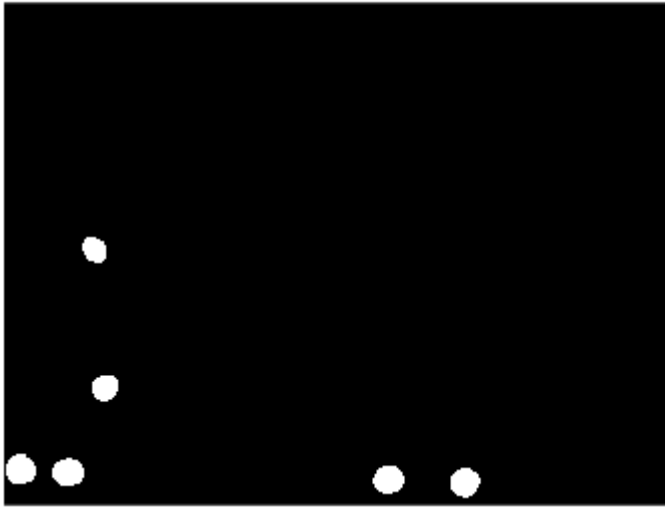Transmission whole image results:

Final Candidates

Transmission no BG results:

Final Candidates

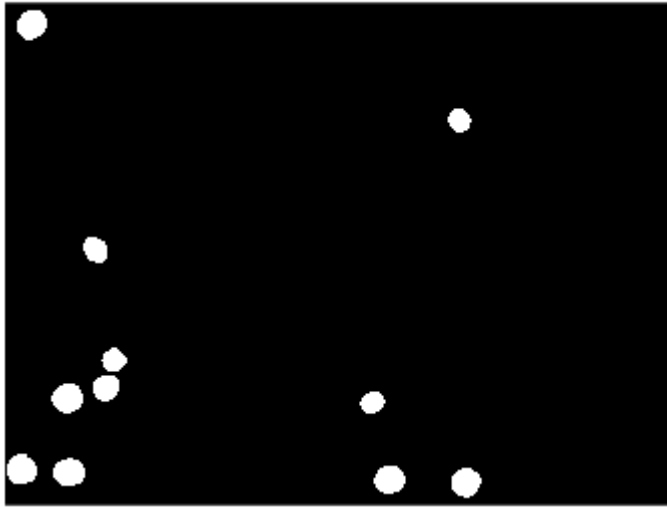Scattering whole image results:

Final Candidates

Scattering no BG results:

Final Candidates

Concatenated Bands whole image results:

Final Candidates

Concatenated Bands no BG results:

Final Candidates