

Nevin Ndonwi

## Computing for Biomedicine Sperm Project Image processing proposal

I am planning on choosing option 2 as a topic, specifically, I plan on working on an interactive tool that will measure the length of a given sperm cell when it is clicked/ interacted with. I plan on using ImageJ and the input will be the image and the output will be the cell length in micrometers using the conversion of 3.06 pixels/micrometer from lecture. I plan on letting the user interact with the image by selecting a region and highlighting all of the sperm cells in that region, clicking on points in the cell to highlight the cell, providing a rough sketch over the cell, etc. I also aim to get my results as close to the ground truth as possible for images in the easy class, medium class, and hard class as well. In my report I plan to include a quantitative evaluation that will entail the deviation of my measurement from the manual measurement for all images that are processed.

In terms of required features I plan on attempting to:

- Use ImageJ to construct the UI so that the user can specify the image input and see the output (the cell length in micrometers using the conversion of 3.06 pixels/micrometer from lecture when a given cell is clicked).
- I plan on letting the user interact with the image by selecting a region and highlighting all of the sperm cells in that region
- I also want to let the user click on points in the cell to highlight the cell.
- I also will attempt to provide a rough sketch over the cell.
- Your GUI should also show the resulting segmented sperm cell (e.g., as a skeleton or a binary mask) overlayed on top of the image, so that the user can check its correctness.

Wish List features:

- Ensure a small deviation from hard truth for the hard images to provide as much robustness as possible.
- Customize the color highlighting for different sperm cells to better label it for researchers.
- Potentially use a more sophisticated front end like react for increased responsibility.

- Create a threshold toggle so that the user can see the selections under different threshold values to gain insights.
- (Ie analyze background components) ,provided an image inverter button to see if different thresholds work better on different images (extendible to other computing for biomedicine projects), making this project extendible to other applications and not just this one depending on the data and the cells that were used.

## Weekly Milestones

October 27-November 1:

- Obtain ground truth data.
- Work on getting python code to read in image data
- Start testing threshold values for sperm cell image data to get values to work for post processing (we have a way of seeing a given image in different thresholds and saving those thresholds )

November 2-November 8:

- Get measuring to work whether it be through the pixels in threshold mode or connecting points in normal mode?
- Use ImageJ to construct the UI so that the user can specify the image input and see the output (the cell length in micrometers using the conversion of 3.06 pixels/micrometer from lecture when a given cell is clicked).
- I want to put points on the image and then connect those points based on the order of the points before it.
- Measure the points out and get the result in micrometers from the pixel conversion
- I want window to show better
- Work on differentiating different cells so that users can interact with them. (You can highlight different connected cells into different colors based on different threshold values)

November 9-November 15:

- Work on differentiating different cells so that users can interact with them.  
(You can highlight different connected cells into different colors based on different threshold values)
- I plan on letting the user interact with the image by selecting a region and highlighting all of the sperm cells in that region (thresholded)
- Lowkey market threshold mode?????
- Work on differentiating different cells so that users can interact with them.  
(You can highlight different connected cells into different colors based on real image (use threshold value set in threshold mode to see different results)) - from the real image
- I plan on letting the user interact with the image by selecting a region and highlighting all of the sperm cells in that region (real image) (it can use the threshold value set in threshold mode as the criteria and also have its own color palette)
- I also will attempt to provide a rough sketch over the cell. (in the real image)
- I also want to let the user click on points in the cell to highlight the cell.
- I also want to let the user click on points in the cell to highlight the cell.  
(You can highlight different connected cells into different colors based on different threshold values)

November 16-November 22:

- Your GUI should also show the resulting segmented sperm cell (e.g., as a skeleton or a binary mask) overlayed on top of the image, so that the user can check its correctness. (real image)
- Your GUI should also show the resulting segmented sperm cell (e.g., as a skeleton or a binary mask) overlayed on top of the image, so that the user can check its correctness. (thresholded image)
- Work on differentiating different cells so that users can interact with them.  
(thresholded)
- Work on differentiating different cells so that users can interact with them.  
(real image)
- I plan on letting the user interact with the image by selecting a region and highlighting all of the sperm cells in that region (thresholded)

- I plan on letting the user interact with the image by selecting a region and highlighting all of the sperm cells in that region (real )
- I also want to let the user click on points in the cell to highlight the cell. (thresholded)**
- I also want to let the user click on points in the cell to highlight the cell. (real)
- I also will attempt to provide a rough sketch over the cell. (real)

November 23-November 29:

- Work on wish list items
- Customize the color highlighting for different sperm cells to better label it for researchers. (thresholded)**
- Customize the color highlighting for different sperm cells to better label it for researchers. (real )
- Create a threshold toggle so that the user can see the selections under different threshold values to gain insights.**
- Ensure a small deviation from hard truth for the hard images to provide as much robustness as possible. (real)
- Work on a quantitative evaluation that will entail the deviation of my measurement from the manual measurement for all images that are processed. [test on all images and pick the ones to present] (real)

November 30-December 1:

- Work on wish list items
- Potentially use a more sophisticated front end like react for increased responsibility. (make more sophisticated python UI????) (NAHHH NO TIME)**
- Ensure a small deviation from hard truth for the hard images to provide as much robustness as possible. (real)
- Work on a quantitative evaluation that will entail the deviation of my measurement from the manual measurement for all images that are processed. [test on all images and pick the ones to present] (real)
- Prepare for my final presentation.

## **December 4: Present my presentation / Demo**

- starts at 2:30pm
- 10 minutes of presenting total
- 8-9 minutes of presenting
- 1-2 minutes of Q and A
- strictly enforced timing
- presentation order will be announced on Monday
- bring my own laptop and make sure there is a usbc connector ( test it on Tuesday or before Tuesday to make sure it works )

Structure: (2-3 slides) + (demo my program)

- go over the problem a bit
- go over the features that I was able to get working
- quantitative analysis that I was able to get finished
- demo the program with a variety of inputs
- use on easy and hard examples
- use user interface features

## **December 5 (work on and complete report and information):**

### **Report and project submission and completion (Due December 7)**

- Work on a quantitative evaluation that will entail the deviation of my measurement from the manual measurement for all images that are processed. (show how it worked on all of the images given as input data (easy , medium, hard))
- Work on the hard dataset
- Also explain how it kinda works
- Also Record wall clock time
- Submit all screenshots
- Submit a zip file or a weblink with all elements and packages and readme instructions to run the project.
- Source code, exe tool, plugin, test data, and results
- Project report containing:
  - What required/wish-list features you have accomplished

- Description of core algorithms, significant coding components from you (other than libraries), GUI development, also explain the libraries I used, also explain my own efforts that I put in the project
- Quantitative analysis of results (if ground truth validation data is available)
- A clearly-written Readme that describes how to use your tool
- Any known bugs and future work

Why is it slow

How does it work?

Data

How does threshold mode work and how does the auto measure mode work?

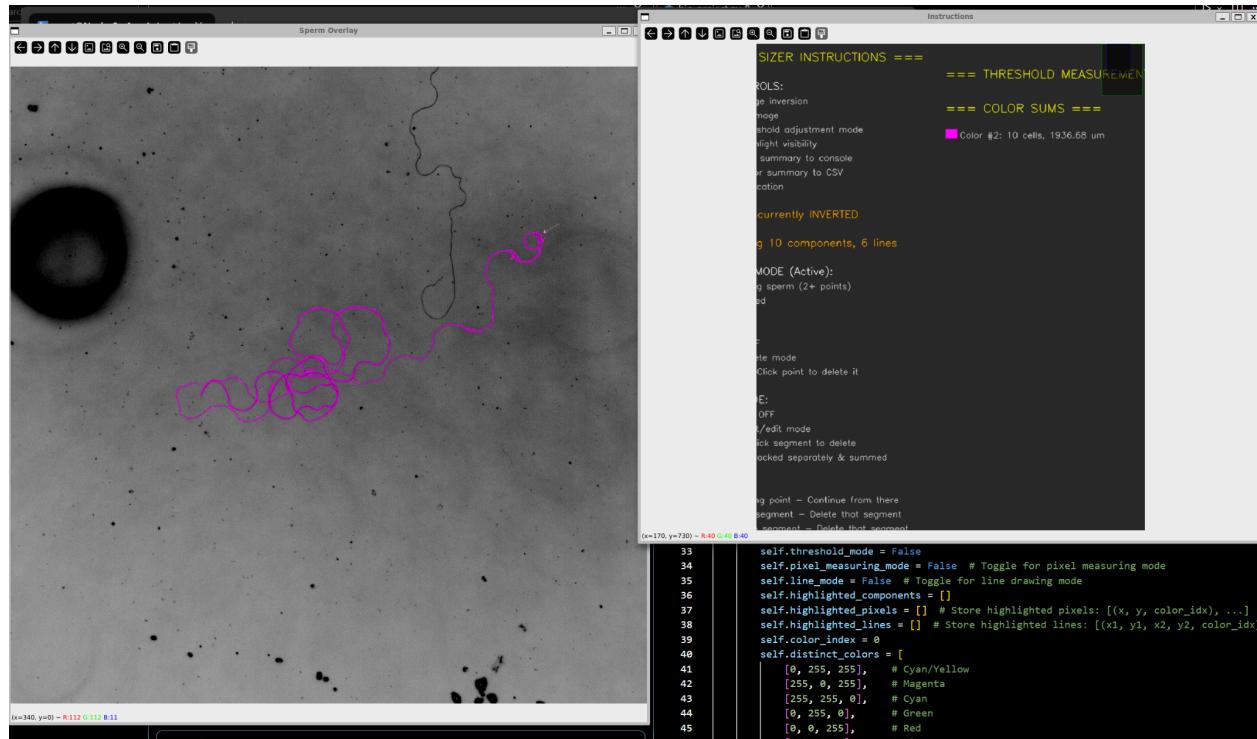
Libraries used

Clockwork out

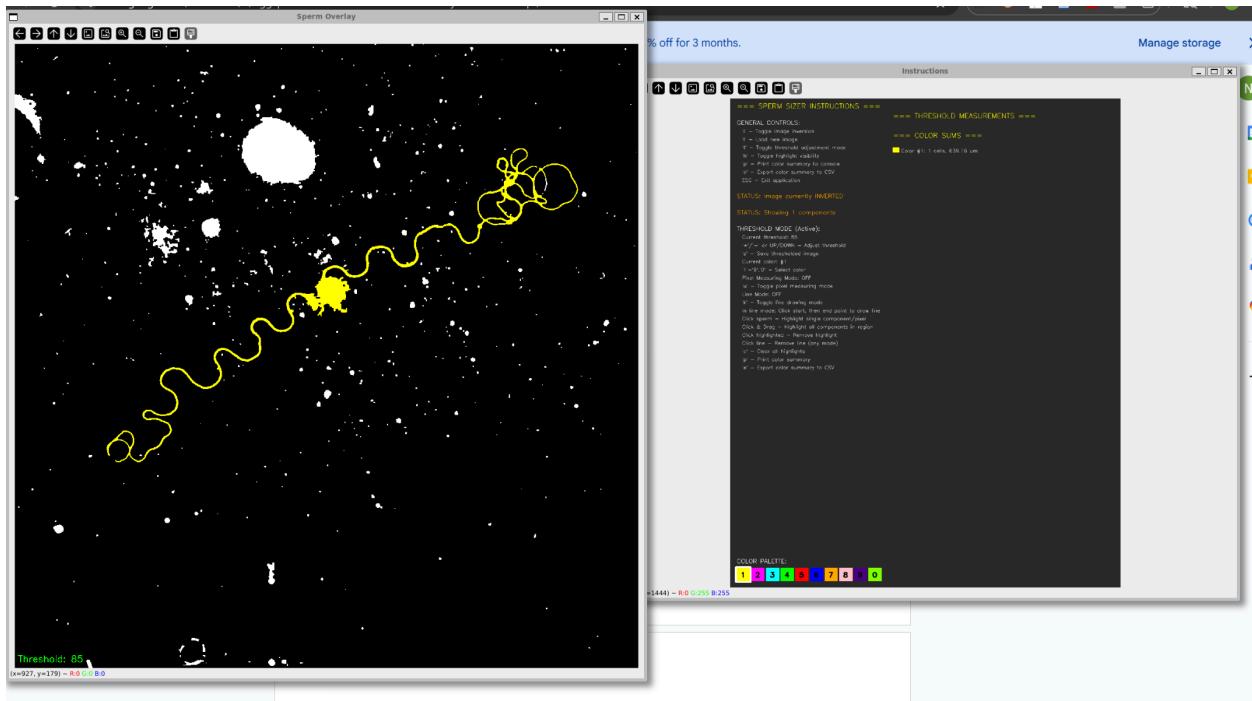
interaction times 0 wall clock time, how long it takes to get measurements , inaccuracies, noise

EASY IMAGES (best screenshots of pre iteration initial testing )

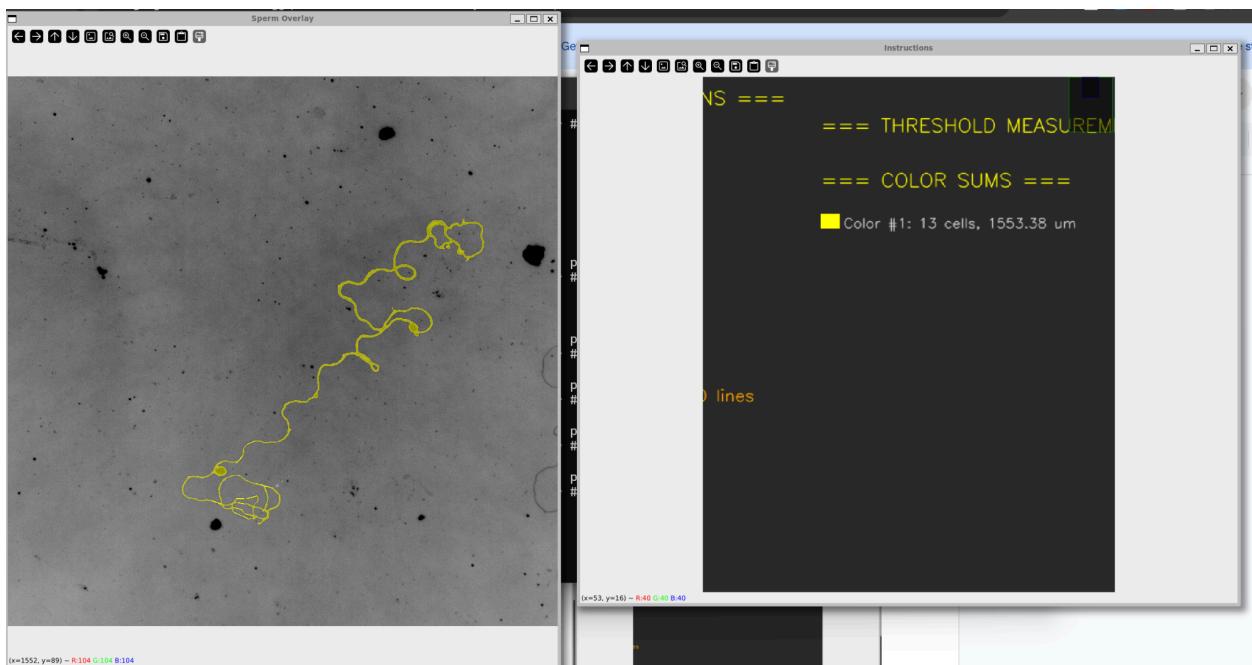
24708.1\_1 at 20X → 1936.66 (expected 1951)



24708.1\_2 at 20X -->



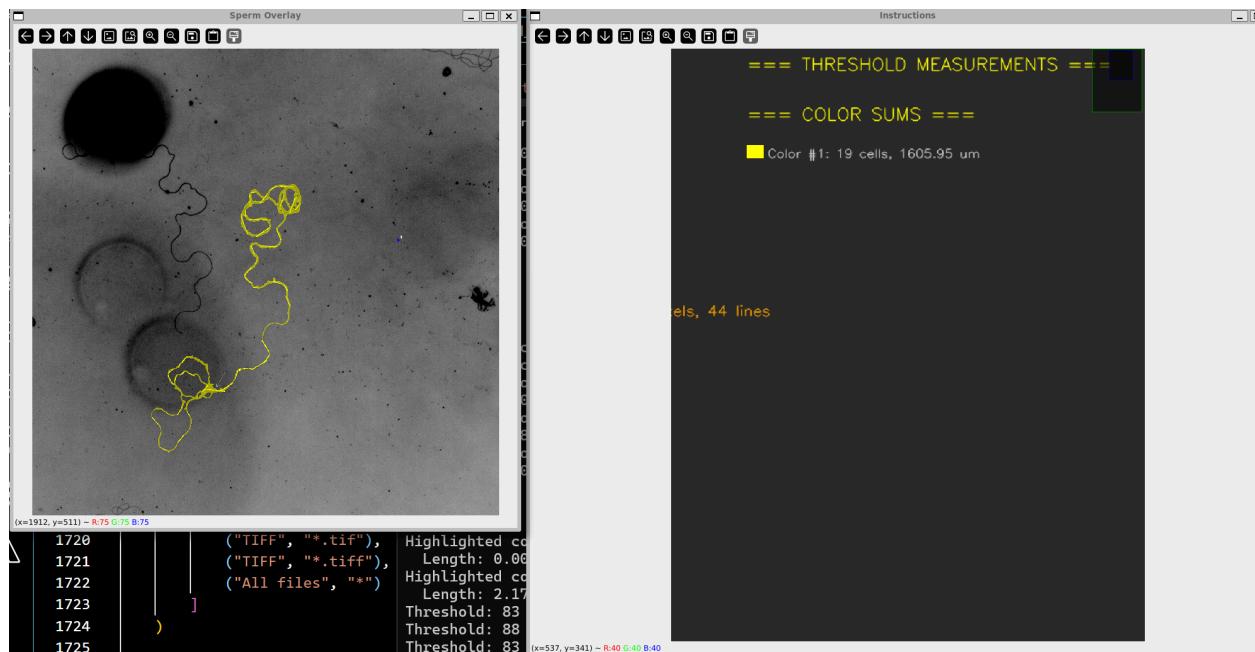
24708.1\_3 at 20X

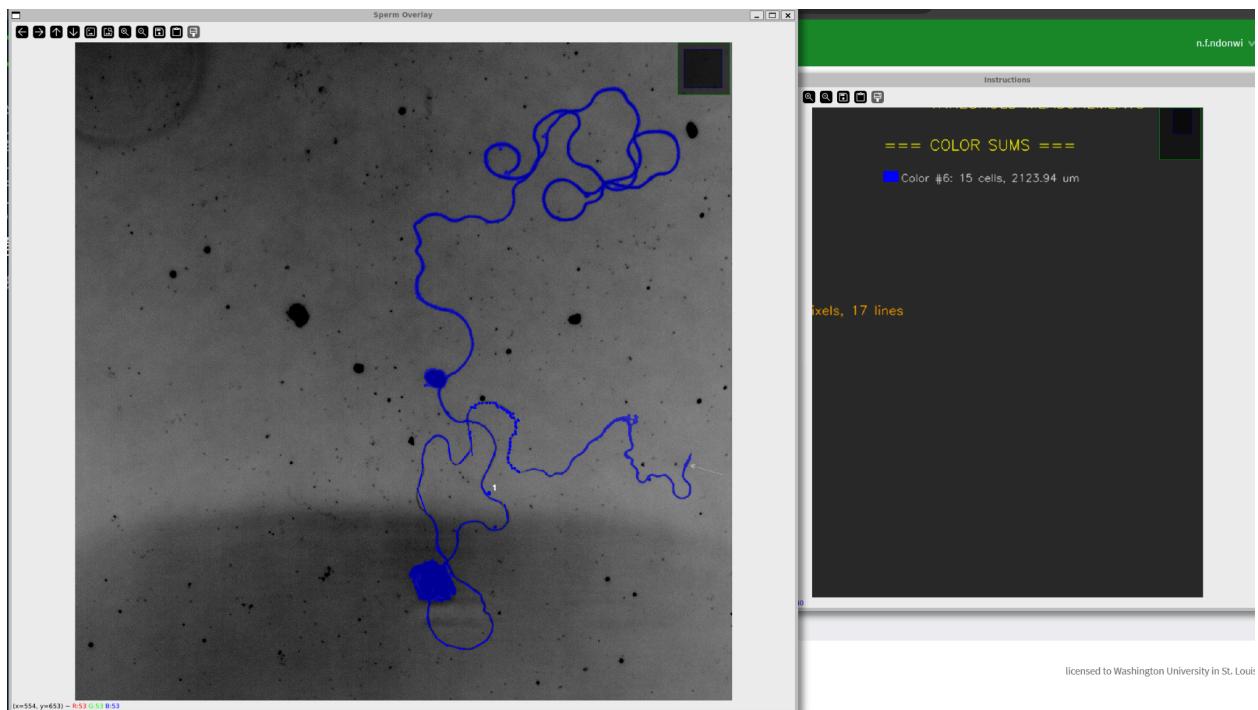


Got 1553.38 expected 1786

## Medium (get screenshots )

24708.1\_4 at 20X -- 1605.95 , expected 1681





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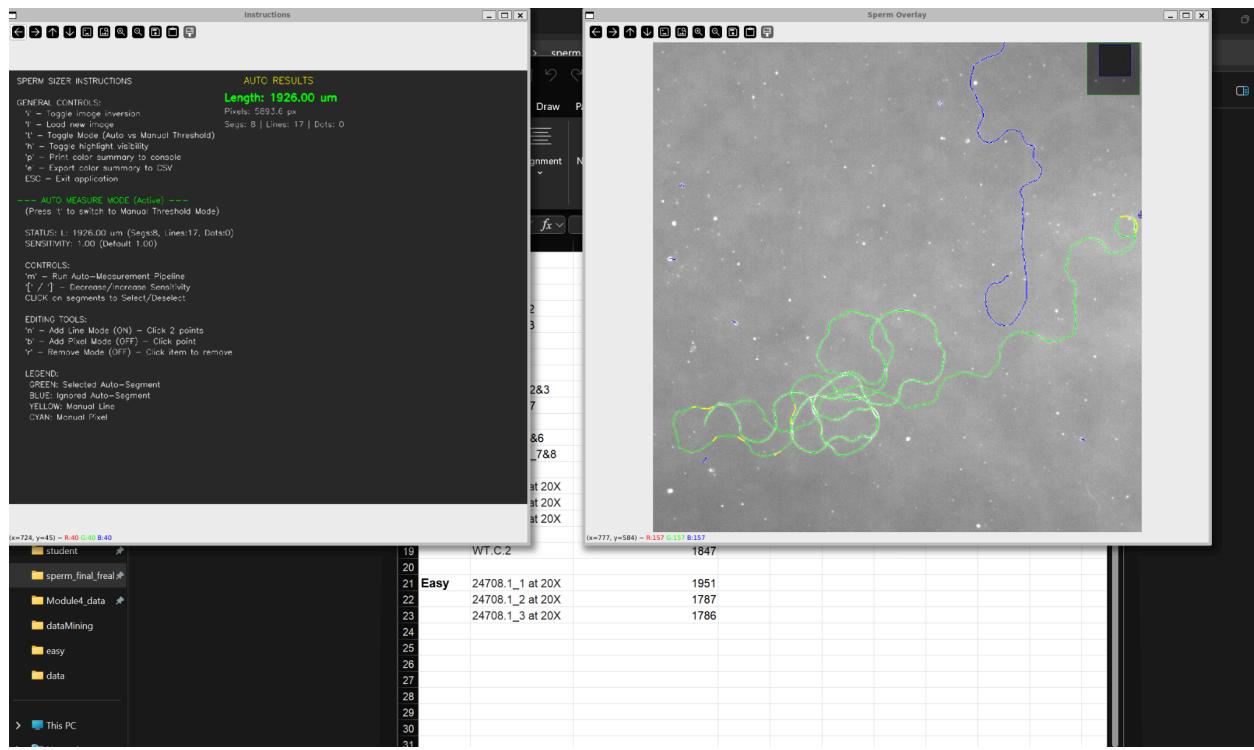
WT.C.1\_20x.jpg -- expected 1090, got 1002



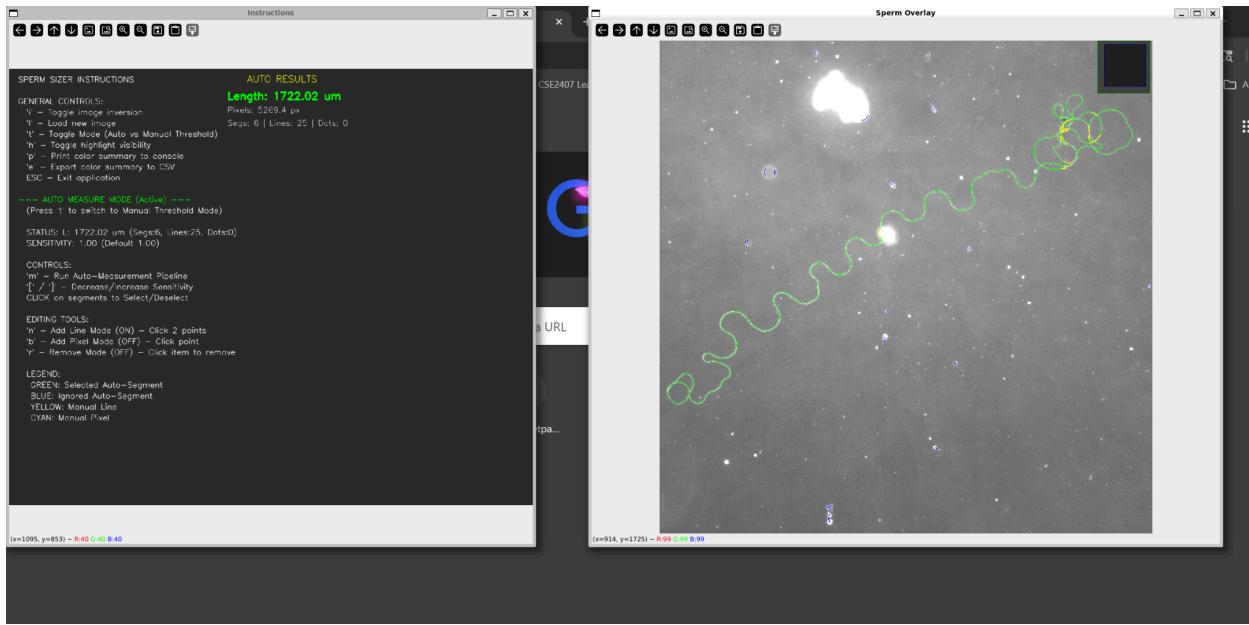
## DA NEW DATA (With Otsu's method and ridge detection / component detection and selection algorithm)

Easy 24708.1\_1 at 20X (GOT 1926, expected 1951)

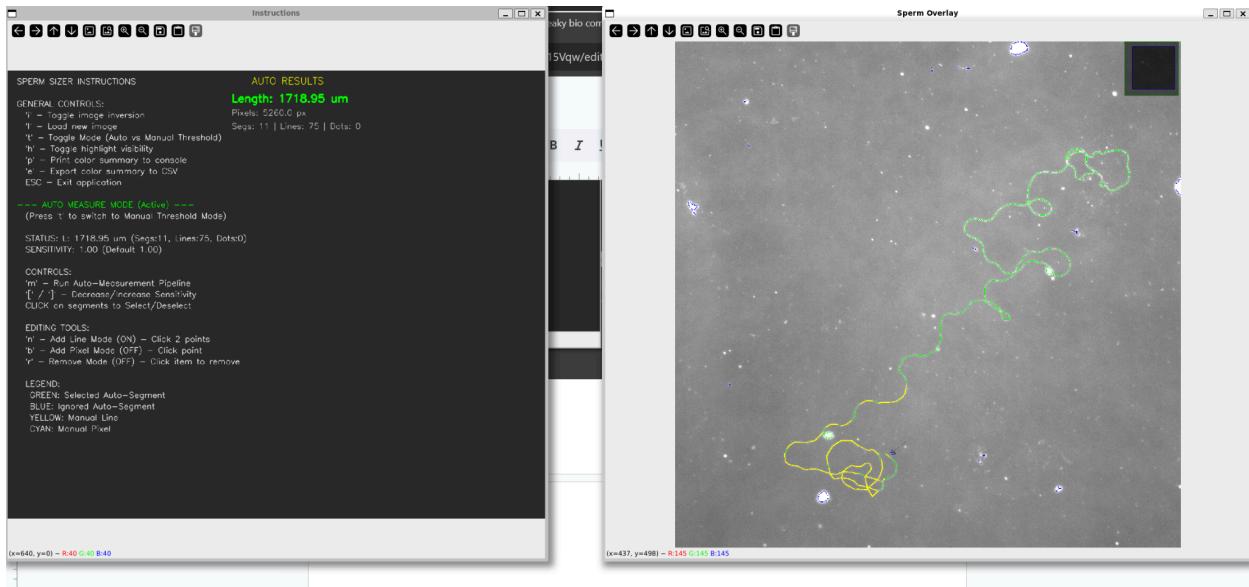
1\_1



1\_2 24708.1\_2 at 20X (GOT 1722.02 expected 1787)

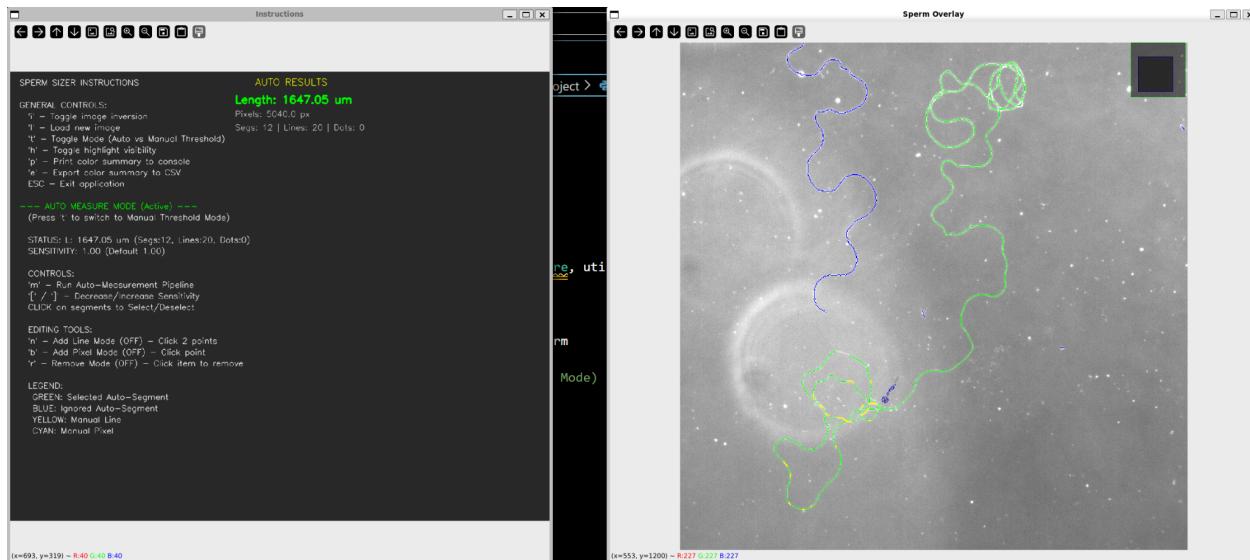


1\_3 24708.1\_3 at 20X (Got 1718.95 but expected 1786)

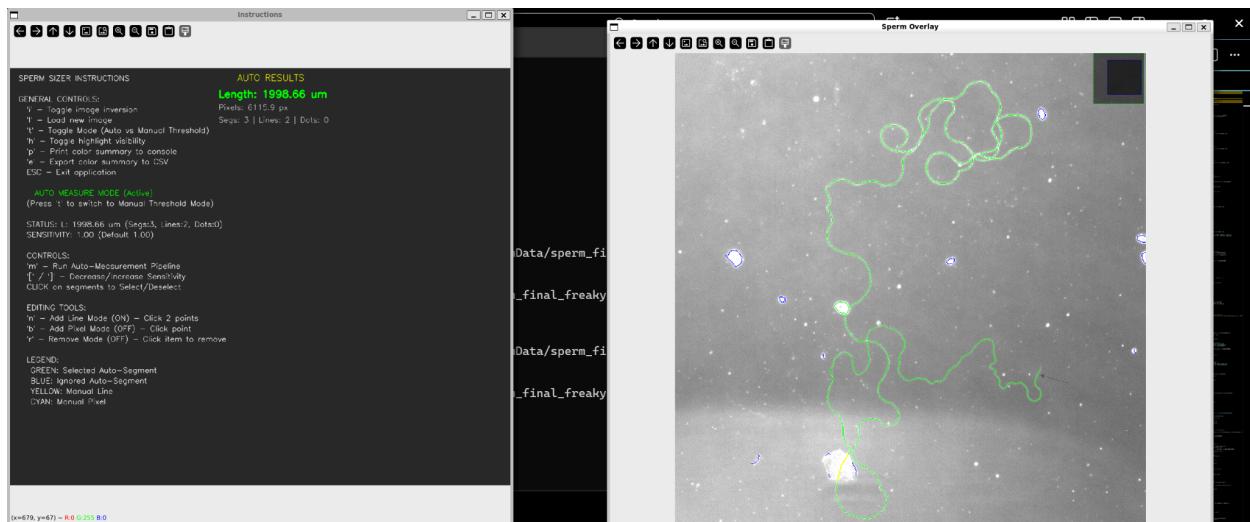


## Medium

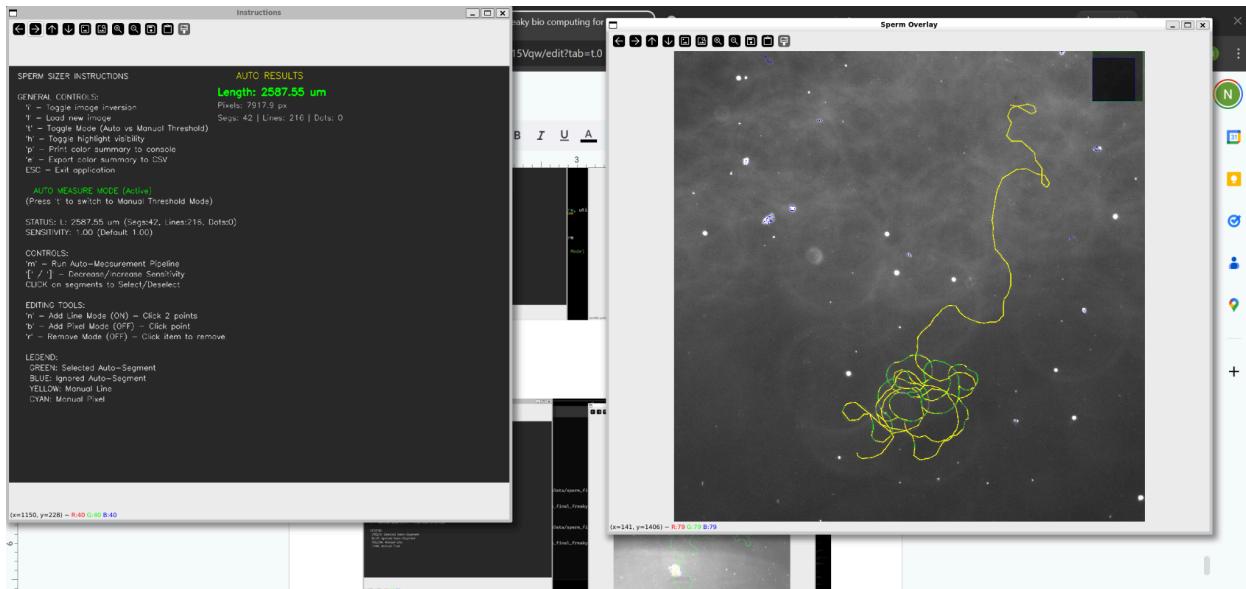
1\_4 24708.1\_4 at 20X (Got 1647.05 but expected 1681)



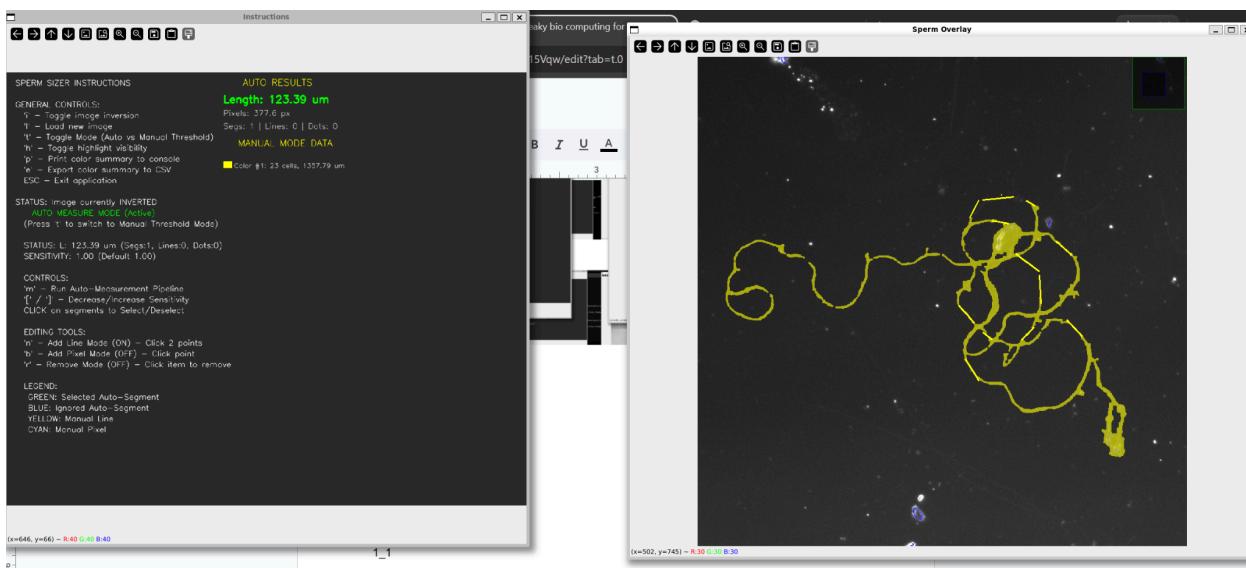
1\_5 24708.1\_5 at 20X (Got 1998.66 but expected 1952)



1\_6 24708.1\_6 at 20X (got 2587.55 but expected 1961)



### C.1 WT.C.1 Got 1357.79 but expected 1090



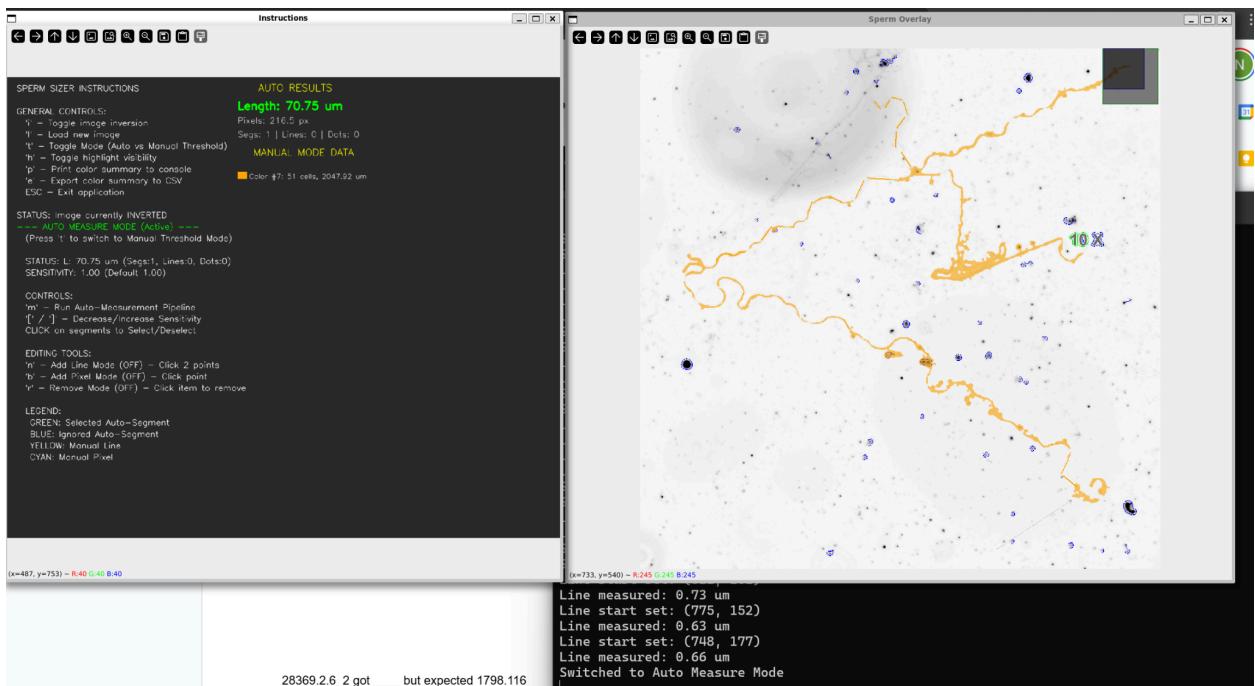
### C.2 WT.C.2 Got 2415.80 but expected 1847



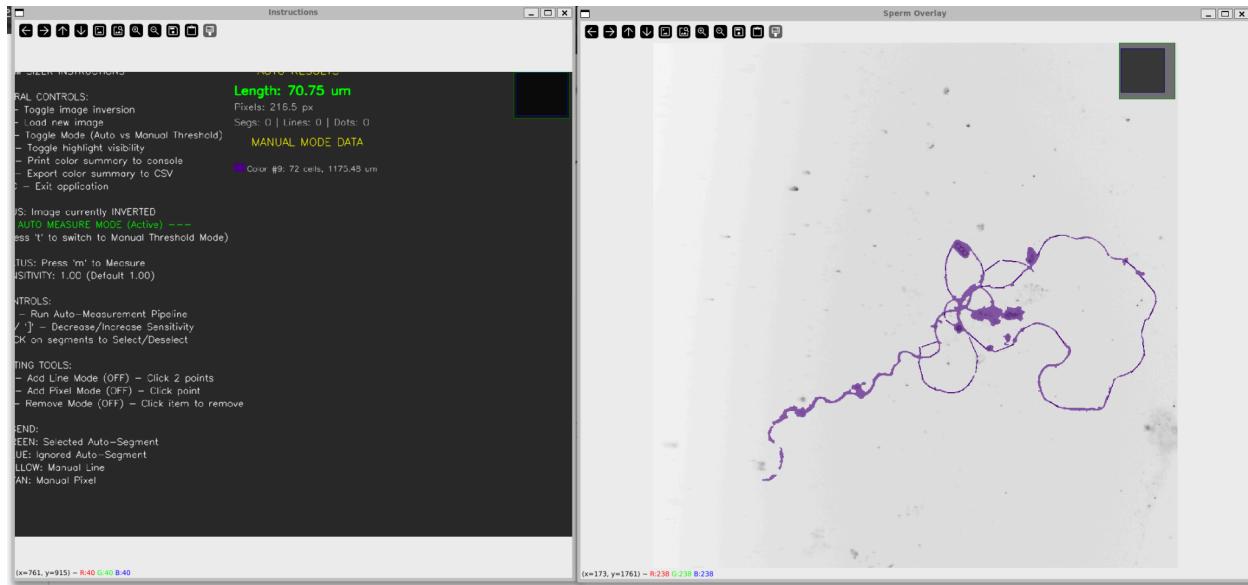
## HARD

(TODO conduct testing on the hard images )

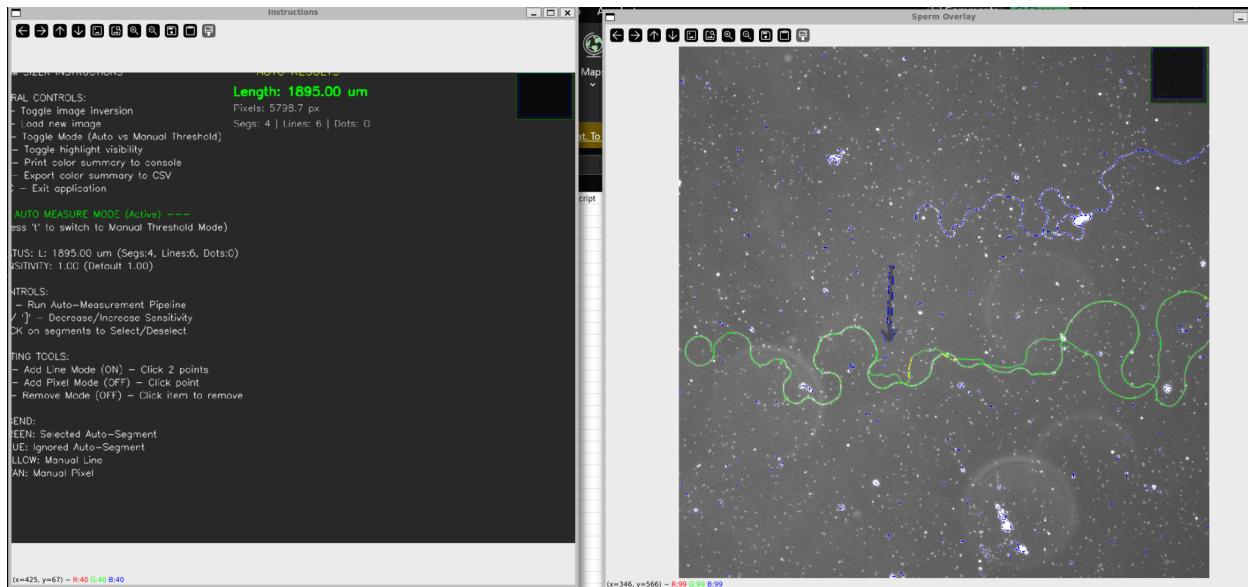
472.1A.1\_1 got 2047.92 but expected 1421.724



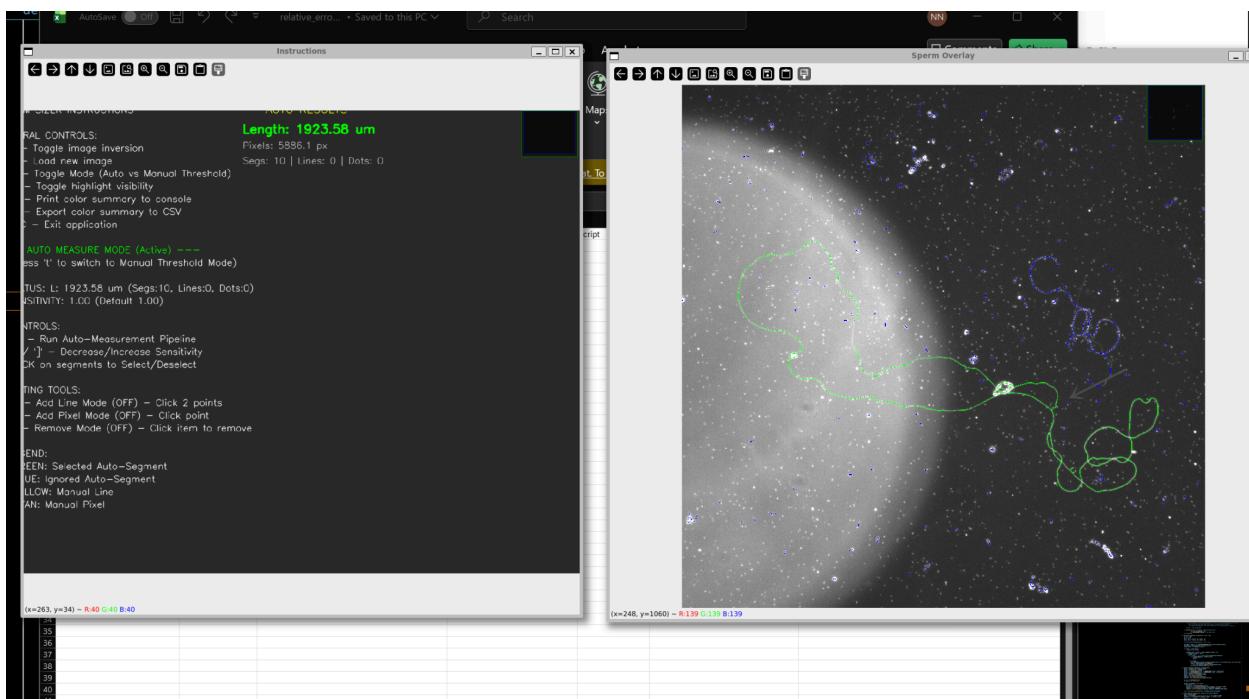
472.1A.1\_2 got 1175.48 but expected 1721.22



28369.2.6\_2 got 1895 but expected 1798.116 (sometimes you have to try inverting the image, mention that as a finding for some)



28369.2.6\_3 got 1923.58 but expected 1820.409



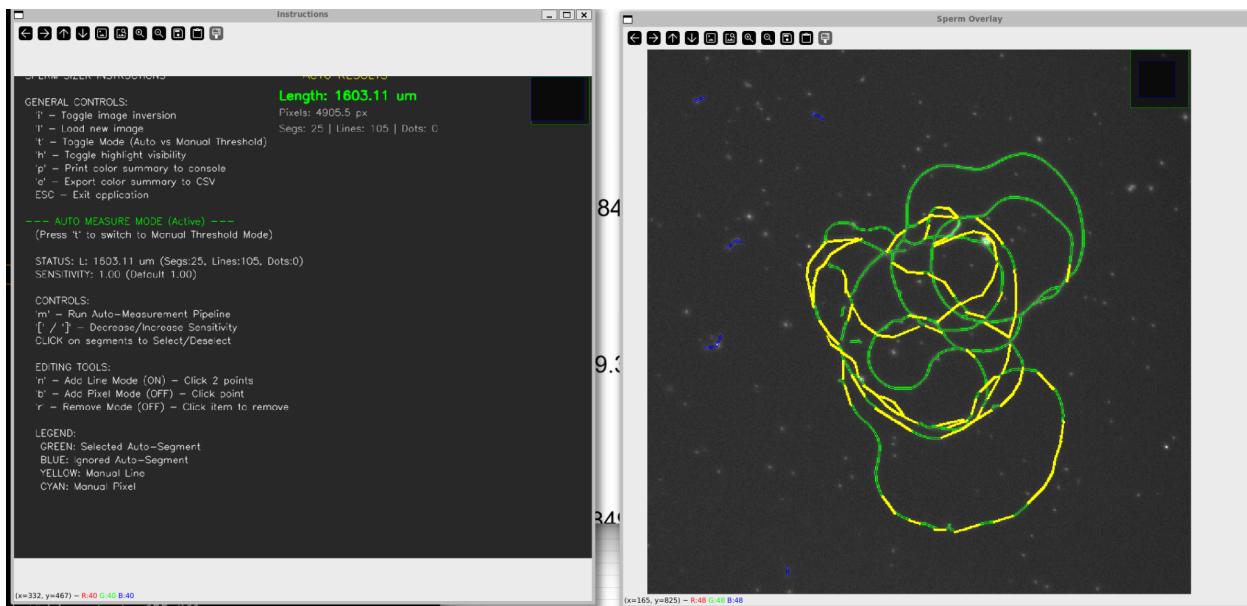
472.1A.1\_5 got 1247.10 but expected 1827.506



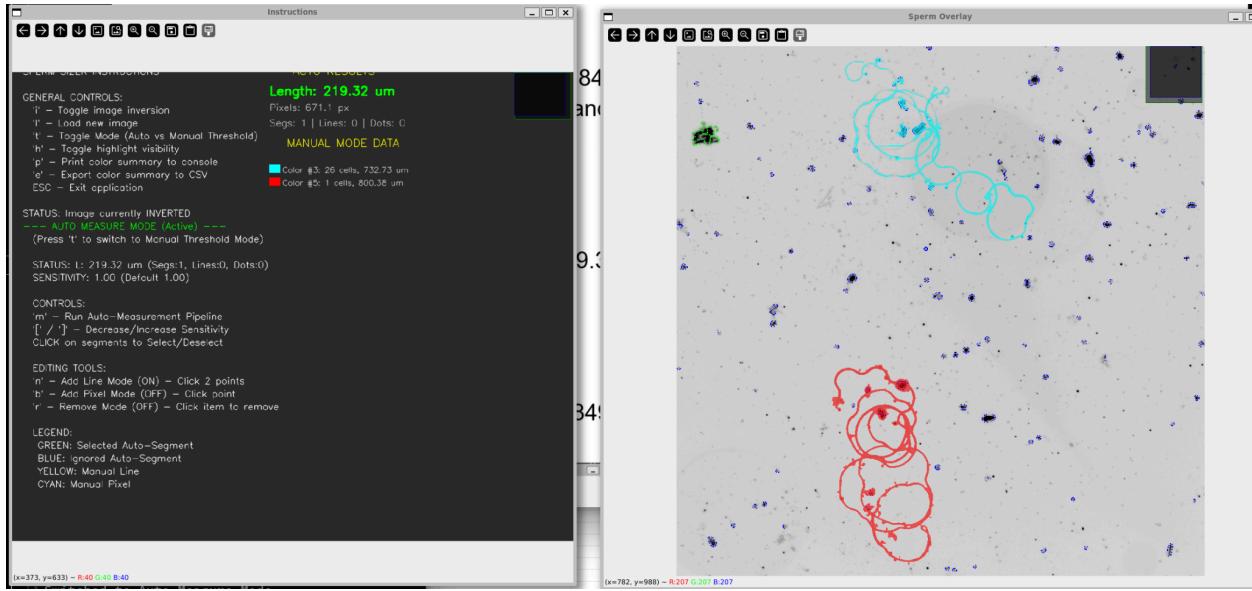
472.1A.1\_4 got 1004 but expected 1836.393



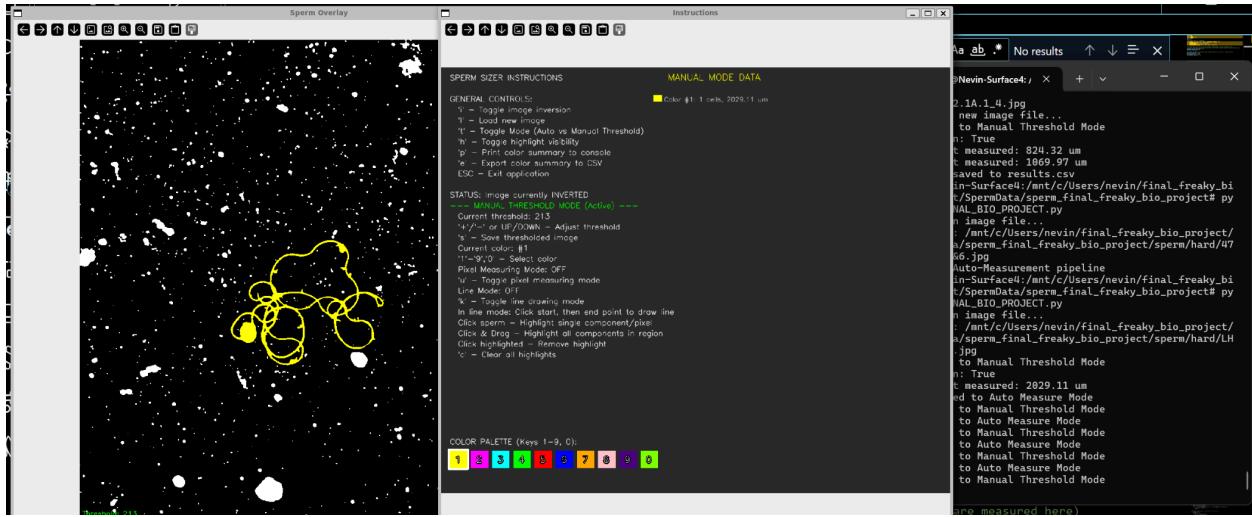
42568.b4.7 got 1603.11 but expected 1840.172



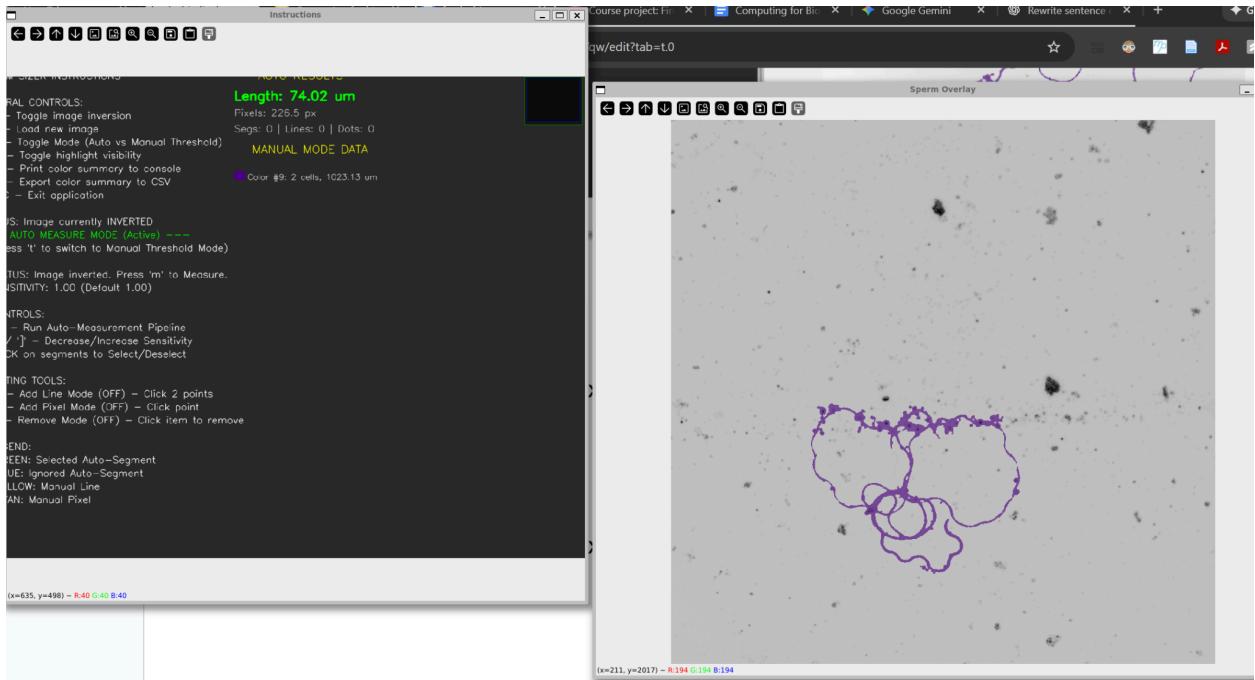
LHM.1B.3\_2&3 got 1000 but expected 1847 (when I relied on threshold mode the accuracy was more off, I think this is due to the pixels and noise that threshold mode has to account for, I have a different pixel - millimeter relationship because I found one that worked better with photos that had more concrete components but it seems to fail at photos where less contrast is present and more noise occurs. )



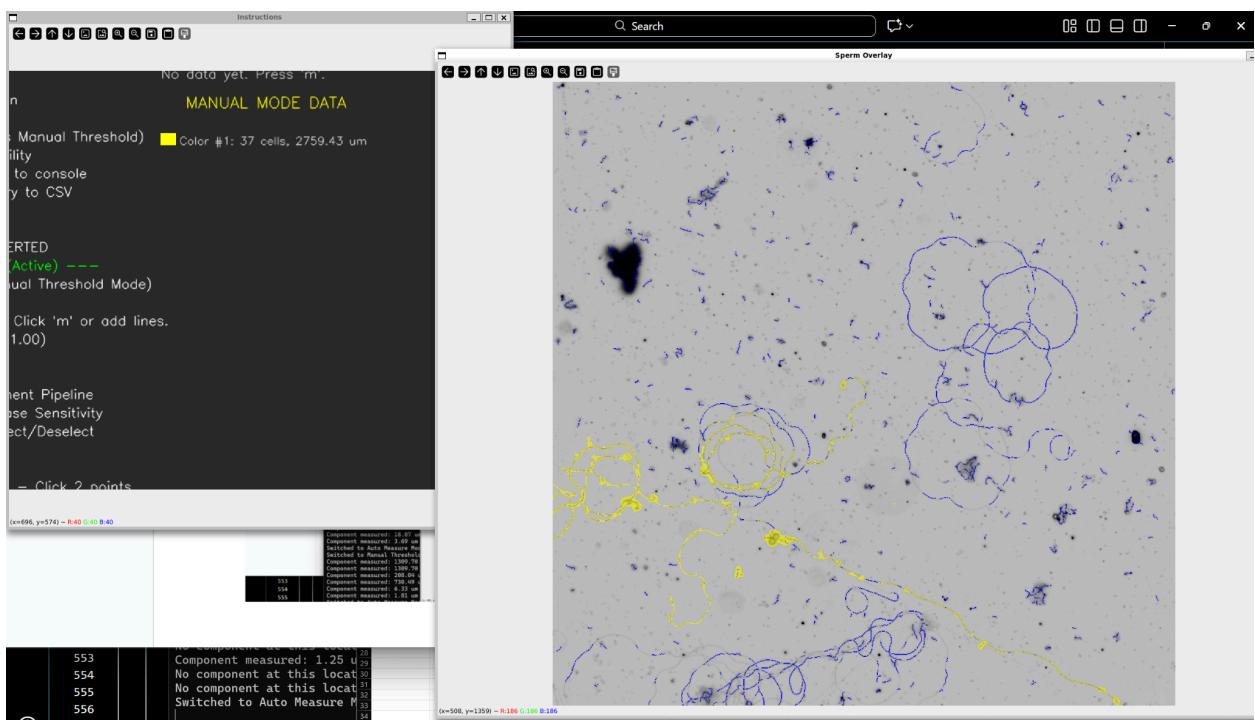
LHM.1B.3\_7 got 2029.11 but expected 1849.383



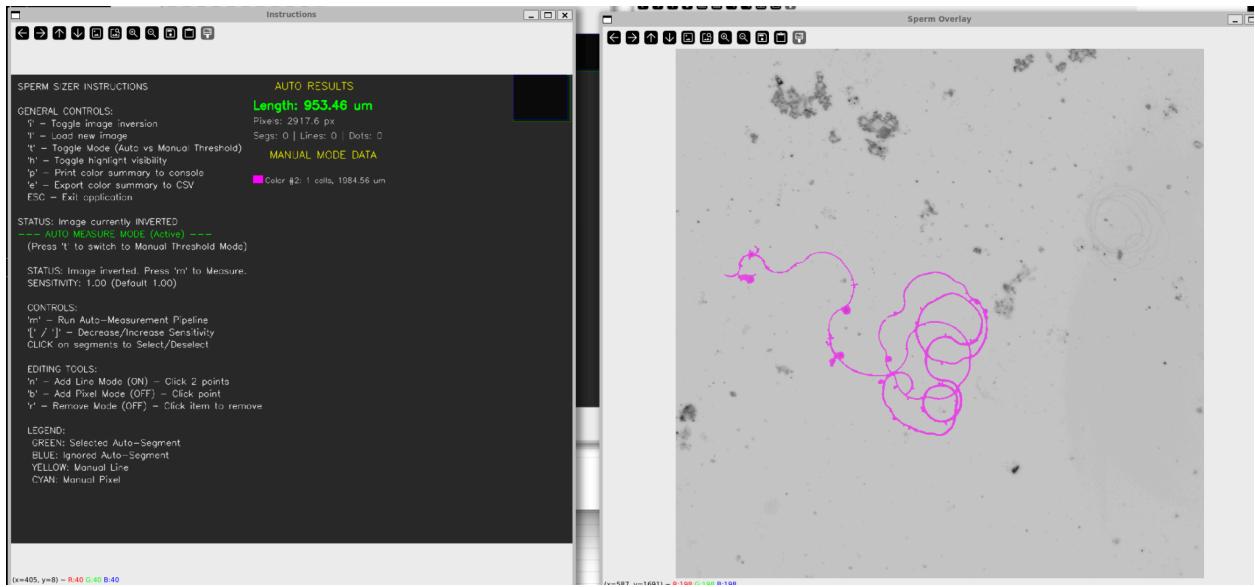
472.1A.1\_3 got 1023.13 but expected 1849.996



472.1B.1\_5&6 got 2759.43 but expected 1870.82



53387.1B.2\_7&8 got 1984.56 but expected 1873.806



Algorithm seems to work better if the sperm is lighter than the background or if the image can be inverted into that scenario.

Next steps , conduct testing and find standard deviation for the rest of the hard samples

I could barely see some of the sperm so i had a hard time tracing them when the algorithm could not find it

Mention threshold level indicated for threshold mode images

```
from sphinx.util import SkipProgressMessage, progress_message
C:\Users\nevin\anaconda3\Lib\site-packages\sphinxcontrib\applehelp\__init__.py:24: RemovedInSphinx80Warning: The 'sphinx.util.progress_message' is deprecated, use 'sphinx.util.display.progress_message' instead. Check CHANGES for API modifications.
from sphinx.util import SkipProgressMessage, progress_message
0.02s - Debugger warning: It seems that frozen modules are being used, which may
0.00s - make the debugger miss breakpoints. Please pass -Xfrozen_modules=off
0.00s - to python to disable frozen modules.
0.00s - Note: Debugging will proceed. Set PYDEVD_DISABLE_FILE_VALIDATION=1 to disable this validation.
C:\Users\nevin\anaconda3\Lib\site-packages\paramiko\transport.py:219: CryptographyDeprecationWarning: Blowfish is deprecated and will be removed in a future release
    "class": algorithms.Blowfish,
2025-12-07 00:59:06.442374: I tensorflow/core/util/port.cc:153] oneDNN custom operations are on. You may see different numerical results due to floating-point round-off errors from different computation orders. To turn them off, set the environment variable `TF_ENABLE_ONEDNN_OPTS=0`.
2025-12-07 00:59:08.250292: I tensorflow/core/util/port.cc:153] oneDNN custom operations are on. You may see different numerical results due to floating-point round-off errors from different computation orders. To turn them off, set the environment variable `TF_ENABLE_ONEDNN_OPTS=0`.
C:\Users\nevin\anaconda3\Lib\site-packages\PyInstaller\building\build_main.py:227: UserWarning:
The numpy.array_api submodule is still experimental. See NEP 47.

1146113 INFO: Extra DLL search directories (AddDllDirectory): ['C:\\\\Users\\\\nevin\\\\AppData\\\\Local\\\\Programs\\\\MiKex\\\\bin\\\\x64\\\\', 'C:\\\\Users\\\\nevin\\\\anaconda3\\\\Lib\\\\site-packages\\\\numpy.lib', 'C:\\\\Users\\\\nevin\\\\anaconda3\\\\Lib\\\\site-packages\\\\cv2\\\\...\\\\x64\\\\vc14\\\\bin', 'C:\\\\Users\\\\nevin\\\\anaconda3\\\\Lib\\\\site-packages\\\\google_crc32c\\\\extra-dll']
1146113 INFO: Extra DLL search directories (PATH): ['C:\\\\Users\\\\nevin\\\\anaconda3\\\\lib\\\\site-packages\\\\cv2\\\\']
```