

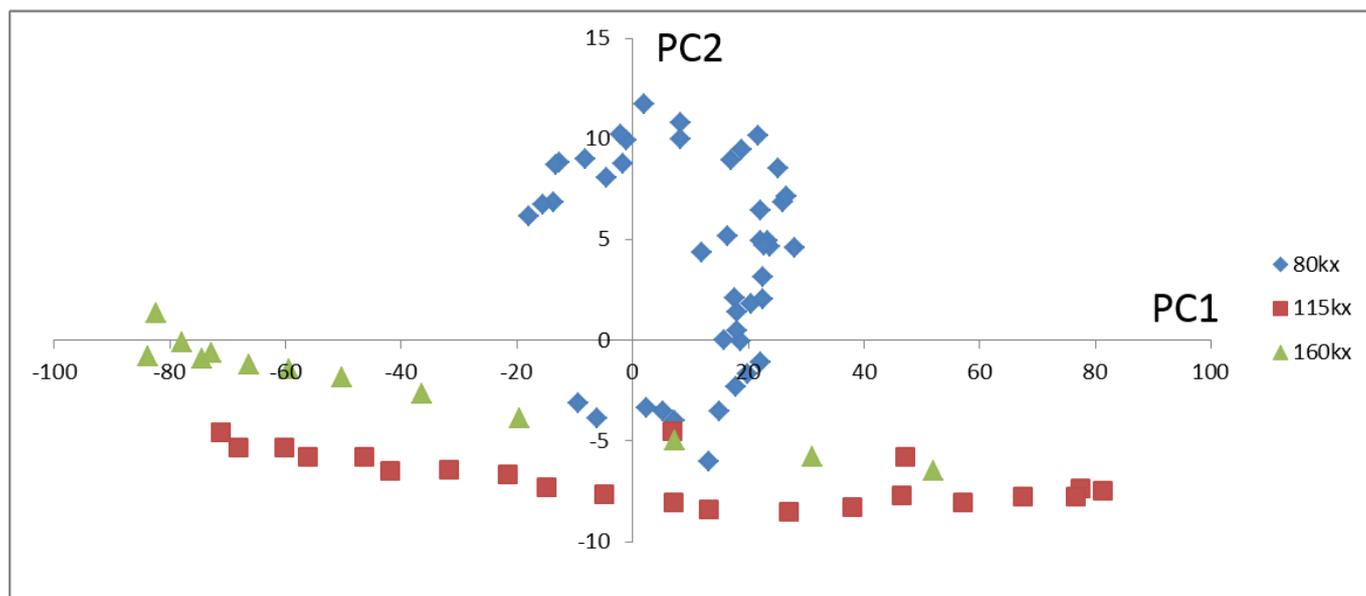
Nanocrystals: Blog Post 10 - Final Blog

Extracting morphological changes in nanocrystals using in situ liquid cell microscopy

Final Blog

This course has been quite the experience. The project presented a lot of unforeseen challenges, but ultimately we feel we were able to overcome most of them and at least establish a potential solution for any we couldn't. By far, the issues we had with image segmentation and binarization were the most difficult. It really slowed us down and put us behind all semester, but in the end we were able to establish a model we were satisfied with. For a detailed walkthrough of our project, follow our previous blogs. We will also post our final presentation at the bottom of this blog for your perusal. For now, we will just discuss some of the insights from our model and some of the takeaways from the class.

Looking at our pc scores in 2d space, we can clearly see clustering and ordering. The data evolve consistently through time and two of the sets follow the same trend. Below you can see the plot.



The green and blue data set both follow a nearly linear trend, while the blue data set is very different. This is actually promising because the literature suggests that there is a threshold dosage at which the growth kinetics transition between diffusion-limited and reaction-limited regimes. So perhaps the blue data sets falls in one regime and the other two data sets fall in the other. Hopefully with further work this model will be a useful tool for verifying kinetic models in the literature.

It would also be great for the model to be further tested with experimental data. We used cross-

validation to see if the model predict pc scores as it should, but the real goal is to be able to predict new results. Feeding the inputs into the model to get the pc scores, then actually running liquid cell microscopy experiments with those parameters to find the real microstructure would rigorously test the model.

Finally, we feel there is always room for improvement in image segmentation and binarization. As we said, it was our single greatest challenge and we recognize the potential for further refinement. The framework to calculate two-point statistics, run PCA, and build a model is there. Further refinement of the segmentation would be an efficient way to improve the model further.

Thank you for following us throughout the project. Below you can find the file for the final presentation. Also, on our wiki project map page, you can find a link to the source code. Please feel free to comment!

[SUPERFINAL_ME8883_Presentation.pptx](#) (5 MB)