

Flow Cytometry Analysis

- Determining cell types using deep learning techniques
- Creating software to allow streamlined process for flow cytometry analysis

The problem

FlowJo

The current standard of analyzing flow cytometry data is the use of the paid application FlowJo, which is very tedious and done manually.

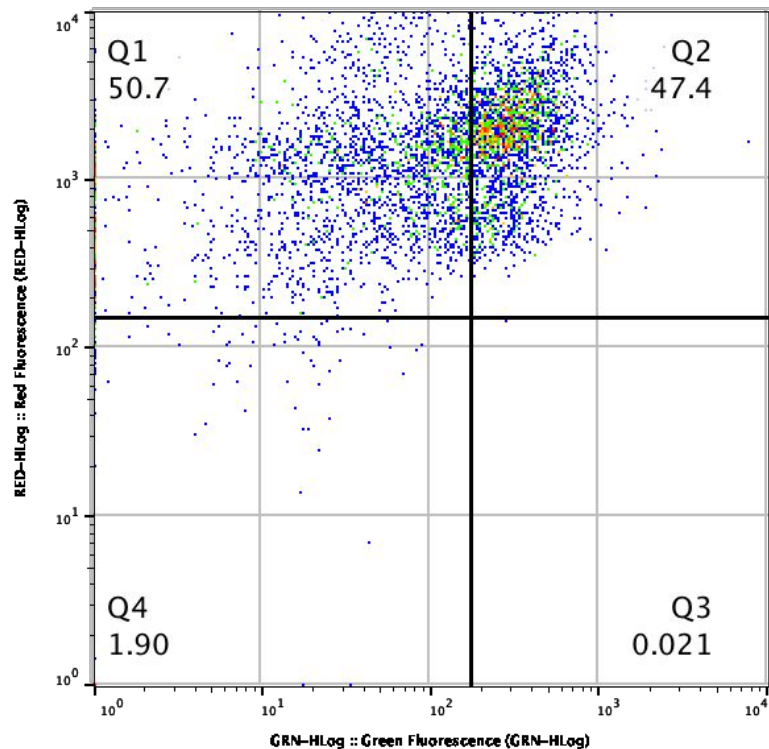
Variability in Data

The method for determining different cell states and types is done by eye, and lacks the capability to determine non-linear patterns. In addition, the multi-channel capabilities of the flow data are not utilized.

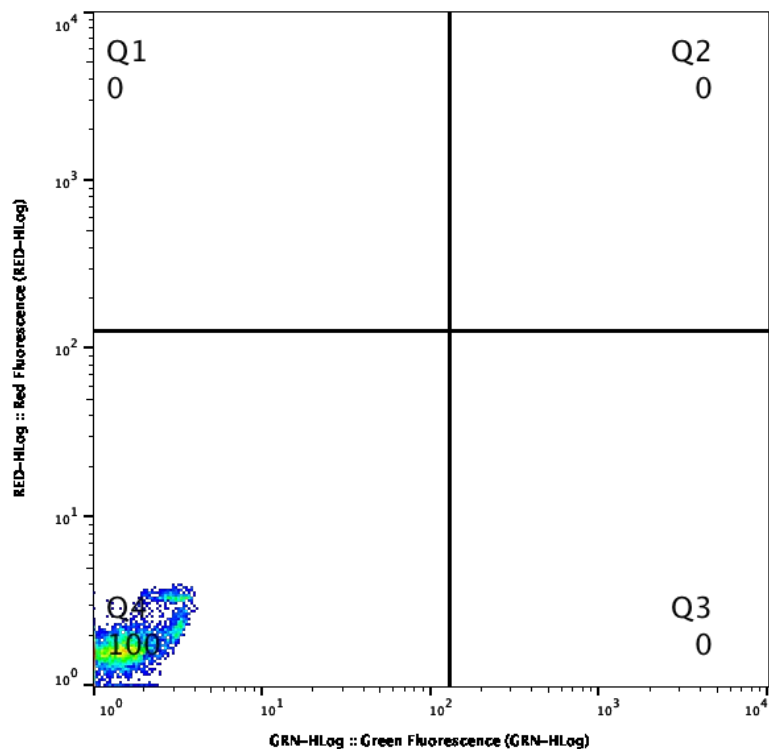
Problem statement

There are significant limitations in the standard ways used to interpret flow cytometry data, and specific learning algorithms can be used to better determine various cell states.

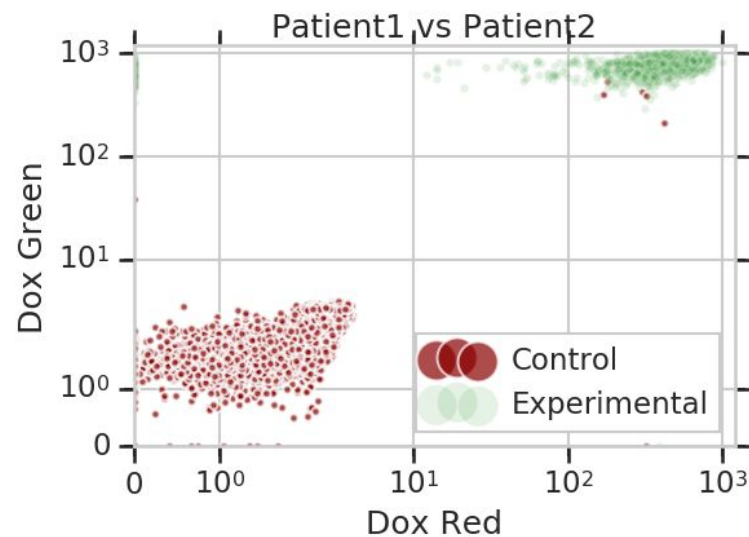
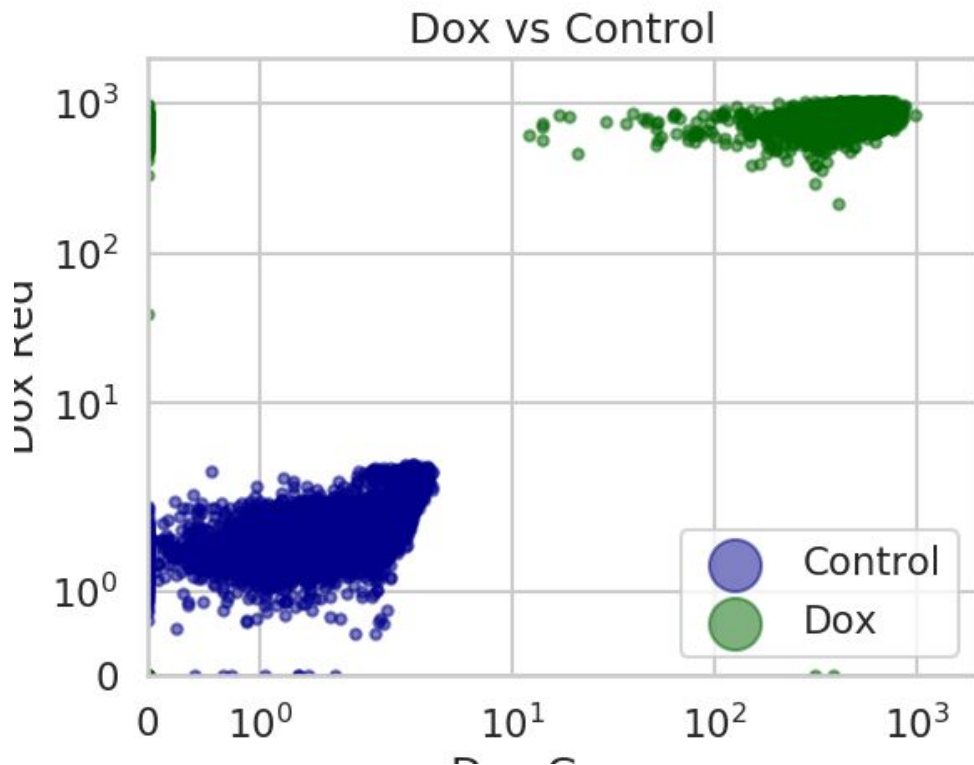
Challenges



	FSC- click to unsroll	FSC- output; double click to unsroll	GRN- click to unsroll	GRN- double click to unsroll	NN	RED- HLin	RED- HLog	RED2- HLin	RED2- HLog	RED2- A	RED2- ALog	RED2- W	SSC- HLin	SSC- HLog	YEL- HLin	YEL- HLog
0	576.0	959.0	43.0	671.0	0	0.0	169.0	0.0	125.0	0.0	155.0	702.0	120.0	785.0	0.0	242.0
1	437.0	928.0	9.0	502.0	0	0.0	228.0	0.0	118.0	0.0	137.0	765.0	106.0	771.0	0.0	0.0
2	289.0	882.0	4.0	412.0	1	0.0	246.0	0.0	79.0	0.0	0.0	493.0	22.0	598.0	0.0	175.0
3	85.0	746.0	285.0	881.0	0	3.0	385.0	1.0	288.0	1.0	298.0	480.0	62.0	712.0	8.0	489.0
4	464.0	935.0	11.0	524.0	0	1.0	253.0	0.0	252.0	0.0	225.0	593.0	123.0	788.0	0.0	114.0



Plotting multiple experiments



Solution: Web application for Flow Cytometry Analysis

The screenshot shows a web browser window with the address bar displaying "https://fcs.nathan2wong.com/upload". The page title is "Flow Cytometry Analysis Tool". Below the title are navigation links: "Home", "Screenshots", "Contact", and "Log Out". The main heading is "Upload FCS Files", followed by a subheading "Upload the .fcs files produced from the flow cytometry experiment." and a note: "Only Red Fluorescence (HLog) and Green Fluorescence (HLog) are supported at this time." A "View Example" button is located below the note. The page is divided into three main sections: "FCS File 1" with the title "Control FCS File" and a "Choose File" button; "FCS File 2" with the title "Experimental FCS File" and a "Choose File" button; and "Upload Files" with an "Email address" input field containing "name@example.com" and a blue "Upload" button. At the bottom, the timestamp "32019-01-23 20:08:03.426098" and the text "Flow Cytometry Analysis Tool created by Nathan." are displayed.

Flow Cytometry Analysis Tool

[Home](#) [Screenshots](#) [Contact](#) [Log Out](#)

Upload FCS Files

Upload the .fcs files produced from the flow cytometry experiment.
Only Red Fluorescence (HLog) and Green Fluorescence (HLog) are supported at this time.

[View Example](#)

FCS File 1

Control FCS File

[Choose File](#) No file chosen

FCS File 2

Experimental FCS File

[Choose File](#) No file chosen

Upload Files

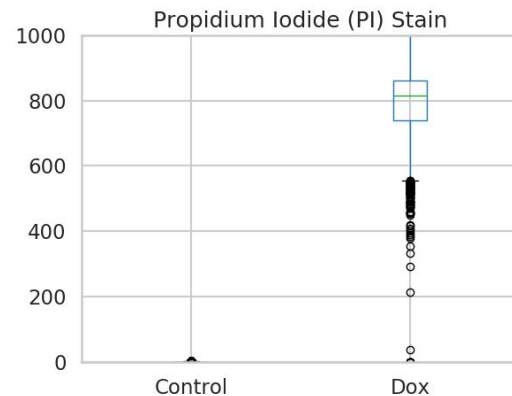
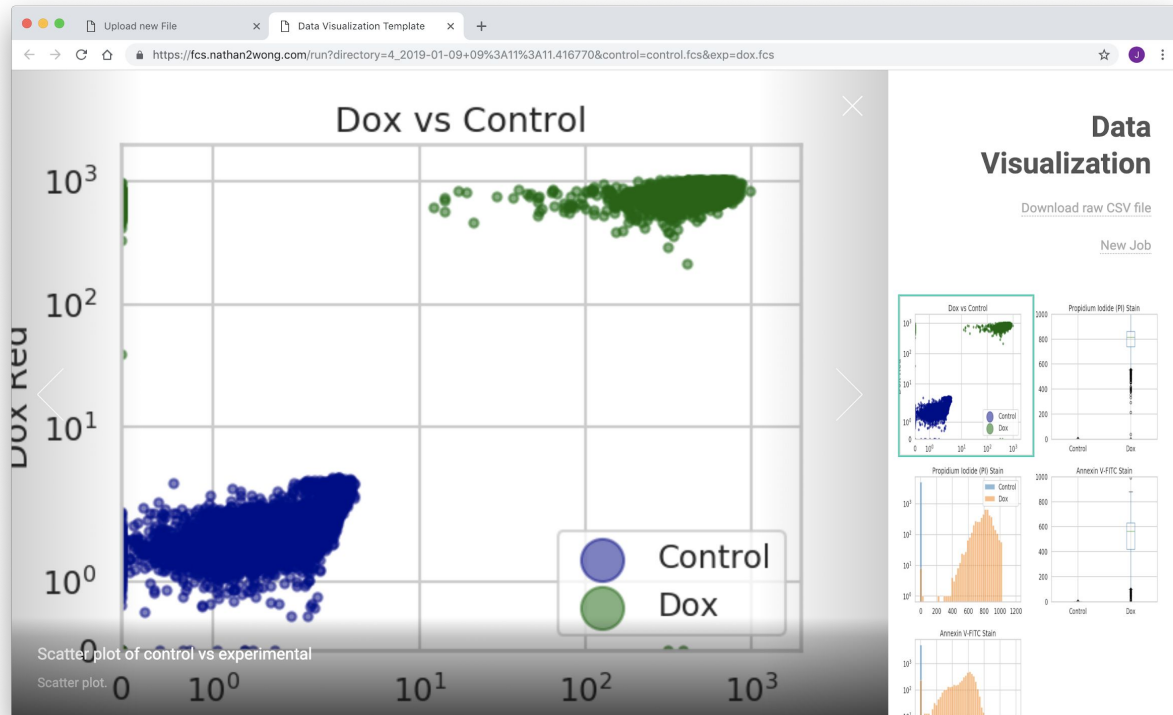
Email address

[Upload](#)

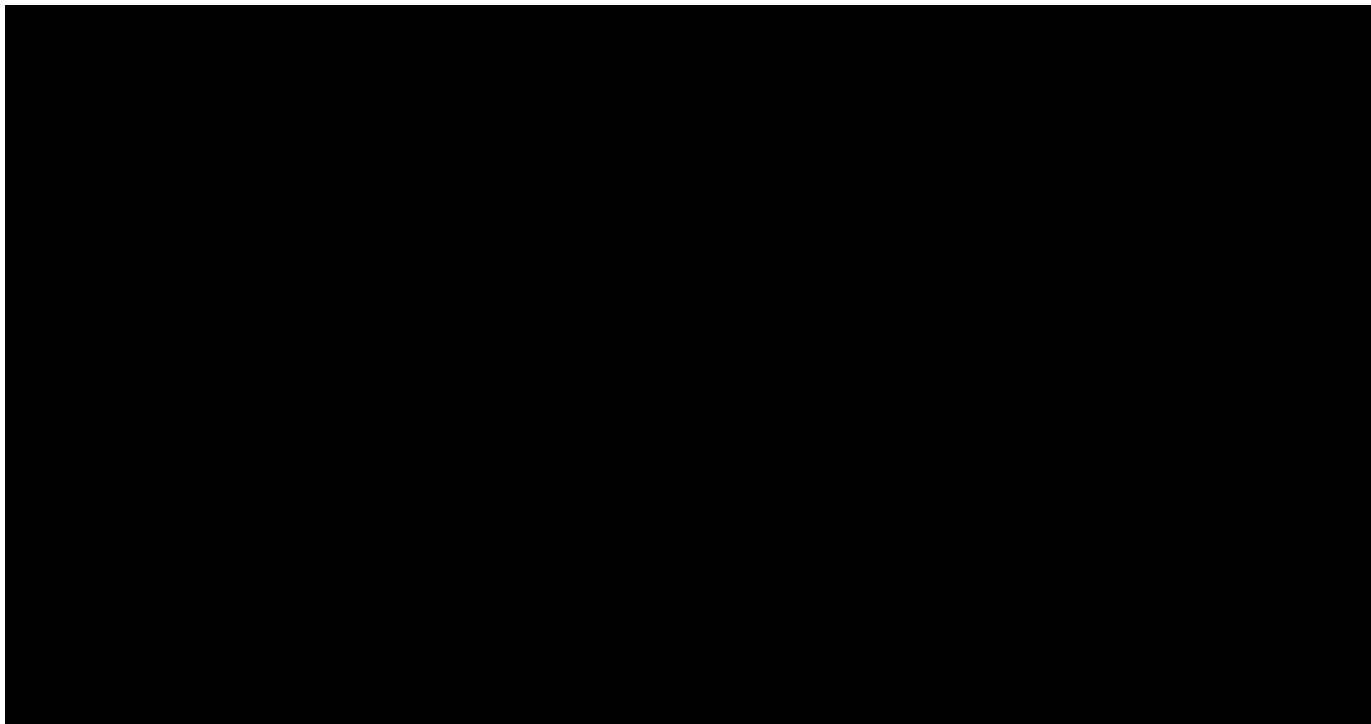
32019-01-23 20:08:03.426098

Flow Cytometry Analysis Tool created by Nathan.

<https://fcs.nathan2wong.com>



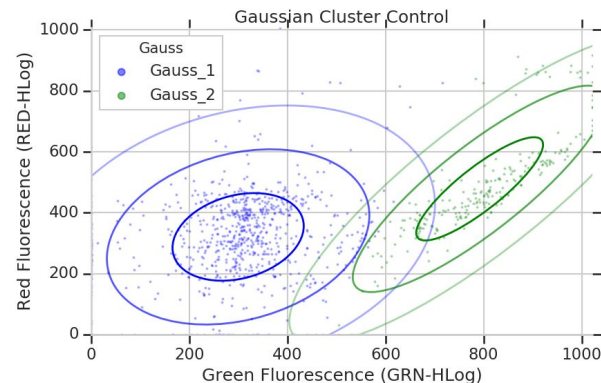
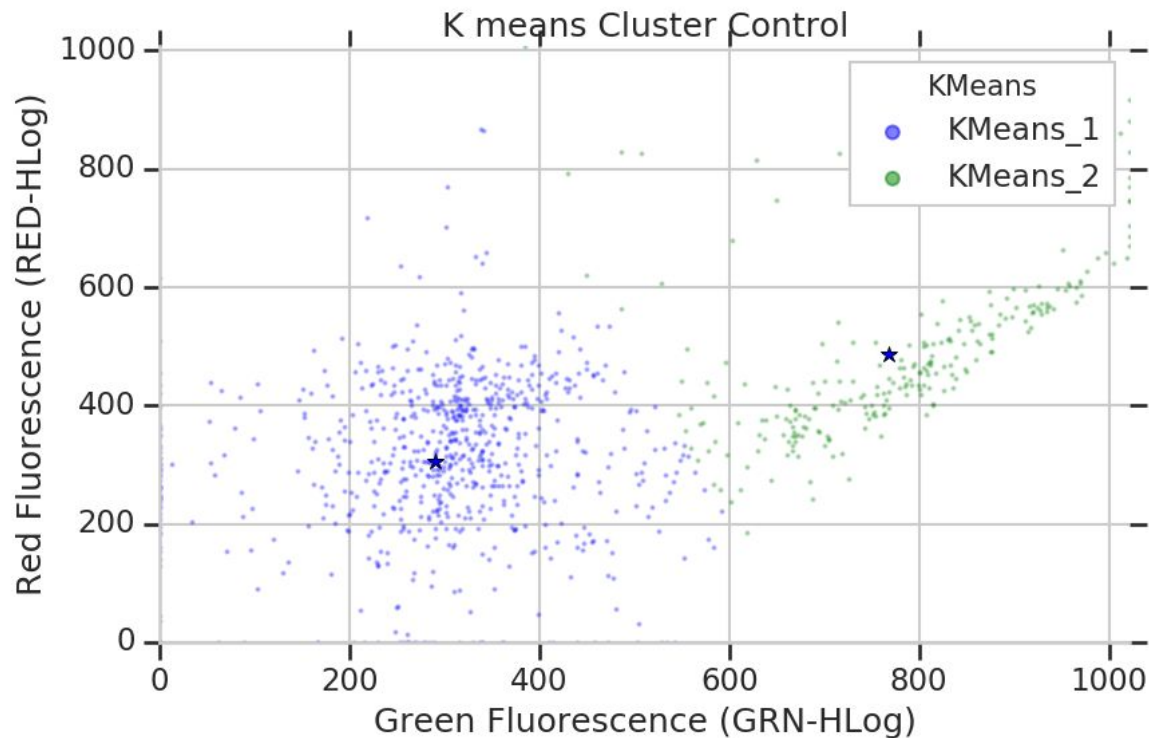
Demonstration Video



Machine Learning and Classification

- Initial goal: determine difference between different samples (ie. Dox vs Nothing)
- Secondary goal: classify into 4 different cell types
- Unsupervised learning, Perceptrons, Decision-trees, Convolutional Neural Networks, Support Vector Machine, K-nearest neighbors, Monte-Carlo Random Walk

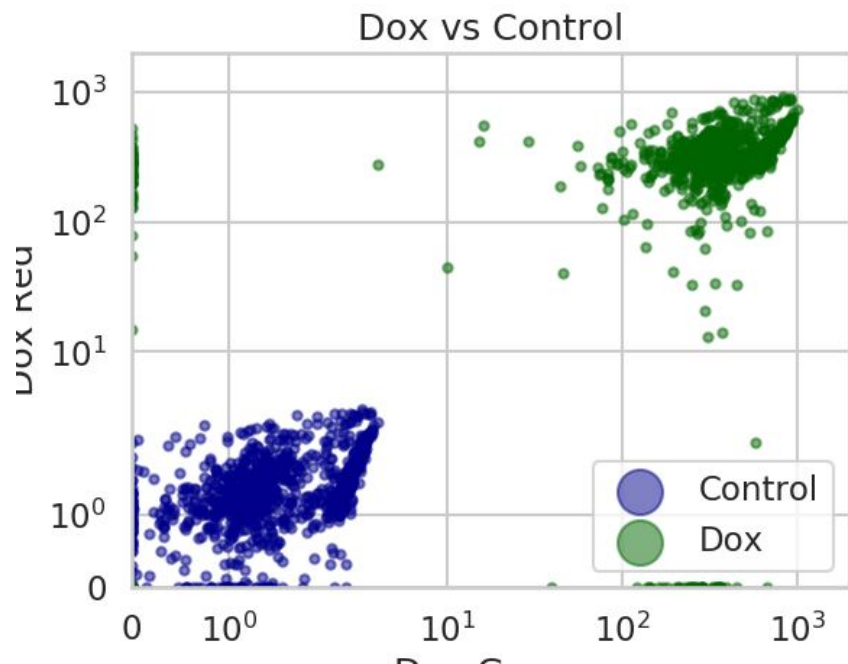
Unsupervised Learning





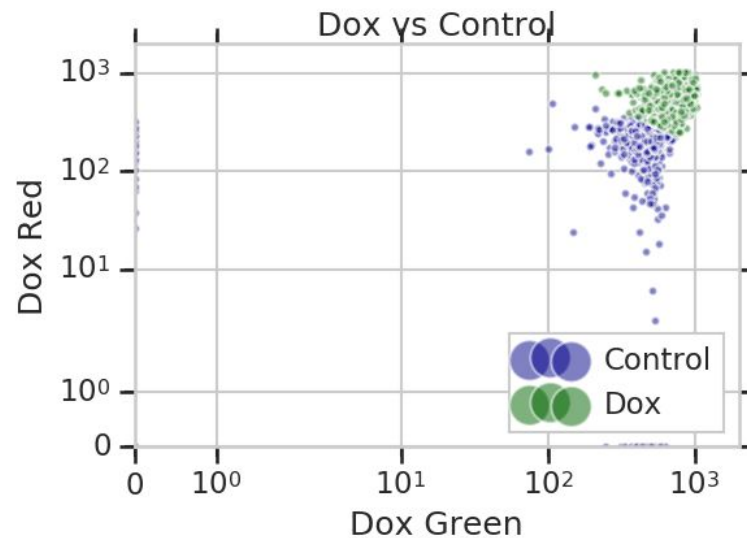
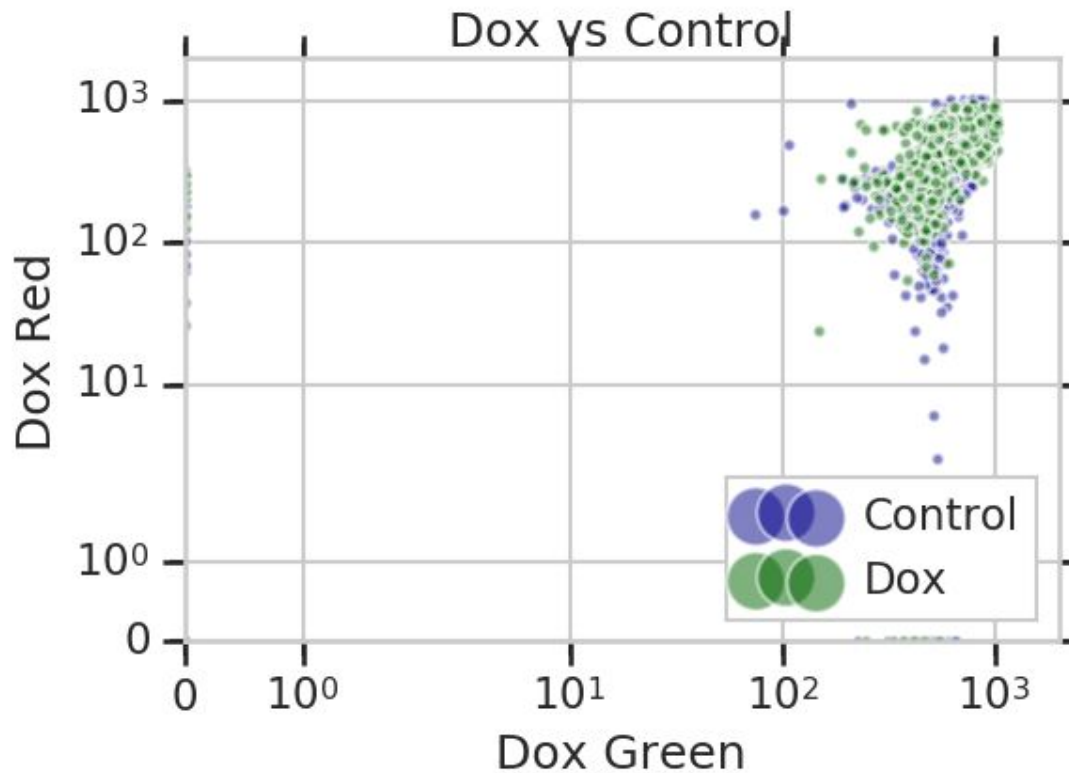
Train to differentiate datasets (ie.
Dox vs Control)

Perceptron: Binary Linear Classifier (~99% accuracy)



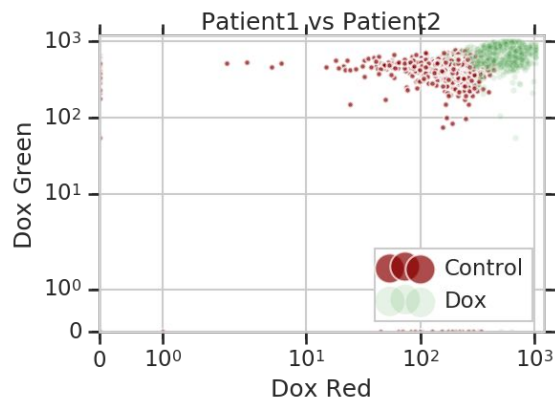
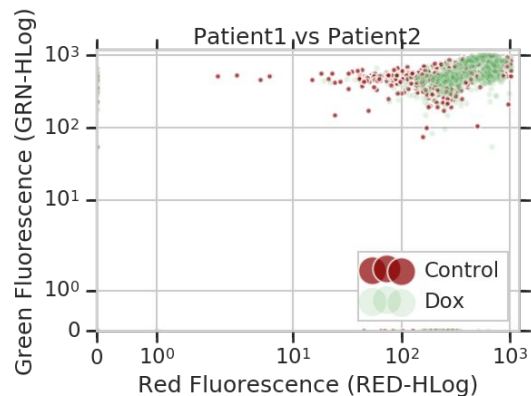
	Red	Green	Label	classifier
click to expand output; double click to hide output				
0	798.575027	599.188782	1	[1]
1	0.599727	2.180591	0	[0]
2	932.756930	346.388988	1	[1]
3	795.294284	124.819488	1	[1]
4	1.961999	0.115012	0	[0]
5	992.634669	381.528351	1	[1]
6	1.773458	2.059145	0	[0]
7	870.866412	502.507863	1	[1]
8	1.916221	-0.019927	0	[0]
9	1.516055	1.693334	0	[0]
10	1.935923	2.216021	0	[0]
11	1.423885	1.832374	0	[0]
12	2.320462	1.099079	0	[0]
13	798.416642	493.536988	1	[1]
14	866.829447	408.425943	1	[1]

Perceptron: Binary Linear Classifier (~74% accuracy)

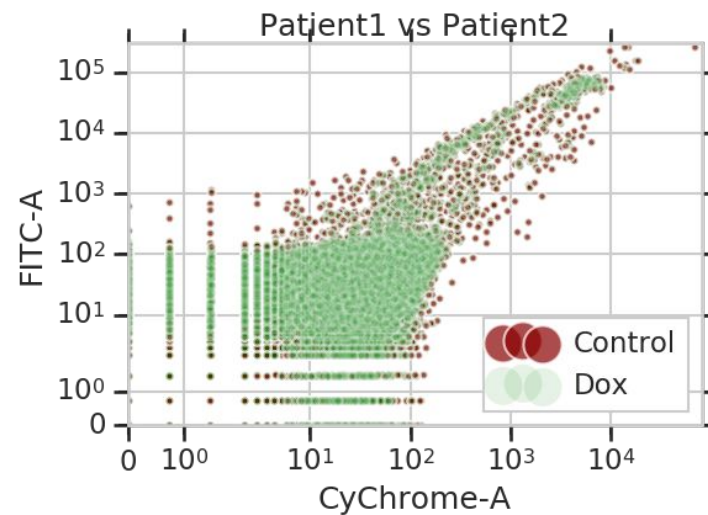
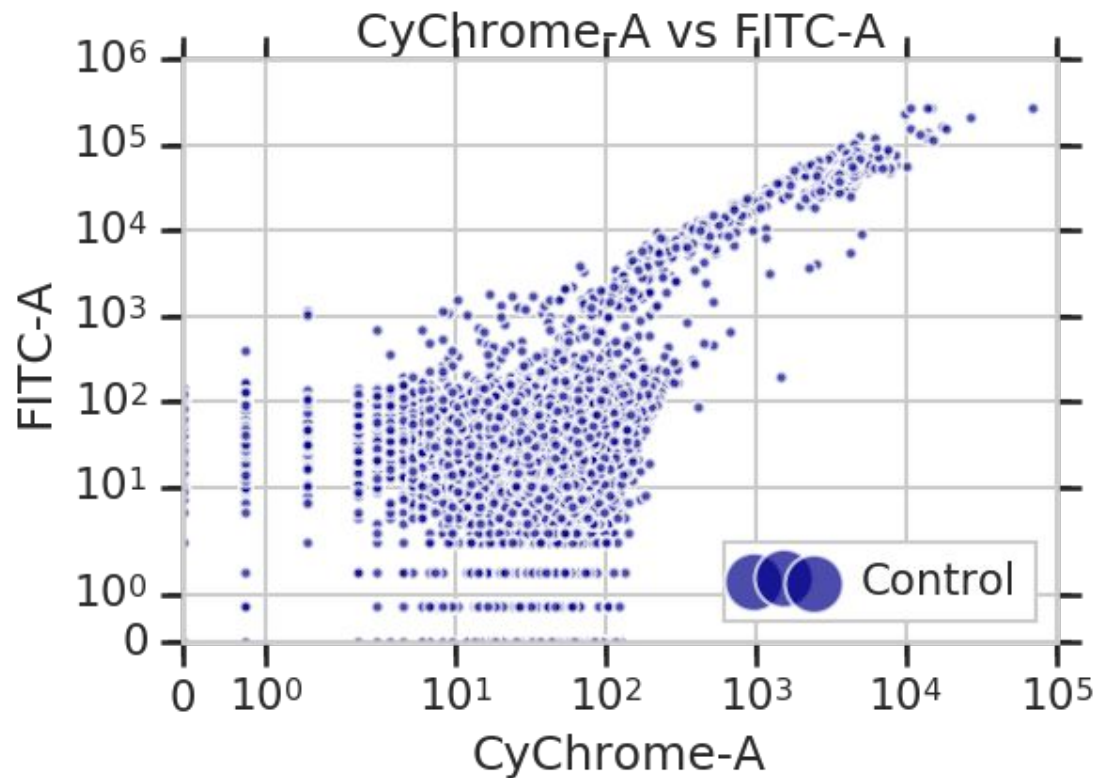


Adding more features (~79% accuracy)

	FSC- HLog	FSC- HLog	GRN- HLog	GRN- HLog	NN	RED- HLog	RED- HLog	RED2- HLog	RED2- HLog	RED2- A	RED2- ALog	RED2- W	SSC- HLog	SSC- HLog	YEL- HLog	YEL- HLog
	click to unscroll output; double click to hide															
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Nature Article Flow Cytometry Data



Other Classifiers (~ 70-75% accuracy)

- Random Forest (Decision tree)
- Hyperparameter regularization for perceptrons
- Convolutional Neural network (10 hidden nodes)

```
Out[64]: [array([-0.02749707, -0.01857512,  0.61941769,  0.16193332,  0.67055136,
                -0.0798152 , -0.27263801, -0.16553927,  0.56553296,  0.05639448,
                0.48302538,  0.32891737, -0.05665307]),
          array([ 0.53320298,  0.43645602, -0.21926395, -0.16611449,  0.16294164,
                -0.53297023,  0.29427769, -0.40827064,  0.29385857, -0.30589829,
                0.33142698,  0.43548104,  0.4418559  ]),
          array([ 0.34050606, -0.18723422,  0.42186015, -0.11689606,  0.06312648,
                0.39428066,  0.06400615,  0.16391696,  0.33636853,  0.48216734,
                0.08656373, -0.07174771,  0.11912515]),
          array([0.44818091, 0.5189298 , 0.10784652])]
```

```
training
INFO:tensorflow:Calling model_fn.
INFO:tensorflow:Done calling model_fn.
INFO:tensorflow:Create CheckpointSaverHook.
INFO:tensorflow:Graph was finalized.
INFO:tensorflow:Restoring parameters from neomodel/train5/model.ckpt-9000
INFO:tensorflow:Running local_init_op.
INFO:tensorflow:Done running local_init_op.
INFO:tensorflow:Saving checkpoints for 9000 into neomodel/train5/model.ckpt.
INFO:tensorflow:loss = 225.01385, step = 9001
INFO:tensorflow:global_step/sec: 105.394
INFO:tensorflow:loss = 163.49983, step = 9101 (0.954 sec)
INFO:tensorflow:global_step/sec: 103.952
INFO:tensorflow:loss = 290.31854, step = 9201 (0.958 sec)
INFO:tensorflow:global_step/sec: 114.036
INFO:tensorflow:loss = 359.3168, step = 9301 (0.885 sec)
INFO:tensorflow:global_step/sec: 113.929
INFO:tensorflow:loss = 147.5505, step = 9401 (0.878 sec)
INFO:tensorflow:global_step/sec: 108.405
INFO:tensorflow:loss = 164.68896, step = 9501 (0.917 sec)
INFO:tensorflow:global_step/sec: 102.552
INFO:tensorflow:loss = 149.77173, step = 9601 (0.977 sec)
INFO:tensorflow:global_step/sec: 108.835
INFO:tensorflow:loss = 289.1897, step = 9701 (0.917 sec)
INFO:tensorflow:global_step/sec: 110.329
INFO:tensorflow:loss = 457.52533, step = 9801 (0.906 sec)
INFO:tensorflow:global_step/sec: 107.603
INFO:tensorflow:loss = 682.356, step = 9901 (0.929 sec)
INFO:tensorflow:Saving checkpoints for 10000 into neomodel/train5/model.ckpt.
INFO:tensorflow:Loss for final step: 433.19727.
```

Challenges and Next Steps

Wet lab side

- Need to re-evaluate goals for this project

Computational

- Develop a reliable method to determine 'true' cell states
 - Sequencing is most reliable method, as described in Nature paper
- Gather more data, with more parameters (MTT can be used)
 - Currently looking into full-well imaging
 - Image Cytometry

Web application

- Expand to fit a library of detection parameters
- Add more visualization capabilities