

StarCellBio Problem Set 2

4/10/2014

Hand drawn flow cytometry histograms:

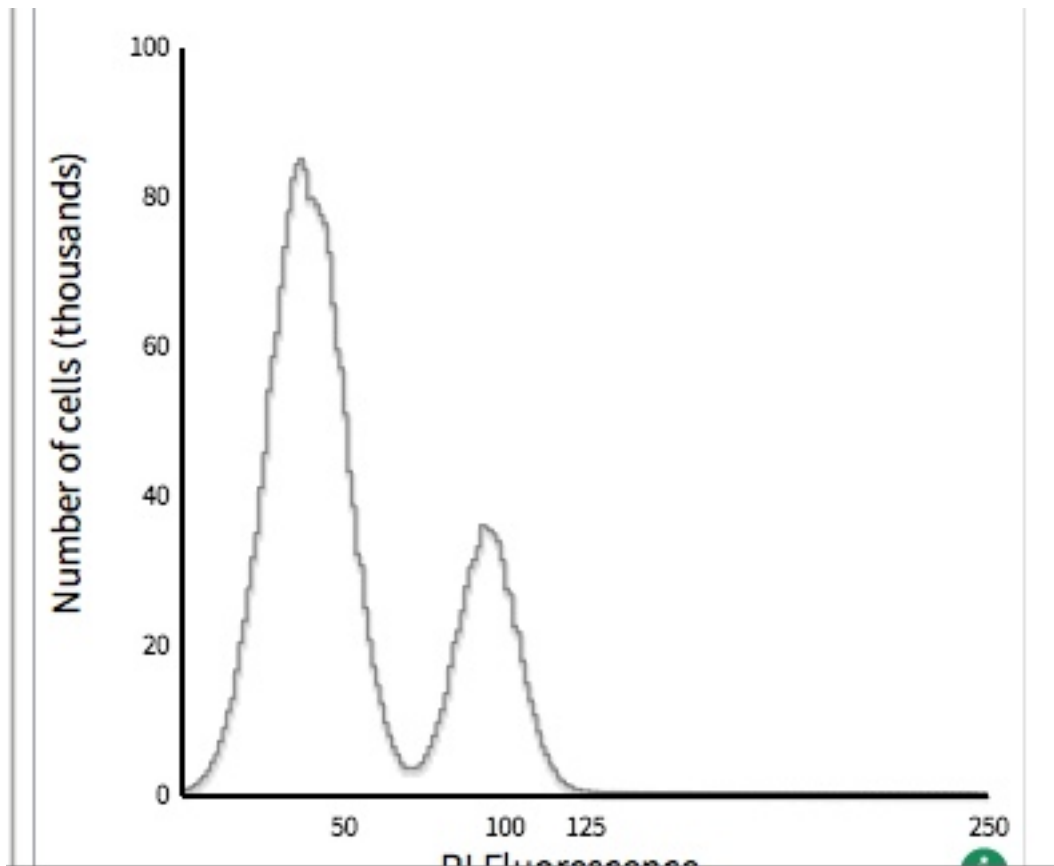
I don't think we need the 125 label on the X-axis. Let's have a 150 and a 200. We can either keep or leave the 250 label. **Don't worry, I'll remove the 125 in the final version.**

Control siRNA S2 cells

The peaks need to be of equal width. The left peak should look the same as the right peak. I think that the peak on the left should be higher than the one on the right.

The ratio between the two peaks should be about 3:1. Done

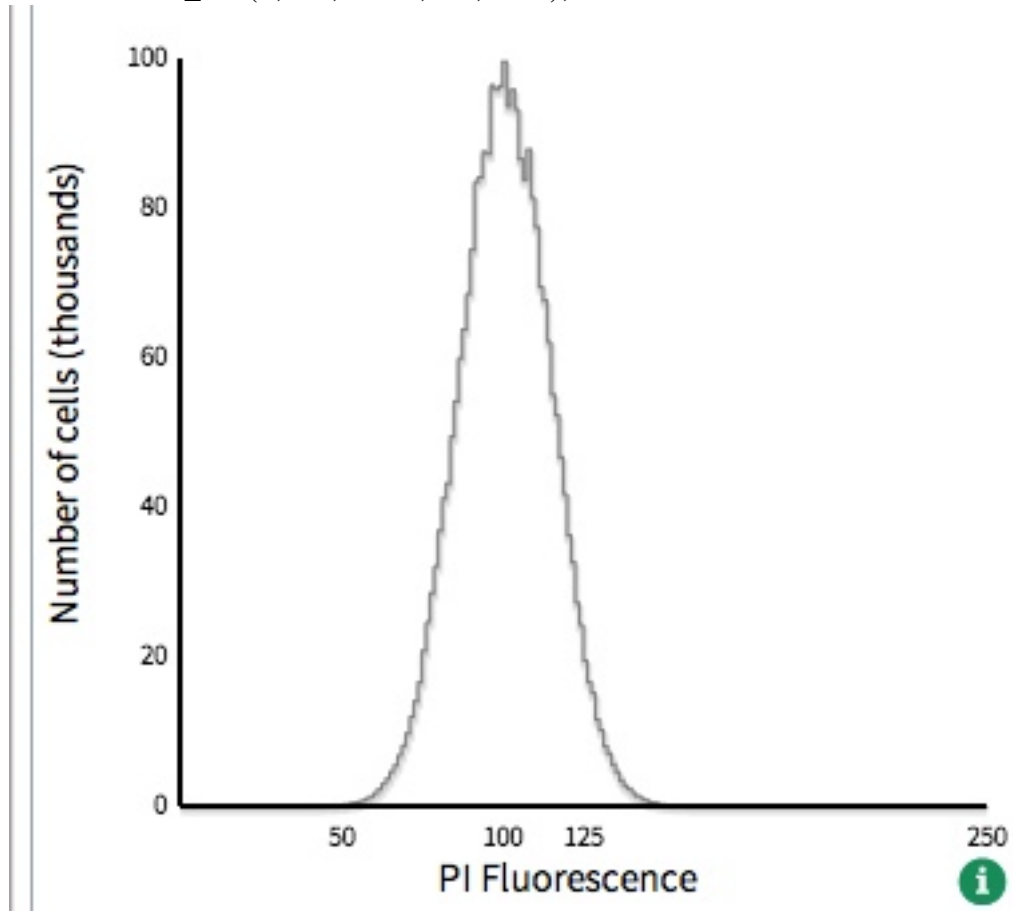
```
return normal_dist(x, 0.8, 0.075, 1, false);  
return normal_dist(x, 0.35, 0.095, 1, false);
```



siRNA Treatment #1, siRNA Treatment #3, & Nocodazole-treated cells

This peak should be steeper on the right side. The shoulder on the left side looks good, but the right side should come down sooner. I made the graph steeper but I thought that this graph should not have shoulders? If it does have shoulders, which side has the shoulder?

```
return normal_dist(x, 0.8, 0.113, 0.5, false);
```

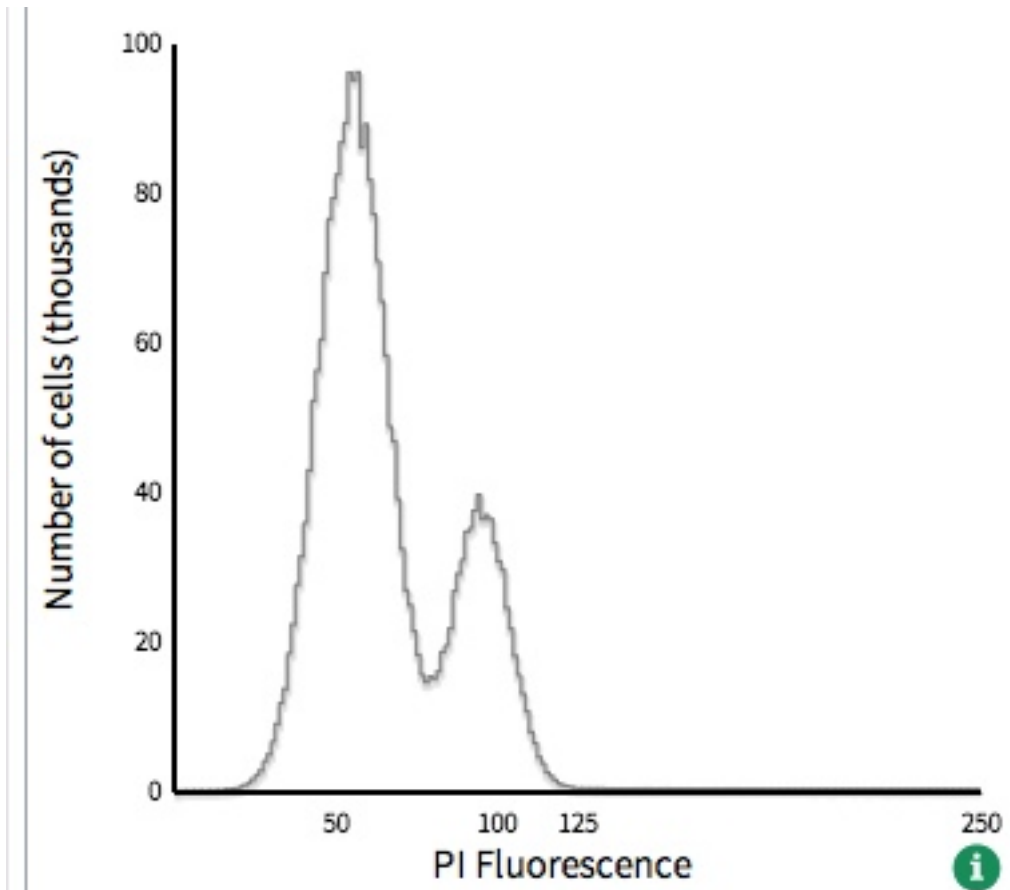


siRNA Treatment #2

The left peak should be equal width to the right peak. The right side of the right peak should hit the x-axis around 125, like the control siRNA treated cells. The left side of the left peak should start at a value of y-axis = 0 and x-axis = 30/40. (The left side of the left peak will be good for siRNA #5, as long as the curve starts at y-axis = 0. But this shoulder for the left peak is what we need for siRNA #5, but not for siRNA #2). The peaks are equal width, but because the x-axis point on the left was shifted, the left graph is taller.

```
return normal_dist(x, 0.75, 0.07, 0, true);
```

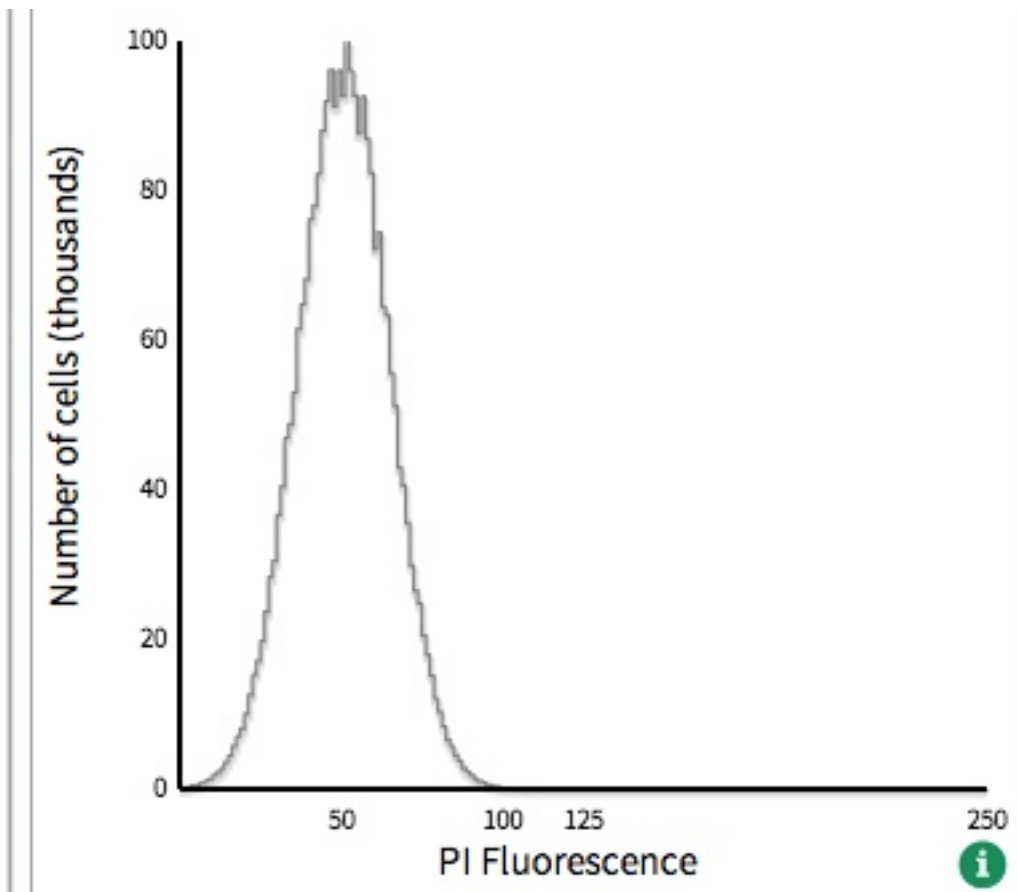
```
return normal_dist(x, 0.43, 0.085, 0, true);
```



siRNA Treatment #4 and Serum-free growth media

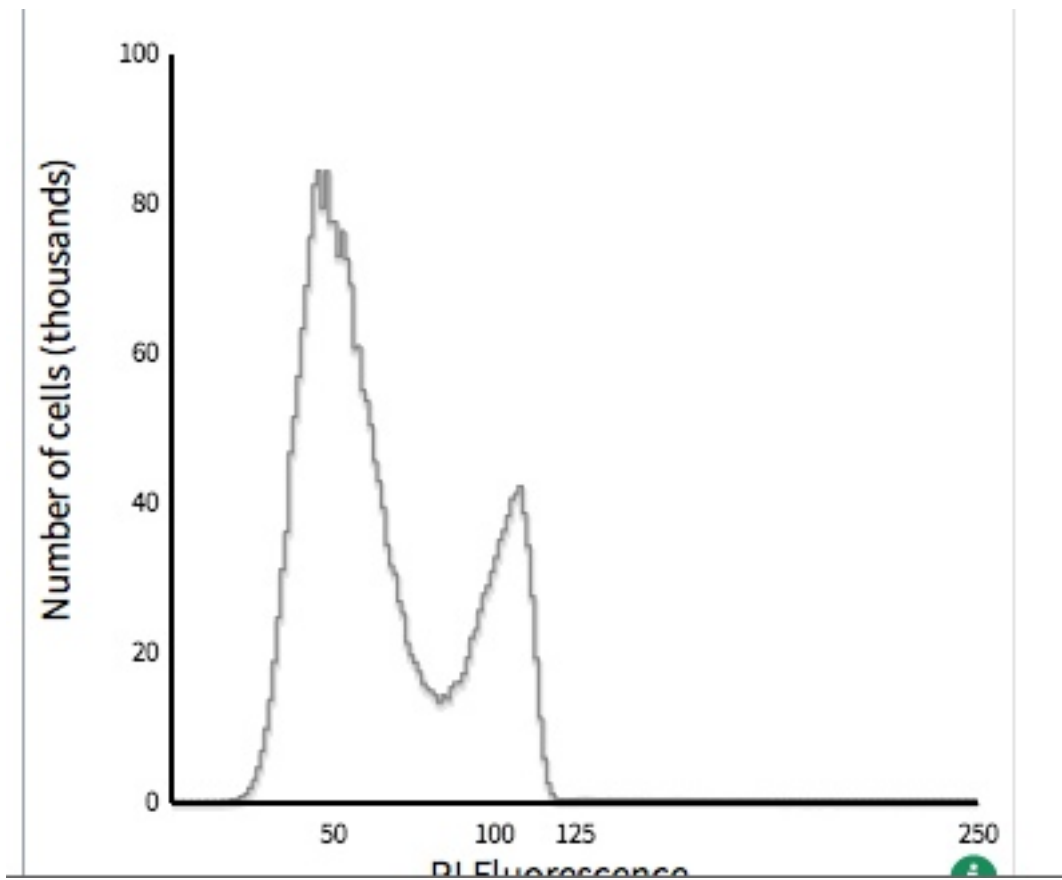
This peak should be more narrow (equal to the peak width of the right peak in the control siRNA treated cells). Otherwise the shape is ok. The narrower the graph, the more likely the peak will reach past the bounds of the graph. Right now, it is very close. I've narrowed the graph, but unless I scale it down, it will go beyond the bounds of the graph.

```
return normal_dist(x, 0.4, 0.113, 0, false);
```



siRNA Treatment #5

```
return normal_dist(x, 0.9, 0.12, 6, true);  
return normal_dist(x, 0.3, 0.16, -3, true);
```



Hydroxyurea-treated cells

```
normal_dist(x, 0.55, 0.216, 5, true);
```

