

Prelim 1 – Problem 1
 CHEME 5440 Spring 2020
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1.

a)

IPTG (mM)	<n> (mRNA/cell)	low	high	IPTG (mM)	<n> (nmol/gDW)	low	high
0	19	18	20	0	0.112719	0.106787	0.118652
0.0005	21	17	26	0.0005	0.124585	0.100854	0.154248
0.005	41	37	44	0.005	0.243237	0.219506	0.261034
0.012	67	65	69	0.012	0.397484	0.385619	0.409349
0.053	86	84	88	0.053	0.510204	0.498338	0.522069
0.216	93	91	95	0.216	0.551732	0.539867	0.563597
1	93	92	94	1	0.551732	0.545799	0.557664

The section in yellow (right) is the converted values.

Conversion was done by multiplying 0.0059326, which is calculated by using $\langle m_c \rangle = 2.8 \times 10^{-13}$ found on bionumbers:

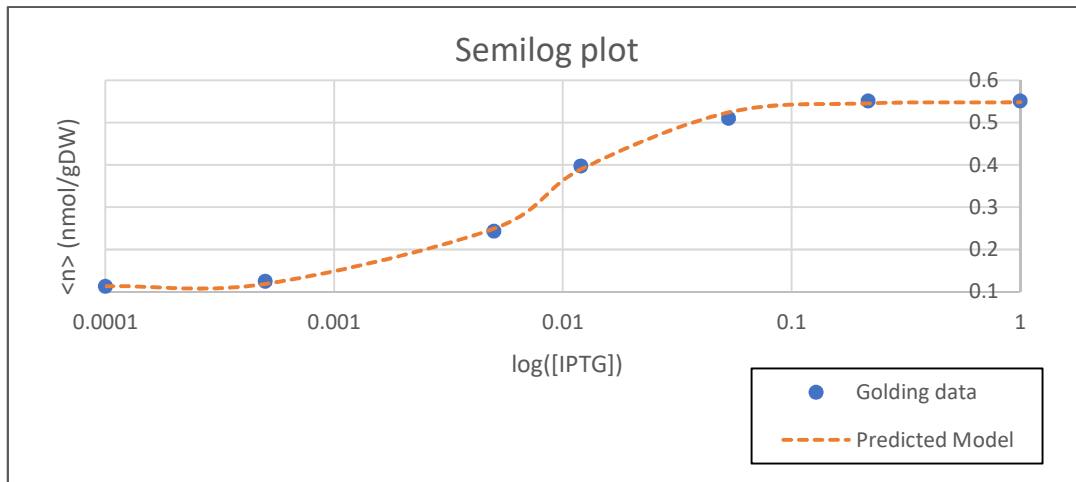
$$\frac{10^9 \text{ nmol}}{1 \text{ mol}} \times \frac{1 \text{ mol}}{6.02 \times 10^{23}} \times \frac{1 \text{ Cell}}{2.8 \times 10^{-13} \text{ gDW}} = 0.0059326$$

Detailed calculations is shown in the problem1 excel file on Github resp.

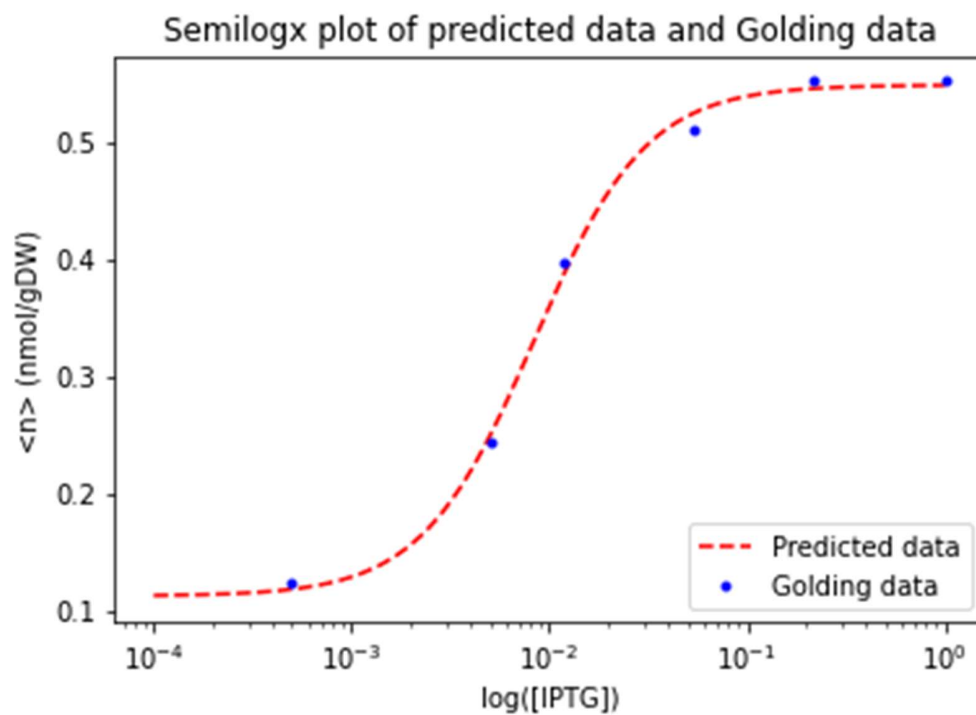
1.

d)

Using Excel, the semilogx plot is plotted as the following:



However, since the data is not continuous, I tried using python to plot it again. Using python, the semilogx plot is plotted as the following:



One can see that the model fits quite well and is in the correct shape.