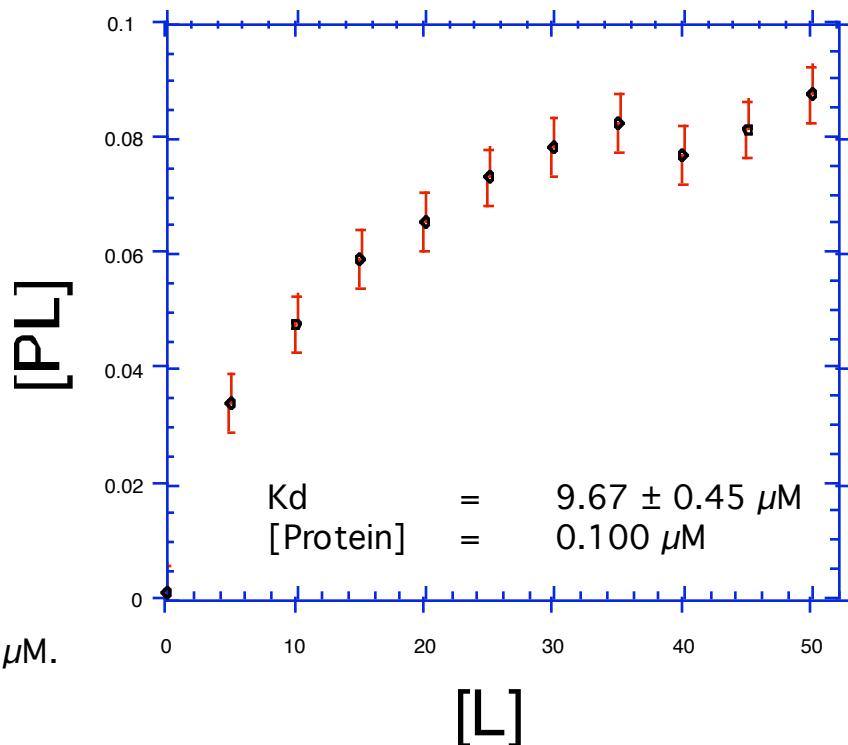


Consider the following:

Titrate 0.100 μM protein with a ligand, L.



The intrinsic value of K_d is $10.0 \mu\text{M}$.

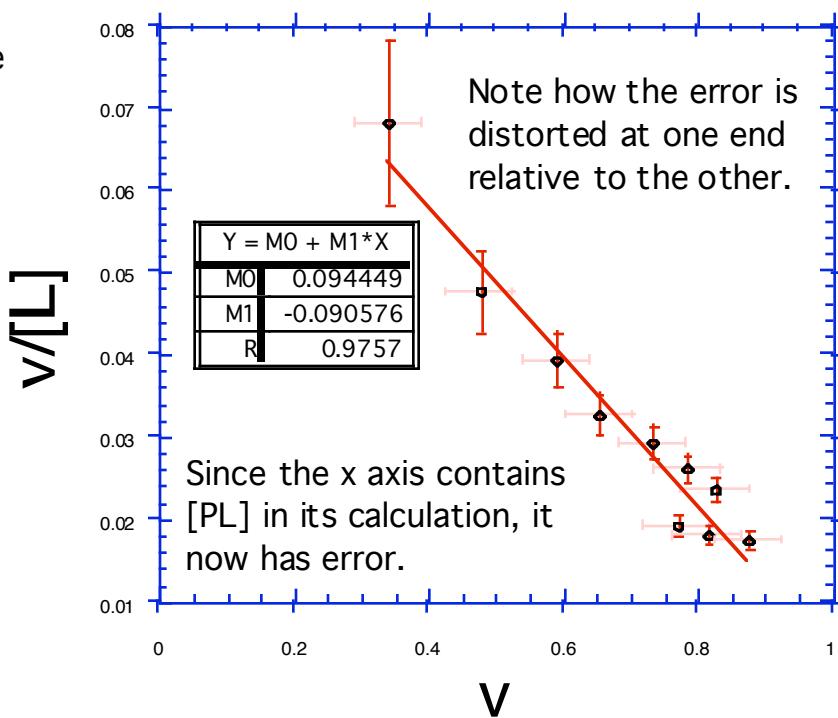
A direct fit of the data yields

$$K_d = 9.67 \pm 0.45 \mu\text{M}$$

A Scatchard analysis of the same data yields

$$K_d = 10.6 \mu\text{M} \text{ (from intercept)}$$

$$K_d = 11.0 \mu\text{M} \text{ (from slope)}$$



Assumes no error in $[L]$.
A full treatment would allow for that as well.