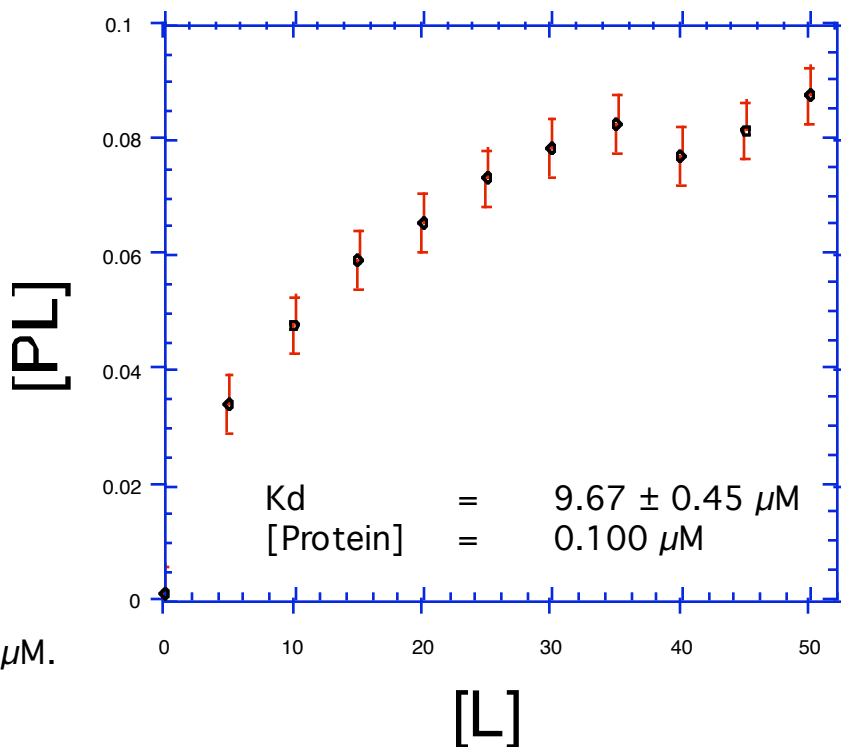


Consider the following:

Titrate 0.100 μM protein with a ligand, L.

The intrinsic value of K_D is 10.0 μM .

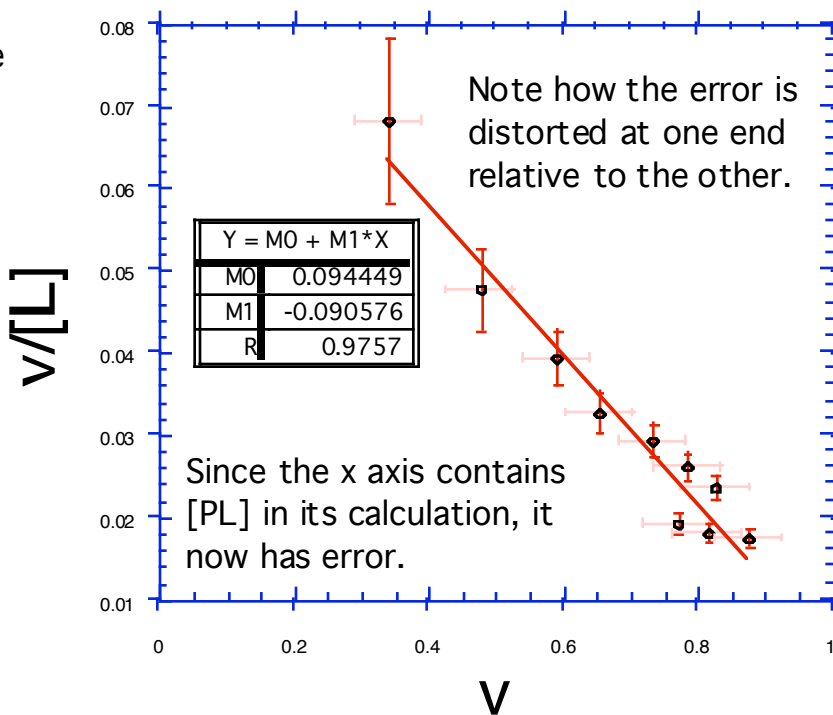


A direct fit of the data yields
 $K_D = 9.67 \pm 0.45 \mu\text{M}$

A Scatchard analysis of the same data yields

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

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



Assumes no error in [L].

A full treatment would allow for that as well.