

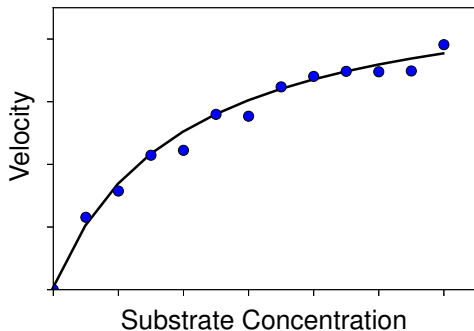
Biological Chemistry Laboratory
Biology 3515/Chemistry 3515
Spring 2017

Lecture 13:

Data Analysis for the V versus $[S]$ Experiment
and Interpretation of the Michaelis-Menten Parameters

21 February 2017
©David P. Goldenberg, 2014
University of Utah
goldenberg@biology.utah.edu

Analysis of Data from the V versus $[S]$ Experiment



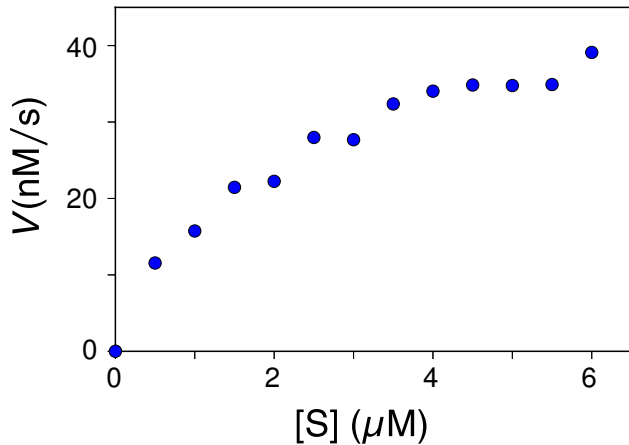
- We want to fit the experimental data to the Michaelis-Menten Equation:

$$V = \frac{[S]V_{\max}}{[S] + K_m}$$

- From the fit, we obtain estimates of K_m and V_{\max} .

Clicker Question #1

Estimate V_{\max} from the graph:



1 30 nM/s

2 40 nM/s *

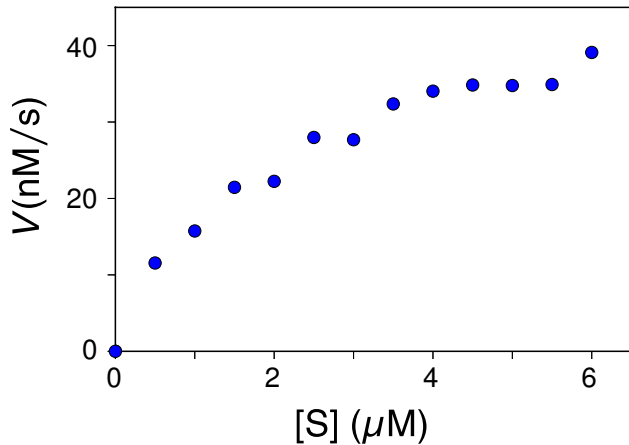
3 50 nM/s

4 80 nM/s

*close enough for credit.

Clicker Question #2

Estimate K_m from the graph:



1 $1 \mu\text{M}$

2 $2 \mu\text{M}$

3 $5 \mu\text{M}$

4 $10 \mu\text{M}$

A Classic Method for Analyzing Enzyme Kinetics Data

- Rearrangement of the Michaelis-Menten Equation:

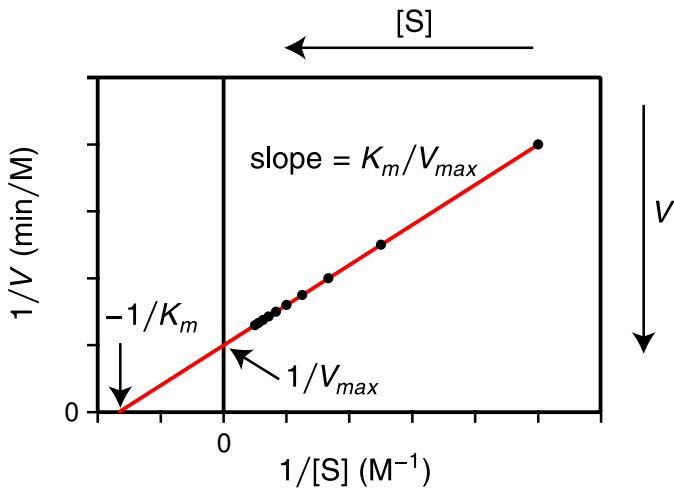
$$V = \frac{[S]V_{\max}}{[S] + K_m}$$

$$\frac{1}{V} = \frac{[S] + K_m}{[S]V_{\max}} = \frac{[S]}{[S]V_{\max}} + \frac{K_m}{[S]V_{\max}}$$

$$\frac{1}{V} = \frac{1}{[S]} \cdot \frac{K_m}{V_{\max}} + \frac{1}{V_{\max}}$$

- A plot of $1/V$ versus $1/[S]$ should generate a straight line with a slope of K_m/V_{\max} and an intercept of $1/V_{\max}$ on the $1/V$ axis.

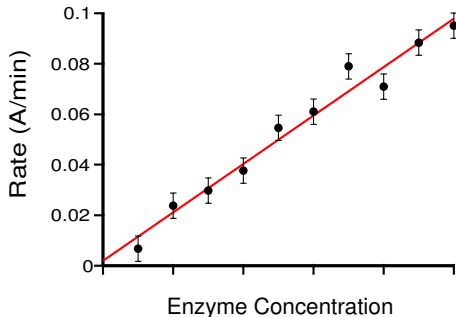
The Lineweaver-Burk Plot



- If the data are perfect, this plot gives good estimates of K_m and V_{max} .
- But, experimental error in V can lead to strange effects!

Experimental Error and Uncertainty

- Error bars for rate measurements are of approximately constant size (e.g., ± 0.005 A/min), rather than a constant percentage of the measurement.



- For 0.1 A/min, ± 0.005 A/min = $\pm 5\%$.
- For 0.01 A/min, ± 0.005 A/min = $\pm 50\%$.
- Least-squares fitting works well if the *absolute* uncertainties of all data points are approximately equal.

What Happens When We Take Reciprocals?

- $V = 0.1 \pm 0.005$

$$\frac{1}{0.105} = 9.52,$$

$$\frac{1}{0.095} = 10.5,$$

$$\frac{1}{V} = 10 \pm 0.5$$

- $V = 0.01 \pm 0.005$

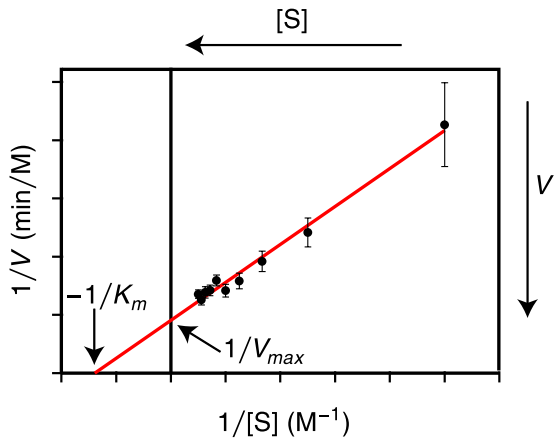
$$\frac{1}{0.015} = 66.7,$$

$$\frac{1}{0.005} = 200,$$

$$\frac{1}{V} = 100 \pm 50$$

- The values of $1/V$ derived from small velocities can have huge absolute errors.

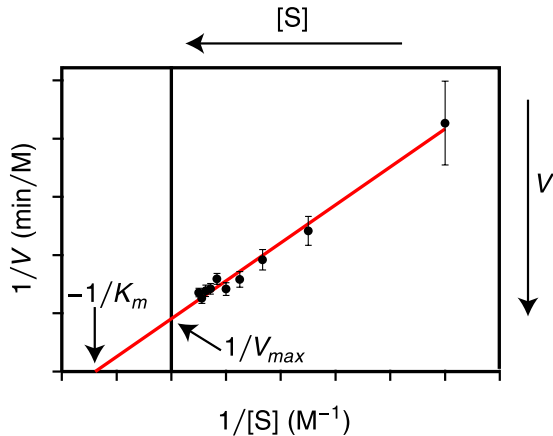
The Effects on a Lineweaver-Burk Plot



- Errors in the least precise measurements (low V) can cause large changes in the line fit to the Lineweaver-Burk plot.

Clicker Question #3

Which parameter is likely to be more sensitive to errors in a Lineweaver-Burk plot?



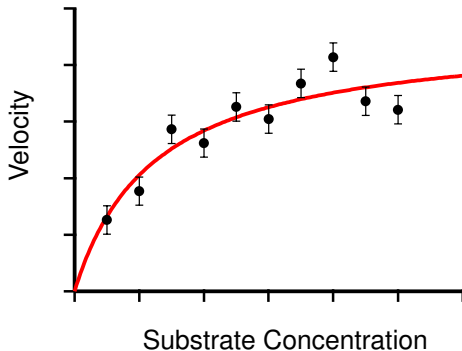
1 K_m *

2 V_{max}

* Provided that values of V approach V_{max} .

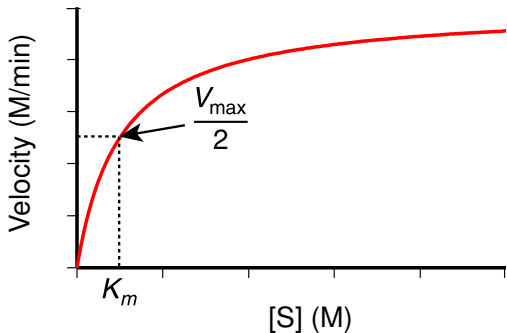
Two Ways to Deal with This Problem

- Use Lineweaver-Burk, but weight data according to uncertainties in $1/V$.
- Fit velocity data directly to the Michaelis-Menten equation using non-linear least-squares method.



- Equal errors in V are weighted equally.

Interpreting K_m



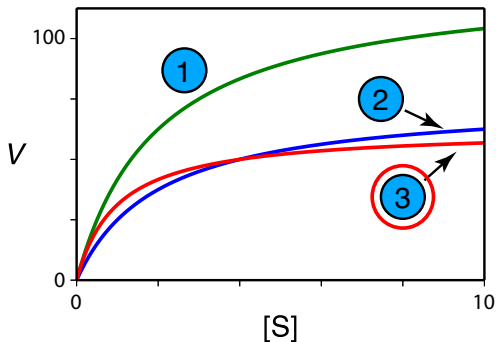
$$K_m = \frac{k_2 + k_{\text{cat}}}{k_1}$$

$$V = \frac{V_{\text{max}}}{2} \quad \text{when} \quad [S] = K_m$$

- When $[S] = K_m$, half of total enzyme has substrate bound.
- The larger K_m is, the more substrate is required to reach $V_{\text{max}}/2$, or any specified fraction of V_{max} .

Clicker Question #4:

Data for three substrates with the same enzyme.



Which substrate binds most tightly to the enzyme?

No wrong answers, for now.

A Closer Look at Binding and K_m : K_m versus K_d



- K_m is defined in terms of the rate constants:

$$K_m = \frac{k_2 + k_{\text{cat}}}{k_1}$$

- K_d is the equilibrium constant for dissociation.

$$K_d = \frac{[E][S]}{[E \cdot S]} = \frac{k_2}{k_1}$$

A large K_d indicates weak binding.

K_m versus K_d

$$K_m = \frac{k_2 + k_{\text{cat}}}{k_1}$$

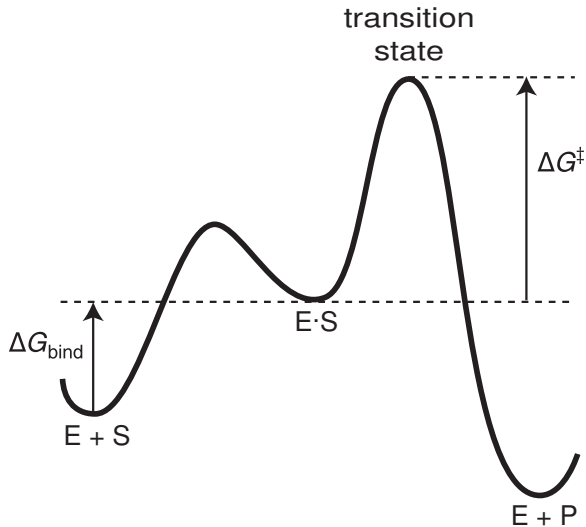
$$K_d = \frac{[E][S]}{[E \cdot S]} = \frac{k_2}{k_1}$$

- If $k_{\text{cat}} \ll k_2$, *i.e.*, the E·S complex is more likely to dissociate than undergo catalysis:

$$K_m \approx \frac{k_2}{k_1} = K_d$$

- In general, $K_m \geq K_d$
- Strength of equilibrium binding may be greater than indicated by K_m .

Energy Profile for an Enzyme-Catalyzed Reaction



- Free-energy change for binding:

$$\Delta G_{\text{bind}} = RT \ln K_d$$

R = Gas constant

T = Temperature

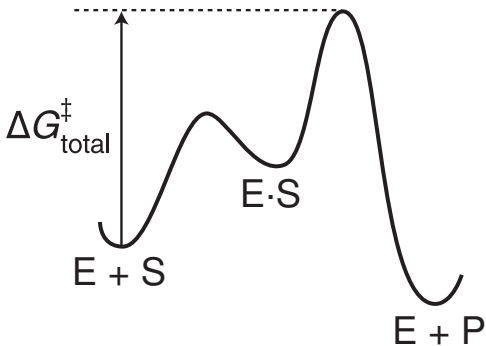
- Free-energy change from $E \cdot S$ complex to transition state:

$$\Delta G^\ddagger = RT \ln \left(\frac{k_b T}{k_{\text{cat}} h} \right)$$

k_b = Boltzmann constant

h = Planck constant

The Significance of k_{cat}/K_m



- Free-energy difference between $E + S$ and the transition state:

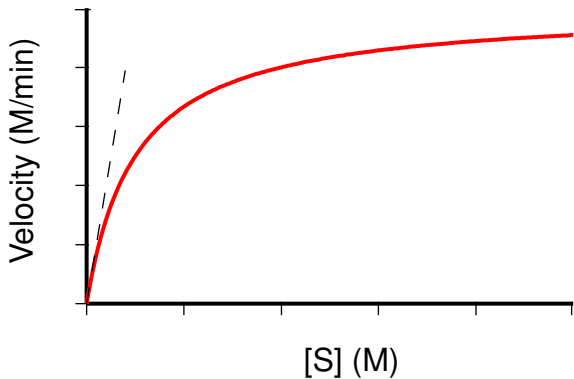
$$\Delta G_{total}^{\ddagger} = \underbrace{RT \ln \left(\frac{k_b T}{h} \right)}_{\text{Constant}} + RT \ln \left(\frac{K_d}{k_{\text{cat}}} \right)$$

- If $k_2 \gg k_{\text{cat}}$, $K_d \approx K_m$:

$$\Delta G_{total}^{\ddagger} = C - RT \ln \left(\frac{k_{\text{cat}}}{K_m} \right)$$

- The ratio k_{cat}/K_m reflects the free energy difference between $E + S$ and the transition state.
- k_{cat}/K_m is commonly interpreted as a measure of enzymatic efficiency.
- Catalytic efficiency is favored by a large value of k_{cat} and a small value of K_m .

k_{cat}/K_m Is Also the Apparent Second-Order Rate Constant at Low Substrate Concentrations



- If $[S] \ll K_m$:

$$V = \frac{[S][E]_T k_{\text{cat}}}{K_m + [S]}$$

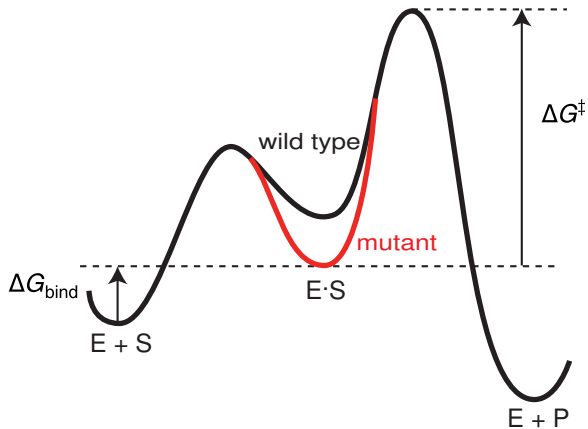
$$V \approx \frac{k_{\text{cat}}}{K_m} [S][E]_T$$

- Units of k_{cat}/K_m

$$\frac{\text{s}^{-1}}{\text{M}} = \text{sec}^{-1}\text{M}^{-1}$$

Is a Low K_m Always Good?

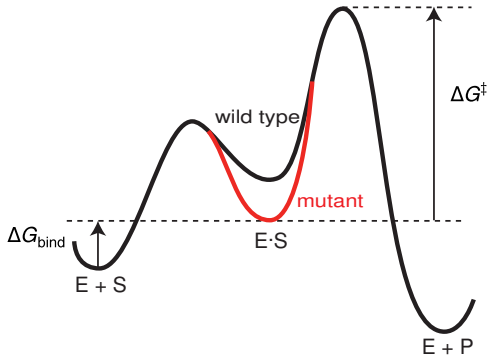
Suppose that we could design a mutant enzyme that forms a more stable complex with substrate.



This will lower K_m , but leave k_{cat}/K_m the same.

Clicker Question #5

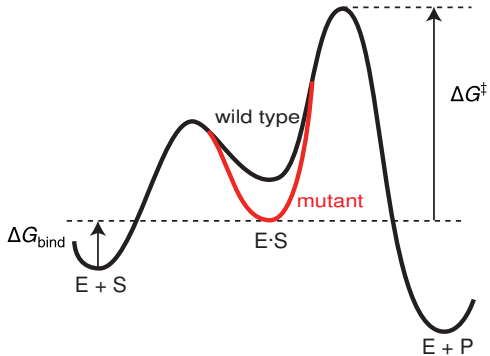
At **low** substrate concentration, will the velocity for the mutant enzyme be greater or less than that of the original enzyme?



- 1 Greater than the original enzyme
- 2 Less than the original enzyme
- 3 The same as the original enzyme

Clicker Question #6

At **high** substrate concentration, will the velocity for the mutant enzyme be greater or less than that of the original enzyme?



- 1 Greater than the original enzyme
- 2 Less than the original enzyme!
- 3 The same as the original enzyme

BPTI is an Extreme Example of a Low- K_m substrate

