In biological systems, enzymes act as catalysts and play a critical role in accelerating reactions, anywhere from $10^3$ to $10^{17}$ times faster than the reaction would normally proceed. Enzymes are high-molecular weight proteins that act on a substrate, or reactant molecule, to form one or more products.

**Michaelis-Menten Enzyme Kinetics**

Enzymes are highly specific catalysts for biochemical reactions, with each enzyme showing a selectivity for a single reactant, or substrate. For example, the enzyme acetylcholinesterase catalyzes the decomposition of the neurotransmitter acetylcholine to choline and acetic acid. Many enzyme–substrate reactions follow a simple mechanism that consists of the initial formation of an enzyme–substrate complex, $\text{ES}$, which subsequently decomposes to form product, releasing the enzyme to react again.

\[
E + S \overset{k_1}{\rightleftharpoons} ES \overset{k_2}{\rightarrow} E + P
\]

where $k_1$, $k_{-1}$, $k_2$, and $k_{-2}$ are rate constants. The reaction’s rate law for generating the product $[P]$ is

\[
\text{rate} = \dfrac{d[P]}{dt} = k_2[ES] - k_{-2}[E][P]
\]

However, if we make measurement early in the reaction, the concentration of products is negligible, i.e.,

\[[P] \approx 0\]

and we can ignore the back reaction (second term in right side of Equation (13.21A)). Then under these conditions, the reaction’s rate is

\[
\text{rate} = \dfrac{d[P]}{dt} = k_2[ES]
\]

To be analytically useful we need to write Equation (13.21) in terms of the reactants (e.g., the concentrations of enzyme and substrate). To do this we use the steady-state approximation, in which we assume that the concentration of $\text{ES}$ remains essentially constant. Following an initial period, during which the enzyme–substrate complex first forms,
the rate at which $\{ES\}$ forms

$$\frac{d[ES]}{dt} = k_1[E] [S] = k_1([E]_0 - [ES])[S] \label{13.22}$$

is equal to the rate at which it disappears

$$\frac{d[ES]}{dt} = k_{-1}[ES] + k_2[ES] \label{13.23}$$

where $([E]_0)$ is the enzyme’s original concentration. Combining Equations \((\ref{13.22})\) and \((\ref{13.23})\) gives

$$[k_1([E]_0 - [ES]) [S] = k_{-1}[ES] + k_2[ES]]$$

which we solve for the concentration of the enzyme–substrate complex

$$[ES] = \frac{[E]_0[S]}{\frac{k_{-1} + k_2}{k_1} + [S]} = \frac{[E]_0[S]}{K_m + [S]} \label{Eq13.24}$$

where $K_m$ is the Michaelis constant. Substituting Equation \((\ref{Eq13.24})\) into Equation \((\ref{13.21})\) leaves us with our final rate equation.

$$\frac{d[P]}{dt} = \frac{k_2[E]_0[S]}{K_m + [S]} \label{Eq13.25}$$

A plot of Equation \((\ref{Eq13.25})\), as shown in Figure \(\PageIndex{1}\), is instructive for defining conditions where we can use the rate of an enzymatic reaction for the quantitative analysis of an enzyme or substrate.

For high substrate concentrations, where $[S] \gg K_m$, Equation \((\ref{Eq13.25})\) simplifies to
\[
\frac{d[P]}{dt} = \frac{k_2[E]_0[S]}{K_m + [S]} \approx \frac{k_2[E]_0[S]}{[S]} = k_2[E]_0 = V_{\text{max}}
\]

where \(V_{\text{max}}\) is the maximum rate for the catalyzed reaction. Under these conditions the reaction is zero-order in substrate and we can use \(V_{\text{max}}\) to calculate the enzyme’s concentration, typically using a variable-time method. At lower substrate concentrations, where \([S] \ll K_m\), Equation \ref{Eq13.25} becomes

\[
\frac{d[P]}{dt} = \frac{k_2[E]_0[S]}{K_m + [S]} \approx \frac{k_2[E]_0[S]}{K_m} = \frac{V_{\text{max}}[S]}{K_m}
\]

where \([E]_0\) is the enzyme concentration and \(k_{\text{cat}}\) is the turnover number, defined as the maximum number of substrate molecules converted to product per enzyme molecule per second. Hence, the turnover number is defined as the maximum number of chemical conversions of substrate molecules per second that a single catalytic site will execute for a given enzyme concentration \([E]_0\).

The Michaelis-Menten model is used in a variety of biochemical situations other than enzyme-substrate interaction,
including antigen-antibody binding, DNA-DNA hybridization, and protein-protein interaction. It can be used to characterize a generic biochemical reaction, in the same way that the **Langmuir equation** can be used to model generic adsorption of biomolecular species. When an empirical equation of this form is applied to microbial growth. The experimentally determined parameters values vary wildly between enzymes (Table \(\PageIndex{1}\)):

**Table \(\PageIndex{1}\):** Enzyme Kinetic parameters

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>(\langle K_m \rangle) (M)</th>
<th>(\langle k_{\text{cat}} \rangle) (1/s)</th>
<th>(\langle k_{\text{cat}}/K_m \rangle) (1/M.s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chymotrypsin</td>
<td>(1.5 \times 10^{-2})</td>
<td>0.14</td>
<td>9.3</td>
</tr>
<tr>
<td>Pepsin</td>
<td>(3.0 \times 10^{-4})</td>
<td>0.50</td>
<td>(1.7 \times 10^{3})</td>
</tr>
<tr>
<td>Tyrosyl-tRNA synthetase</td>
<td>(9.0 \times 10^{-4})</td>
<td>7.6</td>
<td>(8.4 \times 10^{3})</td>
</tr>
<tr>
<td>Ribonuclease</td>
<td>(7.9 \times 10^{-3})</td>
<td>(7.9 \times 10^{2})</td>
<td>(1.0 \times 10^{5})</td>
</tr>
<tr>
<td>Carbonic anhydrase</td>
<td>(2.6 \times 10^{-2})</td>
<td>(4.0 \times 10^{5})</td>
<td>(1.5 \times 10^{7})</td>
</tr>
<tr>
<td>Fumarase</td>
<td>(5.0 \times 10^{-6})</td>
<td>(8.0 \times 10^{2})</td>
<td>(1.6 \times 10^{8})</td>
</tr>
</tbody>
</table>

While \(\langle K_m \rangle\) is equal to the substrate concentration at which the enzyme converts substrates into products at half its maximal rate and hence is related to the affinity of the substrate for the enzyme. The catalytic rate \(\langle k_{\text{cat}} \rangle\) is the rate of product formation when the enzyme is saturated with substrate and therefore reflects the enzyme's maximum rate. The rate of product formation is dependent on both how well the enzyme binds substrate and how fast the enzyme converts substrate into product once substrate is bound. For a kinetically perfect enzyme, every encounter between enzyme and substrate leads to product and hence the reaction velocity is only limited by the rate the enzyme encounters substrate in solution. From Equation \(\langle \text{RefEq13.24}\rangle\), the catalytic efficiency of a protein can be evaluated.

\[
\frac{\langle k_{\text{cat}} \rangle}{\langle K_m \rangle} = \frac{k_2}{K_m} = \frac{k_1k_2}{k_{-1} + k_2}
\]

This \(\langle k_{\text{cat}}/K_m \rangle\) ratio is called the specificity constant measure of how efficiently an enzyme converts a substrate into product. It has a theoretical upper limit of \(10^8\) – \(10^{10}\) /M.s; enzymes working close to this, such as fumarase, are termed superefficient (Table \(\PageIndex{1}\)).

Determining \(\langle V_m \rangle\) and \(\langle K_m \rangle\) from experimental data can be difficult and the most common way is to determine initial rates, \(\langle v_0 \rangle\), from experimental values of \(\langle [P] \rangle\) or \(\langle [S] \rangle\) as a function of time. Hyperbolic graphs of \(\langle v_0 \rangle\) vs. \(\langle [S] \rangle\) can be fit or transformed as we explored with the different mathematical transformations of the hyperbolic binding equation to determine \(\langle K_d \rangle\). These included:

- nonlinear hyperbolic fit (e.g., Figure \(\langle \text{PageIndex1} \rangle\))
- double reciprocal plot (e.g., Lineweaver–Burk plot discussed below)
- Eadie-Hofstee plot
Lineweaver–Burk plot

Another commonly-used plot in examining enzyme kinetics is the **Lineweaver-Burk plot**, in which the inverse of the reaction rate, \(1/r\), is plotted against the inverse of the substrate concentration \(1/[S]\). Rearranging Equation \(\ref{Eq13.26}\),

\[
\frac{1}{r} = \frac{K_M + [S]}{k_2 [E]_0 [S]} = \frac{K_M}{k_2 [E]_0} \frac{1}{[S]} + \frac{1}{k_2 [E]_0} \label{Eq28}\]

The Lineweaver–Burk plot (or double reciprocal plot) is a graphical representation of the Lineweaver–Burk equation of enzyme kinetics, described by Hans Lineweaver and Dean Burk in 1934 (Figure \(\PageIndex{2}\)). The Lineweaver-Burk plot results in a straight line with the slope equal to \(K_M/k_2 [E]_0\) and \(y\)-intercept equal to \(1/V_{max}\) via Equation \(\ref{Eq13.26}\).

![Lineweaver–Burk plot diagram](image)

**Figure \(\PageIndex{2}\):** Lineweaver–Burk plot of Michaelis–Menten kinetics.

The plot provides a useful graphical method for analysis of the Michaelis–Menten equation:

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

Taking the reciprocal gives

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

where

- \((V)\) is the reaction velocity (the reaction rate),
- \((K_m)\) is the Michaelis–Menten constant,
- \((V_{max})\) is the maximum reaction velocity, and
- \(([S])\) is the substrate concentration.

The Lineweaver–Burk plot was widely used to determine important terms in enzyme kinetics, such as \((K_m)\) and \((V_{max})\), before the wide availability of powerful computers and non-linear regression software. The \(y\)-intercept of such
a graph is equivalent to the inverse of \((V_{\text{max}})^{−1}\); the x-intercept of the graph represents \((-1/K_m)\). It also gives a quick, visual impression of the different forms of enzyme inhibition.

Example \((\PageIndex{2})\)

The reaction between nicotineamide mononucleotide and ATP to form nicotineamide–adenine dinucleotide and pyrophosphate is catalyzed by the enzyme nicotineamide mononucleotide adenylyltransferase. The following table provides typical data obtained at a pH of 4.95. The substrate, S, is nicotineamide mononucleotide and the initial rate, v, is the \(\mu\text{mol}\) of nicotineamide–adenine dinucleotide formed in a 3-min reaction period.

<table>
<thead>
<tr>
<th>[S] (mM)</th>
<th>v ((\mu\text{mol}))</th>
<th>[S] (mM)</th>
<th>v ((\mu\text{mol}))</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.138</td>
<td>0.148</td>
<td>0.560</td>
<td>0.324</td>
</tr>
<tr>
<td>0.220</td>
<td>0.171</td>
<td>0.766</td>
<td>0.390</td>
</tr>
<tr>
<td>0.291</td>
<td>0.234</td>
<td>1.460</td>
<td>0.493</td>
</tr>
</tbody>
</table>

Determine values for \(V_{\text{max}}\) and \(K_m\).

**Solution**

Figure 13.12 shows the Lineweaver–Burk plot for this data and the resulting regression equation. Using the y-intercept, we calculate \(V_{\text{max}}\) as

\[
V_{\text{max}} = \frac{1}{y\text{-intercept}} = \frac{1}{1.708 \text{ mol}} = 0.585 \text{ mol}
\]

and using the slope we find that \(K_m\) is

\[
K_m = \text{slope} \times V_{\text{max}} = 0.7528 \text{ mol} \text{M}^{-1} \times 0.585 \text{ mol} = 0.440 \text{ mM}
\]

**Figure 13.12:** Lineweaver–Burk plot and regression equation for the data in Example 13.6.
Exercise (PageIndex(2)): o-diphenyl oxidase

The following data are for the oxidation of catechol (the substrate) to o-quinone by the enzyme o-diphenyl oxidase. The reaction is followed by monitoring the change in absorbance at 540 nm. The data in this exercise are adapted from jkimball.

\[
\text{catechol} \quad \begin{array}{c}
\text{HO} \\
\text{HO} \\
\end{array}
\]

catechol

\[
\text{o-quinone} \quad \begin{array}{c}
\text{O} \\
\text{O} \\
\end{array}
\]
o-quinone

<table>
<thead>
<tr>
<th>[catechol] (mM)</th>
<th>0.3</th>
<th>0.6</th>
<th>1.2</th>
<th>4.8</th>
</tr>
</thead>
<tbody>
<tr>
<td>rate (∆AU/ min)</td>
<td>0.020</td>
<td>0.035</td>
<td>0.048</td>
<td>0.081</td>
</tr>
</tbody>
</table>

Determine values for \(V_{\text{max}}\) and \(K_m\).

Click [here](#) to review your answer to this exercise.

The double reciprocal plot distorts the error structure of the data, and it is therefore unreliable for the determination of enzyme kinetic parameters. Although it is still used for representation of kinetic data, non-linear regression or alternative linear forms of the Michaelis–Menten equation such as the Hanes-Woolf plot or Eadie–Hofstee plot are generally used for the calculation of parameters.

Problems with the Method

The Lineweaver–Burk plot is classically used in older texts, but is prone to error, as the \(y\)-axis takes the reciprocal of the rate of reaction – in turn increasing any small errors in measurement. Also, most points on the plot are found far to the right of the \(y\)-axis (due to limiting solubility not allowing for large values of \(\langle [S]\rangle\) and hence no small values for \(\langle 1/[S]\rangle\)), calling for a large extrapolation back to obtain \(x\)- and \(y\)-intercepts.

When used for determining the type of enzyme inhibition, the Lineweaver–Burk plot can distinguish competitive, non-
competitive and uncompetitive inhibitors. Competitive inhibitors have the same y-intercept as uninhibited enzyme (since \(V_{\text{max}}\) is unaffected by competitive inhibitors the inverse of \(V_{\text{max}}\) also doesn't change) but there are different slopes and x-intercepts between the two data sets. Non-competitive inhibition produces plots with the same x-intercept as uninhibited enzyme (\(K_m\) is unaffected) but different slopes and y-intercepts. Uncompetitive inhibition causes different intercepts on both the y- and x-axes but the same slope.

**Eadie–Hofstee Plot**

The Eadie–Hofstee plot is a graphical representation of enzyme kinetics in which reaction rate is plotted as a function of the ratio between rate and substrate concentration and can be derived from the Michaelis–Menten equation by inverting and multiplying with \(V_{\text{max}}\):

\[
\frac{V_{\text{max}}}{v} = \frac{V_{\text{max}}(K_m+[S])}{V_{\text{max}}[S]} = \frac{K_m+[S]}{[S]}
\]

Rearrange:

\[
V_{\text{max}} = \frac{vK_m}{[S]} + v[S]
\]

Isolate \(v\):

\[
v = -K_m \frac{v}{[S]} + V_{\text{max}}\]

**Figure \(\PageIndex{3}\):** The Eadie-Hofstee plot is a more accurate linear plotting method with \(v\) is plotted against \(v/[S]\).

A plot of \(v\) against \(v/[S]\) will hence yield \(V_{\text{max}}\) as the y-intercept, \(V_{\text{max}}/K_m\) as the x-intercept, and \(K_m\) as the negative slope (Figure \(\PageIndex{3}\)). Like other techniques that linearize the Michaelis–Menten equation, the Eadie-Hofstee plot was used historically for rapid identification of important kinetic terms like \(K_m\) and \(V_{\text{max}}\), but has been superseded by nonlinear regression methods that are significantly more accurate and no longer computationally inaccessible. It is also more robust against error-prone data than the Lineweaver–Burk plot, particularly because it gives equal weight to data points in any range of substrate concentration or reaction rate (the Lineweaver–Burk plot unevenly weights such points). Both Eadie-Hofstee and Lineweaver–Burk plots remain useful as a means to present data graphically.

**Problems with the Method**
One drawback from the Eadie–Hofstee approach is that neither ordinate nor abscissa represent independent variables: both are dependent on reaction rate. Thus any experimental error will be present in both axes. Also, experimental error or uncertainty will propagate unevenly and become larger over the abscissa thereby giving more weight to smaller values of \( v/[S] \). Therefore, the typical measure of goodness of fit for linear regression, the correlation coefficient \( R \), is not applicable.

Contributors

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- World Public Library
- Wikipedia
- Dr. S.K. Khare (IIT Delhi) via NPTEL