Problem 1.
The binding of protein P with ligand L to form complex C is reversible, as told

$$
\mathrm{P}+\mathrm{L} \xrightarrow{\mathrm{k}_{\mathrm{on}}} \mathrm{C} \text { and } \mathrm{C} \xrightarrow{\mathrm{k}_{\text {off }}} \mathrm{P}+\mathrm{L}
$$

We are given a table with various initial concentrations of L in order to estimate $\mathrm{k}_{\text {on }}$ and $\mathrm{k}_{\text {off }}$ and also $K_{d}$ for the reaction.

$$
\frac{\mathrm{dC}_{\mathrm{C}}}{\mathrm{dt}}=\mathrm{k}_{\mathrm{on}} \mathrm{C}_{\mathrm{P}} \mathrm{C}_{\mathrm{L}}-\mathrm{k}_{\text {off }} \mathrm{C}_{\mathrm{C}}
$$

Also from material balances and stoichiometry, we have $\mathrm{C}_{\mathrm{P}}+\mathrm{C}_{\mathrm{C}}=\mathrm{C}_{\mathrm{P} 0}$ and $\mathrm{C}_{\mathrm{L}}+\mathrm{C}_{\mathrm{C}}=\mathrm{C}_{\mathrm{L} 0}$, therefore

$$
\frac{\mathrm{dC}_{\mathrm{C}}}{\mathrm{dt}}=\mathrm{k}_{\mathrm{on}}\left(\mathrm{C}_{\mathrm{P} 0}-\mathrm{C}_{\mathrm{C}}\right)\left(\mathrm{C}_{\mathrm{L} 0}-\mathrm{C}_{\mathrm{C}}\right)-\mathrm{k}_{\mathrm{off}} \mathrm{C}_{\mathrm{C}}
$$

In this problem, we can safely assume that $\mathrm{C}_{\mathrm{L} 0}-\mathrm{C}_{\mathrm{C}} \approx \mathrm{C}_{\mathrm{L} 0}$ since $\mathrm{C}_{\mathrm{L} 0} \gg \mathrm{C}_{\mathrm{P} 0}$ in all three cases of different $\mathrm{C}_{\mathrm{L} 0}$.
Thus, the integrated analytic expression for $\mathrm{C}_{\mathrm{C}}$ becomes

$$
\mathrm{C}_{\mathrm{C}}=\frac{\mathrm{k}_{\mathrm{on}} \mathrm{C}_{\mathrm{P} 0} \mathrm{C}_{\mathrm{L} 0}}{\mathrm{k}_{\mathrm{on}} \mathrm{C}_{\mathrm{L} 0}+\mathrm{k}_{\text {off }}}\left\{1-\exp \left[-\left(\mathrm{k}_{\text {on }} \mathrm{C}_{\mathrm{L} 0}+\mathrm{k}_{\text {off }}\right) \mathrm{t}\right]\right\}=\frac{\mathrm{C}_{\mathrm{P} 0} \mathrm{C}_{\mathrm{L} 0}}{\mathrm{C}_{\mathrm{L} 0}+\mathrm{K}_{\mathrm{d}}}\left\{1-\exp \left[-\left(\mathrm{k}_{\text {on }} \mathrm{C}_{\mathrm{L} 0}+\mathrm{k}_{\text {off }}\right) \mathrm{t}\right]\right\}
$$

where $K_{d} \equiv \frac{k_{\text {off }}}{k_{\text {on }}}$
Therefore, if we plot $C_{C}$ w.r.t time for each cases of $C_{L 0}$, we can fit according to an exponential $\mathrm{y}=\mathrm{a}[1-\exp (-\mathrm{bt})]$, where b is $\mathrm{k}_{\mathrm{on}} \mathrm{C}_{\mathrm{L} 0}+\mathrm{k}_{\text {off }}$, and a is $\frac{\mathrm{C}_{\mathrm{P} 0} \mathrm{C}_{\mathrm{L} 0}}{\mathrm{C}_{\mathrm{L} 0}+\mathrm{K}_{\mathrm{d}}}$. Values for a and b are shown in the following table.

| $\mathrm{L}_{0}(u M)$ | a | b |
| :---: | :---: | :---: |
| 1 | 0.903 | 1.1113 |
| 5 | 1.0436 | 4.7047 |
| 15 | 0.9932 | 15.1079 |

One important observation in this table is that parameter a does not change much when initial ligand concentration is changed, indicating $\mathrm{C}_{\mathrm{L} 0}=1 \mu \mathrm{M}$ is already above the saturating value. Therefore, value for $\mathrm{k}_{\text {off }}$ can not be obtained accurately from this design of experiments. We can only conclusively obtain the value for $\mathrm{k}_{\text {on }}$.
So we fit a linear express of $b$ vs. $C_{L 0}$ to get $k_{\text {on }}$.

$$
\mathrm{k}_{\mathrm{on}}=0.0010 \mathrm{nM}^{-1} \mathrm{sec}^{-1}
$$

An estimate on $\mathrm{k}_{\text {off }}$ would be

$$
0<=\mathrm{k}_{\mathrm{off}} \ll \mathrm{k}_{\mathrm{on}} \mathrm{C}_{\mathrm{L} 0, \min }=0.0010 \mathrm{nM}^{-1} \mathrm{sec}^{-1} * 1 \mathrm{uM}=1 \mathrm{sec}^{-1}
$$

Similarly an estimate on $\mathrm{K}_{\mathrm{d}}$ is
$0<=\mathrm{K}_{\mathrm{d}} \ll \mathrm{C}_{\mathrm{L} 0, \min }=1 \mu \mathrm{M}$.



Cite as: William Green, Jr., and K. Dane Wittrup, course materials for 10.37 Chemical and Biological Reaction Engineering, Spring 2007. MIT OpenCourseWare (http://ocw.mit.edu), Massachusetts Institute of Technology. Downloaded on [DD Month YYYY].

Problem 2.
For a steady state chemostat, the material balance on cell mass yields

$$
D \equiv \frac{F}{V}=\mu
$$

the volumetric productivity is

$$
\mathrm{F}\left(\mathrm{X}-\mathrm{X}_{0}\right)=\mu \mathrm{V}\left(\mathrm{X}-\mathrm{X}_{0}\right)
$$

For a batch reactor, the material balance on cell mass yields

$$
\frac{\mathrm{dX}}{\mathrm{dt}}=\mu \mathrm{X}
$$

where the initial condition is $\mathrm{X}(\mathrm{t}=0)=\mathrm{X}_{0}$.
Therefore, we have $X=X_{0} \exp (\mu t)$
The volumetric productivity is

$$
\frac{\mathrm{V}\left(\mathrm{X}-\mathrm{X}_{0}\right)}{\mathrm{t}+\mathrm{t}_{\text {turn }}}=\frac{\mathrm{V}\left(\mathrm{X}-\mathrm{X}_{0}\right)}{\frac{1}{\mu} \ln \frac{\mathrm{X}}{\mathrm{X}_{0}}+\mathrm{t}_{\text {turn }}}
$$

Therefore, the ratio of the two

$$
\mu \mathrm{V}(\mathrm{X}-\mathrm{X} 0) / \frac{\mathrm{V}\left(\mathrm{X}-\mathrm{X}_{0}\right)}{\frac{1}{\mu} \ln \frac{\mathrm{X}}{\mathrm{X}_{0}}+\mathrm{t}_{\text {turn }}}=\ln \frac{\mathrm{X}}{\mathrm{X}_{0}}+\mu \mathrm{t}_{\mathrm{turn}}
$$

In practice, for chemostat, in order to maximize the productivity of biomass (DX), the operating condition for $\mu$ is close $\mu_{\max }$. Therefore the ratio above is approximately

$$
\ln \frac{\mathrm{X}}{\mathrm{X}_{0}}+\mu_{\max } \mathrm{t}_{\mathrm{turn}}
$$

Problem 3.
The expression that would be suitable to describe the change of protein expression is:

$$
\mathrm{C}_{\mathrm{P}}=\frac{\mathrm{k}_{\mathrm{P}} \mathrm{k}_{\mathrm{r}}}{\gamma_{\mathrm{r}}\left(\gamma_{\mathrm{P}}+\mu\right)}\left\{1-\exp \left[-\left(\gamma_{\mathrm{P}}+\mu\right) t\right]\right\}
$$

where the meaning of each symbol is in accord with what we did in class.
The time required to change from an "off state" to an "on state" ( $95 \%$ of the steady-state value) is

$$
0.95=1-\exp \left[-\left(\gamma_{\mathrm{P}}+\mu\right) t\right] \text { or } t=-\frac{\ln 0.05}{\gamma_{\mathrm{P}}+\mu}
$$

a) if cells are rapidly growing with a doubling time 30 min and stable protein with a degradation half-time one day, i.e.

$$
\frac{\ln 2}{\mu}=30 \min \text { and } \frac{\ln 2}{\gamma_{\mathrm{P}}}=1 \text { day }
$$

So the half-time for switching is the time need to reach

$$
\begin{gathered}
0.95 \times \frac{1}{2}=1-\exp \left[-\left(\gamma_{\mathrm{P}}+\mu\right) t\right] \\
t_{\text {switching }}=\frac{-\ln \left(1-0.95 \times \frac{1}{2}\right)}{\left(\gamma_{\mathrm{P}}+\mu\right)}=\frac{-\ln \left(1-0.95 \times \frac{1}{2}\right)}{\frac{\ln 2}{30 \mathrm{~min}}+\frac{\ln 2}{1 d a y}} \approx 27.9 \mathrm{~min}
\end{gathered}
$$

b) if cells are not growing at all and the protein with a degradation half-time one hour, i.e.

$$
\frac{\ln 2}{\gamma_{\mathrm{P}}}=1 \mathrm{hr}
$$

So the half-time for switching is

$$
t_{\text {switching }}=\frac{-\ln \left(1-0.95 \times \frac{1}{2}\right)}{\left(\gamma_{\mathrm{P}}+\mu\right)}=\frac{-\ln \left(1-0.95 \times \frac{1}{2}\right)}{\frac{\ln 2}{1 \mathrm{hr}}+0}=0.93 \mathrm{hr}
$$

So in both cases, the switching times are much much longer than that of the current electronic circuits, which is on the order of $\sim \mathrm{ns}-\mu \mathrm{s}$. Thus, it would not be promising in realizing a computer for practical uses.

