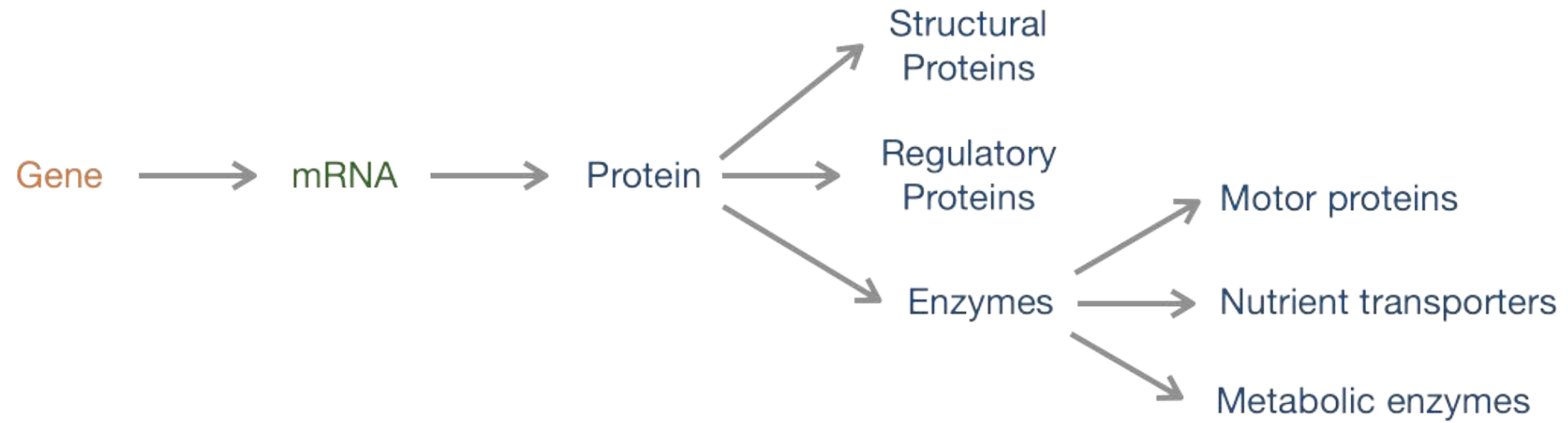


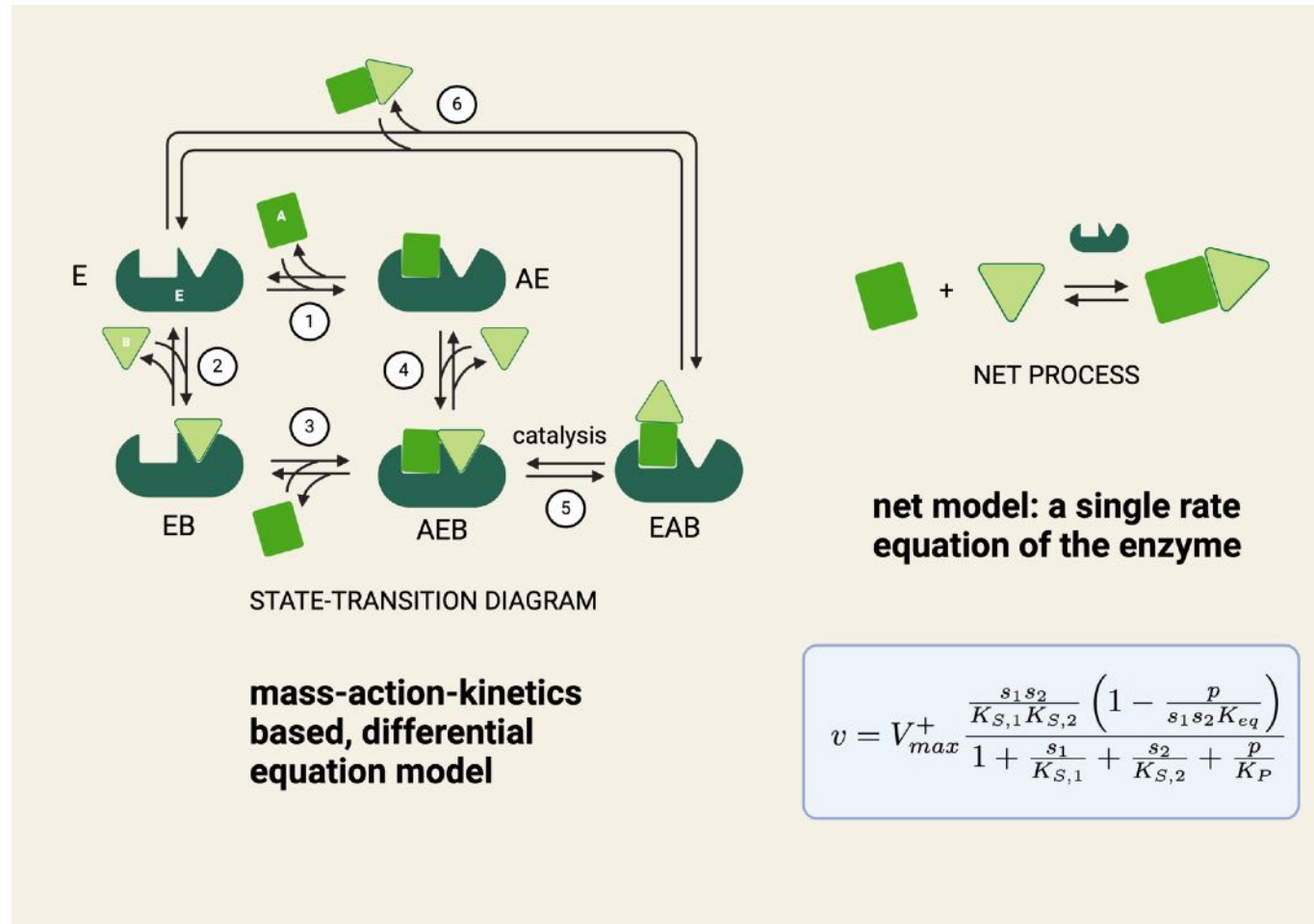
Monomeric/single-subunit Enzyme kinetics

Basic modelling of biological networks

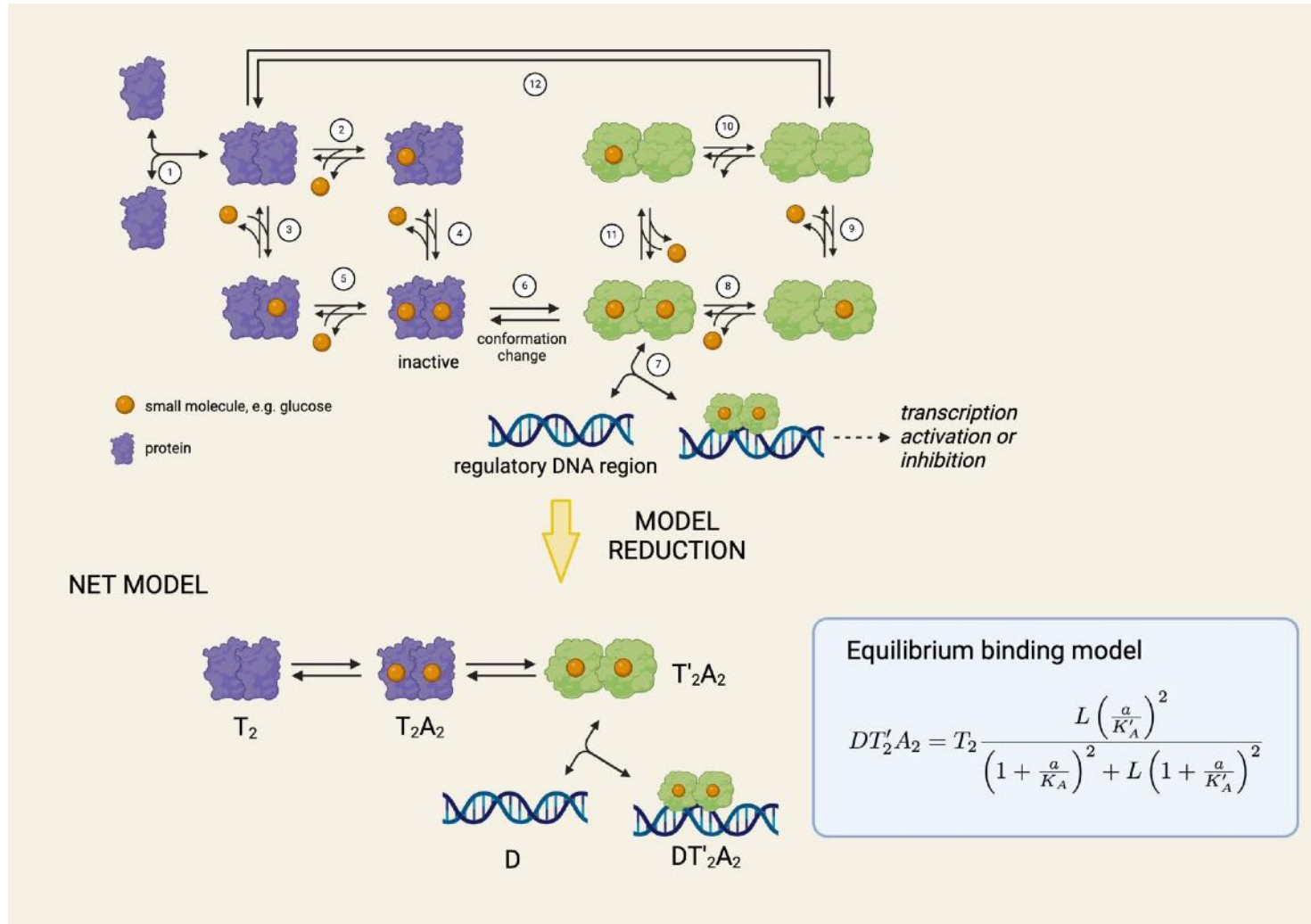
Enzymes



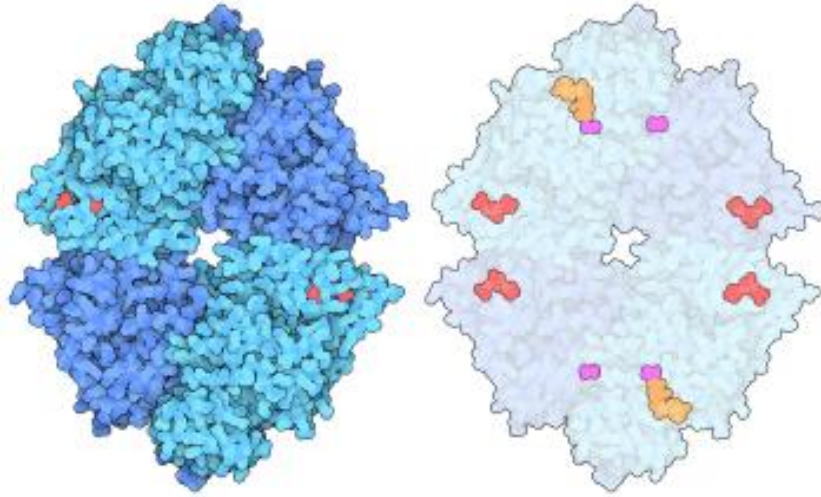
make net models of state-transition diagrams of enzyme catalysis: this week



make net models of state-transition of regulatory proteins: after enzyme kinetics

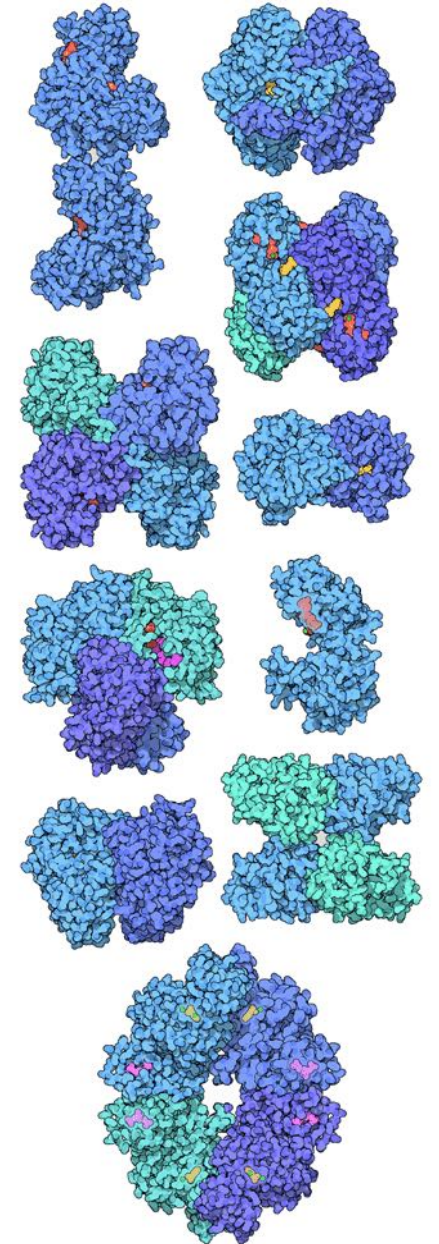


Enzymes: monomers (this week) and multimers (next week)



pyruvate kinase:

1. 4 subunits, a multimer
2. different binding sites on a single subunit
3. conformational changes occur when those sites are occupied
4. regulatory and catalytic sites
5. multimers are enzyme subject to regulation by feedforward and feedback loops
6. more sensitive to regulators than monomer (single subunit enzymes)



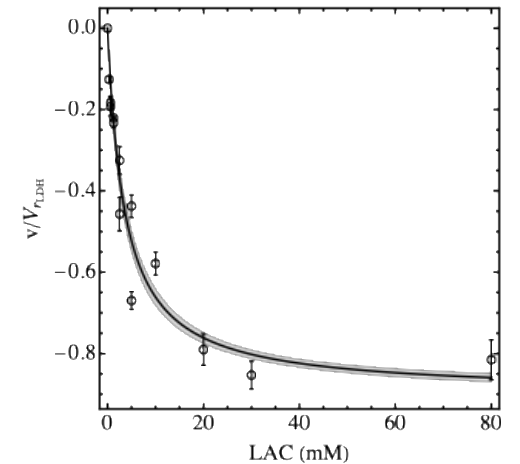
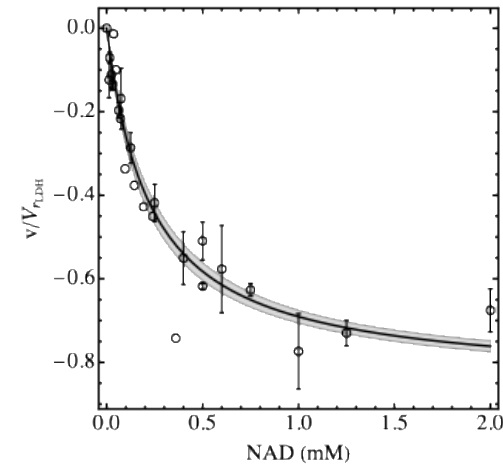
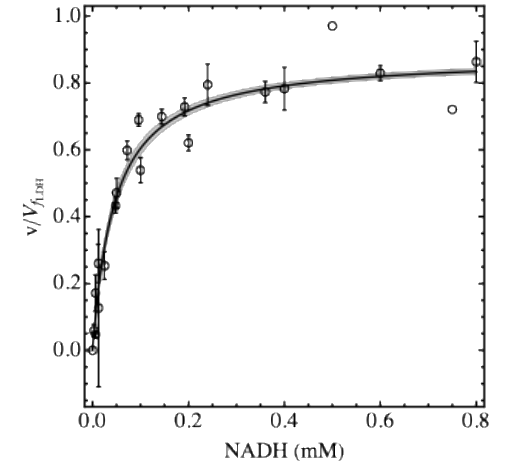
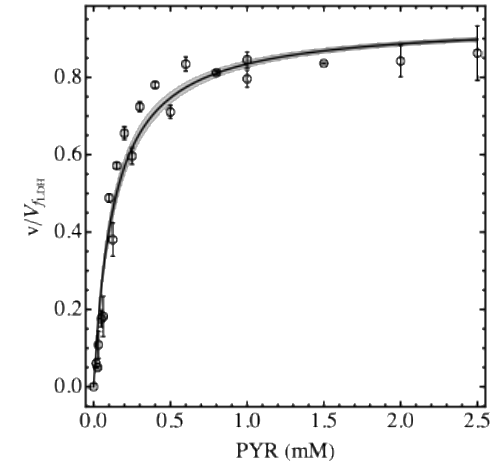
All glycolytic enzymes

Enzyme kinetics: experimental example

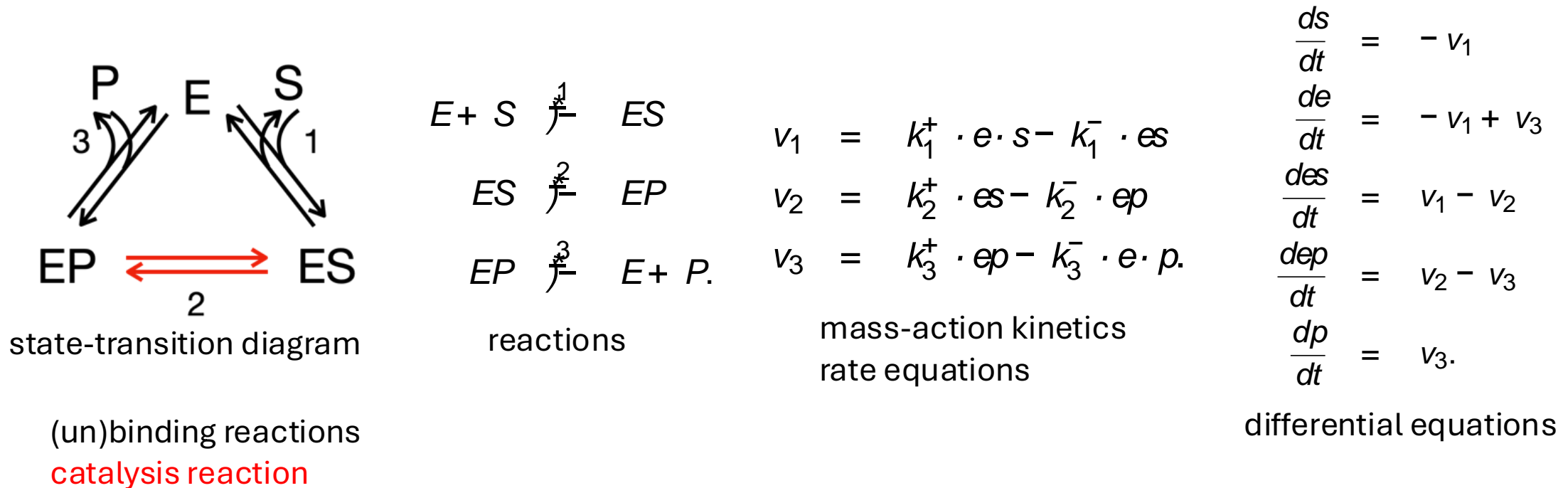
- Lactate dehydrogenase
- Important in cancer cells, Warburg effect
- $\text{NADH} + \text{PYRUVATE} \rightleftharpoons \text{NAD} + \text{LACTATE}$
- Activity measured in cell free extract
- Rate equation to be fitted to data:

$$v = V_{MAX}^+ \frac{\frac{nadh \cdot pyr}{K_{NADH} K_{PYR}} - V_{MAX}^- \frac{nad \cdot lac}{K_{NAD} K_{LAC}}}{\left(1 + \frac{nadh}{K_{NADH}} + \frac{nad}{K_{NAD}}\right) \left(1 + \frac{pyr}{K_{PYR}} + \frac{lac}{K_{LAC}}\right)}$$

- And for us to derive, our first net model of a state-transition diagram of an enzyme.
- Question: what would be a possible state-transition diagram for lactate dehydrogenase?



Derivation of enzyme kinetics: equations

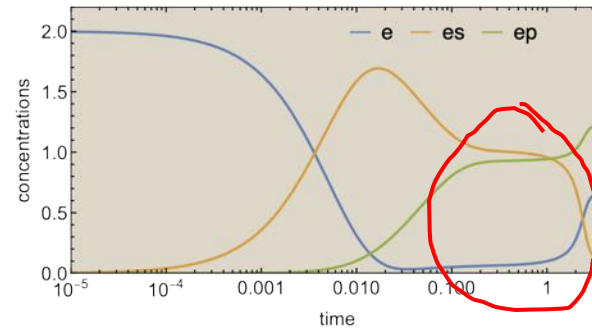
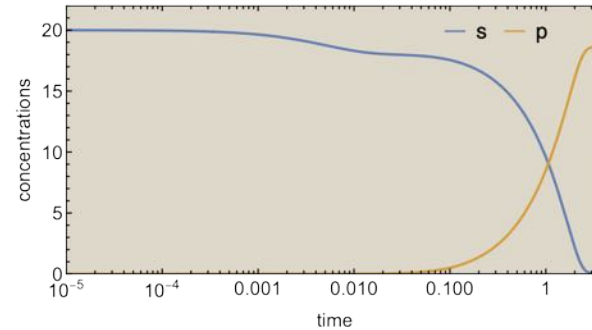
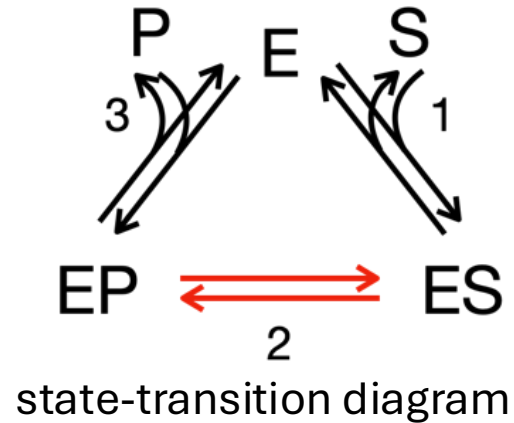


- aim: make net model
- enzyme kinetics derivation
- outcome:

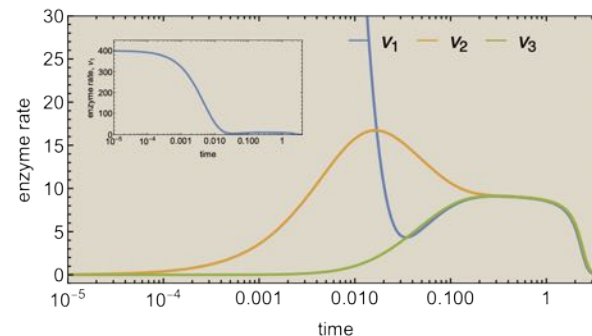
$$v = \frac{V_{max}^+ \frac{s}{K_S} - V_{max}^- \frac{p}{K_P}}{1 + \frac{s}{K_S} + \frac{p}{K_P}}$$

net model

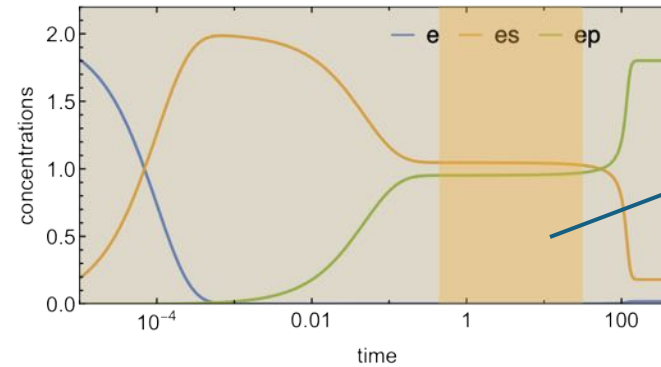
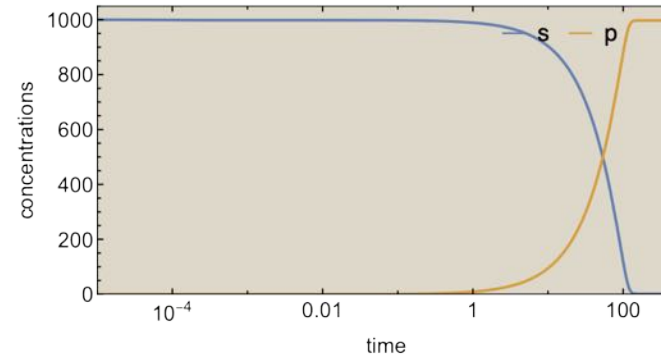
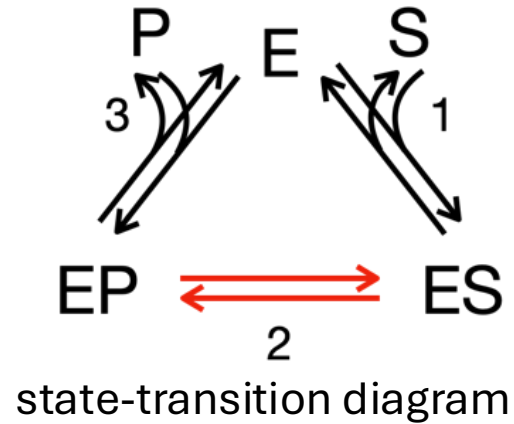
Derivation of enzyme kinetics: emergence of quasi-steady state of enzyme species



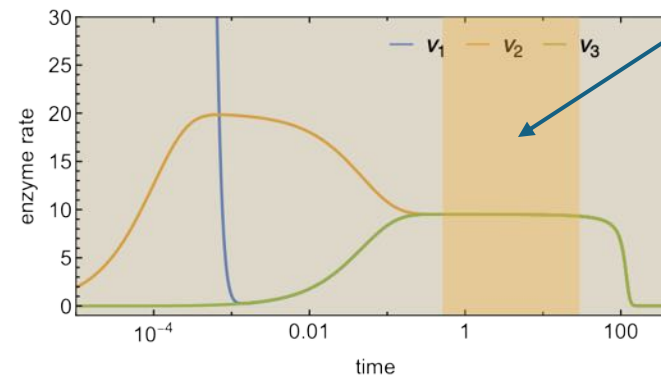
time window
with enzyme-species concentrations
constant: quasi-steady state
i.e. $de/dt \cong 0$, $des/dt \cong 0$, $dep/dt \cong 0$



Derivation of enzyme kinetics: emergence of quasi-steady state of enzyme species, due to substrate excess



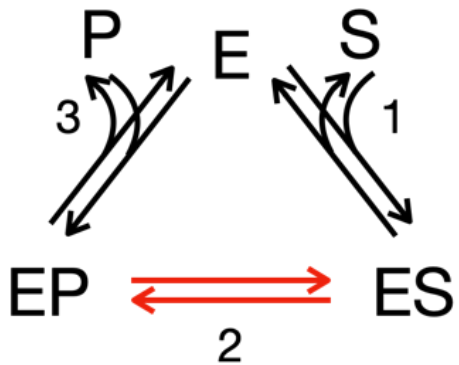
quasi-steady state
of enzyme-species
concentrations



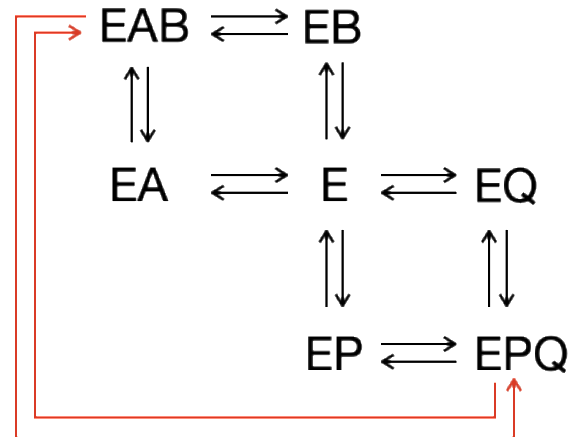
therefore rates constant!

derivation of enzyme kinetics: net model is valid in quasi-steady state regime

- quasi-steady state assumption
 - assume differential equations for enzyme species constant
- quasi-equilibrium assumption
 - assume differential equations for enzyme species constant
 - and, assume that (un)binding rates are zero (equilibrium) (catalysis rate not; so catalysis rate is assumed to be the rate limiting step)

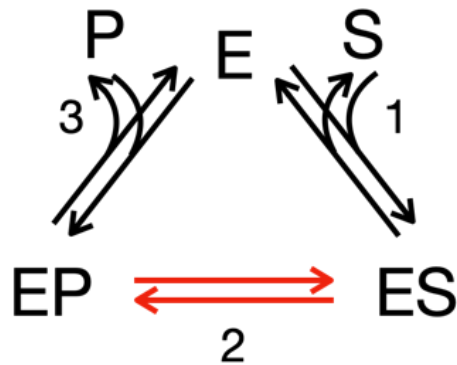


mechanism for
 $A + B \xrightarrow{*} P + Q$



(un)binding reactions
catalysis reaction

we focus on the quasi-equilibrium assumption



- Assume quasi-steady state of enzyme species
- Assume (un)binding reactions as fast and catalysis slow, such that (un)binding reactions are (close to) zero and catalysis reaction not.

• Then: Enzyme rate: $v_2 = k_2^+ es - k_2^- ep$

(un)binding reaction rates at equilibrium: $v_1 = 0$, $v_2 = 0$

Equilibrium conditions $K_1 = K_S = \frac{e \cdot s}{es}$, $K_3 = K_P = \frac{e \cdot p}{ep}$

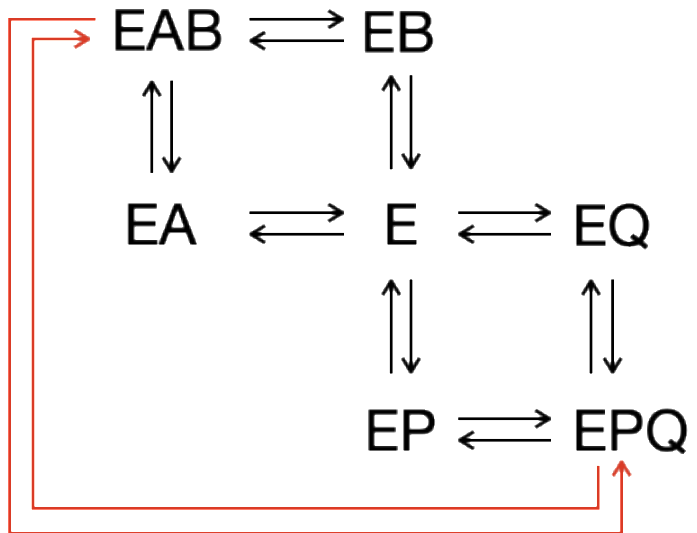
conservation of total $e_T = e + es + ep = e + \frac{e \cdot s}{K_S} + \frac{e \cdot p}{K_P}$

solve for e: $e = e_T \frac{1}{1 + \frac{s}{K_S} + \frac{p}{K_P}}$

solve for es and ep: $es = e_T \frac{\frac{s}{K_S}}{1 + \frac{s}{K_S} + \frac{p}{K_P}}$, $ep = e_T \frac{\frac{p}{K_P}}{1 + \frac{s}{K_S} + \frac{p}{K_P}}$

Enzyme rate equation: $v_2 = k_2^+ es - k_2^- ep = \frac{k_2^+ e_T \frac{s}{K_S} - k_2^- e_T \frac{p}{K_P}}{1 + \frac{s}{K_S} + \frac{p}{K_P}}$

Do the same for:



Do the same for:

