

Lecture 2

5/12/2004

brief review of lecture 1

* similarity between } human designed
control system
adaptation / homeostasis
in biological systems

* human designed syst
control theory well developed
for the design & analysis

examples of application of control theory
to the analysis of biological system
scarce

* basic concepts of control theory
△ block diagram (satellite attitude
control example)

△ 3 basic types of feedback
P I. D controller

△ Laplace transform as a tool
to analyze feedback control systems
differential eq. → algebraic eq.

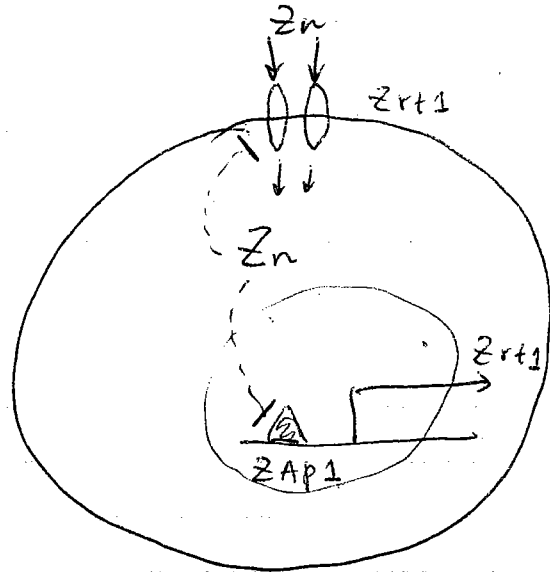
steady state

stability → location of poles

transient dynamics

example - modeling internal nutrient homeostasis, example of zinc

A
Simplified
picture



two different feedbacks

transcriptional: high Zn \rightarrow shut down transcription of transporter

protein degradation: high Zn \rightarrow induce endocytosis of transporter \rightarrow vacuole \rightarrow degraded

A minimal model:

dynamics of

T : transporter

N_i : internal nutrient concentration

with feedbacks

both transcriptional

post-translational

A simple model proposed by
Erin O'Shea & Mike Springer

$$\begin{aligned} \frac{dN_i}{dt} &= k_m k_a T - u \\ \frac{dT}{dt} &= \alpha (R - N_i) - \beta T \end{aligned}$$

↑ transport
↑ usage

↓ transcriptional control
↓ protein degradation

$$k_a = \frac{N_e}{N_e + K_t} \quad \text{fraction bound by external nutrient}$$

k_m : maximum transport rate of a single transporter

R : set point

$$\beta = \beta_0 k_a \quad \text{degradation of nutrient bound transporter}$$

Laplace transform the equations

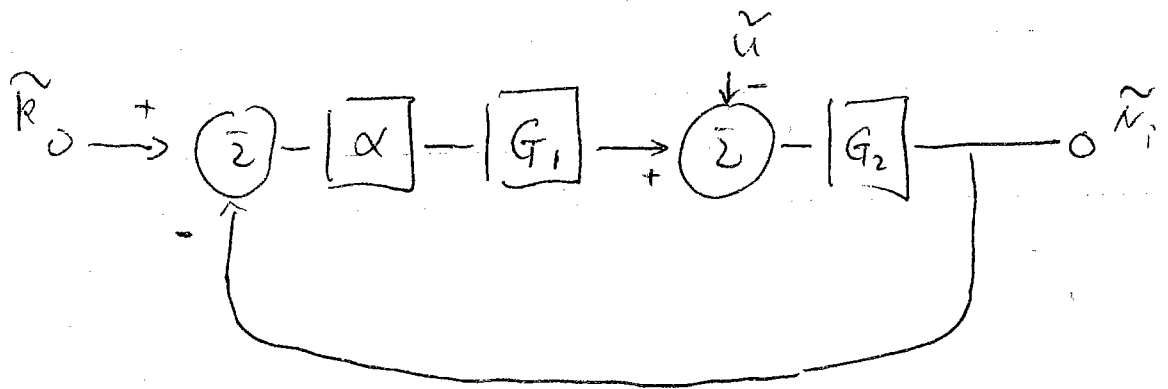
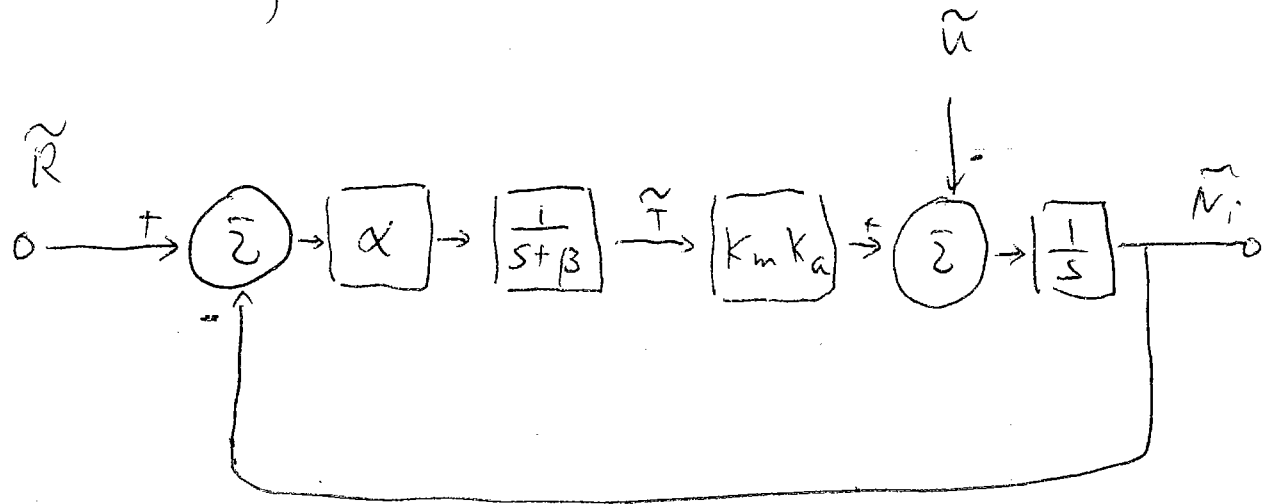
$$s \tilde{N}_i = k_m k_a \tilde{T} - \tilde{u}$$

$$(s + \beta) \tilde{T} = \alpha (\tilde{R} - \tilde{N}_i)$$

$$\tilde{N}_i = \frac{1}{s} (k_m k_a \tilde{T} - \tilde{u})$$

$$\tilde{T} = \alpha \frac{1}{s + \beta} (\tilde{R} - \tilde{N}_i)$$

block diagram



$$G_1 = \frac{k_m k_a}{s + \beta} \quad G_2 = \frac{1}{s}$$

to solve the loop equation

$$[(\tilde{R} - N_i) \alpha G_1 + \tilde{u}] G_2 = \tilde{N}_i$$

$$\tilde{R} \alpha G_1 G_2 - \tilde{u} G_2 = \tilde{N}_i (1 + \alpha G_1 G_2)$$

$$\tilde{N}_i = \frac{\tilde{R} \alpha G_1 G_2 - \tilde{u} G_2}{1 + \alpha G_1 G_2}$$

$$= \frac{\tilde{R} \alpha \frac{k_m k_a}{s + \beta} \frac{1}{s} - \tilde{u} \frac{1}{s}}{1 + \alpha \frac{k_m k_a}{s + \beta} \frac{1}{s}}$$

$$\tilde{N}_i = \frac{\tilde{R} \alpha k_m k_a - \tilde{u} (s + \beta)}{s (s + \beta) + \alpha k_m k_a}$$

steady state

$$\tilde{R} = \frac{R}{s}$$

$$\tilde{u} = \frac{u}{s}$$

$$N_i (t \rightarrow \infty) = \lim_{s \rightarrow 0} s \tilde{N}_i$$

$$= s \cdot \frac{\frac{R}{s} \alpha k_m k_a - \frac{u}{s} (s + \beta)}{s (s + \beta) + \alpha k_m k_a} \quad | \quad s \rightarrow 0$$

$$= \frac{R \alpha k_m k_a - u \beta}{\alpha k_m k_a}$$

$$= R - \frac{u \beta}{\alpha k_m k_a}$$

$$\beta = \beta_0 k_a$$

$$= R - \frac{u \beta_0}{\alpha k_m}$$

not depend on k_a external concentration

stability is given by the poles of \tilde{N}_i or roots of the characteristic equation

$$s^2 + s\beta + \alpha k_m k_a = 0$$

$$s_{1,2} = \frac{-\beta \pm \sqrt{\beta^2 - 4\alpha k_m k_a}}{2}$$

both roots on left hand plane \rightarrow stable

features

external
concentration

* perfect adaptation with respect to M_e
but need fine tuned mechanism
↳ increase in uptake
matches exactly the degradation
increase

* not perfect adaptation w.r.t other
parameters, e.g., usage rate

* increase gain, e.g. α decrease
error, but may induce oscillations

* protein synthesis rate \propto mRNA
which can not jump $\propto (R - N_i)$

?
Alternative model with perfect
adaptation

1) instead of proportional feedback
need integral feedback

model with integral feedback only?

replace $\alpha (R - N_i)$

by $\alpha_I \int (R - N_i) dt$

laplace transform $\frac{\alpha_I}{s} (R - N_i)$

just replace α by $\frac{\alpha_I}{s}$

$$\begin{aligned} \tilde{N}_i &= \frac{\tilde{R} \frac{\alpha_I}{s} \frac{k_m k_a}{s+\beta} \frac{1}{s} - \tilde{u} \frac{1}{s}}{1 + \frac{\alpha_I}{s} \frac{k_m k_a}{s+\beta} \frac{1}{s}} \\ &= \frac{\tilde{R} \alpha_I k_m k_a - \tilde{u} s (s+\beta)}{s^2 (s+\beta) + \alpha_I k_m k_a} \end{aligned}$$

the characteristic equation

$$s^3 + s^2 \beta + \alpha_I k_m k_a = 0$$

with coefficient of s term 0

the system is always unstable
(must exist a root at RHP)

2) proposal 2

PI controller

replace $\alpha (R - N_i)$ by

$$\alpha_p (R - N_i) + \alpha_I \int (R - N_i) dt$$

replace α by $\alpha_p + \frac{\alpha_I}{s}$

$$\begin{aligned} \tilde{N}_i &= \frac{\tilde{R} \left(\alpha_p + \frac{\alpha_I}{s} \right) \frac{k_m k_a}{s+\beta} \frac{1}{s} - \tilde{u} \frac{1}{s}}{1 + \left(\alpha_p + \frac{\alpha_I}{s} \right) \frac{k_m k_a}{s+\beta} \frac{1}{s}} \end{aligned}$$

$$\tilde{N}_i = \frac{\tilde{R} k_m k_a (s \alpha_p + \alpha_I) - \tilde{u} s (s + \beta)}{s^2 (s + \beta) + k_m k_a (s \alpha_p + \alpha_I)}$$

Characteristic equation

$$s^3 + s^2 \beta + k_m k_a \alpha_p s + k_m k_a \alpha_I = 0$$

in lecture 1, we worked out stability criterion

is that $\underbrace{k_m k_a \alpha_I}_{\text{const}} < \underbrace{k_m k_a \alpha_p}_{\text{coeff of linear term}} \cdot \underbrace{\beta}_{\text{coeff of second order term}}$

$$\alpha_I < \beta \alpha_p$$

the steady state

$$N_i(t \rightarrow \infty) = R \quad \text{independent of all parameters}$$

△ how to realize the PI controller

both the transcription factor ZAP1
the transporter Zrt1

are sensing the zinc level

* two zinc fingers in ZAP1 were implicated in zinc sensing →
no. active activation domain

* the mechanism for Zn+1 zinc sensing
less clear

① the integral part:

ZAP1 change activity according to N_i

$$\text{ZAP1 activity} \propto (R - N_i)$$

fast dynamics for
ligand binding

transporter

$$\text{Synthesis} \propto \text{mRNA} \propto \int (R - N_i) dt$$

accumulation of mRNA slow process

② the proportional part

$$\text{degradation rate} = a + bN_i$$

transporter sensing internal nutrient
concentration

$$\frac{dN_i}{dt} = k_m k_a T - u$$

$$\frac{dT}{dt} = \alpha_I \int (R - N_i) dt - (a + bN_i) T$$

non linear eq.

but again $N_i(t \rightarrow \infty) = R$

steady state nothing is changing

Linearize the equation around
steady state

$$N_i = R + \delta N_i$$

$$T = T^*$$

$$\frac{d \delta N_i}{dt} = k_m k_a T - u$$

$$\frac{dT}{dt} = -\alpha_I \int \delta N_i dt - b T^* \delta N_i - (a + bR) T$$

$$= -\alpha_I \int \delta N_i dt - \alpha_p \delta N_i - \beta T$$

$$\alpha_p = b T^*, \quad \beta = a + bR$$

stability condition

$$\alpha_I < \beta \alpha_p = (a + bR) b T^*$$

however T^* is decreasing with
increased external concentration

→ higher external concentra.
less stable

△ An interesting prediction is that
the transporter is sensing internal
concentration instead of
external concentration

① a number of predictions can be tested

* time scale for homeostasis

< mRNA life time for transporter

* transporter senses internal concentration

* stability decrease as external concentration increase

②

a key question is

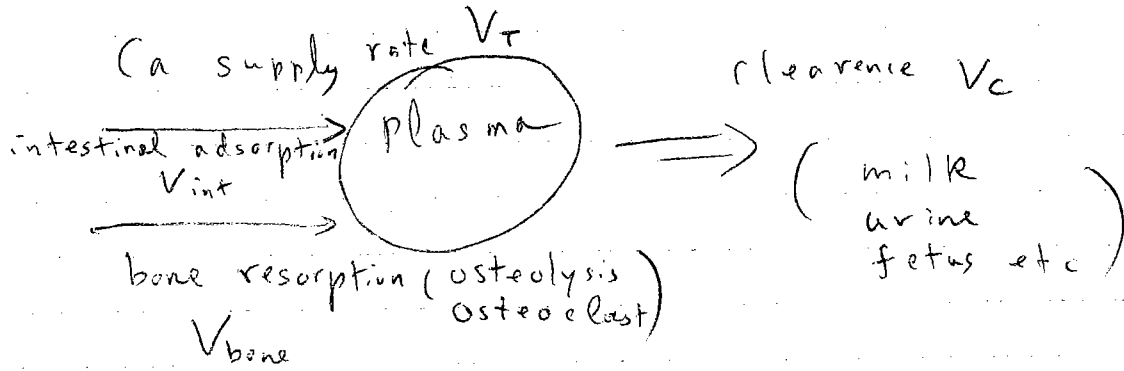
what sets the set point

for transcription factor

response ?

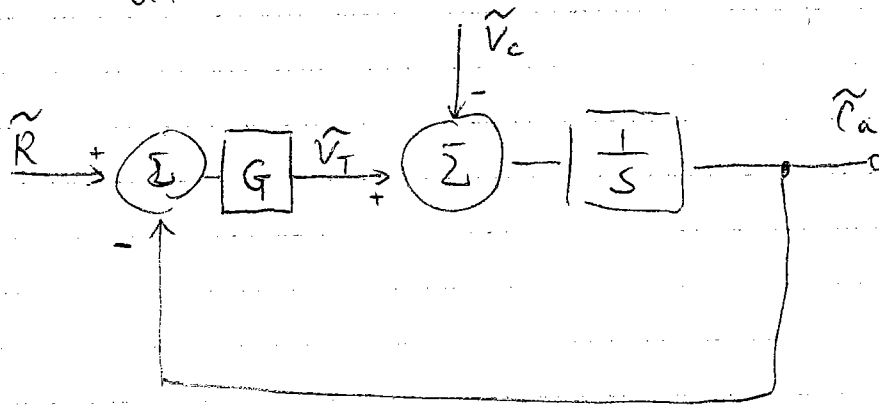
modeling

Example : Calcium homeostasis



$$\frac{dCa}{dt} = V_T - V_c$$

$$V_T = V_{bone} + V_{int}$$



feedback proportional : $V_T = k_p (R - Ca)$

$$G = k_p$$

Solve the loop equation

$$(R - Ca) G/s - V_c/s = Ca$$

$$Ca = \frac{R G/s - V_c/s}{1 + G/s} \rightarrow \text{loop gain}$$

standard model by Ramberg et al.

for proportional feedback

$$G = k_p$$

$$\tilde{C}_a = \frac{\tilde{R} k_p - \tilde{V}_c}{s + k_p}$$

for const
R and V_c

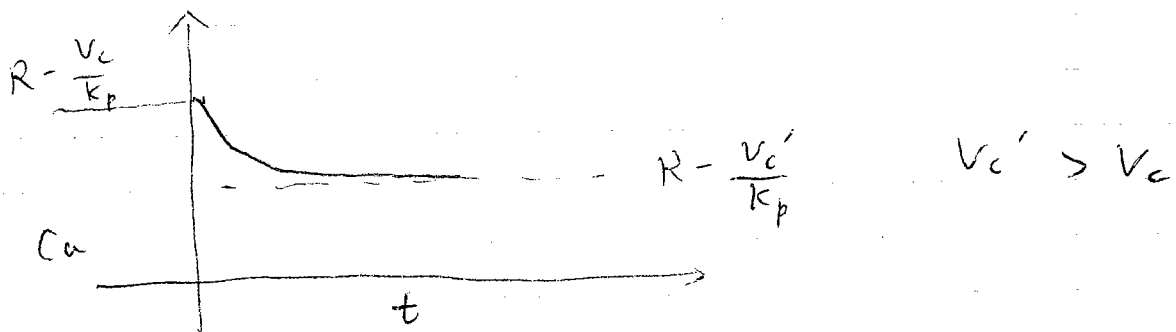
$$\tilde{R} = \frac{R}{s}, \quad \tilde{V}_c = \frac{V_c}{s}$$

Steady state

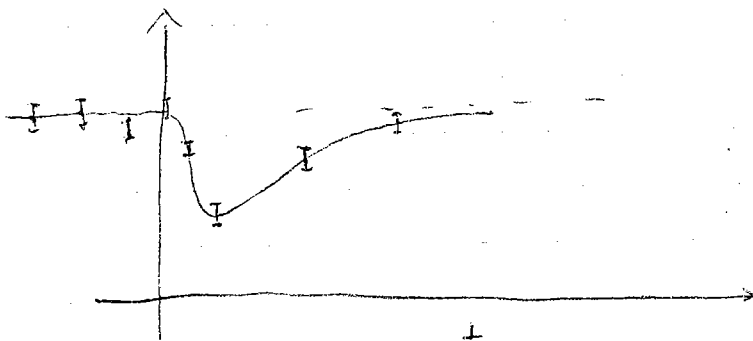
$$C_a(t \rightarrow \infty) = \lim_{s \rightarrow 0} s \tilde{C}_a = \frac{R k_p - V_c}{k_p} = R - \frac{V_c}{k_p}$$

thus a change in clearance rate
lead to a change of steady state
level

the pole is $-k_p$, exponential decay
with time const $\tau = \frac{1}{k_p}$



renal observation



perfect adaptation
shape of
the curve
different

El-Samad et al.
 proposed a PI controller
 model.

$$V_T = k_p (R - a) + k_i \int_0^t (R - a) dt$$

$$G = k_p + \frac{k_i}{s}$$

$$\tilde{a} = \frac{\tilde{R} G/s - \tilde{V}_c/s}{1 + G/s}$$

$$= \frac{\tilde{R} (k_p + k_i/s) \frac{1}{s} - \tilde{V}_c/s}{1 + (k_p + k_i/s)/s}$$

$$= \frac{\tilde{R} (k_p s + k_i) - \tilde{V}_c s}{s^2 + k_p s + k_i}$$

$$\tilde{R} = \frac{R}{s}$$

$$\tilde{V}_c = \frac{V_c}{s}$$

steady state

$$a(t \rightarrow \infty) = \lim_{s \rightarrow 0} s \tilde{a} = \frac{R (k_p s + k_i) - V_c s}{s^2 + k_p s + k_i} \Big|_{s \rightarrow 0}$$

$$= R \quad \text{perfect adaptation}$$

stability

$$\text{roots: } s^2 + k_p s + k_i = 0$$

$$s = \frac{-k_p \pm \sqrt{k_p^2 - 4k_i}}{2}$$

always stable if $k_p^2 \geq 4k_i$
 oscillatory

realization of PI controller by hormones, two hormone scenario

$$V_T = V_A + V_B$$

$$V_A \propto [\text{Hormone A}] \propto \text{error}$$

$$V_B \propto [\text{Hormone B}]$$

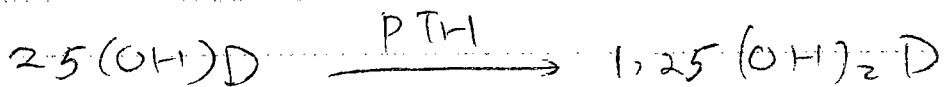
$$\frac{d}{dt} [\text{Hormone B}] \propto [\text{Hormone A}]$$

$$V_T = k_p \text{Error} + k_i \int \text{Error}$$

parathyroid gland $\rightarrow [PTH] \propto \text{Error}$

$\hookrightarrow \propto \text{bone resorption}$

$1,25(OH)_2D \propto \text{intestine adsorption}$



$$\frac{d}{dt} [1,25(OH)_2D] \propto [PTH]$$