

# ***dynamic processes in cells*** ***(a systems approach to biology)***

jeremy gunawardena  
department of systems biology  
harvard medical school

lecture 4  
17 september 2015

## recap

$$a_n \frac{d^n x}{dt^n} + a_{n-1} \frac{d^{n-1} x}{dt^{n-1}} + \cdots + a_1 \frac{dx}{dt} + a_0 = 0$$

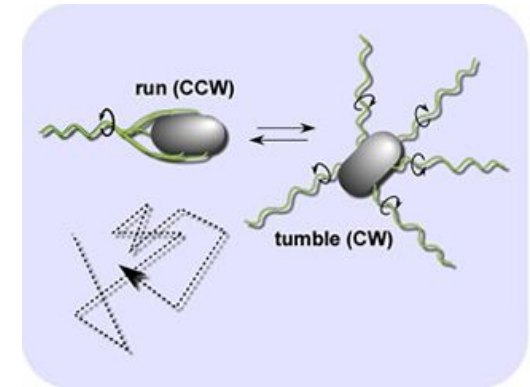
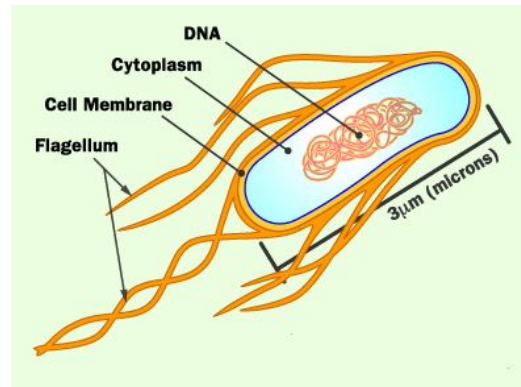
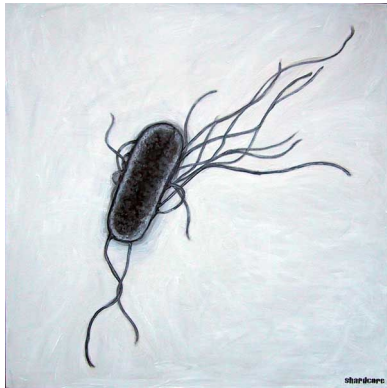
**the Laplace transform converts differentiation by s (or t) into multiplication by t (or s)**

**the solutions of a linear ODE are linear combinations of terms of the form  $t^j e^{z_i t}$  where  $z_i$  are the roots of the characteristic equation**

**stable if, for all roots  $z_i$ ,  $\text{Re}(z_i) < 0$**

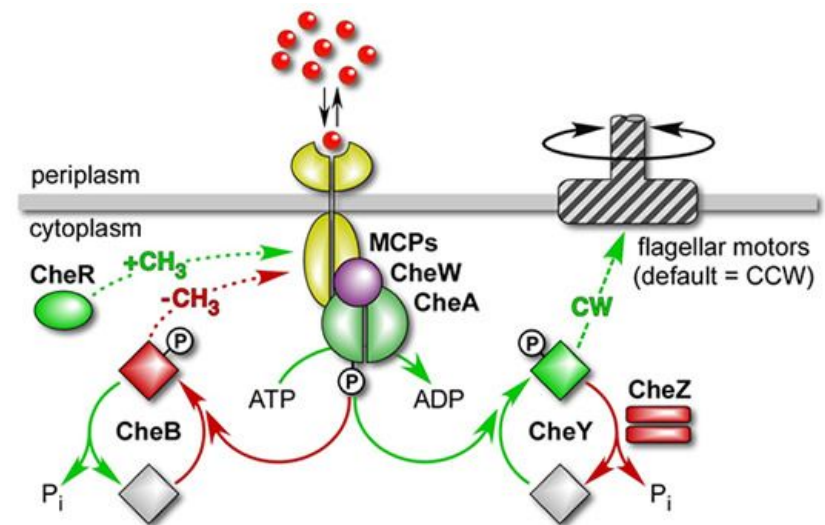
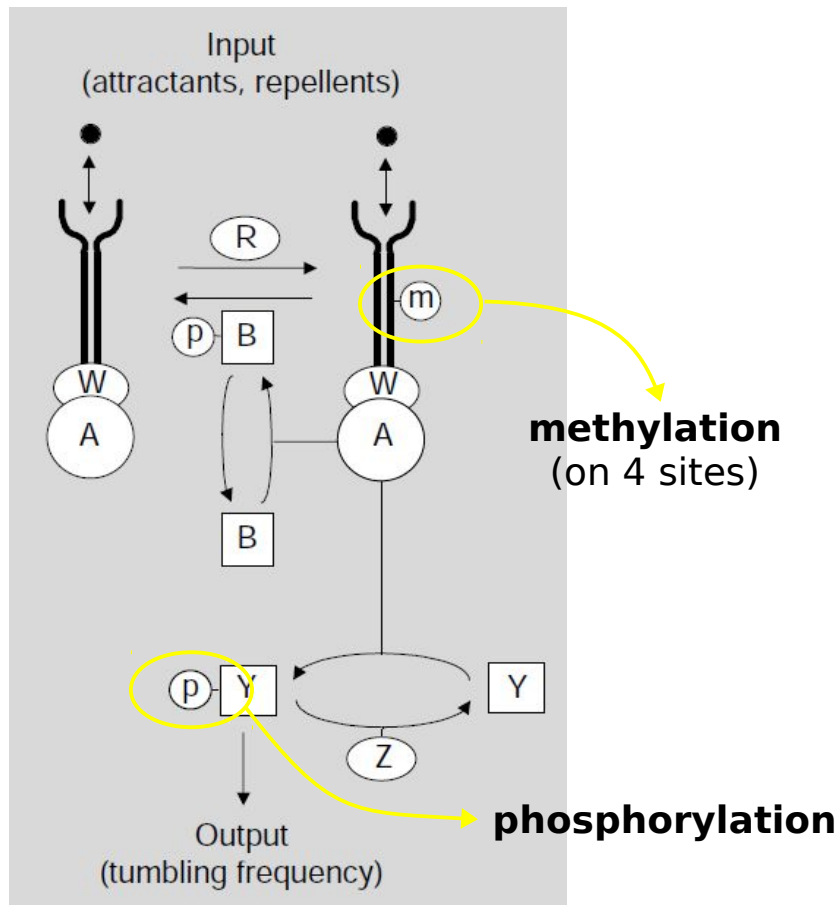
**different kinds of negative feedback have different effects - redundancy can be more apparent than real**

# E coli chemotaxis



E coli navigates towards an attractant, or away from a repellent, by rotating its flagella, alternating between **“runs”** (flagella rotating together) and **“tumbles”** (flagella rotating apart). By changing the tumbling frequency, a bacterium can navigate along a chemotactic gradient.

# molecular circuitry of E coli chemotaxis

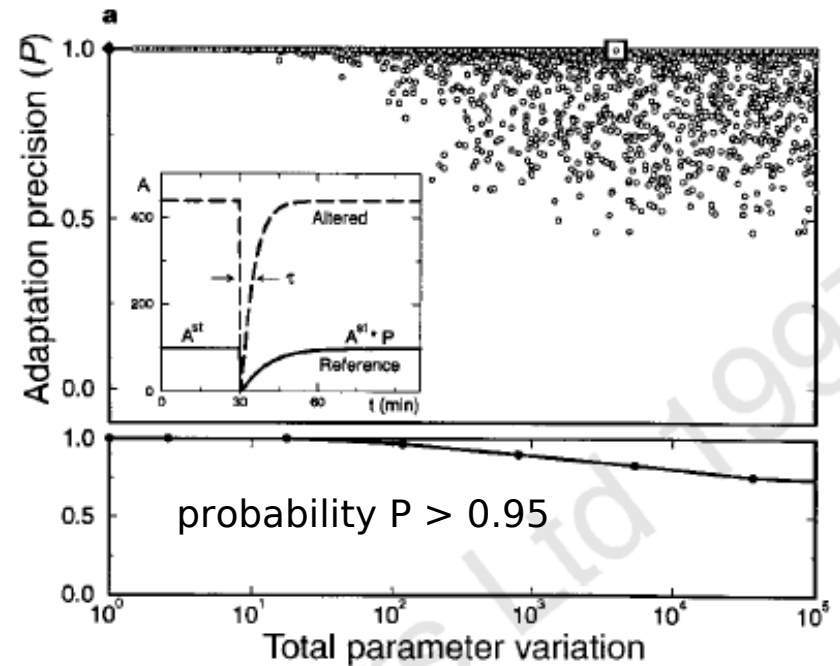
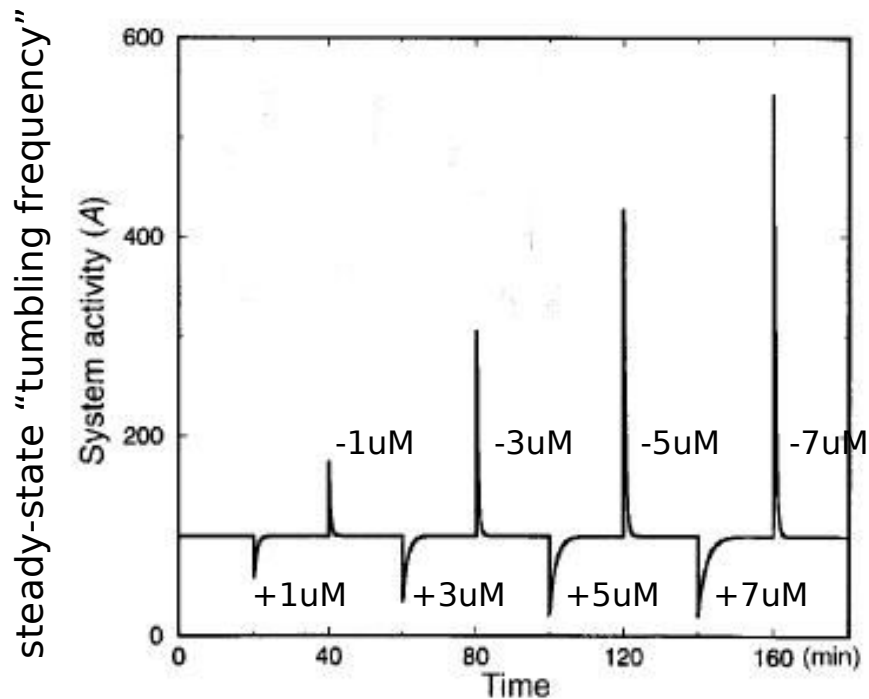


N Barkai, S Leibler, "Robustness in simple biochemical networks", Nature **387**:913-7 1997

right hand image here and on the previous slide from Sandy Parkinson's lab @University of Utah - [chemotaxis.biology.utah.edu/Parkinson\\_Lab/](http://chemotaxis.biology.utah.edu/Parkinson_Lab/)

## perfect adaptation, in theory

steady-state tumbling frequency returns to its set point after a disturbance, with no steady-state error.

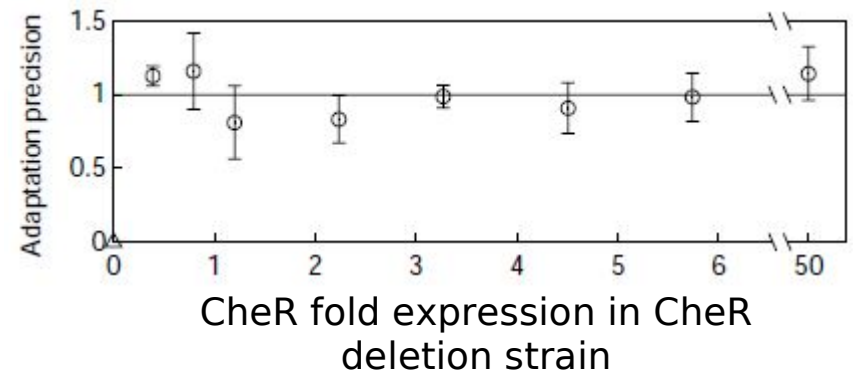
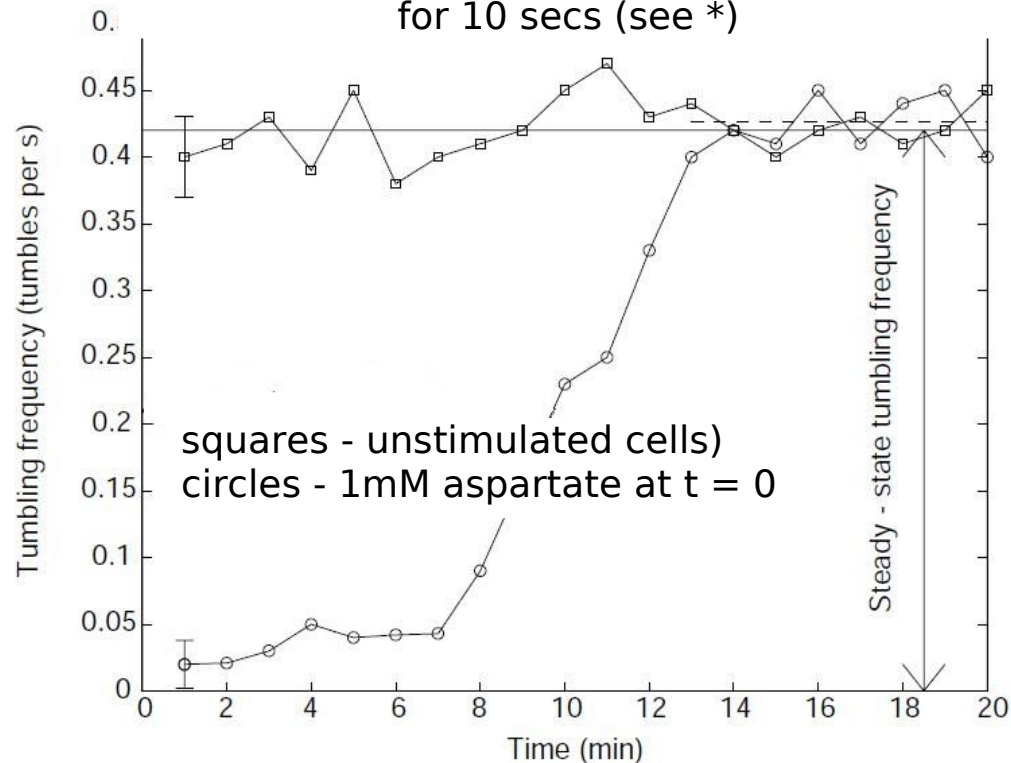


“Figure 3a illustrates the most striking result of the model ... Typically, one can change simultaneously each of the rate constants several fold and still obtain, on average, only a few per cent deviation from perfect adaptation”

# perfect adaptation, in practice

## E coli RP437 strain

each data point averaged over 100-400 cells  
for 10 secs (see \*)



Protein varied	Fold expression	Precision of adaptation
Wild type	1.0	$0.98 \pm 0.05$
CheB*	$0.4 \pm 0.1$	$0.98 \pm 0.12$
CheB*	$12 \pm 3$	$1.09 \pm 0.11$
CheBct	$\sim 11$	$0.90 \pm 0.13$
CheY†	$0.2 \pm 0.1$	$1.04 \pm 0.08$
CheZ	0	$1.1 \pm 0.14$
Tar, Tap, CheR,B,Y,Z§	$5 \pm 2$	$1.04 \pm 0.07$

U Alon, M G Surette, N Barkai, S Leibler, "Robustness in bacterial chemotaxis", Nature **397**:168-71 1999

\* Korobkova, Emonet, Vilar, Shimizu, Cluzel, "From molecular noise to behavioural variability in a single bacterium", Nature **428**:574-8 2004

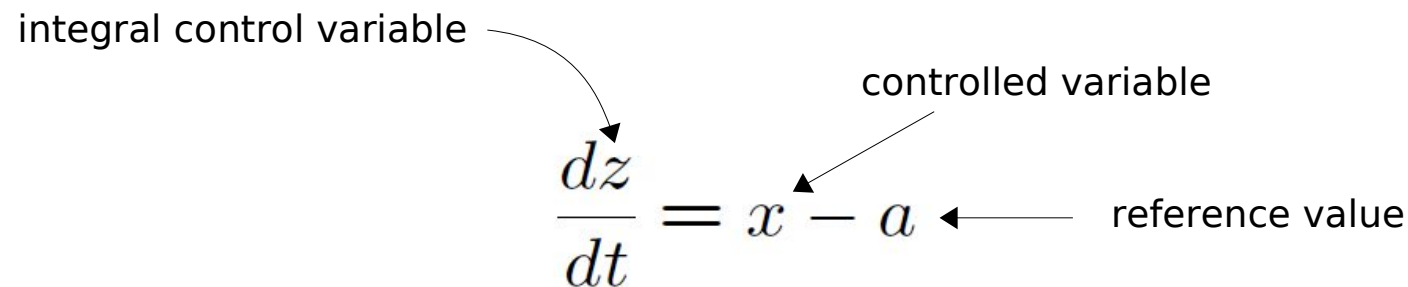
## perfect adaptation arises from integral control

the Barkai-Leibler model implements integral control, in the sense that a generalised variable,  $z$ , can be identified for which

integral control variable

controlled variable

reference value

$$\frac{dz}{dt} = x - a$$
The diagram shows the differential equation  $\frac{dz}{dt} = x - a$ . An arrow points from the text 'integral control variable' to the variable  $z$  in the numerator of the derivative. Another arrow points from the text 'controlled variable' to the variable  $x$ . A third arrow points from the text 'reference value' to the variable  $a$ .

$z$  is approximately the total receptor methylation level in the Barkai-Leibler model

furthermore, perfect adaptation **implies** integral control

T-M Yi, Y Huang, M I Simon, J Doyle, *“Robust perfect adaptation in bacterial chemotaxis through integral feedback control”*, PNAS **97**:4649-53 2000

## matrix formulation

1 component, order n

$$a_n \frac{d^n x}{dt^n} + a_{n-1} \frac{d^{n-1} x}{dt^{n-1}} + \cdots + a_1 \frac{dx}{dt} + a_0 = 0$$

n components, order 1

$$\frac{dx}{dt} = A.x \quad x = (x_1, \cdots, x_n)^t$$

$$x_1 = x, \quad x_2 = \frac{dx}{dt}$$

$$a_2 \frac{d^2 x}{dt^2} + a_1 \frac{dx}{dt} + a_0 x = 0$$

$$\frac{d}{dt} \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} 0 & 1 \\ -\frac{a_0}{a_2} & -\frac{a_1}{a_2} \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \end{pmatrix}$$

put matrix in triangular form by  
Gaussian elimination

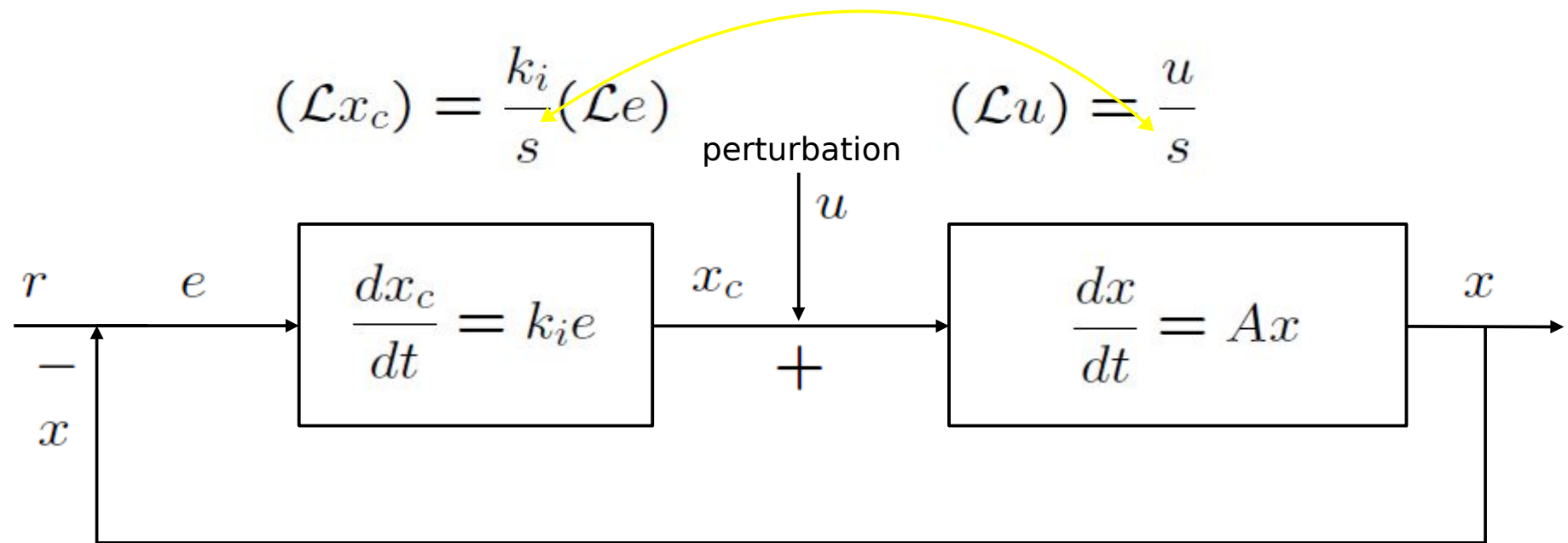
see “Matrix algebra for beginners, Parts I, II & III”





## the internal models principle

a controller which perfectly adapts to an additive perturbation must contain an **internal model** of the perturbation



Francis, Wonham, "The internal model principle of control theory", Automatica 12:457-465 1976; E Sontag, "Adaptation and regulation with signal detection implies internal model", Systems & Control Letters, **50**:119-26 2003; M Kawato, "Internal models for motor control and trajectory planning", Curr Opin Neurobiol **9**:718-27 1999.

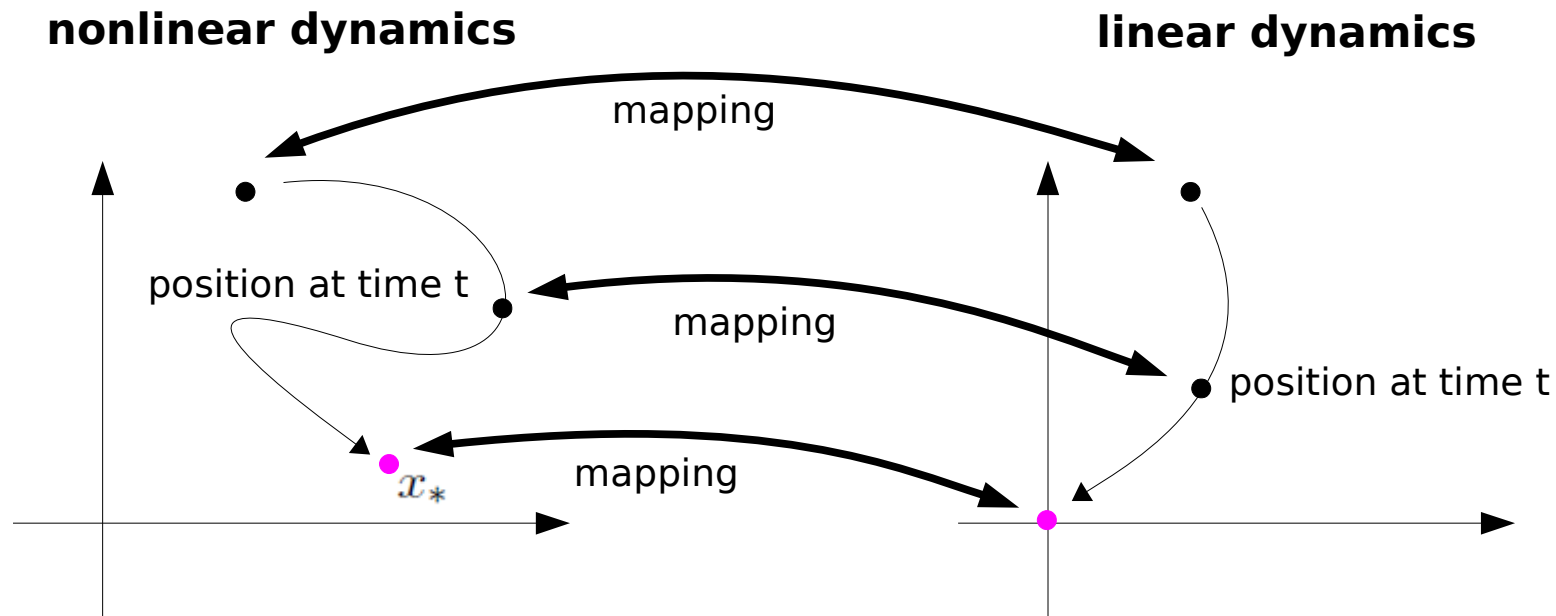
# linear systems approximate nonlinear systems

**HARTMAN-GROBMAN THEOREM** - in the vicinity of a hyperbolic steady state (all eigenvalues of the Jacobian have non-zero real part), a nonlinear system can be qualitatively approximated by a linear one

Jacobian matrix

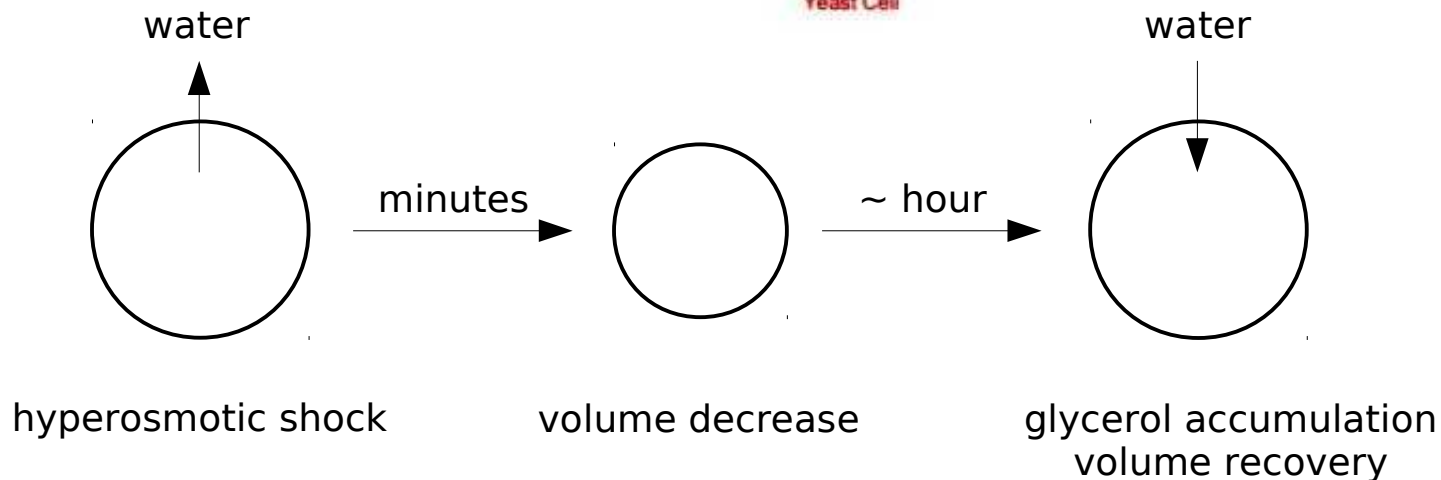
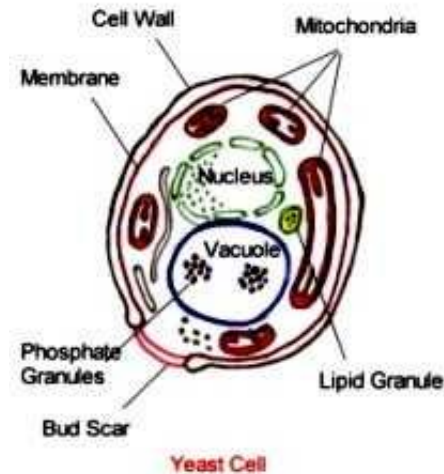
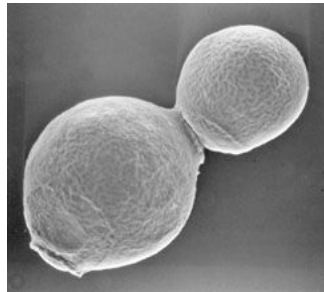
$$\frac{dx}{dt} = f(x) \quad f(x_*) = 0$$

$$\frac{dy}{dt} = A \cdot y \quad A = \left( \frac{\partial f_i}{\partial x_j} \right) \Big|_{x=x_*}$$
$$y = x - x_*$$



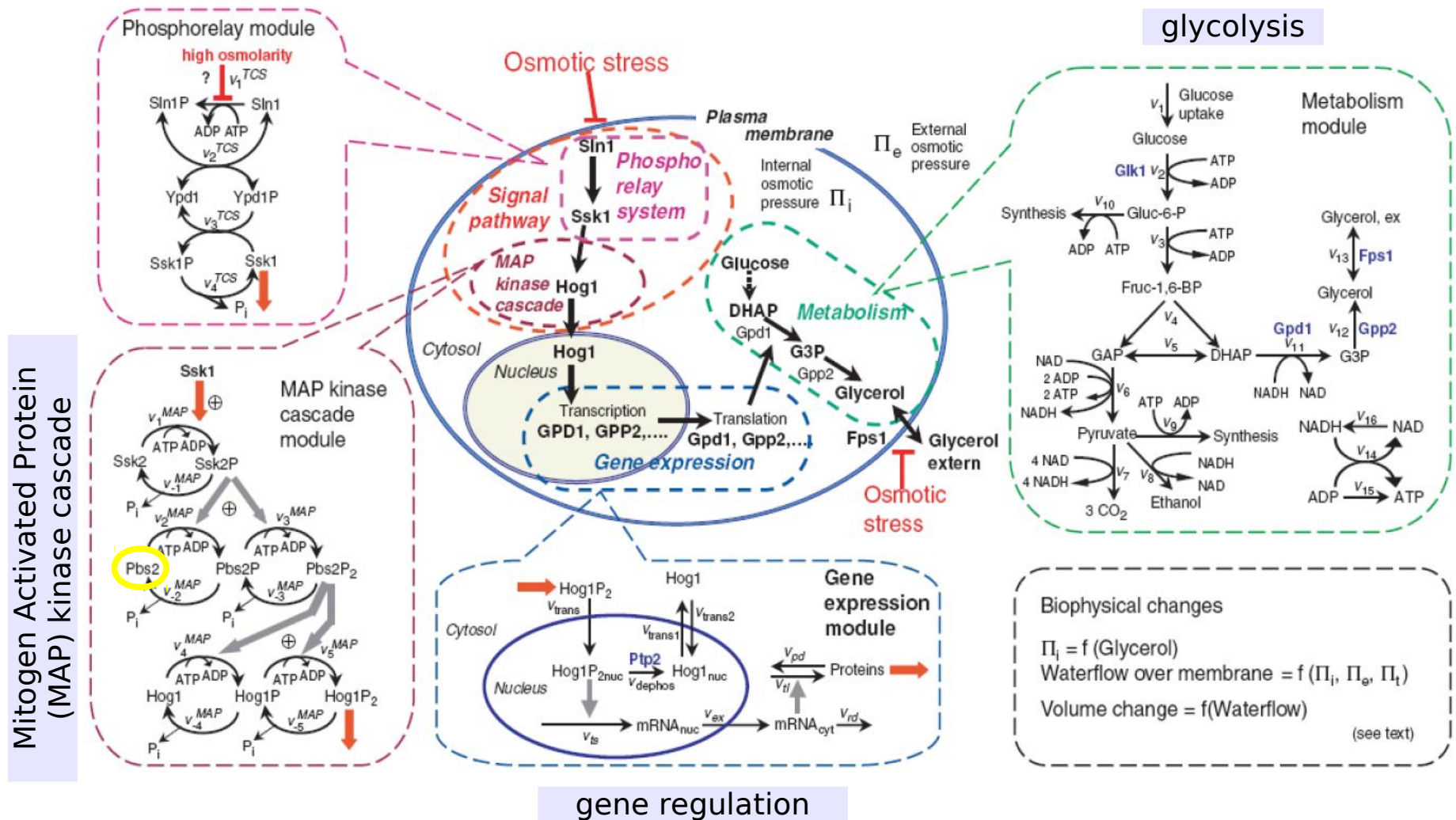
# osmolarity regulation in *S cerevisiae*

yeast are unicellular fungi whose external environment can exhibit changes in osmolarity on fast and slow time scales



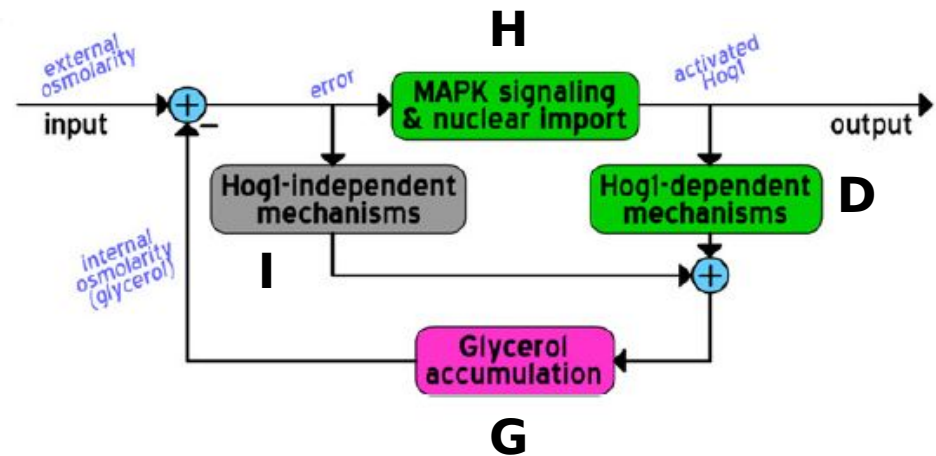
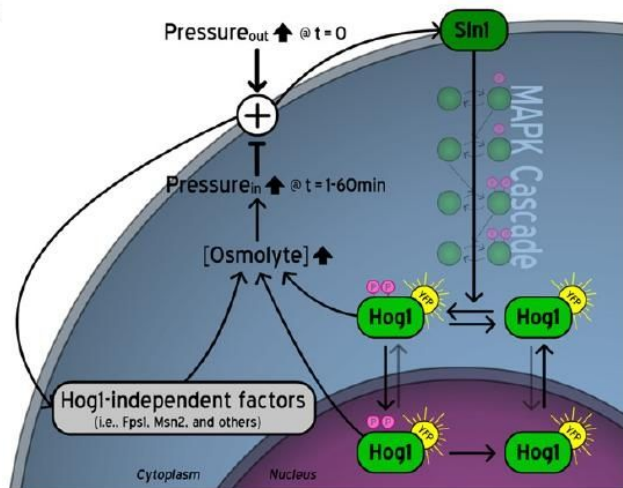
# detailed model of the molecular network

two-component signalling



Klipp, Nordlander, Kruger, Gennemark, Hohmann, "Integrative model of the response of yeast to osmotic shock", Nature Biotech **23**:975-82 2005

# osmolarity regulation as a control system



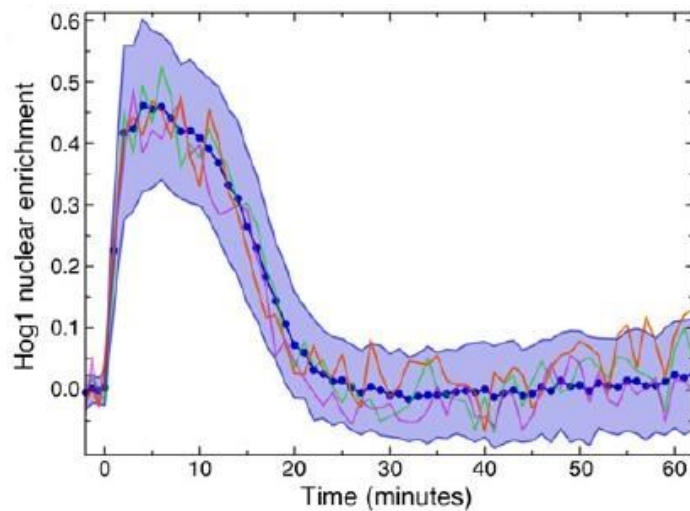
D Muzzey, C Gomez-Urbe, J T Mettetal, A van Oudenaarden, "A systems-level analysis of perfect adaptation in yeast osmoregulation", Cell **138**:160-71 2009

# Hog1 nuclear enrichment shows perfect adaptation

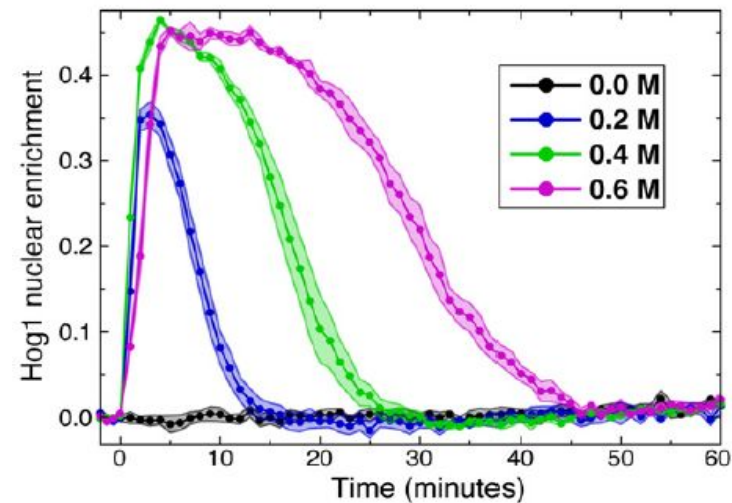
Hog1-YFP, haploid *SHO1*- cells

SHO1 deletion disables the non-Sln1 pathway of Hog1 activation

homeostatic response to step-function increase in external NaCl



cell-to-cell variation is low



population average returns to its set point  
perfect adaptation - no steady-state error

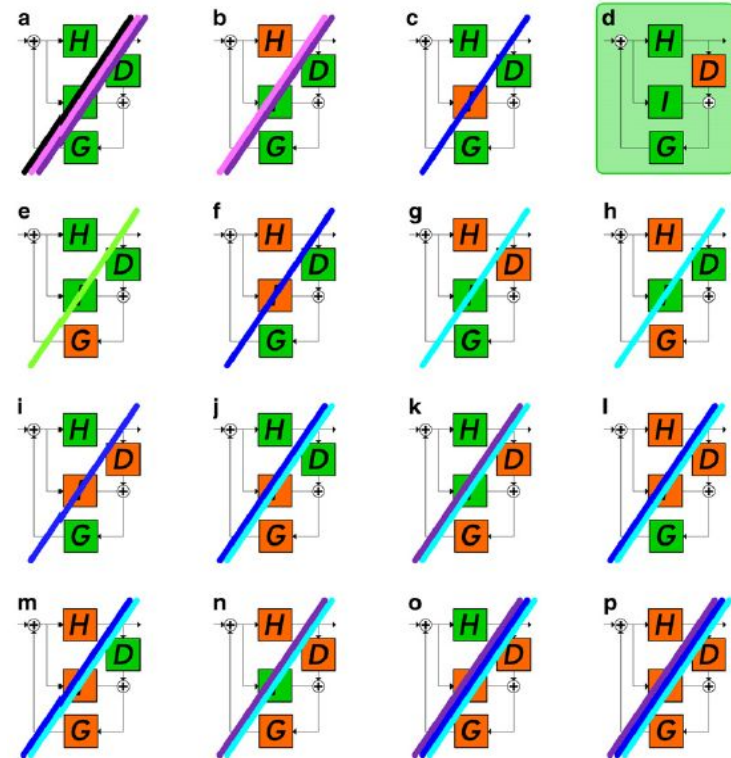
perfect adaptation implies integral control in the linear approximation



# locating the integral feedback

there is a single integrator, localised to the Hog1-dependent module D

integral control requires Hog1 kinase (Pbs2) activity



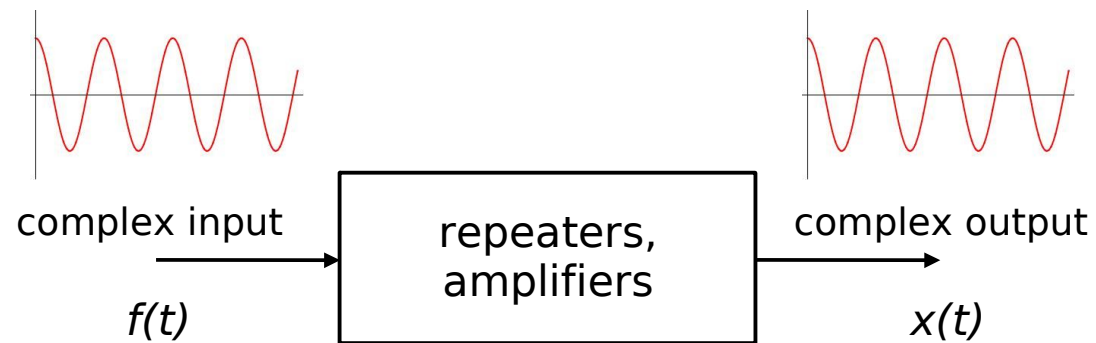
further analysis and extension to *Candida albicans*:

You, ..., Brown, "A systems biology analysis of long and short-term memories of osmotic stress adaptation in fungi", BMC Res Notes **5**:258 2012



## a more complex control problem

trans-continental telephony, early 20<sup>th</sup> century,



$$a_n \frac{d^n x}{dt^n} + \cdots + a_1 \frac{dx}{dt} + a_0 x$$

need to ensure that the output recapitulates the input with “high fidelity”

need to understand the input/output behaviour of a highly complex system without knowing all the internal details

## follow the sines

force the system with a sinusoidal input and look at the output

$$f(t) = e^{i\omega t} \quad (\mathcal{L}f)(s) = \frac{1}{s - i\omega}$$

Harry  
Nyquist



1889-1976

Hendrik  
Bode



1905-1982

$$a_n \frac{d^n x}{dt^n} + a_{n-1} \frac{d^{n-1} x}{dt^{n-1}} + \cdots + a_1 \frac{dx}{dt} + a_0 x = f(t)$$

$$(\mathcal{L}x)(s) = \frac{(\mathcal{L}f) + c(s)}{Z(s)} = \frac{1}{(s - i\omega)Z(s)} + \frac{c(s)}{Z(s)}$$

Hendrik Bode, **Network Analysis and Feedback Amplifier Design**, Van Nostrand, New York 1945

## stable system has output at same frequency

if the system is stable, so that the roots of  $Z(s)$  have negative real parts, then  $i\omega$  cannot be a repeated root

$$\begin{aligned}(\mathcal{L}x)(s) &= \frac{1}{(s - i\omega)Z(s)} + \frac{c(s)}{Z(s)} \\&= \frac{B}{s - i\omega} + \sum_{i=1}^k \left( \sum_{u=1}^{r_i} \frac{C_{i,u}}{(s - z_i)^u} \right) + \sum_{i=1}^k \left( \sum_{u=1}^{r_i} \frac{D_{i,u}}{(s - z_i)^u} \right)\end{aligned}$$
$$x(t) = Be^{i\omega t} + \underbrace{\sum_i C'_i t^{r_i} e^{z_i t} + \sum_i D'_i t^{r_i} e^{z_i t}}_{\rightarrow 0, \text{ as } t \rightarrow \infty} \quad \text{because of stability}$$

**after the transients have died down, the response of a stable linear system to sinusoidal forcing is a sinusoidal output at the same frequency**

## the transfer function

but what is the amplitude, B?

$$\left( a_n \frac{d^n}{dt^n} + a_{n-1} \frac{d^{n-1}}{dt^{n-1}} + \cdots + a_1 \frac{d}{dt} + a_0 \right) (B e^{i\omega t}) = A e^{i\omega t}$$

$$B(a_n(i\omega)^n + a_{n-1}(i\omega)^{n-1} + \cdots + a_1(i\omega) + a_0) = A$$

$$B = \left( \frac{1}{Z(i\omega)} \right) A = G(i\omega) A$$

the **transfer function** is the reciprocal of the characteristic polynomial

## linear frequency analysis

**the amplitude is the transfer function, evaluated at the forcing frequency**

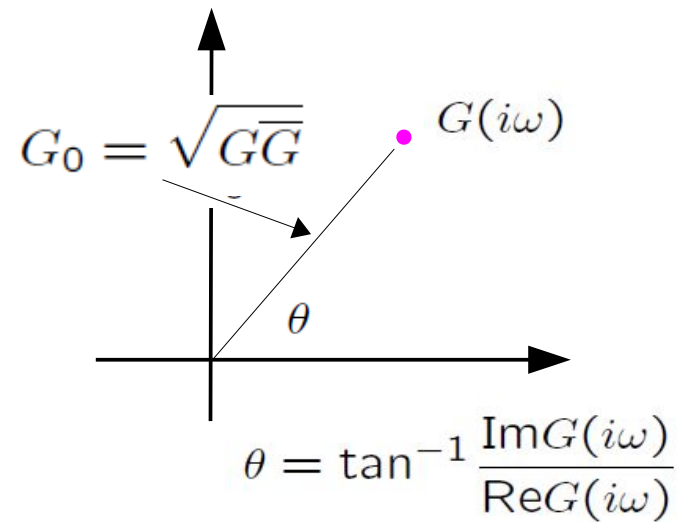
$$f(t) = Ae^{i\omega t} \quad x(t) = G(i\omega)Ae^{i\omega t}$$

$$G(i\omega) = G_0 e^{i\theta}$$

$$x(t) = G_o A e^{i(\omega t + \theta)}$$

gain

phase lag or lead



for high fidelity, the gain and the phase lag/lead should change little with frequency

## second-order linear ODEs

consider a system normalised the way physicists prefer

$$\begin{array}{ccc} \text{positive} & & \text{coefficient of } x \text{ is } +1 \\ \downarrow & & \downarrow \\ \left( \frac{1}{\omega_f^2} \right) \frac{d^2 x}{dt^2} + \left( \frac{2\delta}{\omega_f} \right) \frac{dx}{dt} + x = 0 \end{array}$$

$$\begin{array}{lll} \omega_f > 0 & \text{fundamental frequency} & (\text{time})^{-1} \\ \delta & \text{damping ratio} & \text{dimensionless} \end{array}$$

with these choices the characteristic polynomial has the following two roots

$$s = \omega_f(-\delta \pm \sqrt{\delta^2 - 1})$$

and the system is stable provided that  $\delta > 0$

# Bode plots

decibels (dB)

follow the sines ...

$$\left(\frac{1}{\omega_f^2}\right) \frac{d^2x}{dt^2} + \left(\frac{2\delta}{\omega_f}\right) \frac{dx}{dt} + x = Ae^{i\omega t}$$

$$\beta = \frac{\omega}{\omega_f}$$

$$G(i\omega) = (1 - \beta^2 + 2\delta\beta i)^{-1}$$

$$G_0 = \sqrt{G\bar{G}}$$

