MSc course: Practical Systems Biology

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This course will provide *an introduction to systems biology* by focusing on the behaviours expected from interactions between only a few genes, taking examples from microbes to mammals.

Cells are dynamic systems, and we will build intuition about the types of responses expected from different gene circuits *by running, adapting, and analysing computer simulations*.

For many, systems biology started with this 1999 review

From molecular

to modular cell biology Leland H. Hartwell, John J. Hopfield, Stanislas Leibler and Andrew W. Murray

interacting molecules ... Cellular functions, such as signal transmission, are carried out by 'modules' made up of many species of

General principles that govern the structure and exist to reproduce, whereas, outside religious **behaviour of modules** may be discovered with help from synthetic sciences such as engineering and computer science, from stronger interactions between experiment and theory in cell biology, and from an appreciation of evolutionary constraints. mation, and the information and the

Modelling action potentials. The upper

Mature, 1999

synthesis of one protein, that DNA contains

individual conductivities, Hodgkin and Huxley

Why do we need systems biology?

 $\prod_{i=1}^{n}$

The sequencing of the human genome has given us a list of the parts of the cell (the genes and proteins).

We need to understand how these parts interact to generate cellular behaviour if we wish to improve medicine and biotechnology. (e.g., necessary or sufficient to produce a behavior) than in terms of relevance to the goals of a system. (Lander, 2007)

binding and hydrolysation of one ATP modes in dynamic By discovering how function arises in dynamic interactions, systems biology addresses the missing links between molecules and physiology. (Bruggeman and Westerhoff, 2007)

Cellular behaviour can be remarkable...

More inspiring definitions emerged later

What distinguishes systems biology from earlier traditions is the tendency to define importance less in operational terms

MAPKK

Zooming out...

CellDesigner 2.2

TLR9

Ca signaling 2+

small GTPase

> PIP signaling

It is because biology is so complex that we need a multidisciplinary approach.

TIRAP

MyD88

IKK

MyD88 independent

Apoptosis

TLR7/8

General principles that govern the structure and behaviour of modules may be discovered with help from synthetic sciences such as engineering and computer science, from stronger interactions b from an appreciation of evolutionary constraints. many components. For example, in the tween experiment and
 Having described such concepts, we need to interactions between experiment and theory in cell biology, and *From molecular* to modular cell biology Leland H. Hartwell, John J. Hopfield, Stanislas Leibler and Andrew W. Murray Cellular functions, such as signal transmission, are carried out by 'modules' made up of many species of interacting molecules ...

ne debilitating effects $(0, 0)$. memory loss are por –*V* (mV) –*V* (mV) 100 The debilitating effects of memory loss are portrayed in the movie Momento (C Nolan,

0 80 Nature, 1999

understanding through in silico reconstruction. They

This approach is particularly clear in genet-

these studies, geneticists inferred the exis-

Can cells remember?

Differentiated (specialised) cells "remember" to stay differentiated. They do not spontaneously undifferentiate.

A memory module

Positive feedback can be generated by the synthesis of new proteins that cause their own rate of synthesis to increase.

| Example: maturation of frog oocytes

4000 J.E. Ferrell Jr. et al. / FEBS Letters 583 (2009) 3999–4005

Very large single cells around 1mm in diameter.

Progesterone induces the cells to mature after which they acquire a jelly coat and \parallel are laid by the frog.

The last protein of the cascade becomes more active as levels of progesterone increase. activated p42 MAPK Fig. 1. Xenopus oocyte maturation as a switch between two cell fates. Fig. 1. Xenopus oocyte maturation as a switch between two cell fates. p ϕ is taking place and the M-phase control to ϕ is taking and the M-phase cyclins are present but locked b in inactive complexes with \tilde{c} progesterone practical purposes can be considered to be in G2-phase—transcriparrested indefinitely in this state, with all its various opposing protion is taking place and the M-phase contract but locked and the M-phase contract but locked are present but locked and \sim cesses (protein synthesis/degradation, phosphorylation/dephosin in active complexes with \mathcal{L} phorylation, anabolism/catabolism, etc.) in balance. arrested indefinitely in this state, with all its various opposing pro-In response to go a good pitch from the from the from the from the frog pitch \mathcal{F} cesses (protein synthesis) synthesis/degradation, phosphorylation, phosphorylation, phosphorylation, phosphorylation, p (Mos) progesterone In response to gonadotropins released from the frog pituitary, MEK₁ $(p42$ MAPK) maturation Fig. 2. Signal transduction pathways involved in Xenopus oocyte maturation.

state, carries out the first asymmetrical meiotic division, enters

gression from the G2-arrest state to the meiosis $2-$ arrest state is $2-$ arrest state is $2-$ arrest state is $2-$

As opposed to negative feedback where an effect diminishes itself.

n *on* and an *off* state for the same level of prog terone, the system has $\begin{bmatrix} \n\end{bmatrix}$ active than an ''inactive" CDK2 monomer [9]. But an oocyte poson and an off state for the same level of progesterone, the system has individual complex is perfectly all-or-none in its activity state, the population of cyclin B-CDK1 complexes could, in principle, set-4000 J.E. Ferrell Jr. et al. / FEBS Letters 583 (2009) 3999–4005 With both an *on* and an *off* state for the same level of progesterone, the system has memory.

factor, or ''pre-MPF"). Activated cyclin B-CDK1 complexes then

Cyclin–CDK complexes are thought to function as near perfect switches at the level of the individual complex: for example, a fully activated cyclin A-CDK2 complex is approximately 10⁹

sesses !1010 cyclin B-CDK1 complexes, meaning that even if an individual complex is perfectly all-or-none in its activity state,

tle into a nearly continuous range of graded activities. This raises

-fold more

cause the oocyte to re-enter meiotic M-phase.

 $\mathcal{G}^{\mathcal{G}}(\mathcal{G})$ from the G2-arrest state to the meiosis 2-arrest state is 2-arrest state is 2-arrest state is 2-arrest state is 2-arrest state in

in this arrested state until either it is fertilized, which allows it to

state, carries out the first asymmetrical meiotic division, enters

gression from the G2-arrest state to the meiosis $2-$ arrest state is $2-$ arrest state is $2-$ arrest state is $2-$

state, carries out the first asymmetrical meiotic division, enters

ual ooc oocyte-to-oocyte variability was assumed here to corre-

with progesterone. The first

s to be quantified Microfluidic devices allow the responses of individual cells to be quantified $\qquad \qquad \mid$ for individual oocytes treated in controlled dynamic environments

not to operate in extracts (*8*), whereby MAPK or something downstream from

state phosphorylation of MAPK in 190 in-

With time-lapse microscopy, 100s of cells can be followed.

Yeast change the concentration of glycerol to adapt to osmotic stress

Cells must increase internal osmolytes to recover turgor

Upon hyper-osmotic stress, cells:

first:

(i) stop dividing (ii) divert glycolytic flux towards glycerol synthesis (iii) close glycerol exporters

second:

(i) increase expression of the enzymes for glycerol synthesis

The signalling network has a Y-shaped structure with two input branches leading to activation of a MAP kinase, Hog1

Summary

accumulation in the control of the c
The control of the c

Individual cells can show behaviour far from average responses.

Microfluidics allows the study of single-cell responses in controlled dynamic environments.

Signal transduction systems can specialize to particular dynamics of the cellular environment.

Systems biology goes beyond intracellular behaviour: communication and cooperation in bacteria

Bacterial communication is called quorum-sensing.

Levels of autoinducer only become high for sufficiently dense populations – when the population of cells has reached a threshold size, or quorum.

examp S_{system}
An example of positive An example of posi[.]
 and cost will vary for each signalling pathway. Based on the concentration of signal required for a response, An example of positive feedback generating "all-or-none" behaviour.

The structures of LuxR proteins suggests suggests suggests suggests suggests suggests suggests and

respectively. Costs are also related to the quantity of signal produced, though the relationship between amount

it can generally be stated that the amounts produced are inversely proportional to the production costs. An additional consideration in signal production is the specificity of the signal produced. This is in part a measure of the information content of the signal, and specificity \mathcal{A} generally correlates with the cost of production.

side-chain moiety (Gould et al. 2004, Watson et al. 2004, Watson et al. 2004, Watson et al. 2004, Watson et al

REVIEWS

Figure 1 | **Generic scheme for quorum sensing.** In its

by Vibrio fischeri bacteria. H O O O A Hawaiian bobtail squid is luminescent because of quorum sensing —
av
—

is associated with signal production. The three signalproduction biochemical pathways and their associated metabolic costs are presented in FIG. 2 and TABLE 1,

it can generally be stated that the amounts produced are inversely proportional to the production costs. An additional consideration in signal production is the specificity of the signal produced produced. This is in part a measurement of the signal produced by \sim

The bacteria are supplied with nutrients in an internal organ from predators by controlling the level of bioluminescence of the squid. The squid hunts at night and hides its shadow emitted.

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iti
1 d
Im Erwinia carotovora: expressed to appropriately initiate our.

antibioluminescence. V. fischeri: densities in the squid, not in the **respectively.** The bacteria only reach high nal produced, the relationship between and use quotum

open ocean, and use quorum

Sinorhizobium meliloti:

C4-HSL/RhlI

O

(**Figure 2***a* and Eberhard et al. 1981,

Annu. Rev. Cell Dev. Biol. 2005.21:319-346. Downloaded from www.annualreviews.org by University of Edinburgh on 09/17/12. For personal use only.

from Waters & Bassler, 2005

teins and communicate with AHL signals

Autoinducers:

∗∗

3-OH-C4-HSL/LuxM Vibrio harveyi

AI-2/LuxS V. harveyi

AI-2/LuxS

V. harveyi:

Vibrio cholerae:

S. typhimurium: Lsr tranporter

Salmonella typhimurium

Luminescence, type III secretion

Virulence, biofilm production Vibrio anguillarum: Protease production

Photorhabdus luminescens: Antibiotic production Clostridium perfringens: Toxin production

 \sqrt{N} \sqrt{a} ^C ^C CC CC CC ^C ^C ^C \sim

Such models will be repositories of information and enable the cycle of experiment and prediction that underpins systems biology.

Moving beyond individual modules, the first whole-cell model was published in 2012.

 $S_{\rm 5}$

serve as anchors for spiral waves during reentrant arrhythmias.

DNA

patients with heart failure. The structures of the structures of the SSS in the PSS in the PSS in the PSS in the

genes to cells to wh om genes to cells to whole organs $\begin{array}{|c|c|c|}\hline \text{ } & \text{ } & \text{ } \end{array}$ RNA and protein degradation were models were deduced from MRI data, which will hopefully \parallel The future The future: from genes to cells to whole organs cyclase (AC), leading to the production of cyclic

RNA

via the release of neurotransmitters and hormones by

could be simulated.

strips and isolated myocytes, two common experimental preparations. The model includes phenomeno-

orate gene expression, signal trans electrophysiology with three dimensional models of the whole organ. RNA pol Models of the heart incorporate gene expression, signal transduction, and integrate the 28 submodels into a unified model. Although we and others had previously developed methods to inte- $W_{\rm eff}$ is clear that computational modeling has helpediately has h further our understanding of the mechanisms of \vert map well to the underlying biophysics. Thus, param-

Outcomes of the course

You will be able to:

(i) design a systems approach

(ii) understand and predict the dynamics of simple modules

(iii) formulate and simulate mathematical models

(iv) write programs in Python to test biological hypotheses

Lecture Outlines

Week 1 What is systems biology? The general systems approach with examples. Why a systems approach is important for molecular and cellular biology.

Weeks 2-5 Fundamentals of modelling biochemical networks Mathematical modelling of biochemical reactions, the law of mass action, and a discussion on ultrasensitivity, cooperativity, and Hill numbers.

Weeks 6 Modelling gene expression Modelling the rate of transcription for genes controlled by activators and repressors.

Weeks 7-8 Positive feedback and genetic switches Positive feedback and MAP kinase cascades, bifurcations and hysteresis, cellular memory and bistable genetic networks.

Weeks 9-10 Negative feedback and oscillations Circadian rhythms, the Tyson model of the circadian clock in the fruit fly, relaxation oscillations, and oscillations through positive and negative feedback.

Week 11 **Stochastic simulations and model-fitting** Depending on interest.

complete meiosis and commence embryogenesis, or it undergoes

 \mathcal{I} some respects of an unusual example of an unusual example

Structure of the course the cell responds to an external trigger by undergoing an all-or-2.2. Mos, p42 MAPK, and CDK1 activation Although many details remain to be worked out, in broad Systems biology Pythone-induced biology Pythone-induced biology Pythone-induced b oocyte maturation is well-understood (Fig. 2). Progesterone stimulates the translation of the Mos oncoprotein, a MAP kinase kinase kinase (MAPKKK). Active Mos phosphorylates and activates the MAPKK MEK1, which then phosphorylates and activates ERK2 Modelling biochemical networks | Basic program forms of the proteins can initiate maturation in the absence of pro-**Example 2008** Loops, lists, and functions and the contract of (sometimes termed ''latent MPF", for latent maturation-promoting sesses !1010 cyclin B-CDK1 complexes, meaning that even if an individual complex is perfectly all-or-none in its activity state, the population of cyclin B-CDK1 complexes complexes complexes complexes conditions of \mathbb{R}^n tle into a nearly continuous range of graded activities. This raises the question of how the all-or-none character of oocyte maturation arises. Is the process all-or-none at the level of p42 MAPK activation and/or CDK1 activation? And how do these reversible activation processes culminate in an irreversible cell fate change? 2.3. The all-or-none, irreversible response depends upon positive Python Analysis of individual oocytes treated with various concentrations of progesterone demonstrated that the steady-state response of the oocyte's MAPK cascade is essentially all-or-none (Fig. 3). At ince concentrations of progesterone, individual oocytes \mathbf{p} were found to have either all of their p42 MAPK non-phosphorylated or all of it phosphorylated. Thus, somewhere between the $\frac{1}{2}$ progesters stimulus is converted to a $\frac{1}{2}$ MAPK response. Moreover, the steady-state response of MAPK to microinjected Mos is also all-or-none [10]. This demonstrates that the MAPK cascade can generate an all-or-none response, not simply propagate one. A plausible mechanism for the generation of expression **Explorering** Scientific computing with arrays ¹ There is some disagreement on whether the Mos/MEK/MAPK cascade is required Modelling gene expression Although many details remain to be worked out, in broad outline the signaling network that mediates progesterone-induced oocyte maturation is well-understood (Fig. 2). Progesterone stimukinasy. Active Mos phosphorylates the Mose phosphory MAPKK MEK1, which then phosphorylates and activates ERK2 (which in Xenopus is often called p42 MAPK). Inhibitors of these MAPK cascade proteins inhibit oocyte maturation, and activated phorylation and activation of cyclin B-CDK1 complexes (sometimes termed ''latent MPF", for latent maturation-promoting tle into a nearly continuous range of graded activities. This raises the question of how the all-or-none character of oocyte maturation arises. Is the process all-or-none at the level of p42 MAPK activation and/or CDK1 activation? And how do these reversible activation processes culminate in an irreversible cell fate change? 2.3. The all-or-none, irreversible response depends upon positive \mathbf{A} tions of progesterone demonstrated that the steady-state response of the oocyte's MAPK cascade is essentially all-or-none (Fig. 3). At intermediate concentrations of progesterone, individual oocytes were found to have either all of their p42 MAPK non-phosphory-paper all of the interest of the interest of the lated or all of it phosphorylated. Thus, somewhere between the progesterone receptor and the bottom of the MAPK cascade, a graded ''analog" progesterone stimulus is converted to a ''digital" the MAPK cascade can generate an all-or-none response, not simply propagate one. A plausible mechanism for the generation of the all-or-none response was suggested by the discovery that, in oocytes, p42 MAPK and CDK1 are organized in positive feedback Ultrasensitivity and allostery **and all accord in the Most case is required** in Plotting data or dispensable dispensable data induced on the proteing data Enzyme kinetics Biochemical switches Negative feedback Genetic oscillators Stochastic gene expression Basic programming Generating random numbers Simulating biochemical networks Stochastic simulations Fitting data

 $C_{\rm{C}}$ complexes are thought to function as near perfect to function as near p switches at the level of the individual complex: for example, a fully activated cyclin A-CDK2 complex is approximately 10⁹ active than an ''inactive" CDK2 monomer [9]. But an oocyte pos-

active than an ''inactive" CDK2 monomer [9]. But an oocyte possesses !1010 cyclin B-CDK1 complexes, meaning that even if an individual complex is perfectly all-or-none in its activity state, the population of cyclin B-CDK1 complexes could, in principle, set-

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