



qbio
quantitative
biology

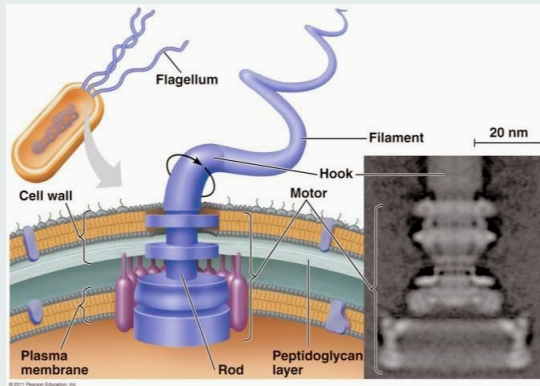
INTRODUCTION TO QUANTITATIVE BIOLOGY

Overview on the field

17TH SEPTEMBER 2024

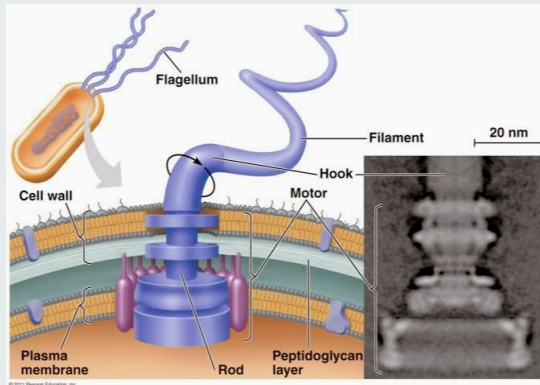
Luca Ciandrini (luca.ciandrini@umontpellier.fr)

Biological System



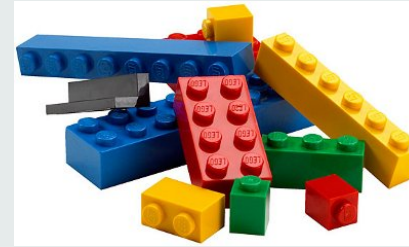
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Biological System



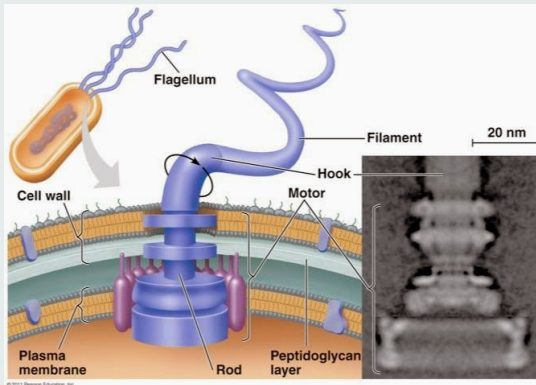
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Components



Characterisation of
biological parts
(Toolkits)

Biological System



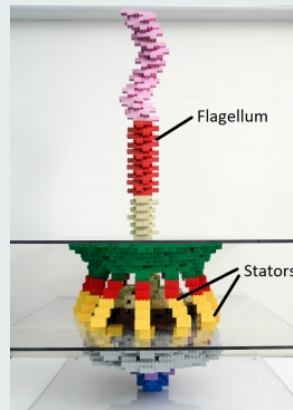
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Components



Characterisation of biological parts (Toolkits)

Systems Biology



Imperial College of London

“Systems biology is the study of biological systems whose behaviour cannot be reduced to the linear sum of their parts’ functions. Systems biology does not necessarily involve large numbers of components or vast datasets, as in genomics or connectomics, but often requires quantitative modelling methods borrowed from physics.”

from nature.com

WHAT IS QUANTITATIVE BIOLOGY?



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qbio \neq biology + number

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numbers and tools to obtain predictions and biological understanding

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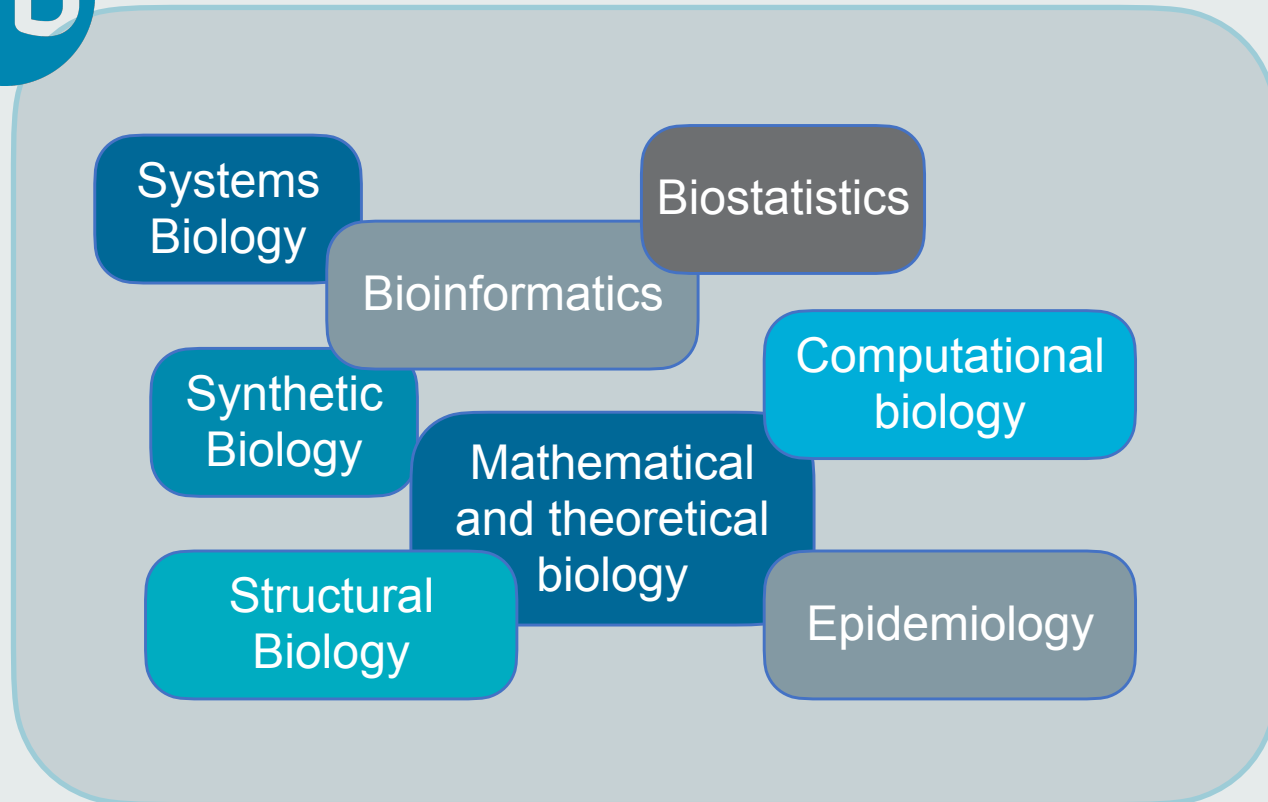
qbio \neq biology + number

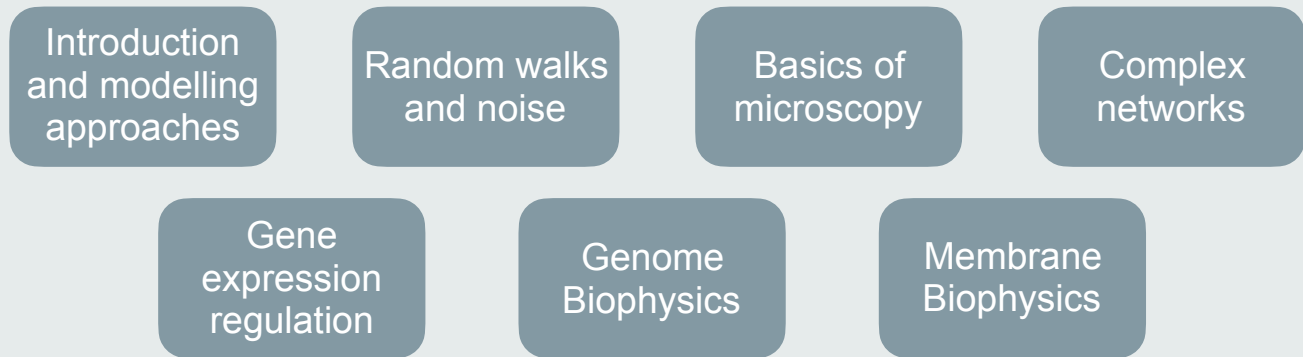
qbio \neq biology + quantitative tools

numbers and tools to obtain predictions and biological understanding



Quantitative Biology





Timetable. Look at our GDoc.

We will give you some material (videos, pdf,...) to revise **before each lecture**.

Please check the GitHub of the course*:

<https://github.com/qbiomaster/qBioMaster-introduction>

IMPORTANT: learn how to manage your time!

**inform us of any incoherence with the GDoc*

Assignments

We mainly *work on projects*, with short reports that you will have to return and that we will grade.

5 assignments x 20%. More in details

- 2 organised by Luca (Modelling, Gene expression,...)
- 2 organised by Marcelo (Genome biophysics, microscopy,...)
- 1 organised by Pierre-Emmanuel (membrane biophysics)

We have different formats (ask the person!)

Week 1

We start from Wilkinson's review



Stochastic modelling for quantitative description of heterogeneous biological systems

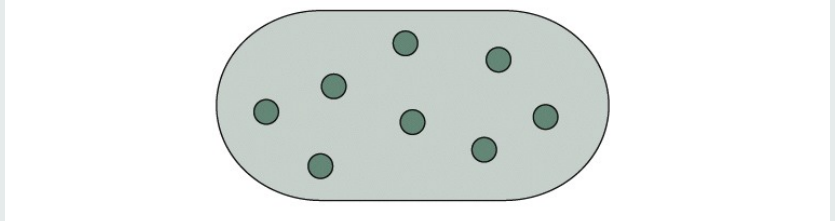
Darren J. Wilkinson

Abstract | Two related developments are currently changing traditional approaches to computational systems biology modelling. First, stochastic models are being used increasingly in preference to deterministic models to describe biochemical network dynamics at the single-cell level. Second, sophisticated statistical methods and algorithms are being used to fit both deterministic and stochastic models to time course and other experimental data. Both frameworks are needed to adequately describe observed noise, variability and heterogeneity of biological systems over a range of scales of biological organization.

NOT EVERYTHING CAN BE MODELLED WITH ODE...



Ex: Cell-to-cell variability



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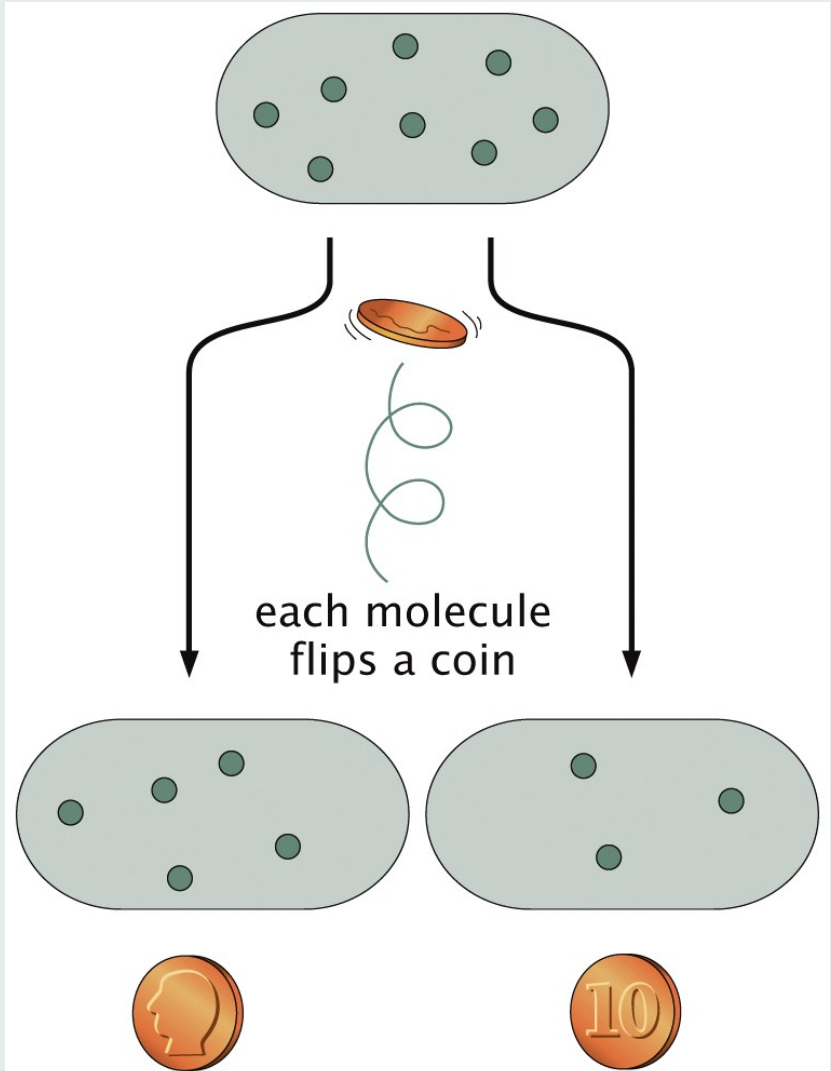


Figure 2.7a Physical Biology of the Cell, 2ed. (© Garland Science 2013)

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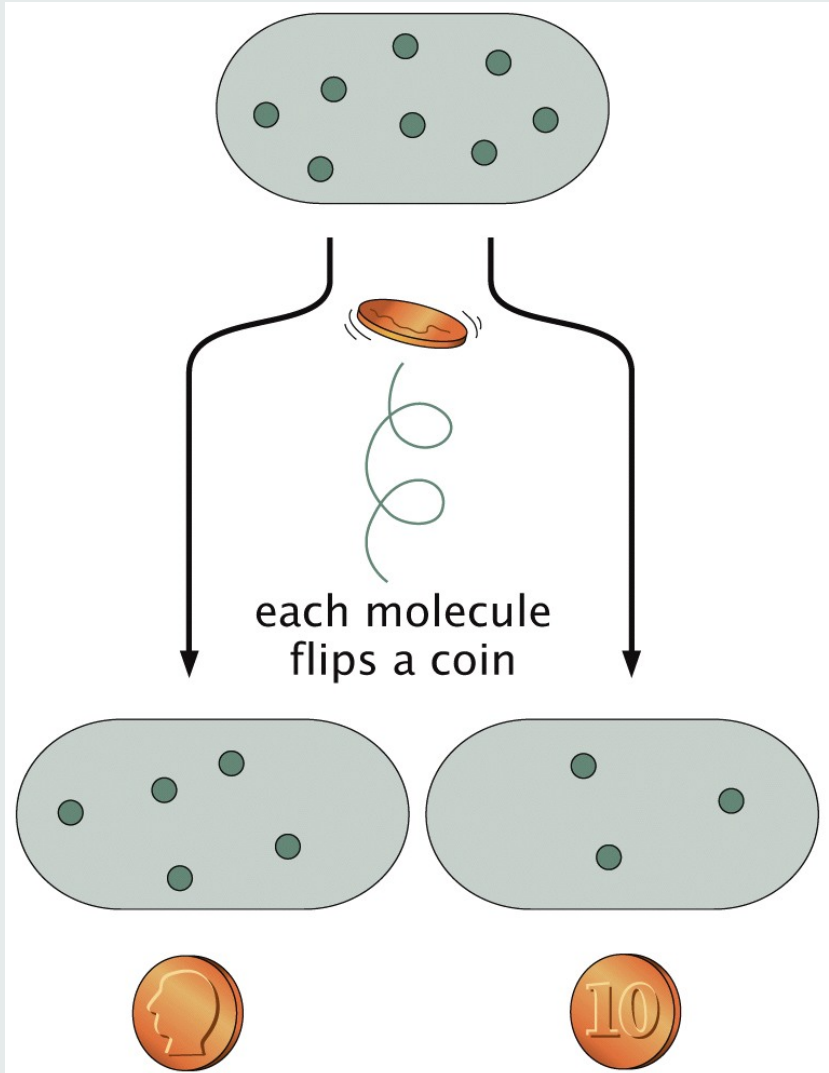
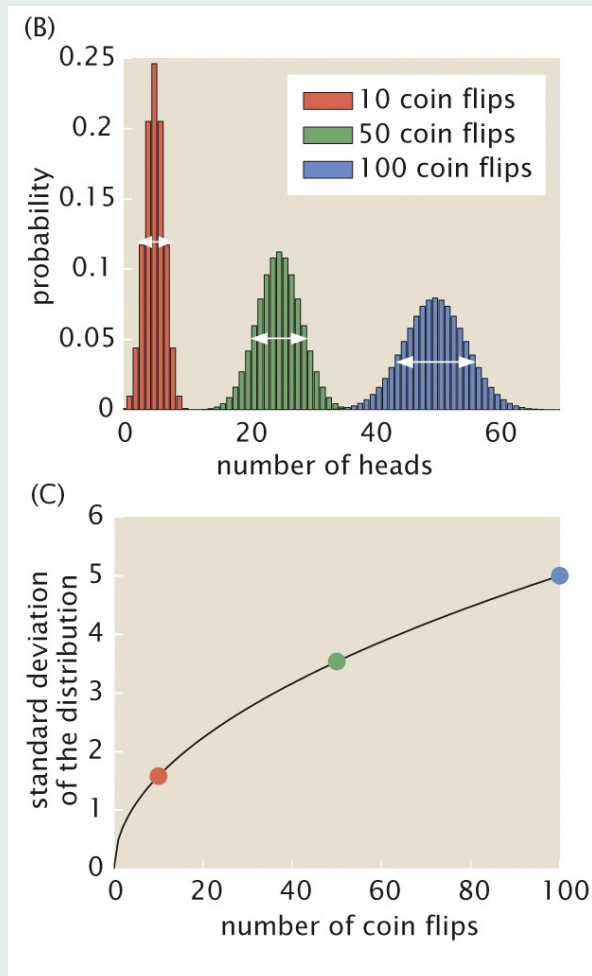


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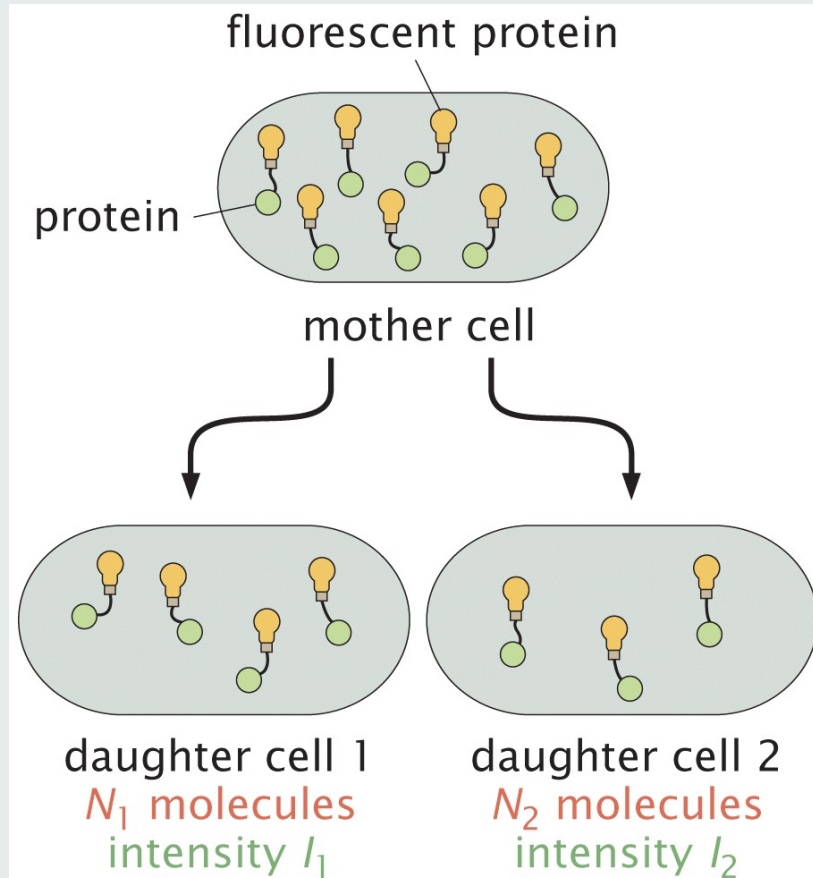


Figure 2.10a Physical Biology of the Cell, 2ed. (© Garland Science 2013)

We can derive that:

$$\langle (I_1 - I_2)^2 \rangle = \alpha I_{tot}$$

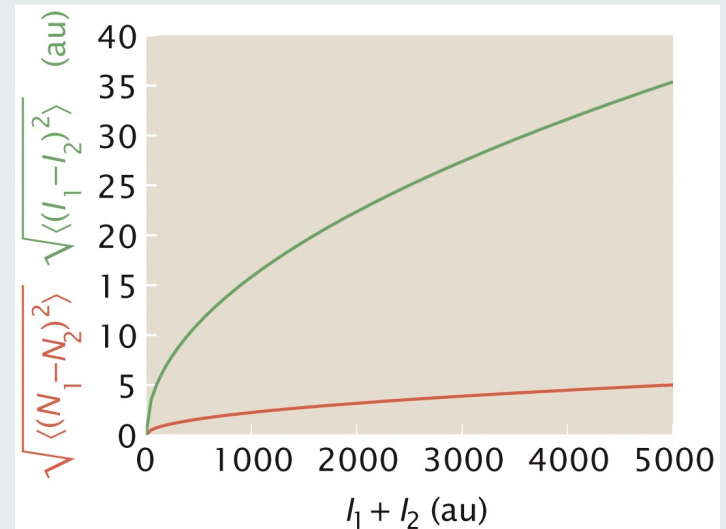


Figure 2.10b Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Data from Rosenfield et al., *Science* 307:1962 (2005)

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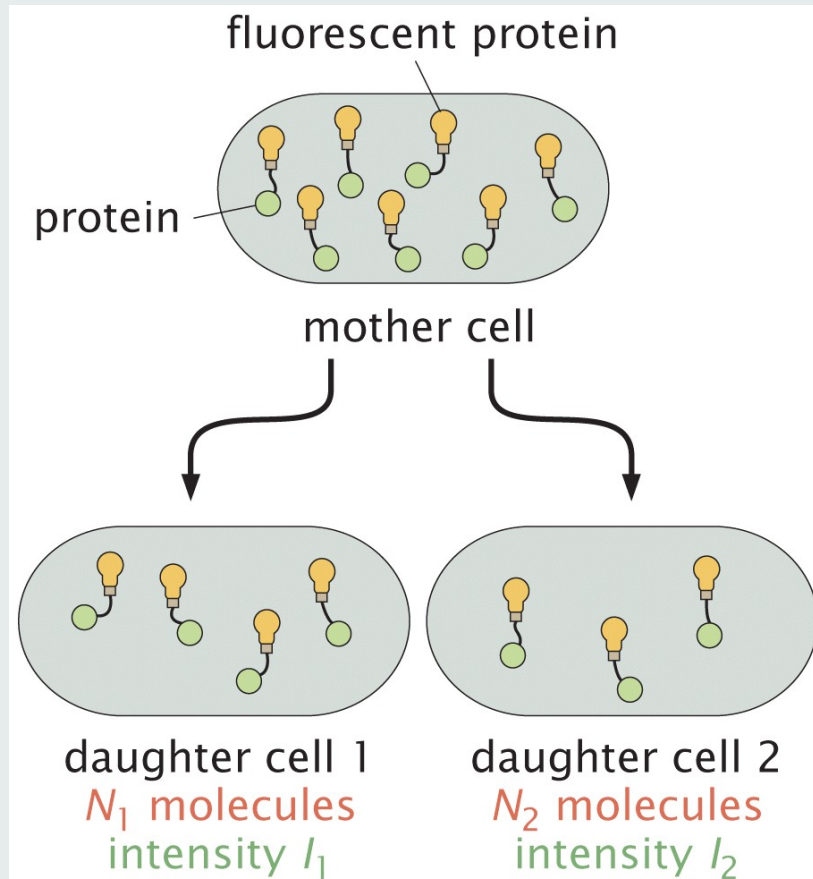


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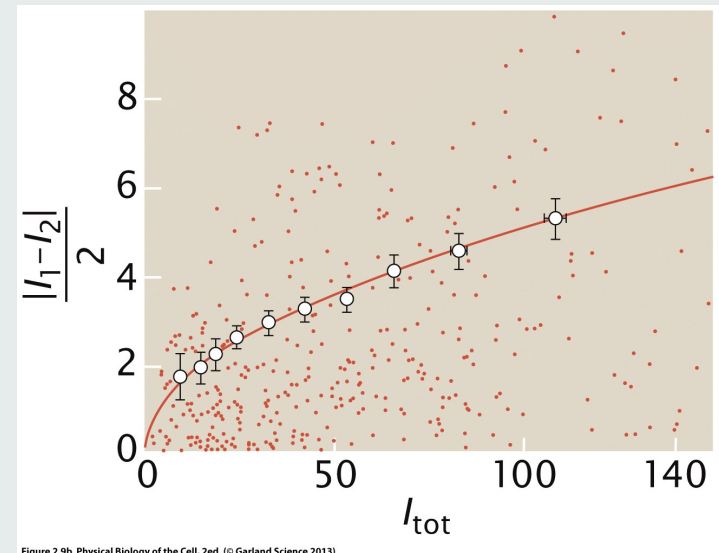


Figure 2.9b Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Data from Rosenfield et al., *Science* 307:1962 (2005)

DO IT YOURSELF (*IN SILICO*)



1. Choose N (and α) and compute I_{tot}
2. Generate N random numbers to mimic cellular repartition (similar to what we did in the bootcamp...)
3. Compute the intensities of daughter cells I_1 and I_2
4. Repeat the “experiment” M times
5. Do the same for a different N

