Institute of Theoretical Physics
São Paulo State University

Precision and Emergence in the Physics of Biological Systems

IV Journeys Into Theoretical Physics
Prof. William Bialek
July 6-12, 2019
Níckolas de Aguiar Alves

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Professor: William Bialek, Princeton University
Notes by: Níckolas de Aguiar Alves

Level: Undergraduate
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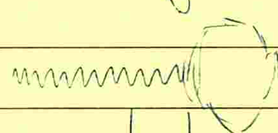
Precision and Emergence in the Physics of Biological Systems

William Bialek - Princeton University

Nicholas Alves
IFUSP
alves.nicholas@usp.br
2019

Biology & Physics recent
Rayleigh: how do we perceive sound? → how do we know where it comes from

Big ~~Small~~ frequency small wavelenght
↳ "acoustic shadow"
↳ higher volume in one ear



low volume
high volume

wbialek@princeton.edu

Small frequency: large wavelenght
↳ only phase differences
↳ we are phase deaf, and thus can't hear where large wavelenghts come from

For a physicist: Biology is interesting, but very messy
→ though biologists act like this is intrinsic, nowadays there is a huge gamma of topics that can be treated with the same organization as in Physics

This talk: precision and emergence

emergence → life is more than the sum of the parts, life is not a molecule
↳ the properties of cells emerge from lots of molecules, the properties of which emerge from lots of parts, and etc
→ known in Physics
↳ Stat Mech

precision → although Bio is messy and sloppy, biological systems are extremely precise
↳ we can see individual photons

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Precision: ecolocation measures 10ns of difference
we can perceive μs of difference between our ears
molecule counting
higher level examples:
"measure" the velocity of movement of something being seen

Precision


catterpillar
↳ Segments with approx same size
How does the animal does it?

Fruit-fly → breeds fast, good to experiment

egg → larva in 1 day
Concentration of certain molecules → measured after 3h

concentration


→ blueprints for the segments

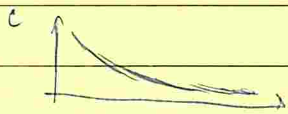
Phys: how much do the peaks vary from embryo to embryo? → $\delta x \lesssim 0.01 L$ ↳ size of embryo
→ "cousin" embryos & no genetic effects

Periodic pattern
Turing: perhaps it comes from random + symmetry?
↳ Nope, for the mother breaks the symmetry at the beginning

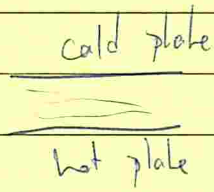

messenger RNA is put at the head-to-be

Concentration
$$\partial_t c = D \nabla^2 c - \frac{c}{\tau}$$
$$-D \left.\frac{\partial c}{\partial x}\right|_{x_0} = Q \text{ (source)}$$
$$c(x, t\to\infty) \approx c_0 e^{-x\lambda}, \quad \lambda = \sqrt{D\tau}$$

Measure the concentration:
develop antibodies to the molecule, add fluorescence. Pick the egg, cook slowly, make holes and add antibodies. Measure fluorescence

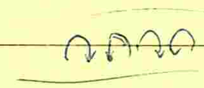


Fluids:



Small gradient: conduction

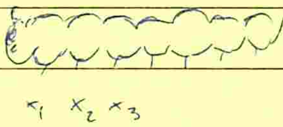
Big gradient: periodic convection

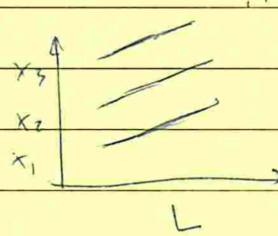


perhaps wrong arrow, but that's the idea

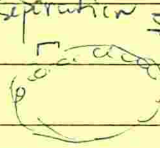
↳ Not the case for Bio → symmetry broken at start

Different sized embryos always the same number of stripes, even if another could be put in





we don't know



separation ~~smaller~~ greater than 0.01 L → each molecule knows where it is

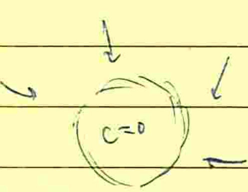
Difference in concentration needed to make a difference: 10%

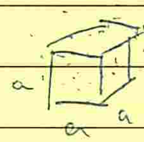
↳ how can different embryos look the same?

↳ bio systems can be precise to that point

What's the smallest Δc you can measure?

c





$\bar{n} = c\, a^3$

$\delta n \sim \sqrt{\bar{n}}$

$\frac{\delta c}{c} \sim \frac{1}{\sqrt{ca^3}} \frac{1}{\sqrt{T/\tau_c}} \sim \frac{1}{\sqrt{Dac\,T}}$

$\nabla c \sim \frac{c}{a}$

$\int d_S \nabla c \cdot D \sim D \frac{c\,a^2}{a}$

$\sim D c a$

wait τ_c for molecules to exchange and get a new sample

$D \tau_c \sim a^2$

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Regulating "gene "expression"

protein $D \sim \mu m^2/s$

$a \sim 3\,nm$

$c \sim nM = 10^{-9} \frac{6 \cdot 10^{23}}{L}$

$\sim 0.6 \frac{1}{\mu m^3}$

$Dac \sim \frac{1}{300}\, Hz \sim \frac{1}{5\, min}$

$\frac{\delta c}{c} \sim 1$ ⇝ we are missing something

(I've skipped somethings)

Where is each cell?

there is also a correlation between the distributions that seems to make out for the confusion

actually, you mightht be a bit confused

the problem

$x \in [0, L]$, $p(x) = \frac{1}{L}$

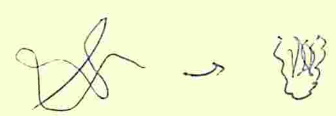
$y = x + \xi$, $\langle \xi^2 \rangle = \sigma^2$

$I(y \to x) = \log\left(\frac{L}{\sigma} \frac{1}{\sqrt{2\pi e}}\right)$

In Physics, we take small deviations seriously

Emergence

i) proteins



protein folding problem

polymer of aminoacids

$aa_1\ aa_2 \dots aa_n$ sequence of aminoacids

For random cases, we would get glass when cooling down

then proteins are organised, and thus they don't look glassy physically

usual folding problem $P(\vec{x} | \{s_i^\alpha\}) = e^{-\beta E(\vec{x}, \{s_i^\alpha\})}$

structure, sequence

but $P(\{s_i^\alpha\} | \vec{x})$? what are the sequences compatible with the structure?

$(s_i^\alpha) \Rightarrow p \sim e^{\sum_{i\alpha} h_i^\alpha s_i^\alpha}$ If we pick some models on the computer and built the proteins, we have problems

$(s_i^\alpha s_j^\beta)$ ↳ the changes we make must be compatible ↳ there is correlation

$$p \sim \exp\left(\sum h_i^\alpha s_i^\alpha + \frac{1}{2}\sum J_{ij}^{\alpha\beta} s_i^\alpha s_j^\beta\right)$$

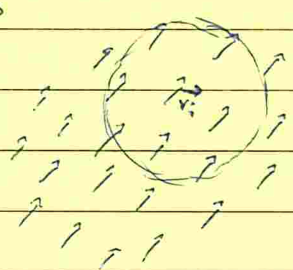
↳ interaction term

Bio: every detail matters ↓ false, we can manipulate and experiment

Phys: details shouldn't matter ↓ false, sometimes things go very wrong

actually, it is somewhere in the middle

ii) Flock of birds



$p(\{\vec{v}_i\})$?

Guess: birds must be trying to make their velocities similar to their neighbors ⟶ local interactions

$$Q = \frac{1}{N}\sum_i \left(\vec{v}_i - \frac{1}{n_c}\sum_{j \in N_i} \vec{v}_j\right)^2 \qquad |N_i| = n_c$$

$$\bar{v} = \frac{1}{N}\sum_i |\vec{v}_i|, \quad \overline{v^2} = \frac{1}{N}\sum_i |v_i|^2$$

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$$p \sim \frac{1}{Z} \exp\left(-\lambda_1 \sum (v_i - \frac{1}{n}\sum_j v_j)^2 - \lambda_2 \sum |v_i| - \lambda_3 \sum |v_i|^4\right)$$

Draw a distribution, compute properties and compare

↳ correlation functions

continuous ✓

Direction: spontaneous symmetry breaking with local interactions

Amplitude: no symmetry