

# Mathematical modelling introduction

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basic models of biological  
networks

# why do we make models?

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# nature and complexity – static pattern formation, simple mechanisms

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Lämmel, M., Meiwald, A., Yizhaq, H. et al. Aeolian sand sorting and megaripple formation. *Nature Phys* **14**, 759–765 (2018).

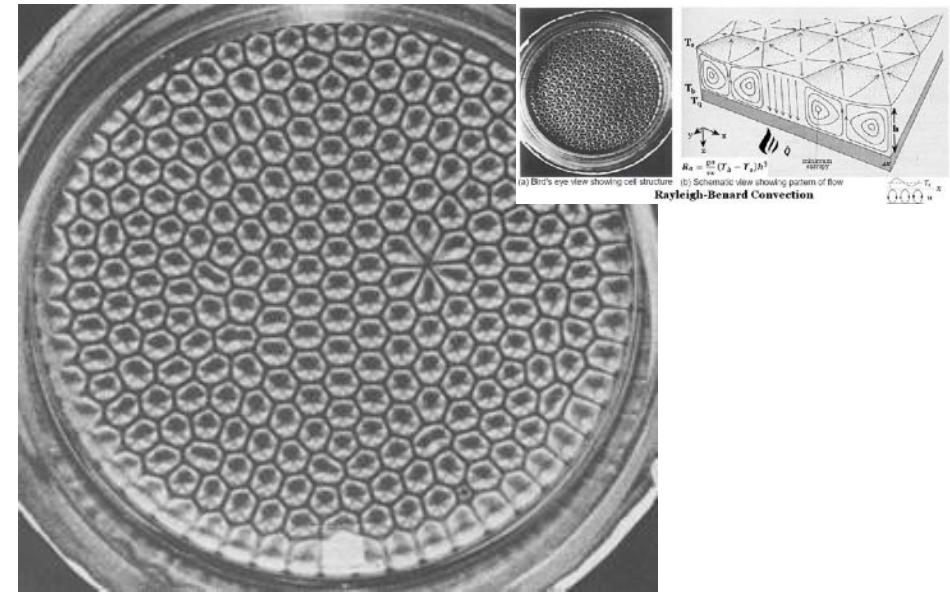


# nature and complexity – dynamic pattern formation, simple mechanisms, physicochemical systems

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Belousov-Zhabotinski reaction  
waves of chemicals in a chemical reaction  
in a lab petri dish



Rayleigh-Bénard convection  
pattern formation in water film exposed  
to temperature gradient

nature and complexity  
– dynamic pattern  
formation, simple  
mechanisms,  
collectives of agents

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a bird flock of starlings



ants making a bridge



a school of fish

nature and complexity –  
static pattern formation,  
unknown mechanisms

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computer generated  
Barnsley fern  
[https://en.wikipedia.org/wiki/Barnsley\\_fern](https://en.wikipedia.org/wiki/Barnsley_fern)

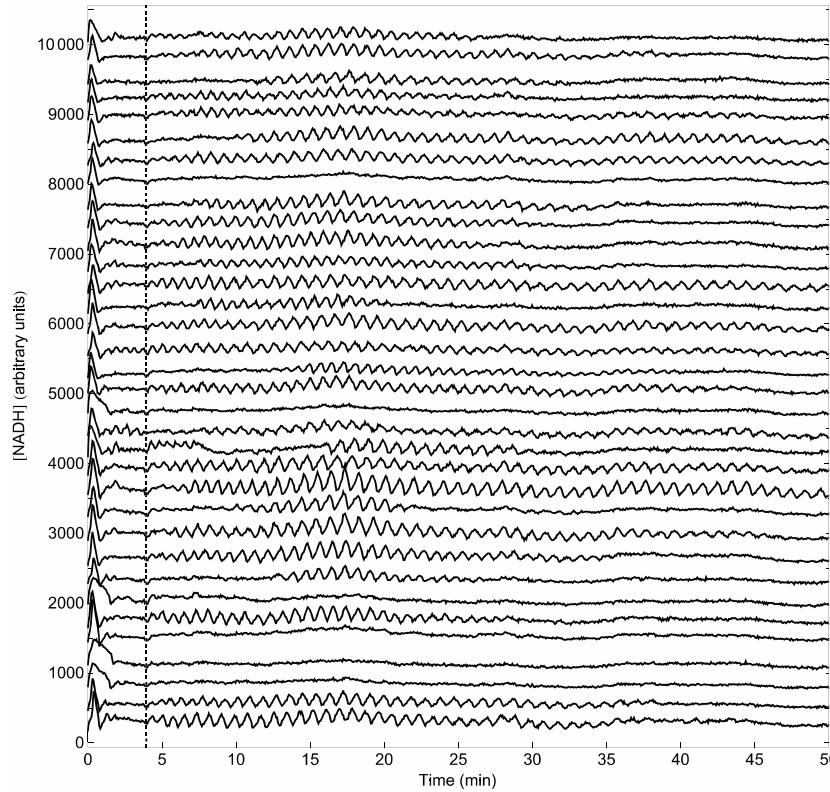


# nature and complexity – dynamic pattern formation, complex mechanisms

## C. elegans worm development

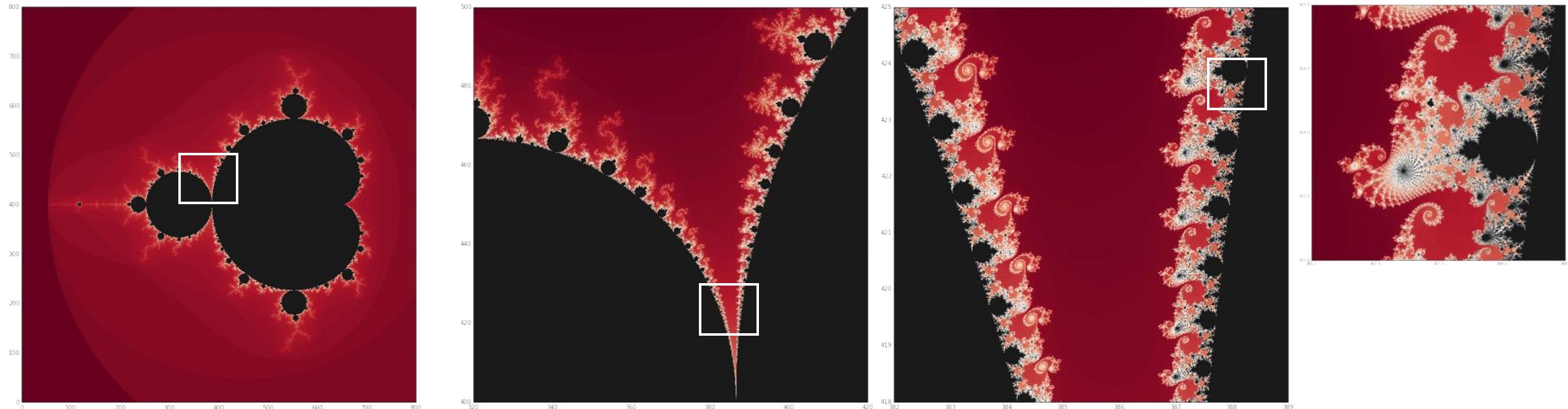
servable oscillations should dampen initially, but subsequently should reappear as the synchronization becomes effective. Fig. 1 shows that reappearance was observed. Because the oscillations in the mixed cell populations were sustained (over 30 cycles; data not shown) and of the same amplitude as before mixing, the re-emergence of oscillations cannot be explained as an interference pattern due to a slight frequency difference between the two subpopulations. This finding and the observation that it takes some time before the oscillations re-emerge after mixing, is at variance with earlier reports concerning transient oscillations in mixed cell populations [7, 17]. This difference with the previous studies may well arise from the rather subtle dependence of the dynamic behaviour of yeast metabolism on the history of the yeast cells [6, 7].

The requirements for any intercellular-signalling mechanism are, (a) the signal has to be sensed by the cells; (b) the signal has to be emitted; and (c) the signal has to pass through the



oscillating yeast cells, communicating with each other

# mathematics and complexity – fractals, Mandelbroth set



# nature and complexity

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complex behavior emerges from interactions

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pattern formation

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self-organisation

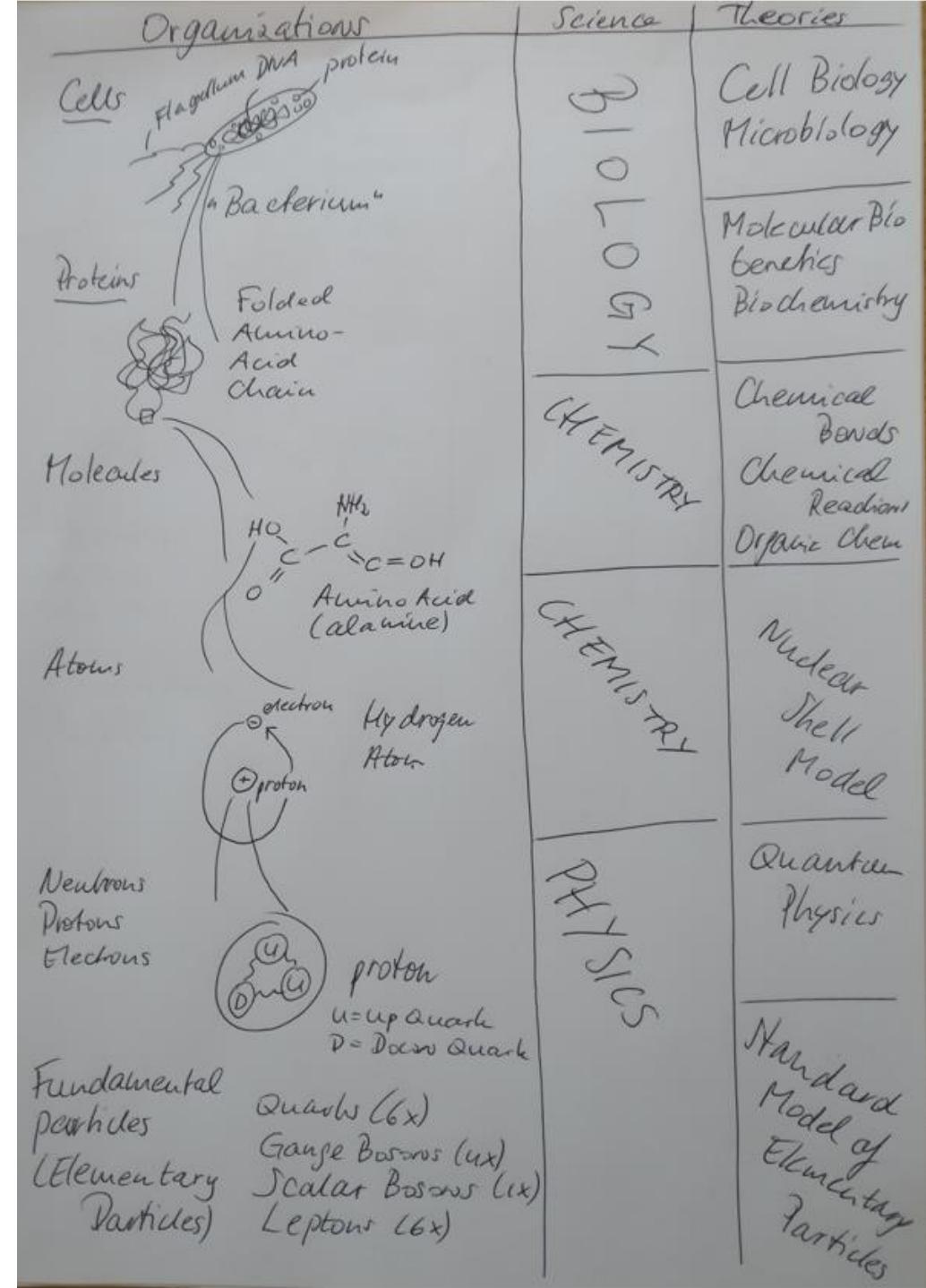
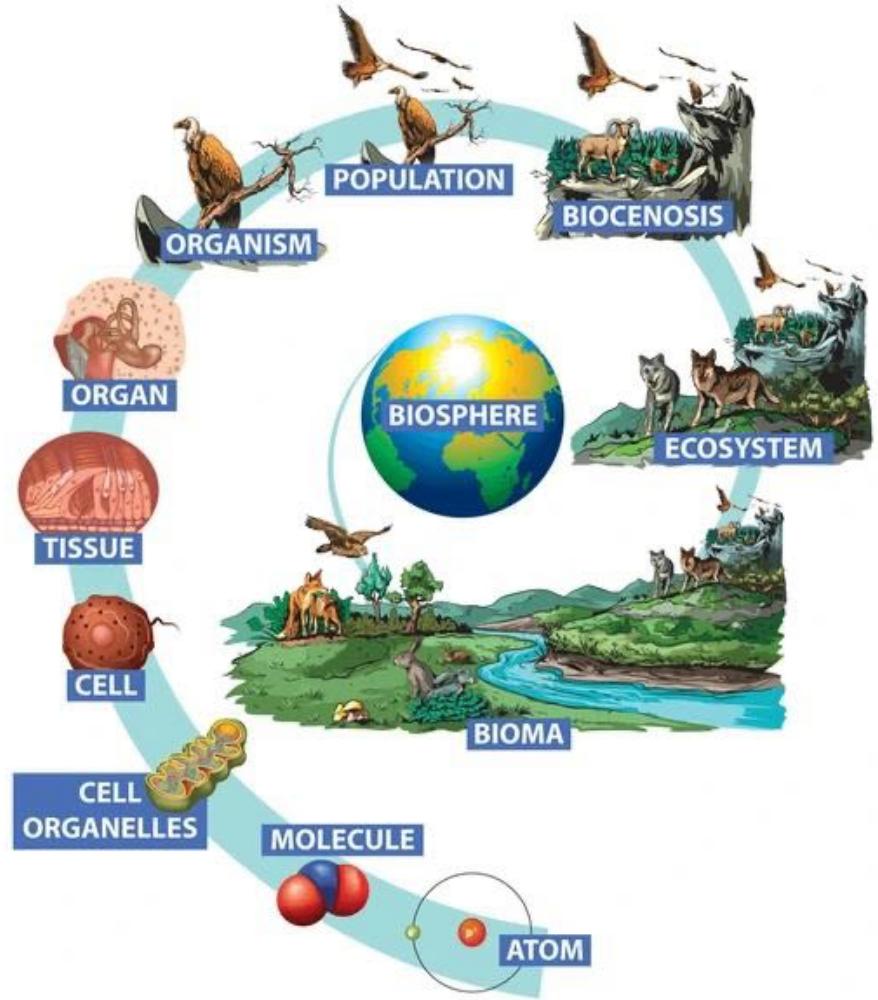
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underlying mechanisms vary from simple to complex

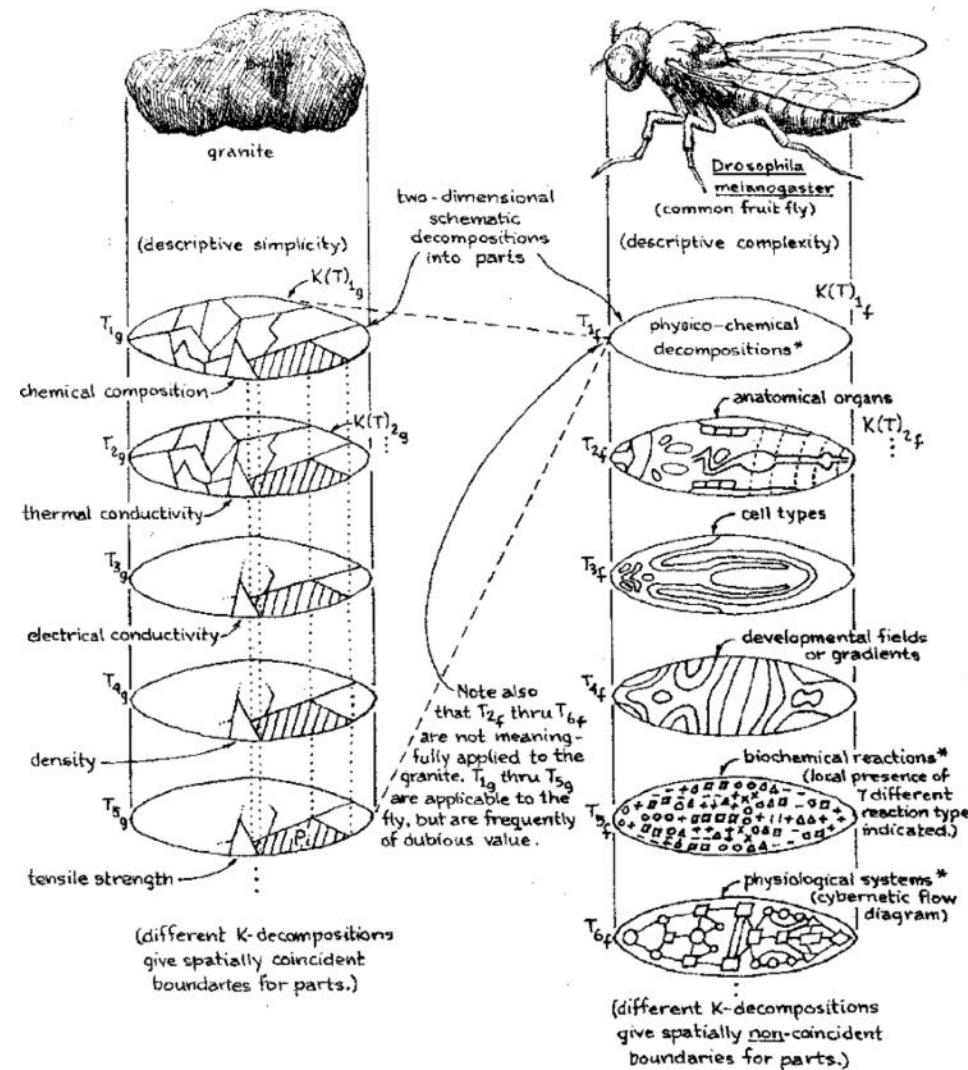
how is nature organised such  
that complexity can arise?

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# nature – a nested hierarchy

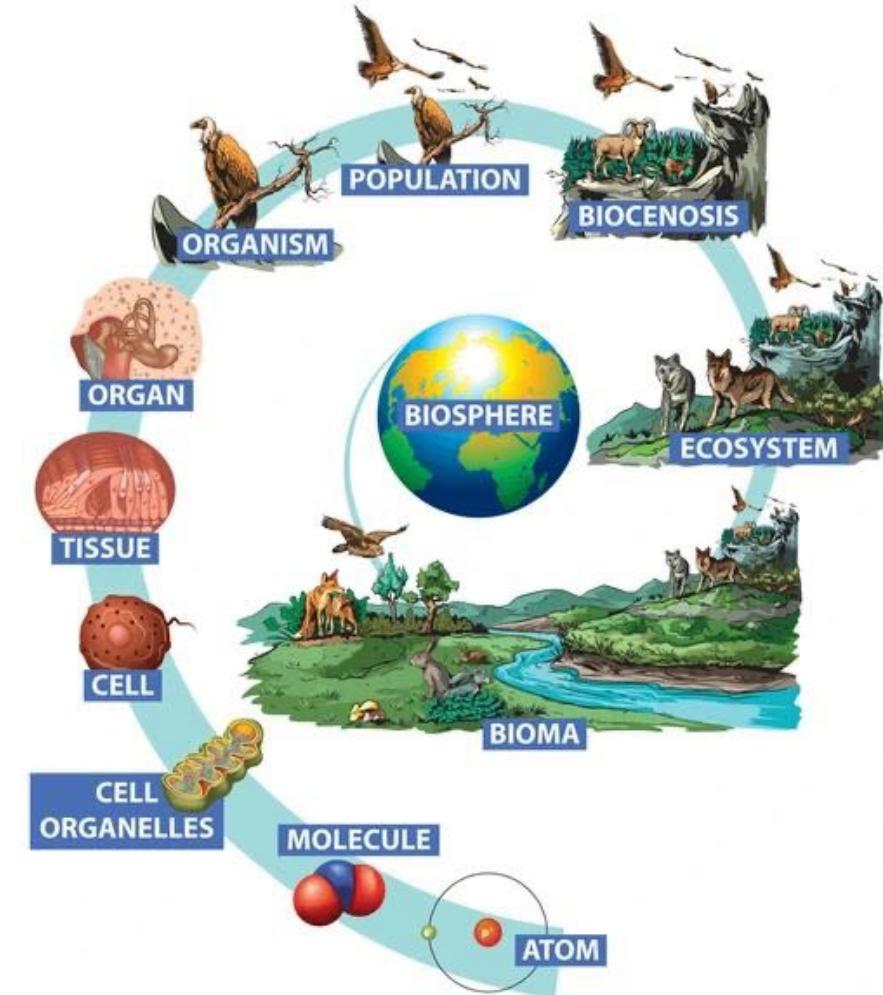


# Complexity – systems vary in complexity



Complexity emerges  
from interactions  
between the lower  
level constituents of  
systems

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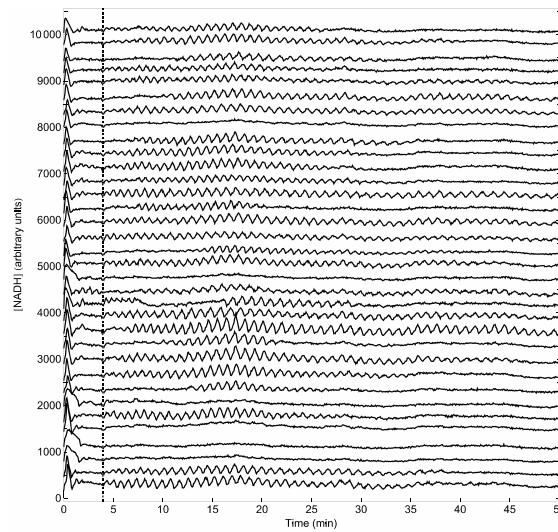
# why do we make models?

- to forecast; to make predictions
- to engineer new technologies and medicine
- to understand the principles of nature
- ....
- ....

many models aim to predict the emergent behavior of systems, given their parts and interactions



chemical reactions  
and diffusion



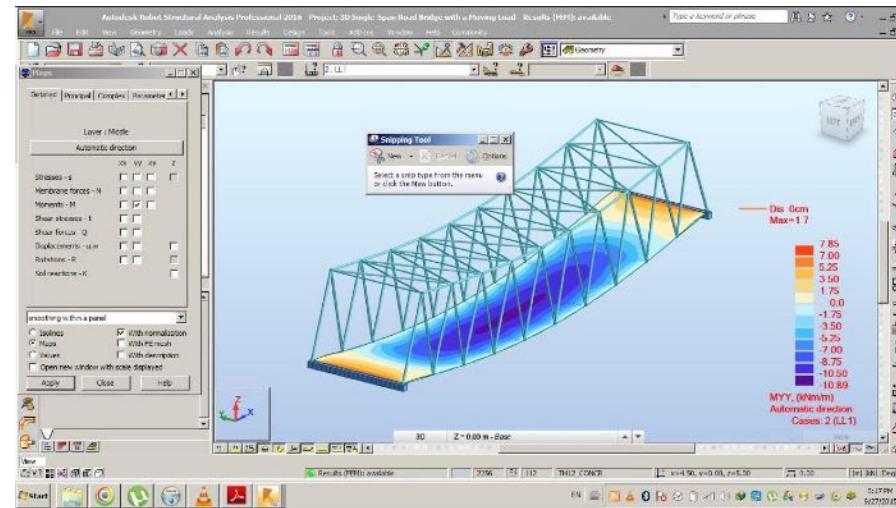
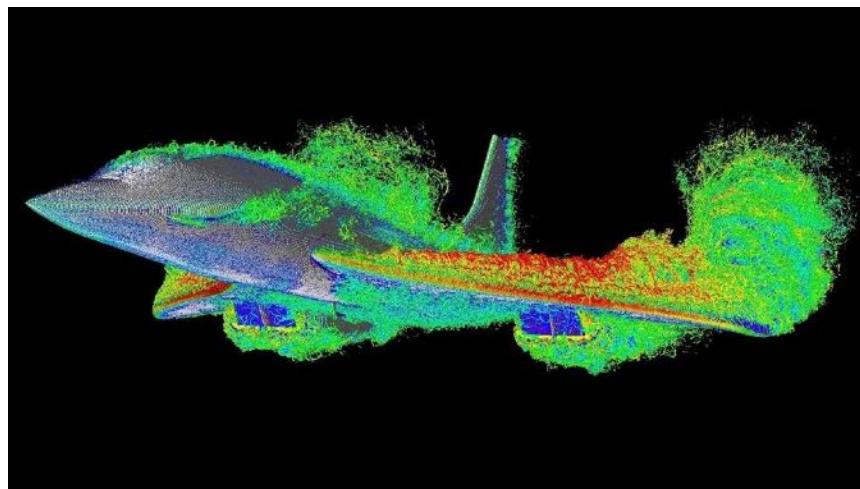
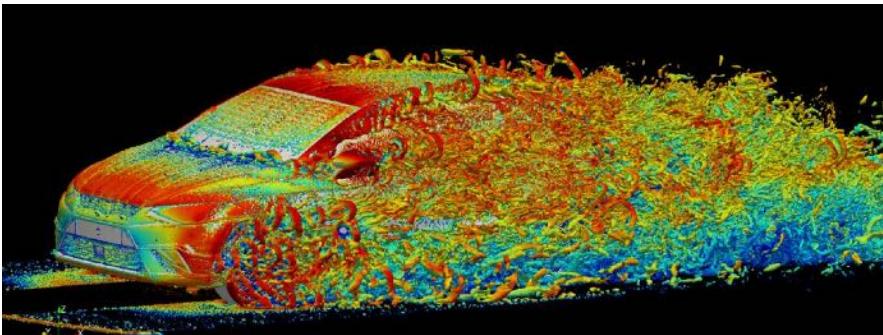
cellular metabolism  
and cell-cell interactions



flying birds and  
neighbour-neighbour interactions (rules)

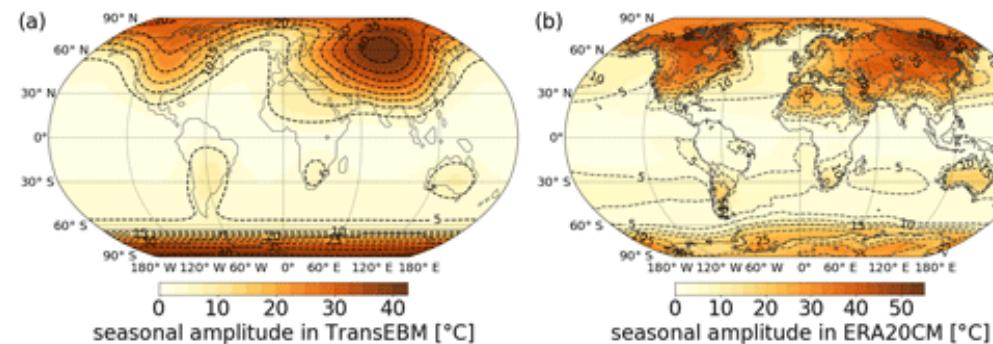
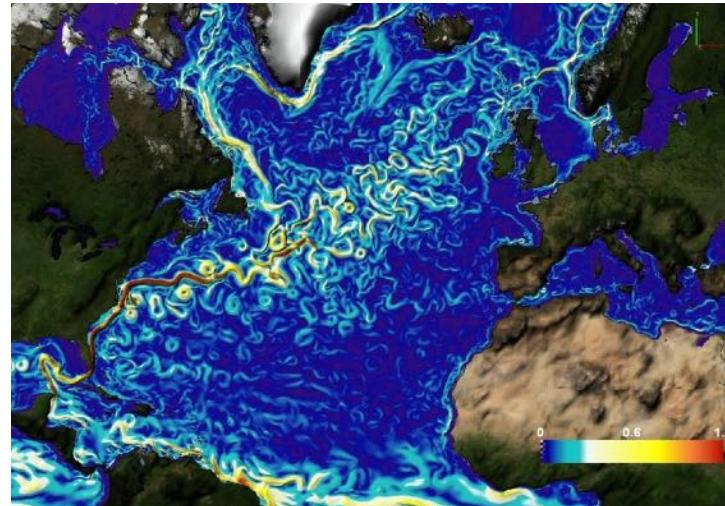
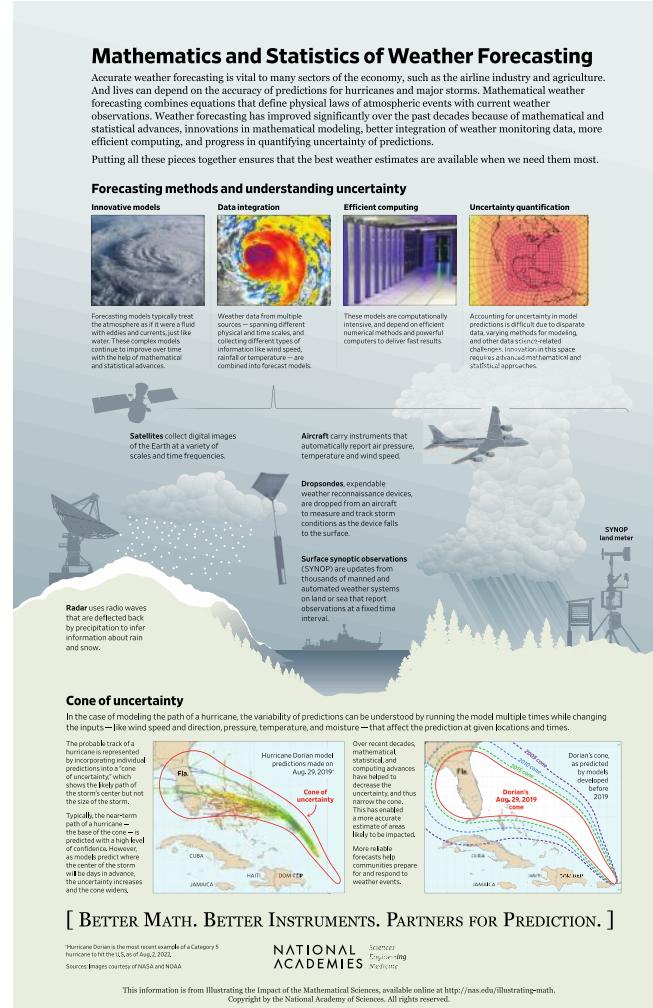
# Models in science and engineering

## *Mechanical engineering*



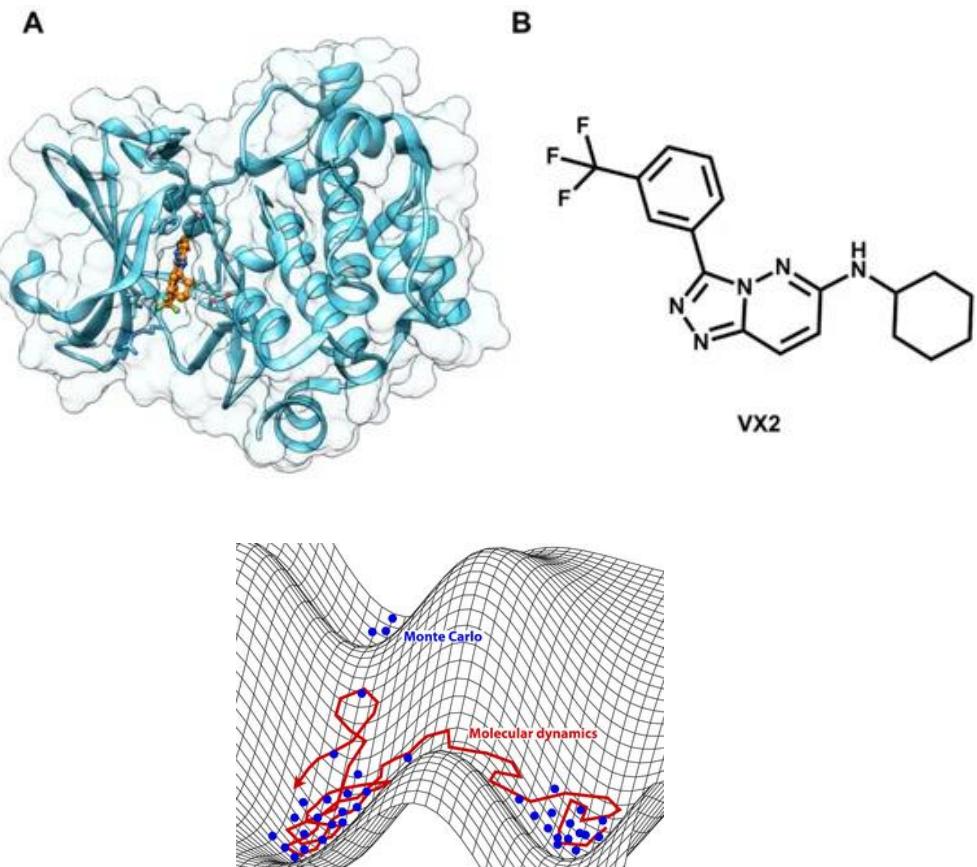
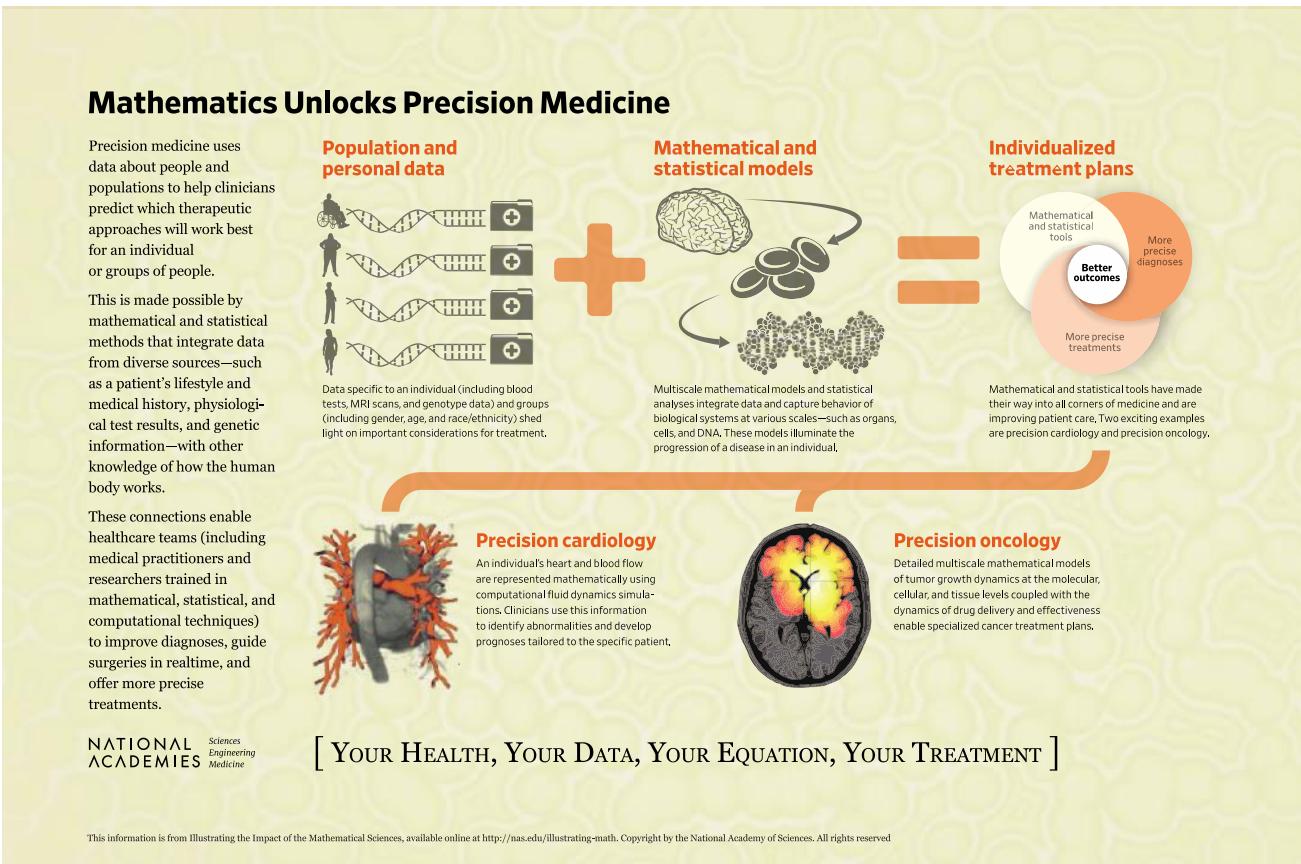
# Models in science and engineering

*Weather forecasting, ocean currents, temperature distribution earth*



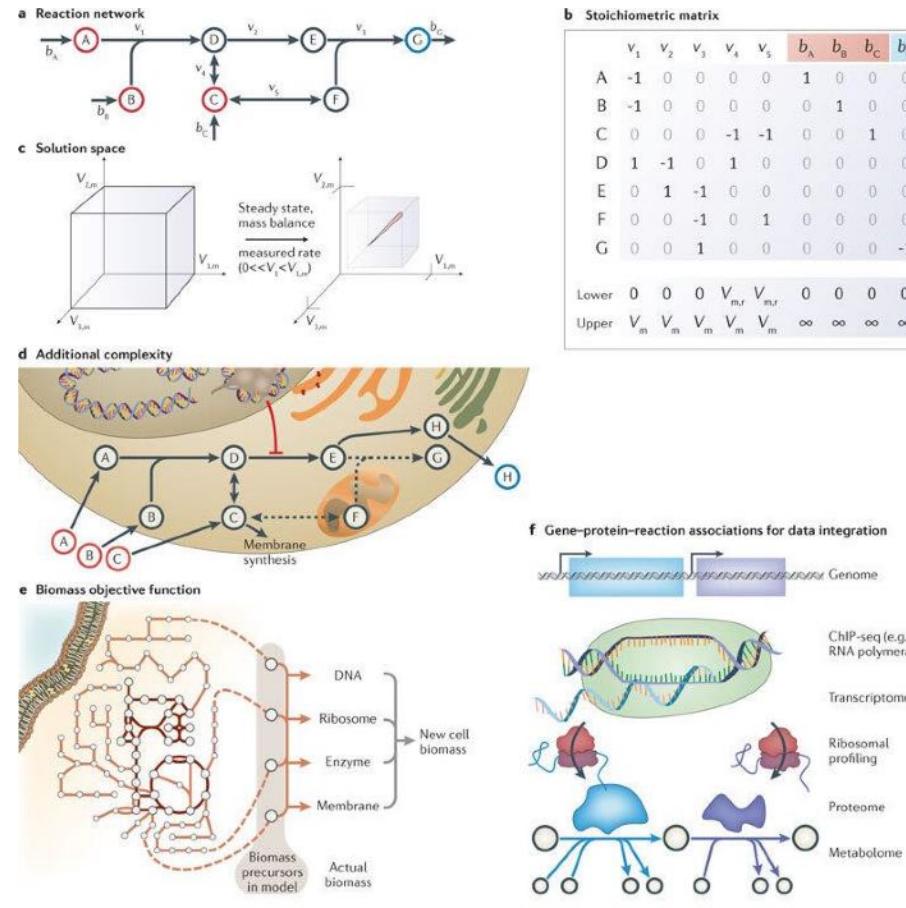
# Models in science and engineering

## Medicine



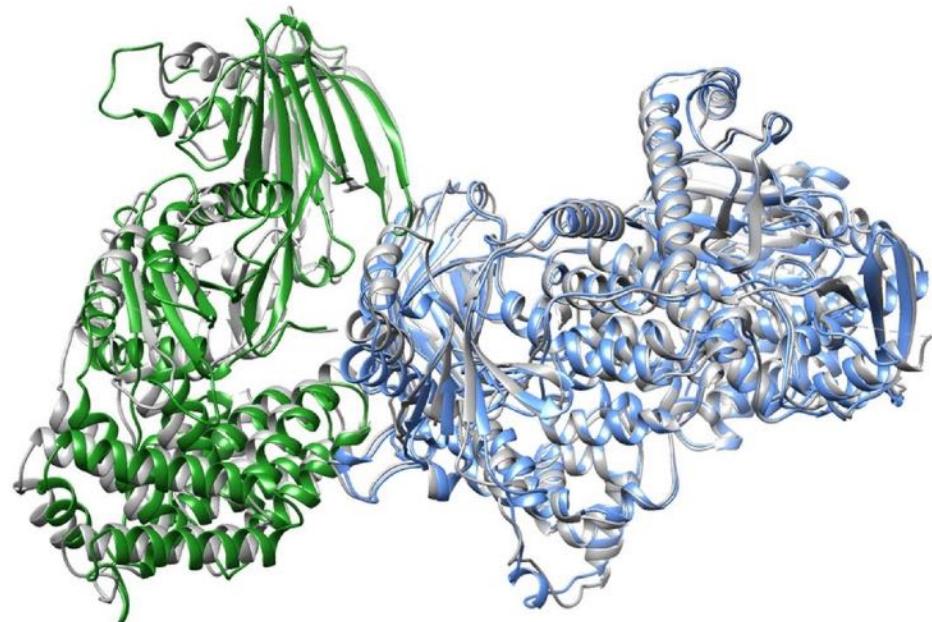
# Models in science and engineering

## Metabolic engineering and biotechnology



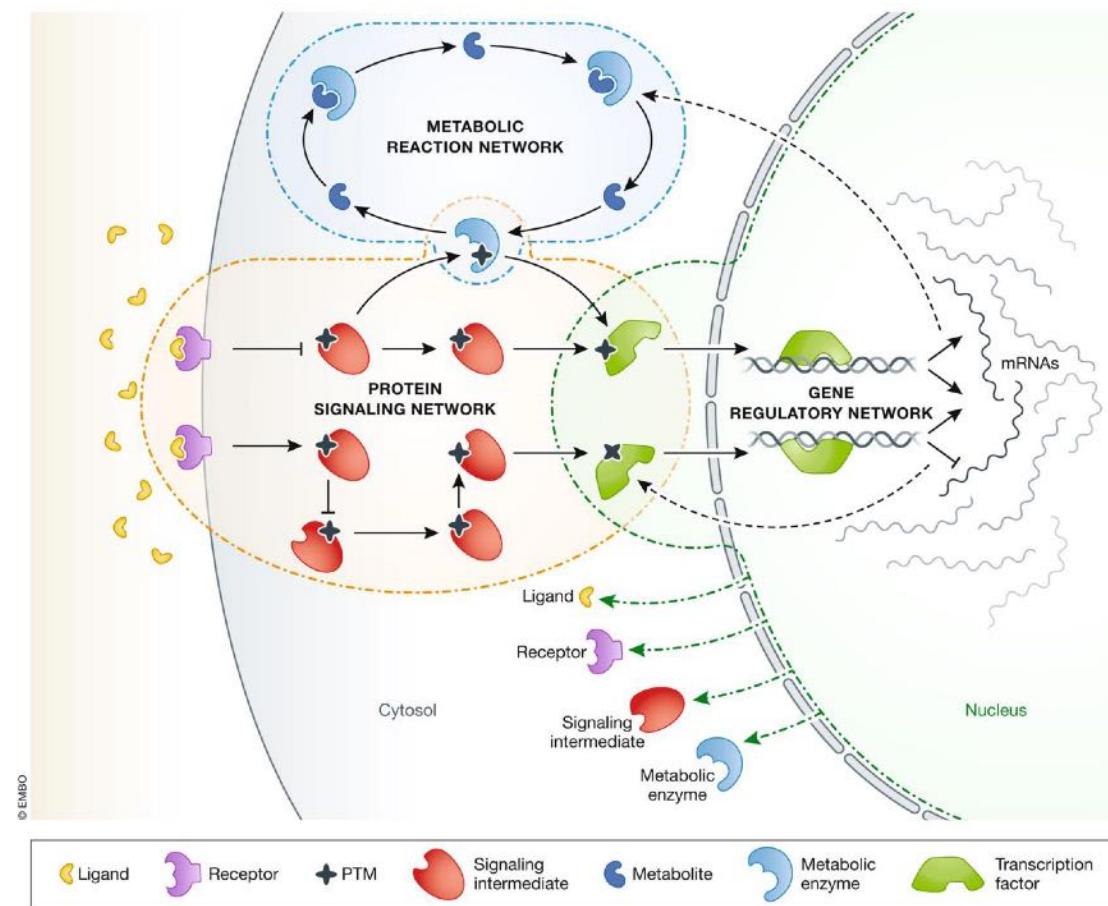
# Models in science and engineering

*AlphaFold and ChatGPT; data-extensive trained neural networks, regression*



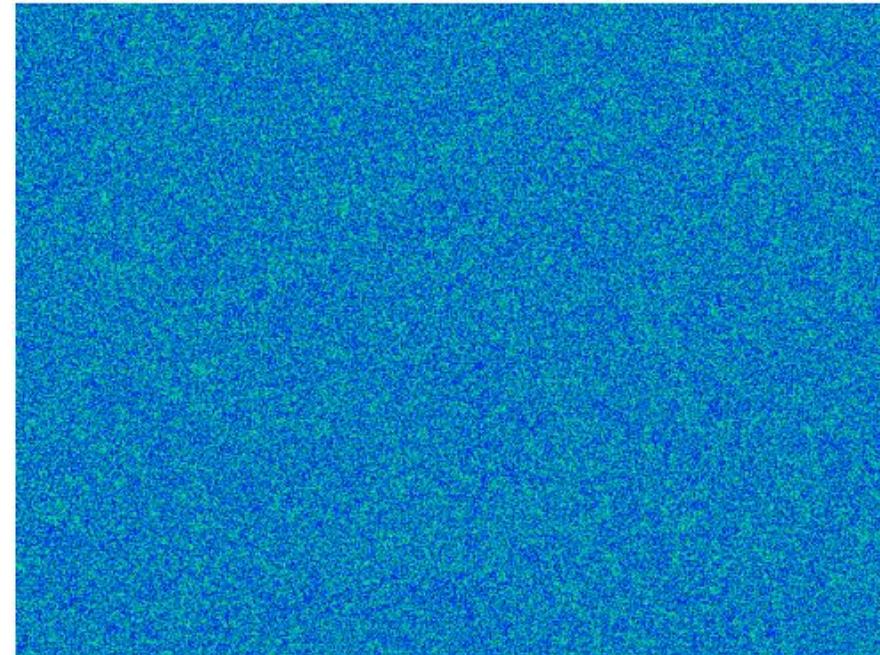
# Models in science and engineering

*Cell biology, biochemistry and drug target identification*



# Models in science and engineering

*Cell biology, biochemistry and drug target identification*



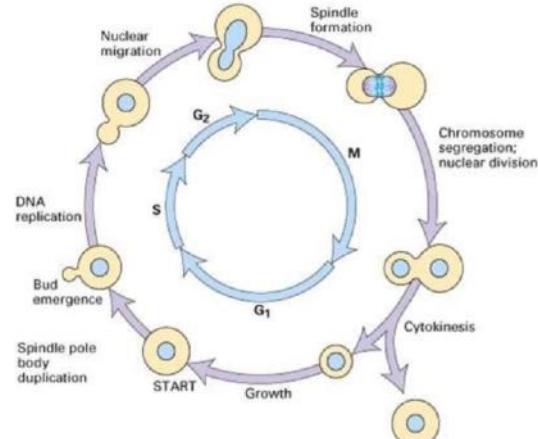
# different types of models (we will consider all of them in this course)

- Equation-based models
  - causal mechanistic models of systems
    - given the properties of the parts of a system
  - phenomenological models
    - given a crude description of a phenomenon generated by a system
  - empirical models
    - given data
- “Equation-free” models
  - neural networks (can approximate any mathematical equation)
    - heavily reliant on the existence of the right set and sufficient data (still rare)

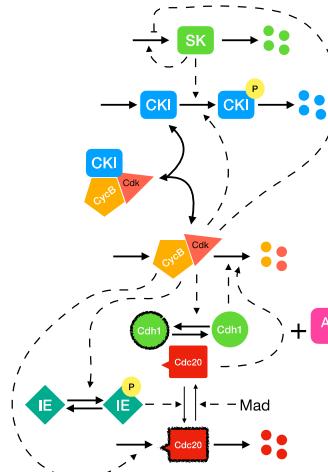
# Dynamic models – we will make many of them

Biological process

A.

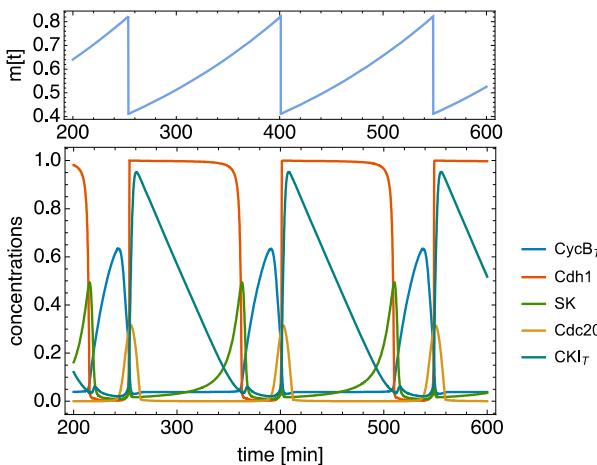


B.

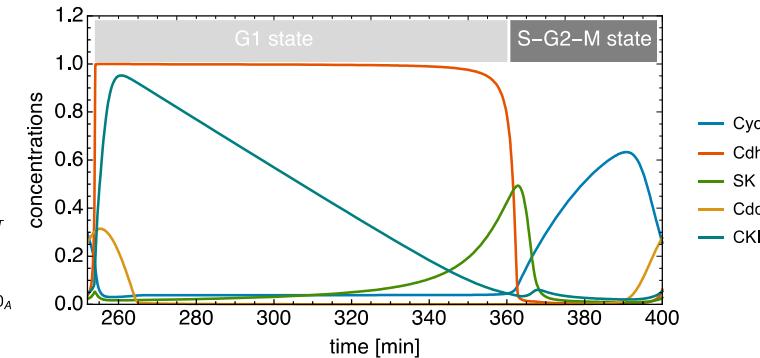


proposed molecular mechanism

C.



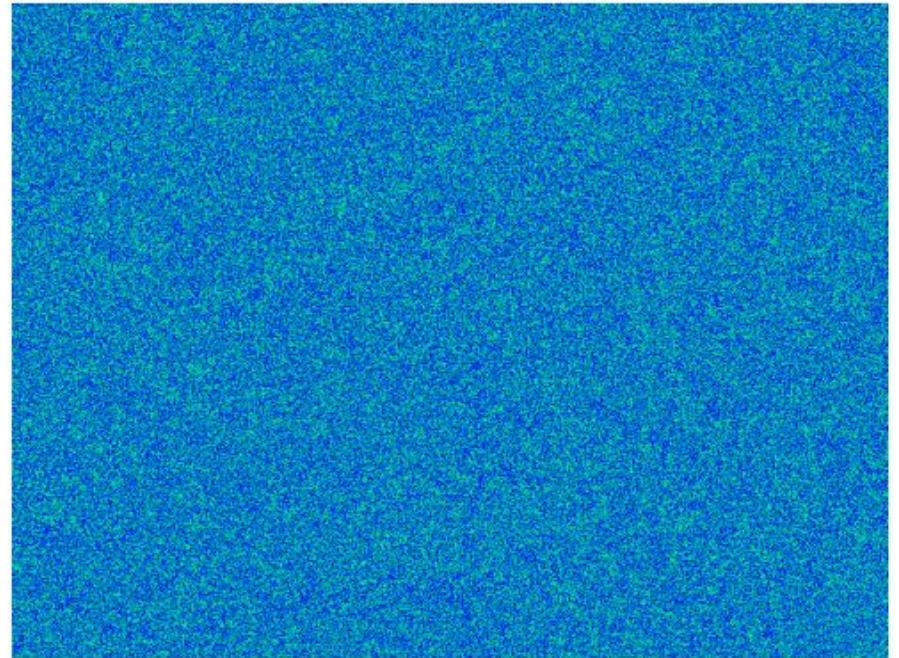
D.



outcome of mechanistic model

# different simulation formalisms of models

- deterministic model
  - as function of time
  - as function of time and space
- non-deterministic (stochastic) models
  - as function of time
  - as function of time and space
- these modelling formalisms are used in biology, engineering, physics, sociology, oceanography, you name it.
- The mathematics and modelling formalisms are discipline independent

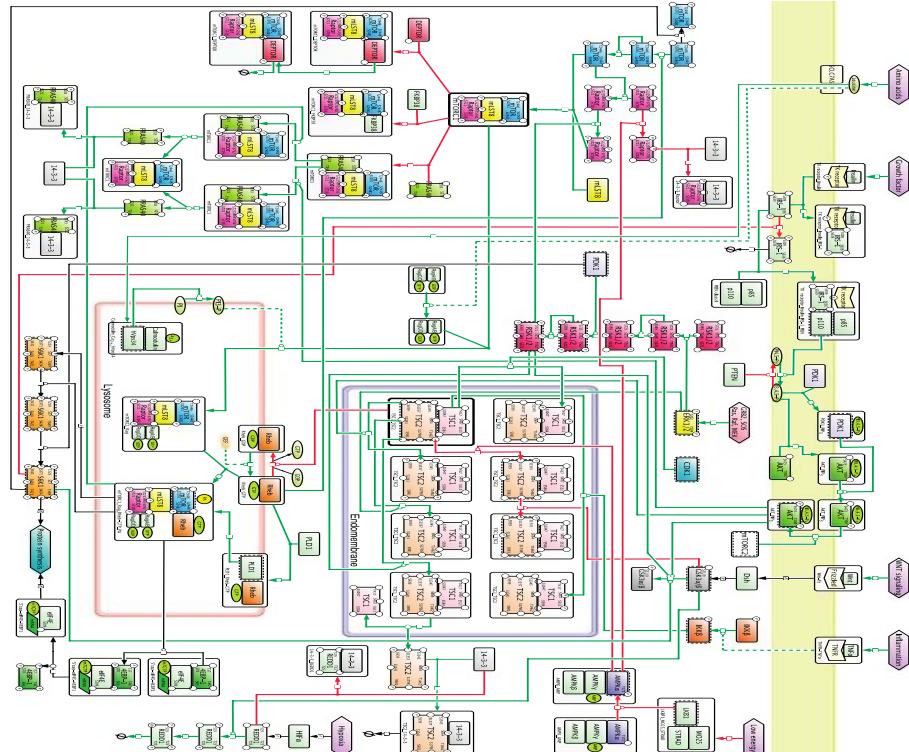


# reduction and explanation

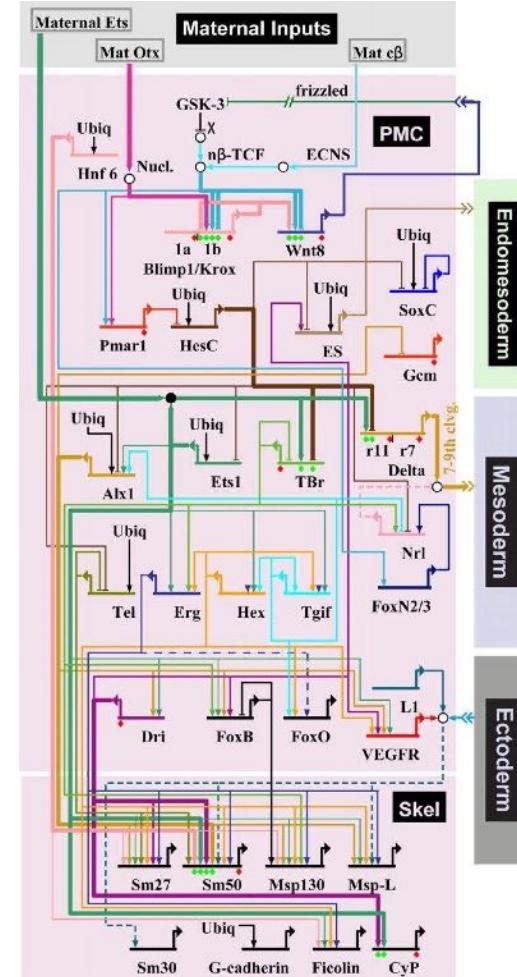


# molecular complexity and a need for simplification

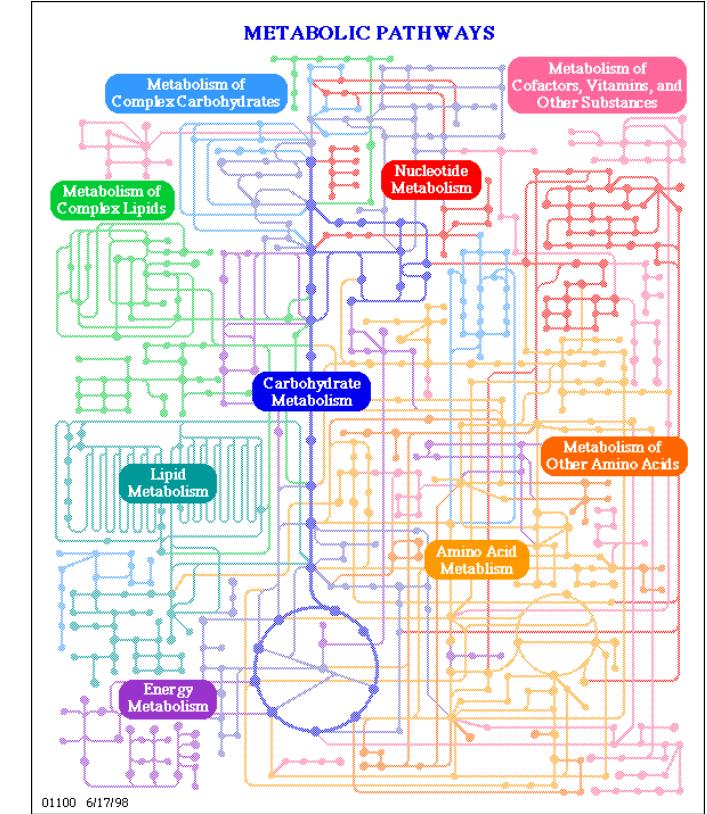
**Figure 3** Upstream regulators of mTORC1 signalling. Species, protein, reactions and cellular components involved in mTORC1 signalling were extracted from the comprehensive mTOR map and illustrated using Sigr. The SBML and PDF files (see supplementary Figure S4) in mTORC1 signalling are available from the URL in the figure caption.



signalling



genetic networks

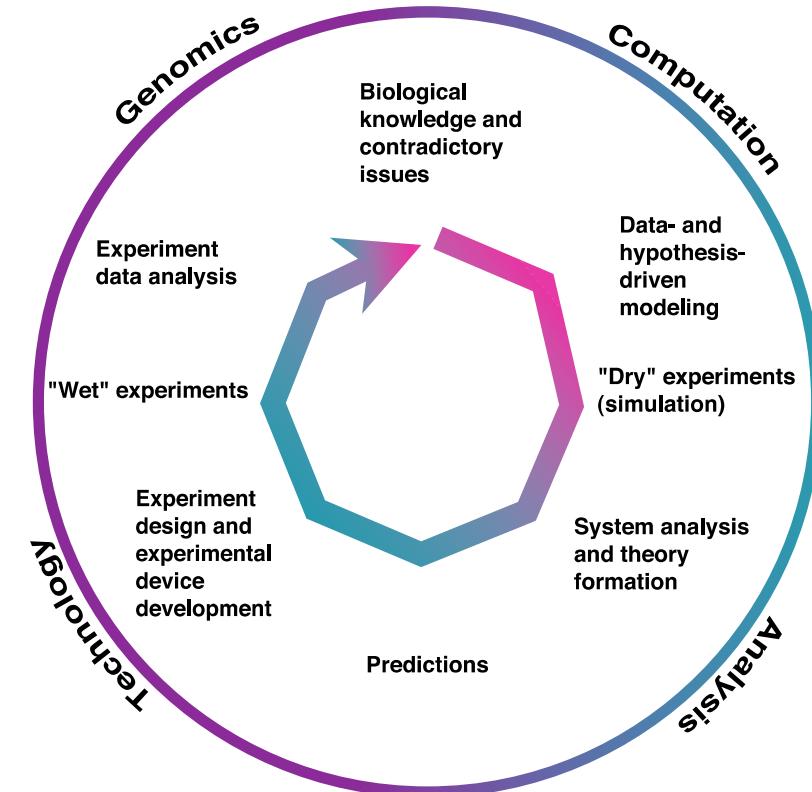


metabolic networks

# Approach – scientific method

**Fig. 1.** Hypothesis-driven research in systems biology. A cycle of research begins with the selection of contradictory issues of biological significance and the creation of a model representing the phenomenon. Models can be created either automatically or manually. The model represents a computable set of assumptions and hypotheses that need to be tested or supported experimentally. Computational "dry" experiments, such as simulation, on models reveal computational adequacy of the assumptions and hypotheses embedded in each model. Inadequate models would expose inconsistencies with established experimental facts, and thus need to be rejected or modified. Models that

pass this test become subjects of a thorough system analysis where a number of predictions may be made. A set of predictions that can distinguish a correct model among competing models is selected for "wet" experiments. Successful experiments are those that eliminate inadequate models. Models that survive this cycle are deemed to be consistent with existing experimental evidence. While this is an idealized process of systems biology research, the hope is that advancement of research in computational science, analytical methods, technologies for measurements, and genomics will gradually transform biological research to fit this cycle for a more systematic and hypothesis-driven science.



# the next approx. 2 weeks

