



“BioQuant Building” by Jürgen Pahle CC BY-SA 4.0

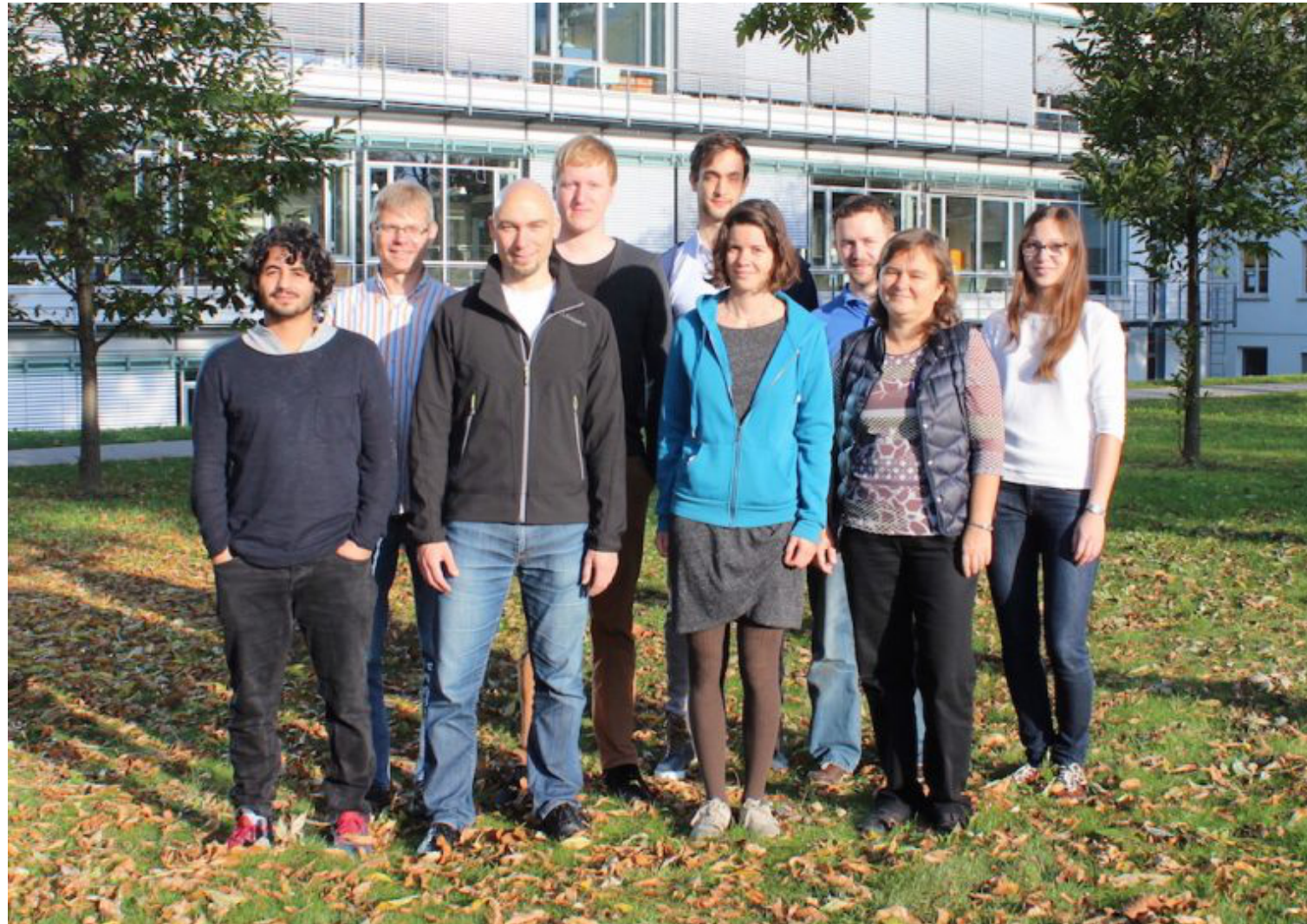
# **Information biology – How to apply Shannon's information theory to biology**

35C3 Leipzig

Jürgen Pahle  
<https://lab.pahle.org>

27<sup>th</sup> December 2018

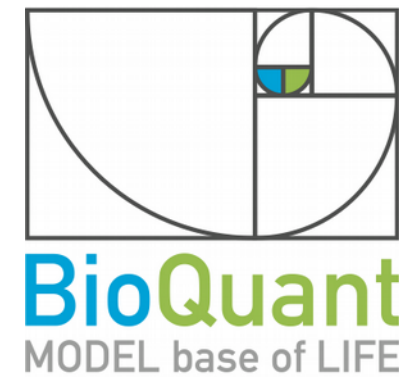
# Pahle Lab @ BioQuant Heidelberg University



“BIP group” by Jürgen Pahle CC BY-SA 4.0



**B**iological **I**nformation  
**P**rocessing Group

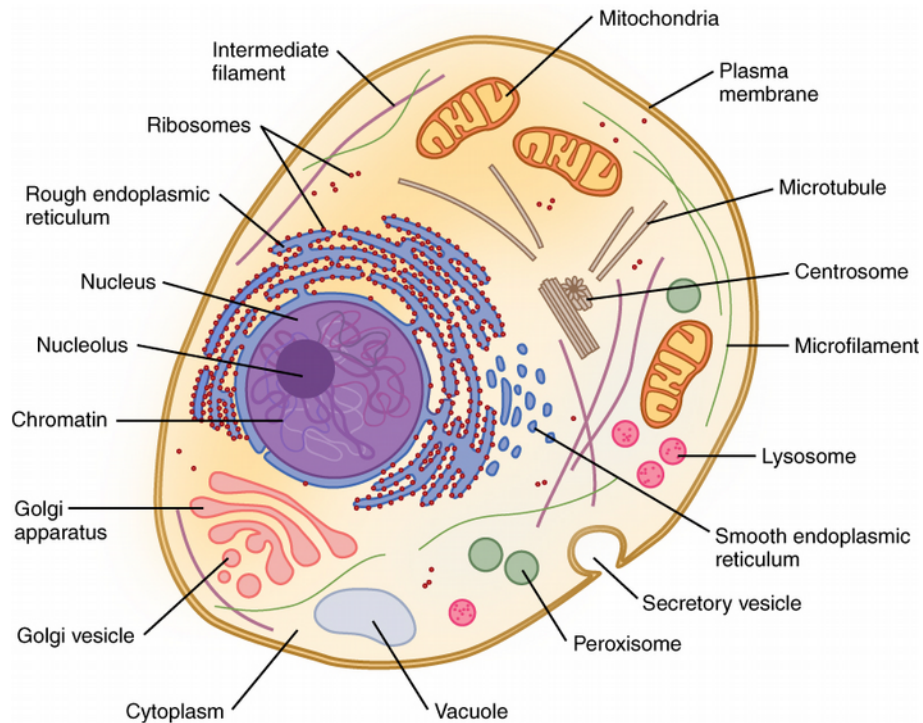


Funded by



- Cellular communication and information processing is everywhere.
- How do cells manage all these computations with relatively unreliable components (proteins, instead of transistors) and (intrinsic) fluctuations in molecular numbers?
- If signalling is impaired severe diseases can be the result, e.g. cancer or epilepsy.
- Cellular signalling pathways have been studied on a molecular level in detail but surprisingly little conceptual work has been done...

# How-to (Biochemical modelling)



- **Compartments** (nucleus, cytosol, ...)
- **Biochemical species** (proteins, enzymes, ions, ...)
- **Reactions** (who reacts with whom?, substrates, products)
- **Kinetics** (velocity of reactions)

Mathematical model

$$\begin{aligned} \frac{dG_\alpha}{dt} &= k_1 + k_2 \cdot G_\alpha - \frac{k_3 \cdot PLC \cdot G_\alpha}{(K_4 + G_\alpha)} - \frac{k_5 \cdot [Ca^{2+}] \cdot G_\alpha}{(K_6 + G_\alpha)} & G_\alpha(t_0) &= 0.01 \text{ nmol} \\ \frac{dPLC}{dt} &= k_7 \cdot G_\alpha - \frac{k_8 \cdot PLC}{(K_9 + PLC)} & PLC(t_0) &= 0.01 \text{ nmol} \\ \frac{d[Ca^{2+}]}{dt} &= k_{10} \cdot G_\alpha - \frac{k_{11} \cdot [Ca^{2+}]}{(K_{12} + [Ca^{2+}])} & [Ca^{2+}](t_0) &= 0.01 \text{ nmol} \end{aligned}$$

## Simulation:

How does the system change over time?

## Analysis of the model:

Which parts influence the behavior most?

Which states are stable (steady state, oscillations)?

"All models are wrong but some are useful"

Box, G.E.P. (1979) "Robustness in the strategy of scientific model building" in Robustness in Statistics (R.L. Launer and G.N. Wilkinson, Eds.), Academic Press

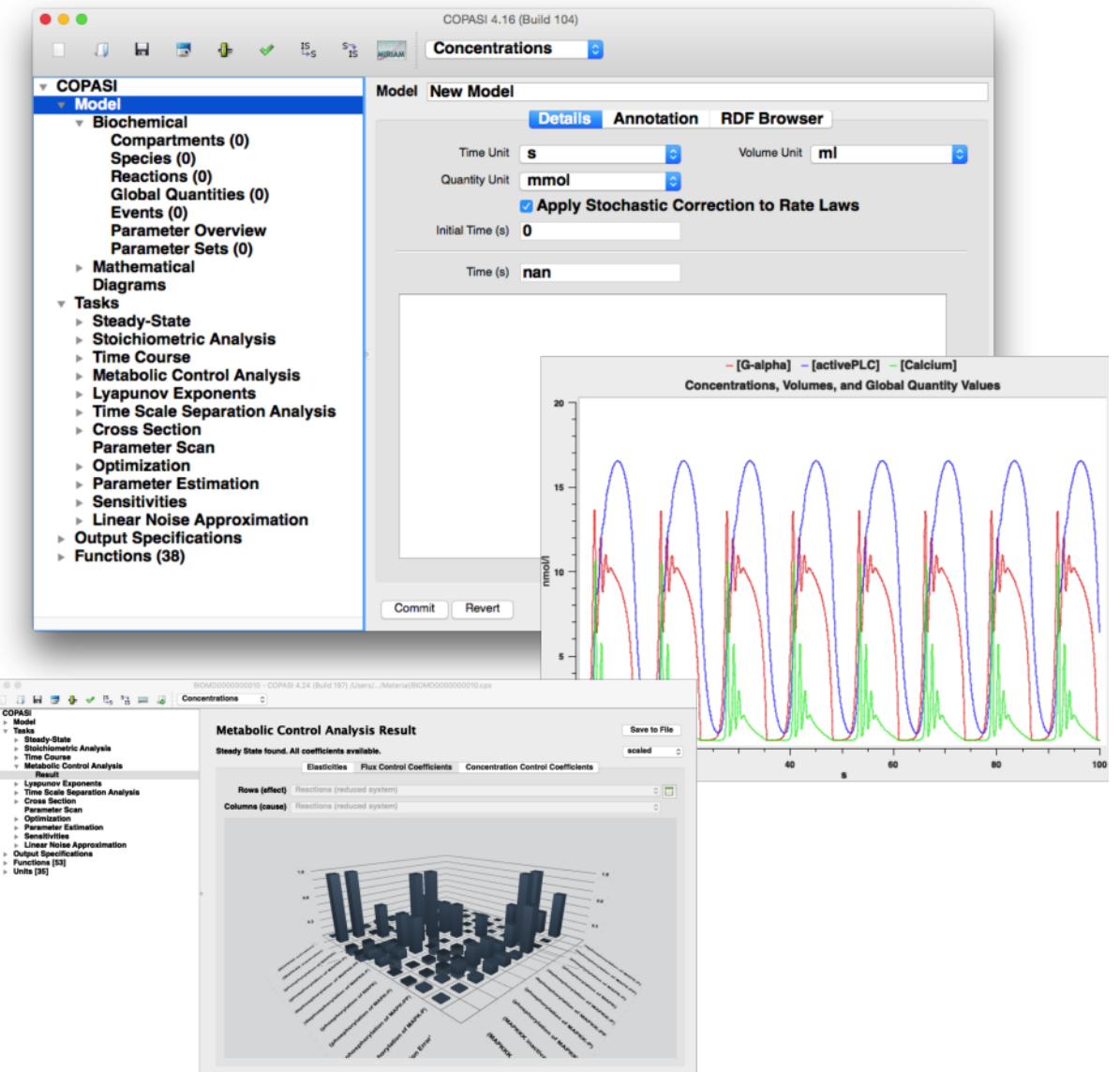
"[..] the practical question is how wrong do they have to be to not be useful"

Box, G.E.P. & Draper, N.R. (1987). Empirical Model-Building and Response Surfaces. Wiley. pp. 74



<http://www.copasi.org>

- COPASI (COMplex PATHWAY SIMULATOR)
- Stand-alone software for the modelling, simulation and analysis of biochemical networks
- “Tool kit” with a variety of different methods:
  - Deterministic, **stochastic and hybrid simulation methods**
  - Metabolic Control Analysis, Elementary Flux Mode Analysis, Sensitivity Analysis, Cross-sections, etc.
  - Parameter Scanning, Optimization, Parameter Fitting
  - User-friendly **GUI**, runs under Mac, Linux, Windows and **command line version**
  - Non-commercial, freely available, open-source (**Artistic license**). Can be used via APIs.
  - Reads and writes the Systems Biology Markup Language (**SBML**), and allows annotations etc.





# CoRC – Copasi R Connector [jpahle.github.io/CoRC](https://jpahle.github.io/CoRC)

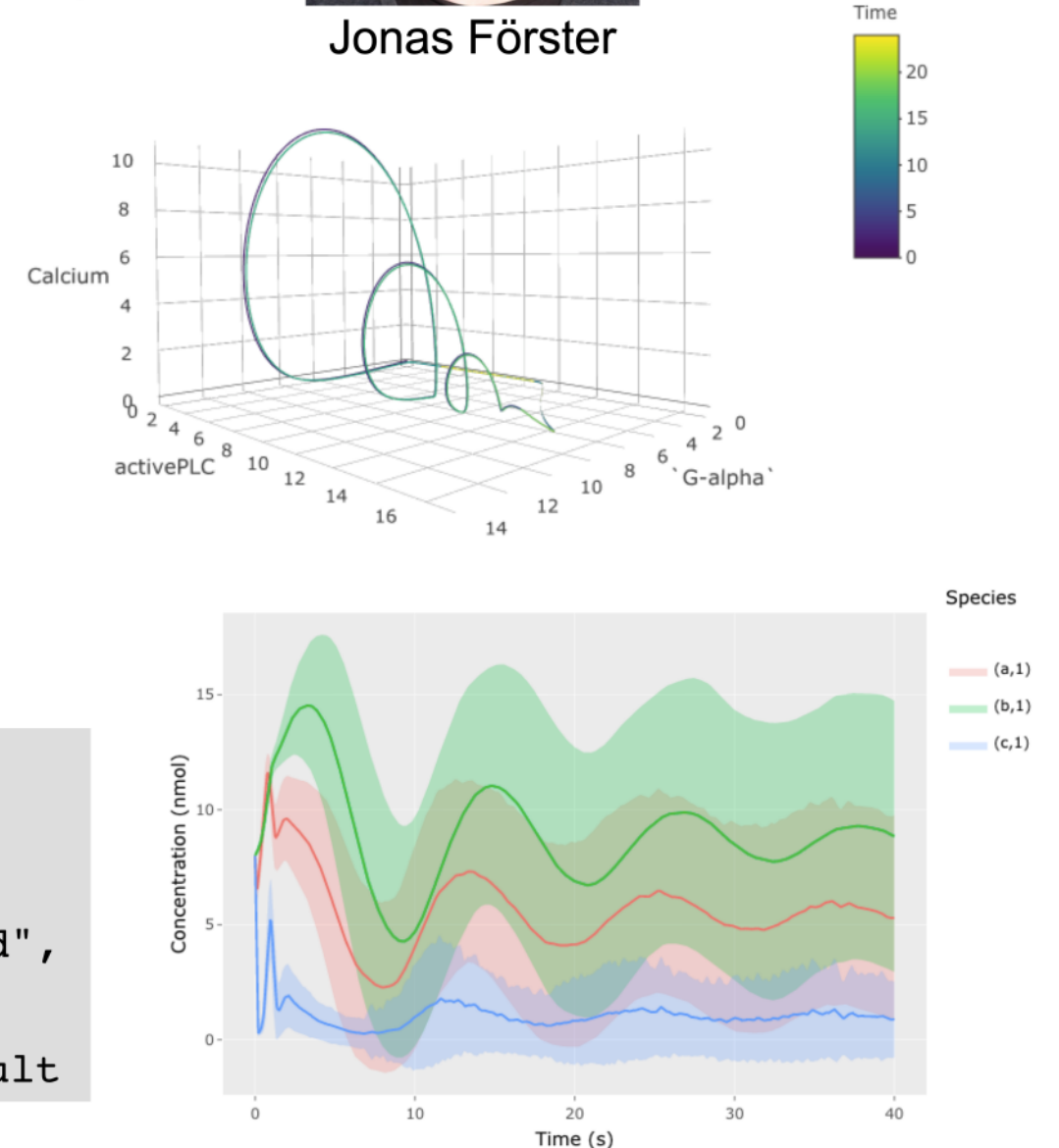


Jonas Förster

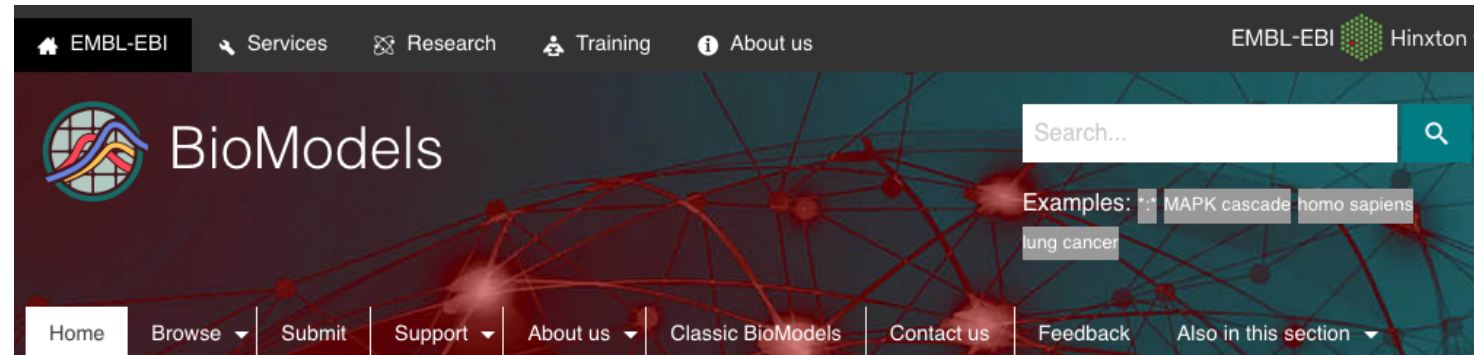
CoRC connects the

- Complex Pathway Simulator COPASI ([copasi.org](https://copasi.org)) and the
- (statistical) programming environment R ([r-project.org](https://r-project.org)).
- Free and open-source

```
loadSBML("http://www.ebi.ac.uk/biomodels-main/download?
mid=BIOMD0000000329")
setTimeCourseSettings(24, intervals = 10000)
timecourse <- runTimeCourse(method = list(method = "directMethod",
                                          use_random_seed = T,
                                          random_seed = 1))$result
```



# Biomodels.net



Repository for published biochemical models

- 727 manually curated models
- 7901 non-curated models

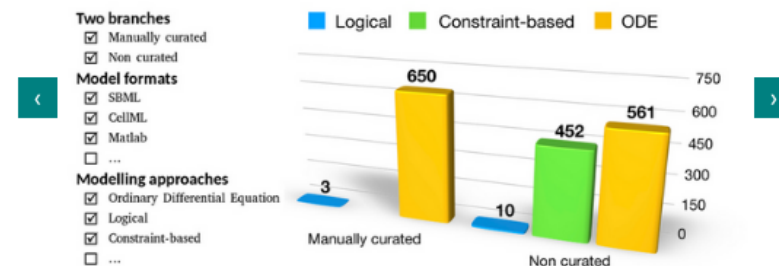
BioModels is a repository of mathematical models of biological and biomedical systems. It hosts a vast selection of existing literature-based physiologically and pharmaceutically relevant mechanistic models in standard formats. Our mission is to provide the systems modelling community with reproducible, high-quality, freely-accessible models published in the scientific literature. More information about BioModels can be found in the [FAQ](#).

## Recently published

- Abroudi2017 - Mammalian Cell Cycle Control Model\_1
- Goldbeter1996 - Cyclin Cdc2 kinase Oscillations
- Gerard2009 - An Integrated Mammalian Cell Cycle Model
- Li2009- Assymmetric Caulobacter cell cycle
- A quantitative model of

## Features

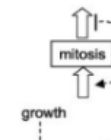
### What is available in BioModels?



## Model of the month

### December, 2018

Chen2004 integrated the various known components of yeast cell cycle control and dynamics and succeeded in forming a model that could predict the phenotypes of over hundred deletion strains.



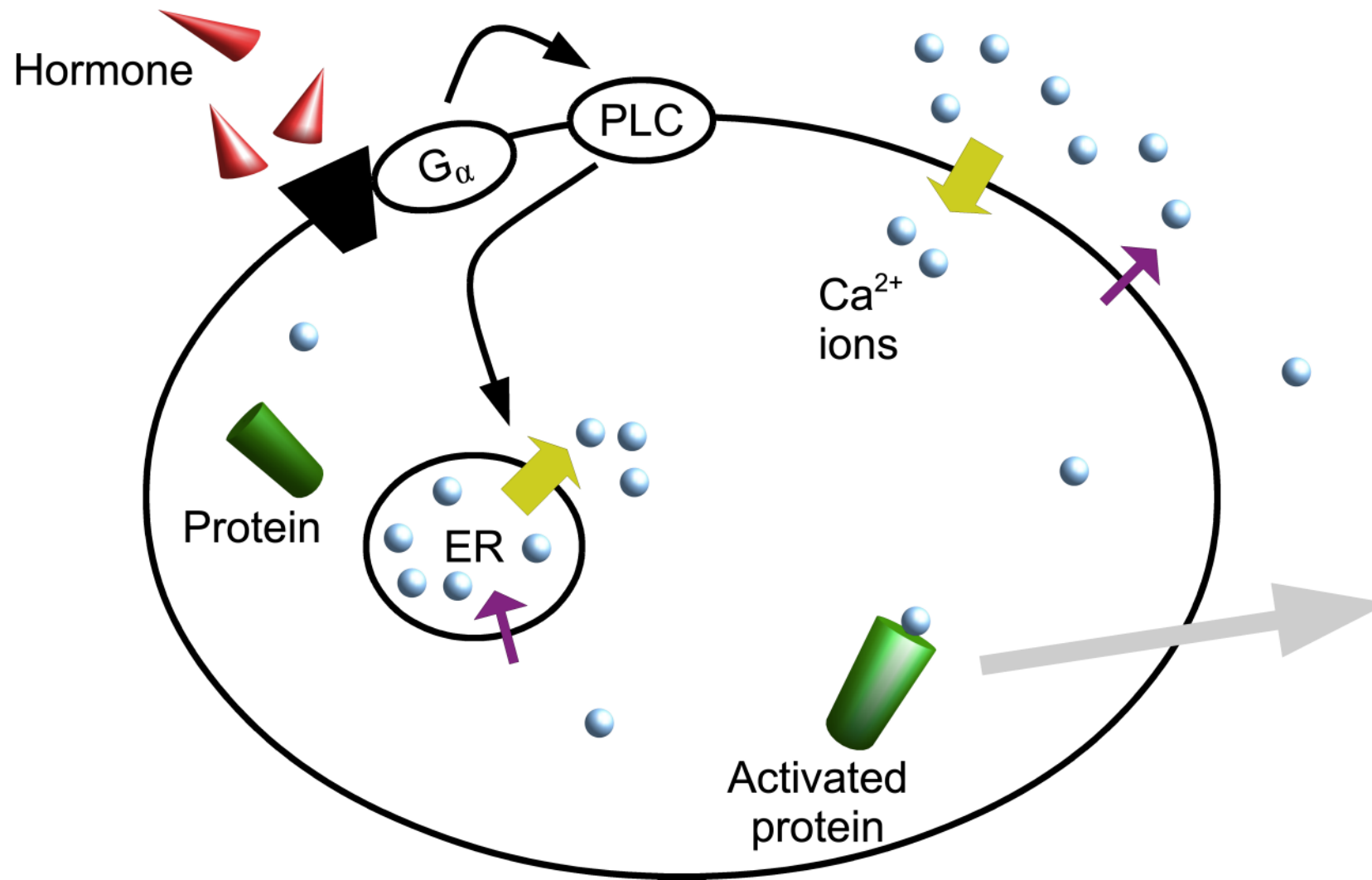
[Access this model of the month](#) | [View all Model of the Month entries](#)

[News](#) [Help](#)

Calcium oscillation model: [Biomodel 329](#)



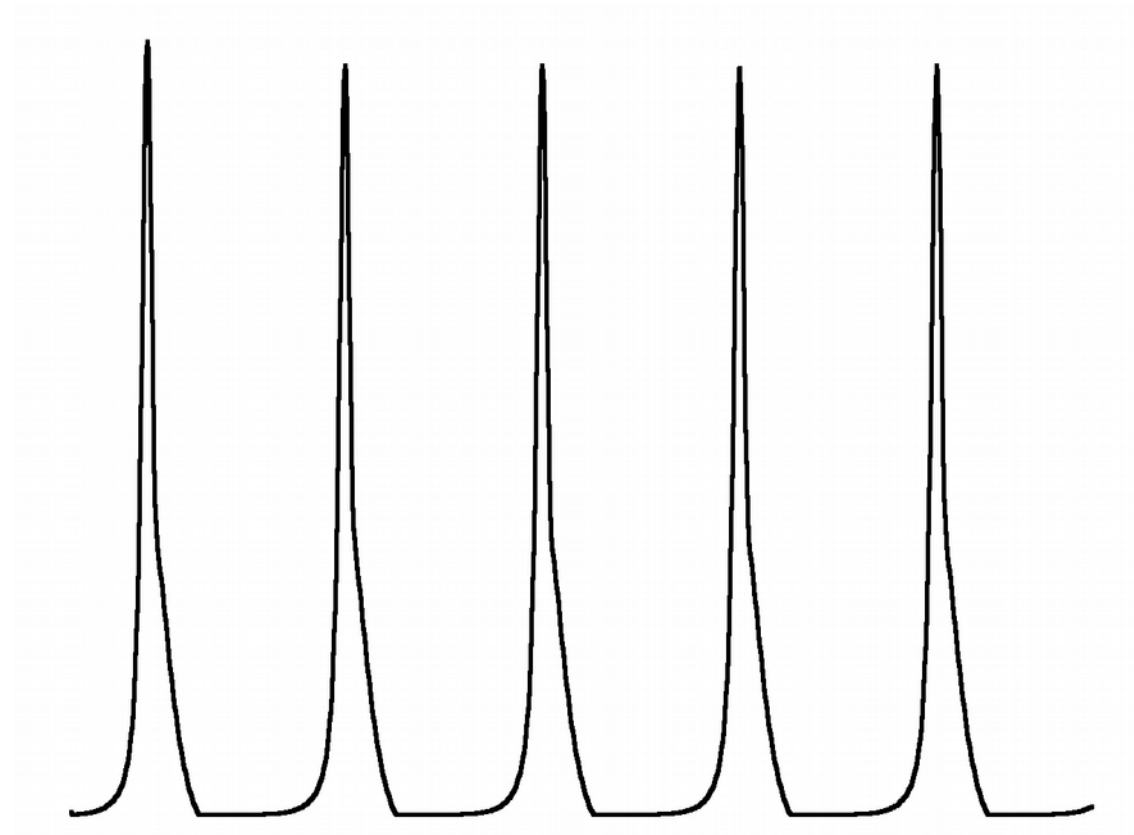
# Signal transduction via $\text{Ca}^{2+}$ ions



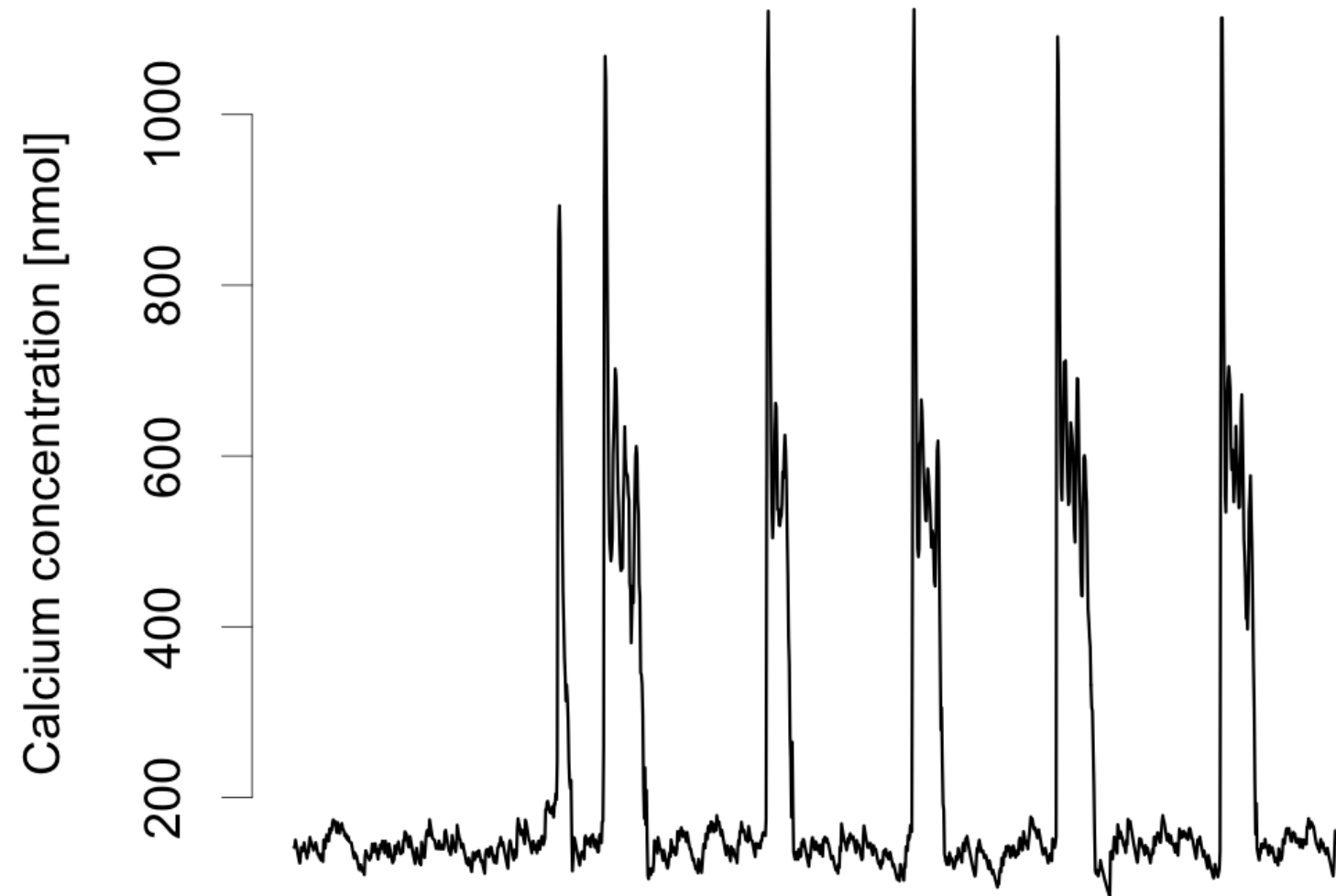
- **Movement:** muscle contraction
- **Learning:** long-term potentiation in neurons
- **Regulation** of metabolism etc.
- **Secretion** of neurotransmitters and others
- **Fertilization**
- ...

# Calcium dynamics (simulated deterministically)

Spiking



# Experimental time series



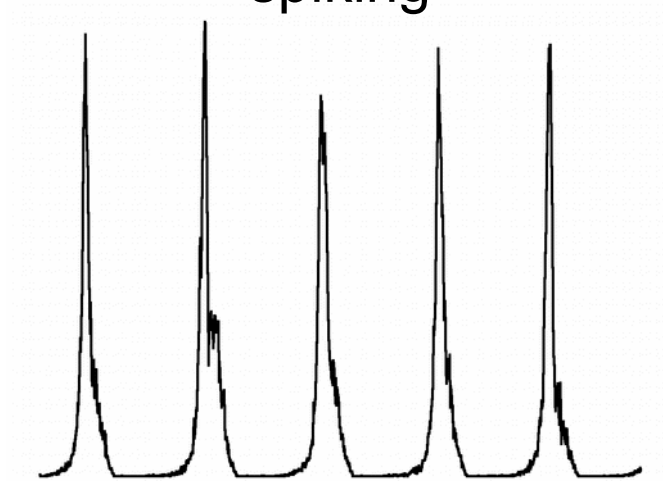
Calcium concentration oscillations in single rat hepatocytes stimulated with ATP (1.5  $\mu\text{M}$ ).  
(data from: Pahle et al. (2008), *BMC Bioinformatics* **9**:139, [doi:10.1186/1471-2105-9-139](https://doi.org/10.1186/1471-2105-9-139))

# Gillespie algorithm

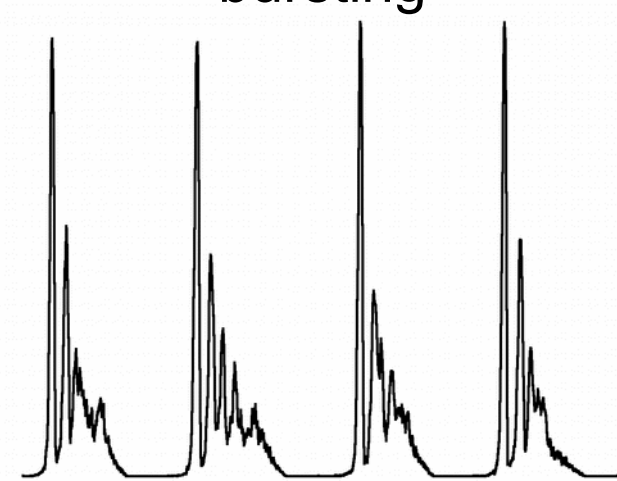


"Gillespie St" by Jürgen Pahle CC BY-SA 4.0

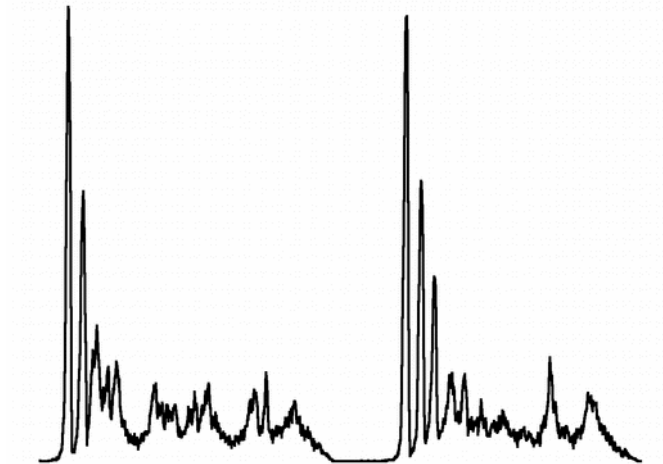
spiking



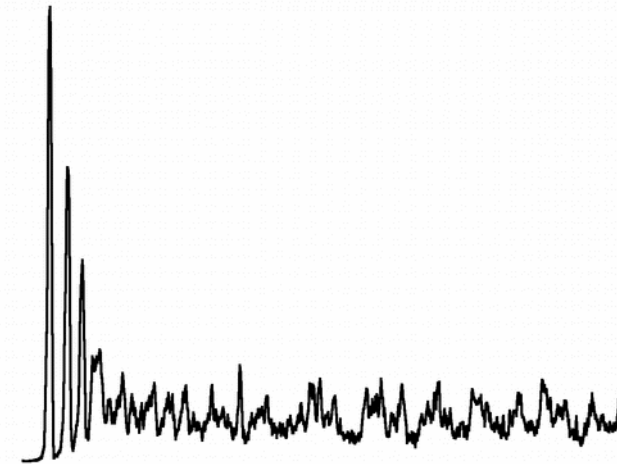
bursting



irregular/chaotic



overstimulation

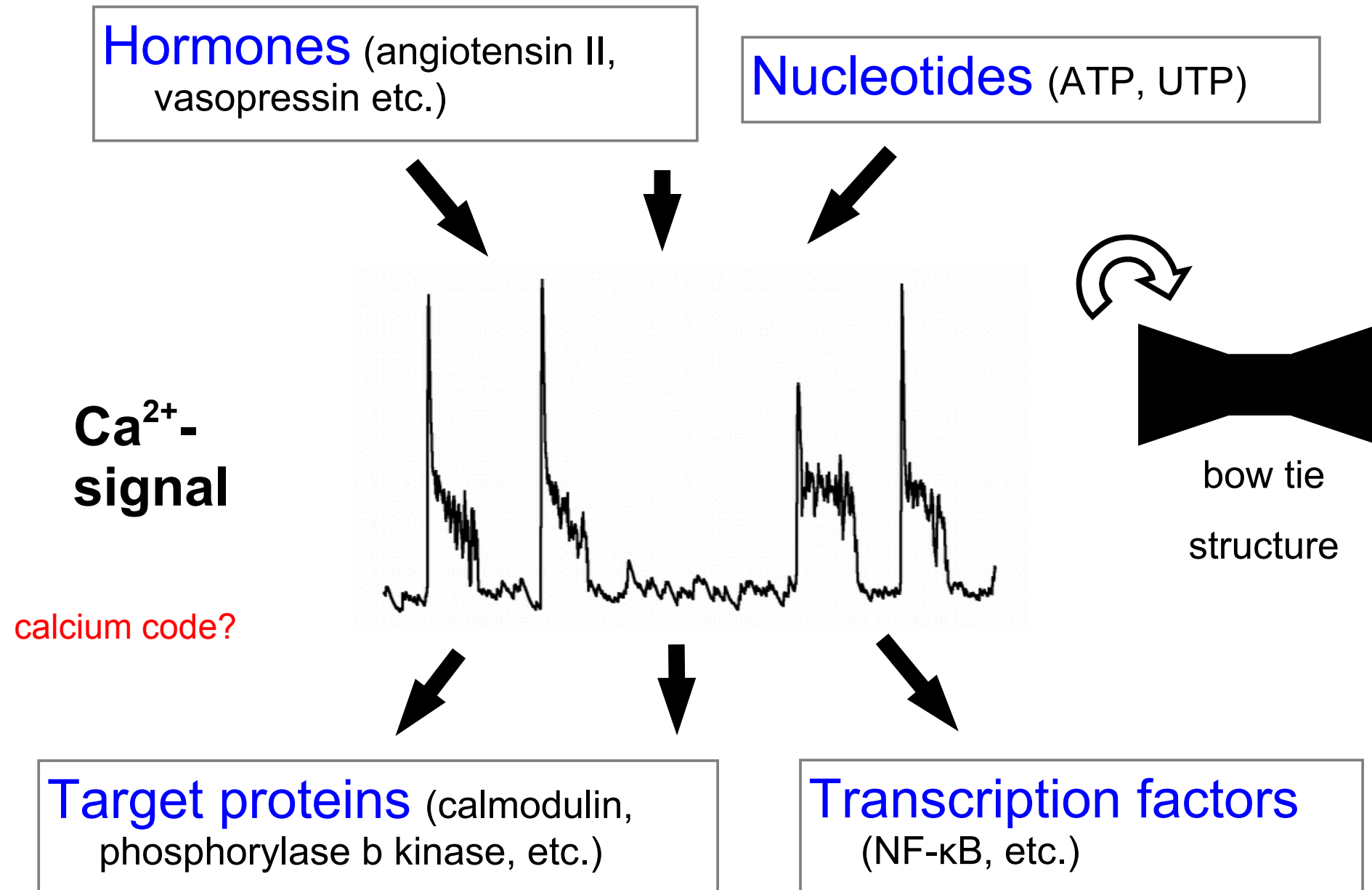


## Monte Carlo simulation algorithms

D.T. Gillespie (1976) *J. Comp. Phys.*  
**22**(4):403,  
[doi:10.1016/0021-9991\(76\)90041-3](https://doi.org/10.1016/0021-9991(76)90041-3)

and extensions thereof...

# Signal transduction via Calcium



# The calcium code

- Intracellular targets sense only the  $\text{Ca}^{2+}$ -concentration inside the cell  
(plus possibly other signalling pathways, “cross-talk”)
- How is the information from different hormones encoded in the calcium signal?
- How is the calcium signal decoded again at the target proteins?

# The calcium code

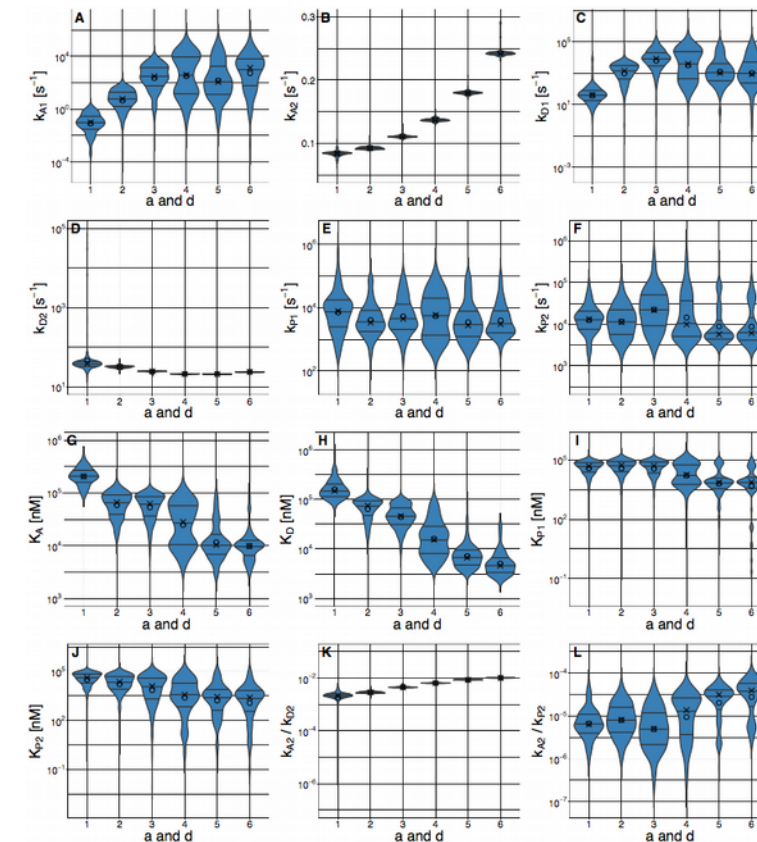
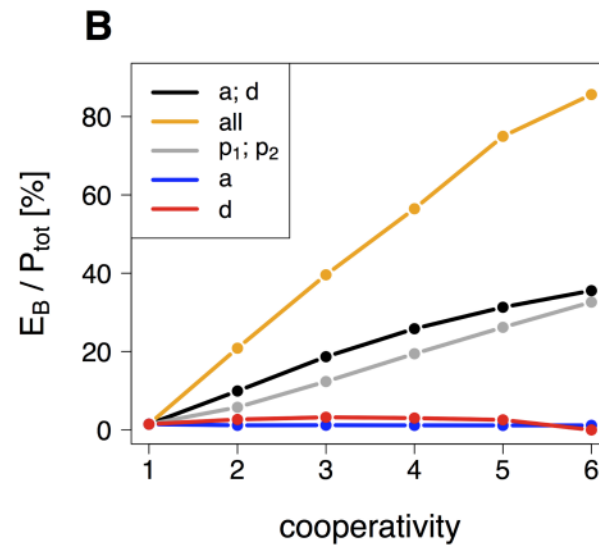
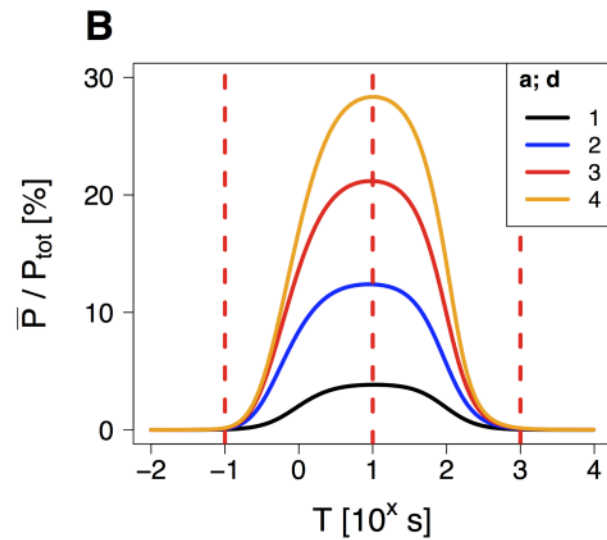
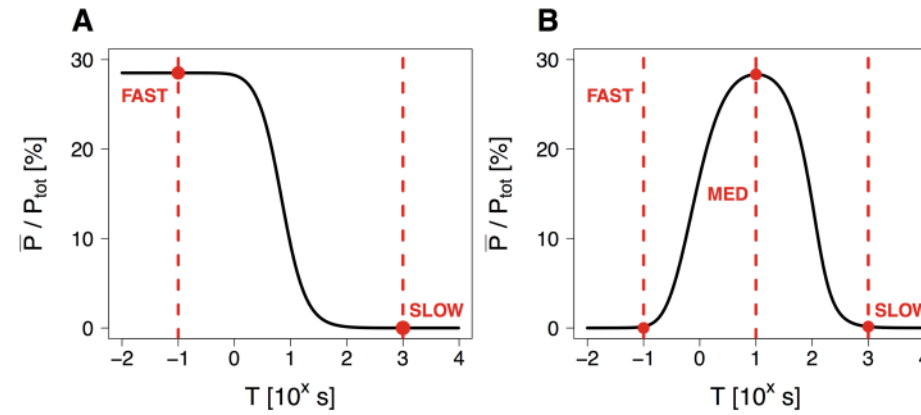
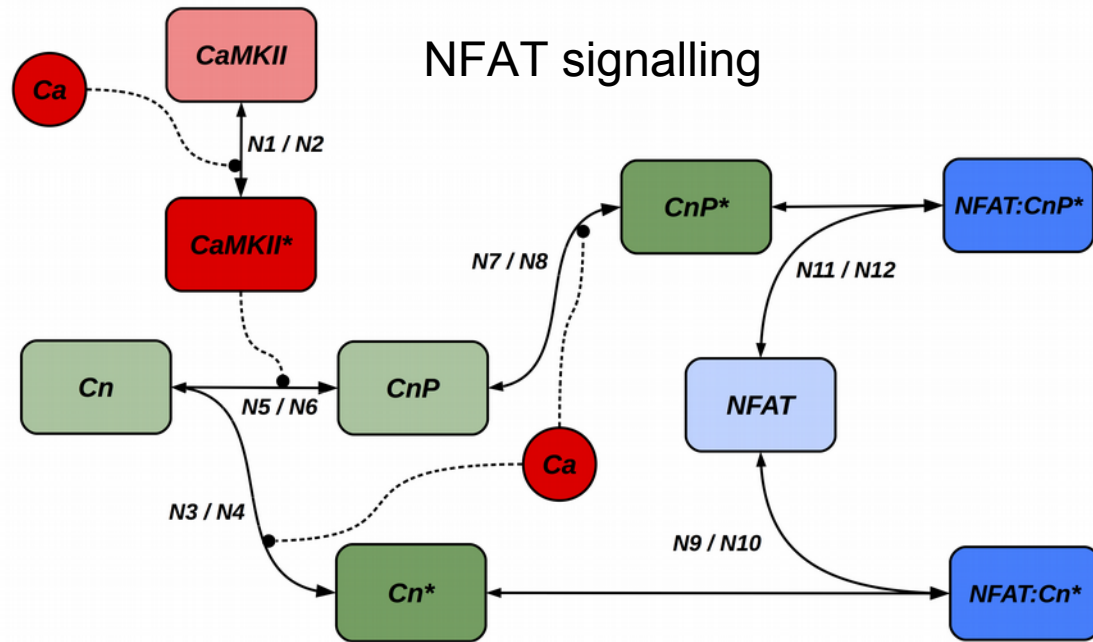
- Intracellular targets sense only the  $\text{Ca}^{2+}$ -concentration inside the cell  
(plus possibly other signalling pathways, “cross-talk”)
- How is the information from different hormones encoded in the calcium signal?
- How is the calcium signal decoded again at the target proteins?
- Specific information seems to be encoded in the
  - amplitude (AM)
  - frequency (FM)
  - duration
  - waveform

# Band-pass activation



Arne Schoch

NFAT gets only activated by calcium oscillations of a certain frequency.





# Signalling speeds

Telekom Broadband ~ 25 – 1000 Mbit/s



4G / LTE ~ 150 – 1200 Mbit/s

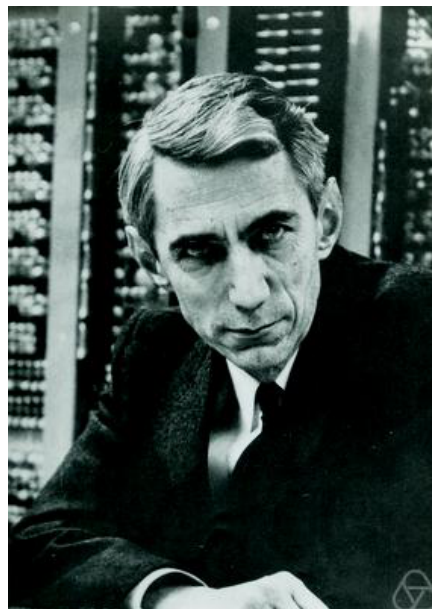


# Biological signalling

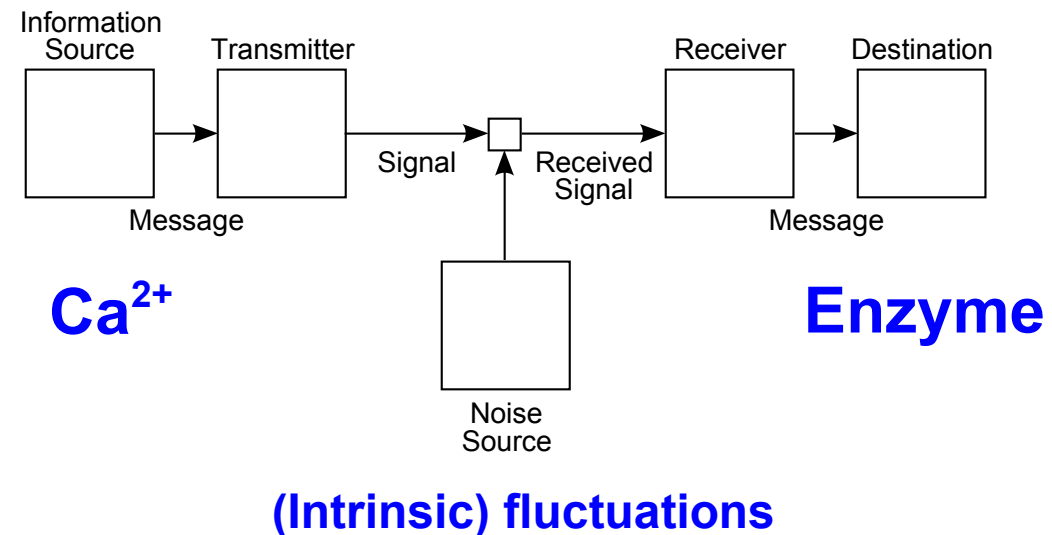
(Intracellular) calcium signalling operates at roughly 0.39 bit/s

# Information theory

- Claude E. Shannon (1916-2001)  
“Mathematical Theory of Communication” (1948)
- Information theory can answer questions about limits of faithful information transfer over a given (noisy) channel etc.



“Shannon, Claude” by  
Konrad Jacobs CC BY-SA 2.0 DE



“Shannon communication system” by  
Wanderingstan, public domain

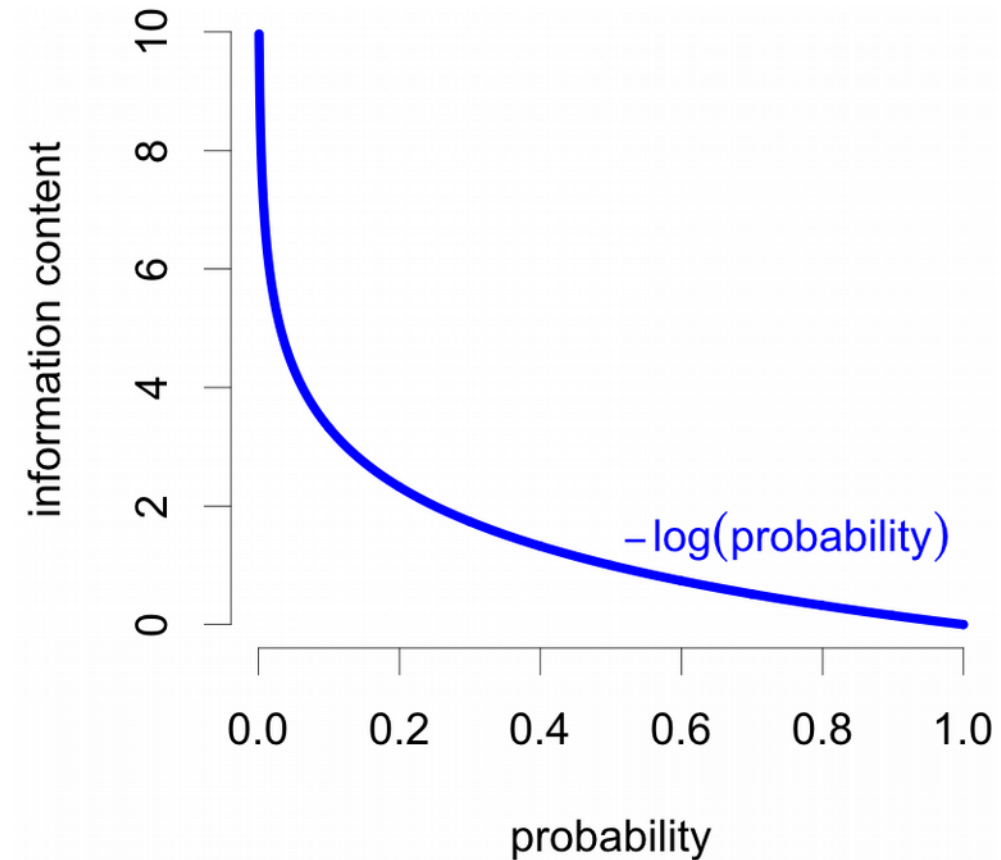
# Information theory 101: How to quantify information?

Information content of  
an event

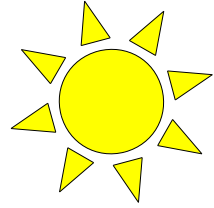
→ **Uncertainty / Surprisal**  
(negative log of probability)

Average uncertainty of all possible  
events → **Entropy**

**Information** = **Decrease** in uncertainty



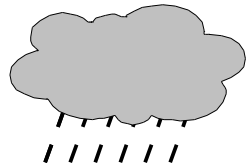
# Weather example



50%

Probability(sunny) =  $\frac{1}{2}$

→ Uncertainty(sunny) = 1.0



50%

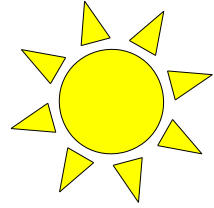
Probability(rainy) =  $\frac{1}{2}$

→ Uncertainty(rainy) = 1.0

On average (entropy of the weather)

→ 1.0 [bit/day]

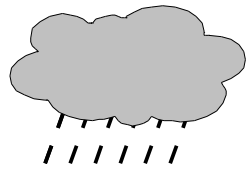
# Weather example



100%

Probability(sunny) = 1.0

→ **Uncertainty(sunny) = 0.0**



0%

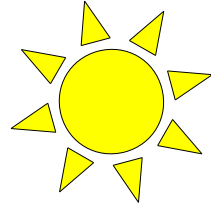
Probability(rainy) = 0

→ **Uncertainty(rainy) = 0.0** per convention

On average (entropy of the weather)

→ **0.0** [bit/day]

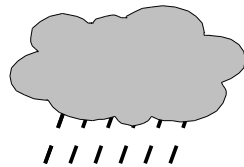
# Weather example



80%

Probability(sunny) = 0.8

→ Uncertainty(sunny) = 0.32



20%

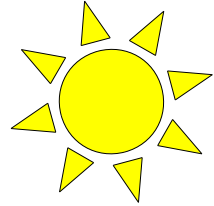
Probability(rainy) = 0.2

→ Uncertainty(rainy) = 2.32

On average (entropy of the weather)

→ 0.64 [bit/day]

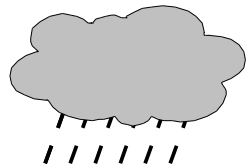
# Weather example (Leipzig)



266/365

Probability(sunny) = 0.73

→ Uncertainty(sunny) = 0.32



99/365

Probability(rainy) = 0.27

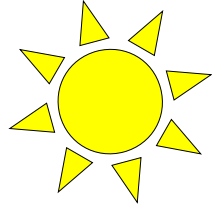
→ Uncertainty(rainy) = 1.88

On average (entropy of the weather in Leipzig)

→ 0.84 [bit/day]



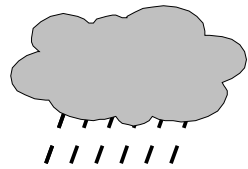
# Weather example



$p\%$

Probability(sunny) =  $p$

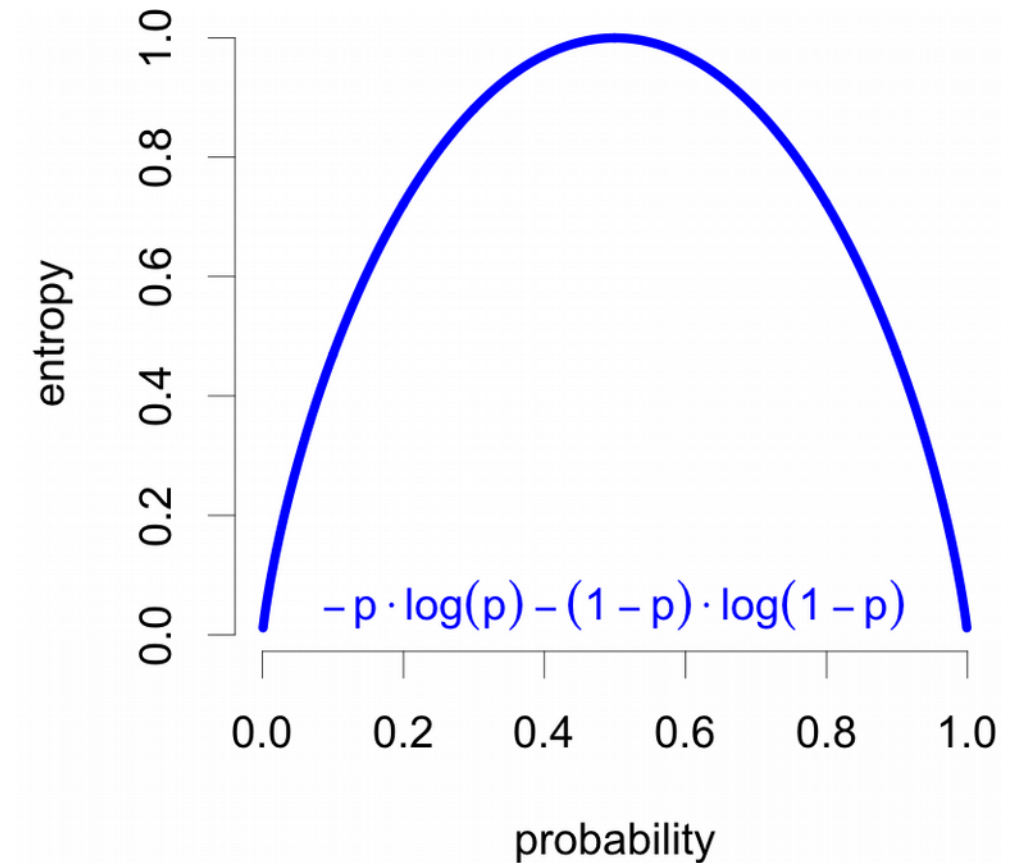
→ **Uncertainty(sunny) =  $-\log_2(p)$**



$(1-p)\%$

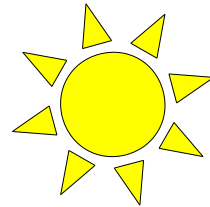
Probability(rainy) =  $1-p$

→ **Uncertainty(rainy) =  $-\log_2(1-p)$**



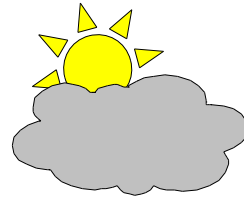
On average (entropy of the weather)  
[bit/day]

# Weather example



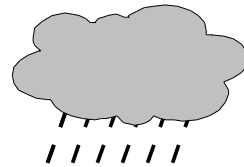
Probability(sunny) = 0.25

→ Uncertainty(sunny) = 2.0



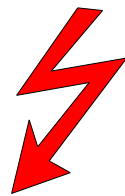
Probability(cloudy) = 0.25

→ Uncertainty(cloudy) = 2.0



Probability(rainy) = 0.25

→ Uncertainty(rainy) = 2.0



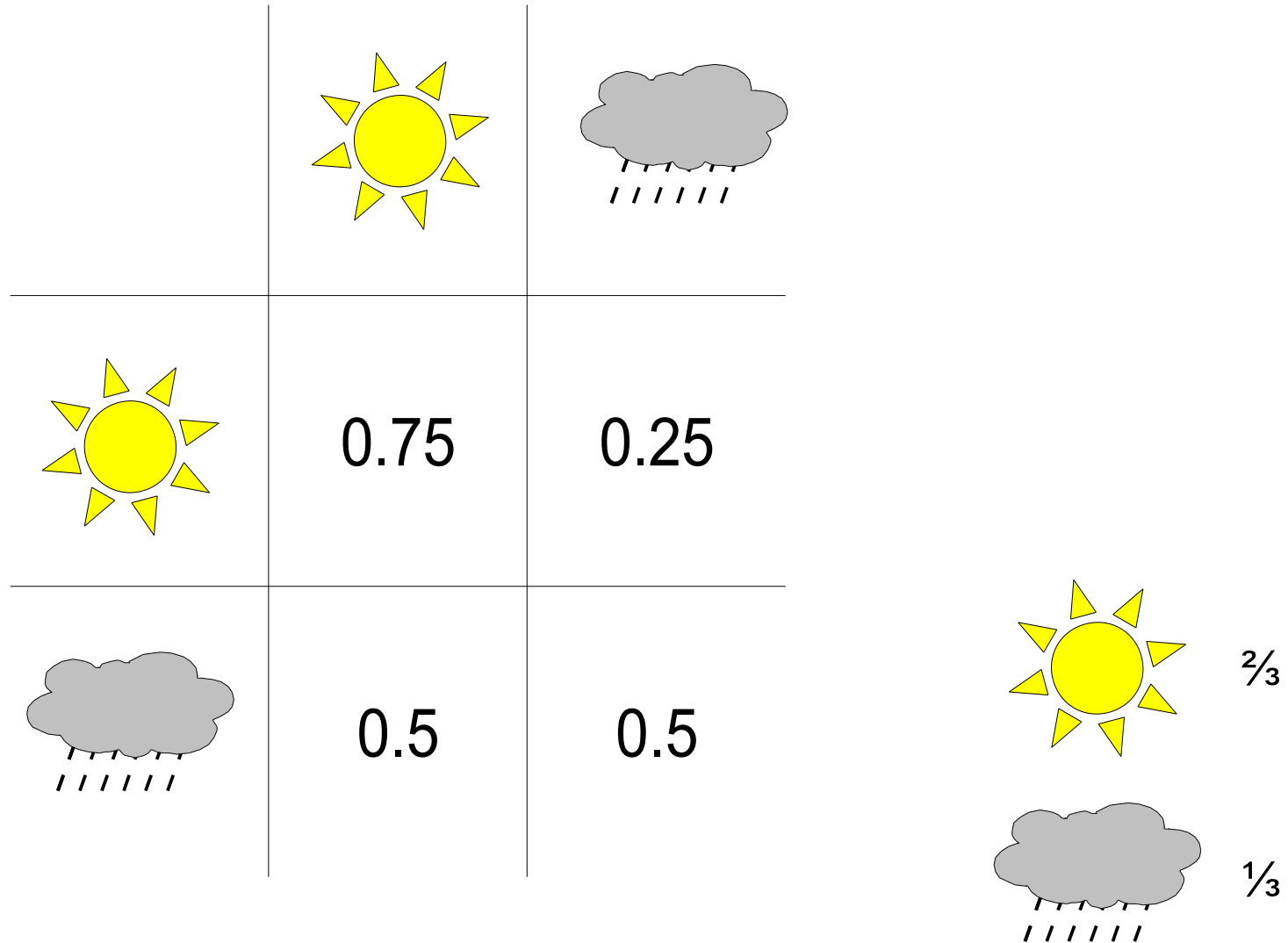
Probability(thunderstorm) = 0.25

→ Uncertainty(thunderstorm) = 2.0

On average (entropy of the weather)

→ 2.0 [bit/day]

# Weather dynamics



# Markov process

- Markov process can not remember former states, future is only dependent on the current state.
- Markovian modeling is used in a variety of fields:
  - Communication:  
Telephone system (Hidden Markov models)
  - Hard disks (error correction)
  - Language recognition
  - PageRank algorithm of Google
  - Biological modeling: Population dynamics, etc.
  - Games of chance (chutes and ladders)



Andrey A. Markov (1856-1922)

# Information/Entropy-rate

The information gained by observing tomorrow's weather, when the today's weather is known:

Entropy(tomorrow's weather | today's weather)

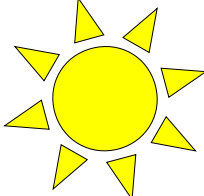
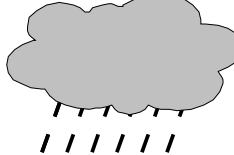
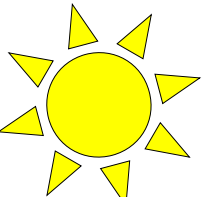
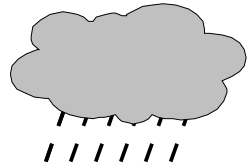
→ conditional probabilities

In our example:

Entropy(tomorrow's weather) = 0.92 [bit/day]

Entropy(tomorrow's weather | today's weather) = 0.87 [bit/day]

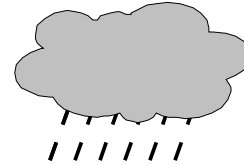
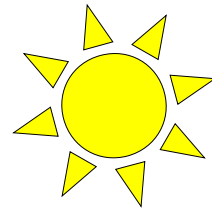
# Weather dynamics

			
	high	0.9	0.1
	low	0.6	0.4
	high	1	0
	low	0	1



# Weather dynamics (Leipzig)

26.12.2018, 10:00:  
1029 hPa → high

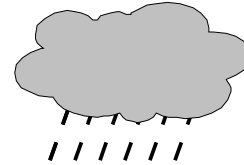
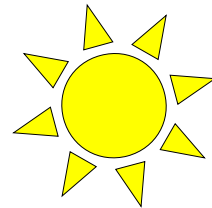


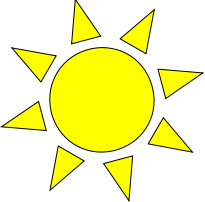
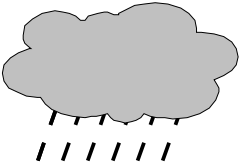
	high	0.9	0.1
	low	0.6	0.4
	high	1	0
	low	0	1



# Weather dynamics (Leipzig)

26.12.2018, 10:00:  
1029 hPa → high



	high	0.9	0.1
	low	0.6	0.4
	high	1	0
	low	0	1





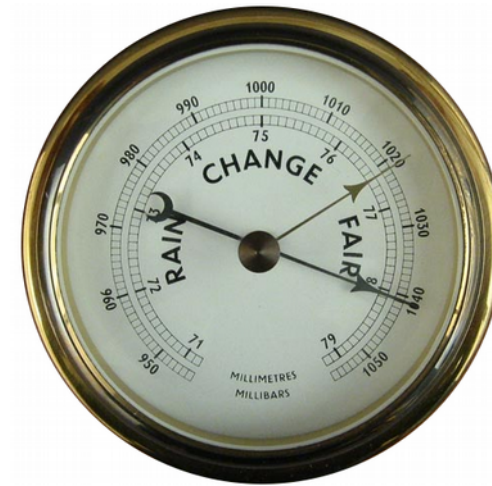
# Information provided by the barometer

Information =

Uncertainty (without barometer)

minus

Uncertainty (with barometer)



Assumption Probability(high) = Probability(low) = 0.5

# Information provided by the barometer

Information =

Uncertainty (without barometer)

minus

Uncertainty (with barometer)



Assumption Probability(high) = Probability(low) = 0.5

Information = 0.39 [bit/day]

# Coming back to calcium

Enzyme dynamics is influenced by calcium

How much of the uncertainty about the enzyme dynamics is taken away, if we know the calcium signal?

→ information transferred  
from calcium to target enzyme



# Transfer Entropy

Quantifies the information transferred by calculating how much uncertainty is lost (or information gained) about a dynamic stochastic process, when the value of the driving signal is known

## Kullback-Leibler-form

T. Schreiber (2000), *Phys. Rev.* **85**(2), 461

$$T_{J \rightarrow I} = \sum p(i_{n+1}, i_n^{(k)}, j_n^{(l)}) \log \left( \frac{p(i_{n+1} | i_n^{(k)}, j_n^{(l)})}{p(i_{n+1} | i_n^{(k)})} \right)$$

Practical problems:

- Signals are not discrete:  
Sums  $\rightarrow$  integrals, probabilities  $\rightarrow$  **Probability densities**
- Probability densities are not known  $\rightarrow$  **Estimation (kernel density, Kraskov, rank-based histogram,...)**
- Confounding variables  $\rightarrow$  **Additional conditioning, influence of history length**

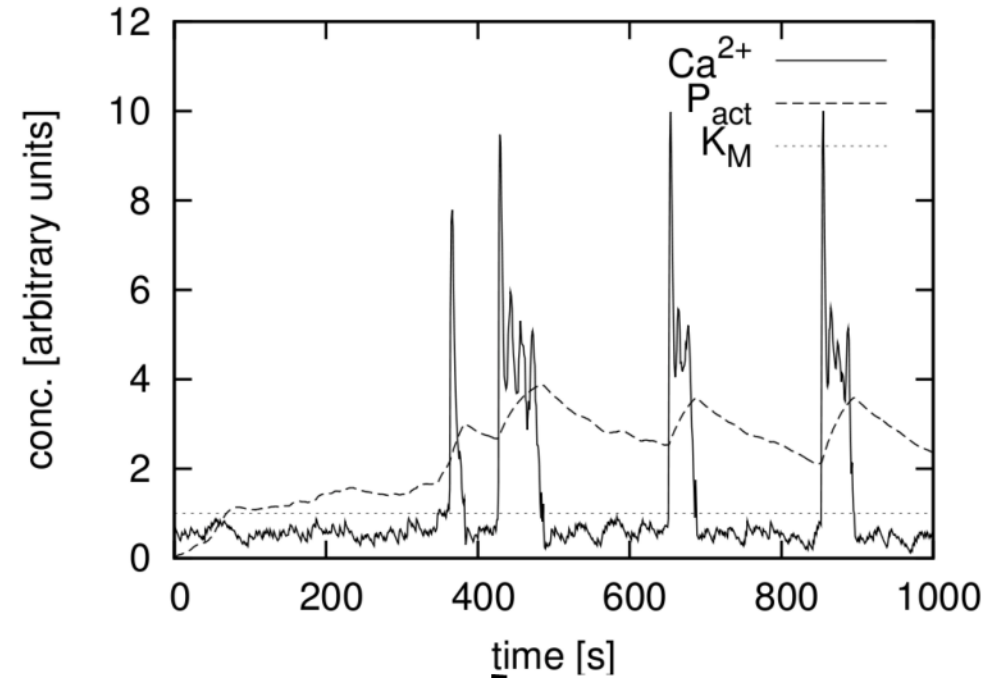
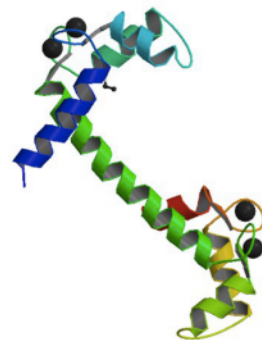
# Coupled protein activation



stochastic coupling  
to a simulated  
protein

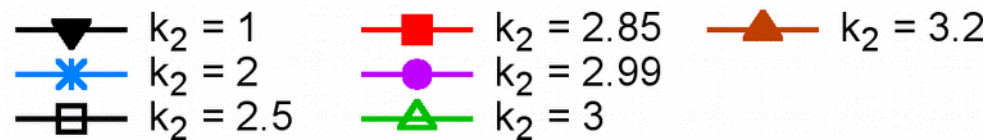
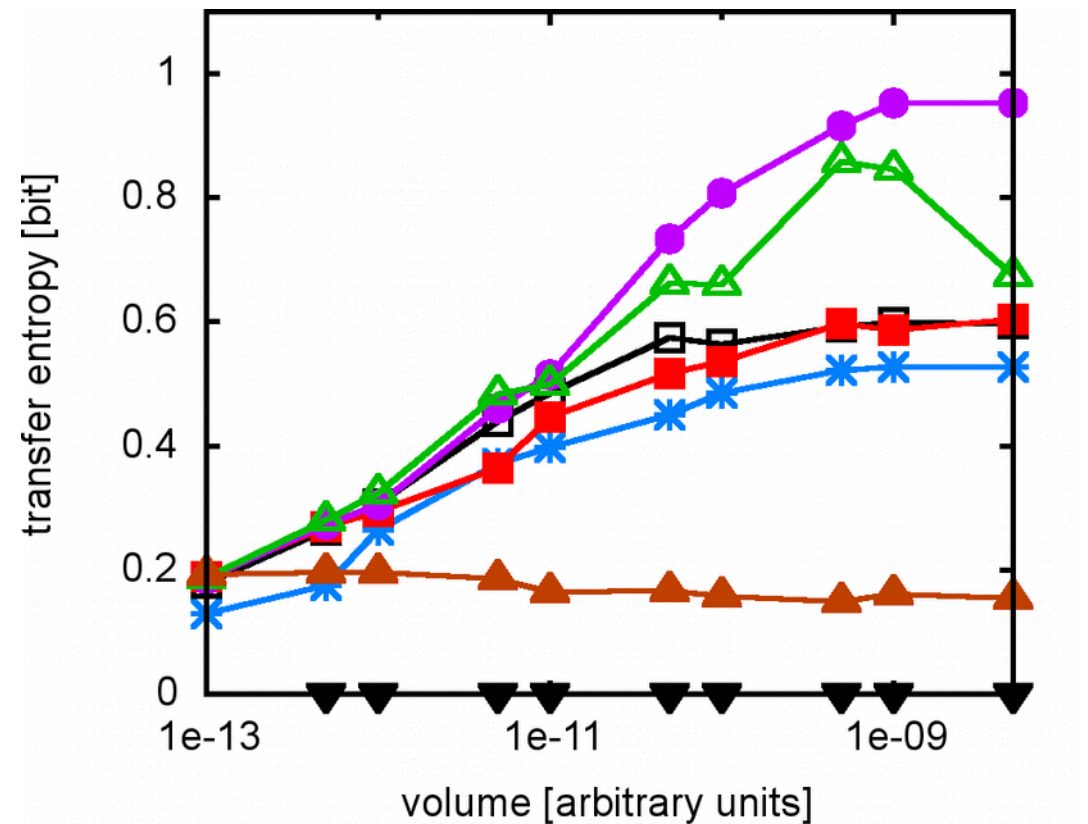
$$\frac{d[P_{\text{act}}]}{dt} = \frac{k_{\text{act}} \cdot [Ca^{2+}]^p}{K_M^p + [Ca^{2+}]^p} \cdot [P_{\text{inact}}] - k_{\text{inact}} \cdot [P_{\text{act}}]$$

e.g.  
calmodulin



estimation of transfer entropy  
(box-assisted) kernel-density estimation  
using rectangular or Gaussian kernels  
rank-based adaptive histogram method

# Information transfer increases with system size



Rate of information transfer increases with increasing system size (particle number)

Bursting: max. rate  $\sim 0.6$  bit/sample

Slight increase in transfer entropy (TE) from spiking to more complex bursting oscillations

In the case of a (elevated) steady state drop to very low values

$k_2$	Dynamics	TE
1	under-stimulation	0.00
2	spiking	0.52
2.5	Bursting	0.59
2.85	Bursting	0.60
2.99	elevated oscillations	0.95
3.2	elevated steady-state	0.15

# Proteins can be tuned to certain characteristics of the calcium input



3D structure

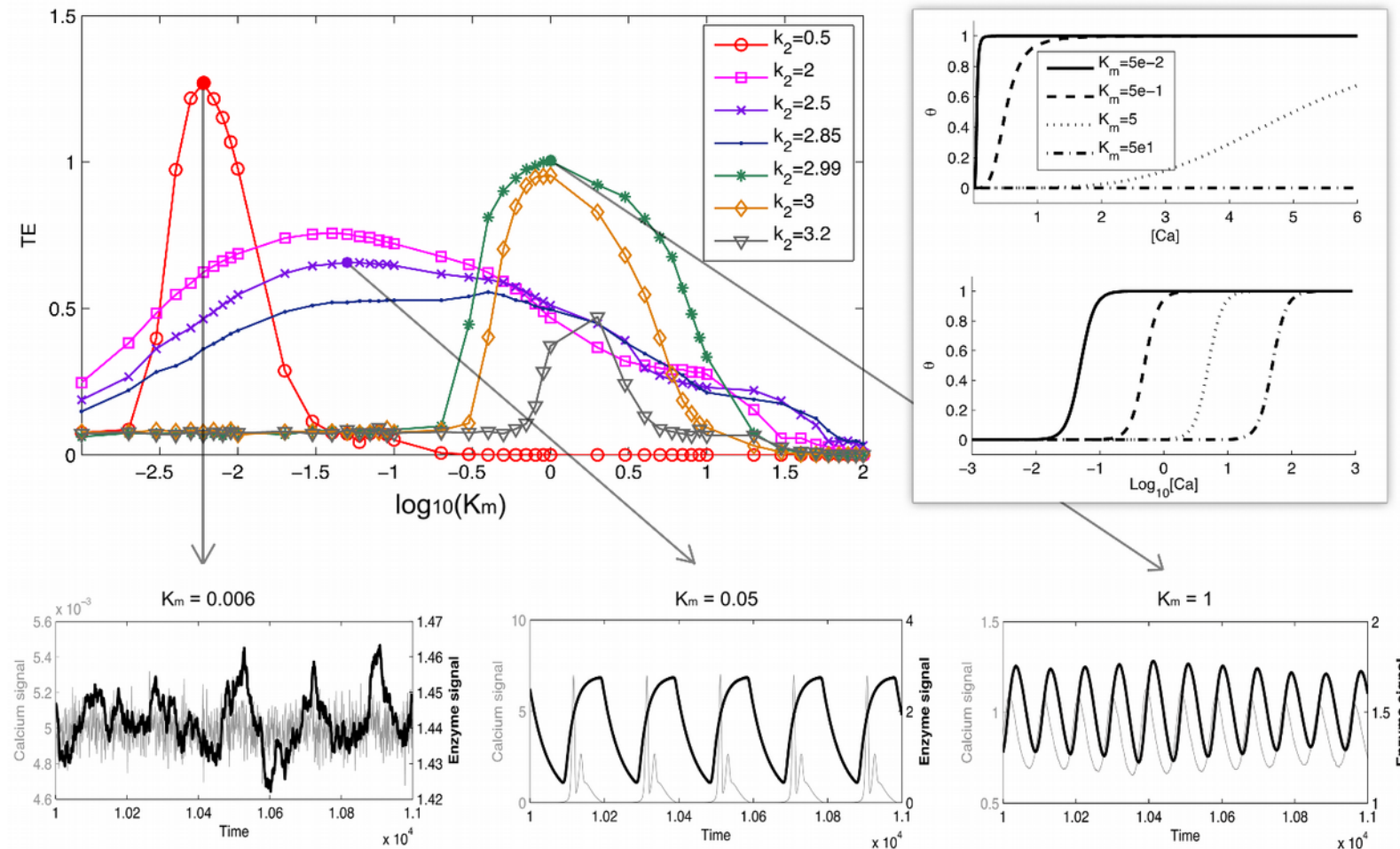


Dynamic behaviour of protein



Which feature of the calcium input influences the activation of a protein most?

→ Differential regulation of proteins!

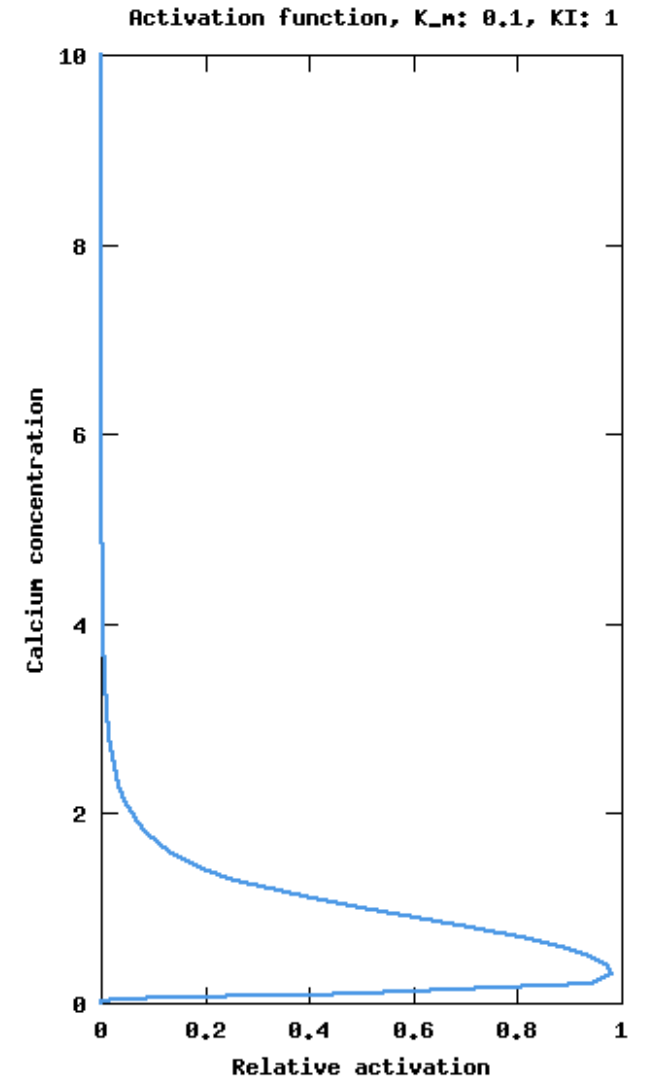
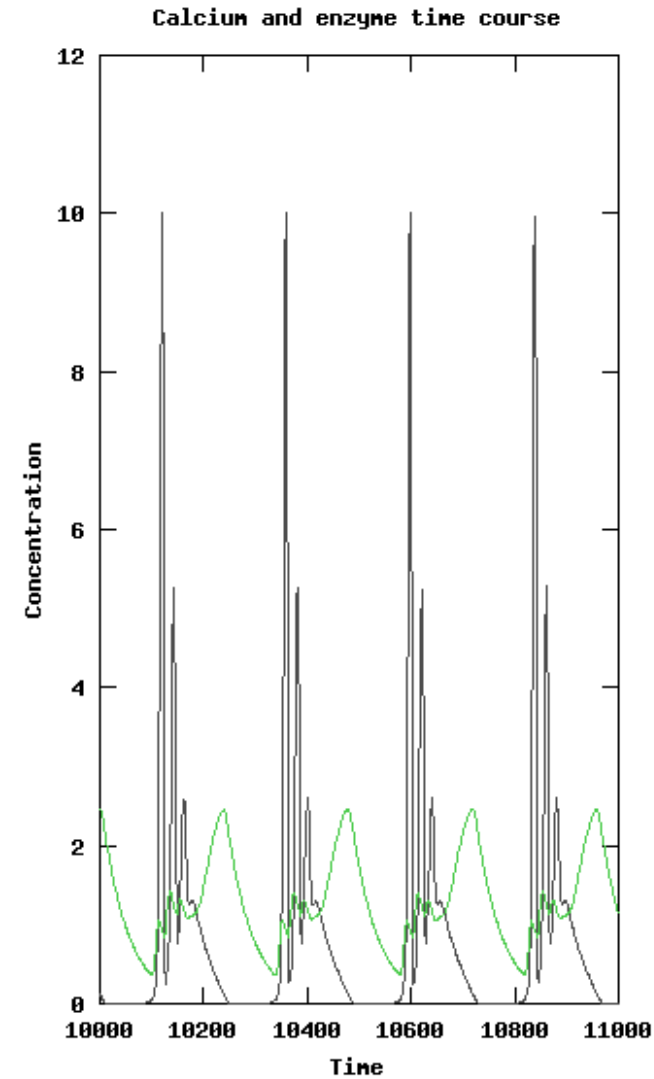
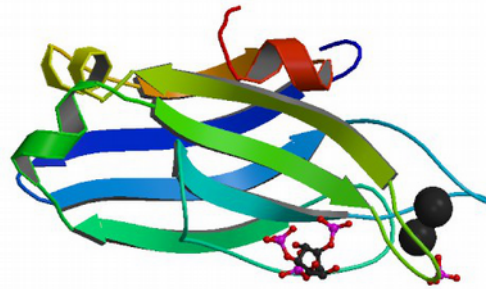


Activation of differently parameterised calmodulin-like proteins by different calcium input oscillations

# More complex proteins allow higher information transfer

(additional inhibitory mechanism)

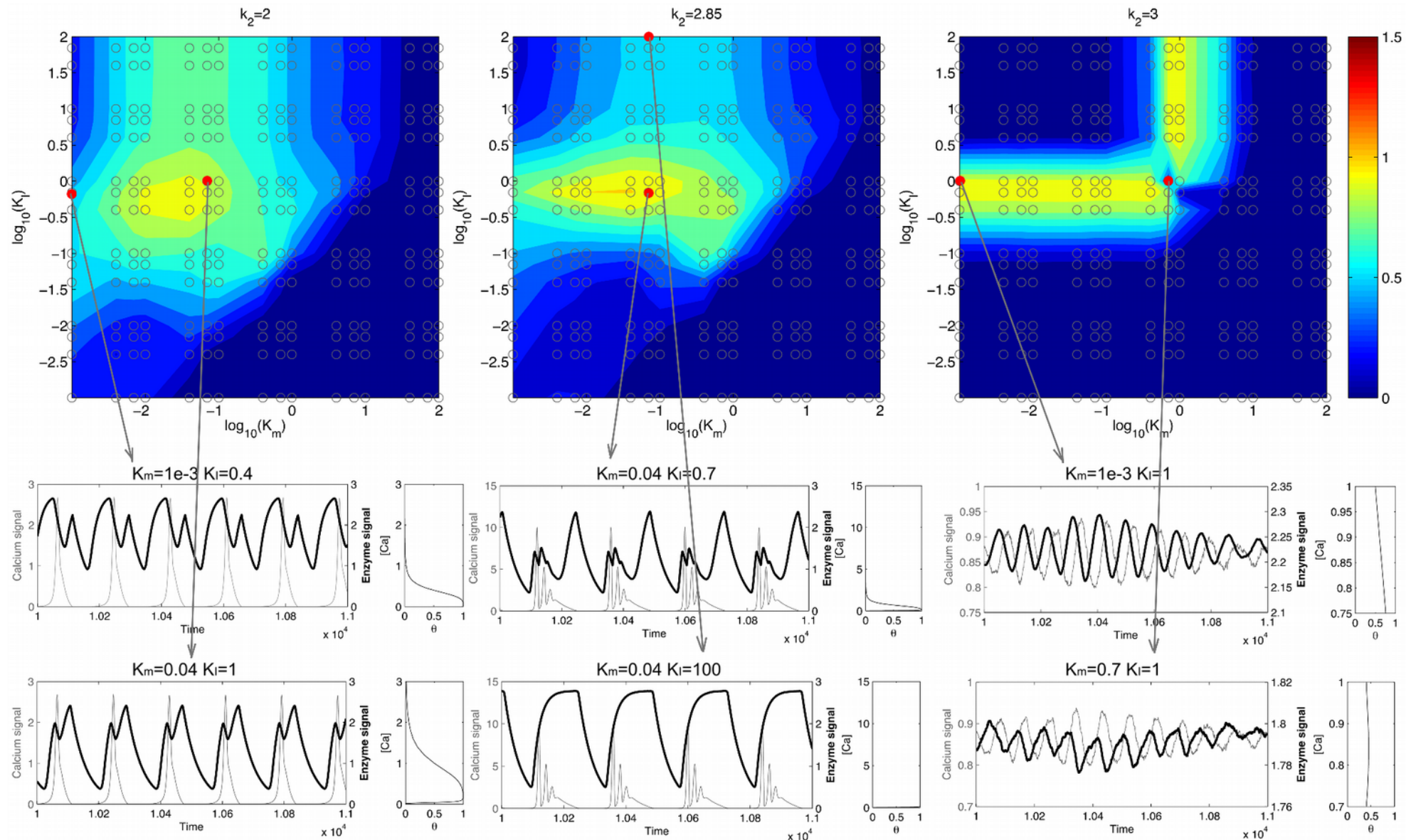
e.g. Protein kinase C (PKC- $\alpha$ )



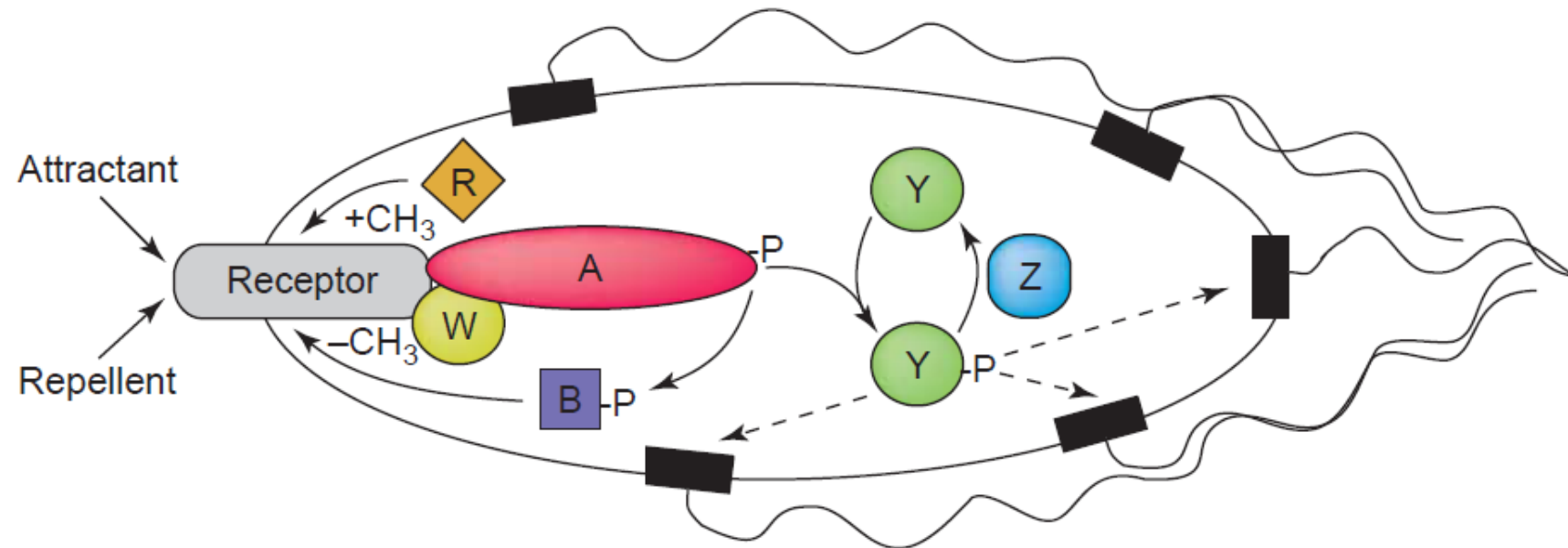
$$\frac{d[P_{act}]}{dt} = \frac{k_{act} \cdot [Ca^{2+}]^p}{K_M^p + [Ca^{2+}]^p} \cdot \frac{K_I^p}{[Ca^{2+}]^p + K_I^p} \cdot [P_{inact}] - k_{inact} \cdot [P_{act}]$$



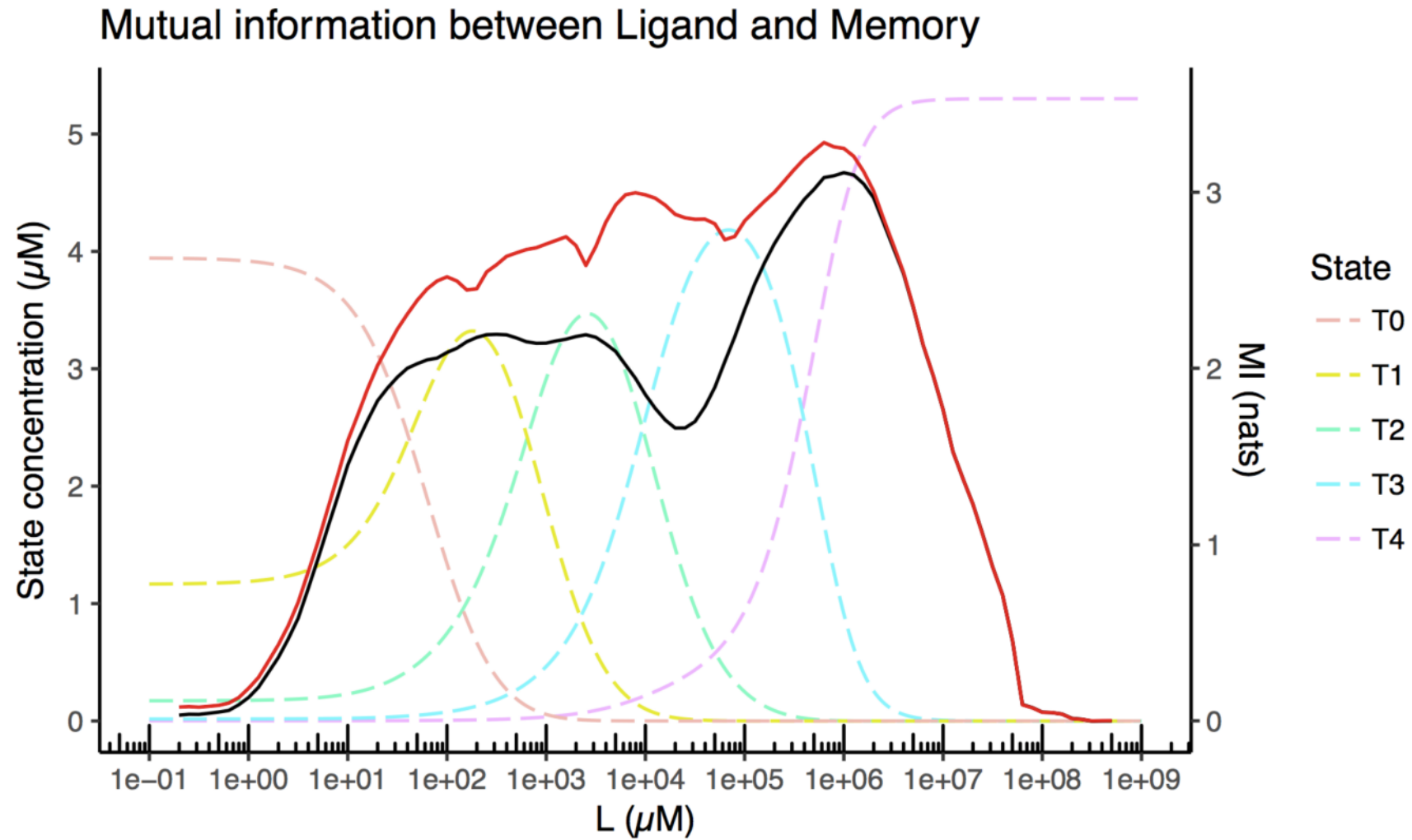
# More complex proteins allow higher information transfer (additional inhibitory mechanism)



# Memory and information flow in *E. coli* chemotaxis

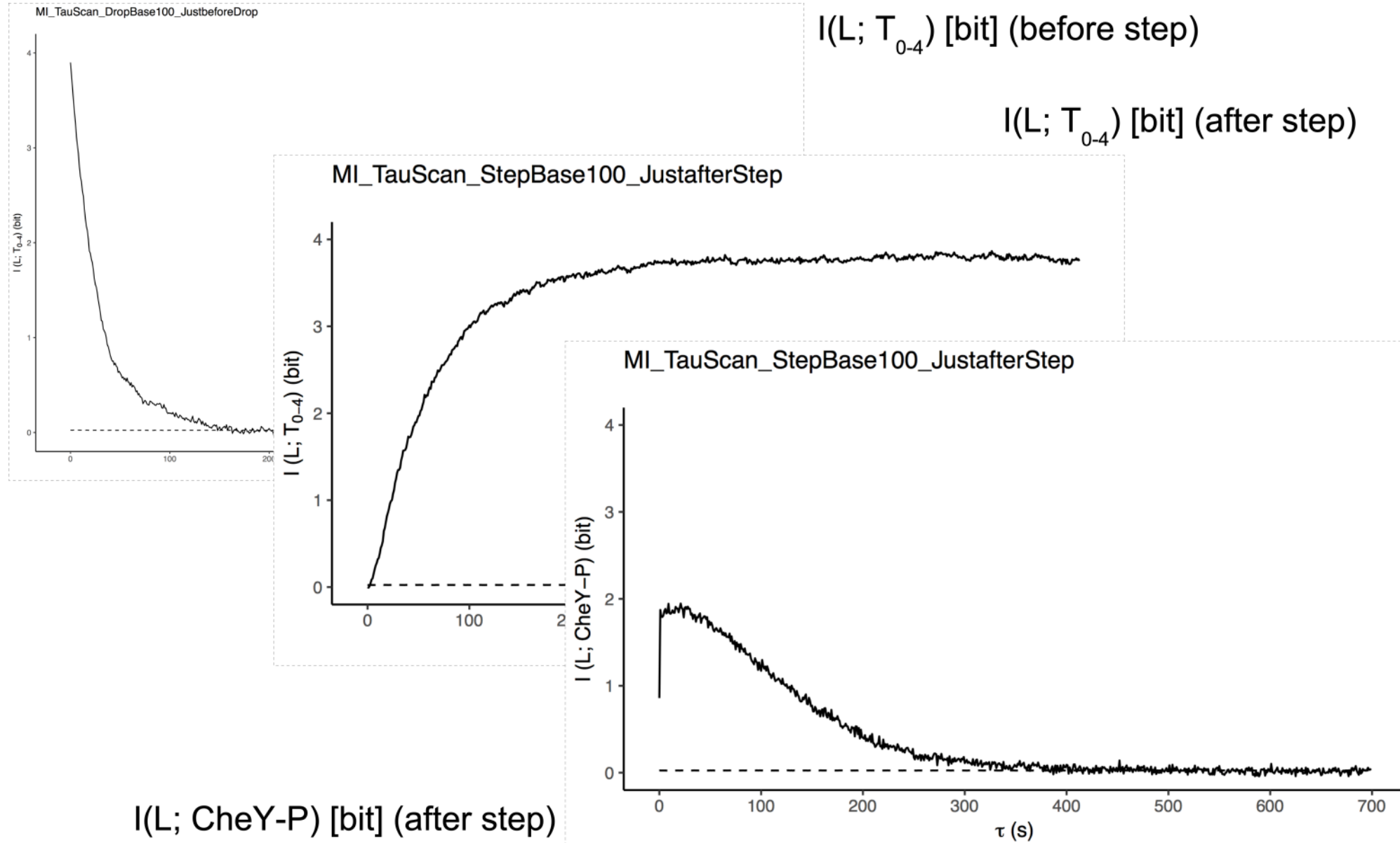


# E. coli memory: Internal representation of outside nutrient (ligand) levels



Memory is in the methylation levels (T0 – T4) of the receptors

# Time- scales of memory building / forgetting / adaptation



# Conclusion

- Information theory can be applied in biology. For instance, this allows to quantify the performance of cellular signalling systems under different conditions.
- Targets of signalling systems can be tuned to the input, such that communication channels are effectively turned on or off depending on the shape of the input.
- Study what features of biological signals carry information (that is relevant for a disease and how to target these) during information transfer (communication in space) and memory (communication in time).
- Estimating and interpreting information-theoretic functionals can be a tricky business.

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# Questions?

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## Links

[lab.pahle.org](http://lab.pahle.org) (BIP group website)

[www.copasi.org](http://www.copasi.org) (biochemical modelling and simulation software)

[jpahle.github.io/CoRC](https://github.com/jpahle/CoRC) (scripting for COPASI)

[OscillatorGenerator](#) (R-package for the generation of artificial oscillatory input signals)

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