

N7: Computational approaches

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HTML Slides: <https://sje30.github.io/n7> (CC BY 4.0 license)

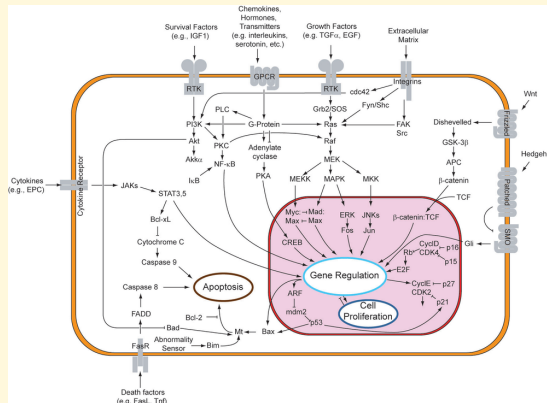
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Part one: introduction

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Why model?

- Everyone models.
- Model system (zebrafish / mouse / organoids).
- I just happen to use the language of maths/computers rather than verbal arguments.



https://en.wikipedia.org/wiki/Cell_signaling

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What can we do with modelling

- Quantitative modelling: test that theories hold true, or test their limits.
- Qualitative modelling: make abstract models to capture essence of a system. (cf. epidemiological modelling since 2020).
- Experiments test for *necessity*; models test for *sufficiency*.
- Make predictions about novel situations.
- Made postdictions to explain past data sets (Abbott 2008).

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Part two: Physiological models

We start with classic Hodgkin and Huxley (1952) model.

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Mathematical description of ion channels

Voltage-gated channels: gating variables $[0,1]$ to represent flow of ions.

For given voltage, e.g. K channel activation, gated by n :

(1- n) Gates switch from closed state to open state with rate α .

(n) Gates switch from open state to closed state with rate β .

i.e.

$$\frac{dn}{dt} = \alpha(1 - n) - \beta n$$

The terms α and β themselves depend on membrane voltage

Similar expressions can be created for sodium activation (m) and inactivation (h).

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Ionic flow determines membrane voltage.

We can derive an expression:

$$c_m \frac{dV}{dt} = -g_L(E_L - V) - g_{Na}m^3h(E_{Na} - V) - g_Kn^4(E_K - V) + I_e$$

where the g terms are the maximal conductances for each channel, and the E terms are the resting potentials for each channel.

This leads to four coupled differential equations.

Solving these requires methods of *numerical integration*.

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Demonstration

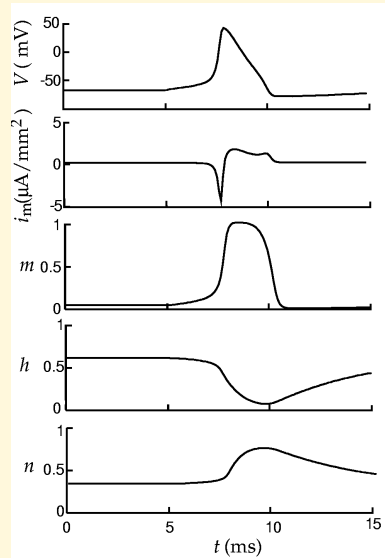
Live demo of all-or-nothing behaviour:

<https://demonstrations.wolfram.com/HodgkinHuxleyActionPotentialModel/>

As you vary external stimulus you can see emergence of an action potential.

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Dynamics of channels and membrane voltage



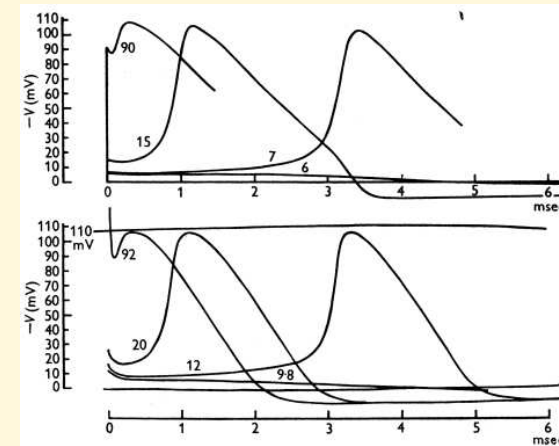
Dayan and Abbott (2002) fig 5.11.

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Goodness of fit

Hodgkin and Huxley(1952). Reproduced from David Sterratt. Upper trace: model; numbers give initial depolarisations (in mV); recordings at 6~C.

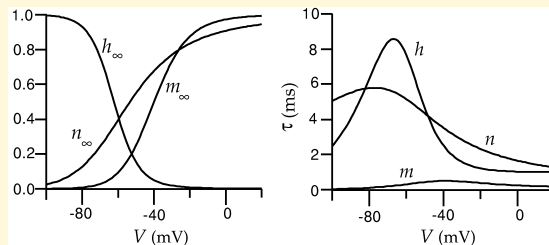
Data taken from squid giant axon; much wider axonal diameter (800 μm) than normal (2 μm) for rapid signal propagation [escape behaviour].



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Simplifications to H-H framework

Two observations (Rinzel, 1985):



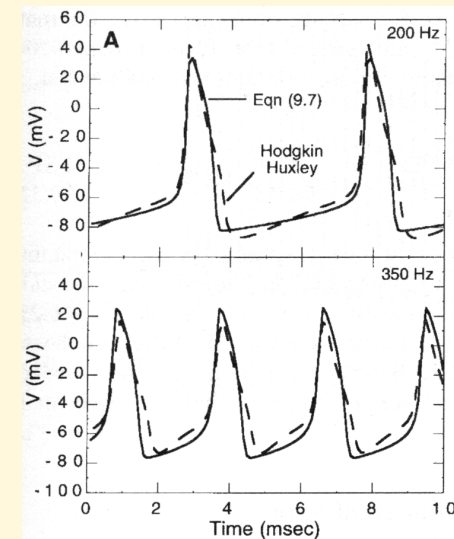
1. m reaches steady-state almost instantaneously.
2. h and $1 - n$ have similar voltage dependence, so model just one of them.

Dayan and Abbott (2002) fig 5.10.

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Rinzel simplification vs HH model

Wilson (1999) Fig 9.3. Comparison of HH model with Rinzel approximation (eqn 9.7). Both systems produce a reduced spike amplitude at higher frequencies.

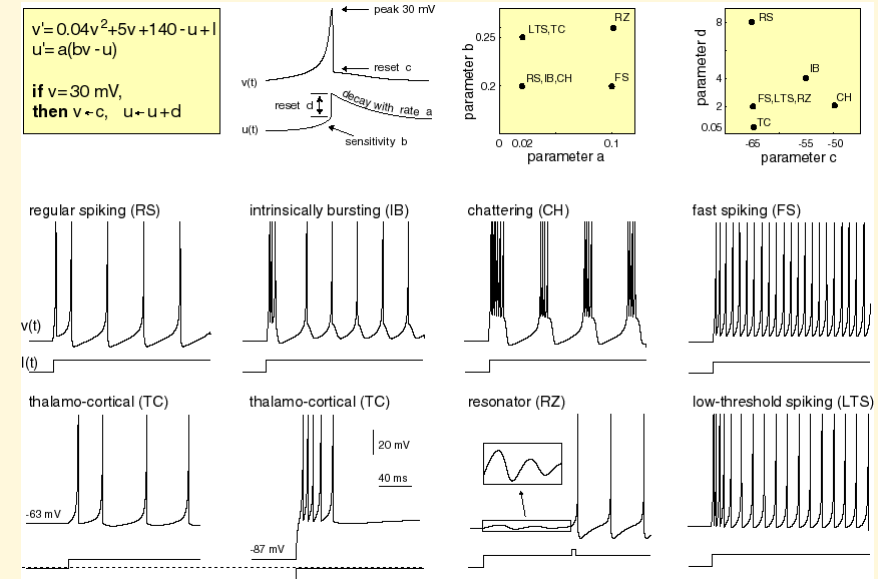


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What is the 'right model' to use?

Various simplifications to Hodgkin-Huxley (Izhikevich, 2004; Figure 2):

What is the Izhikevich (2003) model?



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Application of Izhikevich model neurons

We can now build model circuits using these neurons. e.g. Tomkova et al 2015:
<https://paperpile.com/app/p/5529195b-9246-0d04-8449-09b3cc7289db>

Dynamic clamp

Dynamic clamp takes membrane voltage, and simulates current that will pass through a particular channel; that channel is injected real-time, as if that channel existed on the neuron.

This allows us to use biology to worry about all the other conductances, rather than a modeller using poor estimates of the conductances.

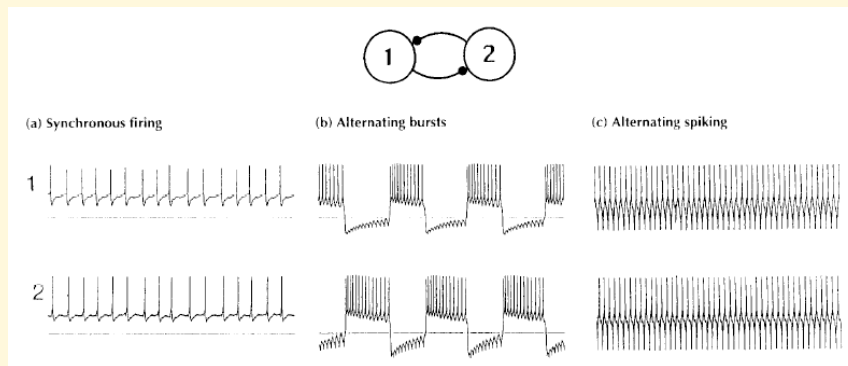
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Dynamic clamp application

Can two mutually inhibitory neurons fire in synchrony?

Use dynamic clamp to *virtually* connect two neurons.

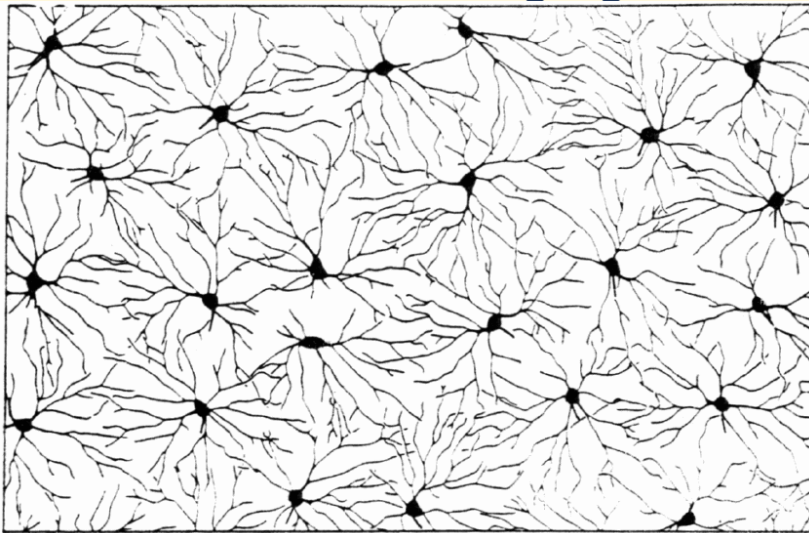


Marder and Abbott 1995, Fig 2

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Part three: Anatomical models

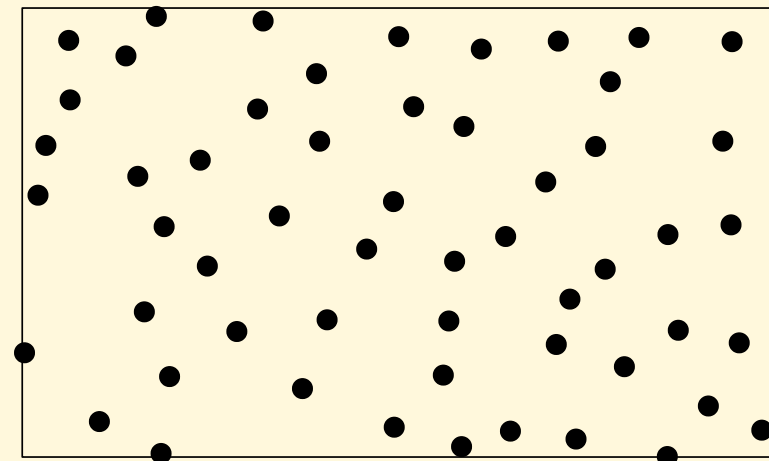
Retinal mosaics: α retinal ganglion cells



1.7 \times 1.2 mm staining of cat retina (Wässle et al., 1981).

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Minimal distance (d_{min}) serial model



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