

# Proposal for MATH3888 project

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# The Hodgkin-Huxley and Hindmarsh-Rose models

The Hodgkin-Huxley model is:

$$C_m \frac{dv}{dt} = -\bar{g}_K n^4 (v - v_K) - \bar{g}_{Na} m^3 h (v - v_{Na}) - \bar{g}_L (v - v_L) + I_{app}$$
$$\frac{di}{dt} = \alpha_i (1 - i) - \beta_i i \quad \text{for each } i \in \{m, h, n\}$$

where  $\alpha_m, \alpha_n$  are of the form  $(a - v)/e^{(b-v)/c} - 1$ ,  $\beta_m, \beta_n, \alpha_h$  are  $ae^{-bv}$  and  $\beta_h$  is of the form  $1/e^{(b-v)/c} + 1$ . The original values of the parameters are  $\bar{g}_{Na} = 120$ ,  $\bar{g}_K = 36$ ,  $\bar{g}_L = 0.3$ ,  $C_m = 1$ . Below is the three-variable submodel of the above given by Rose and Hindmarsh:

$$\frac{dv}{dt} = y - av^3 + bv^2 + I - z$$
$$\frac{dy}{dt} = c - dv^2 - y$$
$$\frac{dz}{dt} = r(s(v - x_1) - z)$$

where  $y = \delta w$  and  $w = r + z$  for a membrane potential  $v$ ,  $r$  recovery variable and  $I$  a non-constant external current. A steady state  $x_1$  is included to ensure consistency with a two-variable system ignoring  $w$ .  $a, b, c, d, s, \delta$  are all constants. This model constitutes replacing the constant  $I_{app}$  with a variable  $I$  and using terms cubic in  $v$ , rather than  $m$  and  $n$ . This gives five points of interest in bifurcation.

## Submodels

There are many submodels to the Hodgkin-Huxely<sup>1</sup> equations, these include things like the Izhikevich<sup>2</sup> model for neuronal spiking, the Moris-Lecar model<sup>3</sup>, which was designed for  $Ca^{2+}$  and  $K^+$  oscillations, and the Hindmarsh-Rose model<sup>4</sup>, which was also designed to model neuronal spiking.

These are all examples of models that are derived from the Hodgkin-Huxely model for the purpose of speciality. The potential of comparing these and other various derivations for this project is interesting; not least for furthering our understanding of the different situations in which to use these models, as well as to further classify the physicality of these models in alternative contexts. This analysis could be done in terms of seeing whether these models, when set up to model the same system, converge in the same time, have similar cycles, bifurcate at different points etc,etc, and to then compare which model best suits a particular situation.

Additionally, if in the course of this analysis we would be able to derive alternatively specialised models that would certainly be extremely interesting.

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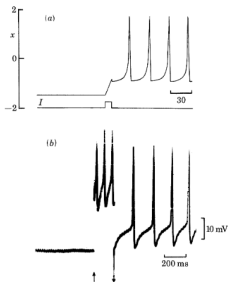
<sup>1</sup>hodgkinhuxely.

<sup>2</sup>izhikevich.

<sup>3</sup>morislecara.

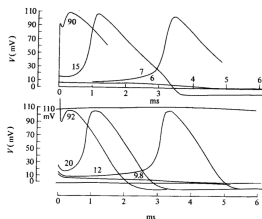
<sup>4</sup>hindmarshrose.

# Comparative analyses



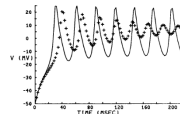
(a) Figure from the paper of Hindmarsh and Rose<sup>a</sup> comparing the models result (top) and experimental data (bottom)

<sup>a</sup>hindmarshrose.



(b) Figure of the Hodgkin-Huxley paper<sup>a</sup> comparing experimental data versus that generated by their model

<sup>a</sup>hodgkinhuxely.



(c) Figure from the Moris-Lecar<sup>a</sup> paper comparing experimental data (solid line) and their models result (dotted line)

<sup>a</sup>morislecar.

All of these figures from their respective initial papers demonstrate the high suitability and accuracy of these models, comparing these models and their usability is of interest.

## Conclusion and bibliography