**FACULITY OF ENGINEERING**

**A PURKINJE CELL MODEL THAT SIMULATES COMPLEX SPIKES**

**BY**

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Declaration and statements of student in respect of their submitted work

I declare that the work in this dissertation was carried out in accordance with the requirements of the University’s Regulations and Code of Practice for Taught Programmes and that it has not been submitted for any other academic award. Except where indicated by specific reference in the text, this work is my own work. Work done in collaboration with, or with the assistance of others, is indicated as such. I have identified all material in this dissertation which is not my own work through appropriate referencing and acknowledgement. Where I have quoted or otherwise incorporated material, which is the work of others, I have included the source in the references. Any views expressed in the dissertation, other than referenced material, are those of the author.

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**Abstract**

Purkinje cells are the principal neurons of the cerebellar cortex. One of their distinguishing features is that they fire two distinct types of action potential, called simple and complex spikes, which interact with one another. Simple spikes are stereotypical action potentials that are elicited at high, but variable, rates (0 − 100 Hz) and have a consistent waveform. Complex spikes are composed of an initial action potential followed by a burst of lower amplitude spikelets. Complex spikes occur at comparatively low rates (∼ 1 Hz) and have a variable waveform. Although, they are critical to all motor coordination in the cerebellar cortex, a simple model that describes the complex spike waveform is lacking. ++

**Keywords: Purkinje cells, neurons, mathematical model, complex spikes, simulation**

Word count: N/A

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1. ***Introduction***

Located in the cerebellum and being amongst the largest neurons in the central nervous system [1], Purkinje cells(PCs) are extraordinary and instantly distinguishable from other brain neurons for their complex planar dendritic trees and for their ability to fire to distinct types of action potential, namely simplex and complex spikes. With over 100,000 input synapses, far most than most other cell types [2] PCs have gathered the interest of many neuroscientists of their potential and capabilities. The mossy fibre connects to the parallel fibre via the granule cell where the parallel fibre pathway regulates the simple spike activity of PCs, ranging from 0 – 100 Hz . On the other hand, climbing fibre input directly triggers complex spikes (CS) at a remarkably low frequency (~1 Hz) [3] with one climbing fibre per PC. CSs can induce long-term depression at parallel fiber synapses on PCs, which may be involved in cerebellum-dependent learning and motor coordination [4] [5].

Despite the existence of a range of computational models to address various features of Purkinje cells, a simple model that captures complex spike generation, waveform variability. In the current paper we explore through simulation the hypothesis that a restricted number of channel-dynamics can explain complex spike waveform. One model is presented: a three-current model that shows that three channels, a leak channel and two active channels, are sufficient to simulate the complex spike waveform. These models serve as a description of the essential ion-channel dynamics supporting complex spike production and should enable further analysis of complex spiking and its relationship to simple spiking. In this way, the models complement the large and detailed models described by Veys et al. (2013); Zang et al. (2018) and give a starting point for a model which also incorporates the interaction between simple spike rate and complex spike waveform described in Burroughs et al. (2017).

1. ***Methods***

In this paper a model of the Purkinje cell somatic voltage dynamics is presented with a three-current model, which has a leak channel and two voltage-gated channels:

( )

where Cm = 1 μF / cm2 is the membrane capacitance, is a leak current,

( )

with = 0.3 mS / cm2 and = 10.613 mV. INa and IK stand for the sodium current and the potassium current. The most commonly used sign convention in neural modeling is that ionic current flowing out of the cell is positive and ionic current flowing into the cell is negative [6].

* 1. **Ion channels**

The current through the sodium channel was modelled using a Markovian scheme developed by Raman and Bean [7] , as seen in Table 1. This scheme models the dynamics of both the transient and resurgent gate. The sodium current is:

( )

Where *o* is the fraction of gates in the open state O, = 120.0 mScm−2 and VNa = 115 mV

Diagram, schematic

Description automatically generated with medium confidence

Table : Current through the resurgent sodium channel is described using a Markovian Scheme.

Where

( )

( )

( )

and γ = 150 ms−1 , δ = 40 ms−1 , ε = 1.75 ms−1 , D = 0.005 ms−1 , U = 0.5 ms−1 , N = 0.75 ms−1 , F = 0.005 ms−1 with

( )

The potassium current is:

( )

Where , = 36.0 mScm−2 and VK = -12 mV. *n* is described with the usual Hodgkin-Huxley channel equations(Eq 17, Eq 18) described in 2.2.

* 1. **Hodgkin-Huxley model**

The **Hodgkin–Huxley model**, or **conductance-based model**, is a mathematical model that describes how action potentials in neurons are initiated and propagated. It is a set of nonlinear differential equations that approximates the electrical characteristics of excitable cells such as neurons. It is a continuous-time dynamical system.

The typical Hodgkin–Huxley model treats each component of an excitable cell in this case a Purkinje cell as an electrical element. The lipid bilayer is represented as a capacitance (Cm). Voltage-gated ion channels are represented by electrical conductances (, for the potassium channel and for the sodium channel) that depend explicitly on voltage. Leak channels are represented by linear conductances (). Finally, the membrane potential is denoted by *Vm,* and it is time dependent.

Thus, for a cell with sodium and potassium channels, the total current through the membrane is given by:

( )

The Hodgkin and Huxley developed a model in which the properties of an excitable cell are described by a set of four ordinary differential equations. Together with the equation for the total current mentioned above, these are:

( )

( )

( )

( )

where *I* is the current per unit area, and α{\displaystyle \alpha \_{i}} and {\displaystyle \beta \_{i}}β are rate constants for the each ion channel, which depend on voltage but not time. There are three gating variables: n for the Potassium channel activation, m for the Sodium channel activation (opening) and h for the Sodium channel inactivation (closing). The value of a gating variables is dimensionless and will vary between 0 and 1; 0 indicates that the channel is closed, whereas 1 indicates that the channel is open. The gating variable fraction is an indication of the conductance of a certain ion at a given time and membrane voltage

( )

( )

( )

(n,m,h)∞ are the steady state values for activation and are usually represented as a function of Vm.

Chart, histogram

Description automatically generated

Figure : Potassium and Sodium channels as function of time{\displaystyle V\_{m}}

One representation of the Hodgkin–Huxley model can be thought of as a differential equation system with four state variables, {\displaystyle V\_{m}(t),n(t),m(t)}V(t), n(t), m(t) and h(t){\displaystyle h(t)}, that change with respect to time{\displaystyle t}. The system is difficult to study because it is a nonlinear system and cannot be solved analytically. However, certain properties and general behaviors, such as limit cycles(closed trajectories), can be proven to exist using numerical methods. A picture containing chart

Description automatically generated

Figure : Limit cycles of the gating variables as a function of Voltage

Channel kinetics are described with the original Hodgkin-Huxley channel equations and constants with, α, β being the forward and backwards rate in ms-1, respectively.

( 17 )

( 18 )

( 19 )

( 20 )

( 21 )

( 22 )

If Eqs. 23 and 24 above are compared with Eqs. 12 and 13 from the original paper (Hodgkin and Huxley, 1952), you will note that the sign of the membrane voltage has been changed to correspond to the modern convention (see subsection on Voltage Conventions above). Hodgkin and Huxley used similar functional forms to describe the voltage dependence of the m and h gates of the sodium channel:++--

One other technical note is that certain function forms can become indeterminate at certain voltage values(Nelson05-ElectrophysModels). Given a specific voltage, an(Vm) and am (Vm) may evaluate to the indeterminate form 0/0. The solution to this problem is to apply L’Hospital’s rule [8], which states that if f(x) and g(x) approach zero as x approaches a, and f ‘(x)/ g’(x) approaches L as x approaches a, then the ratio f (x)/ g(x) approaches L as well. Using this rule, it can be shown that an(10) = 0.1 and am(25) = 0.430825375 . Hence, the limits for every case are hand-tuned for simplicity and efficiency.

All the input parameters listed in Table 2, are defined in Python.

|  |  |  |
| --- | --- | --- |
| ***Parameters*** | ***Chosen Value*** | ***Reference*** |
| Cm (μF/cm2) | 1.0 | [9] |
| (mS/cm­­2) | 120.0 | [9] |
| (mS/cm­­2) | 36.0 | [9] |
| (mS/cm­­2) | 0.3 | [9] |
| Vm (mV) | 0.0 | [9] |
| VNa (mV) | 115.0 |  |
| VK (mV) | -12.0 |  |
| Vl (mV) | 10.613 |  |
| VThreshold (mV) | 55.0 |  |
| Iinj (μA/cm2) | 10.0 |  |
| Tmax (ms) | 35.0 |  |

Table 2: Experimental Constants for the Hodgkin and Huxley model

Chart, line chart

Description automatically generated

Figure 3: Neuron potential as a function of time

Simulations were run in Python 3.9.10, OS on a CPU. Models were simulated as ordinary differential equations and integration was performed explicitly using the scipy.integrate.odeint package suitable for stiff problems or non-stiff problems of first order ode-s. One second of Purkinje cell activity can be simulated in N/A minute N/A seconds.

Optimization was performed using a mixture of error minimization and hand-tuning techniques.

1. ***Results***
2. ***Discussion***

**Code Availability Statement:**

The Python source code used to create the figures and the modelling is available at github.com/PurkinjeCell.

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