

Abstract

The small (1 mm) nematode *Caenorhabditis elegans* has become widely used as a model organism; in particular the *C. elegans* connectome has been completely mapped, and *C. elegans* locomotion has been widely studied (c.f. <http://www.worm-book.org> Corsi [1]). We describe a minimal reaction-diffusion model for the *C. elegans*, which results in similar behaviour to the neuromechanical model of Izquierdo & Beer [2]. This may be considered as a simple model for Xu et al.'s "descending pathway" description of the *C. elegans* central pattern generator (CPG) Xu et al. [3] and Wen et al. [4]. Olivares et al. [5] present a likely more realistic model which relies on small networks of neurons, and presents a distributed model of the CPG. In particular, we use simulation methods to show that a small network of FitzHugh [6]-Nagumo et al. [7] neurons (one of the simplest neuronal models) can generate key features of *C. elegans* undulation (see Magnes et al. [8]), and thus locomotion. Finally, we recreate the required oscillations and coupling with a network of coupled Keener [9] analog neurons. Olivares et al. [5]

A minimal reaction-diffusion neural model generates *C. elegans* undulation

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1 Introduction

The small (1 mm) nematode *Caenorhabditis elegans* (*C. elegans*) has become widely used as a model organism [1], and has been among the most widely studied biological models of neuronal development, locomotion and the central pattern generator [10]. The *C. elegans* connectome has been completely mapped [11] and, as described below, its locomotion has been widely studied (Corsi [1]). There are a variety of neuronal models which can generate such undulation, “When crawling on a solid surface, the nematode *C. elegans* moves forward by propagating sinusoidal dorso-ventral retrograde contraction waves. A uniform propagating wave leads to motion that undulates about a straight line.” [12]. A different type of locomotion, often called swimming, occurs when nematodes are submerged in a liquid medium. The nematodes “switch” between these two gaits, under the regulation of particular serotonergic and dopaminergic neurons.

The purpose of this paper is to describe a minimal, biomimetic, reaction-diffusion model for the *C. elegans* central pattern generator (CPG) [3, 4]. We use simulation methods to show that a small network of FitzHugh [6]-Nagumo *et al.* [7] neurons (one of the simplest neuronal models) based on a skeleton model of the *C. elegans* CPG can reproduce key features of *C. elegans* undulation [8] and thus locomotion.

In addition to simulating the CPG, we also implemented a modified version of the FitzHugh-Nagumo neuron, originally proposed by Keener [9], as an analog circuit. This circuit solves the Keener differential equations, and we adjusted it to allow diffusive coupling between neurons. We made a small network with these “neuro-mimetic” circuits, and showed that their behaviour replicates FitzHugh-Nagumo simulated behaviour.

There are many other models for the CPG; for example, a 2019 preprint by [5] proposes a distributed network of oscillating systems, instead of a structured chain like our proposed CPG. The point of this paper is to create a minimal working model, though, and not to strive for full realism.

Olivares *et al.* [5] recently created a more biologically relevant model for the CPG, which argues that the CPG is a network of connected, self-oscillating systems. The role of this paper is to show a very minimal model, and our approach has been to create a small and

computationally cheap model.

2 The model central pattern generator

A central pattern generator is a small neural circuit which generates and regulates the movement of complex organisms. This structure is present in different forms in many animals, and it regulates many types of periodic motion. Xu *et al.* [3] proposed an architecture for the CPG of *C. elegans* which is described below in figure ??.

In more complex animals, like horses or dogs, there is only one CPG; the dynamics of the CPG change depending on the gait of the animal [13]. The mode of locomotion depends on the sequence in which the neurons fire, but the network’s topology remains the same. We show later that breaking the symmetry of the CPG model can lead to radical changes in behaviour.

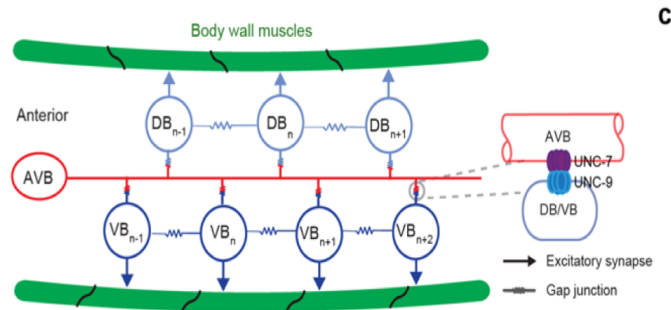


Figure 1: The central pattern generator proposed by Xu *et al.* [3]. Note the structure of the neurons, especially the head oscillator driving the descending pathway.

The central pattern generator has two principal components. First is the **head oscillator**. As described by Gjorgjieva *et al.* [14], the head oscillator consists of two “head neurons” with mutually inhibitory coupling. Oscillations are generated when this coupling destabilizes an excitable steady state.

In the terms of dynamical systems analysis, the oscillations destabilize to a stable limit cycle. The mutual inhibition and symmetry between neuron pairs leads to a phase lock of 180° . This provides out-of-phase stimuli which propagate through the descending pathway, with the inhibition between neuron pairs keeping the oscillations stable.

Second is the **descending pathway**, which consists of pairs of coupled, excitable, dorsal and ventral neurons. These follow the body of the worm, and are linked to motor neurons and muscles. The head oscillator drives the descending pathway, and the pathway is kept in sync by mutual inhibitory coupling between neurons.

While *C. elegans* has twelve pairs of motor neurons, we have only used six pairs in our model. An equivalent result could be obtained with more neurons, by increasing the coefficient of diffusion along the pathway, causing a shorter phase lag between neuron pairs. Figure ?? on the next page is a depiction of our simplified model as a graph, wherein neurons are nodes, and the arrows between them symbolize connections.

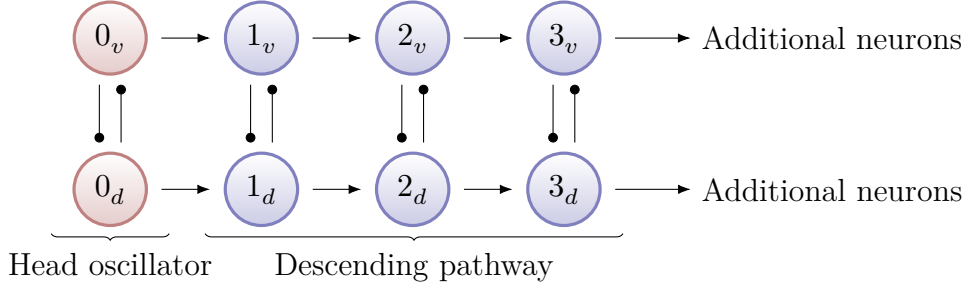


Figure 2: Our simplified central pattern generator model. Descending coupling (shows inhibitory connections, and potential flows through gap junctions, not necessarily symmetric)

3 The FitzHugh-Nagumo Neuronal Model

In accord with the goal of this paper, we sought the simplest relevant neuronal model. The classical Hodgkin-Huxley[15] model of squid neurons has led to a variety of simpler conduction models, including the Morris-Lecar[16] and Fitzhugh-Nagumo (FHN) models.

The FHN model consists of two dynamical variables; a fast activator variable v corresponding to the (rescaled) membrane potential, and a slow inhibitor variable w corresponding to a generalized gating variable.

$$\begin{aligned}
 dv &= f(v) + w - I_{\text{ext}} \\
 dw &= \epsilon(a - bv) \\
 f(v) &= \frac{v^3}{3} - v
 \end{aligned} \tag{1}$$

The parameter I_{ext} is an external driving current, and can also be used to increase excitability. In the analog implementation, this is an integral component of tuning the neuron's frequency response.

In this system, $f(v)$ can be any function which retains the appropriate dynamics, in that it has the same general shape as the cubic $f(v)$. In our analog implementation, we use a piecewise linear approximation to the cubic, in order to simplify the circuit and avoid using expensive components. Here, the position of the w -nullcline is controlled by a , and the vertical translation of the v -nullcline is controlled by I_{ext} .

Xu et al. described a simplified two-variable model consisting of a fast, cubic-like activator variable (see the V-nullcline) and a slow, non-linear inhibitor variable (see the n-nullcline). The Fitzhugh-Nagumo model has similar activator nullclines.

The original system was meant to model one neuron only. Following ***, we used generalized diffusion coupling between FHN neurons to mimic synapses. A positive coefficient would simulate a gap junction, or an excitatory synapse; a negative coefficient would simulate inhibitory coupling (Collins & Richmond [13]).

The equations, when modified for synaptic connections, look like this:

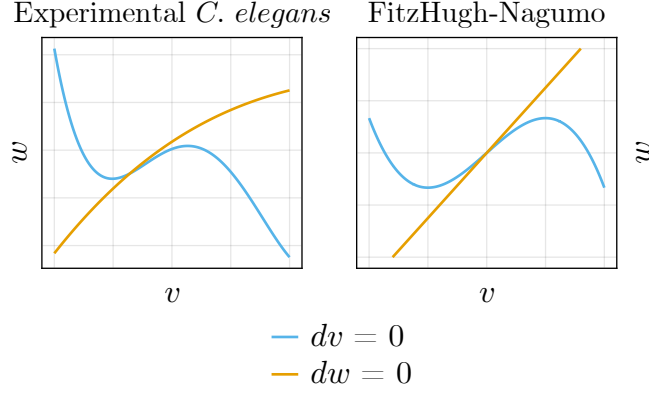


Figure 3: Nullclines of several different neuronal models; on the right is the biological model of Xu et al, in the centre is the Morris-Lecar model, and to the right is the FitzHugh-Nagumo model. These have been arranged in order of decreasing complexity.

$$\begin{aligned}
 dv &= f(v) + w - I_{\text{ext}} + D(\Delta v) \\
 dw &= \epsilon(a - bv) \\
 f(v) &= \frac{v^3}{3} - v
 \end{aligned} \tag{2}$$

where Δv is the difference in voltage between the driving and driven neurons, essentially $\Delta v = v_{\text{driven}} - v_{\text{driving}}$.

4 Simulation

We performed the simulations in Python, using the standard SciPy ODE solvers, which wrap LSODA.

4.1 Methods

See the appendix, or attached code, for how we simulated this motion. It will be published on Github with embedded plots, so people can see it.

We realize the network shown in Figure ?? on the preceding page into a system of ODEs, and solve it. The equations are integrated, giving a timeseries of neuronal potentials. These were passed through filters to simulate muscular movement and the resistance of the medium. We used Gaussian smoothing and B-splines for this purpose.

We generated a video by fixing the head of a worm to the origin, and re-normalizing the coordinates resulting from the filtering.

4.2 Generating undulation from neuron potential

The CPG network which we created is of the same form as the 2-D musculature of our simulated worm. Each neuron is attached to a muscle; when it fires, it causes the attached muscle to contract. We model the muscles as leaky integrators of the neuron’s voltage; therefore, Gaussian smoothing of the neuron’s voltage works to “create” an effective muscle contraction signal. Through Gaussian smoothing, the movement is heavily dependent

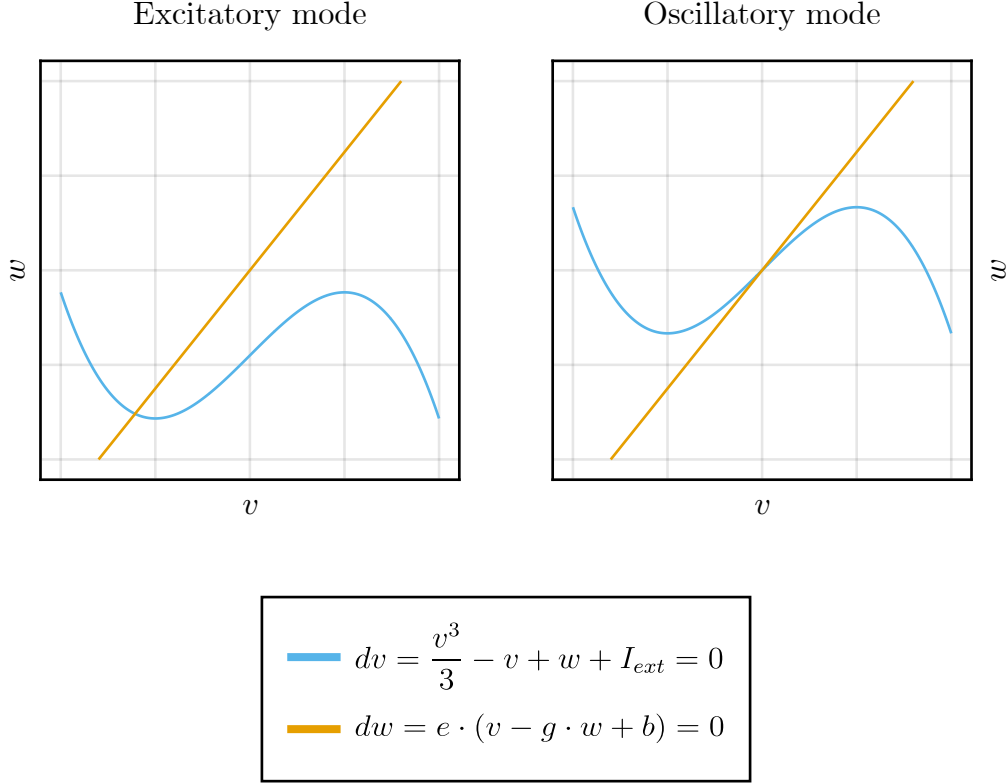


Figure 4: The nullclines of the FitzHugh-Nagumo neuron. Nullclines are isoclines where the derivative of a variable is zero. Here we show an oscillatory mode and an excitable one. In an oscillating cell, the stable equilibrium is replaced by an unstable equilibrium (open circle) around which it circles indefinitely. See Parsons & Huizinga [17] for a clear explanation of the dynamics of oscillatory biological systems.

on the current state of the neuron but also dependent somewhat on the history.

Much like Izquierdo & Beer [2] did, we take a segment-based approach to the worm model. Pairs of muscles on either side determine the overall angular displacement per segment. The magnitude of the “contraction” resulting from the smoothing is interpreted as an angular displacement for that segment. We use a cubic spline interpolation to smoothen the worm body.

Each neuron is assumed to be connected to a muscle; when it fires, it should cause that muscle to contract. Pairs of neurons on either side determine the overall angular displacement per segment. Gaussian smoothing and a cubic spline are used to mimic muscle movement and medium resistance. The magnitude of the “contraction” resulting from the smoothing is interpreted as an angular displacement for that segment.

In this model, muscles can be seen as “leaky integrators” (Boyle et al. 2012) – the movement is heavily dependent on the current state of the neuron but is also dependent somewhat on the history.

4.3 Comparison to real worm

Cite the paper which Jenny sent here. It can be seen that our model closely approximates an unconstrained worm, specifically of the wild type.

While the angle which a worm crawling on agar subtends tends to be oblique, as the constraint on the worm decreases, the angle becomes more and more acute - consider the videos. It is not hard to see that a fully unconstrained worm might behave much like our model does.

The worm undulates in a sinusoidal manner, both in simulation and reality.

5 Analog implementation

Nagumo *et al.* [7] proposed a circuit to simulate a FitzHugh-Nagumo neuron, shown in Figure 5. It used a tunnel diode to achieve a cubic-like activation function, and an inductor to differentiate the K current. However, this approach presents several complications. Tunnel diodes are rare, and rather expensive; inductors cannot be used in proximity because of mutual inductance effects, and are quite large.

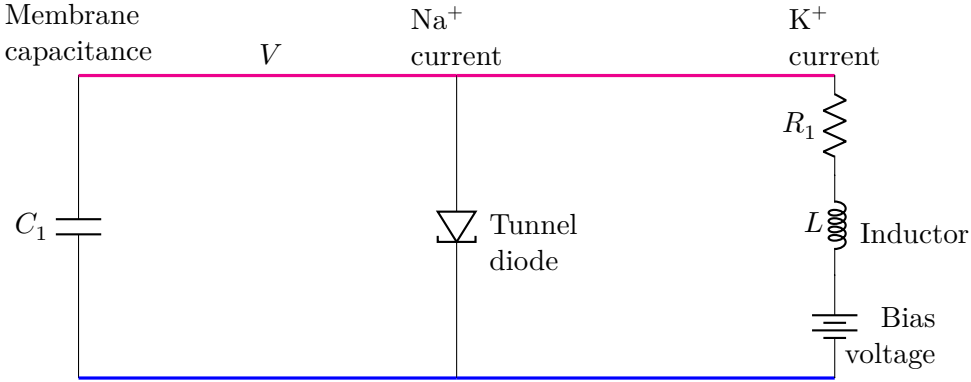


Figure 5: The original circuit proposed by Nagumo *et al.* [7]. Note the use of inductors for differentiation, and the tunnel diode to supply a cubic-like V-I curve. Our circuit, based off Keener [9], is arranged in the same layout, to make the similarities and differences more explicit.

The sodium channel in the FitzHugh-Nagumo equations has a negative resistance regime, wherein the current decreases as the voltage increases. Nagumo's tunnel diode exhibits this behaviour, but it may be replaced by any device with a similarly nonlinear V-I curve. The necessary feature is that in the oscillatory regime, the system is a relaxation oscillator, and that it has an excitable regime.

Keener [9] proposed a modified Nagumo circuit which used the saturation properties of operational amplifiers ("op-amps") to achieve cubic-like non-linearity in the FHN model. He also used an op-amp and a capacitor to simulate the inductor in the original Nagumo circuit.

As a result of the piecewise linear approximation to the cubic, the nullclines of the circuit system differ slightly from the original FitzHugh-Nagumo nullclines. However, in experiments this did not cause a significant change in the dynamics of the individual neuron, or many connected together - the nullclines are sufficiently similar that the dynamics are effectively the same.

Our modifications to Keener's proposed circuit are mainly concerned with diffusive coupling between neurons. If each individual circuit is thought of as a single neuron, then we implemented diffusive coupling methods between those neurons. We also found that you

don't need separate power supplies, and you can get finer control by adjusting the bias voltage and input through a separate mechanism.

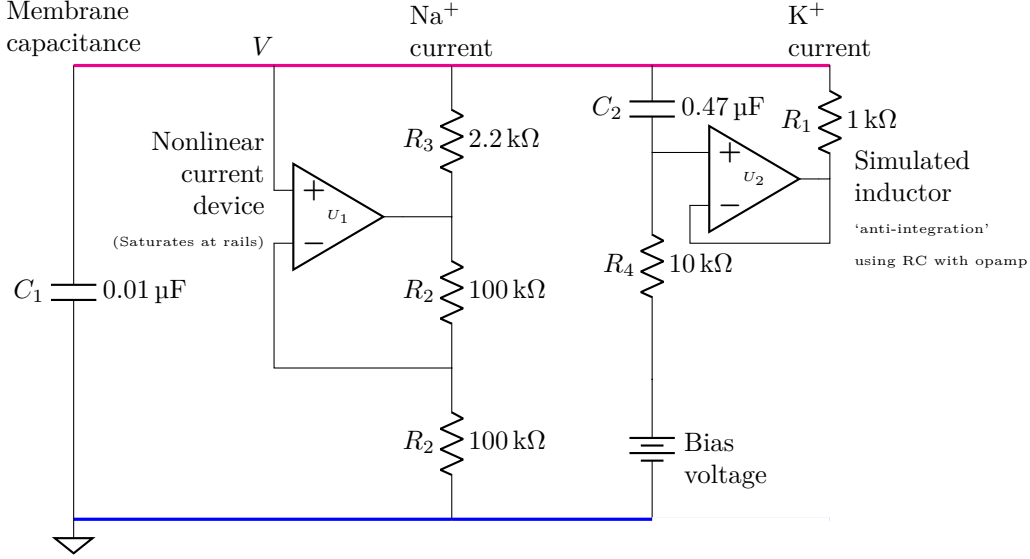


Figure 6: The circuit we created, based of Keener [9]. Note the use of operational amplifiers in place of the inductor and tunnel diode; though this circuit looks more complex, in practice it is quite simple to implement.

However, this is only one neuron. In order to implement a full central pattern generator, we implemented diffusive coupling mechanisms. These mechanisms are shown in Figure ?? on page ??. We implemented a positive diffusion coefficient by passing the voltage through a resistor (to simulate D), and then a diode (to simulate $\max(\Delta v, 0)$). The negative diffusion coefficient was implemented by using an inverting amplifier with a small gain, and then passing through a diode.

5.1 Comparison of analog and simulation

To compare the analog implementation with our simulated model, we will focus on the timeseries output of the neurons, and not on the end worm. Include the relevant figure here - you can see clearly that the effect is the same. There are some differences in the waveform because of the different activation function in the circuit (linear interpolation).

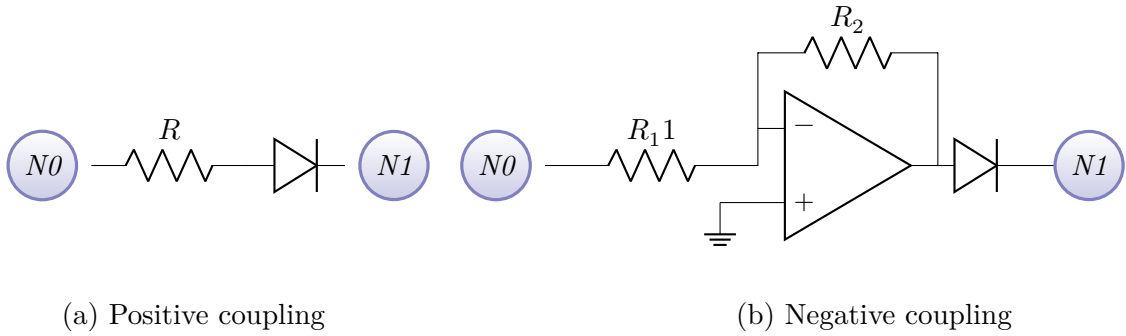


Figure 7: Coupling methods

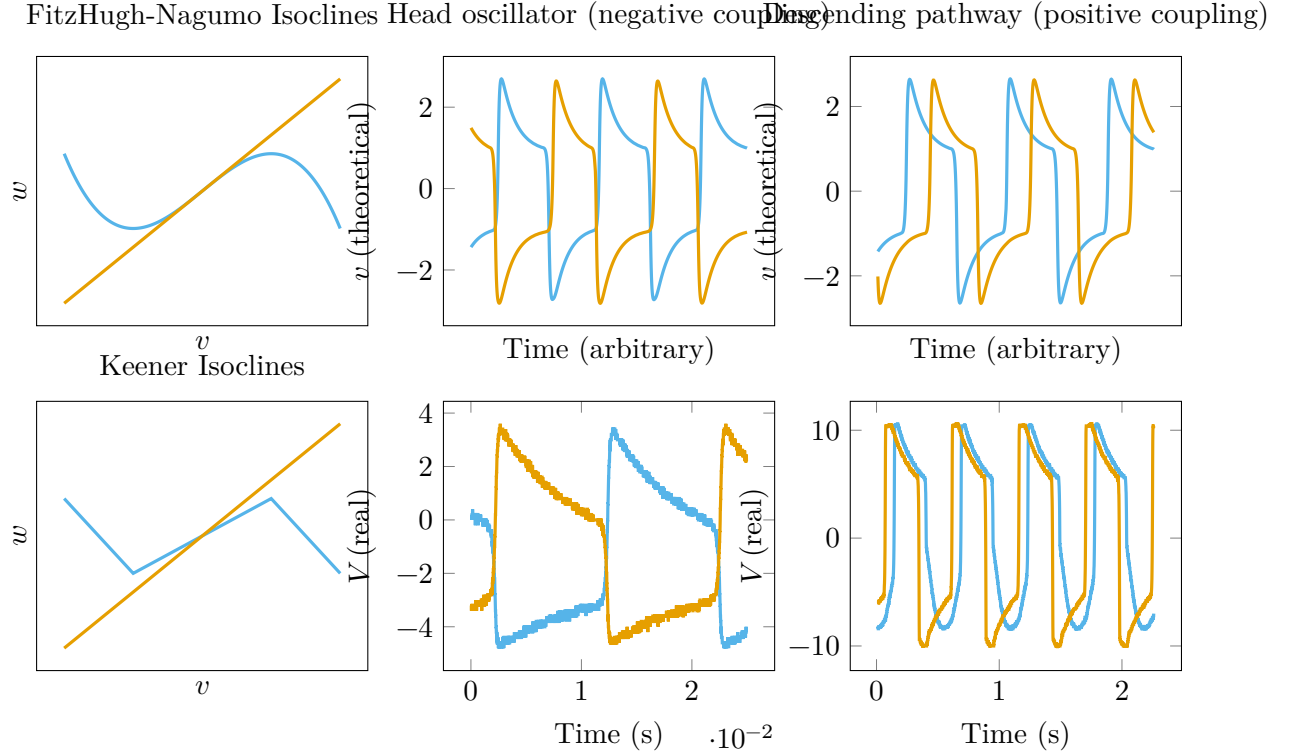


Figure 8: Comparison between simulated dynamics (top row) and observed dynamics in circuit (bottom row).

5.2 Relevance of Izquierdo & Beer [2] to our model

The Izquierdo & Beer [2] model is based on physical realities, and was generated using an evolutionary modelling process to find the structure of the descending neural network which controls muscular motion. As a result, the model, while realistic, is complex, and differs from ours in several places. First, the model is not a simple descending linked chain but a complex graphlike structure with repeating, complex self-oscillatory systems of neurons.

Our goal in modelling *C. elegans* is not to produce a very physically accurate model, but rather to replicate those behaviours which are essential - and only those - to the movement of the nematode. As such, we have the liberty of producing a simpler and more easily quantifiable model.

6 Conclusion

We have shown that the undulatory motion of *C. elegans* can be simulated using a structured central pattern generator, and simple, biomimetic neurons. This system is computationally cheap, and translates to a simple analog circuit.

Our model of the nematode is surprisingly similar to real unconstrained motion. While most measurements of *C. elegans* are taken on horizontal agar sheets, observations made in clear, water-filled cuvettes where the worm floats freely seem to resemble our simulated worm more.

Given the flexibility of the model, by introducing defects and asymmetries into the topology, we can study how mutations affect the nematode’s motion, as well as the structures underlying differences in phenotypes.

Reference some connections to Adamatzky *et al.* [18] - the neural system as a computational system. Also cite similarity between B-Z and FHN.

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