

# OpenWorm: Aggregating biological simulations in an open science project

Stephen Larson, Ph.D

Project Coordinator

OpenWorm.org



# OpenWorm is building a *c. elegans* simulation

Open science

Computational  
(neuro)biology  
& software  
engineering



Scientific  
approach



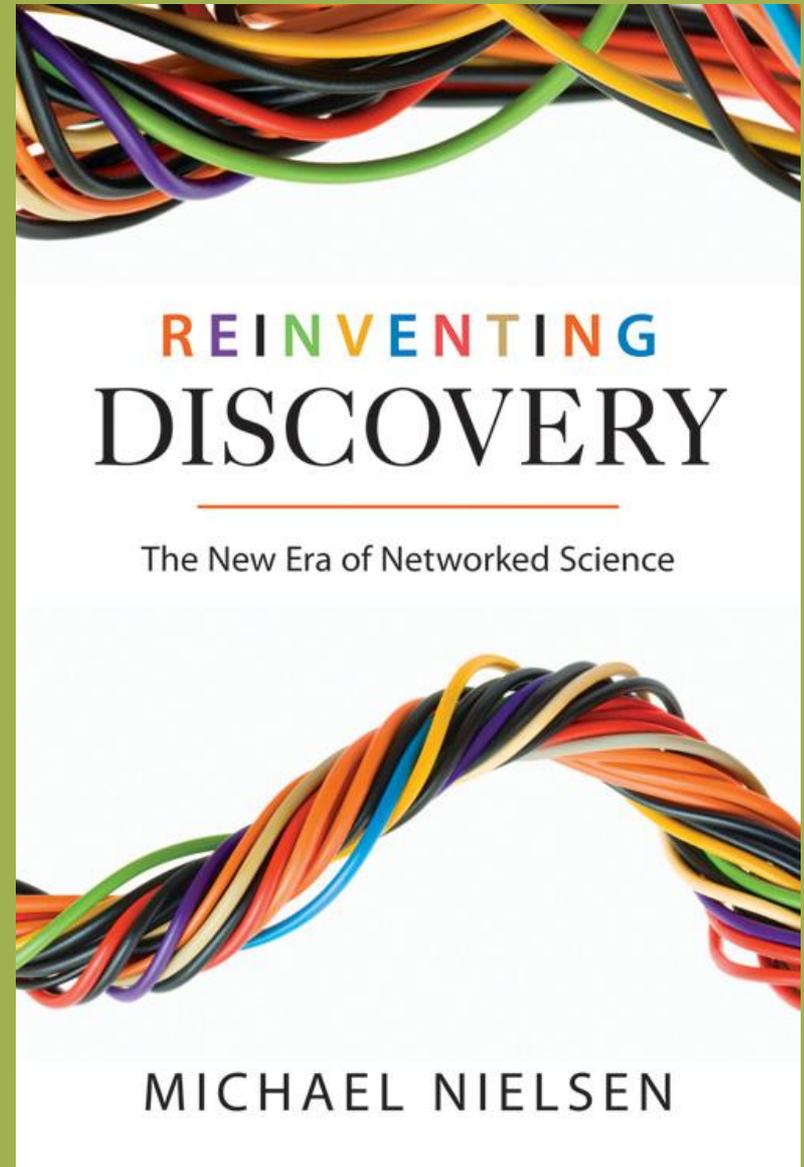
# OpenWorm's goal

- Long term: Full scale **simulation** of a **C. elegans**
- Medium term: Accurately predict **WormBehavior** database using **3D neuromechanical model**



# OpenWorm

- Independent international **open science** community started in 2011
  - 9 **core members**
  - 36 **contributors** across 12 **countries**
  - 24 **GitHub repos** & 220 **GitHub followers**
  - 300 **mailing list** members
- Community open source construction
  - Every line of code posted on GitHub
- Hosted 40+ online meetings last year
  - Streamed on YouTube



# People

Imagine working with a group of super-motivated wizards coming together for a common goal. It's amazing what talented people can achieve when their creativity is unleashed.

## Core team



Our Superheroes.

Andrey  
Palyanov

Balazs  
Szigeti

Giovanni  
Idili

Jim  
Hokanson

Matteo  
Cantarelli

Michael  
Currie

Padraig  
Gleeson

Sergey  
Khayrulin

Stephen  
Larson

## Contributors



Helping us with amazing support. Thanks!

Alexander  
Dibert

Andrew  
Leifer

Andrew  
Papadopoli

Bóris Marin

Charles  
Cooper

Christian  
Grove

Chris  
Jensen

Crystin  
Slade

Dan  
Knudsen

David  
Dalrymple

Deanne  
Taylor

Dmitriy  
Shabanov

Dmitar  
Shterionov

Eviatar  
Yemini

Gaston  
Gentile

Gleb  
Kuznetsov

Jay Coggan

Jesus  
Martinez

John  
Hurliman

John White

Jordan  
Boyle

Jinze Yu

Marius  
Buibas

Mariusz  
Sasinski

Matt Olson

Mike Vella

Mei Zhen

Netta  
Cohen

Pedro  
Tabacof

Peter  
McCluskey

Petr Baudis

Rayner  
Lucas

Rich Stoner

Steven  
Cook

Timothy  
Busbice

Vanessa  
Adelmann

# Posted challenge on GitHub

slarson opened this issue 8 months ago

Edit

## Create HivePlot data set from connectome

 tabacof is assigned 

Milestone: **Data visualization**



A [HivePlot](#) is a great way to visualize complex networks. To better understand what these are, check out [the general introduction slides](#).

The *c. elegans* connectome is the connectivity graph of all of the neurons of its simple "brain". Visualizing this graph has yielded [some insight into its structure](#), but it is still hard to pull patterns out of this graph as it is highly complex.

As far as I can find, HivePlots have not yet been applied to connectomes. This is a great opportunity to start.

- Take the [connectivity graph data from our spreadsheet](#) (first sheet only to start)
- [Download the java HivePlot program](#)
- Open an example under this program to understand the format:

```
A [attribute1=100 attribute2=1000] # node 'A'  
B [attribute1=200 attribute2=2000] # node 'B'  
C [attribute1=400 attribute2=4000] # node 'C'  
A -> B [attribute1=100 attribute2=1000 attribute3=positive] # edge from 'A' to 'B'  
B -> C [attribute1=200 attribute2=2000 attribute3=negative] # edge from 'B' to 'C'
```

- Write a python script to convert the connectivity graph data into this format.
- Load the data up, play with different ways of creating the hive plot for this data set, generate images & share.

# A volunteer emerges

Personal contribution to the project



Inbox x

Boomerang x

Forums x



**Pedro Tabacof** <tabacof@gmail.com>

Feb 27 ☆



to info ▾

Hello,

I really like the idea of this project and I was wondering how I could contribute. I'm a computer engineer with scientific computing experience (C/C++, Python, Matlab), including work with ODE integrators (Cvode, Lsoda), neural networks (Matlab toolbox), evolutionary computing, nonlinear optimization (Minpack, NLOPT) and system identification/optimal control (CasADi). I have some above average knowledge in neurobiology, though I'm very rusty on this aspect.

How should I start? I must admit I don't have much free time on my week, so I will need some time before I gather enough knowledge to do anything worthwhile.

Thanks,  
Pedro Tabacof.  
School of Electrical and Computer Engineering,  
State University of Campinas, Brazil.

# Pedro Tabacof, citizen scientist



**Pedro Tabacof**

tabacof

 Unicamp

 Brazil

 Joined on Aug 14, 2012

 Contributions

 Repositories

 Public Activity

★ [tabacof](#) starred [casadi/casadi](#) 3 months ago

★ [tabacof](#) starred [openworm/OpenWorm](#) 3 months ago

 [tabacof](#) created repository [casadi](#) 5 months ago

 6 months ago  
[tabacof](#) pushed to master at [openworm/data-viz](#)  
 [2db6df4](#) Creation of the hive plot folder

★ [tabacof](#) starred [openworm/OpenWorm](#) 6 months ago

# Three weeks later, a result!

PUBLIC  **openworm / data-viz** Unwatch 32 ★ Star 1 Fork 2

### History for **data-viz / HivePlots**

**May 17, 2013**

 **Update readme.txt**  
slarson authored 3 months ago 6e668c40e7 [Browse code](#)

**Mar 07, 2013**

 **Updated readme with some examples**  
slarson authored 6 months ago 5fc9e9117e [Browse code](#)

 **Creation of the hive plot folder**  
tabacof authored 6 months ago 2db6df4ae0 [Browse code](#)

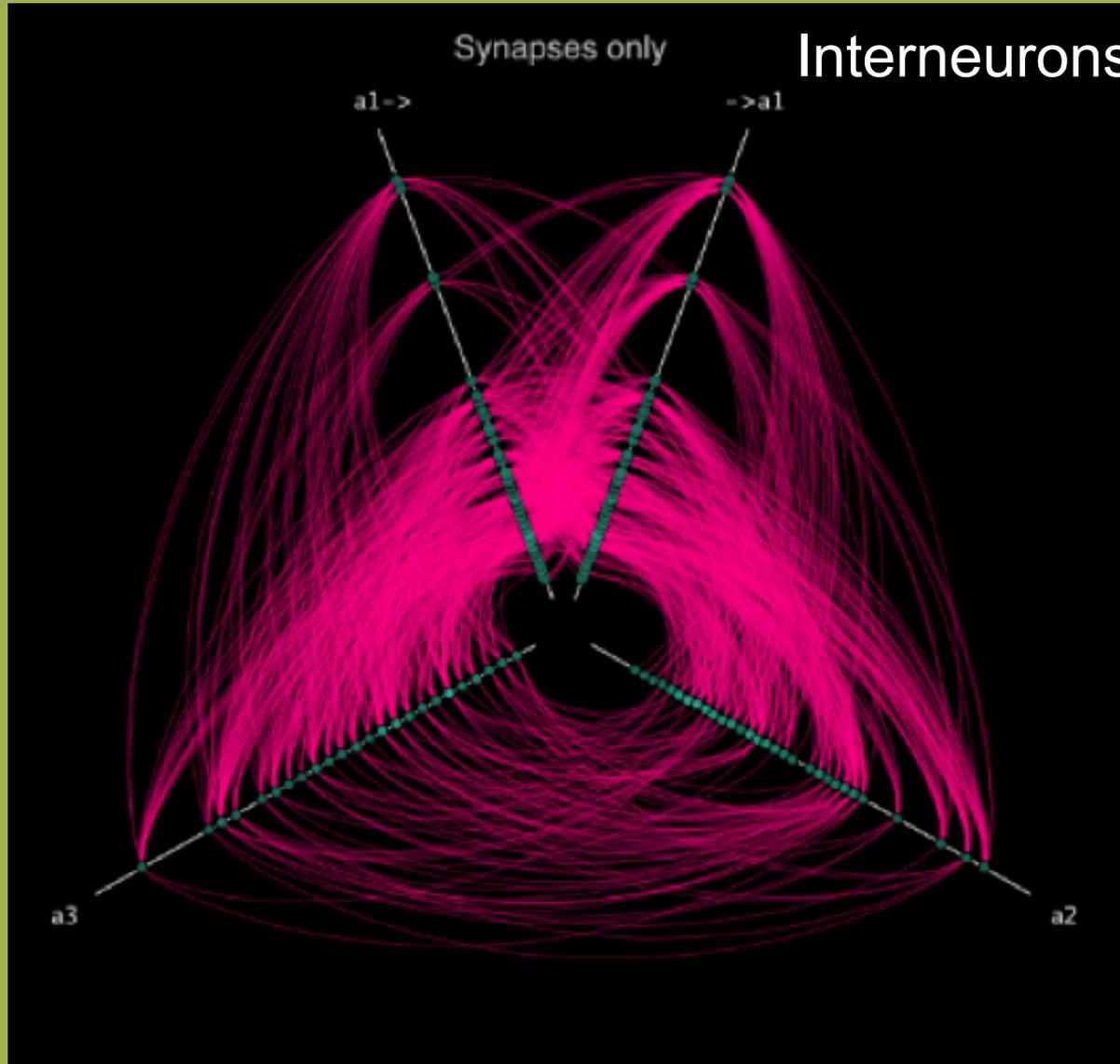


**Creation of the hive plot folder**  
tabacof authored 6 months ago

# Chemical synapse connectome

image  
produced  
using JHive

Sensory  
neurons

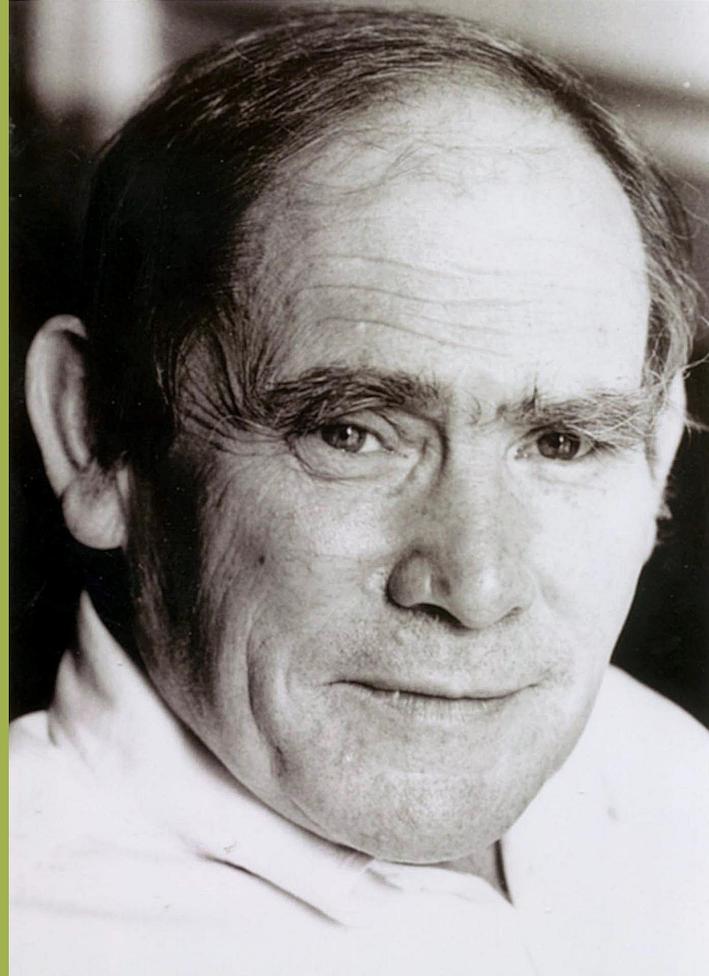


Motor  
neurons

# Why *C. elegans*?



# Dr Sydney Brenner



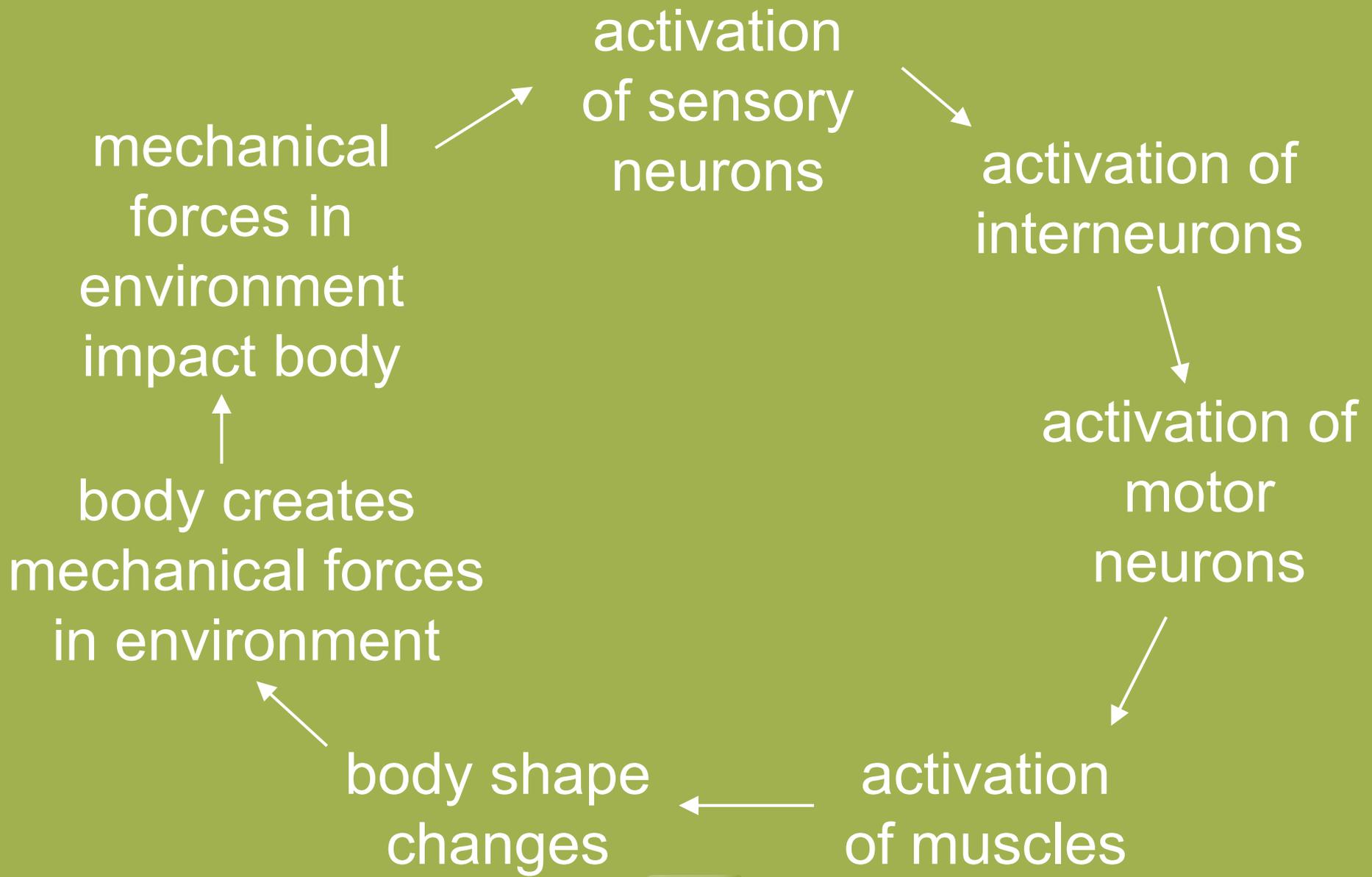
# C. elegans background

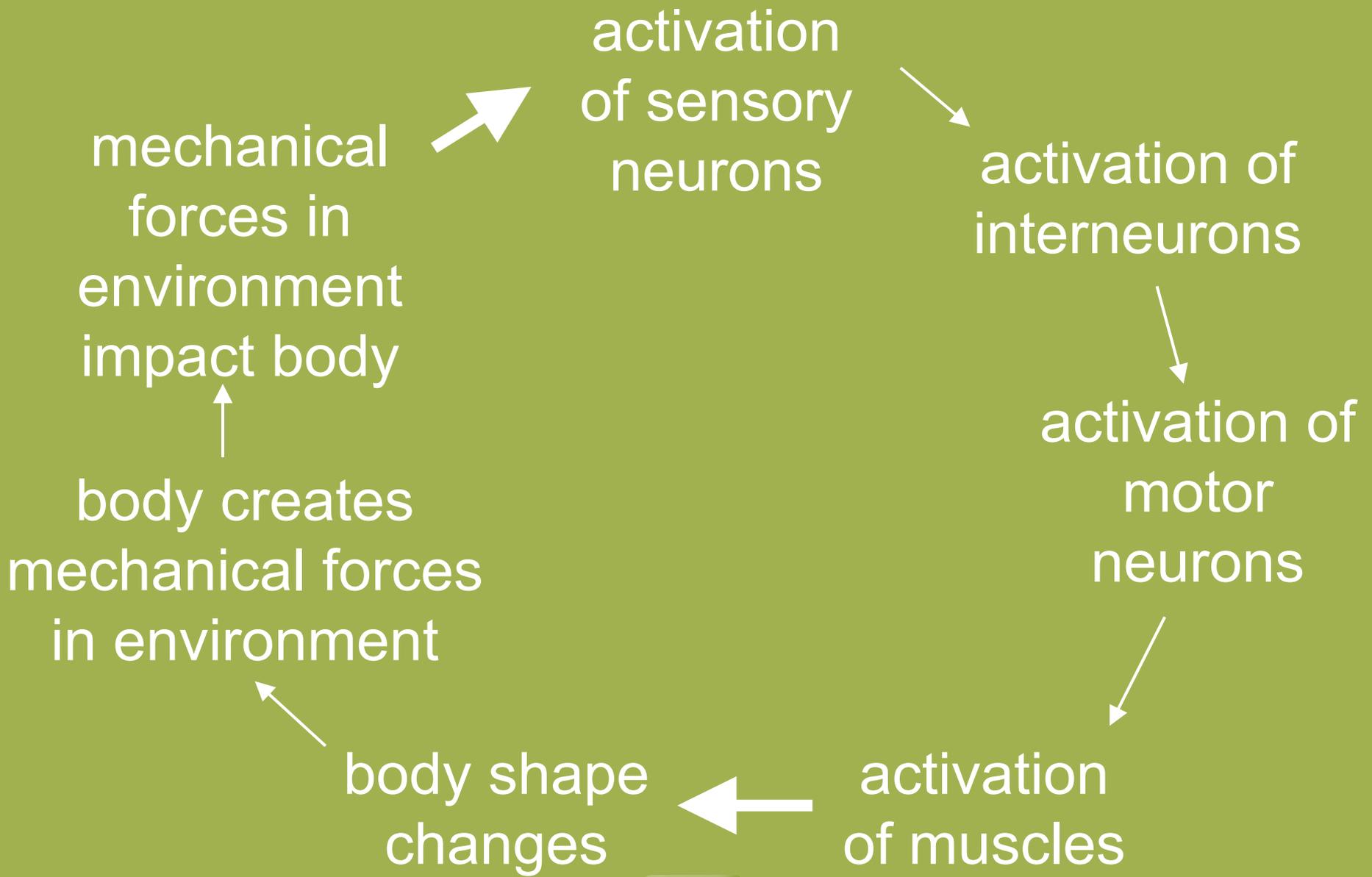
- Behavior
  - Seeks out food & mates
  - Avoids predators & toxins
  - Has social behaviors
- Genomics
  - First fully sequenced organism
- Cellular anatomy
  - 302 neurons, 95 muscle cells, ~1000 total cells
  - Every cell division from fertilized egg to adult is known
- Connectome
  - Only full organism connectome completed to date.



**C. elegans**  
**represents a *huge***  
**opportunity for**  
**computational**  
**biology**









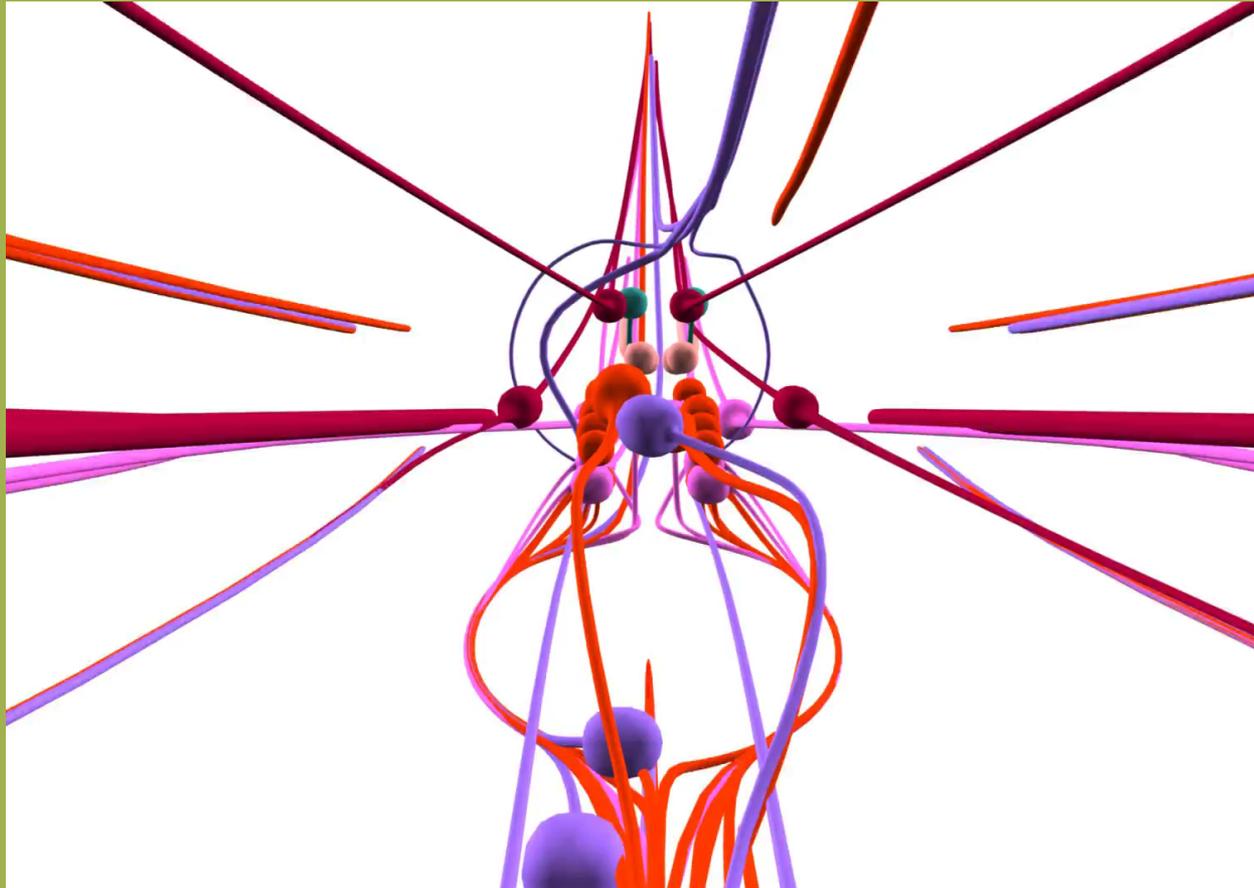
**Data about structure are available**

:)



# C. elegans connectome 2013

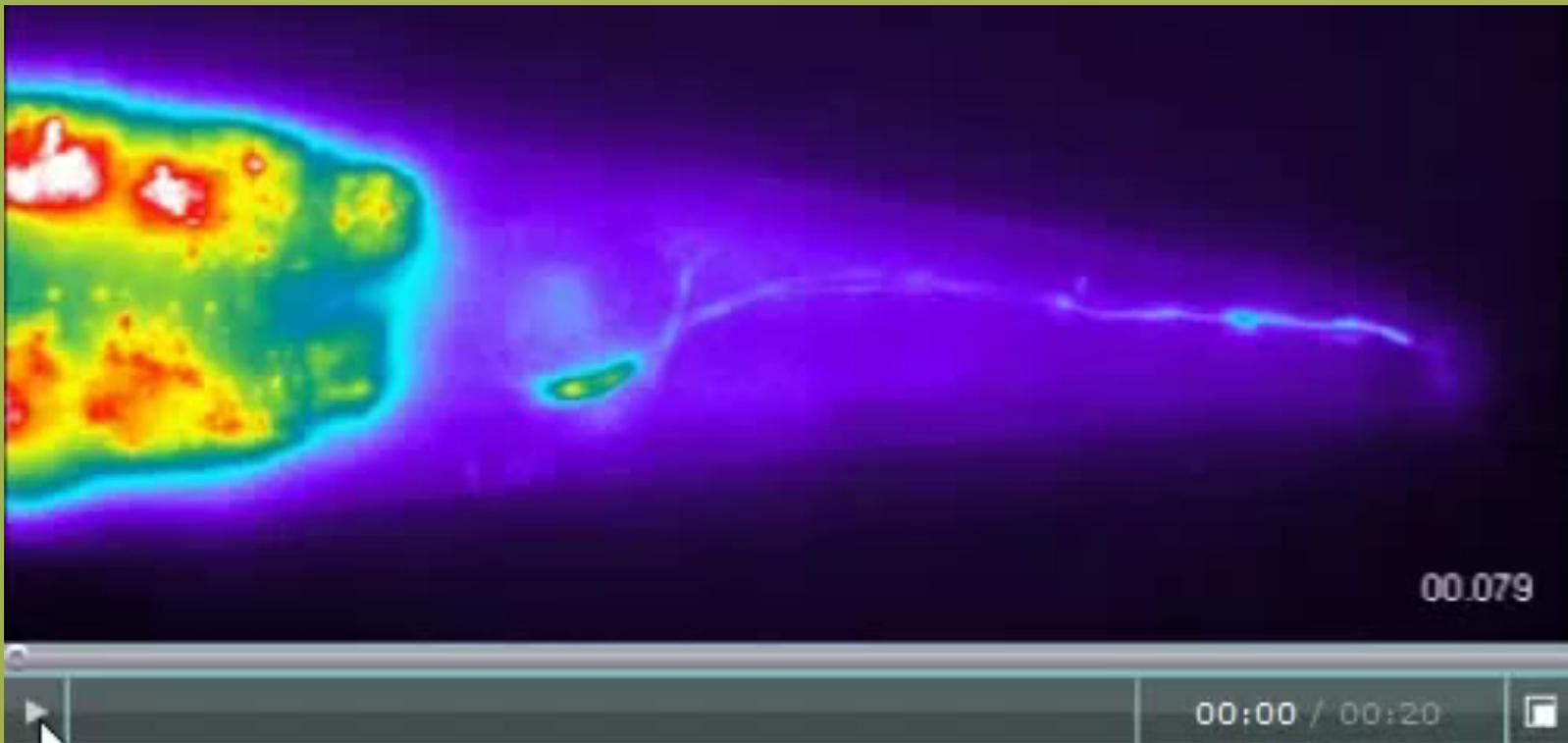
[NeuroML  
representation  
of c. elegans  
connectome on  
OpenSource  
Brain](#)



Christian Grove,  
Wormbase



# Data on dynamics of neurons in *c. elegans* is being revolutionized by optical imaging



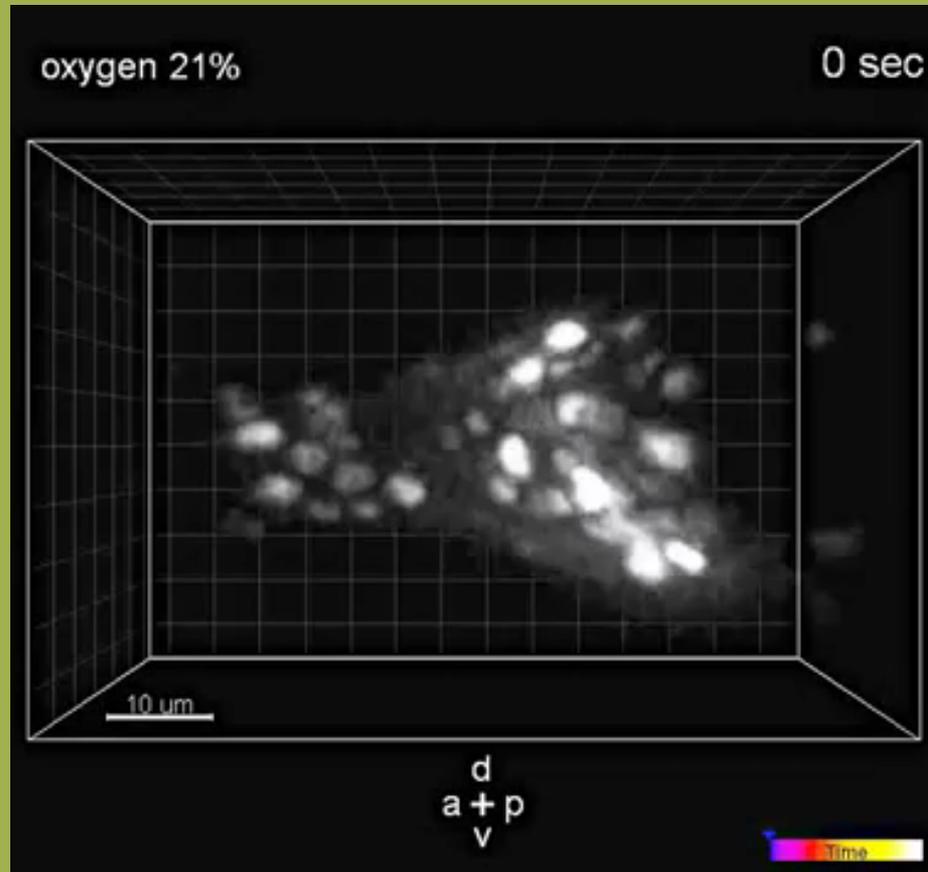
Dr. Sreekanth Chalasani,  
Salk Institute

# Data on dynamics of neurons in *C. elegans* is being revolutionized by optical imaging



Dr. Andrew Liefer,  
Princeton University

# Data on dynamics of neurons in *c. elegans* is being revolutionized by optical imaging



# Data about structure & dynamics are available

:) :)

body creates  
mechanical forces  
in environment



body shape  
changes

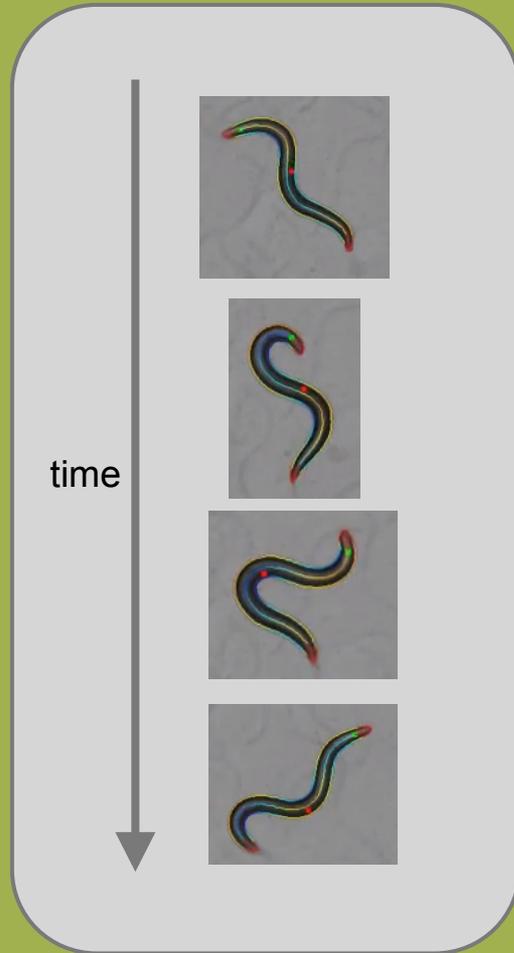


# Worm Behavior Database training data

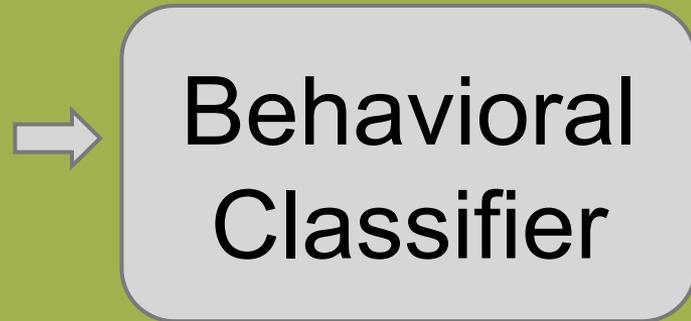


Yemini et al.,  
Nat. Methods 2013

# Worm behavior classifier



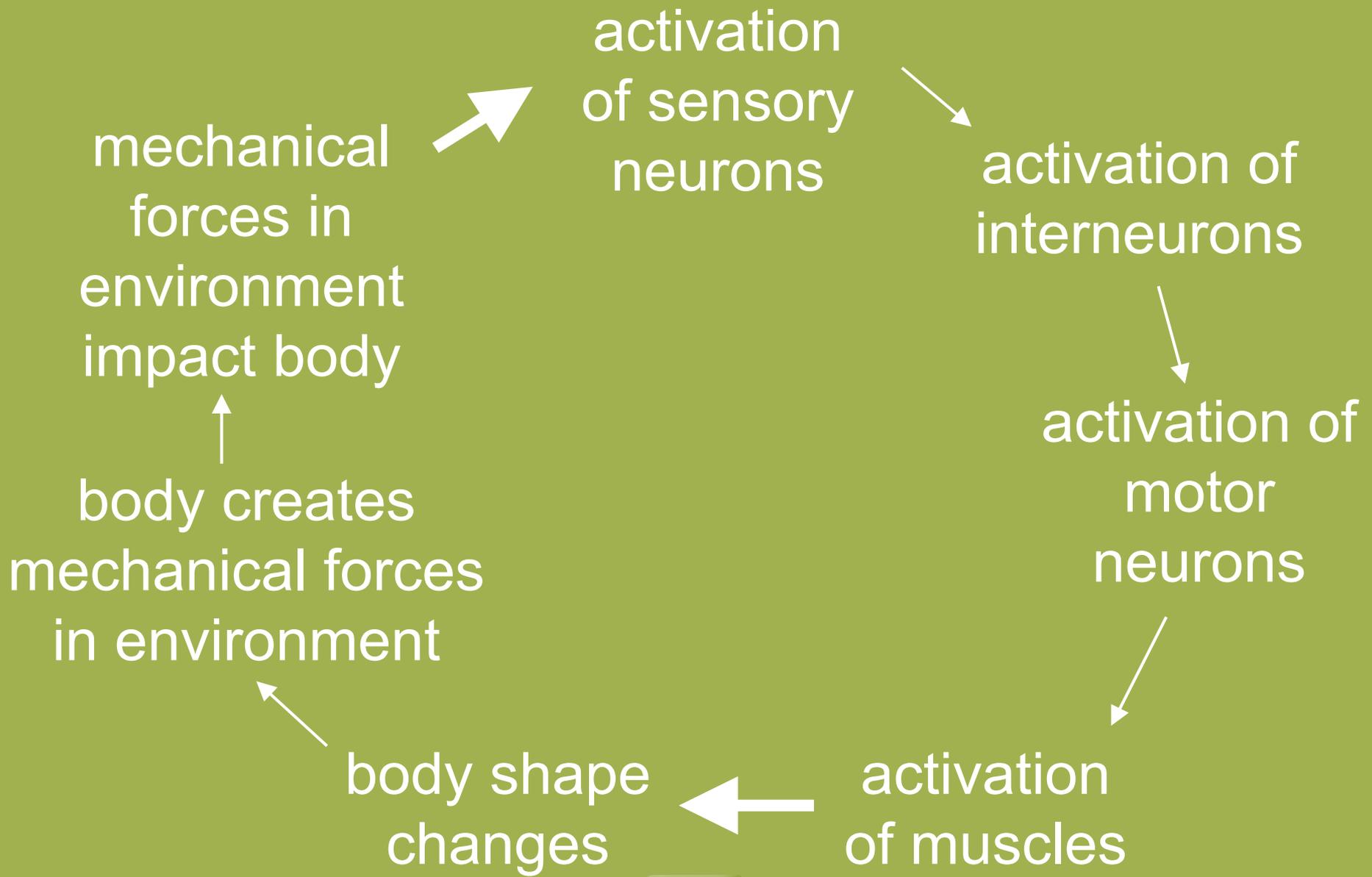
Simulated worm  
snapshots



Derived from  
observations of real  
worms



Jim Hokanson  
Michael Currie



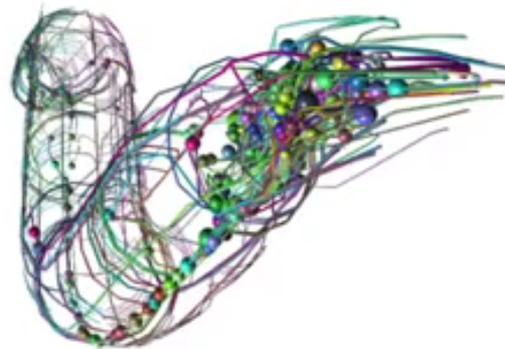
# Cyber Elegans



Palyanov et al.,  
In Silico Biology, 2012

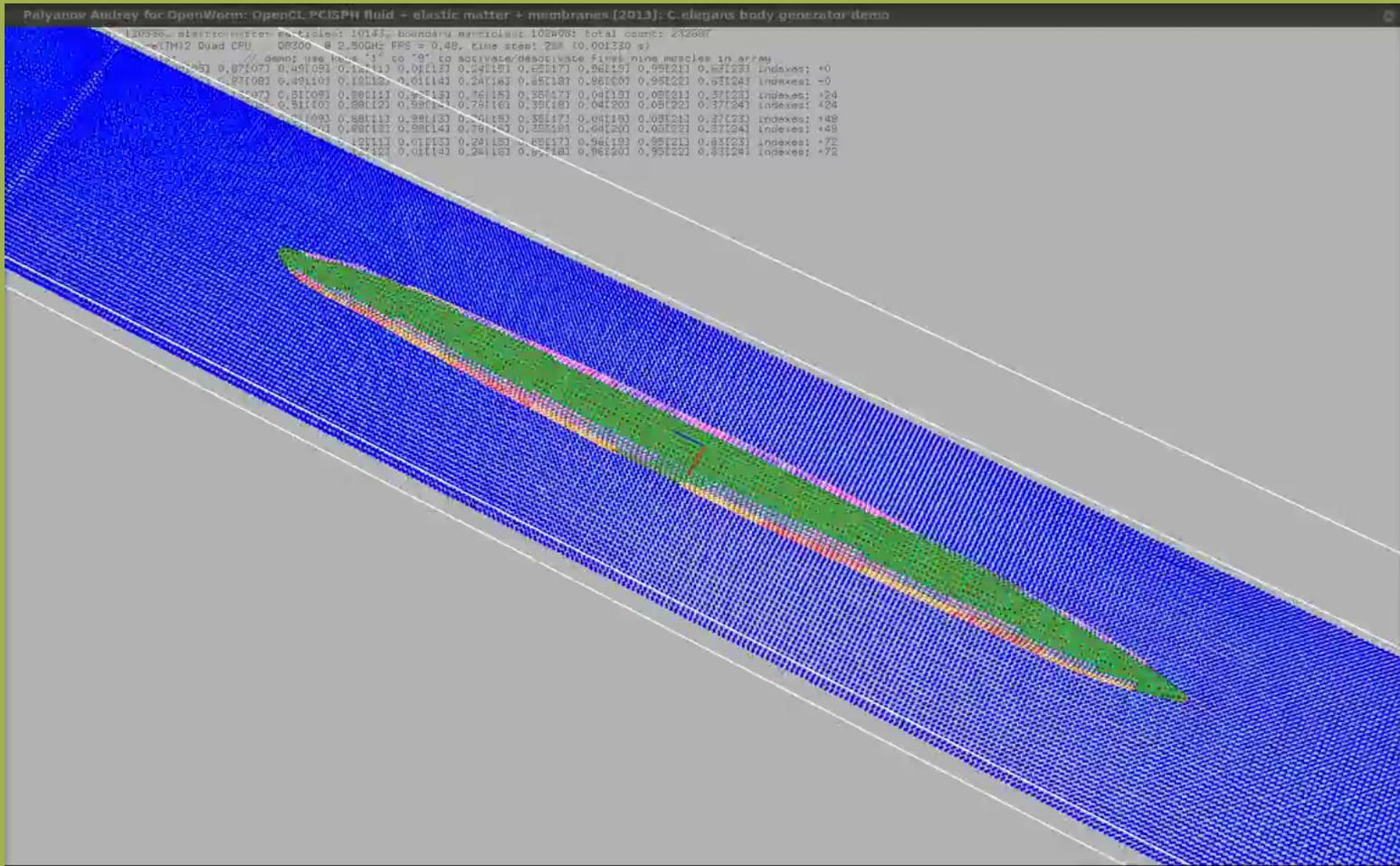
# C. elegans connectome 2013

[NeuroML  
representation  
of c. elegans  
connectome on  
OpenSource  
Brain](#)



Padraig Gleeson  
Tim Busbice  
Matteo Cantarelli

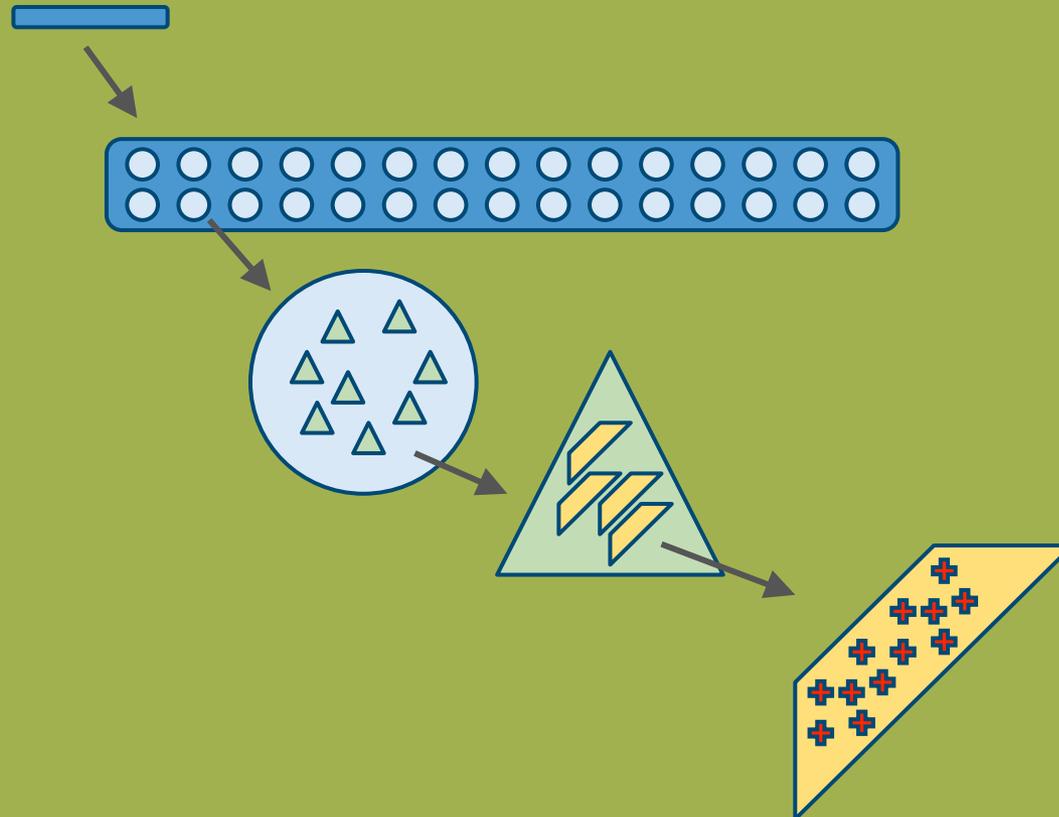
# Mechanical prototype: “Sibernetic”



Andrey Palyanov  
Sergey Khayrulin  
Mike Vella

# Bridging multi-scale models via software engineering

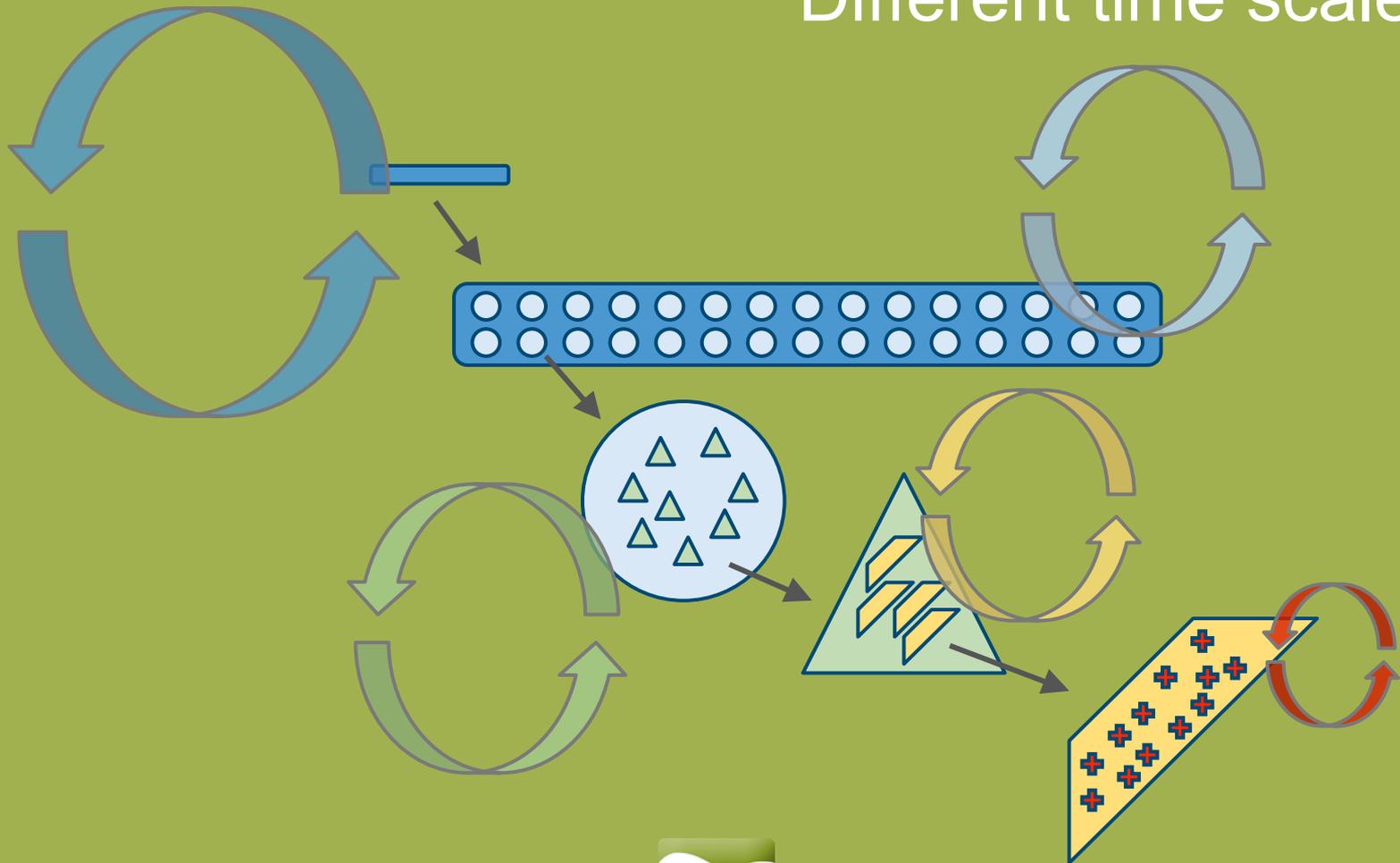
Different spatial scale



Diverse models and algorithms

# Bridging multi-scale models via software engineering

Different time scales



# Geppetto.org is open source and online



Highlights

Features

Gallery

Testimonials

Get Involved

FAQ



geppetto  
Simulate the future.

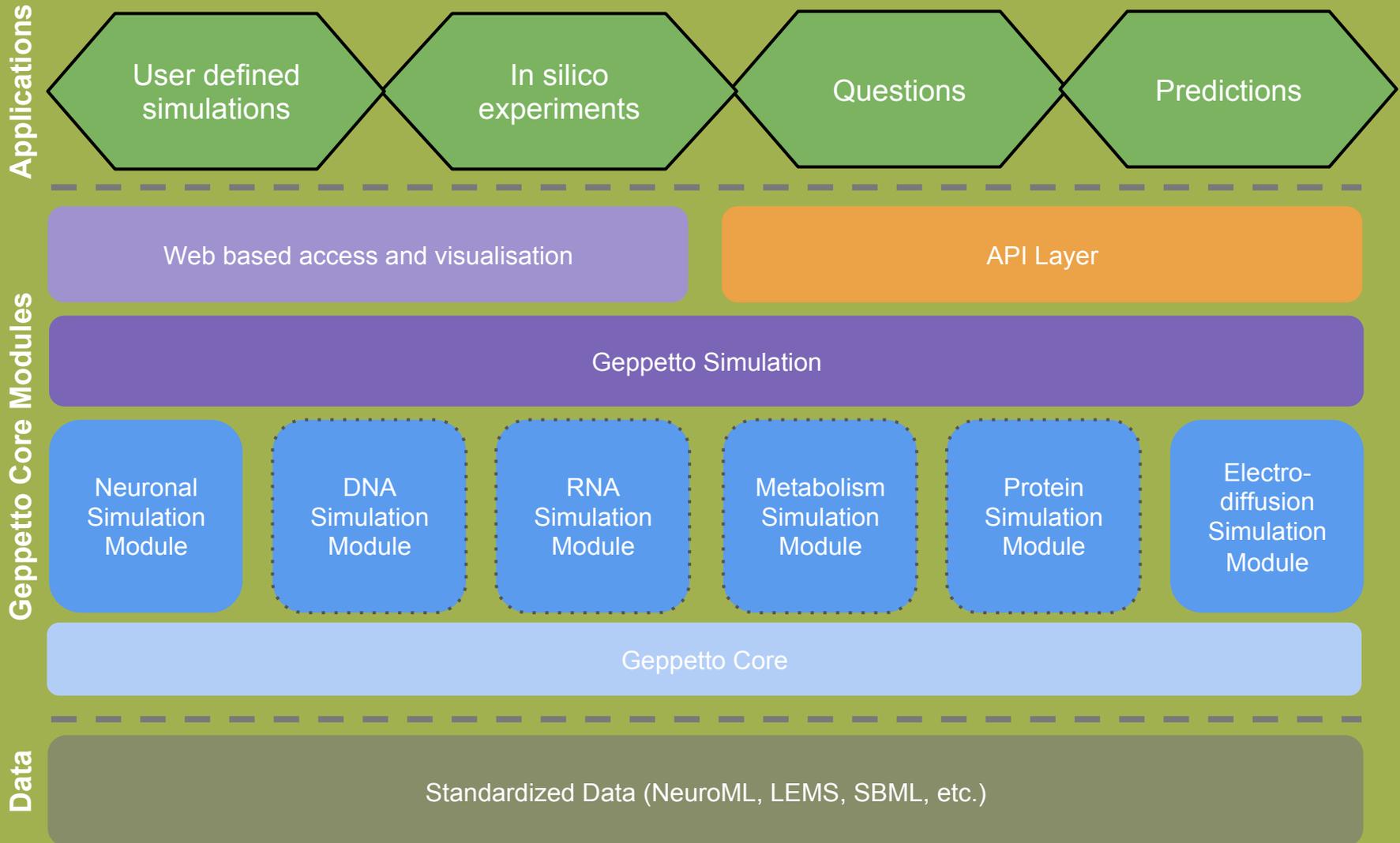
Download 

Wiki 



Giovanni Idili  
Matteo Cantarelli  
Jesus Martinez

# Geppetto architecture



# In Progress

- Past
  - Palyanov et al. 2012
  - OpenWorm Browser - WebGL & iOS
  - Spatial Connectome in NeuroML
- Present
  - Sibernetic integration
    - First step towards "virtual embodiment"
    - C. elegans motor system & muscle cells
  - Plugging the nervous system into the body model
    - More serious inference around ion channels
  - Building the worm classifier
  - Geppetto
    - Web-Based Service Oriented Architecture
    - Fluid mechanics Solver (PCI-SPH, OpenCL)
    - Single compartment Neurosolver (HH, OpenCL)



# New initiative in EU: Si Elegans

- FP7 funded
- Aims to reproduce c. elegans behavior using FPGA models, one per neuron
- More info: <http://www.si-elegans.eu>



# Other *c. elegans* modeling initiatives

- Lab of Netta Cohen, Leeds University
- Lab of Cori Bargmann & Larry Abbott, Columbia University
- Lab of Shawn Lockery, Univ. of Oregon
- NemaLoad project, David Dalrymple



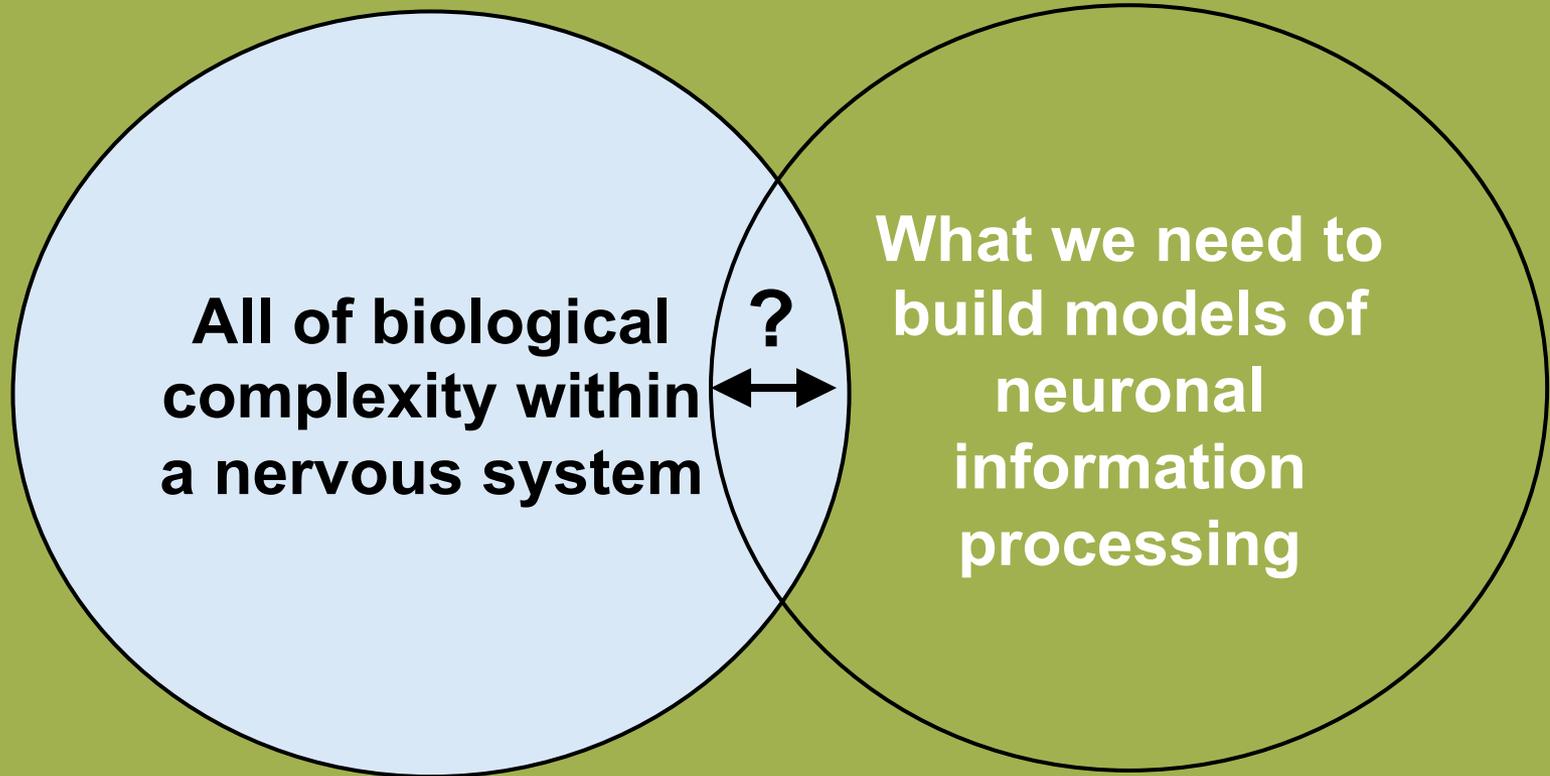
The **transistor** is the  
**fundamental**  
**information processing**  
**unit**  
of the computer



The neuron is the  
**transistor of the brain,**  
but we don't have a  
model of a neuron that  
**predicts all known  
biophysical data**

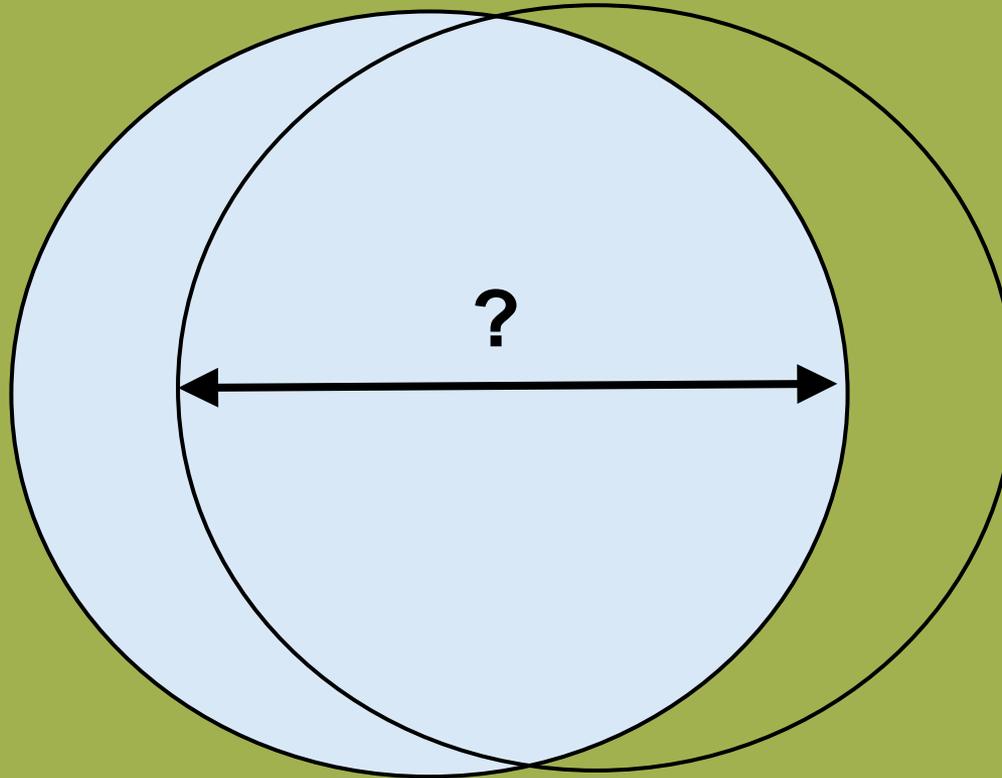


# Principal challenge



# Principal challenge

All of  
biological  
complexity  
within a  
nervous  
system



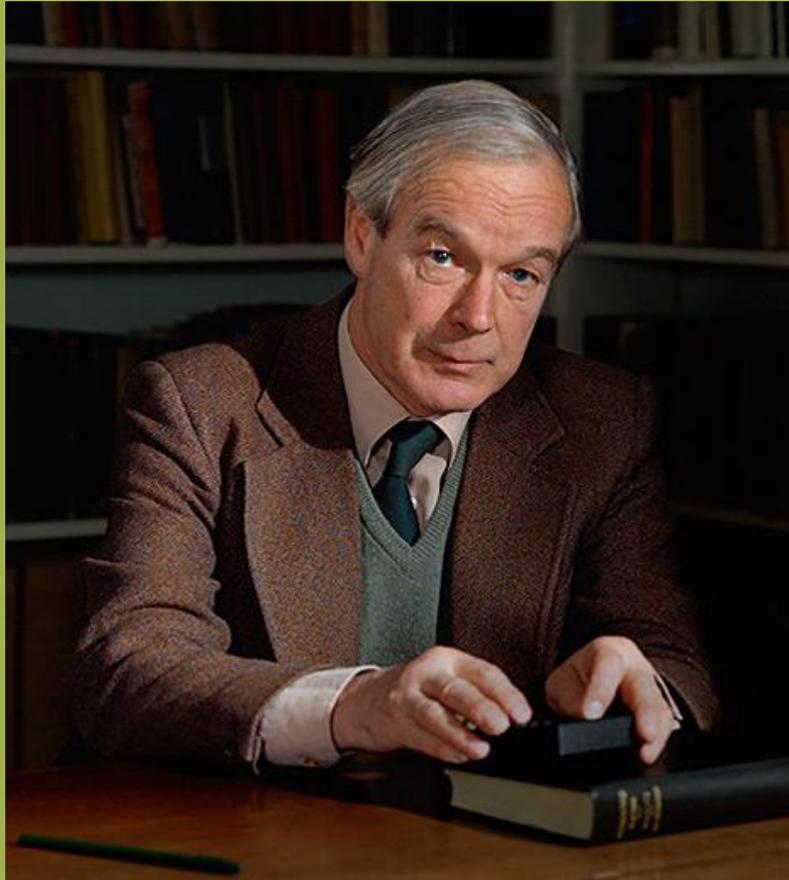
What we need  
to build  
models of  
neuronal  
information  
processing

# Why not *C. elegans*?

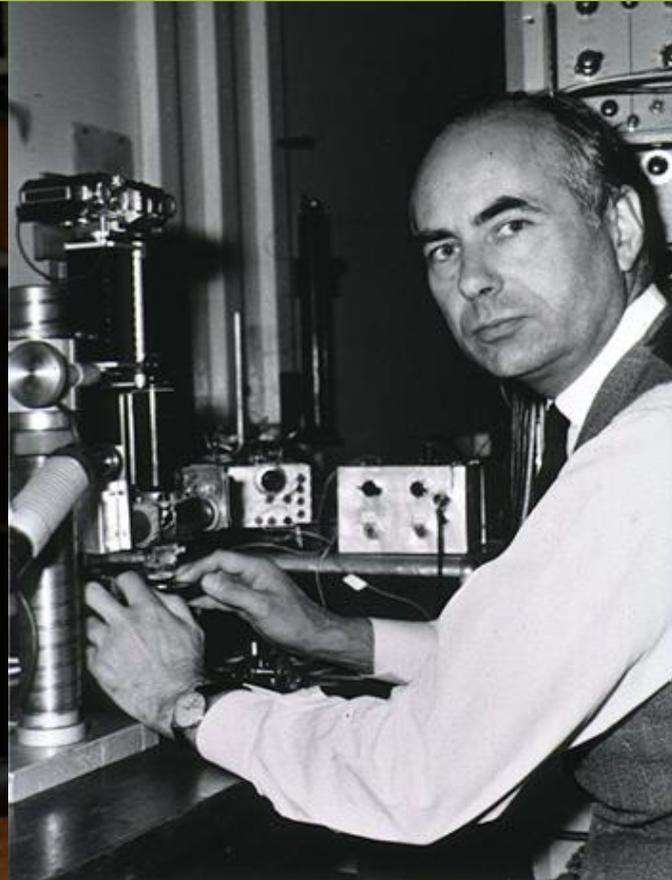


- Does it have neurons? Yes.
- Do the neurons have action potentials? No.
- Do the neurons still operate using similar biophysical processes? Yes.

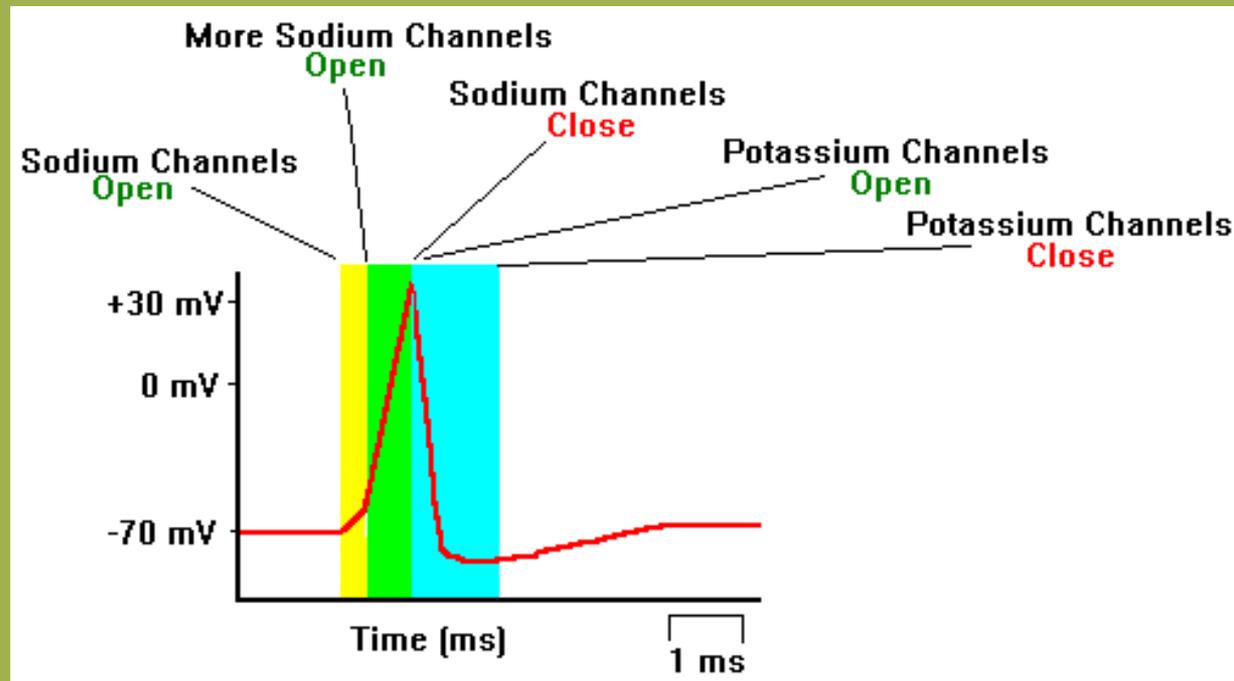
# Sir Alan Lloyd Hodgkin



# Sir Andrew Fielding Huxley

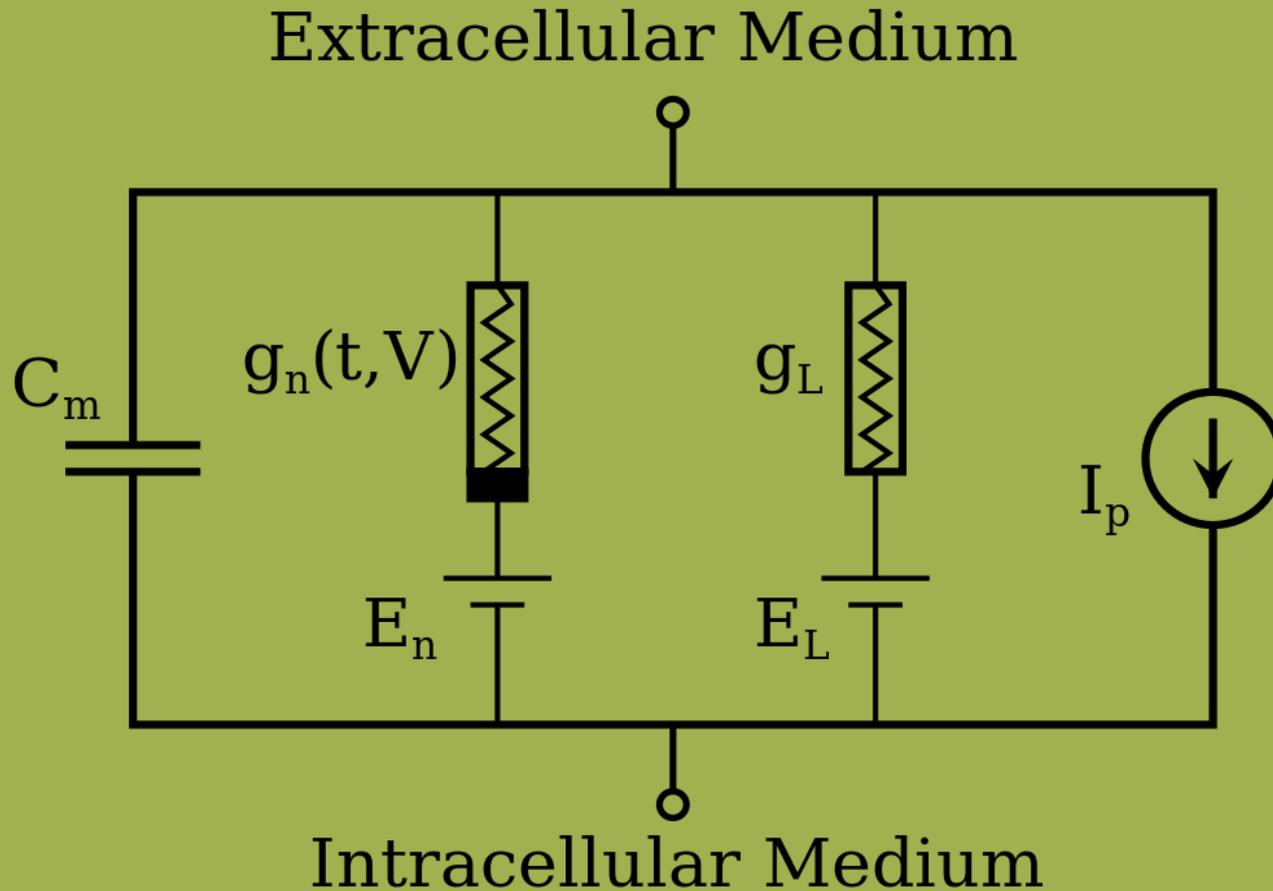


# Hodgkin–Huxley model



- 1952 work by two British physiologists
- Awarded the 1963 Nobel Prize in Physiology / Medicine
- Describes how action potentials in neurons are initiated and propagated
- A set of nonlinear ODEs that approximates the electrical characteristics of excitable cells

# Hodgkin–Huxley model



The functional atom of  
a neuronal signal is **not**  
**a “spike”**,  
it is a  
**change in membrane**  
**potential**



The structural atom of a  
neuron is **not** a  
**node in a graph,**  
it is an  
**ion channel**



# Dynamics in HH-based models

- Signalling more complex than excitation and inhibition
- Action potentials with different widths
- Neuropeptide signalling
- Re-bound inhibition
- Calcium dynamics
- Dendritic spikes
- Back-propagating action potentials
- ...also lends itself better to multiple-compartments



With an accurate  
biophysical model of a  
neuron, we could discard  
details based on  
principles rather than  
pragmatism



# Tradeoffs in neuromorphic computing

Partial models of  
complex neuronal  
systems

vs

Holistic models of  
simpler neuronal  
systems



# Response to the charge

- Why would one invest in neuro-inspired / neuromorphic computing over other alternative computing technologies?
  - Efficient computing architectures are embodied within neurons
  - Biological information processing is the result of billions of years of evolution -- tapping into a lot of valuable solutions to problems of information processing
- What are the big wins?
  - Building neuronal models that do what physics models do: accurately predict reality
- How long will it take to get there?
  - ?
- What are the critical path objectives?
  - Better data, more detailed modeling, more validation of detailed models against real data



# Contributions

- Introduced the open science initiative of OpenWorm
- Explained the value of *c. elegans* as a model organism
- Described the target of closing the brain – body loop in *c. elegans*
- Showed past progress of the OpenWorm project
- Described over-arching ideas behind the pursuit of neuronal models that reproduce real behavioral output



# Contact Info

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[info@openworm.org](mailto:info@openworm.org)

