



Topic: Ecology and Evolution

**400A - Sun, Jun 29**  
7:00 PM - 10:00 PM Alpha Course  
The evolution of complex life in aquatic environments  
Lecturers: Jeffrey J. Labadie

**B - Mon, Jun 30**  
10:00 AM - 12:00 PM  
The evolution of complex life in aquatic environments  
Lecturers: Jeffrey J. Labadie

**C - Tue, Jul 01**  
10:00 AM - 12:00 PM  
The evolution of complex life in aquatic environments  
Lecturers: Jeffrey J. Labadie

## Methods

**Silbernetic & OpenWorm Software with Monte Carlo Simulator**

**Features:**

1. Real-time simulation of the neural network.
2. Real-time simulation of the worm's movement.
3. Real-time simulation of the worm's sensory input.
4. Real-time simulation of the worm's output.
5. Real-time simulation of the worm's internal state.

**Simulation Results:**

The simulation results show that the worm's movement is highly correlated with its sensory input. The worm's output is also highly correlated with its internal state. The worm's internal state is highly correlated with its sensory input.

**Conclusion:**

The simulation results show that the worm's movement is highly correlated with its sensory input. The worm's output is also highly correlated with its internal state. The worm's internal state is highly correlated with its sensory input.

**References:**

1. Silbernetic & OpenWorm Software with Monte Carlo Simulator. (2010). [Online]. Available: <http://www.silbernetic.com>

2. Silbernetic & OpenWorm Software with Monte Carlo Simulator. (2010). [Online]. Available: <http://www.openworm.com>

3. Silbernetic & OpenWorm Software with Monte Carlo Simulator. (2010). [Online]. Available: <http://www.monte-carlo-simulator.com>

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## INTRODUCTION

### Background

Endosymbiont (2012) first proposed **symbiotic theory** for the evolution of **mitochondria** in eukaryotic cells. It is the theory that **mitochondria** during the prokaryotic-to-eukaryotic transition 200 million years ago. Comparative study of entire genomes of *Leishmania* and *Trypanosoma* revealed that they share 45 percent amino-acid sequence homology. This suggests that these two species share a common ancestor. **Leishmania** and *Trypanosoma* are parasites that live inside animal cells.

**Research Question**












































The smallest worm *Caenorhabditis elegans* was used to study the evolution of mitochondria. The question was: **What homologous genes could possibly drive the mitochondrial evolution of another marine worm to perform a similar role?**

### Purpose

The purpose of this study was to determine whether *Caenorhabditis elegans* could perform a similar function as the *Leishmania* and *Trypanosoma* species. The study was to determine if the *Caenorhabditis elegans* could perform a similar function as the *Leishmania* and *Trypanosoma* species.

### Hypothesis

The hypothesis was that the *Caenorhabditis elegans* could perform a similar function as the *Leishmania* and *Trypanosoma* species.



## DISCUSSION

### Validation in Silico: Monte Carlo Simulation of Somatic Tumor

#### Theories Matching Simulation Results

Three models were presented to allow researchers to search for the best model to fit the data. The three models were:

- 1. **Stochastic models** (20) (Hill, 1982), (21) (Hill, 1982), (22) (Hill, 1982)
- 2. **Stochastic models** (23) (Hill, 1982), (24) (Hill, 1982), (25) (Hill, 1982)
- 3. **Stochastic models** (26) (Hill, 1982), (27) (Hill, 1982), (28) (Hill, 1982)

The results showed that the stochastic models (20) (Hill, 1982), (21) (Hill, 1982), (22) (Hill, 1982) were the best fit to the data. The stochastic models (23) (Hill, 1982), (24) (Hill, 1982), (25) (Hill, 1982) were the best fit to the data. The stochastic models (26) (Hill, 1982), (27) (Hill, 1982), (28) (Hill, 1982) were the best fit to the data.

#### Review of Known Facts About C. Elegans

The results of the simulation were compared to the known facts about C. elegans. The results showed that the stochastic models (20) (Hill, 1982), (21) (Hill, 1982), (22) (Hill, 1982) were the best fit to the data. The stochastic models (23) (Hill, 1982), (24) (Hill, 1982), (25) (Hill, 1982) were the best fit to the data. The stochastic models (26) (Hill, 1982), (27) (Hill, 1982), (28) (Hill, 1982) were the best fit to the data.

#### Unexplained Challenges

There are several challenges that remain to be explained. These challenges are:

- 1. **Stochastic models** (20) (Hill, 1982), (21) (Hill, 1982), (22) (Hill, 1982)
- 2. **Stochastic models** (23) (Hill, 1982), (24) (Hill, 1982), (25) (Hill, 1982)
- 3. **Stochastic models** (26) (Hill, 1982), (27) (Hill, 1982), (28) (Hill, 1982)

#### Required Tools

The results of the simulation were compared to the known facts about C. elegans. The results showed that the stochastic models (20) (Hill, 1982), (21) (Hill, 1982), (22) (Hill, 1982) were the best fit to the data. The stochastic models (23) (Hill, 1982), (24) (Hill, 1982), (25) (Hill, 1982) were the best fit to the data. The stochastic models (26) (Hill, 1982), (27) (Hill, 1982), (28) (Hill, 1982) were the best fit to the data.

**METHODS**

**1. Experimental Design**

Starting with *C. elegans*, adjust model parameters for biochemically matter and environment to evolve

Generate new generations of worms across the day if any such happens, when given beautiful food sources (as they see on the first fish after a given period, or 30)

grow into big fat Ascarids without any synaptic trace?

**Beautiful Food!**

**Nematode (before)**

**Ascarid (after)**

**Synaptic trace**

**A Real Fish (after) growing into a real Ascarid**

**You fish? A big fish?**

**You fish? A big fish?**

[illegible]

### RESULTS

#### 1. Collaboration: "The Smallest Worm Will Turn." (Shakespeare, "Henry VI", 1591).

Host	Protein	Host	GP2	Recovery	Recovery	Total Seed	Run Time	OK
Medicago sativa	3-Alpha-Naphthol MD	12-Alpha-GP1	15.128	13.76				<input checked="" type="checkbox"/>
102 Medicago sativa	3-Alpha-Naphthol MD	Receptor GP2 128	15.128	13.76	6010	100 sec		<input checked="" type="checkbox"/>
103 Medicago sativa	3-Alpha-Naphthol MD 2.128	12-Alpha-GP1	15.128	13.76	6010	100 sec		<input checked="" type="checkbox"/>
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137 Medicago sativa	3-Alpha-Naphthol MD	12-Alpha-GP1	15.128	13.76	6010	100 sec		<input checked="" type="checkbox"/>
138 Medicago								

2. Visualization: "The Worm Did Turn, It Turned on itself." (Klimasauskas, 2013)

Worm movement visualization showing a sequence of frames (0000 to 0009) and a corresponding grid of movement data. The grid is divided into four sections: M000, M020, M040, and M060. The grid shows the worm's path (orange) and position (yellow) over time. The worm's movement is characterized by a series of turns, with the path and position changing significantly over time.

## CONCLUSIONS

### Underwater Buoyancy Drives Somatic Twist of Marine Invertebrates

- Somatic twist theory of Sherrin (1971) offers a testable hypothesis for how conical trunks become twisted.
- My results of decussate orientation in anemone maritima and the conical trunks of *Hydra* support the twist theory.
- My experimental buoyancy tests show *Hydra* animals twist in warm currents when food was plentiful.
- My construction, twist design of a bamboo tube can track equator and position during Sherrin's identity when decussate insertion has passed.
- A biomechanical model has been given for *Hydra* control and twist with mechanical trunks and a structural submerged twist an anemone.
- Moses Carlo illustrates three great new approaches to conducting experiments in *Hydra* when combined with Sherrin's

## REFERENCES


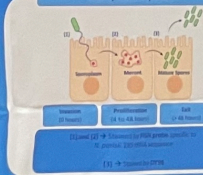
1. Krasnowska-Wojcik, H., Tomaszek, B., & Szust, J. (2010). *Wzrost i zdrowie dzieci w Polsce*. Warszawa: Państwowy Zakład Wydawnictw Lekarskich.
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7. Krasnowska-Wojcik, H., Tomaszek, B., & Szust, J. (2010). *Wzrost i zdrowie dzieci w Polsce*. Warszawa: Państwowy Zakład Wydawnictw Lekarskich.
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10. Krasnowska-Wojcik, H., Tomaszek, B., & Szust, J. (2010). *Wzrost i zdrowie dzieci w Polsce*. Warszawa: Państwowy Zakład Wydawnictw Lekarskich.

399A - Sun, Jun 29  
416B - Mon, Jun 30  
433C - Tue, Jul 01

## Department of Molecular G

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### Life Cycle of *N. parisii*



**Project Goals**

**INITIAL STATE**  
 Evaluate measures affecting differential competitiveness in 4 areas of Competitiveness capabilities

**AIM 1**  
 Characterize differences in industries, markets and Competitiveness capacity

**AIM 2**  
 Estimate activities in 4 areas across world segments

**AIM 3**  
 Use interpretation lines to identify 4 progress (Measurement requires 40% increase, identify





# 25<sup>th</sup> International Worm Meeting

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## CERTIFICATE OF PRESENTATION

This certifies that the person listed below attended and presented at the 25<sup>th</sup> International Worm Meeting, June 28-July 2, 2025, at the University of California, Davis, United States.

Name: Adam Cheong

Affiliation: Proof School

Title of Talk: Monte Carlo simulation of somatic twist in ancient marine worms

Session: Ecology and Evolution



Anne Marie Mahoney  
Senior Director of Conferences



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March 19, 2025

Adam Cheong, High School  
Proof School  
973 Mission Street  
San Francisco, CA 94103  
United States

Dear Adam Cheong,

On behalf of the Program Committee, you are cordially invited to participate in the 25<sup>th</sup> International Worm Meeting to be held June 28-July 2, 2025 at the University of California, Davis, in Davis, California. The organizers greatly appreciate the important contribution that you will make to the meeting. We expect approximately 1,600 scientists and students from all over the world with interests in Worm genetics to participate. All meeting attendees are required to pay a meeting registration fee and are responsible for all travel costs. The total cost of registration, housing and meals for the conference depends on the type of accommodations reserved and your registration category. Your abstract entitled "**Monte Carlo simulation of somatic twist in ancient marine worms**" has been accepted and will be programmed.

The Genetics Society of America is a professional membership organization for an international community of biologists advancing the field of genetics. The purposes of the Society are 1) to facilitate communication between geneticists, 2) to promote research that will bring new discoveries in genetics, 3) to foster the training of the next generation of geneticists so they can effectively respond to the opportunities provided by our discoveries and the challenges posed by them, and 4) to educate the public and their government representatives about advances in genetics and the consequences to individuals and to society.

The National Academies has a useful web site concerning obtaining a visa ( <http://nationalacademies.org/visas>) for international participants. As part of new security procedures, many applications are being sent to the State Department in Washington where they are reviewed, with assistance from other agencies. Because of the number of visas being processed and the need to be thorough with the reviews, this can take as much as 3 to 4 months or more. Therefore, we advise scientists intending to come to the United States to apply for their visa as early as possible. Please contact me with any questions. We look forward to your participation in the meeting

Please contact me with any questions. We look forward to your participation in the meeting.

Sincerely,

*Anne Marie Mahoney*

Anne Marie Mahoney  
Senior Director of Conferences

## Monte Carlo simulation of somatic twist in ancient marine worms

A somatic twist was thought to occur during the invertebrate-to-vertebrate transition 550 million years ago, resulting in a dorsoventrally inverted body plan for all vertebrates leading to decussation in the corticospinal tracts (Kinsbourne, 2013). Our research explored the plausibility of an evolutionary pathway that connects ancient marine worms to the protochordate *Pikaia* (aka the 'first fish'). But what force(s) could possibly drive the biomechanical tissues of ancient marine worms to perform a somatic twist?

To recreate evolutionary events inside a computer, our experimental design requires Monte Carlo simulation of feast and famine cycles. Our research purpose is to observe how the first digital *C. elegans* worm from the OpenWorm Project evolves *in silico* to become the first fish, whose fossil was initially thought to be that of a "big fat annelid worm" when first discovered in the Burgess Shale, with a dorsoventrally inverted body plan after a somatic twist when given bountiful food sources over evolutionary time. Our hypothesis that underlies the simulation: underwater buoyancy from generations of feeding drove the somatic twist of ancient marine worms.

We downloaded an open source worm model from the OpenWorm Project and installed the SiberNet software, which provides visualization of worm locomotion driven by a physics engine that simulates the hydrodynamics interaction between the environment and the body of the worm. We gathered model parameters for biomechanical matter within an aquatic environment and adjusted them according to cycles of feast and famine, in order to evolve successive generations of marine worms. We modeled feast and famine cycles stochastically using a Markov chain to drive proportionate changes of parameters characterizing each ring of the marine worm: body mass and volume, thus density and buoyancy based on the Archimedes' Principle. Our approach of integrating Monte Carlo simulation of feast and famine cycles over evolutionary time with a hydrodynamics engine for worm locomotion is a novel aspect of our research.

Monte Carlo simulation shows great promise as a practical new approach to conducting evolutionary biology experiments *in silico* when combined with SiberNet and OpenWorm. Our research work is ongoing and we would like to share our interim progress in various design aspects of evolutionary modeling for a digital worm as well as practical computational challenges encountered along the way. We hope to ultimately be able to provide *in silico* validation for Kinsbourne's somatic twist theory, supported in turn by our hypothesis that underwater buoyancy force drove somatic twist in marine worms during evolutionary times when food was bountiful.

### References:

Kinsbourne, M. (2013). Somatic twist: A model for the evolution of decussation. *Neuropsychology*, 27(5), 511–515. <https://doi.org/10.1037/a0033662>

**Project Description:** A somatic twist was thought to occur during the invertebrate-to-vertebrate transition 550 million years ago, resulting in a dorsoventrally inverted body plan for all vertebrates. My hypothesis is that underwater buoyancy force drove the biomechanical tissues of ancient marine worms to perform a somatic twist. My experimental design requires Monte Carlo simulation to recreate evolutionary events inside a computer, so that I can observe how the first digital worm organism evolves to become the first fish when given bountiful food sources.