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 Sibernetic 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 Sibernetic 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.

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March 19, 2025

Adam Cheong, High School
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Dear Adam Cheong,

On behalf of the Program Committee, you are cordially invited to participate in the 25th 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

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Sincerely,

Anne Marie Mahoney

Anne Marie Mahoney
Senior Director of Conferences