

Structural Simulation of Jellyfish Propulsion*

Jacob Kaminsky and Jake Kremer

Abstract—This report details the structural simulation of jellyfish propulsion modeled using Python. The study replicates the contraction-relaxation cycle by employing a node-based framework that simulates the movement of the jellyfish bell. The simulation operates in a high Reynolds number regime, accounting for fluid dynamic forces like drag. Key results include the cyclical velocity profile and vertical displacement of the nodes. Applications of this research include advancements in biomimetic robotics and fluid dynamics. Proposed future improvements include refining the model by increasing node density and incorporating tentacles to better simulate natural dynamics.

I. INTRODUCTION

Jellyfish are renowned for their energy-efficient propulsion, achieved through a unique contraction-relaxation cycle of their bell. During contraction, water is expelled, propelling the jellyfish forward, while the passive recovery phase conserves energy by allowing elastic recoil to restore the bell's shape. Understanding this mechanism through computational modeling has potential applications in bio-inspired robotics and underwater propulsion systems. This study focuses on simulating the structural dynamics of jellyfish propulsion using Python, with an emphasis on the interaction between structural mechanics and fluid forces.

II. BACKGROUND

Previous research has extensively explored the fluid dynamics of jellyfish swimming but has paid less attention to the structural mechanics enabling their movement. Jellyfish rely on flexible tissues in their bell, which facilitate elastic recovery during the relaxation phase. This elasticity minimizes energy expenditure while maintaining propulsion. Modeling these structural dynamics is critical to replicating the efficiency of jellyfish propulsion. Additionally, jellyfish operate in a high Reynolds number environment, where inertial forces dominate over viscous forces, making drag a significant factor in their movement.

III. IMPLEMENTATION

The simulation models the jellyfish bell as a system of interconnected nodes, with motion driven by periodic changes in node angles. The primary phases of the simulation are the contraction and relaxation of the bell, modeled using trigonometric functions.

The body and position of a simulated jellyfish with 9 nodes is shown below in Figure 1.

*This work was completed under the advisement of Professor M. Khalid Jawed with the University of California, Los Angeles: Department of Mechanical and Aerospace Engineering

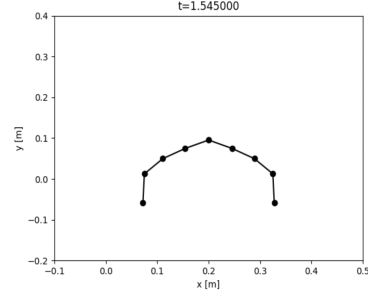


Fig. 1. Jellyfish Structure with 9 Nodes

As displayed, the length of the jellyfish's bell is distributed along n nodes. In this figure, 9 nodes are shown. The simulation was also carried out for 5 and 7 nodes using the same bell length of 40 cm.

A. Node Angle Calculation

The adjustment angle for each node, $k(t)$, is defined as a function of time t and its relative position to the midpoint:

$$k = \begin{cases} MA \cdot \sin\left(\frac{\pi}{2} \cdot \frac{t_{mod}}{A}\right), & \text{if } 0 \leq t_{mod} < A, \\ MA \cdot \cos\left(\frac{\pi}{(P-A) \cdot CS} \cdot (t_{mod} - A)\right), & \text{if } A \leq t_{mod} < P \end{cases} \quad (1)$$

where P is the total cycle period, A is the contraction duration, MA is a predetermined maximum angle, CS is an adjustment factor, and t_{mod} is the modulus of the current time. The angle varies non-linearly across nodes, with the midpoint experiencing the greatest adjustment.

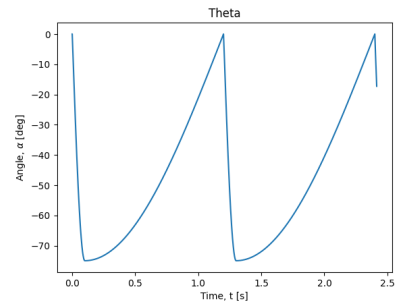


Fig. 2. Angle Between Side Node, Middle Node, and Horizontal Axis

The node-specific adjustment, k_{Node} , distributes the contraction angle across all nodes along the jellyfish bell. The function ensures that the angle is at a maximum at the edges and decreases non-linearly toward the center. This scaling captures the natural biomechanics of jellyfish movement,

where the central nodes experience the minimum adjustment, while the outermost nodes contribute the largest angular deformation. The midpoint of the bell represents the transition point, ensuring a smooth and realistic deformation profile.

$$k_{\text{Node}} = \frac{\text{MidIndex}}{2} + \frac{\text{MidIndex} - (\text{MidIndex} \cdot 0.1) \cdot |\text{Node} - \text{MidIndex}|^2}{\text{MidIndex}} \quad (2)$$

where MidIndex is the index of the middle node and Node is the index of the current node being adjusted for.

B. Drag Force and Velocity Direction

Jellyfish operate in a high Reynolds number regime. The drag force F_D acting on each node is given by:

$$F_D = -C_D A \cdot 0.5 \rho v^2 \hat{v} \quad (3)$$

where C_D is the drag coefficient, A is the effective projected area, ρ is the fluid density, v is the velocity magnitude, and \hat{v} is the unit velocity vector. The effective projected area is further defined as:

$$A = dL \cdot r_0 \quad (4)$$

where dL is the distance between nodes and r_0 is the radius of each member. The velocity vector for each node is calculated as the change in position between successive time steps, normalized to ensure proper alignment of the drag force.

$$\mathbf{v}_{\text{dir}} = \begin{bmatrix} q_{\text{new}}[2 \cdot \text{node}] - q_{\text{old}}[2 \cdot \text{node}] \\ q_{\text{new}}[2 \cdot \text{node} + 1] - q_{\text{old}}[2 \cdot \text{node} + 1] \\ 0 \end{bmatrix} \quad (5)$$

$$\hat{\mathbf{v}} = \begin{cases} \frac{\mathbf{v}_{\text{dir}}}{\|\mathbf{v}_{\text{dir}}\|}, & \text{if } \|\mathbf{v}_{\text{dir}}\| \neq 0 \\ \mathbf{0}, & \text{if } \|\mathbf{v}_{\text{dir}}\| = 0 \end{cases} \quad (6)$$

C. Time-Stepped Simulation

The simulation iteratively updates node positions, angles, and velocities at each time step. The primary algorithm follows these steps:

- 1) Run Objective Function to find the new configuration.
- 2) Compute the node angles $k(t)$ using the defined trigonometric functions.
- 3) Calculate node displacements based on their angles and positions relative to the midpoint.
- 4) Adjust velocities and ensure drag forces are correctly applied.

The displacements in x and y (x, y) relative to the midnode using trigonometric relationships are defined by:

$$x = |(\text{midNode} - 1) - i| \cdot \Delta L \cdot \cos\left(|\theta_{\text{Node}}| \cdot \frac{\pi}{180}\right) \quad (7)$$

$$y = |(\text{midNode} - 1) - i| \cdot \Delta L \cdot \sin\left(|\theta_{\text{Node}}| \cdot \frac{\pi}{180}\right) \quad (8)$$

The found displacements are then applied to the correct node with respect to the middle node. The relationships

slightly differ for node positions left and right of the middle node.

For nodes left of the midpoint ($i < \text{midNode} - 1$):

$$q[2i] = q[2 \cdot \text{midNode} - 2] - x \quad (9)$$

$$q[2i + 1] = q[2 \cdot \text{midNode} - 1] - y \quad (10)$$

For nodes right of the midpoint ($i > \text{midNode} - 1$):

$$q[2i] = q[2 \cdot \text{midNode} - 2] + x \quad (11)$$

$$q[2i + 1] = q[2 \cdot \text{midNode} - 1] - y \quad (12)$$

IV. RESULTS

Displayed below are the results gathered from the simulation using 5, 7 and 9 nodes to construct the jellyfish. Figures 3, 5 and 7 show the vertical displacement of the middle node while Figures 4, 6 and 8 show the vertical velocity of the middle node for each simulated jellyfish.

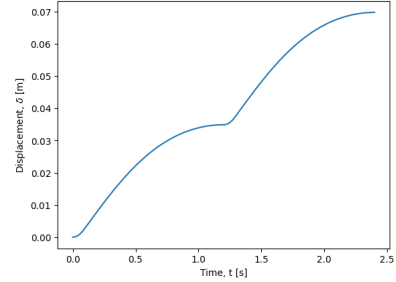


Fig. 3. 5 Node Case: Displacement of Middle Node

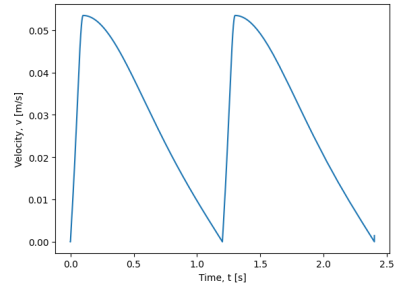


Fig. 4. 5 Node Case: Velocity of Middle Node

As shown in Figures 3, 5 and 7, the vertical displacement of the middle node demonstrates a clear cyclical pattern that corresponds to the contraction-relaxation motion of the jellyfish. Figures 4, 6 and 8 show the velocity in the y -direction also oscillating over time, consistently reaching zero at the end of each contraction cycle. This behavior reflects the interplay between the elastic recoil of the jellyfish bell and the fluid dynamic forces acting on it. The zero-velocity points mark the transition between contraction and relaxation, serving as a reset mechanism for the propulsion cycle.

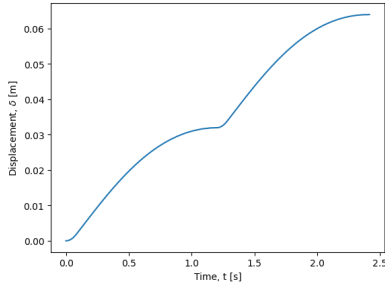


Fig. 5. 7 Node Case: Vertical Displacement of Middle Node

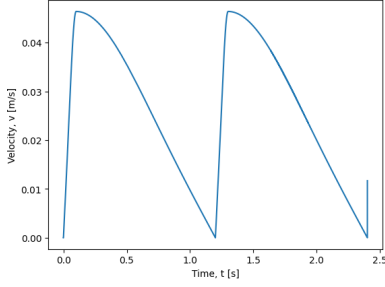


Fig. 6. 7 Node Case: Velocity of Middle Node

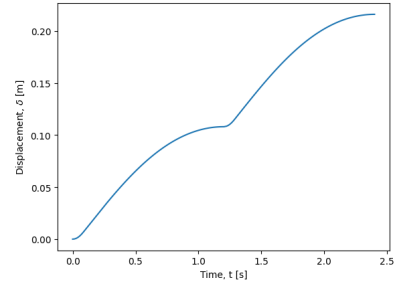


Fig. 7. 9 Node Case: Displacement of Middle Node

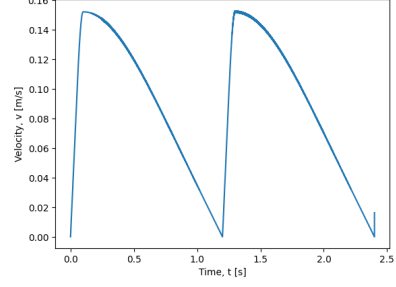


Fig. 8. 9 Node Case: Velocity of Middle Node

The overall displacement of the center node during one complete cycle with 5 and 7 nodes is about the same for both at around 3 cm. Using 9 nodes results in an overall single cycle displacement of around 7 cm. This discrepancy is most likely due to the increased angle of the outer two nodes, as explained in implementation, which results in a much greater contraction thrust produced and thus a greater displacement.

V. DISCUSSION ON VELOCITY DYNAMICS

During each contraction cycle, the velocity of the jellyfish in the y-direction reaches zero. This occurs at the end of the contraction phase, when the drag force fully counteracts the forward momentum. Our model experiences this result because at the end of each cycle, the angle is brought back to 0° such that the model is completely perpendicular to the direction of movement, resulting in a large area and thus drag force. While this behavior is not realistic to jellyfish as they never completely flatten out, for the purpose of our model it allows for a good simulation of the movement cycle.

VI. FUTURE IMPROVEMENTS

To improve the accuracy and applicability of the simulation, several enhancements are proposed. First, increasing the number of nodes in the model would allow for a more refined structural representation of the jellyfish. Second, the addition of trailing tentacles could provide more realistic dynamics by simulating the natural flow interactions observed in real jellyfish. Third, the model should be tested under varying parameters, such as fluid density, bell length, and elastic modulus, as well as different contraction functions for the angle θ . These improvements would increase the fidelity of

the simulation and broaden its potential applications in understanding and designing bio-inspired propulsion systems.

REFERENCES

- [1] S. Dabiri and M. Gharib, "Jellyfish as a Model for Underwater Propulsion," *Annual Review of Marine Science*, vol. 12, 2020, pp. 93–118.
- [2] R. M. Alexander, "Elastic Structures and Movement in Aquatic Organisms," *Journal of Experimental Biology*, vol. 213, no. 7, 2010, pp. 1031–1039.
- [3] E. Kanso, "Bio-inspired Flexible Structures in Fluid Dynamics," *Journal of Biomechanics*, vol. 49, no. 11, 2016, pp. 2196–2203.
- [4] Z. J. Olsen and K. J. Kim, "Design and Modeling of a New Biomimetic Soft Robotic Jellyfish Using IPMC-Based Electroactive Polymers," *Frontiers in Robotics and AI*, vol. 6, 2019, p. 112. doi: 10.3389/frobt.2019.00112. PMID: 33501127; PMCID: PMC7805721.
- [5] B. J. Gemmell, J. H. Costello, S. P. Colin, C. J. Stewart, J. O. Dabiri, D. Tafti, and S. Priya, "Passive energy recapture in jellyfish contributes to propulsive advantage over other metazoans," *Proceedings of the National Academy of Sciences*, vol. 110, no. 44, 2013, pp. 17904–17909. <https://doi.org/10.1073/pnas.1306983110>.
- [6] P. J. Yang, M. Lemons, and D. L. Hu, "Rowing jellyfish contract to maintain neutral buoyancy," *Theoretical and Applied Mechanics Letters*, vol. 8, no. 3, 2018, pp. 147–152. ISSN: 2095-0349. [<https://www.sciencedirect.com/science/article/pii/S2095034918301028>].
- [7] D. Mould, "Aesthetic Flows in Fluid Simulation," *Graphics Interface*, 2005. [<https://gigl.scs.carleton.ca/sites/default/files/davidmould/jelly.pdf>].