## Enhanced Posture Tracking Reveals Common Dimensionality in Crawling and Swimming *C. elegans*

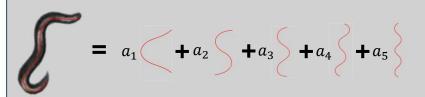


Jacob M. Wheelock  $^{1,2}$ , Hang Lu  $^{1,3}$ 

1. Interdisciplinary Program in Bioengineering, 2. School of Electrical and Computer Engineering, 3. School of Chemical and Biomolecular Engineering, Georgia Institute of Technology

## **Background**

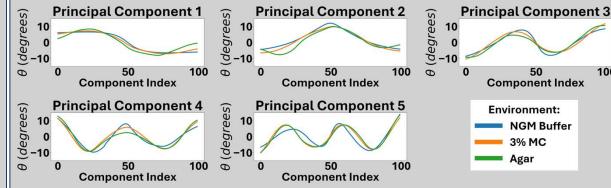
Quantitative posture tracking in *C. elegans* is crucial for understanding behavior. Principal Component Analysis (PCA) reduces complex postures into a few principal components called "eigenworms," which reduce the complexity of detailed behavior analysis [1,2].



We introduce a robust posture tracking algorithm that overcomes previous limitations in handling self-occluding poses. This advancement allows for accurate posture analysis in various environments, improving understanding of *C. elegans* locomotion and behavior.

## Results

In this study, we analyzed the principal component (PC) shapes of *C. elegans* in three environments with increasing resistance: NGM buffer, 3% methylcellulose, and agar. Ten worms were recorded freely moving in each environment for ten minutes and each worm's principal components were averaged within environments and plotted below. Interestingly, similar eigenworms describe the worm's posture across all environments.



## **Posture Tracking Pipeline**



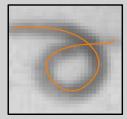
1. Annotate Images and Train Bounding Box Detection Network



4. Skeletonize and Order Points



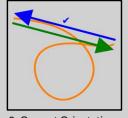
**2.** Automatically generate Rough Masks and Train Mask Detection Network



Fit Splines

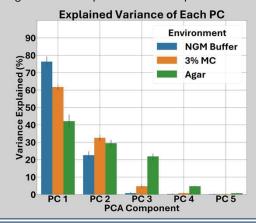


**3.** Detect and Generate Clean Masks on New Dataset

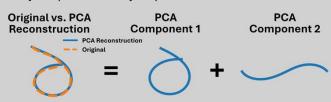


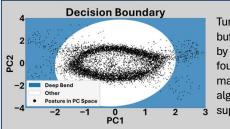
Correct OrientationBased on Previous Frame

Though worms in each environment are well represented by similar eigenworms, those in less resistive environments require fewer eigenworms to explain most of their postures.



Only two principal components were needed to explain well over ninety-five percent of body shape variance in NGM buffer





Turning behaviors in NGM buffer are well classified by a decision boundary found by a supervised machine learning algorithm known as a support vector machine

This work was funded by NIH R01MH130064 and NIH R01NS115484 from the National Institutes of Health

[1]. Stephens, G. J., Johnson-Kerner, B., Bialek, W., & Ryu, W. S. (2008). Dimensionality and dynamics in the behavior of C. elegans. PLoS Computational Biology, 4(4), e1000028. [2]. Broekmans, O. N., Rodgers, J. B., Ryu, W. S., & Stephens, G. J. (2016). Resolving coiled shapes reveals new reorientation behaviors in C. elegans. eLife, 5, e17227