Three New Software Tools for Tracking Worms, Visualizing Neural Networks and Displaying Gene Structures

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Several software programs exist that can identify and track a population of worms on a Petri plate (e.g. Ramot et. al, PLOS One 2008). I developed a new Matlab-based worm tracking program to record and analyze macroscopic worm behavior, including movement speed, movement direction and body size. We have used this software to process multi-hour, 1 frame/second videos of bright worms against a dark background. The software identifies objects as worms based on their shape, rather than relying on movement inferred from frame subtraction. This approach has the advantage of tracking severely uncoordinated mutants (i.e. fewer false negatives) but the disadvantage of identifying non-moving curvy objects as worms (i.e. more false positives). Nonetheless, in practice it has proved to be more accurate, more robust and more flexible than the previous worm tracker used in the lab.

I have also written a web application that enables interactive visualization and analysis of the *C. elegans* neural network. Built from existing datasets, this application enables you to: (1) view as a radial graph the immediate synaptic partners of an individual neuron or neuron class; (2) find the shortest anatomical paths (via synapses and gap junctions) between two neurons; (3) zoom out to view interconnected neurons more than one synapse away; and (4) view and add accessory information about each neuron, such as gene expression figures, physiology figures, ablation phenotypes and gene over- and under-expression phenotypes.

Third, I developed a web application that generates a proportional publication-quality graphic of a gene's exons and introns. By simply pasting a gene's nucleotide sequence from Wormbase, you can generate a vectorized PDF that includes a gene's 5' UTR, coding sequence, 3' UTR, and mutations and deletions.

Both the neural network visualization and the exon-intron graphic maker are available at www.wormweb.org.

Poster

Topic: Technical Advances

Keywords:

No. characters (counting spaces): 1,968