

Nemo: A computational tool for analyzing nematode locomotion

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AF3. Algorithms and File List

1. Algorithms used to extract image and information data

- a. `extract_all_objects.m`: This algorithm incorporates other routines in this section leading to an automated extraction of image information. It requires a minimum intervention from the user (introduction of input values).
- b. `extract_object.m`: Applies morphological operations to animals. After thresholding and removal of smallest objects in the image, the mask and the skeleton of the animal are derived as binary images.
- c. `correct_skeleton.m`: Given the coordinates of the worm in the previous image, the algorithm determines which of the two endpoints of the animal can be associated with 'head' and 'tail'.

- d. `point_segment.m`: Segmentation procedure carried out according to the number of segments defined by the user.
- e. `area_calculation.m`: The area occupied by the animal is calculated (in pixels).
- f. `length_elegans.m`: The actual length (in pixels) of the worm considering neighbouring points along the spine ('skeleton') is computed.
- g. `thickness_automatic.m`: The thickness of particular animal sections are calculated. Thickness is given for every segment in pixels.
- h. `cm_total.m`: The centroid of the animal is calculated.
- i. `manual_correction`: If the worm skeleton contains branches, they are removed using this algorithm.
- j. `extract_all_objects_amc.m`: An automated procedure used to obtain the revised information related to the skeleton, length, and other features of the worm (see previous steps).
- k. `Nemo.m`: File that contains commands to perform specific actions when the Graphical User Interface is used.
- l. `Nemo.fig`: File that loads the GUI.

2. Generated files

- a. thickness_image=A_segment=B.txt: text file containing values that represent half the width (in pixels) of segment B in image A .
- b. skeleton_A: binary image that contains the skeleton of the animal.
- c. skeleton_A_point=B: text file that contains the coordinates of the centroid of the segment B in image A .
- d. skeleton_A_total_point=B: the location of the centre of mass of the animal in image A after the animal has been segmented in B parts.
- e. mask_a: binary image of the animal mask.
- f. number_of_time_points.txt: text file that contains the number of segments in which the animal has been divided.
- g. length_A.txt: actual length of animal skeleton (in pixels) considering the spine.
- h. frames_per_sec.txt: images taken in the unit of time.
- i. edge_A.txt: matrix with the location of the endpoints of the skeleton in images A and $A+1$.
- j. background_row_column.txt: text file containing values corresponding to the threshold (to generate a binary image) and size of every image.