Identification of posture in C. Elegans using Template Matching

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***Abstract*—Caenorhabditis Elegans, a model organism in biology is used to study the behavior of the neural activity. The locomotion behavior of the nematode is determined to understand the behavior of the nematode which in turn reflects the neural activity. In this study, the posture exhibited by the nematode is studied and is classified either omega turn or not. The study uses template matching techniques from image processing to determine the posture of the nematode. The study performs thresholding, denoising, and different filtering as a part of preprocessing. The study uses template matching using correlation of the input image and the template to identify the postures and shows that the template matching algorithm could succeed when the orientation and the scale is taken into consideration. The study shows that it is very imperative to build a model which is invariant of scale and orientation.**

***Index Terms*—physician gaze, primary care visits, patient-physician interaction, healthcare technology, computer vision**

I. Introduction

C Elegans is a microscopic roundworm of length 1mm long and is usually found in temperate soil environment. The nematode has a simple neural structure and a well-connected cell lineage. The nematode has 302 neurons as compared to over 100 billion neurons in humans and over 3 trillion connections. Because of its simple structure, transparent nature and well-connected cell lineage, the cell differentiation and cell activity could be easily studied. C Elegans are very useful in understanding biological mechanism of the nervous system. It is considered as a model organism as it shares many of the essential biological characteristics that are central problems of human biology. It is very useful to understand basic biological mechanisms and to study basic mechanisms of disease that translate to understanding how to fight disease in humans.

The locomotion behavior of C. Elegans is very important as the behavior of the nematode ultimately reflects the neural activity. The locomotion behavior could be defined as the changes of movement and postures over time. Hence, it is imperative to understand the postural change in the C. Elegans nematode. Our study focuses on the omega bends, a significant posture exhibited by the nematode. Various studies identify the biological reason behind the omega bend posture. Hence, our study aims to determine if the nematode exhibits an omega turn or not, given an input image.

II. Related Work

Various studies tried to determine the posture of the C. Elegans nematode. Huang et.al., [1] described a novel algorithm which could detect the omega bends in the nematode by extracting the skeleton of the nematode. The head and tail of the nematode were also identified and the angle between the head, tail and the center of the body were used to determine the posture of the worm. Nagy et al., [2] presents an automated process of detection of complex postures in the nematode Caenorhabditis elegans. Their work is based on a generative statistical model and a coarse-to-fine strategy. In this study, first a small set of characteristic features for the head and body regions is defined as functions of oriented edges in the image. With these features a coarse outline of the worm is obtained. Then, the statistical model uses the edge information in the image to enable precise identification of the postures. This study shows that the both simple and complex postures in the given input image can be determined and also show the flexibility and usability of the model.

Schwarz et al., [3] proposes a discrete representation of behavior to understand the locomotion behavior of the nematode C. elegans. The worm's posture is approximated by its closest matching template from a set of 90 postures and locomotion is represented as sequences of postures. The locomotion was studied over time and its posture were recorded as a set. The worm locomotion was recorded on different environments to study their change in behavior. Although previous works aimed to determine the posture of the worm, there hasn't been any template matching technique to identify the postures. Hence, our work would be to identify posture of the worm using template matching.

III. Data

Daf2, a genetic variant of the nematode C. Elegans was allowed to crawl on the surface of an agar plate. Any presence of food was removed from the agar plate and the activity of the worm was recorded every other day. The worm was tracked using an in-house worm tracker [provide reference] under laboratory conditions. Total of 10 daf2 worms were recorded every other day until death. Our data reports 10000 images extracted from the first 6 minutes of video recorded on day 3 of one daf2 worm. From the 10000 images, templates were extracted and were used to compare with other images.

IV. Methodology

An overview of the methodology is shown in 1. The raw input images first undergo a series of processing as a part

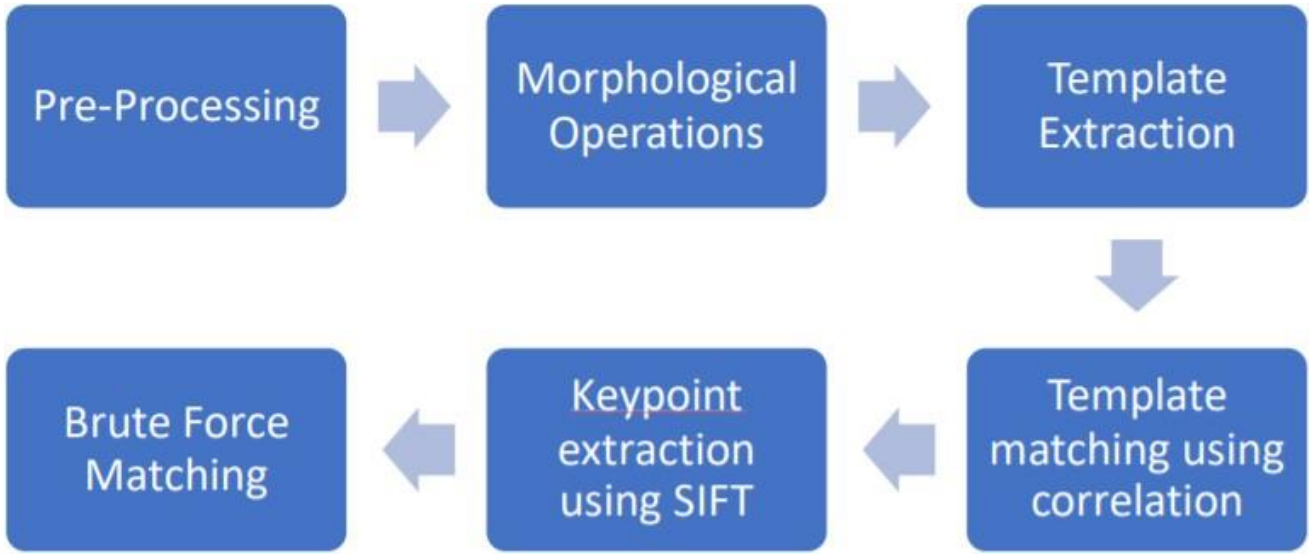

Fig. 1. Overall methodology of the study

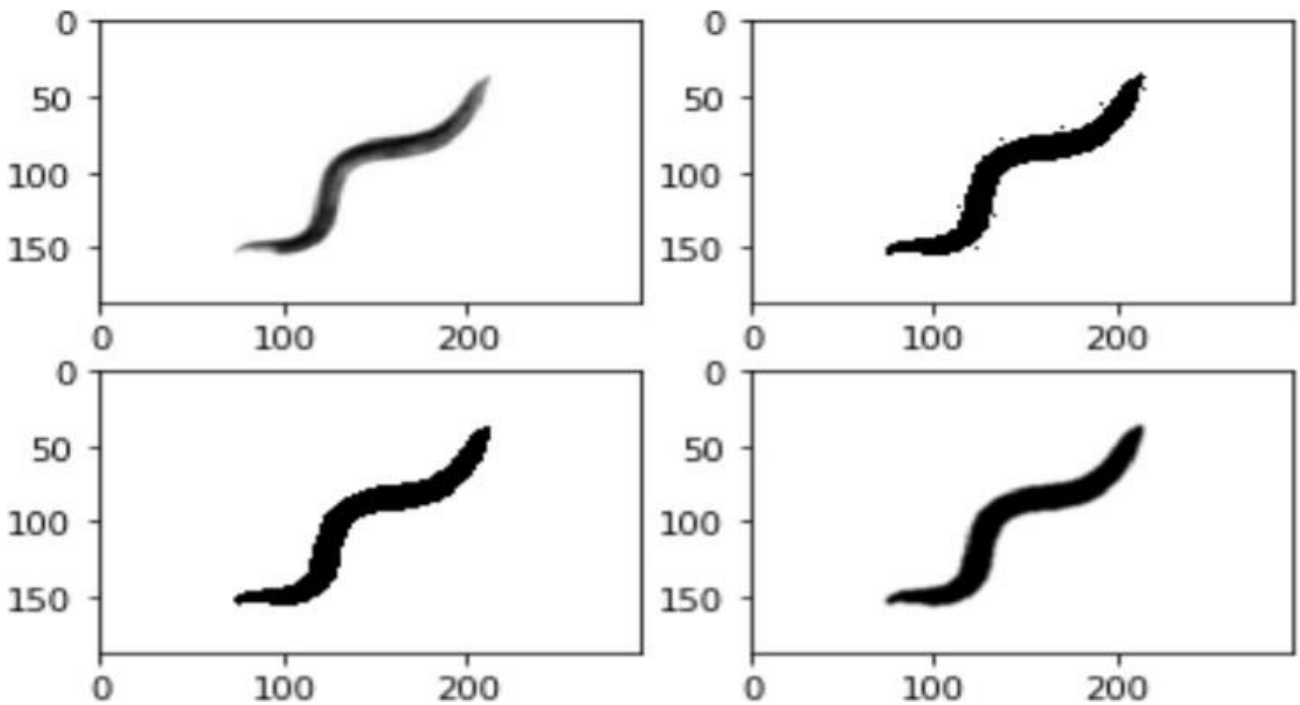

Fig. 2. The results of various pre-processing techniques. Top left: shows the original input image; Top right: shows the binary image reproduced by binary thresholding; Bottom left: shows the output of a 5*5 median filter applied on the binary image; bottom right: shows the output of a 5*5 Gaussian filter applied on the denoised image.

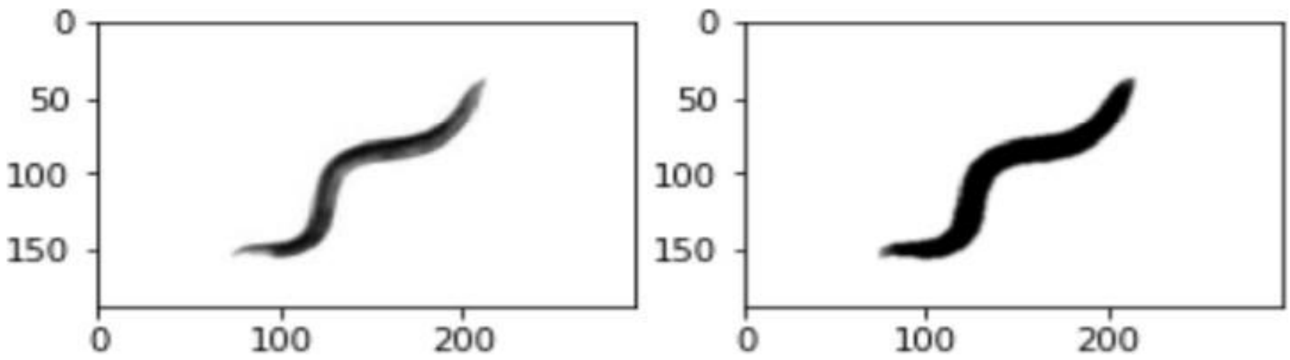

Fig. 3. Original image (left) and the image after morphological operations (right) were performed

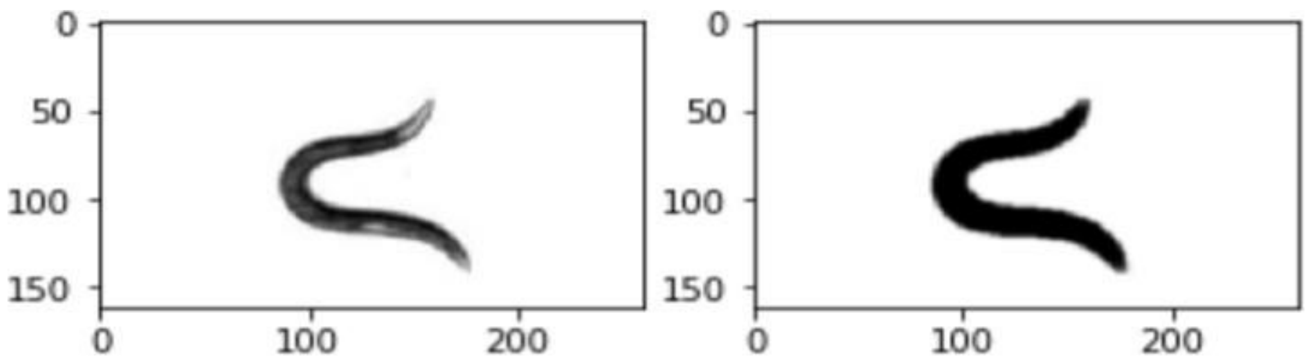

Fig. 4. The template extracted from the original dataset (left) and pre-processed image (right) of the template

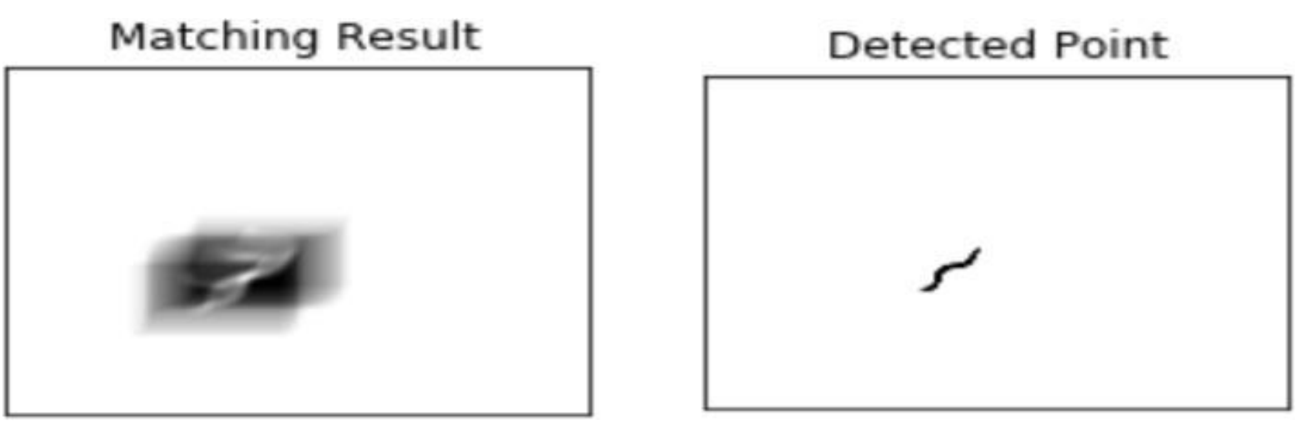

Fig. 5. The result of the template matching algorithm using correlation

Fig. 6. The worm marked as an omega turn by the algorithm

of data preparation. New set of data are extracted as a result of preprocessing. This new set of data was used to extract the template. This set of templates was then compared to our data following the methods of TM_CCORR_Normed template matching algorithm. To make the algorithm invariant of scale and orientation, key points were extracted from the template and the input image and were used to comparisons. The key points were extracted by SIFT algorithm. The key points from input and template were then matched using Brute-Force matching technique.

A. Pre-Processing

The input image was then converted to a binary image by thresholding. The input image has only the worm and the background with some noise in the background. Hence, binary thresholding was easy to apply. Threshold of 250 was used for binary thresholding. We chose this threshold because we know that the background was almost white with few gray values close to 250. The binary image was then denoised using a 5*5 median filter to remove the noise prevalent in the background/ agar plate. Further, a 5*5 Gaussian filter was used to smoothen the edges.

B. Morphological Operations

To close the holes or gaps in the nematode's body, dilation followed by erosion also known as a closing operation was performed on the denoised binary image. The morphological closing operation was chosen because of its effectiveness in filling the holes in the body structure of the nematode.

C. Template Extraction

For determining the posture of the nematode, we had to classify the whether the nematode exhibited omega turn or not. There are several ways to find it. The skeleton of the nematode could be extracted and the angle between the head and tail could give the posture of the nematode. Alternatively, a nematode exhibiting an omega turn could be used as a template and could be compared against the input image to find if the nematode exhibits omega turn or not. For this purpose, we had to extract a template where the nematode exhibited an omega turn. Four different templates were extracted from the dataset.

D. Template Matching using Correlation

In our study, we performed template matching using the correlation method. The template is slid over the input image and the correlation between the input and the template is calculated. The correlation between the input and the template is calculated using the following formula

Where R(x, y) stores the match metric for each location of the template over the input image.

The brightest match or the location with the highest correlation is found using the MinMaxLoc function in opencv python. A threshold of 0.7 was determined to be the matching criteria in our study. There is no solid reason for this thresholding. The thresholding was determined as an intuitive way by the author. Any correlation above than 0.7 is considered to be a match and the nematode is considered to exhibit an omega turn.

E. Keypoint Extraction using SIFT

As the nematodes crawl in the surface of the agar plate in different directions, the orientation of the template becomes important in identifying the posture of the nematode. Since, the nematode crawls in all 360 degrees possible, the template becomes variant of the orientation and naive approach of template matching could potentially lead to high number of false negatives in the study. It is also known that the nematode grows and widen as the nematode ages. Also, because of the video captured techniques and scaling of the template and the input image, the template is prone to variability due to scaling. Both scaling and orientation of the nematode in the input image and the template could potentially affect the outcome of our study.

Hence, to address these challenges, we aim to extract keypoints and descriptors using the Scale Invariant Feature Transform (SIFT) algorithm. The SIFT algorithm is invariant of scale and orientation and hence could be used in feature matching as we proceed further. Our study leverages the SIFT algorithm to make our model invariant of scale and orientation.

F. Brute Force Matching

The keypoints from the template and the images from the dataset were compared to match the posture of the worm. Similar keypoints from the input and the template would be matched together. For the brute force matching, we again used a good match ratio of 0.7 or 70% which matches the keypoints with 75% accuracy.

V. RESULTS

Figure 2 shows the input image and the results of relevant techniques. As a first step, the input image underwent series of pre-processing. First the input image was converted to a binary image by a thresholding method. The resulting binary image had a lot of noise in the background of the nematode. The agar plate has some noise which was captured by the binary thresholding. And hence to denoise the binary image, a 5*5 median filter was further applied. This resulted in removing all the noise from the image. However, the edges of the nematode were affected as a result. Therefore, further a 5*5 Gaussian filter was used to smoothen the image. Because of the prevalence of holes in the nematode's body, a morphological closing operation was performed. The closing operation was successfully able to fill the holes in the body of the nematode as show in figure 3. Figure 3 shows the original image and the image after morphological operations were performed. It was visible from the image that the body of the nematode has no holes and is also well characterized from the background. The template extracted from the dataset is shown in figure 4. The template has the nematode exhibiting an omega turn. The template also had to be pre-processed and closed for consistency.

The result of the naive method of template matching which uses the correlation between the template and the input image is shown in figure 5. With a threshold of 0.7, the algorithm was able to detect the template in the image to a fair extent. Because of the shape of the nematode during its movement, most of the forward motion were matched as an omega turn. This lead to a high number of false positives. With a threshold of 0.7, the algorithm matched the posture in figure 6 to be an omega turn when it is clearly not. However, the threshold of 0.7 was set to have some flexibility when the orientation of the worm is different to that of the template. This algorithm failed badly when the orientation of the nematode and the template were different. Most of the omega turns were falsely marked negative increasing the number of false negatives.

The keypoints of the template and the input images were extracted using the SIFT algorithm. However, the keypoints from the set of templates never matched with any of the image in the dataset. The possible reason for failure was hard to understand. Different thresholding and sets of template were tried to improvise the algorithm, but failed.

VI. CONCLUSION AND FUTURE WORK

From our study, it is very clear that the model built has to be invariant of scale and orientation in order for the model to succeed. Hence, would be my future work. The aim would be improve the model by extracting features from the template and matching them with the input image.

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