

# Behavior Tracking of Medaka based on Rotation Invariant Features

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## 1 Introduction

Recent advances in genetics are remarkable, and it is elucidated most of the DNA sequence of medaka (*Oryzias latipes*) matches the DNA sequence of human (*Homo sapiens*) as in Refs. [1]. Currently, visual measurement by experts is commonly used for behavior analysis of medaka. However, the time cost and misidentification by human eye evaluations is often problematic. In order to deal with the above problem, we suggest a method based on image processing technology. When we treated data which is taken by a camera, such as we need to note the change of brightness and sudden speed change and direction change of target (medaka). To remove these influence, we introduce new tracking method which combined central difference orientation code matching and particle filter as in Refs. [2] and [3]. Further, we show effectiveness of the proposed method through experimentation.

## 2 Our proposed algorithm

In this chapter, we introduce an algorithm of our proposed method. This algorithm is roughly composed of four steps such as pre-processing, particle filter, central difference orientation code matching and decision of the target position. First, we perform four processes including grey-scale processing as pre-processing. Then, we derive the detected position and the estimated position of target using by central difference orientation code matching and particle filter. Finally, we determine the target position by integrated evaluation the detected position and the estimated position.

## 3 The detection method of target position

In the proposed method, we use orientation code as a

feature quantity. Then, we detect the target position by performing orientation code matching. Moreover, in order to cope with direction change of target, we calculate central difference orientation code and use for detection.

### 3.1 Orientation code

First, we describe orientation code. In here, we defined the brightness value  $I(i, j)$  of a target pixel at position  $(i, j)$  and calculate horizontal gradient  $\nabla I_i$  and vertical gradient  $\nabla I_j$  based on Sobel filter. Then, the direction  $\theta_{ij}$  in which the luminance gradient is the maximum is derived from  $\nabla I_i$  and  $\nabla I_j$ . Further, orientation code  $c_{ij}$  is obtained by using gradient quantization  $\theta_{ij}$  quantized by quantization width  $\Delta\theta$  as follows:

$$c_{ij} = \begin{cases} \theta_{ij}/\Delta\theta & \text{if } |\nabla I_i| + |\nabla I_j| > \Gamma \\ N = 2\pi/\Delta\theta & \text{otherwise} \end{cases} \quad (1)$$

In equation (1), quantization width  $\Delta\theta$  is  $\pi/8$ , and  $\Gamma$  is a threshold that determined in order to remove a low gradient.

### 3.2 Central difference orientation code

Since orientation code fluctuates due to the rotation, we calculate central difference orientation code. First, in order to calculate the rotation angle of the template image and the target image, we create the radar chart by applying the crossing method to the histogram based on orientation code derived from each image. Further, we derive the principal axis of inertia based on the plot area of radar chart as shown in Fig. 1. Then, the angle of principal axis of inertia is defined as the rotation angle  $\phi$ , and each image are rotated as shown in Fig. 2. Finally, we derive the central orientation code in each image after rotation  $O_{ij}$ .

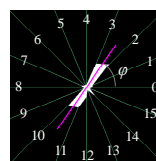


Figure 1: Radar chart

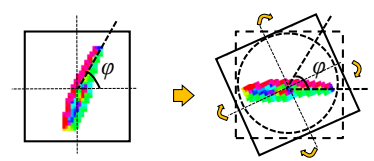


Figure 2: Rotation of the image

### 3.3 Central difference orientation code matching

We perform matching between rotated images. Below, we explain method of matching using equation (2)-(4).

$$d(a, b) = \begin{cases} \min\{|a-b|, N-|a-b|\} & \text{if } a \neq N, b \neq N \\ N/2 & \text{if } a = N, b = N \\ N/4 & \text{otherwise} \end{cases} \quad (2)$$

$$D_{kij} = \sum_{K=k-n}^{k-1} \left( \frac{d(a, b) - 4}{4} \right) \quad (3)$$

$$d_{Rkij} = \left( \sum_{j=1}^M \sum_{i=1}^M D_{kij} \cdot R_{ij} \right) / \left( \sum_{j=1}^M \sum_{i=1}^M R_{ij} \right) \quad (4)$$

In this paper, we use multiple templates which are weighted for matching. First, we calculate the mean of absolute residuals  $d(a, b)$  based on central difference orientation code  $a$  and  $b$  at the position  $(i, j)$  of each  $n$  templates and the target image from equation (2). Then, we define the average of the mean of absolute residuals  $D_{kij}$  from equation (3). Finally, we derive evaluation value of matching from equation (4). In here,  $R_{ij}$  means a weight value, and  $k$  means time.

### 4 The estimation method of target position

In this chapter, we describe the estimation method. The algorithm of particle filter consists of three steps such as particle transition, calculate likelihood and resampling. In particle transition, the transition range is set based on the maximum swimming power of target which is known to cope with the sudden speed fluctuation of target. Further, we calculate two types of likelihood for each transitioned particle given by equation (5) and (6). Then, a particle position at which the likelihood becomes maximum is determined as the estimated position of target. Finally, we perform resampling on low-likelihood particles based on Mahalanobis distance.

$$L_m^{(l)} = \exp\left(-\frac{D_l^2}{2\sigma_D^2}\right), \quad D_l = \sqrt{(i_k - i_p^{(l)})^2 + (j_k - j_p^{(l)})^2} \quad (5)$$

$$L_c^{(l)} = \exp\left(-\frac{Ew_l^2}{2\sigma_{Ew}^2}\right), \quad Ew_l = 4E_{wij} + 4 \quad (6)$$

### 5 The observation method of medaka

We describe observation method of medaka which combined methods described in chapter 3 and 4. First, we set the search area around the estimated position. Then, we apply orientation code matching within its area. Further, we extract an arbitrary number as a candidate region in order from a target region having a small average of the mean of absolute residuals  $d_{Rkij}$ . Furthermore, we calculate distance evaluation value  $\lambda_s$  based on distance between the center position of candidate area and the estimate position. In here,  $s$  means candidate number.

Below, we define the evaluation formula in equation (7).

$$E_s = \alpha \cdot \frac{D_{Rkij} + 1}{2} + (1 - \alpha) \cdot \lambda_s \quad (7)$$

In equation (7),  $\alpha$  means a weight value representing the priority of the evaluation value and takes a value 0 to 1. An area where the integrated evaluation value  $E_s$  is the minimum is detected as the position of target.

## 6 Experiment

We show effectiveness of our proposed method through experiment. In here, we apply the proposed method to 8 targets swimming in herd in a vessel, and generate a swimming trajectory in each individual. Below, we show the experimental parameters. The video image size is  $720 \times 480$  pixels, number of images are 1800, the search area size is  $19 \times 19$  pixels, the template size is  $9 \times 9$  pixels, the threshold value of orientation code  $\Gamma$  is 2, number of the template images are 5, number of particle are 60 and weight value  $\alpha$  is 0.84. Further, we show the experimental results in Fig. 3.

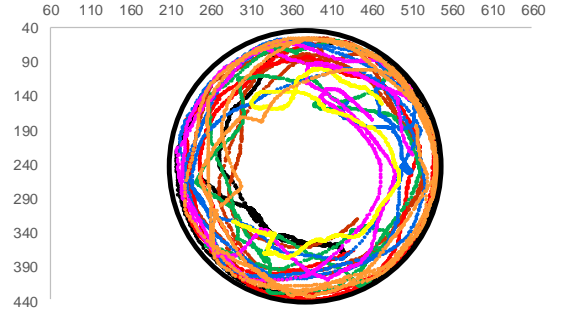


Figure 3: Swimming trajectory of each target

Fig. 3 is shown the swimming trajectories of each target generated throughout the frame. Our proposed method was able to obtain the swimming trajectories of each target without erroneous detection for 1 minute moving image.

## 7 Conclusion

In this paper, we proposed method of behavior tracking of medaka. We dealt the change of brightness, sudden speed change and direction change of target by using method which combined detection method and estimation method. Furthermore, we show effectiveness of our proposed method through experiment.

### References

- [1] M. Kasahara et al., "The medaka draft genome and insights into vertebrate genome evolution", *nature*, Vol.449, No.7145, pp.255-382, 2007
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