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HEAD TRACKING AND FLAGELLUM TRACING FOR SPERM MOTILITY ANALYSIS

H.-F. Yang[†], X. Descombes[‡], S. Prigent[§], G. Malandain[‡], X. Druart[¶], F. Plouraboué^{||}

ABSTRACT

Sperm quality assessment plays an essential role in human fertility and animal breeding. Manual analysis is time-consuming and subject to intra- and inter-observer variability. To automate the analysis process, as well as to offer a means of statistical analysis that may not be achieved by visual inspection, we present a computational framework that tracks the heads and traces the tails for analyzing sperm motility, one of the most important attributes in semen quality evaluation. Our framework consists of 3 modules: head detection, head tracking, and flagellum tracing. The head detection module detects the sperm heads from the image data, and the detected heads are the inputs to the head tracking module for obtaining the head trajectories. Finally, a flagellum tracing algorithm is proposed to obtain the flagellar beat patterns. Our framework aims at providing both the head trajectories and the flagellar beat patterns for quantitatively assessing sperm motility. This distinguishes our work from other existing methods that analyze sperm motility based merely on the head trajectories. We validate our framework using two confocal microscopy image sequences of ram semen samples that were imaged at two different conditions, at which the sperms behave differently. The results show the effectiveness of our framework.

Index Terms— object detection, object tracking, flagellum tracing, sperm motility analysis, confocal microscopy

1. INTRODUCTION

Sperm quality assessment plays an important role in human fertility and animal breeding. One of the most important attributes for evaluating semen quality is sperm motility, according to the World Health Organization (WHO) report [1]. When performed manually, semen analysis based on sperm motility is labor-intensive and subject to intra- and inter-observer variability. Computer-assisted sperm analysis (CASA) systems, in contrast, provide rapid and objective semen fertility assessment. In addition, they also offer a means of statistical analysis that may not be achieved by visual assessment. Hence, automated sperm motility analysis systems are highly desirable.

To analyze the sperm motility, algorithms that obtain the trajectories of sperm heads have been developed in the CASA systems, which are mainly for evaluating the velocity of individual sperms. Such algorithms are based on template matching [2], particle filtering [3], and motion template [4]. While great effort has been made to

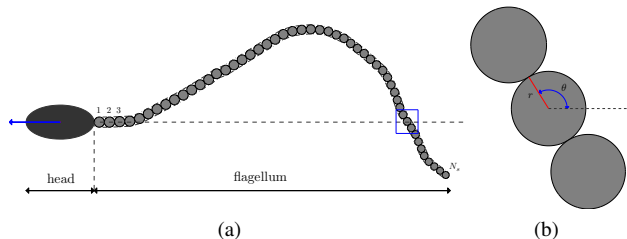


Fig. 1. Representation of a spermatozoon. (a) A spermatozoon consists of a head and a flagellum. The head is represented by an ellipse. The direction of its major axis indicates the direction of sperm movement (the blue arrow). The red point is the head center. The flagellum is made up of a sequence of N_s circles. (b) Close-up of the circles in the bounding box in (a) is shown. Each circle is parameterized by a radius (r) and an angle (θ).

develop head tracking algorithms, relatively little attention has been given to obtaining the shapes of flagellar beat. In biology, it is established that the shapes of flagellar beat determine the moving path of a sperm cell [5], so retrieving the flagellar beat patterns, as well as the head trajectories, from image data will help shed new insight on the sperm motility assessment.

In this paper, we present a computational framework designed to track the heads and trace the tails for quantitative analysis of sperm motility. Our framework includes 3 modules: head detection, head tracking, and flagellum tracing. These modules are performed sequentially to obtain the head trajectories and flagellar beat patterns. First, the head detection module detects the sperm heads every 100 frames using a Multiple Birth and Cut (MBC) algorithm [6]. The detections are the inputs to the head tracking module for obtaining the head trajectories and angles of head rotation. We use a block matching method [7] to register the heads in the subsequent images with respect to the positions and angles of those detected heads. This is different from other tracking methods that consider only the head positions. Finally, we propose a flagellum tracing algorithm, based on a Markov chain Monte Carlo (MCMC) sampling method, to obtain the flagellar beat patterns.

2. METHOD

2.1. A Spermatozoon Model

Modeling of a spermatozoon is essential to extraction and analysis of its movement. We consider a model that represents a spermatozoon as an assembly of a head and a flagellum. Figure 1(a) illustrates this modeling scheme. An ellipse is used to represent the head, and the direction of its major axis is parallel to the direction of sperm movement (the blue arrow). The flagellum is made of a sequence of N_s circles. Each circle is tightly connected to its adjacent neighbors and is represented by a radius (r) and an angle (θ). θ is defined as the angle between the straight line connecting the centers of two adjacent circles and the direction of sperm movement. This circle

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[†]Univ. Nice Sophia Antipolis, CNRS, I3S, UMR 7271, 06900 Sophia Antipolis, France.

[‡]INRIA, 06900 Sophia Antipolis, France.

[§]Univ. Nice Sophia Antipolis, CNRS, INSERM, iBV, UMR 7277, 06100 Nice, France.

[¶]INRA, CNRS-Université de Tours-Haras Nationaux, 37380 Nouzilly, France.

^{||}IMFT UMR 5502 CNRS/INPT/UPS, 31400 Toulouse, France.

✉H.-F. Yang, X. Descombes, S. Prigent, and G. Malandain are in the team MORPHEME, INRIA/I3S/iBV, 06903 Sophia Antipolis, France.

representation is shown in Figure 1(b). Hence, given a chain of N_s circles, each with (r_i, θ_i) , the flagellum length will be $\sum_{i=1}^{N_s} 2r_i$.

2.2. Head Detection

This module aims at segmenting sperm heads from a 2D image. Our modeling uses an ellipse to represent a head. Hence, a head is represented by 5 parameters, denoted as (x, y, a, b, ϕ) , where (x, y) are coordinates of the center point, a and b are the lengths of the major and minor axes, respectively, and ϕ is the angle between the major axis and the horizontal direction. Using such a representation, the goal of the head detection then becomes to detect an unknown number of ellipse-shaped objects. To achieve this goal, an improved Multiple Birth and Cut (MBC) algorithm based on marked point processes [6] is used. We perform the head detection every 100 frames in order to address the concern that if the sperms are missed by the detection algorithm on the previous frames, they can be detected on a later frame.

2.3. Head Tracking

Heads are tracked by co-registering every couple of successive images. For each couple, a subimage is defined around the head in the first image and registered with the second image: this yields the displacement of the head (rotation and translation) that is used in turn to define a sub-image in the second image for the next co-registration. The composition of computed transformations allows to track the head through the sequence. The registration process, built on a block matching technique, iterates two stages in a multi-scale manner [7]. Given a reference image I and a floating image J , for each small block in the floating image, the first stage finds the most similar sub-region in the reference image based on a similarity criterion. Then, the second stage estimates the global rigid transformation that best describes the obtained correspondences.

2.4. Flagellum Tracing

We present a new flagellum tracing method to extract the shapes of flagellar beat from the image sequence in which the sperm head is registered. According to our modeling of a spermatozoon introduced in Section 2.1, the flagellum is made of a sequence of N_s circles, $C = (c_1, \dots, c_{N_s})$, where c_i represents the i th circle with parameters (r_i, θ_i) . The goal of flagellum tracing is to find the most probable sequence of circles, \hat{C} , given the image data D , which is

$$\hat{C} = \underset{C}{\operatorname{argmax}} p(C|D). \quad (1)$$

Based on the Bayes' rule, Equation (1) can be rewritten as

$$p(C|D) \propto p(D|C)p(C), \quad (2)$$

where $p(D|C)$ is the observation likelihood, and $p(C)$ is the prior.

2.4.1. Circle Prior

We assume that the prior, $p(C)$, follows a Markov process, that is, circle c_i depends only on its previous circle c_{i-1} . So the prior can be factorized as

$$\begin{aligned} p(C) &= p(c_1) \prod_{i=2}^{N_s} p(c_i|c_{i-1}) \\ &= p(r_1, \theta_1) \prod_{i=2}^{N_s} p(r_i, \theta_i|r_{i-1}, \theta_{i-1}). \end{aligned} \quad (3)$$

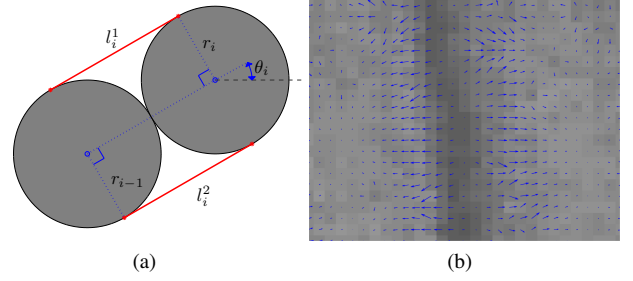


Fig. 2. Illustration of computation of the observation likelihood. (a) Let l_i^1 and l_i^2 be the two line segments that connect the tangent points of circles c_{i-1} and c_i . The gradient likelihood considers the normal to the image level lines at each point on lines l_i^1 and l_i^2 . Please refer to the text for more detail. (b) The vector fields are diverging from the centerline of a tail (dark) and thus the centerline has positive divergence.

We also assume that the radius r_i and orientation θ_i are independent of each other. Then, Equation (3) becomes

$$p(C) = p(r_1)p(\theta_1) \prod_{i=2}^{N_s} p(r_i|r_{i-1}) \prod_{i=2}^{N_s} p(\theta_i|\theta_{i-1}). \quad (4)$$

Under such a Markov assumption, the radius r_i and orientation θ_i are more likely to be similar to those of the previous circle. Thus, $p(r_i|r_{i-1})$ and $p(\theta_i|\theta_{i-1})$ are modeled using a Gaussian centered around the r_{i-1} and θ_{i-1} , respectively. Mathematically, they are represented as

$$\begin{cases} p(r_i|r_{i-1}) \propto \exp(-\lambda_r (r_i - r_{i-1})^2) \\ p(\theta_i|\theta_{i-1}) \propto \exp(-\lambda_\theta (\theta_i - \theta_{i-1})^2), \end{cases} \quad (5)$$

where λ_r and λ_θ are constant parameters. For the first circle, its orientation is determined by the detected head, and its radius is estimated from the image data by testing possible radii in a user-defined range. Thus, we set $p(r_1) = 1$ and $p(\theta_1) = 1$.

2.4.2. The Observation Likelihood

The observation model incorporates two constraints: gradient and divergence constraints. Both constraints consider the interaction between pairs of adjacent circles, so we factorize $p(D|C)$ as

$$p(D|C) = \prod_{i=2}^{N_s} p_g(D|c_{i-1}, c_i) \prod_{i=2}^{N_s} p_d(D|c_{i-1}, c_i), \quad (6)$$

where $p_g(\cdot)$ and $p_d(\cdot)$ are the gradient and divergence likelihoods, respectively.

Gradient Constraint Before defining this constraint, we first introduce a contrast invariant energy $G(\cdot)$. It is defined over the normal to image level lines, aiming to well locate the object boundary in microscopy images [6]. Specifically, for two adjacent circles c_{i-1} and c_i as shown in Figure 2(a), we extract two line segments, l_i^1 and l_i^2 , whose endpoints are the tangent points of the circles. Given these two lines, $G(l_i^1, l_i^2)$ is then defined as

$$G(l_i^1, l_i^2) = \frac{1}{|l_i^1| + |l_i^2|} \int \left\langle \frac{\nabla g(x)}{\|\nabla g(x)\|}, \mathbf{n}(x) \right\rangle dx, \quad (7)$$

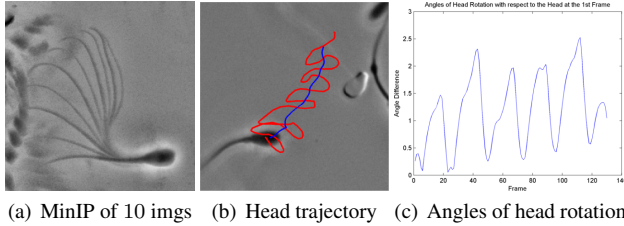


Fig. 4. (a) Minimum Intensity Projection (MinIP) of head-registered images of a sperm, (b) its head trajectory (red) and average path (blue), and (c) angles of head rotation with respect to the head on the first frame.

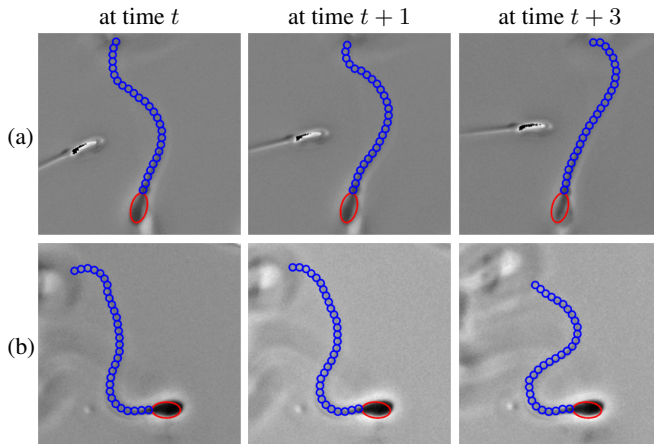


Fig. 5. Flagellum tracing results. (a) Results of a sperm in the control group. (b) Results of a sperm under bME effects. The obtained sequences of circles, along with the ellipses, are overlaid on the images at different times. Visually, the tracing module successfully traces the tails.

and the high concentration of bME conditions. By visual observation, the sequences of circles are lined up well with the flagella in the images, indicating that the proposed method successfully traces the flagella even when the sperms exhibit different beat patterns. More tracing results are shown in Figure 6.

We compared the computer-generated traces against the manual annotations to evaluate the performance of flagellum tracing. The metrics used were missed detection rate (MDR) and false detection rate (FDR) [9]. MDR is the percentage of pixels in the annotation that are more than d pixels away from the computer-generated result; FDR is the percentage of pixels in the generated result that are more than d pixels away from the annotation. We set d to 3, and the MDR and FDR were 6.12% and 1.78%, respectively, for 4 selected sperms, each of which was traced for 10 images.

We further compared the sperm behaviors at the normal and bME conditions, which is summarized in Table 2. It shows that the sperms under the effects of a high concentration of bME are of lower beat cross frequency and tail beat frequency and thus move slower.

4. CONCLUSIONS AND FUTURE WORK

We presented a framework that performs head detection, head tracking, and flagellum tracing to track the sperm heads and trace the tails for sperm motility analysis. The experimental results demonstrated the effectiveness of our method. In the future, we plan to further

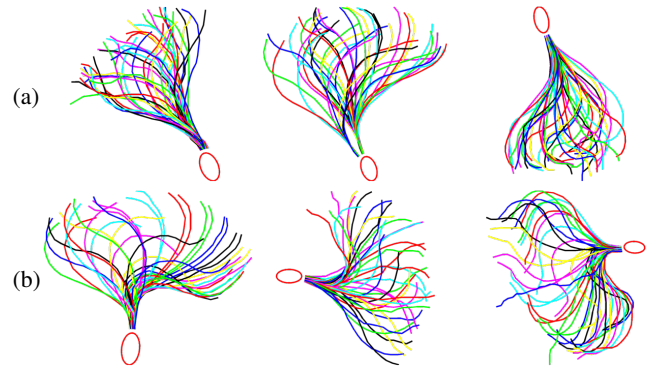


Fig. 6. Flagellar beat patterns of sperms under different conditions. Sperms are (a) at normal condition (control) and (b) at a high concentration of bME. Sperms under the high concentration of bME show larger beat amplitudes. Forty traces for each sperm are shown.

Table 2. Comparison of the Straight Line Velocity (VSL), Beat Cross Frequency (BCF), and Tail Beat Frequency (TBF) of Sperms at the Normal Condition and at the High Concentration of bME. The numbers are represented as mean \pm STD.

	VSL ($\mu\text{m/s}$)	BCF (Hz)	TBF (Hz)
Normal	95.33 ± 37.56	52.15 ± 8.67	25.59 ± 4.30
bME	83.61 ± 21.48	29.17 ± 5.82	14.58 ± 2.91

analyze the head trajectories and flagellar beat patterns to better understand the mechanisms that govern the sperm motility.

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