User Manual - Sperm Simulator V.06.00

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Contents

Chapter 1

Introduction

Sperm Simulator has been developed to assess the performance of sperm detection and sperm tracking algorithms. Using this simulation, one can generate a semen image for testing of Computer-Assisted Semen Analysis (CASA) systems and algorithms. There are four types of swimming modes for the sperm cells available for simulation. The four types are: (1) circular, (2) linear-mean, (3) hyperactive, and (4) immotile. An example of simulated image is shown in figure 1.1. Figure 1.1a shows the simulated image and figure 1.1b shows the same image with the previous locations of each cell shown in blue. For detailed explanation of the process of simulation, please refer to [].

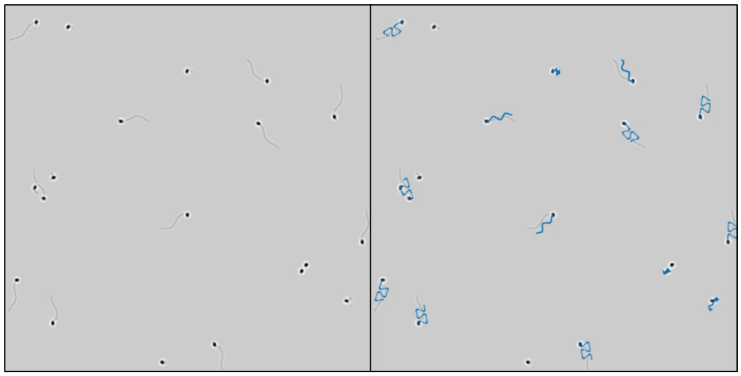

Figure 1.1: An example of a simulated image. (a) Without previous track. (b) With previous track shown in blue.

The simulator is provided as (1) a Windows application and as (2) MATLAB files. The graphical user interface (GUI) has been developed for ease of use. Detailed explanation about each component of the GUI is given in Section II. Any parameters not available in

the GUI can be changed by accessing the MATLAB files.

In chapter 2, detailed explanation about each component in GUI is explained. In chapter 3, method of starting and using the sperm swim simulator is given. In the appendix, the equations for the model of sperm cell and swimming modes of sperms are given.

If you find this software useful in your research, please cite us using the following .bib entry:

```
@articleChoi2021Sim,
 title={An assessment tool for Computer-Assisted Semen Analysis (CASA) algorithms},
 author={Choi, Ji-won and Alkhoury, Ludvik and Urbano, Leonardo and Masson, Puneet
 and VerMilyea, Matthew and Kam, Moshe},
 journal={},
 volume={},
 pages={},
 year={},
 publisher={}}
```

If you have any questions or would like to report on a bug, please write to us via email (jc423@njit.edu or jichoi0222@gmail.com).

Chapter 2

Graphical User Interface

The graphical user interface (GUI) for sperm simulator version 6.00 is shown in figure 2.1.

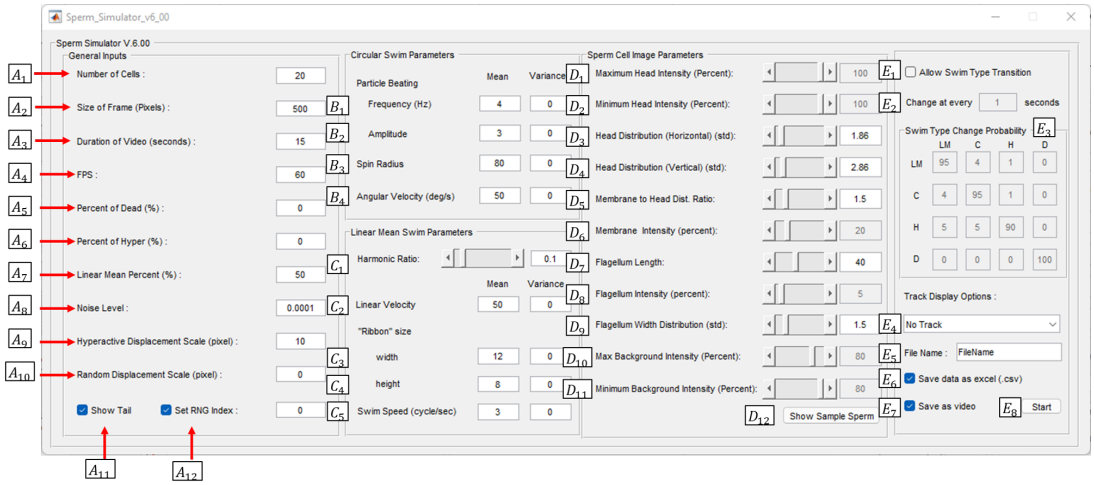

Figure 2.1: Sperm Simulator (Version 6.00) Graphical User Interface with notations

The explanation of the components of the GUI are provided below:

- General inputs
  - A_1: Number of cells in the simulated image
  - A_2: Size of the image (the width and the length of the frame)
  - A_3: Duration of the simulated image (seconds)
  - A_4: Frame rate of the simulated image (fps)
  - A_5: Percent of dead cells within the total number of cells defined in A_1

  - A_6: Percent of hyperactive cells within the total number of cells defined in A_1
  - A_7: Percent of linear mean swimming cells within the total number of cells defined in A_1
  - A_8: Variance of additive zero-mean Gaussian noise in the simulated image
  - A_9: Diffusion coefficient (σ_b, see table A.4) of the hyperactive swimming cells (Brownian motion)
  - A_{10}: standard deviation of zero-mean Gaussian noise added to the position of each cell
  - A_{11}: Option to show flagella of cells in the time-lapse image (check - YES, blank - NO)
  - A_{12}: Option to set random number generator index for reproducibility (check - YES, blank - NO)

- Circular Swim Parameters (see table A.1)
  - B_1: Mean and variance of the frequency of sinusoid modulating on the circular path (f_s) defined in circular swimming cells (Hz)
  - B_2: Mean and variance of the amplitude of sinusoid modulating on the circular path (a) defined in circular swimming cells (pixels)
  - B_3: Mean and variance of radius of circular path (r_c) defined in circular swimming cells (pixels)
  - B_4: Mean and variance of angular velocity on the circular path (f_c) (rate of cycle per second) in circular swimming cells (degrees per second (360 degrees: one cycle))

- Linear Mean Swim Parameters (see table A.2)
  - C_1: Ratio (A_{har}) between the third and the first harmonics of the ribbon (third/first)
  - C_2: Mean and variance of straight line path velocity (V) defined in linear mean swimming cells (pixels/second)
  - C_3: Mean and variance of ribbon width (r_h) (horizontal oscillatory movement) defined in linear mean swimming cells (pixels)
  - C_4: Mean and variance of ribbon height (r_v) (vertical oscillatory movement) defined in linear mean swimming cells (pixels)
  - C_5: Mean and variance of angular velocity (f_l) on the ribbon-like path defined in linear mean swimming cells (ribbon cycles per second)

* the ribbon cycle velocity is assumed to be independent of the overall linear velocity in this simulation

- Sperm Cell image Parameters (see table A.5 and figure A.1)
  - D_1: Maximum sperm head intensity (grayscale) of cells
  - D_2: Minimum sperm head intensity (grayscale) of cells
  - D_3: Standard deviation of the head intensity horizontal distribution (σ_{x_G})
  - D_4: Standard deviation of the head intensity vertical distribution (σ_{y_G})
  - D_5: Ratio of the distance of head to the membrane (halo) (distribution of membrane/distribution of head) ($\sigma_{x_L}/\sigma_{x_G} = \sigma_{y_L}/\sigma_{y_G}$)
  - D_6: Intensity (grayscale) of the membrane
  - D_7: Standard deviation of the f_3 distribution (σ_f)
  - D_8: Length of flagellum (equal to the wavelength λ of circular swim model)
  - D_9: Intensity (grayscale) of the flagellum
  - D_{10}: Maximum background intensity (grayscale, varies between 0 and 1) (B_L)
  - D_{11}: Minimum background intensity (grayscale, varies between 0 and 1) (B_L)
  - D_{12}: Show a sample image of a cell
- Additional Parameters
  - E_1: Option to allow sperm transition to another type of swim (check - YES, blank - NO)
  - E_2: Time interval (sec) that triggers a change in swim type with probability specified in E_3
  - E_3: State transition probability matrix for cell swim types (sum of each row must equal to 100)
  - E_4: Option to show track of the cells in the time-lapse image (No track, 0.5 sec track, 1 sec track, show all track)
  - E_5: Name of the saved data and/or time-lapse video file
  - E_6: Option to save the simulation data as a csv file (check - YES, blank - NO)
  - E_7: Option to save the simulation as a video (check - YES, blank - NO)
  - E_8: Button to start the simulation

Chapter 3

Operation Manual

3.1 Starting the Sperm Simulator Application

Users have two choices to start the Sperm Simulator Application. (1) Users that does not have access to MATLAB can use the stand-alone application, *SpermSimulator.exe*, and (2) users with access to MATLAB can use the MATLAB files to run the simulator.

3.1.1 Sperm Simulator Application (Windows)

3.1.1.1 Installing the Sperm Simulator application

1. To begin the installation, open the Sperm Simulator V6.00 installer executable (shown in figure 3.1).

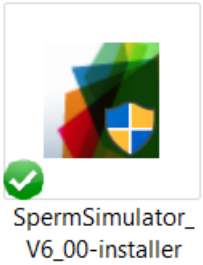

Figure 3.1: Sperm Simulator V6.00 Installer Executable

2. An installer for the Sperm Simulator software should open as one shown in figure 3.2. Click "Next" to proceed with the installation.

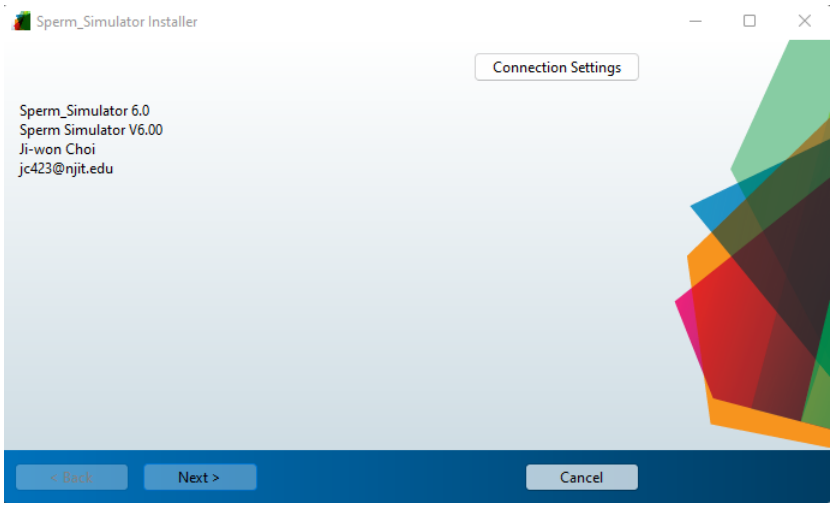

Figure 3.2: Sperm Simulator V6.00 Installer (Step 2)

3. Specify the location where the software should be installed to (shown in figure 3.3). Once the path has been specified, click "Next" to proceed.

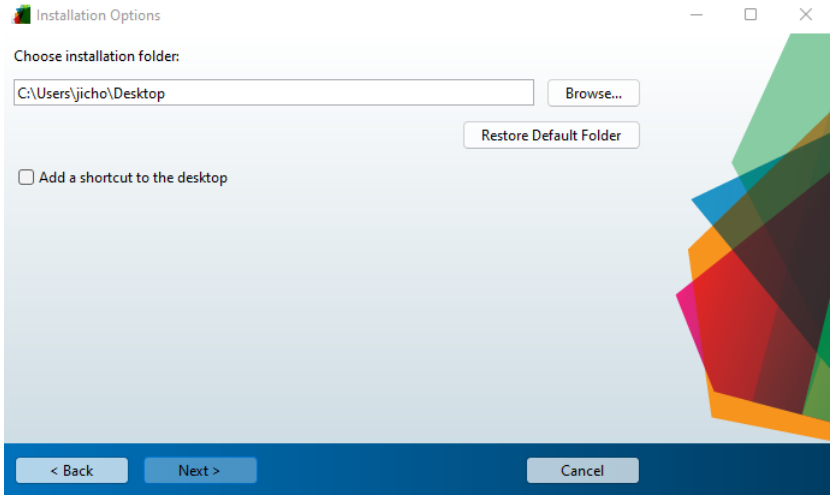

Figure 3.3: Sperm Simulator V6.00 Installer (Step 3)

4. To use the application (Sperm Simulator Version 6.00), one is required to have version 9.9 (R2020b) of the MATLAB Runtime installed on one's computer. The user should be prompted to install the MATLAB Runtime when the installer is excuted (shown in figure 3.4).

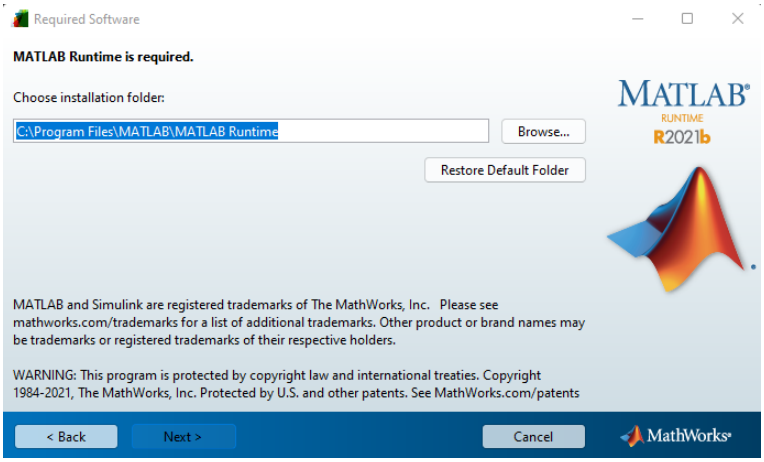

Figure 3.4: Sperm Simulator V6.00 Installer (Step 4)

Specify the path location where the MATLAB Runtime will be installed to. One can also install the MATLAB Runtime by entering the command >> *mcrinstaller* in the MATLAB prompt (requires one to already have MATLAB installed to one's computer). Click "Next" to proceed.

5. Accept the license agreement as shown in figure 3.5 and click "Next" to proceed.

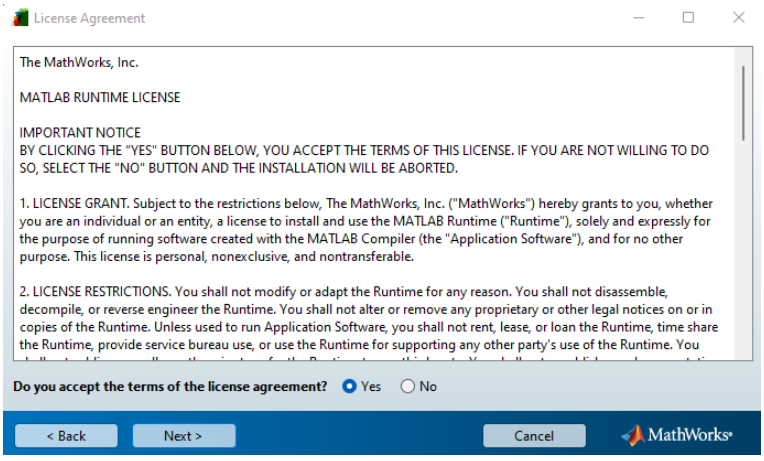

Figure 3.5: Sperm Simulator V6.00 Installer (Step 5)

6. A confirmation page will be shown in the installer (figure 3.6). Click “Install” to begin the installation process. One should be able to see the progress of the installation process as shown in figure 3.7.

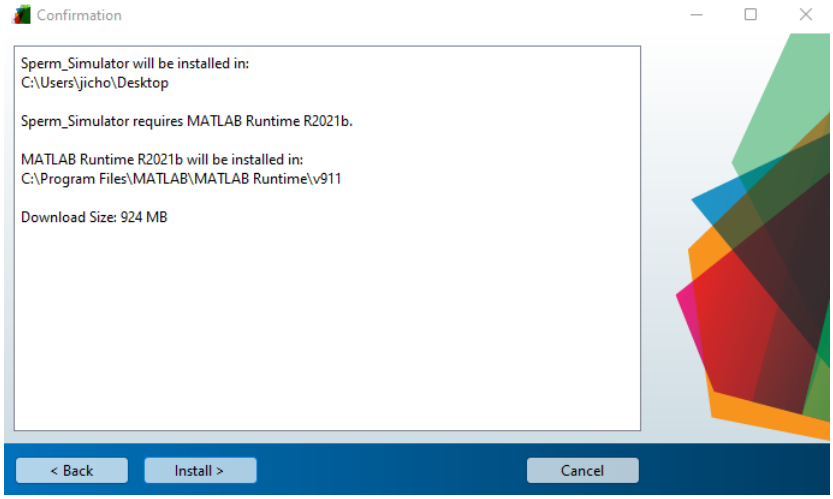

Figure 3.6: Sperm Simulator V6.00 Installer (Step 6-1)

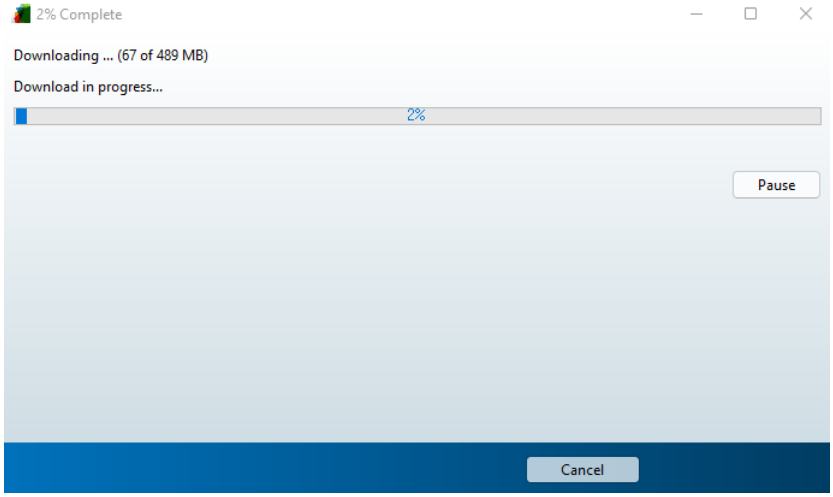

Figure 3.7: Sperm Simulator V6.00 Installer (Step 6-2)

7. When the installation is finished, the installer will prompt the user that the installation has been completed (figure 3.8).

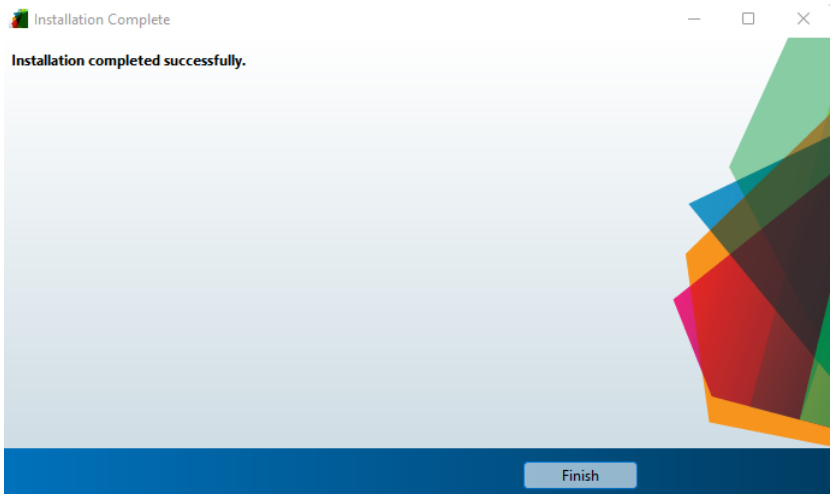

Figure 3.8: Sperm Simulator V6.00 Installer (Step 7)

Go to the location specified in (Step 3) and one should find three folders: "appdata," "application," and "uninstall." Open the "application" folder.

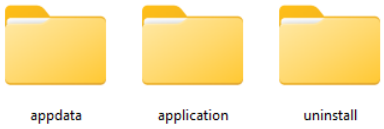

Figure 3.9: Contents of the Sperm Simulation software

Four files will be inside the folder: "default_icon," "readme," "Sperm_Simulator," and "splash." Open "Sperm_Simulator" to start the software.

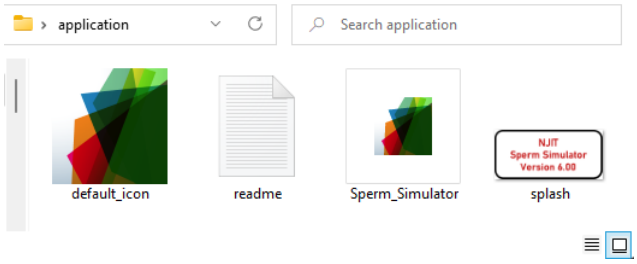

Figure 3.10: Files located in application folder

3.1.2 MATLAB file

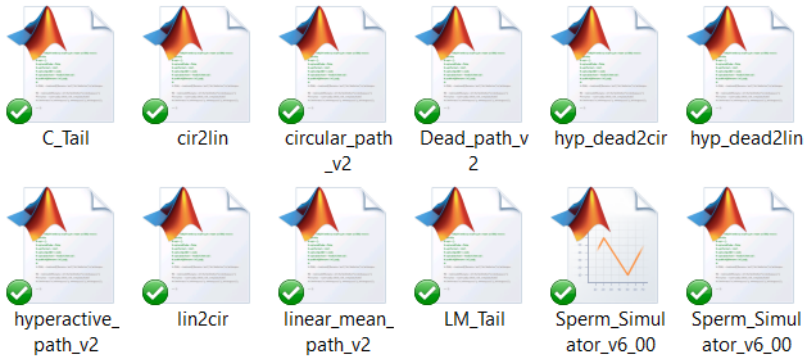

Figure 3.11: MATLAB files required to run sperm swim simulator

The simulation package consists of 12 MATLAB files:

- C_Tail.m
- cir2lin.m
- circular_path_v2.m
- Dead_path_v2.m
- hyp_dead2lin.m
- hyperactive_path_v2.m
- lin2cir.m
- linear_mean_path_v2.m
- LM_Tail.m
- Sperm_Simulator_v6_00.fig
- Sperm_Simulator_v6_00.m

To start the simulation software, run the Sperm_Simulator_v6_00.m file on MATLAB.

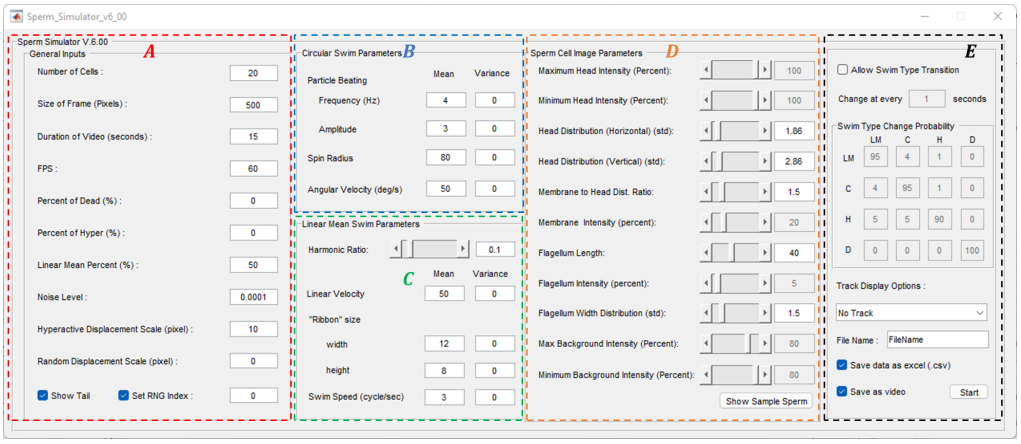

Figure 3.12: Sperm Simulator (Version 6.00) Graphical User Interface

3.2 Using the Sperm Simulation Application

In either methods, the graphical user interface (shown in fig. 3.12) for sperm simulator will open. The general inputs of the simulator is given on the left side of the simulator (zone A, red dotted box). Here, user is able to define the distribution of the cell swimming types. As a default, 50 percent of the cells are linear mean swimming cells, and the rest (50 percent) of the cells are circular swimming cells.

In zone B, blue dotted box, the parameters used for circular swimming cells (B_1 to B_4) can be defined, and in zone C, the green dotted box, the parameters used for linear mean swimming cells (C_1 to C_5) can be defined. Each cell's swimming parameters are distributed normally distributed with mean and variance defined in B_1 - B_4 and C_2 - C_5. If the swimming parameters need to be set the same for all the cells, please set the variance to be zero. Harmonic Ratio C_1 can be changed either using the slider or by specifying the exact value inside of the box left of the slider.

Parameters related to the image of the simulated sperm can be found in zone D, orange dotted box. The user is also able to press D_{12} to get a sample image of the cell. Please adjust the value of each parameter by moving the slider or by specifying the exact value inside of the box left of each slider (available for D_3, D_4, D_5, D_7, and D_9).

In zone E, black dotted box in Fig. 3.12, some additional parameters and options can be found. On the top, the user is given an option to allow the transition of swim mode of each cell in the simulation (E_1). When the option to enable swim type transition as shown in Fig. 3.13, the user is given the option to define the swim transition probabilities (percent), E_3, and transition occurrence interval (seconds), E_2. In the box for swim type change probability, E_3, swim types listed in the left most column indicate the current swim

type and the swim types listed in the upper most row indicate the next swim state. For example, in Fig. 3.13b, every one second all linear mean swimming (LM) cells will change into circular (C) swimming cells (100%), all circular (C) swimming cells will change into hyperactive (H) swimming cells (100%), all hyperactive (H) swimming cells will change into dead (D) cells (100%), and all dead (D) cells will change into linear mean (LM) swimming cells (100%). Default setting shown in Fig. 3.13a will allow all the cells to have transition every second as follows:

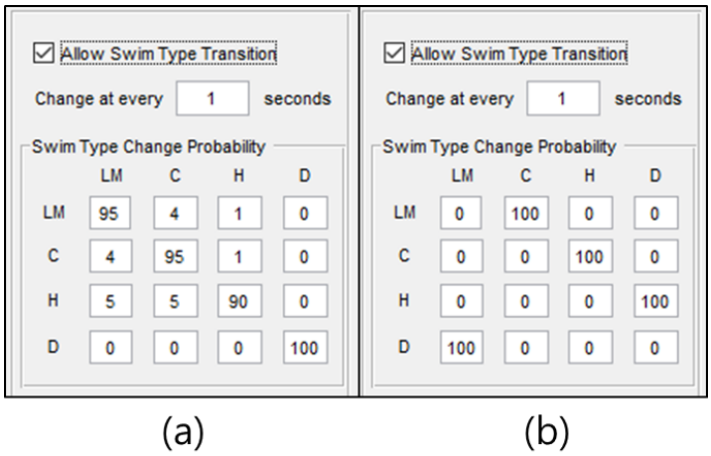

Figure 3.13: Swim type transition option; (a) default probability setting, (b) an example of user defined probability setting

Linear mean swimming cell will

- have 95% chance of staying as linear mean swimming cell
- have 4% chance to change into circular swimming cell
- have 1% chance to change into hyperactive swimming cell

Circular swimming cell will

- have 95% chance of staying as circular swimming cell
- have 4% chance to change into linear mean swimming cell
- have 1% chance to change into hyperactive swimming cell

Hyperactive swimming cell will

- have 90% chance of staying as hyperactive swimming cell
- have 5% chance to change into linear mean swimming cell

- have 5% chance to change into circular swimming cell

Dead cell will

- have 100% chance of staying as dead cell

On the bottom in zone E, the user is able to have the tracks of the cells plotted on the simulated image (E_4). An example of images with different options for E_4 is shown in figure 3.14. Each options for figure 3.14a-3.14d are shown in table 3.1.

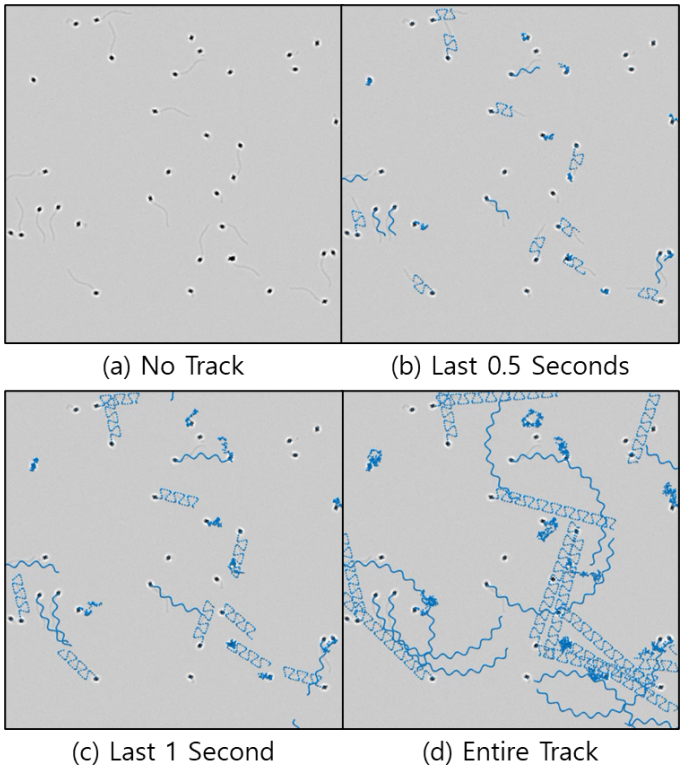

Figure 3.14: Track display options. (A) No track. (B) Show tracks of cell locations in the last 0.5 seconds. (C) Show tracks of cell locations in the last 1 second. (D) Show tracks of all the past locations of cells.

Table 3.1: Track options set for example shown in figure 3.14

	E_4	Effect
a	No Track	Show no track
b	0.5 seconds	Show tracks of past locations of cells for the last 0.5 seconds
c	1 second	Show tracks of past locations of cells for the last 1 second
d	Show the Entire Track	Show tracks of all the past locations of cells

The user is also able to select an option to save the data as an excel file (E_6) and an option to save the simulation as video (E_7). Lastly, the user can press start (E_8) to start the simulation.

3.2.1 Simulation Output Example

3.2.1.1 Video File Output

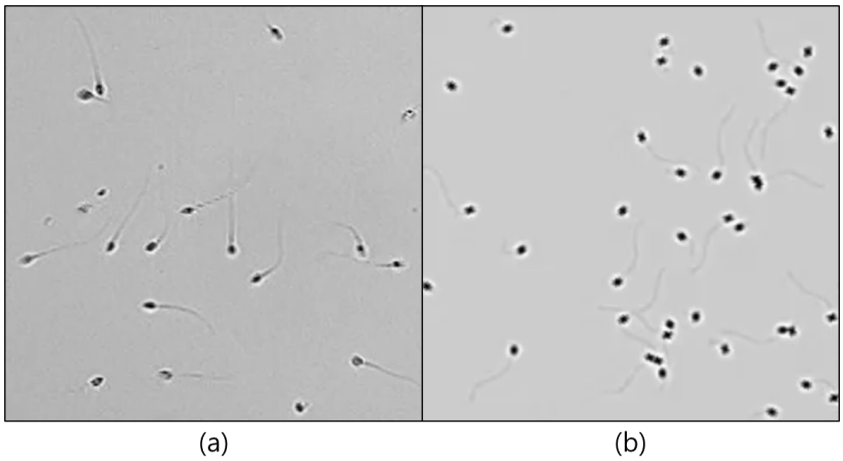

Figure 3.15: (a) Image of real sperm cells (b) image of simulated sperm cells

A sample of an output image (.mp4) is shown in figure 3.15b next to an image of a real semen sample in figure can be seen figure 3.15a. The simulated sperm cells have dark center and is surrounded by a white membrane. This is to resemble the look of real sperm cells. A sperm cell consists of a dark center, and a white ring, or a halo, which is the membrane surrounding the sperm head.

3.2.1.2 Data File Output

An example of csv file output is shown in Fig. 3.16. First column indicates the index of cell/particle, second column is the x-coordinate of the particle, third column is the y-coordinate of the particle, fourth column is the angle of the cell's head, fifth column is the frame number, sixth column indicates the cell's swim type (0 = circular, 1 = linear mean, 2 = hyperactive, 3 = dead), and the seventh column indicates if the direction of swim has been renewed (only applicable for linear mean swimming cells; when a linear mean swimming cell exit the frame, the cell is relocated to a random location in the edge of the frame to swim back into the frame).

	Particle index	x coordinate	y coordinate	Head angle	Frame number	Swim type	Direction renewal
	A	B	C	D	E	F	G
1	1	357.3	219.39	-112.44	1	0	0
2	2	175.47	152.73	-108.58	1	0	0
3	3	130.38	286.62	-66.647	1	0	0
4	4	394.92	82.927	-99.72	1	0	0
5	5	220.85	255.42	-37.676	1	0	0
6	6	110.33	364.37	49.564	1	0	0
7	7	112.78	315.37	84.059	1	0	0
8	8	307.84	106.87	100.24	1	0	0
9	9	121.74	297.34	179.76	1	0	0
10	10	354.93	264.43	-168.95	1	0	0
11	11	390.01	171.24	-99.798	1	1	0
12	12	91.196	152.13	135.46	1	1	0
13	13	77.583	96.221	121.54	1	1	0
14	14	231.82	378.42	-74.31	1	1	0
15	15	75.18	11.585	157.21	1	1	0
16	16	246.56	217.74	133.42	1	1	0
17	17	145.71	345.75	-24.272	1	1	0

Figure 3.16: Example of generated data file (.csv format)

3.2.2 Simulation Image Parameters

In this section, the functionalities of sperm cell image parameters in zone D are described and shown.

3.2.2.1 Head Intensity

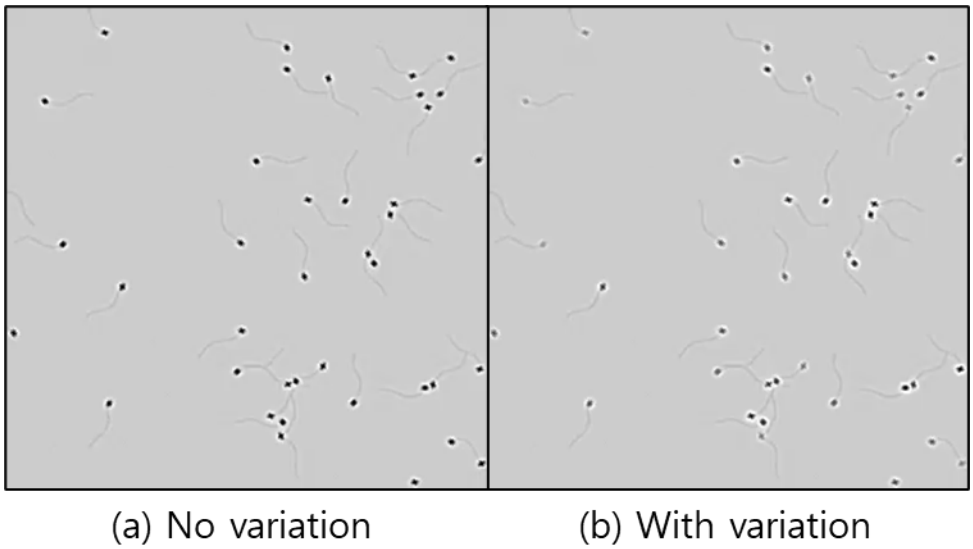

Figure 3.17: Effect of changing minimum head intensity. (A) Default: Maximum 100%, Minimum 20%. (B) Maximum 80%, Minimum 20%.

The parameters D_1 and D_2 determine the intensity of sperm heads. 100% represents

completely dark center (grayscale value of 0) and as the intensity percent gets lower, the head intensities become lower. If the maximum and minimum value of the intensity values are different, each cell in the image is assigned to a random value between the maximum and the minimum intensity values (randomly selected from uniform distribution between the minimum and maximum value). An example of this is shown in figure 3.17. In figure 3.17a, maximum and minimum intensity values are assigned to 100%. In In figure 3.17b, maximum intensity value is 100% and the minimum intensity value is 20%.

3.2.2.2 Head Distribution

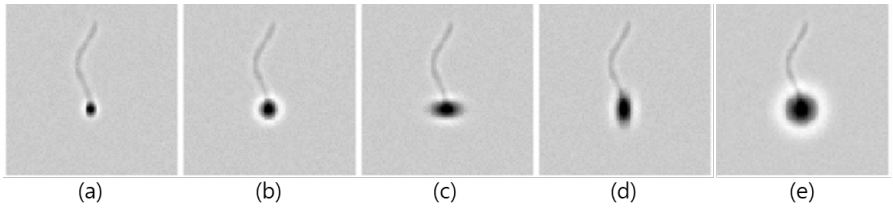

Figure 3.18: Effect of changing head distribution (size). (A) Default: Horizontal std = 1.86, Vertical std = 2.86. (B) Horizontal std = 5, Vertical std = 5. (C) Horizontal std = 15, Vertical std = 5. (D) Horizontal std = 5, Vertical std = 15. (E) Horizontal std = 15, Vertical std = 15.

The parameters D_3 and D_4 determine the size of the sperm heads. D_3 and D_4 are standard deviation of the head intensity distribution in horizontal (σ_{x_G}) and vertical (σ_{y_G}) directions, respectively. In simple terms, one can set D_3 and D_4 to have the sperm heads in one's desired size. In figure 3.18, an example of sperm heads with different values of D_3 and D_4 are shown. The values of D_3 and D_4 for figure 3.18 are shown in table 3.2. The values of D_3 and D_4 can be changed either using the slider or by specifying the exact values inside the box.

Table 3.2: Value of D_3 and D_4 for figure 3.18

	D_3	D_4
A (default)	1.86	2.86
B	5	5
C	15	5
D	5	15
E	15	15

3.2.2.3 Membrane to Head Distance Ratio

The parameter D_5 determines the ratio between the head and the membrane. Higher value of D_5 will cause the membrane to appear farther away from the center of the cell head.

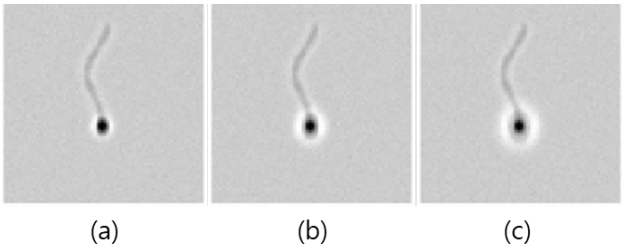

Figure 3.19: Effect of changing the ratio between the membrane and the head. (A) Default: Membrane to Head Dist. Ratio = 1.5. (B) Membrane to Head Dist. Ratio = 3. (C) Membrane to Head Dist. Ratio = 5.

An example is shown in figure 3.19. $D_5 = 1.5$ in figure 3.19a, $D_5 = 3$ in figure 3.19b, and $D_5 = 5$ in figure 3.19c.

3.2.2.4 Membrane and Tail Intensity

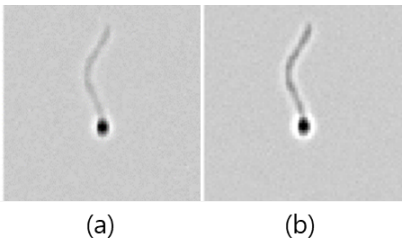

Figure 3.20: Effect of changing intensity of membrane and flagellum. (A) Default: Membrane Intensity 20%, Tail Intensity 5%. (B) Membrane Intensity 30%, Tail Intensity 10%.

The parameters D_6 and D_8 determines the intensity of the membrane and the flagellum, respectively. High values of D_6 and D_8 will cause the membrane and the flagellum to be more pronounced in the produced image. An example is shown in figure 3.20. $D_6 = 20$ and $D_8 = 5$ in figure 3.20a and $D_6 = 30$ and $D_8 = 10$ in figure 3.20b. As one can see, the membrane and the flagellum is more distinct in figure 3.20b compared to the membrane and the flagellum in figure 3.20a.

3.2.2.5 Tail Width

The parameter D_9 determines the width of the flagellum. An example is shown in figure 3.21, where $D_9 = 1.5$ in figure 3.21a and $D_9 = 2$ in figure 3.21b. High value of D_9 will cause the flagellum to appear thicker.

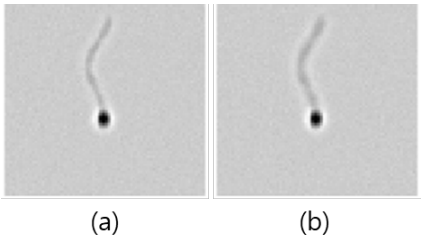

Figure 3.21: Effect of changing flagellum width (std). (A) Default: flagellum width (std) = 1.5. (B) flagellum width (std) = 2.

3.2.2.6 Background Intensity

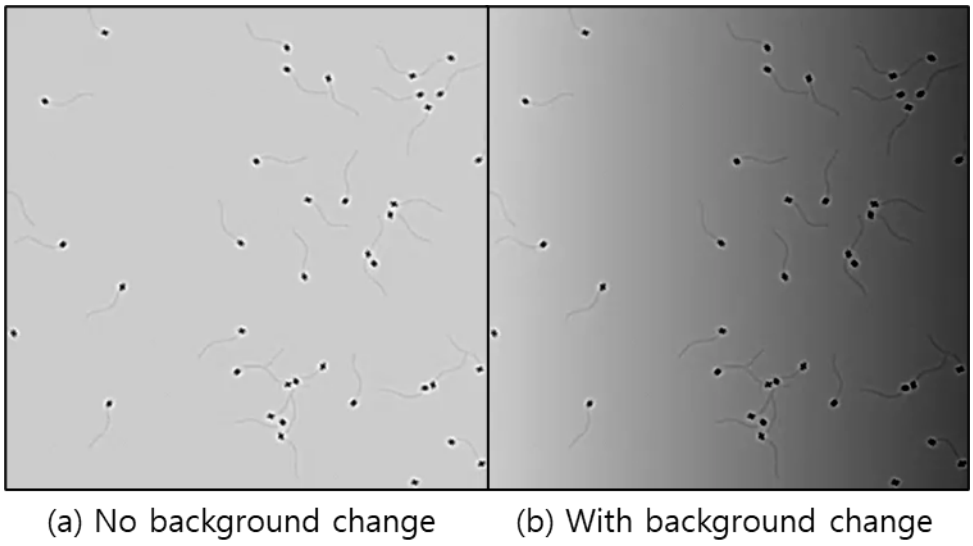

Figure 3.22: Effect of changing minimum background intensity. (A) Default: Maximum 80%, Minimum 80%. (B) Maximum 80%, Minimum 20%.

The parameter D_{10} and D_{11} determines the intensity of the background. If the D_{10} and D_{11} are set to 100%, the background will be completely white (grayscale value of 255). The default values of D_{10} and D_{11} are 80%. In real cases, the semen image will have differences in lighting in the frame. To mimic this effect, the value of D_{10} and D_{11} can be set to different values. The background intensity value in the frame are set to change linearly from left to right from the value D_{10} to D_{11} respectively. An example of this is shown in figure 3.22, where $D_{10} = 80$ to $D_{11} = 80$ in figure 3.22a (no variation in background) and $D_{10} = 80$ to $D_{11} = 20$ in figure 3.22b (variation in background or lighting).

Appendix A

Sperm Swimming Model Equations

Table A.1: Simulation of a Circular Swimming Cell

Circular Swim Model - Head	$x_{H_C}(t) = (r_c + a\sin(2\pi f_s t))\cos(2\pi f_c t) + C_{x_c}$	(A.1a)
	$y_{H_C}(t) = (r_c + a\sin(2\pi f_s t))\sin(2\pi f_c t) + C_{y_c}$	(A.1b)
	$x_{T_c}(k,t) = b(k)\sin\left[2\pi\left(\frac{k}{M} - f_s t\right)\right]$	(A.2a)
	$y_{T_c}(k) = -\lambda\frac{k}{M}$	(A.2b)
Circular Swim Model - Flagellum	$\begin{bmatrix} x_{tail_C} \\ y_{tail_C} \end{bmatrix} = R(2\pi f_s t)\begin{bmatrix} x_{T_c} \\ y_{T_c} \end{bmatrix} + \begin{bmatrix} x_{H_C} \\ y_{H_C} \end{bmatrix}$	(A.3)
	$R(\cdot) = \begin{bmatrix} \cos(\cdot) & -\sin(\cdot) \\ \sin(\cdot) & \cos(\cdot) \end{bmatrix}$	(A.4)
	$b(k) = a\left(\alpha\frac{\lambda k}{M} + \beta\right),\ \alpha = 0.02,\ \beta = 0.8$	(A.5)

(x_{H_C}, y_{H_C}) : head position of circular swimming cell
r_c : radius of the circular path
a : amplitude of the sinusoid modulated on the circular path
f_s : frequency of the sinusoid modulated on the circular path (Hz)
f_c : frequency of the circular cycle (cycle/sec)
(C_{x_c}, C_{y_c}) : vertical and horizontal offset constant
(x_{Tail_C}, y_{Tail_C}) : a set of k points along the center of the flagellum of circular swimming cell
λ : wavelength of flagellum (distance between the start and the end of the flagellum)
$R(\cdot)$: rotation matrix
$b(\cdot)$: local variation in beating amplitude along the flagellum

Table A.2: Simulation of a Linear Mean Swimming Cell

Linear Mean Swim Model - Head

$$\begin{bmatrix} x_c \\ y_c \end{bmatrix} = \begin{bmatrix} V\cos(\theta_r)t + C_{x_L} \\ V\sin(\theta_r)t + C_{y_L} \end{bmatrix} \tag{A.6}$$

$$P = \begin{bmatrix} P_x(t) \\ P_y(t) \end{bmatrix} = \begin{bmatrix} \frac{r_v}{2}\sin(4\pi f_l t) \\ \frac{r_h A_c}{2}[\sin(2\pi f_l t) + A_{har}\sin(6\pi f_l t)] \end{bmatrix} \tag{A.7}$$

$$A_c = \frac{1}{\max\limits_{\theta}(\sin(\theta) + A_{har}\sin(3\theta))} \tag{A.8}$$

$$\begin{bmatrix} x_{H_L} \\ y_{H_L} \end{bmatrix} = R(\theta_r)P + \begin{bmatrix} x_c \\ y_c \end{bmatrix} \tag{A.9}$$

Linear Mean Swim Model - Flagellum

$$\begin{bmatrix} x_o(k,t) \\ y_o(k,t) \end{bmatrix} = \begin{bmatrix} b_1(k)x_T(k,t) \\ b_2(k)y_T(k,t) \end{bmatrix} \tag{A.10}$$

$$x_T(k,t) = \frac{r_v}{2}\sin\left(4\pi\left(\frac{k}{M} + f_l t\right)\right) \tag{A.11a}$$

$$y_T(k,t) = \frac{r_h}{2}\sin\left(2\pi\left(\frac{k}{M} + f_l t\right)\right) \tag{A.11b}$$

$$\begin{bmatrix} x_{LM}(k,t) \\ y_{LM}(k,t) \end{bmatrix} = \begin{bmatrix} x_o(k,t) \\ y_o(k,t) \end{bmatrix} - \begin{bmatrix} \frac{\lambda k}{M} \\ 0 \end{bmatrix} \tag{A.12}$$

$$y_{LM_2}(k,t) = y_{LM}(k,t) - [P_y(t) - y_T(0,t)]b_3(\psi) \tag{A.13}$$

$$\begin{bmatrix} x_{tail_{LM}} \\ y_{tail_{LM}} \end{bmatrix} = R(\theta_r)\begin{bmatrix} x_{LM} \\ y_{LM_2} \end{bmatrix} + \begin{bmatrix} x_{H_L} \\ y_{H_L} \end{bmatrix} \tag{A.14}$$

$$b_1(k) = \frac{1}{1 + e^{(\alpha k/M + \beta)}} \tag{A.15a}$$

$$b_2(k) = e^{-\gamma_1 k/M} \tag{A.15b}$$

$$b_3(k) = 1 - e^{-\gamma_2 k/M} \tag{A.15c}$$

(x_{H_L}, y_{H_L}) : position of the sperm head of linear swimming cell
(C_{x_L}, C_{y_L}) : horizontal and vertical offset constant (pixels)
V : straight line path velocity (pixels/sec)
f_l : rate of change in ribbon angle (Hz)
r_h, r_v : width and height of ribbon (pixels)
A_{har} : user defined ratio between the first and the third harmonics
A_c : correction constant for defined width of the ribbon
θ_r : direction of the forward movement (radian)
$(x_{Tail_{LM}}, y_{Tail_{LM}})$: a set of k points along the center of the flagellum of linear mean swimming cell
$b_1(k), b_2(k)$: local horizontal and vertical variation in beating amplitude along the flagellum
$b_3(k)$: flagellum position correction function

Table A.3: Simulation of a Hyperactive Swimming Cell

Hyperactive Swim Model - Head	$x(t) = \mu_x t + \sigma_{x_b} W(t)$ and	(A.16a)
	$y(t) = \mu_y t + \sigma_{y_b} W(t)$	(A.16b)
	$x_{H_H}(t) = x_{H_H}(t-T) + \sigma_b W(T)$ and	(A.17a)
	$y_{H_H}(t) = y_{H_H}(t-T) + \sigma_b W(T)$,	(A.17b)
Hyperactive Swim Model - Flagellum	$(x_{tail_H}(k,t), y_{tail_H}(k,t)) =$ Linear interpolation on a set of points $[(x_{H_L}(0), y_{H_L}(0)), (x_{H_L}(1), y_{H_L}(1)), (x_{H_L}(2), y_{H_L}(2)), ..., (x_{H_L}(n), y_{H_L}(n))]$ where $x_{H_L}(n) = x_{H_H}(t-nT)$, $y_{H_L}(n) = y_{H_H}(t-nT)$	(A.18)

(μ_x, μ_y) : drift coefficients of Brownian motion
$(\sigma_{x_b}, \sigma_{y_b})$: diffusion coefficients of Brownian motion
$W(t)$: standard 1-dimensional Brownian motion ($W(t) \sim N(0,t)$)
(x_{H_H}, y_{H_H}) : position of the sperm head of hyperactive cell
T : the difference in time between each simulation frame
(x_{Tail_H}, y_{Tail_H}) : a curve along the center of the flagellum of hyperactive cell

Table A.4: Simulation of an Immotile Cell

Immotile Cell Model - Head	$x_{H_I}(t) = x_{H_I}(0)$ and	(A.19a)
	$y_{H_I}(t) = y_{H_I}(0)$	(A.19b)
Immotile Cell Model - Flagellum	$(x_{tail_I}(k,t), y_{tail_I}(k,t)) =$ Linear interpolation on a set of points $[(x_{I_L}(0), y_{I_L}(0)), (x_{I_L}(1), y_{I_L}(1)), (x_{I_L}(2), y_{I_L}(2)), ..., (x_{I_L}(n), y_{I_L}(n))]$ where $x_{I_L}(n) = x_{H_H}(-nT)$, $y_{I_L}(n) = y_{H_H}(-nT)$	(A.20)

(x_{H_I}, y_{H_I}) : position of the sperm head of immotile cell
(x_{Tail_I}, y_{Tail_I}) : a curve along the center of the flagellum of immotile cell

Table A.5: Equations for Generating Image of Sperm Cell

$$I_1(x,y,t) = \begin{cases} 255 & (x,y) \in \{(x_{H_C}(t), y_{H_C}(t)), (x_{H_L}(t), y_{H_L}(t)), \\ & \qquad (x_{H_H}(t), y_{H_H}(t)), (x_{H_I}(t), y_{H_I}(t))\} \\ 0 & \text{otherwise} \end{cases} \tag{A.21}$$

$$I_2(x,y,t) = \begin{cases} 255 & (x,y) \in \{(x_{tail_C}(k,t), y_{tail_C}(k,t)),\ (x_{tail_L}(k,t), y_{tail_L}(k,t)), \\ & \qquad (x_{tail_H}(k,t), y_{tail_H}(k,t)),\ (x_{tail_I}(k,t), y_{tail_I}(k,t))\}, \\ & \qquad k = 1,2,3,...,M, \\ 0 & \text{otherwise} \end{cases} \tag{A.22}$$

$$f_1(x,y) = \frac{1}{2\pi\sigma_{x_G}\sigma_{y_G}} exp\left(-\left[\frac{(\frac{x}{\sigma_{x_G}})^2 + (\frac{y}{\sigma_{y_G}})^2}{2}\right]\right) \tag{A.23}$$

$$g(x,y) = \nabla^2\left(\frac{1}{2\pi\sigma_{x_L}\sigma_{y_L}} exp\left(-\left[\frac{(\frac{x}{\sigma_{x_L}})^2 + (\frac{y}{\sigma_{y_L}})^2}{2}\right]\right)\right) \tag{A.24}$$

$$f_2(x,y) = \max(0, g(x,y)) \tag{A.25}$$

$$f_3(x,y) = \nabla^2\left(\frac{1}{2\pi\sigma_f^2} exp\left(-\left[\frac{(\frac{x}{\sigma_f})^2 + (\frac{y}{\sigma_f})^2}{2}\right]\right)\right) \tag{A.26}$$

(x_{H_C}, y_{H_C}): the locations of sperm heads of cells engaged in circular swimming.
(x_{H_L}, y_{H_L}): the locations of sperm heads of cells engaged in linear mean swimming.
(x_{H_H}, y_{H_H}): the locations of sperm heads of cells engaged in hyperactive swimming.
(x_{H_I}, y_{H_I}): the locations of sperm heads of cells engaged in no swimming (immotile cells).
(x_{tail_C}, y_{tail_C}): the points along the curve of sperm flagellum of circular swimming cell.
(x_{tail_L}, y_{tail_L}): the points along the curve of sperm flagellum of linear mean swimming cell.
(x_{tail_H}, y_{tail_H}): the points along the curve of sperm flagellum of hyperactive cell.
(x_{tail_I}, y_{tail_I}): the points along the curve of sperm flagellum of immotile cell.
$(\sigma_{x_G}, \sigma_{y_G})$: Standard deviations of the point spread function f_1 (determine the width and the length of the sperm head)
$(\sigma_{x_L}, \sigma_{y_L})$: Standard deviations of the point spread function f_2 (determine the width and the length of the membrane surround the sperm head).
σ_f: Standard deviation of the point spread function f_3 (determines the width of the flagellum).

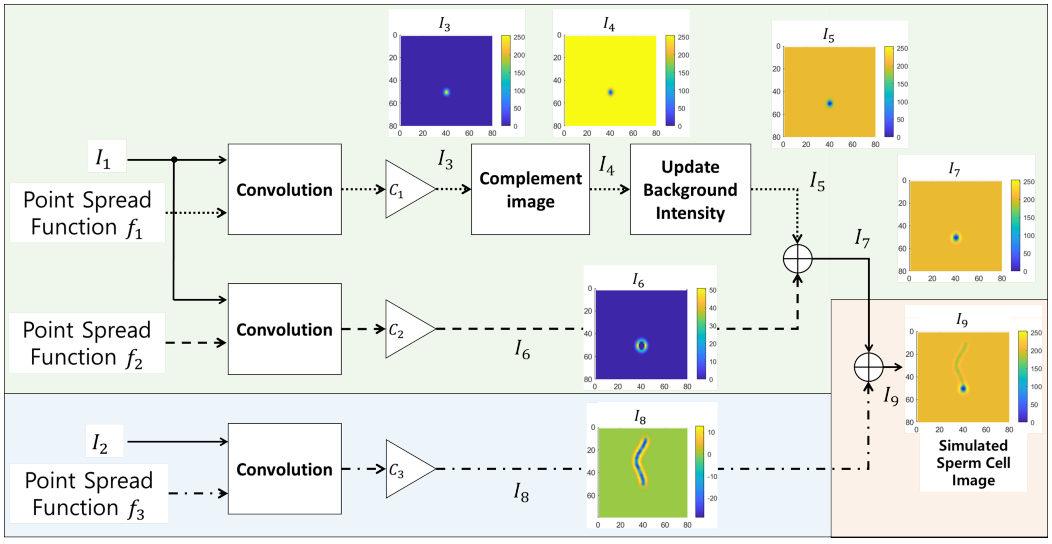

Figure A.1: Sperm Image Generation Process