Detection of Abnormal Human Sperm Morphology Using Support Vector Machine (SVM) Classification

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ABSTRACT

Abnormal sperm morphology is a key indicator of male infertility, making its accurate detection crucial for reproductive health assessments. This study explores the application of Support Vector Machine (SVM) classification to automatically detect abnormalities in human sperm morphology. A dataset of microscopic sperm images was collected and labelled based on normal and abnormal morphological features, including head shape, midpiece defects, and tail irregularities. Feature extraction techniques were employed to quantify key morphological characteristics, which were then used to train the SVM model. The proposed SVM-based approach demonstrated high accuracy in classifying normal versus abnormal sperm morphology, significantly reducing the time and error associated with manual analysis. This method provides an efficient, automated solution for andrology laboratories and fertility clinics, enhancing diagnostic consistency and reliability. By incorporating machine learning techniques, this system holds promise for improving the precision of sperm morphology analysis, ultimately contributing to better fertility treatments and outcomes

1. Introduction

Men's reproductive health is a crucial aspect in the pursuit of optimal fertility. One of the key indicators of men's reproductive health is sperm morphology, which encompasses the shape and structure of sperm [1]. Abnormalities in sperm morphology, such as abnormal head shapes, defects in the midpiece, and irregularities in the tail, have been shown to significantly contribute to infertility issues [2]. According to data from the World Health Organization (WHO), approximately 30-40% of male infertility cases can be attributed to sperm morphology disorders [3]. Therefore, accurate and rapid detection of these abnormalities is essential for proper diagnosis and management.

Manual analysis of sperm morphology is often time-consuming and prone to human error. This process typically involves microscopic examination that requires specialized skills and high precision [4]. Additionally, variations in interpretation by different technicians can lead to inconsistencies in diagnosis. With the increasing demand for more efficient and accurate methods, machine learning technology, particularly Support Vector Machine (SVM), has emerged as a

promising solution. SVM is an effective machine learning algorithm for classification and regression and has been used in various medical applications, including image analysis [5].

The state of the art in this research indicates that although several approaches have been applied to detect sperm morphology, many of these methods still rely on manual analysis or less efficient techniques. Previous studies have demonstrated the potential of using machine learning algorithms in medical image analysis; however, their application in detecting sperm morphology remains limited. Some studies have attempted to use deep learning techniques [6][7][8], but challenges such as the need for large datasets and model complexity often pose obstacles. Therefore, this research aims to explore and develop an automated method using SVM to detect abnormalities in sperm morphology with high accuracy.

The primary objective of this study is to develop an SVM-based classification system that can automatically identify normal and abnormal sperm based on morphological characteristics. By using a labeled dataset of microscopic images, this research aims to enhance the efficiency and accuracy of sperm morphology analysis while reducing the time and errors associated with manual analysis. Furthermore, this study seeks to provide new insights into how machine learning techniques can be integrated into clinical practice to improve infertility diagnosis and treatment.

In conclusion, this research is expected to make a significant contribution to the field of fertility diagnosis by offering an automated solution that can enhance consistency and reliability in sperm morphology analysis. Thus, the outcomes of this research will not only benefit andrology laboratories and fertility clinics but may also contribute to improved fertility treatment outcomes overall. The implementation of this system is anticipated to assist doctors and fertility specialists in making more accurate and timely decisions, providing new hope for couples facing fertility challenges.

2. Method

The research methodology follows a systematic approach, beginning with data acquisition, which includes sample collection, sample preparation, coloring (optional), as the image preprocessing. Following this, feature extraction is performed on the processed images, and the dataset is split into training and testing sets. The SVM model is trained using the available training data, and then tested using the testing data. The classification results are analyzed and presented as output for further evaluation. At this stage, the author found a framework that can be used as a reference for conducting detection systems of abnormal human sperm morphology. The methodology used is as in Figure 1.

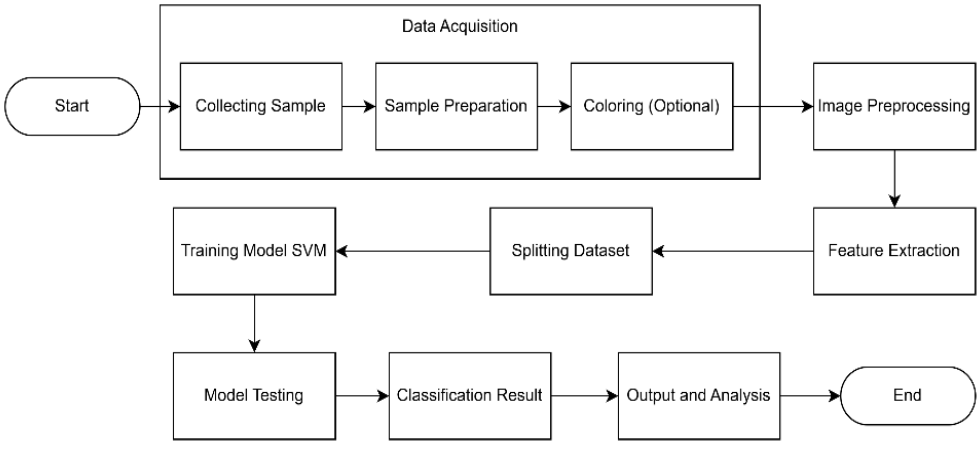

Fig. 1. Research Methodology

2.1. Data Acquisition

In this study, the data used consists of microscopic images of sperm that were manually taken at the Biology Laboratory. The data collection was carried out using an optical microscope connected to a digital camera to capture images of the sperm, with the assistance of laboratory

technicians or experts in the field. Sperm samples were obtained from individuals who provided consent through masturbation into a sterile container to ensure cleanliness and avoid contamination. After collection, the samples were immediately transported to the laboratory at room temperature to maintain sperm viability, with the transport time not exceeding 30 minutes. In the laboratory, the samples were mixed with an appropriate culture medium to enhance sperm motility and were allowed to sit for 30 minutes so that the sperm could swim freely. To improve contrast and facilitate the identification of morphology, sperm samples may be stained using specific dyes such as eosin-nigrosin [9].

The imaging process was conducted using the OptiLab IRIS-4 microscope, where sperm images were captured with the OptiLab Advance Plus camera at appropriate magnifications (e.g., 40x or 100x) to capture detailed sperm morphology, including the head, midpiece, and tail. Figure 1 shows the primary data collected from the sperm samples, displaying various sperm morphologies, both normal and abnormal. These images include normal sperm, characterized by ideal morphology such as an oval head, slim midpiece, and long, straight tail, as well as abnormal sperm, which exhibit variations such as round or conical heads, wide or irregular midpieces, and bent or short tails.

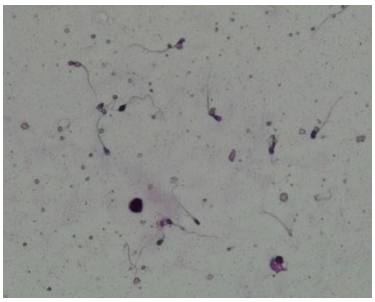

Fig. 2. Example Image from Dataset

This dataset (Figure 2) includes hundreds of images that have been labeled by andrology experts based on criteria established by the WHO, providing a solid foundation for further analysis using classification techniques such as Support Vector Machines (SVM). These images are not only representative but also of high quality, enabling the development of automated systems for more accurate sperm morphology detection.

2.2. Processing Stages

The image data collected from the microscopic imaging process will undergo further processing before it can be used for more in-depth analysis and input into the classification model. This stage is referred to as image preprocessing, which aims to enhance the quality of the images so that they are easier to process by machine learning models and yield more accurate predictions [10]. The common preprocessing steps in image processing begin with converting the original image to grayscale, where the colored images are transformed into grayscale images to reduce data complexity [11]. For example, for pixels at coordinates (*x*,*y*), the grayscale value can be calculated using the formula as Equation (1):

$$I_{gray}(x,y) = 0.2989 \cdot R(x,y) + 0.5870 \cdot G(x,y) + 0.1140 \cdot B(x,y) \quad (1)$$

To include the results of the calculations for each equation mentioned in the above narrative, we can assume the RGB values for the pixel at coordinates (x,y) as follows:

- R(x,y)=100
- G(x,y)=150
- B(x,y)=200

Therefore, the calculation for grayscale becomes as Equation (2):

$$I_{gray}(x,y) = 0.2989 \cdot 100 + 0.5870 \cdot 150 + 0.1140 \cdot 200 = 140.74 \quad (2)$$

Next, various techniques are applied to smooth the image, aiming to minimize random variations that can obscure important features. This is often achieved by analyzing the pixel values in local areas of the image and adjusting them to reduce discrepancies [12]. With a cleaner image, the likelihood of misidentifying features due to noise-related artifacts is diminished. This leads to better accuracy in detecting and classifying objects, which is crucial in fields like biological imaging. Noise removal is performed using filtering techniques such as Gaussian Blur, which can be expressed by the formula as Equation (3):

$$I_{blur}(x,y) = K_1 \sum_{i=-k}^{k} \sum_{j=-k}^{k} I_{gray}(x+i, y+j) \cdot G(i,j) \quad (3)$$

Where G(i, j) is the Gaussian kernel and *K* is the normalization factor. For example, let's assume a simple Gaussian kernel is used with $k = 1$ and $K_1 = 16$, and it has the grayscale values I_{gray} around the pixel (x, y) as follows.

- $I_{gray}(x-1, y-1) = 140$
- $I_{gray}(x-1, y) = 145$
- $I_{gray}(x-1, y+1) = 150$
- $I_{gray}(x, y-1) = 155$
- $I_{gray}(x, y) = 160$
- $I_{gray}(x, y+1) = 165$
- $I_{gray}(x+1, y-1) = 170$
- $I_{gray}(x+1, y) = 175$
- $I_{gray}(x+1, y+1) = 180$

And the value for the Gaussian Kernel G(i, j) for $k = 1$ is:

$$\begin{bmatrix} 1 & 2 & 1 \\ 2 & 4 & 2 \\ 1 & 2 & 1 \end{bmatrix} \cdot \frac{1}{16}$$

Therefore, the calculation for blur becomes:

$$I_{blur}(x,y) = \frac{1}{16}\,(1 \cdot 140 + 2 \cdot 145 + 1 \cdot 150 + 2 \cdot 155 + 4 \cdot 160 + 2 \cdot 165 + 1 \cdot 170$$
$$= 140 + 290 + 150 + 310 + 640 + 330 + 170 + 350 + 180$$
$$= \frac{1}{16}\,(2560) = 160$$

After the image is processed, the next step is feature extraction to obtain relevant morphological information. The extracted features include shape features, which measure dimensions and form, as well as texture features using methods such as Histogram of Oriented Gradients (HOG) [13][14]. HOG can be calculated with the formula as Equation (4):

$$HOG\,(x,y) = \sum_{i=0}^{N} \sum_{j=0}^{M} \sqrt{(I_x(i,j))^2 + (I_y(i,j))^2} \quad (4)$$

Where I_x and I_y are the image gradients in the x and y directions. Suppose the image gradients are as follows:

- $I_x = \begin{bmatrix} 1 & 2 \\ 3 & 4 \end{bmatrix}$
- $I_y = \begin{bmatrix} 4 & 3 \\ 2 & 1 \end{bmatrix}$

Therefore, the HOG calculation becomes:

$$HOG = \sqrt{(1^2 + 4^2)} + \sqrt{(2^2 + 3^2)} + \sqrt{(3^2 + 2^2)} + \sqrt{(4^2 + 1^2)}$$
$$= \sqrt{1 + 16} + \sqrt{4 + 9} + \sqrt{9 + 4} + \sqrt{16 + 1}$$
$$= \sqrt{17} + \sqrt{13} + \sqrt{13} + \sqrt{17}$$
$$= 4{,}123 + 3{,}606 + 3{,}606 + 4{,}123 = 15{,}458$$

The extracted features are then normalized to ensure that all features are on the same scale. Normalization is performed using the formula:

$$X_{norm} = \frac{X - \mu}{\sigma} \quad (5)$$

Where X is the original feature value, μ is the mean of the feature, and σ is the standard deviation of the feature. Suppose the feature value X = 160, the mean (μ) = 150, and the standard deviation (σ) = 10

$$X_{norm} = \frac{160 - 150}{10} = \frac{10}{10} = 1$$

2.3. Modelling Stages

After the data acquisition and preprocessing stages, the dataset is split into two primary subsets: a training set and a testing set. This split is crucial to ensure that the model can generalize well to unseen data. In this research, a common ratio such as 80% for training and 20% for testing is used. The training set is used to train the model, while the testing set evaluates its performance. Once the dataset is split, the Support Vector Machine (SVM) model is trained using the training data. In this stage, the SVM algorithm learns to classify sperm morphology based on the features extracted during the preprocessing phase [15]. The objective of the SVM is to find a hyperplane that best separates the data points into different classes (normal or abnormal sperm in this case). After training, the model is tested on the testing set, which was kept aside during the splitting phase. The testing data is new to the model, meaning it hasn't been used for training. This step evaluates how well the trained SVM model can classify unseen samples. Performance metrics like accuracy, precision, recall, and F1-score are typically calculated during this phase to measure how well the model performs in classifying sperm morphology.

3. Results and Discussion

The results of the study are represented by evaluation metrics. The model's average recall and precision are 91%, with an F1-Score of 90%. These results indicate that the developed Support Vector Machine (SVM) model performs very well in classifying normal and abnormal sperm morphology. With an average recall of 91%, the model is able to detect most abnormalities in

sperm, meaning only a few abnormal samples are missed. Precision, also at 91%, shows that the model rarely produces false positives or misclassifies normal sperm as abnormal. Furthermore, the F1-Score of 90% reflects a balance between precision and recall, indicating that the model is both stable and effective in its classification tasks. Overall, these evaluation metrics demonstrate that the developed automated system can be used as an accurate tool for detecting abnormalities in sperm morphology and has the potential to replace manual methods, which tend to be slow and prone to human error. Therefore, the implementation of this system in andrology laboratories or fertility clinics is expected to improve diagnostic accuracy and accelerate decision-making in handling male infertility issues.

Table 1. Classification Reports

Kelas	Metrik Evaluasi		
	Presisi	*Recall*	*F1-Score*
1	0.89	0.99	0.94
0	0.97	0.65	0.77
Total	0.91	0.91	0.90

4. Conclusion

The conclusion of this research highlights the effectiveness of the Support Vector Machine (SVM)-based system in accurately detecting abnormalities in sperm morphology. With high precision, recall, and F1-Score metrics, the model demonstrated strong performance in classifying normal and abnormal sperm cells. This automated approach not only enhances the accuracy and consistency of sperm morphology analysis but also reduces the time and potential for human error associated with manual examination. The findings suggest that the developed system can be a valuable tool for andrology laboratories and fertility clinics, improving the diagnostic process and aiding in the early detection of male infertility issues. Furthermore, the study provides a foundation for future advancements in integrating machine learning techniques into clinical practices, promoting more reliable and efficient fertility diagnostics.

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