Literasi Nusantara
vol.5 no. 1, November 2024 – February 2025
https://journal.citradharma.org/index.php/literasinusantara/index
ISSN 2746-8208 (Online)
ISSN 2746-3575 (Print)

Identification of Abnormal Spermatozoa Motility Using the SVM Algorithm

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DOI : *https://doi.org/10.56480/jln.v5i1.1324*

Received: August 24, 2024
Revised: September 29, 2024
Accepted: October 23, 2024

Abstract

Spermatozoa motility is one of the key indicators in determining male fertility quality. Manual assessment of motility abnormalities often requires significant time and effort, thus necessitating a more efficient and accurate automated approach. This study aims to identify abnormalities in spermatozoa motility using the Support Vector Machine (SVM) algorithm, utilizing microscopic video data analyzed through TrackPy for spermatozoa trajectory tracking. The analysis process involves data acquisition, spermatozoa detection in each frame, sperm trajectory construction, and trajectory classification into normal or abnormal categories. The SVM model was trained using a dataset derived from spermatozoa trajectories classified based on parameters such as average velocity and trajectory linearity. The results show that the method achieved the highest accuracy of 89 percent in identifying spermatozoa motility abnormalities in HD resolution videos with a frame rate of 30 fps.

Keywords– *Spermatozoa, Motility, TrackPy, SVM*

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1. Introduction

Spermatozoa motility is a key indicator in assessing sperm quality and male fertility levels (Aristoteles & Lumbanraja, 2023). Directional and efficient movement is crucial for the fertilization process, as spermatozoa must achieve optimal speed and specific movement patterns to reach the egg (Ratnawati et al., 2019). Spermatozoa that do not move at adequate speeds or exhibit irregular movement patterns are generally considered infertile (Akbar et al., 2021; Baharuddin & Irmawati, 2021). Infertility, with a global prevalence of 15%, poses a significant challenge, with approximately 40% of cases attributed to male factors, according to WHO (WHO, 2021). Sperm motility analysis, which involves measuring speed, trajectory patterns, and linearity, is a crucial step in evaluating sperm quality (Mortimer, 2020; Menkveld, 2001). However, manual methods for analyzing motility remain inefficient and prone to subjective errors (Dai et al., 2021).

With advancements in technology, the Computer-Aided Sperm Analysis (CASA) system has been developed to analyze motility automatically (Van der Horst, 2020). Previous research by Masdiyasa et al. (2018) used the Gaussian Mixture Model (GMM) for background subtraction in sperm motility analysis, showing good detection accuracy with an f-measure of 0.8265, but facing limitations in video quality and computational complexity. A follow-up study by Masdiyasa et al. (2024) employed matching-based algorithms and GMM to determine spermatozoa motility abnormalities, achieving a highest tracking accuracy of 77.3% and an average abnormality detection accuracy of 87.7%. However, this method still struggles with high variation data, such as low-quality videos, rapid spermatozoa movement, and real-time analysis complexity.

Statistical analysis plays a crucial role in sperm motility research. This process involves collecting, processing, and interpreting data to identify patterns and relationships in spermatozoa movement (Rifa'i, 2023). With the integration of machine learning, statistical analysis now enables the handling of large datasets more efficiently and accurately (Judijanto, 2024). In this study, the Support Vector Machine (SVM) algorithm will be used to classify spermatozoa

motility patterns into "normal" and "abnormal" categories. SVM is known for its reliability in handling high-dimensional data and producing robust classification models (Chandra & Bedi, 2021).

This study also utilizes the TrackPy library, designed to accurately track particle trajectories (Allan et al., 2021). With features such as trajectory detection, clustering, and movement pattern analysis, TrackPy facilitates efficient processing of spermatozoa motility data. The research dataset includes spermatozoa videos with a duration of 15 seconds, a resolution of 1920 x 1080 pixels, and a frame rate of 30 FPS. The combination of SVM and TrackPy is expected to improve the accuracy of detecting spermatozoa motility abnormalities, reduce classification errors, and provide a more effective solution for automated and quantitative male fertility analysis.

2. Method

The methods used in this study include the Python library TrackPy for spermatozoa detection and the Support Vector Machine (SVM) algorithm for identifying abnormalities. The methods are illustrated in the flowchart shown in Figure 2.1 below.

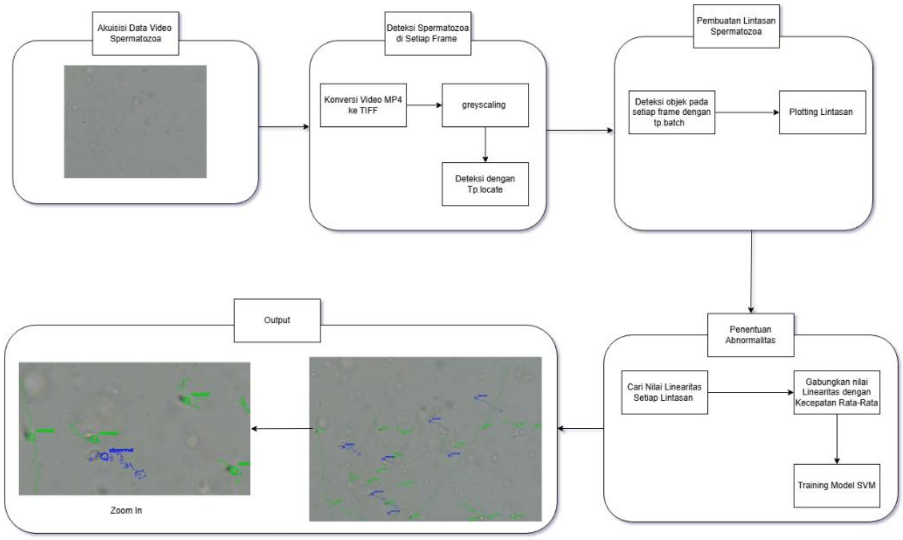

Figure 1. System Design

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The flowchart in Figure 2.1 illustrates the complete process of analyzing spermatozoa motility, starting from data acquisition to abnormality determination using the Support Vector Machine (SVM) algorithm. The process begins with the acquisition of spermatozoa video data recorded using a microscope. The video is then converted into a multi-frame TIFF format to facilitate further data processing. Afterward, the images are converted to grayscale to improve the efficiency of object detection. Spermatozoa detection in each frame is performed using the TrackPy library with the tp.locate function, which identifies particles based on morphological features and pixel intensity.

Once the objects are detected, the next step is linking the spermatozoa trajectories using the tp.batch function. This function identifies the same particles across multiple frames, forming continuous trajectories. Trajectory visualization is conducted to validate the detection results and ensure that the generated trajectories correspond to the movement of spermatozoa. The next step is trajectory analysis, where the linearity and average velocity values are calculated for each trajectory. Linearity reflects the straightness of the movement path, while average velocity indicates the intensity of spermatozoa movement.

The results of this trajectory analysis are used as input data to train the SVM model. The SVM algorithm is then used to classify spermatozoa trajectories into "normal" or "abnormal" categories. This process produces an output in the form of labeled trajectory visualizations, where normal trajectories are marked in green and abnormal trajectories in blue. This visualization provides a clear depiction of spermatozoa movement patterns, facilitating clinical diagnosis and sperm quality evaluation. This approach combines statistical analysis and machine learning to enhance the accuracy and efficiency of sperm motility analysis.

3. Result and Discussion

The output of this study is a video with annotations on spermatozoa labeled as normal and abnormal.

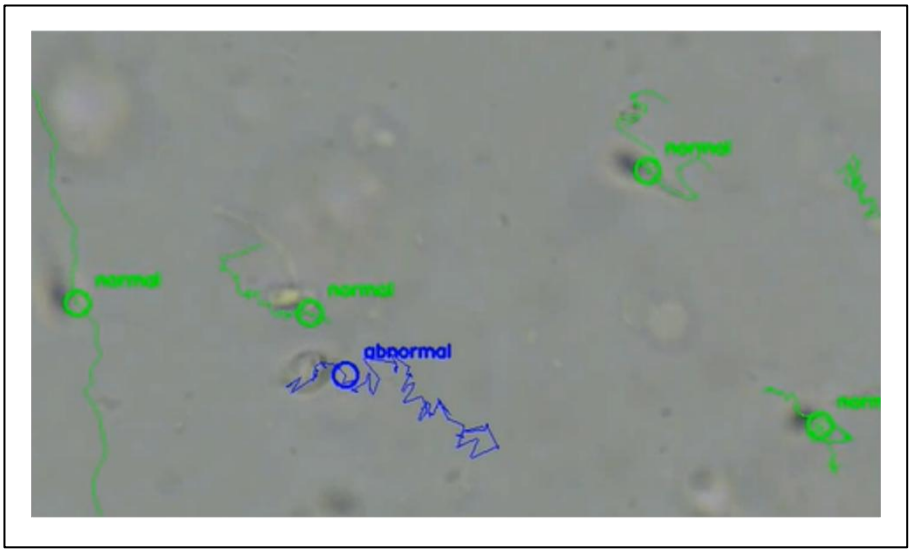

Figure 2. Abnormality Determination Result

The image shows the visualization results of spermatozoa movement trajectory analysis using TrackPy and SVM. Each spermatozoa trajectory is represented by colored lines, with green indicating normal movement trajectories and blue indicating abnormal ones. In normal trajectories, spermatozoa movement tends to be directional and linear, whereas abnormal trajectories display random and irregular movement patterns. This visualization is designed to facilitate the identification and evaluation of spermatozoa movement patterns based on parameters such as average velocity and linearity. With the "normal" and "abnormal" labels, these results support further classification processes, which can be used to quantitatively analyze sperm quality. The visualization demonstrates the system's ability to accurately detect trajectories while also identifying spermatozoa with deviant movement patterns.

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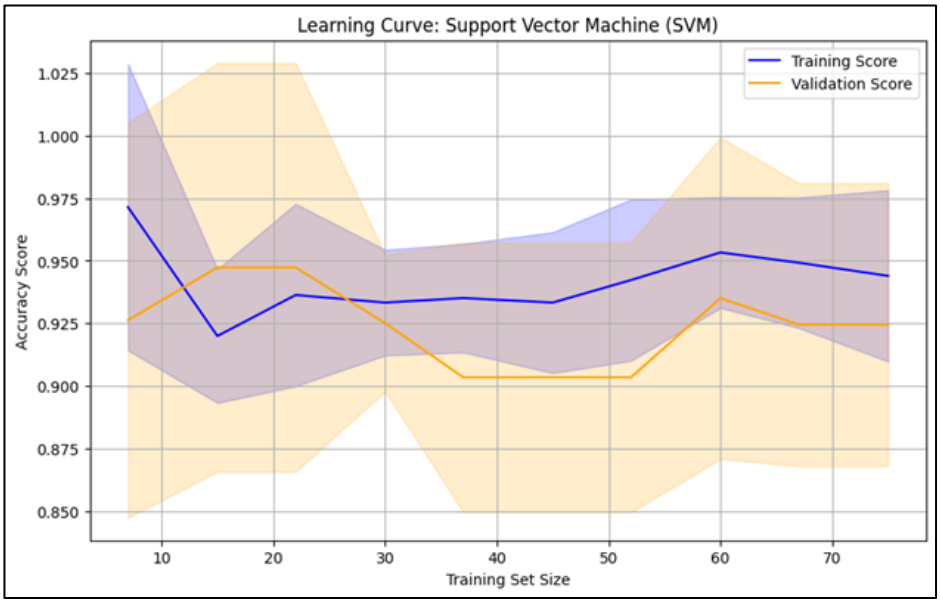

Figure 3. SVM Model Learning Curve

The learning curve graph in Figure 2.3 illustrates the performance of the SVM model based on the size of the training dataset. The blue line represents accuracy on the training data, while the orange line shows accuracy on the validation data. With a smaller dataset, the training score is high but the validation score is low, indicating overfitting. However, as the training dataset size increases, both scores approach a stable value of around 0.95, indicating good model generalization. The variation in validation scores (represented by the shaded orange area) shows fluctuations, but these decrease with larger datasets, signifying improved model stability. These results demonstrate that the SVM model performs optimally with an adequate amount of training data.

Table 1. Classification Report

	Precision	**Recall**	**F1-Score**	**Support**
Abnormal	0.71	1.00	0.83	5
Normal	1.00	0.86	0.92	14
Accuracy			0.89	19
Macro Avg	0.86	0.93	0.88	19
Weighted Avg	0.92	0.89	0.90	19

The table illustrates the evaluation results of the classification model's performance in detecting spermatozoa movement trajectories, categorized into two groups: "Abnormal" and "Normal." For the "Abnormal" category, precision reaches 0.71, meaning that 71% of all "Abnormal" predictions are correct. Recall is 1.00, indicating that the model successfully identified all truly abnormal trajectories. The F1-Score for this category is 0.83, representing the harmonic mean of precision and recall.

For the "Normal" category, precision is 1.00, signifying that all "Normal" predictions are correct. Recall for this category is 0.86, meaning the model detected 86% of trajectories that were truly normal. The F1-Score for this category is 0.92, reflecting an excellent balance between precision and recall.

Overall, the model achieves an accuracy of 0.89, indicating an 89% success rate in classifying spermatozoa trajectories. The macro average (Macro Avg) of precision, recall, and F1-Score are 0.86, 0.93, and 0.88, respectively, providing an overview of the model's performance across both categories without considering the data distribution in each category. The weighted average (Weighted Avg), which accounts for the data distribution in each category, yields precision of 0.92, recall of 0.89, and F1-Score of 0.90, demonstrating consistent model performance across both categories.

4. Conclusion

In this study, a series of procedures were implemented to detect and determine abnormalities in spermatozoa movement using the Python library TrackPy and the SVM algorithm. The research involved testing scenarios with video data at a frame rate of 30 FPS. The TrackPy library successfully annotated and tracked spermatozoa movement, providing coordinate and velocity data, which were subsequently used for abnormality analysis with the SVM algorithm.

The results of determining spermatozoa movement abnormalities using the SVM algorithm showed that videos with a frame rate of 30 FPS achieved the highest average accuracy of 89%. One of the weaknesses identified in using TrackPy is the detection of non-sperm particles, which can affect model accuracy

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and data distribution during training. This factor can lead to bias in the analysis results, particularly in cases of low-quality video, overlapping or intersecting particle trajectories, and frames that are not properly recorded.

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