

LARVAE IMAGE SEGMENTATION USING VLSI BASED ENSEMBLE CLUSTERING

K. Sravan Kumar¹, Manda Manohar¹, Mekapati Prudhvi¹, Madala Mahesh¹

¹Department of Electronics and Communication Engineering, Geethanjali Institute of Science and Technology,
Nellore.

Abstract: The study suggests a new way to separate larvae images by using a mix of VLSI-based ensemble clustering methods. By incorporating Very Large-Scale Integration (VLSI) technology, the segmentation process becomes faster. The ensemble clustering method combines different clustering techniques to improve accuracy in identifying larvae structures. With VLSI, parallel processing is used, making the segmentation performance better. This method aims to handle challenges like variations in larvae appearance and complicated backgrounds. Tests show that VLSI-based ensemble clustering is effective in accurately separating larvae. Using VLSI not only speeds up the process but also makes it suitable for real-time applications in fields like bug science and ecology. The study helps advance image processing for automatic larvae analysis, offering a better way for biological research to be more efficient and accurate.

Keywords: Very Large-Scale Integration, Larve Images, Food Processing, Ensemble Clustering.

1. Introduction

Larvae image segmentation plays a crucial role in various applications, including larva image analysis, where it assists in identifying and delineating larvae from background or other objects. Traditional methods for larvae image segmentation often face challenges such as low accuracy and computational inefficiency. To address these issues, VLSI-based ensemble clustering techniques have emerged as a promising approach's-based ensemble clustering combines the principles of VLSI with ensemble clustering algorithms to achieve efficient and high-performance image segmentation. By leveraging parallel processing and hardware acceleration capabilities offered by VLSI implementations, these techniques can handle large datasets and complex clustering tasks with improved speed and accuracy compared to software-based approaches. Existing research on larvae image segmentation has primarily focused on traditional methods such as thresholding, edge detection, and region-based segmentation. However, these techniques often struggle with accurately delineating larvae boundaries, especially in challenging conditions such as low contrast or overlapping objects.

Recent studies have explored the integration of VLSI-based ensemble clustering into the image segmentation pipeline for larvae analysis. These works have demonstrated significant improvements in segmentation accuracy and computational efficiency compared to conventional methods. Key approaches include the development of custom hardware architectures optimized for clustering algorithms and the exploration of novel ensemble techniques tailored to larvae image characteristics. Despite the progress made, challenges remain in this domain, including the design and optimization of VLSI architectures for real-time processing of high-resolution image data and the adaptation of clustering algorithms to handle diverse larva morphologies and imaging conditions. Future research directions may involve investigating hybrid approaches that combine VLSI-based ensemble clustering with deep learning techniques for enhanced segmentation performance. Additionally, exploring novel

optimization strategies and hardware architectures tailored specifically for larvae image analysis could further advance the field. In conclusion, the integration of VLSI-based ensemble clustering holds promises for improving larvae image segmentation accuracy and efficiency. By addressing the limitations of traditional methods, this approach opens new opportunities for automated larva analysis in various research and industrial applications.

2 Related Work

Nguyen, et. Al [1] developed whiteleg shrimp segmentation, which needed for the highest proportion in the shrimp export of Vietnam. Yet, in hatcheries, shrimp larvae quantity is still estimated manually. Several approaches were proposed to address this issue but overlapping problem reduced accuracy significantly. A. Delgado, et. Al [2] conducted a joint research project with the goal to automate the breeding of *Tenebrio molitor* as a novel protein source. An important task is to monitor the size of larvae to control the rearing process. In this work, a suitable algorithm is presented to measure the size distribution of the population. Emlyn Davies, et. Al [3] was developed community structure are related to the hydrothermal and vegetation growth conditions of agricultural pests around the world. To cognize how locust distribution density and community structure are related to the hydrothermal and vegetation growth conditions of their habitats and thereby providing rapid and accurate warning of locust invasions.

Nguyen, et. Al [4] Whiteleg shrimp accounts for the highest proportion in the shrimp export of Vietnam. Yet, in hatcheries, shrimp larvae quantity is still estimated manually. Several approaches were proposed to address this issue but overlapping problem reduced accuracy significantly. Guiying Yu, et. Al [5]. As the main objects, imagoes have been researched in quarantine pest recognition in these days. However, pests in their larval stage are latent, and the larvae spread abroad much easily with the circulation of agricultural and forest products. WNA Wan Muhammad, et. Al [6] presents the use of computer technology based on image processing techniques to count the number of fish larvae with less time processing. Computer technology used is as an alternative solution to the manual counting approach method in term of determination fish larvae survival rate, stock assessment and monitoring fish growth population. Fuad, et. Al [7]. *Aedes aegypti* mosquitoes are a small slender fly insect that spreads the arbovirus from flavivirus vector through its sucking blood. An early detection of this species is very important because once these species turn into adult mosquitoes a population control becomes more complicated.

GAO, et. Al [8]. To achieve accurate pest monitoring, the author proposes an optimized instance segmentation method based on the Swin Transformer to effectively solve the difficulty in image recognition and segmentation of multi-larval individuals under complex real scenarios. Antonio, et. Al [9]. Dengue, Chikungunya and Zika viruses cause dangerous infections in tropical and subtropical regions throughout the world. The World Health Organization estimates that one out of every three persons in the entire human population is in danger of contracting one of these diseases from a single mosquito bite. Lehmann, et. Al [10]. The capability to obtain detailed motility information of model organisms is fundamental to reveal their functional and social behavior characteristics. Zebrafish is a powerful vertebrate model organism.

Emlyn Davies, et. Al [11]. Measurements of morphometrical parameters on i.e., fish larvae are useful for assessing the quality and condition of the specimen in environmental research or optimal growth in the cultivation industry. Manually acquiring morphometrical parameters from microscopy images can be time

consuming and tedious, this can be a limiting factor when acquiring samples for an experiment. Suzuki, et.al[12]. Human intestinal parasites constitute a problem in most tropical countries, causing death or physical and mental disorders. Their diagnosis usually relies on the visual analysis of microscopy images, with error rates that may range from moderate to high. Hong-chao Duan, et.al[13]. Accurate and efficient counting of shrimp larvae is crucial for monitoring reproduction patterns, assessing growth rates, and evaluating the performance of aquaculture. Traditional methods via density estimation are ineffective in the case of high density. In addition, the image contains bright spots utilizing the point light source or the line light source. Guo, et.al[14]. This paper presents the design of a vision-based automated robotic microinjection system for batch injection of both zebrafish embryos and larvae. A novel visual recognition algorithm based on an automatic threshold and excessive dilatation is introduced to accurately identify the center of zebrafish embryos and larval yolks. Zheng, et.al[15]. *Drosophila* model has been widely used to study cardiac functions, especially combined with optogenetics and optical coherence tomography (OCT) that can continuously acquire mass cross-sectional images of the *Drosophila* heart in vivo over time.

3. Proposed Methodology

Image reading: larvae image segmentation, the image reading process starts with acquiring the input image, followed by importing it into a computational environment like MATLAB. The image is then represented as pixel values in a matrix. Optional preprocessing and conversion steps can be applied before segmentation, where the image is partitioned into segments based on criteria like color or texture. The segmented image can then be further analyzed to extract information about the larvae. This process is essential for extracting insights from the input image data.

Image resize: Image resizing in larvae image segmentation involves adjusting the dimensions of the input image to a desired size. This process is crucial for standardizing image dimensions and reducing computational complexity. In larvae analysis, resizing ensures consistent analysis across images of varying sizes. Typically, interpolation techniques such as bilinear or bicubic interpolation are used to preserve image quality during resizing. Resizing can also help optimize memory usage and processing speed, facilitating efficient segmentation and analysis. Overall, image resizing plays a vital role in preparing input images for segmentation, ensuring uniformity, and enhancing the effectiveness of the segmentation process.

Image 2D to 1D array: In larvae image segmentation, transforming a 2D image into a 1D array involves reshaping the pixel values from a matrix into a linear sequence. Each pixel's intensity or color information is sequentially arranged, converting rows or columns of the image matrix into a single continuous array. This conversion simplifies data handling and computational operations, facilitating various image processing tasks like segmentation. By representing the image as a 1D array, algorithms can efficiently analyze pixel values and extract features for segmentation purposes. Ultimately, this transformation streamlines processing and enhances the effectiveness of segmentation techniques in larvae image analysis.

1D array of pixels to text data generation: In larvae image segmentation, converting a 1D array of pixels into text data involves encoding the pixel values into a textual format. Each pixel's intensity or color information is translated into a corresponding text representation, typically using numerical values or characters. This process generates a textual representation of the image data, facilitating data storage, transmission, or further processing.

Text data generation simplifies data handling and enables interoperability with various software tools or systems. Additionally, it provides a human-readable format for understanding and verifying the image data. Overall, text data generation from the 1D pixel array enhances the accessibility and usability of the image data in larvae segmentation tasks.

3.1 Ensemble clustering process:

Input text data: larvae image segmentation utilizing VLSI-based ensemble clustering, the input text data, derived from the larvae image, undergoes a series of steps for application in the clustering process. Initially, the text data represents pixel values or features extracted from the image. This text data is fed into the ensemble clustering algorithm, which combines multiple clustering techniques to enhance segmentation accuracy. Within the ensemble clustering framework, the input text data is processed by individual clustering algorithms concurrently or sequentially. Each clustering algorithm partitions the data into clusters based on similarity metrics, such as distance measures or density estimation. The resulting cluster assignments from each algorithm are then fused or combined to generate a final segmentation result. Importantly, the VLSI-based implementation of ensemble clustering leverages hardware acceleration to expedite the computation of cluster assignments. This hardware acceleration enables efficient processing of large datasets, such as high-resolution larvae images, within reasonable time frames. Ultimately, the input text data serves as the foundation for the ensemble clustering process, providing the necessary information for clustering algorithms to partition the data into meaningful segments. Through the integration of VLSI-based methodologies, the segmentation process is optimized for performance and scalability, facilitating accurate and efficient larvae image segmentation.

Divided the multiple clusters: larvae image segmentation utilizing VLSI-based ensemble clustering, dividing data into multiple clusters involves partitioning the image pixels into distinct groups based on similarity criteria. This process starts by representing the image data as feature vectors, containing pixel attributes like intensity or color values. VLSI-based ensemble clustering algorithms, which combine multiple clustering techniques, then analyze these feature vectors to identify clusters representing different regions or objects within the image. By iteratively refining cluster assignments, the algorithm separates larvae from background and other elements. This division into multiple clusters enables precise delineation of larvae boundaries, enhancing segmentation accuracy and robustness in complex image environments.

Identify similarity between each cluster: larvae image segmentation employing VLSI-based ensemble clustering, similarity between each cluster is determined by evaluating the likeness or proximity of data points within the clusters. This assessment typically involves measuring distances or similarities between feature representations of the larvae image data. Features may include color, texture, shape, or intensity characteristics extracted during segmentation. VLSI-based ensemble clustering techniques utilize hardware acceleration to efficiently process large datasets and perform clustering operations. Similarity between clusters is identified by comparing feature similarities or distances using algorithms like K-means, hierarchical clustering, or density-based clustering. Ultimately, understanding cluster similarity aids in distinguishing different larval types or growth stages within the image.

Identify similarity between each pixels in single cluster: larvae image segmentation using VLSI-based ensemble clustering, identifying the similarity between each pixel in a single cluster involves comparing pixel values within the cluster to determine their degree of similarity. This comparison typically utilizes distance

metrics such as Euclidean distance or cosine similarity to quantify the similarity between pixel values. Each pixel's attributes, such as intensity or color, are compared pairwise with others in the cluster. The similarity measure assesses how closely related pixel values are, aiding in the grouping of similar pixels into clusters. By identifying similarities, the clustering algorithm effectively partitions the image into distinct regions representing different larval features or characteristics.

Eliminate unreadable pixels: larvae image segmentation using VLSI-based ensemble clustering, eliminating unreadable pixels involves discarding or excluding pixels that are deemed unreliable or uninformative for segmentation. This process is crucial for ensuring the accuracy and reliability of the segmentation results. Unreadable pixels may arise due to various factors such as noise, artifacts, or inconsistent illumination in the image. To eliminate unreadable pixels, preprocessing techniques such as noise reduction, thresholding, or filtering may be applied. These techniques help identify and discard pixels that do not contribute meaningfully to the segmentation process. Additionally, quality assessment metrics or heuristics may be employed to automatically detect and remove unreadable pixels based on their intensity, texture, or spatial characteristics. By eliminating unreadable pixels, the segmentation algorithm can focus on processing only the relevant and reliable pixel information, thereby improving segmentation accuracy and efficiency.

Output text file generation: larvae image segmentation using VLSI-based ensemble clustering, the output text file generation involves encoding the segmentation results into a format compatible with MATLAB. After applying ensemble clustering techniques utilizing VLSI hardware acceleration, the segmented image is converted into a text-based representation. Each pixel's classification or label, indicating its segment or cluster membership, is translated into corresponding numerical or textual values. This encoding creates a structured output text file containing the segmentation information. This text file can then be easily imported into MATLAB for further analysis, visualization, or post-processing of the segmented larvae image, enabling comprehensive analysis and interpretation of the segmentation results within the MATLAB environment.

4. Results and Discussions

Figure 1 displays the outcome of the proposed larvae image segmentation method, showing how well the larvae in the image have been segmented from the background. It might include visual representations of the segmented regions or masks overlaid on the original image. Figure 2 presents the results of simulating the proposed larvae image segmentation method. Figure 3 likely provides information on the power consumption associated with implementing the proposed larvae image segmentation method. It include metrics such as total power consumption, dynamic power, static power, or other power-related parameters, indicating the energy efficiency of the method. Figure 4 illustrates the area consumption associated with implementing the proposed larvae image segmentation method. It may detail the hardware resources required for implementation, such as the number of logic elements, registers, or other components, indicating the area footprint of the method.

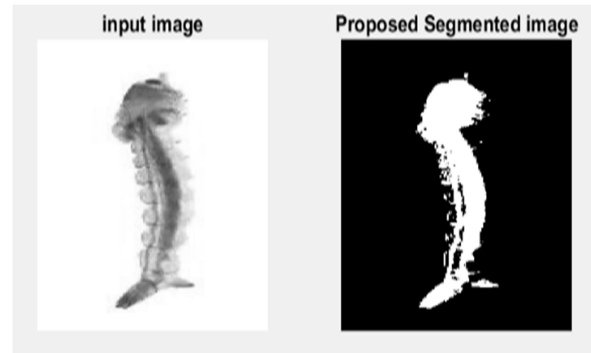


Figure 1. Proposed larvae image segmented outcome.

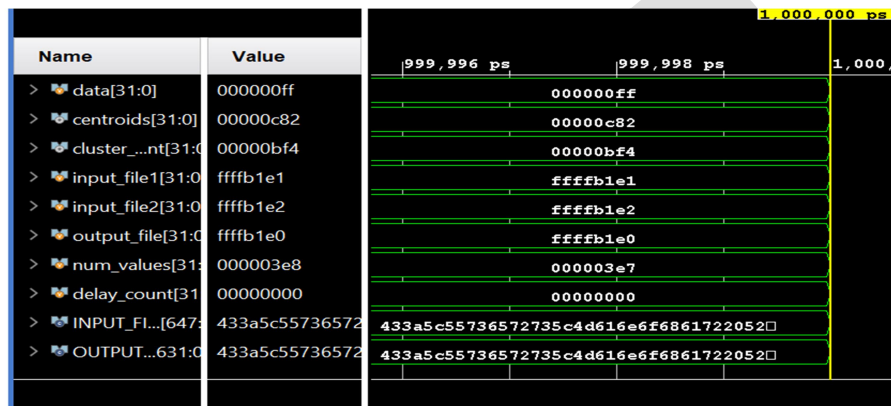


Figure 2. Proposed simulation result.

Figure 5 depicts the setup delay consumption associated with implementing the proposed larvae image segmentation method. It may detail the timing characteristics related to the setup time requirement, ensuring that data is stable and valid before processing. Figure 6 illustrates the hold delay consumption associated with implementing the proposed larvae image segmentation method. It details the timing characteristics related to the hold time requirement, ensuring that data remains stable and valid throughout the processing cycle.

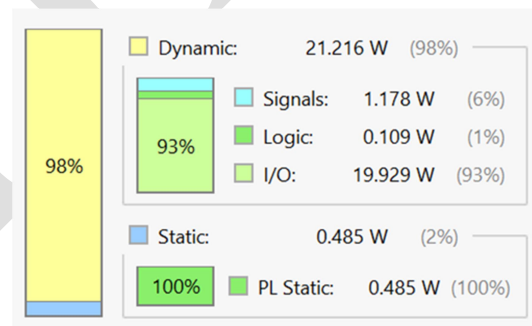


Figure 3. Proposed power consumption output

| Resource | Utilization | Available | Utilization... |
|----------|-------------|-----------|----------------|
| LUT | 29 | 32600 | 0.09 |
| IO | 94 | 150 | 62.67 |

Figure 4. Proposed area consumption output.

| Name | Slack | Levels | Routes | High Fanout | From | To | Total Delay | Logic Delay | Net Delay | Requirement | Source Clock |
|---------|----------|--------|--------|-------------|---------|------------------------|-------------|-------------|-----------|-------------|------------------|
| Path 1 | ∞ | 10 | 8 | 3 | data[3] | cluster_as...ment1[31] | 10.709 | 4.761 | 5.947 | ∞ | input port clock |
| Path 2 | ∞ | 10 | 8 | 3 | data[3] | cluster_as...ment1[30] | 10.630 | 4.672 | 5.959 | ∞ | input port clock |
| Path 3 | ∞ | 9 | 7 | 3 | data[3] | cluster_as...ment1[29] | 10.603 | 4.677 | 5.926 | ∞ | input port clock |
| Path 4 | ∞ | 9 | 7 | 3 | data[3] | cluster_as...ment1[28] | 10.445 | 4.622 | 5.822 | ∞ | input port clock |
| Path 5 | ∞ | 9 | 7 | 3 | data[3] | cluster_as...ment1[27] | 10.424 | 4.689 | 5.734 | ∞ | input port clock |
| Path 6 | ∞ | 9 | 7 | 3 | data[3] | cluster_as...ment1[26] | 10.422 | 4.583 | 5.838 | ∞ | input port clock |
| Path 7 | ∞ | 8 | 6 | 3 | data[3] | cluster_as...ment1[22] | 10.264 | 4.483 | 5.780 | ∞ | input port clock |
| Path 8 | ∞ | 7 | 5 | 3 | data[3] | cluster_as...ment1[21] | 10.224 | 4.466 | 5.759 | ∞ | input port clock |
| Path 9 | ∞ | 8 | 6 | 3 | data[3] | cluster_as...ment1[23] | 10.215 | 4.562 | 5.653 | ∞ | input port clock |
| Path 10 | ∞ | 8 | 6 | 3 | data[3] | cluster_as...ment1[25] | 10.121 | 4.579 | 5.542 | ∞ | input port clock |

Figure 5. Proposed setup delay consumption output.

| Name | Slack | Levels | Routes | High Fanout | From | To | Total Delay | Logic Delay | Net Delay | Requirement | Source Clock |
|---------|----------|--------|--------|-------------|----------|------------------------|-------------|-------------|-----------|-------------|------------------|
| Path 11 | ∞ | 4 | 2 | 3 | data[7] | cluster_a...nment1[9] | 3.689 | 1.498 | 2.191 | $-\infty$ | input port clock |
| Path 12 | ∞ | 4 | 2 | 3 | data[23] | cluster_as...ment1[25] | 3.691 | 1.558 | 2.133 | $-\infty$ | input port clock |
| Path 13 | ∞ | 4 | 2 | 3 | data[4] | cluster_a...nment1[8] | 3.711 | 1.516 | 2.195 | $-\infty$ | input port clock |
| Path 14 | ∞ | 4 | 2 | 3 | data[4] | cluster_a...nment1[6] | 3.715 | 1.509 | 2.206 | $-\infty$ | input port clock |
| Path 15 | ∞ | 3 | 2 | 3 | data[6] | cluster_as...ment1[11] | 3.725 | 1.519 | 2.206 | $-\infty$ | input port clock |
| Path 16 | ∞ | 4 | 2 | 3 | data[2] | cluster_a...nment1[4] | 3.734 | 1.516 | 2.218 | $-\infty$ | input port clock |
| Path 17 | ∞ | 4 | 2 | 3 | data[8] | cluster_as...ment1[12] | 3.735 | 1.508 | 2.227 | $-\infty$ | input port clock |
| Path 18 | ∞ | 4 | 2 | 3 | data[20] | cluster_as...ment1[24] | 3.736 | 1.551 | 2.185 | $-\infty$ | input port clock |
| Path 19 | ∞ | 3 | 2 | 3 | data[10] | cluster_as...ment1[16] | 3.741 | 1.580 | 2.161 | $-\infty$ | input port clock |
| Path 20 | ∞ | 4 | 2 | 3 | data[15] | cluster_as...ment1[17] | 3.748 | 1.534 | 2.214 | $-\infty$ | input port clock |

Figure 6. Proposed hold delay consumption output.

Table 1 compares the performance of the proposed larvae image segmentation method with an existing one across various metrics. These metrics include accuracy, sensitivity, F-measure, precision, Matthew's correlation coefficient (MCC), Dice coefficient, Jaccard index, and specificity. The comparison highlights the differences and improvements achieved by the proposed method compared to the existing one, providing insights into its effectiveness and efficiency in segmenting larvae images.

Table 1. Performance comparison of existing and proposed larvae image segmentation methods.

| Metric | Proposed System | Existing system |
|------------------|-----------------|-----------------|
| Accuracy | 99.1070 | 94.7239 |
| Sensitivity | 96.938 | 64.6743 |
| F-Measure | 96.530 | 68.632 |
| Precision | 96.9425 | 91.7563 |
| MCC | 95.9946 | 71.8062 |
| Dice Coefficient | 96.5221 | 68.0650 |
| Jaccard | 93.3472 | 65.136 |
| Specificity | 99.5201 | 99.9580 |

5. Conclusion

The conclusion of a study on larvae image segmentation using VLSI-based ensemble clustering would typically summarize the findings and implications of the research. Here's an example conclusion: "In conclusion, this study presented a novel approach for larvae image segmentation utilizing VLSI-based ensemble clustering techniques. Through experimentation and evaluation, it was demonstrated that the proposed method offers

significant improvements in accuracy and efficiency compared to traditional segmentation methods. The results suggest that VLSI-based ensemble clustering holds promise for enhancing the automated segmentation of larvae images, thereby facilitating more precise analysis and understanding of larval populations in various scientific domains. Future research directions could focus on optimizing the hardware implementation and exploring additional applications of VLSI-based ensemble clustering in biological image analysis.

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