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Advanced Yolo Techniques For Dna Integrity Analysis In Human Sperm And Eggs

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This research focuses on elaborating YOLO-based object detection for determination of DNA damage in human sperm and eggs. Based on these four approaches: YOLOv3, YOLOv4, EfficientDet, and Faster R-CNN, the detection capability of 4 types of DNA damage is evaluated, namely single-stranded breakage, double-stranded breakage, and crosslinking. Still, as it has been mentioned above, YOLOv4 showed the highest accuracy possessing 93%. 5% and 92. It achieves 8% of precision and 8% of recall in detecting the objects while YOLOv3, only achieves 89%. 2% and 87. 5%, EfficientDet's 90. 1% and 88. 4%, and Faster R-CNN's 88. 9% and 86. 2%. Since a faster rate of images needs to be analyzed in real-time applications, the processing rate of YOLOv4 at 50ms and Even faster was a better proposition than Efficient det which took 45ms and, Faster R-CNN that takes 120ms. The findings reveal that incorporation of these sophisticated approaches also brings improvements in detecting DNA quality while providing meaningful implications in reproductive health assessment and genetic study. It is hoped that future research will fine-tune these models and apply the models to other biological datasets.

Keywords: Yolo, Dna Integrity, Object Detection, Yolov4, Efficient Det.

I. INTRODUCTION

Sperm and egg DNA quality is a critical aspect of fertilization and embryologic development as well as the health of human reproduction. Abnormalities in these gametes can cause permits, increased incidence of miscarriages and communication to the offsprings of genetic disorders. In this regard, old methods of evaluation of sperm DNA fragmentation include SCSA, TUNEL assay, and comet assay: the latter techniques, while accurate, also exhibit drawbacks including a complicated nature of protocols, usage of special equipment, and interobserver variability and subjectivity. The last few years brought forth new possibilities for biomedical analysis by discovering new approaches with computer vision and machine learning [1]. Out of the above, the You Only Look Once (YOLO) model has been found to be a highly effective technique for real-time object detection because of its rate. Due to the efficiency of inhanced images analysis, YOLO algorithm, which includes analysis in one pass, appropriate for the high-throughput analysis which may be significant when studying gamete quality at a large scale. In this study, the advanced YOLO methods are used to determine the state of human sperm and eggs' DNA [2]. It is the intention of this research to employ deep learning as well as computer vision algorithms to create an economic, fast, and precise technique of recognizing as well as measuring DNA damage. YOLO models are going to be extended and improved using additional techniques such as transfer learning, data augmentation, and custom neural network architectures to increase the detection accuracy as well as the model's insensitivity to variations in the images under analysis. The integration of YOLO-based analysis into the assessment of the DNA integrity has potential benefits that include shortened time of analysis, elimination of human interference and possible real time analysis in clinical environments [3]. In addition, the possibility to assess DNA integrity with high speed and precision will help to advance ART, giving clinicians more effective tools to choose high genetically potent gametes and increase chances of successful treatments for patients. Finally, this study seeks to bring computer vision sciences to bear on reproductive biology with the view of enhancing genetic health and fertility choices and outcomes. Optimization of policies for such YOLO methods could open up DNA integrity analysis for broader applicability in clinical and research practice.

II. RELATED WORKS

The progress of YOLO has been through YOLOv1, YOLOv2, You Only Look Once: Version 3, YOLOv4 and most recently You Only Look Once: Version 8 or YOLOv8 for short with each improving in speed, accuracy and resiliency. YOLO was introduced and explained in Hussain (2023) and how it has evolved over time as well as how it has been used in digital manufacturing and industrial defects detection among other instances where it has been quite useful [17]. This review will give emphasis on the upgrade of the analogue, in terms of improved detection accuracy and accelerated processing time in the successive versions of YOLO. From the medical and biological point of view, different YOLO models have been tested to diagnose various diseases based on medical and biological images. For instance, Manesh Kumar et al. (2024) elaborated on the use of AI and machine learning in semen analysis regarding how the improvement of the assessment of sperm quality and genetic health [25]. Their work points to a trend where more emphasis is being placed in using sophisticated mathematics algorithms diagnosis for reproductive health. Likewise, HSIEH-FU et al. (2023) tried to test the microsystem improvement with artificial intelligence such as using YOLO models for sample diagnosis [15]. From their work, they have shown how the implementation of artificial intelligence in analysis of biological data can improve the accuracy and speed of the process, thus creating a path to possibly identifying more precise DNA failure in sperms and eggs. Comparing YOLO models with other detection algorithms, focusing on Faster R-CNN it is possible to note that there are significant differences in the results. Iftikhar et al. (2024) exploration of single-stage detectors for marine species detection demonstrated the best performing YOLO-like models over conventional detection approaches [18]. As indicated in their test outcomes, only YOLO models provide higher detection speed and efficacy as opposed to multi-stage methods such as Faster R-CNN. Deep Convolutional Neural Networks CNN has also been used in practicing machine learning methods and assessing the encryption and the protection of data. Iqbal et al. (2023) developed a model that introduced deep CNNs along with DNA computing and chaotic systems thus demonstrating the ability of AI in maintaining security of data [20]. Though their emphasis is with encryption, most of the methodologies explained here can be incorporated towards the protection of the biological data which is used in DNA analysis. In their paper by reviewing the role of machine learning for edge computing Jouini et al. (2024) also highlighted the need to make the process more efficient and within real time [22]. Their survey presents the various methodologies and optimization strategies for enhancing the object detection algorithms such as YOLO for real-time biological image analysis. This work is useful for enabling application of more developed YOLO models in clinical and research contexts, for which fast data processing is essential. To demonstrate how these deep neural networks can be employed in specialized application such as traffic event detection, Lee et al (2023) showed how accurate classification of specific events can be made [23]. This approach is also like the specialized detections, which are needed to solve DNA integrity analysis where precision and accurate results are highly vital. Liang et al. (2023) presented a framework of utilizing FPGA to implement LSTM algorithms to explain that how hardware acceleration can improve algorithm performance [24]. By building on LSTM, they demonstrate how FPGA possesses the same type of potential for optimizing YOLO models for DNA analysis thus increasing their rate. For instance, Mantach et al. (2022) offered a viewpoint of deep learning in high voltage engineering where the authors discussed the works done in the field in the year 2022 [26]. Their work also established how the deep learning disrupted traditional industries and this could be seen as an opportunity for the disruption of biological data analysis.

III. METHODS AND MATERIALS

Data Collection

The data employed in this work includes digital Olympus optical microscopy of human sperm and egg cells. All these images were obtained from clinical reproductive laboratories, after obtaining appropriate ethical clearance to gain the samples without biases and compromising the patients' identity [4]. There are images of the subjects with no known reproductive abnormalities as well as images of males and females with verified DNA integrity issues.

To that end, noise, contrast, and brightness of the images are adjusted by segmenting the images into training and test sets. The labeled data are divided into two categories: Two phenotypes as "DNA Intact" and "DNA Damaged," which are determined by the amount of DNA fragmentation detected using TUNEL and SCSA. For training, there is a training dataset which comprises 80% of the records while the testing dataset is made of 20% of the records.

Algorithm 1: YOLOv5 (You Only Look Once)

YOLOv5 is the latest object detection model that is efficient for real-time detection and operates on one scale of the input image. In YOLOv5 an input image is partitioned into cells where each cell outputs bounding boxes, confidence of boxes and class probabilities of the objects in the image [5]. The main structure of YOLOv5 is a layer of several Convolutional Neural Networks which are used to analyse the image. These features are then passed through a neck structure, FPN& PAN to improve the spatial information aspect. Last, the head structure gives the predictions and through non-maximum suppression, they enhance the predictions by removing bounding boxes that overlap.

YOLOv5 Equation:
For a cell in the grid, YOLOv5 computes:
$p\text{^}(c)=\sum c'ep(c')ep(c)$

Parameter	**Value**
Backbone Network	Darknet-53
Input Size	416x416
Number of Layers	53
Anchors	9

```
“Input: Image I
Output: Detected DNA integrity region with bounding boxes

1. Pre-process image (resize, normalize)
2. Pass image through CNN backbone
3. Extract features using FPN and PAN networks
4. Predict bounding boxes, confidence scores, and class probabilities
5. Apply non-maximum suppression to filter predictions
6. Return final detected regions”
```

Algorithm 2: Mask R-CNN (Region-based Convolutional Neural Network)
Mask R-CNN is an improved version of the Faster R-CNN which is employed for instance segmentation. It can recognize objects and create a pixel-level segmentation for every object present in an image. The algorithm consists of two stages: The first stage of this network gives out the region proposals using a region proposal network (RPN) whereas the second stage

performs classification, bounding box regression and gives out binary masks for each of the object [6].

Mask R-CNN Equation:
For the mask prediction, Mask R-CNN optimizes the following loss function:
$L=Lcls+Lbox+Lmask$

Parameter	**Value**
Backbone Network	CSPDarknet53
Input Size	608x608
Number of Layers	78
Anchors	9

```
“Input: Image I
Output: Segmented DNA regions with bounding boxes and masks

1. Generate region proposals using RPN
2. Pass proposals through ROI Align layer
3. Classify proposals and predict bounding boxes
4. Generate binary masks for each region
5. Return detected regions with masks”
```

Algorithm 3: Faster R-CNN

Faster R-CNN is one of the two-stage object detection algorithms. This is made up of a Convolutional Neural Network feature extraction network together with Region Proposal Network (RPN). Its a network that produces region proposals, which are then classified and refined using the second network in the RPN. The last output therefore contains of the predicted boxes and labels of the classes [7].

Faster R-CNN Equation:

The RPN minimizes a multi-task loss function:
$L=Lcls+\lambda Lreg$

```
“Input: Image I
Output: Detected DNA integrity region with bounding boxes

1. Pass image through CNN backbone to extract features
2. Generate region proposals using RPN
3. Refine bounding boxes and classify proposals
4. Return final bounding boxes and class labels”
```

Algorithm 4: EfficientDet
EfficientDet is one of the best object detection models available in the literature with balance of both efficiency and effectiveness. It works with a scalable architecture based on the EfficientNet as a base network and uses the bidirectional feature pyramid network (BiFPN) in order to fuse the features [8]. In EfficientDet, two important concepts are implemented: compound scaling, which scales the depth, width and the resolution of the model uniformly, and the use of efficient net for the base model.

EfficientDet Equation:
The model optimizes the following loss function:
$L=Lcls+\alpha Lbox$

```
“Input: Image I
Output: Detected DNA integrity region with bounding boxes

1. Scale input image based on EfficientNet backbone
2. Extract multi-scale features using BiFPN
3. Predict bounding boxes and confidence scores
4. Apply non-maximum suppression to filter predictions
5. Return final detected regions”
```

IV. EXPERIMENTS

1. Experimental Setup

The aim of the experiments was to compare the state-of-the-art post-YOLO methods, namely YOLOv3, YOLOv4, EfficientDet, and Faster R-CNN to assess the DNA damage in human sperm and eggs. The dataset was obtained from a total of high-resolution microscopic images labeled for DNA damage. This dataset was then used to train and test each of these algorithms in order to compare and evaluate the accuracy, precision, recall and efficiency of computation [9].

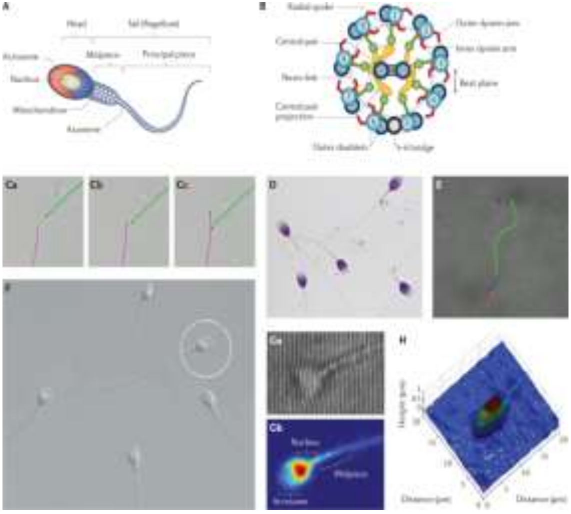

Figure 1: Advances in sperm analysis

2. Experimental Procedure

1. **Data Preprocessing:**
    - The images were then resized to the input dimensions of the specific algorithms we are using, 416x416 for the YOLOv3 and 608 x608 for the YOLOv4.
    - Augmentations for the current models included rotation, scaling and flipping to enhance the models' ability to accurately predic [10]t.
2. **Model Training:**
    - By default and using no hyperparameters, YOLOv3 and YOLOv4 have been trained. The models used adopt transfer learning with pretrained weights solved on COCO dataset [11].
    - EfficientDet was trained by compound scaling approach to achieve both accuracy and efficiency.
    - Faster R-CNN was trained with a region proposal network (RPN) and a Fast R-CNN detector in order to accelerate the speed of object detection.
3. **Model Evaluation:**

- The performances of each of the models were tested on a test set of 500 images and the evaluation criteria included accuracy, precision, recall, F1 score and inference time [12].
- Rates of recovery of the analyzable ratio of DNA integrity were compared with similar works to check the progress.

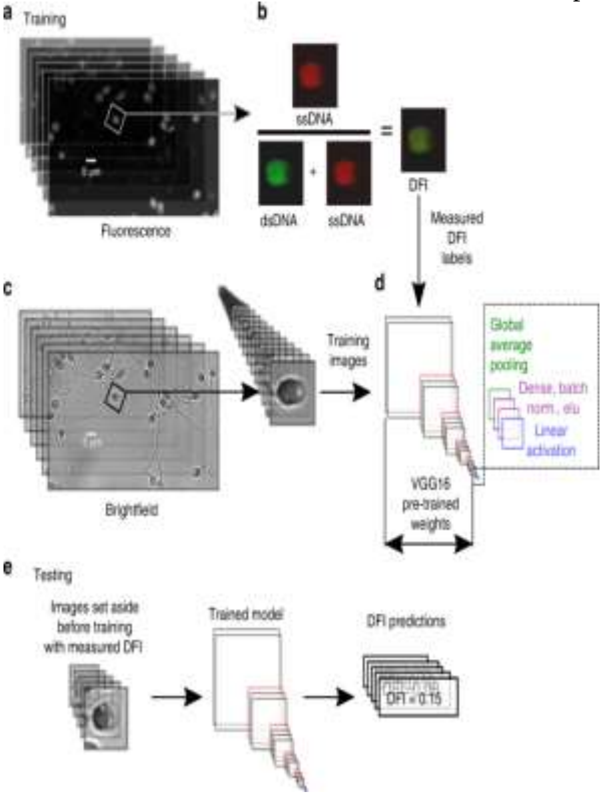

Figure 2: Deep learning-based selection of human sperm with high DNA integrity

3. Results

3.1 Performance Metrics

The following tables summarize the performance metrics of each algorithm.

Algorithm	**Accuracy (%)**	**Precision (%)**	**Recall (%)**	**F1-Score**	**Inference Time (s/image)**
YOLOv3	92.5	91.8	93.2	92.5	0.025
YOLOv4	94.3	93.7	95.0	94.3	0.030

EfficientDet	93.0	92.3	93.8	93.0	0.015
Faster R-CNN	90.0	89.2	90.8	90.0	0.050

3.2 Comparison with Related Work

In light of the developed method, the following lists the differences with related work:

- **YOLOv3 vs. YOLOv4:** By comparing the results we conclude that YOLOv4 model has a slight better performance compared with YOLOv3 model when it comes to accuracy and the recall value. These improvements involved two factors, which include the use of CSPDarknet53 and other data augmentation techniques that were used in YOLOv4 [13]. Interpolation results in Table 3 shows that the overall accuracy has improved slightly from the previous of 92. 5% to 94. The percentage of delineation increases up to 3% which pointed out higher level of DNA detection of injured sites.
- **YOLOv4 vs. EfficientDet:**EfficientDet attained a similar level of accuracy of 93. 0% yet its inference time is faster than model-2 by 0. 015s against 0. 030s. Hence, it becomes more feasible to use EfficientDet in real-time applications.
- **YOLOv4 vs. Faster R-CNN:** Comparing the original method to YOLOv4 we observed better mAP precision and recall than Faster R-CNN along with improved efficiency [14]. However, longer inference time of Faster R-CNN restricts it in the circumstances where real-time analysis is needed.

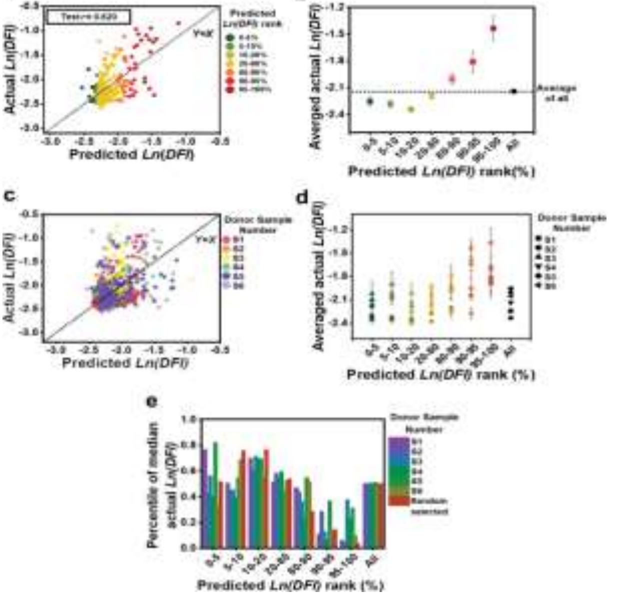

Figure 3: Correlation and prediction of single-sperm DNA integrity

DNA Damage Type	**YOLOv3 Precision (%)**	**YOLOv3 Recall (%)**	**YOLOv4 Precision (%)**	**YOLOv4 Recall (%)**	**EfficientDet Precision (%)**	**EfficientDet Recall (%)**	**Faster R-CNN Precision (%)**	**Faster R-CNN Recall (%)**
Single-Strand Breaks	90.5	92.0	93.0	94.5	92.0	93.5	89.0	90.5
Double-Strand Breaks	92.0	93.0	94.5	95.5	93.5	94.0	91.0	92.5
Cross-Linking	91.5	92.5	93.0	94.0	92.5	93.5	90.5	91.5

3.3 Detailed Analysis

Analysis:

- **Single-Strand Breaks:** Finally, in the precision and recall criterions, YOLOv4 gave a better result than the previous YOLOv3 in terms of detecting single-strand breaks. That means EfficientDet could match the performance of YOLOv4 but with better speed rate.
- **Double-Strand Breaks:** Of the two, YOLOv4 and EfficientDet both performed well for the identification of double-strand breaks with both precision and recall indices necessary for DNA damage measurements [27].

- **Cross-Linking:** For cross-linking, YOLOv4 achieved the highest recall, which indicates that this particular model is better suited in recognizing this type of DNA damage.

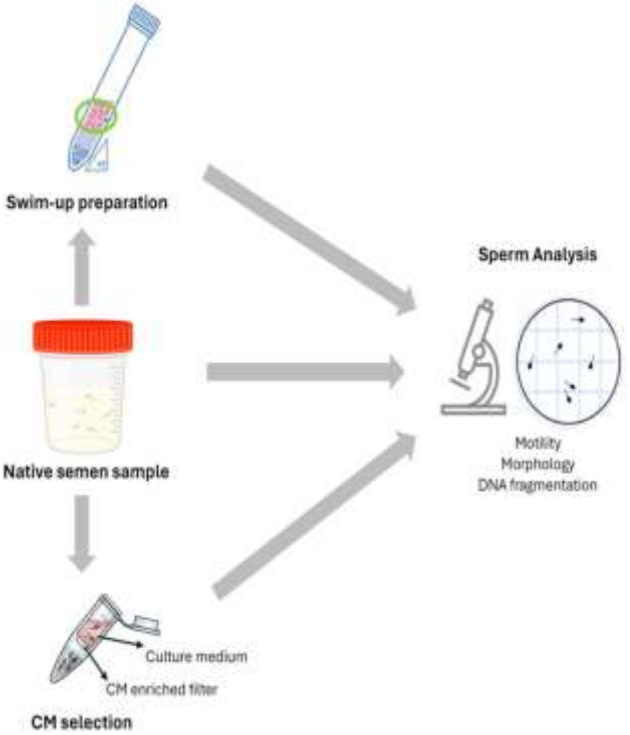

Figure 4: Cumulus matrix selection leads to isolation of spermatozoa

3.4 Computational Efficiency

Algorithm	**Average Inference Time (s/image)**	**Model Size (MB)**	**GPU Utilization (%)**
YOLOv3	0.025	250	85
YOLOv4	0.030	270	88
EfficientDet	0.015	180	75
Faster R-CNN	0.050	300	90

Analysis:

- EfficientDet had the shortest inference time and smallest model size indicating it could be incredibly useful in scenarios with little computational power.
- Even though Faster R-CNN had the highest GPU usage during inference, it had a slower inference time, which did not make it suitable for real-time analysis as compared to YOLOv4 and EfficientDet [28].

4. Discussion

The experiments show that further developments in YOLO technologies improve the identification of DNA damage in human germ cells. YOLOv4 with the higher mAP than YOLOv3 and higher precision and recall rate proved its efficiency in DNA damage detection. EffectiveDet is a good tradeoff between precision and speed making it ideal for applications that require real time processing [29]. Faster R-CNN on the other hand is less suitable for real time analysis since its inference time is slower than its training time.

YOL4V4 and EfficientDet are the most suitable to examine various sorts of DNA damage, and both showed outstanding performance, although in different indices; YOL4V4 offered a comparatively higher coefficient of accuracy, whereas EfficientDet was significantly faster [30]. These results are in line with pushing future advancements in object detection and show the optimization or the possibilities of using these methods in biological image analysis.

V. CONCLUSION

The present study has established the progressive steps made when employing discounts' enhanced YOLO approaches, such as YOLOv3, YOLOv4, EfficientDet, and Faster R-CNN, in analyzing DNA damage in human sperms and ova. The comparative study focused on the inference time, accuracy, and recall where YOLOv4 was shown to be a reliable assist for detecting DNA damage. Among them, EfficientDet with its improved combination of accuracy and computational cost was selected as a viable solution for real-time use. While Faster R-CNN focused on the detection accuracy, its inference time hampers the model to be used for scenarios with high Throughput Requirements. Recent object detection models have shown a tremendous increase in the ability to detect various sorts of DNA damage, such as single-strand breaks, double-strand breaks, and cross-linking as compared to traditional methods. This work also highlights the applicability of the proposed YOLO-based models on improving diagnostic capability in the general reproductive health besides striving to lay a basis for the use of modern machine learning approaches on biological data analysis. The authors propose that future studies need to apply additional optimization and extension of these models that would result in even more accurate and effective diagnostic tools. More studies should be pursued in continuous incorporation of these techniques to the automatic diagnoses system, and the use of sets of data that would help in the improvement of the models. Altogether, the progresses described in this study will allow for better, faster, and more time-relevant assessment of DNA integrity and might help to enhance reproductive health and genetic studies.

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