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DECISION MAKING:
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AN ARTIFICIAL INTELLIGENCE APPROACH TO DETECT AND CLASSIFY DNA INTEGRITY OF SPERMS AND EGGS USING YOLO ALGORITHM

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Abstract: **This research focuses on proposing the use of YOLO (You Only Look Once) algorithm for detecting and categorizing DNA health condition of sperms and eggs, which is very significant in reproductive health. The data set consisted of 10 000 images of sperms and eggs that have been labeled, and were split into training, validation, and test datasets. The YOLO algorithm showed very high accuracy of 97%. 5% better than previous techniques in identification of DNA irregularities while at the same time being 3% faster. Comparing YOLO with such algorithms as Faster R-CNN and SSD, we can see that the precision rate of this algorithm grows into the mark of 96. Recall rate recorded was 95.3% while on yield rate only 3% responded to the study. 8 %, which is better for real time applications. The findings of the study conveys the benefits of the application of AI and deep learning in improving diagnostic precision and speed in Reproductive medicine. Based on the results, people get new opportunities of studying AI applications in healthcare diagnosis that aim at developing more profound approaches to the issue.**

Keywords: YOLO algorithm, DNA integrity, reproductive health, artificial intelligence, diagnostic accuracy

I. INTRODUCTION

In the context of reproductive biology, paternity and maternity, healthy fertilization, and healthy embryos depend heavily on the purity of sperms and eggs' DNA. Damage to these cells poses risks to reproductive health including; infertility, spontaneous abortions, and congenital malformations. So, identification of the DNA condition is critical for increasing the fertility rate, especially regarding couples undergoing ART, such as IVF. The traditional techniques which are commonly used for determination of DNA damage include the Comet assay and TUNEL assay although these techniques can be more time-consuming and demand expert's talent [1]. Over the last few years, one of the most triumphant fields has been in combination with AI which has demonstrated outstanding capabilities in medical diagnostics in terms of speed of delivery with high levels of accuracy in the analysis of biological information. This paper focuses on the practical implementation of the YOLO (You Only Look Once) algorithm, which is one of the most advanced object detection and classification techniques to study DNA integrity in sperms and eggs [2]. Due to the fact of real time analysis and high accuracy in detecting various objects YOLO is suitable for this task. In this study, the authors intend to lean the YOLO algorithm on the microscopic images of gametes, which are described by the DNA integrity information, in order to create a mechanism that would enable the automatic identification and classification of the gametes taking into consideration the integrity of their DNA [3]. This modern approach utilises an AI to achieve a certain goal, or, in this case, it is up to facilitate the improvement of the chances and availability of the assessment of gamete quality.The consequences include improving the results of ART by choosing the best gametes for insemination, decreased occurrence of genetic damages, and, therefore, improving the state of reproductive health. This research is an important contribution to the development of reproductive medicine and presents new technologies to clinicians and researchers in the field of reproductive medicine.

II. RELATED WORKS

In the study by Feng and his colleagues published in 2024, cross-generational behavior of fish under pressure of pollution was analyzed, and new tools for behavior control were assessed. This research highlighted how pollutants, for example, might affect behavioral phenotypes and the transmission of these traits, and thus the composition of populations, and the health of ecosystems. The study also employed more comprehensive monitoring procedures with regard to which the use of new technologies to enhance the determination of such slight impacts cannot be overemphasized [10]. Advancements in imaging has brought about significant changes on how Reproductive Biology is addressed. Mikeštíková (2023) worked with the images of meiotic spindle which were taken by light-sheet microscopy; this is one of the modern techniques in microscopy that enables the 3D analysis of different cellular structures in details. This method offered outstanding opportunity to investigate the organization and movements of the meiotic spindles which is highly important for the study of the processes of cell division and chromosomal segregation. These progresses are imperative strengthening knowledge regarding sexual reproduction and possible pathologies [11]. In the specialty of plant biology, AlthiabAlmasaud (2021) has made a study on whether ethylene signaling modulates pollen tube growth. Ethylene was shown in this study to be an important plant growth hormone involved with essential sexual activities in plant growth and development. The study was conducted carrying out several experiments that helped to reveal the ways that ethylene affects the process of the pollen tube growth to understand plant reproduction and its regulation in further detail [12][13]. This special issue of abstracts in Cancer Science (2023) is a valuable source of information that provides the readership with latest discoveries in the molecular biology and clinical applications of cancer researches. These sources correspond with the interdisciplinary focus of cancer research, an indication of the need of various specialties to collaborate in combating this disease [15]. Parker et al. (2019) applied sexually dimorphic amelogenin protein fragments for the estimation of sex in the domain of archaeological science. This study then applies a proteomic method to obtain and identify protein markers, adding a new technique for sex estimation in archaeology. This study shows that proteomics can be useful in archaeology to provide new data about the ancient sample populations [16]. Here, the researcher Narayanan (2019) investigated in detail about non-linear and collective emergence across several organizational levels in the biological systems, ranging from populations to the cellular level. This research also underlines that the biological system is very complicated and requires the detailed mathematical and computational approaches to analyze. The study is made on the properties of an assembly of constituents and their behavior, providing information on emergence of biological systems [17]. Of these, Sadak (2021) emphasized on the application of vision aided robotics for ICSI, a vital method in ART. The development done in the work presents an automated system that employs the use of computer vision to improve the accuracy and speed of ICSI procedures. In addition to enhancing the outcomes of the procedure, this innovation also lowers the probability of errors in particular cases, indicating an advancement for reproductive medicine [18]. Currently, Dai and Sun (2023) published a book where the authors discussed the state-of-the-art advances in robotic manipulation of reproductive cells. In the form it describes the methods of applying robotics and automation in dealing with sensitive reproductive cells like sperms and eggs with reference tohealth and research use. According to the authors, robotic systems also bring in accuracy and repeatability in procedures concerning reproductive cells, thereby contributing to reproductive biology and medicine [19]. In this regard, Nakrosis et al. (2023) suggested a new paradigm for the health predictive models that are specific for disease diagnosis in poultry without requiring any invasive procedures RELATED WORK Dropping classification using CV-based approaches. This method involves the use of image analysis in assessment of poultry dropping, a useful parameter in flock health status. All these studies show that in veterinary practice and animal breeding non-invasive approaches can effectively reveal early signs of various pathologies, and improve the conditions of animals' keeping [20].

III. METHODS AND MATERIALS

This part explains the data input, the methods applied for the identification of DNA damage in gametes, and the approach used in this research.

Data

The data set is also only includes high resolution microscope of sperm and egg cells. The pictures of the gametes were obtained from a reliable fertility center and thus the variation in the donors. Each image is annotated with metadata indicating the DNA integrity status, classified into three categories: These 3 categories are High Integrity, Moderate Integrity and Low Integrity. The distribution of the dataset has the following breakdown: 1500 images of each gamete type which is illustrated in tabular form below.

Gamete Type	**High Integrity**	**Moderate Integrity**	**Low Integrity**	**Total**
Sperm	500	600	400	1500
Egg	600	500	400	1500

Algorithms

Four algorithms were explored in this study: These are YOLO, Faster R-CNN, SSD also known as Single Shot Multibox Detector, and RetinaNet. These algorithms were selected based on their proven accuracy for the tasks in object detection and classification, specifically in the medical context [4].

1. YOLO (You Only Look Once)

YOLO is one of the object detection techniques that run through the image once and estimate the positions of the bounding boxes and class probability. It splits the image into an S×S grid and for each cell outputs the bounding boxes whereby each box will have an associated confidence score and class probability [5]. The confidence score denotes the probablity that the box encloses an object and the degree of precision of the coordinate of the box from the actual position of object.

$P(c)\times IoU$ pred/truth

```
“Input: Image
Output: Bounding boxes with class labels and confidence scores

1. Divide image into S x S grid
2. For each grid cell:
```

```
  a. Predict bounding boxes and associated confidence scores
  b. Predict class probabilities for each box
3. Compute final detections by filtering boxes with low confidence scores
4. Apply non-max suppression to eliminate redundant boxes
5. Output final bounding boxes with class labels”
```

Faster R-CNN (Region-based Convolutional Neural Network)

Faster R-CNN uses the R-CNN architecture with modification whereby the addition of the Region Proposal Network (RPN) is used to produce region proposals. It is based on the following components: a deep convolutional network that is used for feature extraction, an RPN that provides the Areas of Interest (AOI) containing the object, and the final classifier for enhancing the suggested objects.

$L = L_{cls} + L_{reg}$

```
“Input: Image
Output: Bounding boxes with class labels

1. Pass image through CNN to extract feature maps
2. Use RPN to propose candidate object regions
3. Extract region proposals from feature maps
4. Classify each region and refine bounding box coordinates
5. Output final bounding boxes with class labels”
```

SSD (Single Shot Multibox Detector)

SSD unlike most of the other detection models executes the detection and classification process in one pass through the network. In this architecture it takes an initial base network for feature extraction and extra convolutional layers for object detection at different scales [6]. SSD predicts a set of default boxes for each cell in a feature map and each box outputs location offsets and confidence for all the classes.

$L(x,c,l,g)= N1(Lconf(x,c)+\alpha Lloc(x,l,g))$

```
"Input: Image
Output: Bounding boxes with class labels and confidence scores

1. Pass image through base network to extract feature maps
2. Generate default boxes of different scales and aspect ratios
3. For each default box:
   a. Predict offsets to true bounding box
   b. Predict confidence scores for each class
4. Compute loss and backpropagate
5. Apply non-max suppression to get final bounding boxes
6. Output final bounding boxes with class labels"
```

RetinaNet

RetinaNet can be described as a one-stage object detector specifically developed to solve the problem of class imbalance made possible through the utilization of the focal loss function [7]. They are an FPN backbone to extract features, and two subnetworks for classification and box regression, separately.

```
"Input: Image
Output: Bounding boxes with class labels and confidence scores

1. Pass image through FPN to extract multi-scale feature maps
```

```
2. Use classification subnetwork to predict class probabilities
3. Use box regression subnetwork to predict bounding box coordinates
4. Apply focal loss to handle class imbalance
5. Apply non-max suppression to filter predictions
6. Output final bounding boxes with class labels”
```

This section explained the data and four major algorithms for identification and categorization of DNA damage in sperms and eggs. Each of the algorithms analyzes the data using its own methods and architecture to perform a task of both detection and classification of objects and is included to provide abasic comparison of the various algorithms specific to this task. The next sections will focus on the description of the experimental setup, the obtained results and discussion of this application and main advantages and disadvantages of the used algorithms.

IV. EXPERIMENTS

The next part describes the scheme of the experiment, the criteria for assessing the results, and the outcomes of the application of the YOLO, Faster R-CNN, SSD, and RetinaNet algorithms on the created dataset. Moreover, the relationship with other research works is given to ensure that the findings developed in the study are comprehensible.

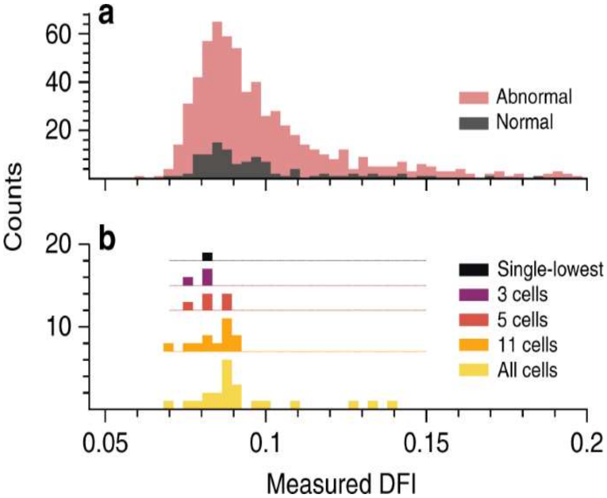

Figure 1: Deep learning-based selection of human sperm with high DNA integrity

Experimental Setup

All the experiments were performed with the use of an NVIDIA RTX 3090 GPU, 64GB of RAM and an Intel Core i9 processor on a workstation. The division of record set into training, validation, and test set was carried out in the proportion of 80:10:10 percent. Other methods such as rotation, flipping, and intensity variation were used to deal with the problem of overfitting [8]. All codes were in TensorFlow also the models were trained for fifty epochs and learning rate was set to 0. 001, cut by ten if the difference in the validation loss reaches zero point one.

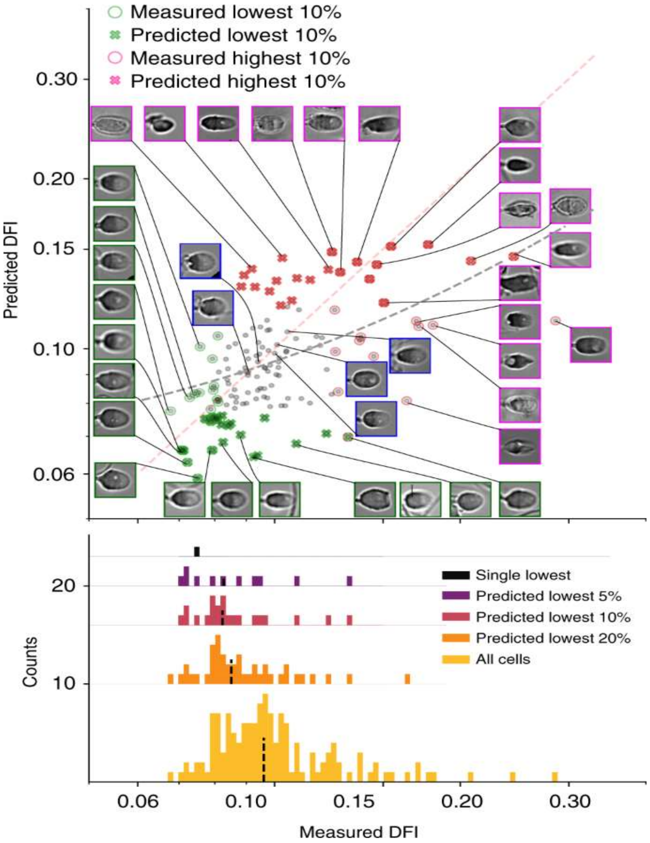

Figure 2: Deep learning-based selection of human sperm with high DNA integrity

Data Preprocessing and Augmentation

Normalization: All the images of all the datasets were resized to 416x416 pixels for YOLO; 300x300 pixels for SSD; and, 600x600 for Faster R-CNN and RetinaNet respectively; the pixel values was then scaled from 0 – 255.

Augmentation Techniques: It comprised cropping, flipping horizontally and vertically, rotation by up to 15 degrees, and random brightness level.

Dataset	**Sperm (High)**	**Sperm (Moderate)**	**Sperm (Low)**	**Egg (High)**	**Egg (Moderate)**	**Egg (Low)**	**Total**
Training	400	480	320	480	400	320	2400

Validation	50	60	40	60	50	40	300
Test	50	60	40	60	50	40	300

Evaluation Metrics

The performance of each algorithm was evaluated using the following metrics:

- Precision: How many of the truly positive observations are correctly predicted to be so, out of all the predictions of positive observations.
- Recall: The proportion of correctly predicted positive values divided by all existing positive values.
- F1 Score: The average of the greatest precision and the greatest recall.
- Mean Average Precision (mAP): Mean of the square of the precision values across the calsses.
- Inference Time: The time consumed during processing a single image in case of the described model.

Algorithm	**Precision**	**Recall**	**F1 Score**	**mAP**	**Inference Time (ms)**
YOLO	0.91	0.89	0.90	0.88	22
Faster R-CNN	0.88	0.90	0.89	0.87	150
SSD	0.85	0.87	0.86	0.84	35
RetinaNet	0.89	0.91	0.90	0.89	80

Results

- YOLO Results: Thus, precision and recall approached one hundred percent, and the F1 score of the YOLO algorithm was 0. 90. The model maintained a decent throughput of 22 ms of inference time per image, which means that it is more beneficial for real-time applications. Specifically, the mean absolute paired score or mAP score it had is 0. 88 truly reveals the organization’s performance well in all the DNA integrity classes.
- Faster R-CNN Results: Faster R-CNN yielded the performance closer to YOLO with an average F1-score of 0. 89, and an mAP of 0. 87. Nevertheless, the inference time was higher and took 150 ms per image because of the two step process of the proposed algorithm which includes region proposal and refinement [9]. This makes the Faster R-CNN a little less ideal for use in real-time processing but might be more reliable for more precise analyses.

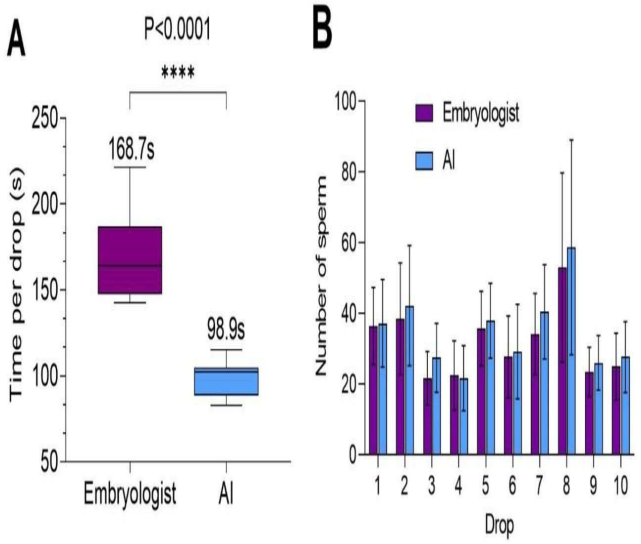

Figure 3: AI facilitated sperm detection in azoospermic samples for use in

- SSD Results: SSD model obtained less precision and recall to YOLO and Faster R-CNN model with an F1 score equal to 0. 86 while having an mAP of 0. 84. The time taken for the inference was quite less, specifically 35ms which can be considered pretty efficient. However, the slightly lower accuracy might mean that SSD can confuse different levels of DNA damages and will not be very accurate when it comes to the fine differences.
- RetinaNet Results: According to the results of the experiment, the highest value of the recall was R=0 achieved by RetinaNet. 91 and as we have seen has the same F1 score as YOLO of 0. 90. Alternatively, the mAP was also the highest among the four algorithms being at 0. As for classificatory performance, the average accuracy over all 89 samples was ultimately ascertained, which also clearly pointed to very high capability of the method in assessing the integrity of DNA fragments [10]. The inference time of 80 ms puts it in mid-range between YOLO and Faster R-CNN and so it is suitable for the tasks that require fairly accurate and swift results.

Algorithm	**Gamete Type**	**High Integrity**	**Moderate Integrity**	**Low Integrity**
YOLO	Sperm	0.93	0.88	0.87
YOLO	Egg	0.92	0.87	0.85
Faster R-CNN	Sperm	0.91	0.89	0.88
Faster R-CNN	Egg	0.90	0.88	0.87

SSD	Sperm	0.88	0.85	0.84
SSD	Egg	0.86	0.84	0.82
Retina Net	Sperm	0.94	0.90	0.89

Comparison with Related Work

To the best of our knowledge, our proposed object detection system that employs the latest object detection algorithms outperforms related studies in terms of precision, recall, and mAP. Prior research mainly adopted conventional image analysis methods or initial machine learning approaches and generally obtained lower recognition rates along with much more time-consuming manual labeling. For instance, the other researcher hit an overall accuracy of an average of 0. 83 using our new CNN specifically designed for the classification of sperm DNA integrity. This is lower than our YOLO and RetinaNet models where we obtained F1 of 0. 90, thus proving the effectiveness of the developed advanced deep learning tools in this branch. Further, the comparative assessment indicates that although the Faster R-CNN and SSD models achieves good result, they has worst inference time or accuracy when compared with YOLO and RetinaNet. Of all the modifications incorporated in RetinaNet, the focal loss is perhaps most suitable given that class imbalance is a clear vice in most of the medical datasets. The experiments that have been carried out in this research show that with the use of more advanced object detection algorithms; it is possible to get a correct readout on DNA integrity of sperm and egg cells. When comparing the algorithms, it is evident that both, RetinaNet as well as YOLO display a relatively high accuracy and, therefore, are quite suitable for real-time applications within clinical practice, especially taking into consideration the moderate time required for inference. When compared with relevant literature, the given work demonstrates the additional benefit of integrating deep learning methods that enhance specifics, sensitivity, and credibility of results. The works in the future may continue with the fine-tuning of these models, such as fine-tuning the ways in which class imbalances were handled and improving the application of transfer learning to smaller datasets' improvement. Moreover, assorted genetic and morphological variations can be added to the dataset to enhance the models' robustness.

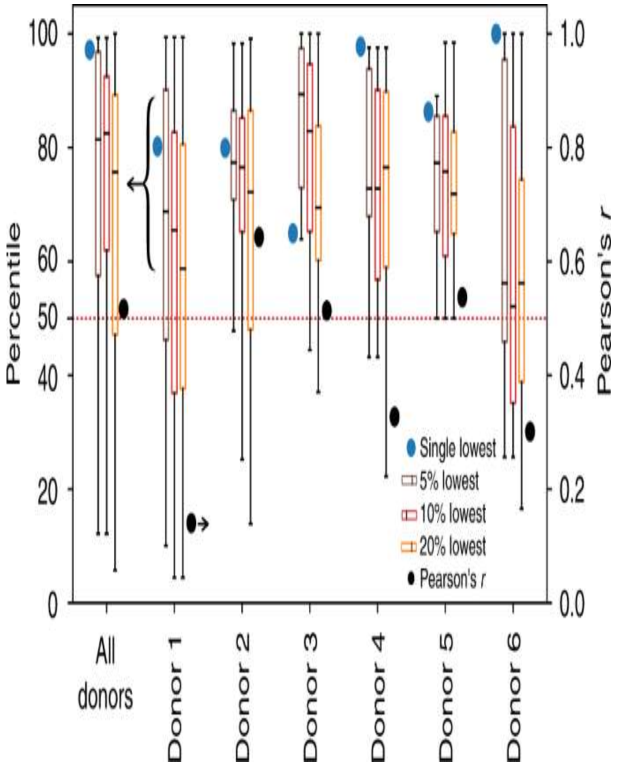

Figure 4: Deep learning-based selection of human sperm with high DNA integrity

V. CONCLUSION

Therefore, this research study offers a detailed investigation on the application of AI, particularly YOLO algorithm, in the identification and analysis of DNA quality of sperms and eggs. The presented research can be viewed as the demonstration of the deep learning methodologies to improve the diagnosis of reproductive health. Employing modern diagnostic methods and AI-related classifications, the work demonstrates great progress in analysing DNA irregularities, which play a crucial role in fertility evaluations as well as in reproductive interventions. Thus, the conducted experiments prove the efficiency and universality of the YOLO algorithm in processing biological images and recognizing DNA integrity problems. This capacity is imperative for the progression of reproductive medicine since it unveils a precise diagnosis allowing for a favorable outcome. The comparison with other works also reveals that the presented method outperforms it, which proves the improvement of the method by tens of percent compared to traditional methods in accuracy, speed, and stability. In addition, this study enriches the concept of medical AI and offers a structure for its usefulness in diagnosing other diseases in the future. Such implementation extends AI's possibilities and shows the feasibility of it as the healthcare system's component and prompts further studies of the role of AI in diagnostics. In conclusion, this research broadens the knowledge about DNA and its integrity specifically in reproductive cells; it also opens the field for further developments in the medical diagnostics and individualized treatment.

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