A ROBUST ENSEMBLE MODEL FOR
PARASITIC EGG DETECTION AND CLASSIFICATION
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ABSTRACT
Intestinal parasitic infections, as a leading causes of morbid-
ity worldwide, still lacks time-saving, high-sensitivity and
user-friendly examination method. The development of deep
learning technique reveals its broad application potential in
biological image. In this paper, we apply several object
detectors such as YOLOv5 and variant cascadeRCNNs to
automatically discriminate parasitic eggs in microscope im-
egages. Through specially-designed optimization including raw
data augmentation, model ensemble, transfer learning and
test time augmentation, our model achieves excellent perfor-
mance on challenge dataset. In addition, our model trained
with added noise gains a high robustness against polluted
input, which further broaden its applicability in practice.

Index Terms— Object detection, biological images, en-
ssemble learning, robustness.

1. INTRODUCTION
Intestinal parasitic infections (IPIs) remain a main disease
severely threatening human health around the world [1], lead-
ing to a heavy financial burden especially in less developed
countries. In WHO’s four-part strategy of IPIs controlling, di-
agnosis acts as a key component and a significant prevention,
where stool examination for parasitic ova is one of the most
convinving and effective standard in laboratories [2]. How-
ever, the requirement of massive examination cost and experi-
enced medical laboratory technologist is still a main obstacles
in practice.

With the rise of deep learning technology in computer vi-
sion, artificial intelligence becomes an effective solution to
many image-related tasks such as image classification [3, 4, 5]
and object detection [6, 7, 8]. The huge success of deep learn-
ing technique reveals its broad application prospects in bio-
logical fields [9, 10]. Learning from a given set of labeled
data, a well trained AI model can easily accomplish certain
biological tasks. Google use a deep learning model “in silico
labeling (ISL)”[11] to perform dichroic fluorescent labeling
of microscope cell images. Vijayalakshmi and Rajesh [12]
utilize a transfer learning approach to identify infected falci-
parum malaria parasite in microscope images.

In this paper, we apply YOLOv5 and variant cascadeRC-
NNs to address the problem of automatic parasitic eggs de-
tection and examination, which are mainstream approaches
in object detection tasks. Since these models are not spe-
cially designed for biological tasks while differences exist be-
tween natural images and biological images [13], we make a
further improvement of the models’ applicability to micro-
scope images, including data augmentation, model ensemble
and other training strategies. Considering possible interfer-
ence to images in practical application scenarios, we also train
our model to gain a certain robustness against various noises
added on test examples. Experimental results demonstrate
that our model achieves excellent performance on test set with
more than 0.956 mAP (0.5:0.95). Even with noise-polluted
test examples, our model can still achieve 0.967 mAP (0.5).
2. BASIC ALGORITHM

In this paper, we apply YOLOv5 [8] and cascadeRCNN [14] as our basic algorithm. The further modification and improvement are accomplished on these models.

**YOLOv5** is a series of mainstream object detection algorithms developed from [6], among which YOLOv5x has the largest model structure and best performance, making it particularly suitable for detecting tiny objective in high-resolution images.

**CascadeRCNN** is developed from FasterRCNN [15], which presents a cascaded R-CNN structure with different IoU thresholds at different levels. It overcomes the defect that selection of IoU threshold in the R-CNN part has a significant impact on the quality of final detection bboxes. A cascadeRCNN contains three modules: backbone, neck and head with three detection bboxes, where backbone module is replaceable with other feature extractors according to practical requirement.

3. DATA AUGMENTATION

Since this challenge focus on robustness and accuracy in data-driven technologies, we make various data augmentations in the given dataset. Including normal augmentation, biological data augmentation and robust data augmentation.

**Normal Data Augmentation.** In standard training procedure, regular data augmentation methods are used to increase models’ generalization ability, including resizing, random flipping, normalization, Mixup and padding, etc.

**Biological Data Augmentation.** Compared with natural images, microscope images has its unique contribution such as more regular background, more similar objective structure and smaller objective area, which means their features are more indistinguishable between classes. Object detector for natural images may be incapable of effectively accomplishing this challenge. Hence, we augment original data with Contrast Limited Adaptive Histogram Equalization (CLAHE) [16], and Enhancement in Mixed Space [17] to enlarge feature difference between classes, as illustrated in Fig. 2. Our augmentation significantly improves model’s discriminate ability to object features.

**Robust Data Augmentation.** To improve our models’ robustness against possible interference occurs on microscope images in practical scenario, our model is fed with both clean and perturbated examples during the training procedure. Multiple perturbation added on images including salt and pepper noise, Gaussian noise, fog and blur. After training with mixed data, our model has gained robustness to various interference, as shown in Fig. 3.

4. IMPLEMENTATION

4.1. Pre-processing

The original dataset contains 11,000 images of 11 classes, each of which contains 1,000 examples. We randomly select 200 examples from each class respectively to construct our validation set with total 2,200 images. The rest of original dataset is our training set, i.e., the training-validation ratio is 4:1. During data processing, we apply the techniques mentioned in Sec. 3 and related parameter settings are listed in Tab. 1.
4.2. Training Procedure

**YOLOv5:** We pre-train YOLOv5x and YOLOv5l on Coco dataset [18]. Then the models are trained on our divided training set. We use SGD with momentum = 0.937, and weight decay is $5 \times 10^{-4}$. The initial learning rate is $1 \times 10^{-2}$ and updated by cosine cyclical learning rate strategy. Total training epoch is 300 with early stop and warm-up epoch is 3.

**CascadeRCNN:** We substitute the backbone in cascadeRCNN with swin-transformer [19] to better extract object features. The variant cascadeRCNNs are first pretrained on Coco dataset. In training procedure, we use Adam with weight decay $5 \times 10^{-4}$. The initial learning rate is $1 \times 10^{-4}$ and updated by multi-step decay strategy. Total training epoch is 30.

4.3. Post-processing

When testing the model, we apply a multi-scaled strategy, i.e., the test examples are scaled into several sizes and predicted separately. In addition, we set different confidence threshold for different classes and only retain results whose confidence is larger than its corresponding threshold. If an anchor has a large area in a large-scale image, we consider it as a wrong prediction and discard it. Same principle is applied to small anchor in the small images.

4.4. Model Ensemble

After all models are tested, we apply Weighted Boxes Fusion (WBF) [20] as our ensemble strategy, which is a state-of-the-art approach of ensemble detection. After ensemble, our model can predict a more accurate anchor on the object with higher confidence. The entire procedure of our implementation is illustrated in Fig. 3.

5. ABLATION STUDIES

The main results of two representative models (YOLOv5x and cascadeRCNN with swin transformer) on test set are summarized in Tab. 2 and Tab. 3. We notice that except for robust augmentation, all strategies are beneficial to the model’s performance, among which biological augmentation is particularly effective, suggesting that specially designed augmentation methods is necessary in biological-related tasks.

Compared with YOLOv5x, cascadeRCNN’s performance is highly related to backbone selection. After substitute its backbone with swin transformer, cascadeRCNN outperforms YOLOv5x. This improvement encourages us to construct an ensemble cascadeRCNN with different backbones for a better performance.

6. ROBUSTNESS AGAINST NOISES

Though training with perturbated data will slightly damage models’ performance on clean test set, it can significantly improves models’ performance when test inputs are polluted.
Table 2. Experimental results of YOLOv5x on test set. Ticked item represents that corresponding strategy is applied during the training procedure. Aug. represents data augmentation.

| Normal | Biological | Robust | Pre | Large | Multi | Transfer | Precision | Recall | mAP (0.5) | mAP (0.5:0.95) |
|--------|------------|--------|-----|-------|-------|----------|-----------|--------|-----------|----------------|
| Aug.   | Aug.       | Aug.   | Train | Size | -scale| Learning|           |        |           |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.931     | 0.919  | 0.926     | 0.860          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.970     | 0.962  | 0.969     | 0.890          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.983     | 0.973  | 0.977     | 0.899          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.977     | 0.961  | 0.974     | 0.895          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.989     | 0.990  | 0.998     | 0.921          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.992     | 0.991  | 0.996     | 0.927          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.992     | 0.994  | 0.998     | 0.936          |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓        | 0.994     | 0.995  | 0.999     | 0.945          |

Table 3. Experimental results of cascadeRCNN on test set. Ticked item represents that corresponding strategy is applied during the training procedure. Backbone represents substituting the original backbone with swin transformer.

| Normal | Biological | Robust | Pre | Back | Large | Multi | Transfer | mAP (0.5) | mAP (0.75) | mAP (0.5:0.95) |
|--------|------------|--------|-----|------|-------|-------|----------|-----------|-------------|----------------|
| Aug.   | Aug.       | Aug.   | Train | bone | Size  | -scale| Learning|           |             |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.940     | 0.930  | 0.858      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.963     | 0.950  | 0.872      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.970     | 0.958  | 0.880      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.970     | 0.955  | 0.881      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.984     | 0.977  | 0.905      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.992     | 0.981  | 0.931      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.994     | 0.987  | 0.938      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.996     | 0.990  | 0.945      |                |
| ✓      | ✓          | ✓      | ✓    | ✓     | ✓     | ✓     | 0.999     | 0.996  | 0.952      |                |

Table 4. mAPs (0.5) of YOLOv5 trained with (Y - R) and without (Y - N) augmented data. The first row represents the noise added on test images.

| Noise    | None | Gaussian | Salt & Pepper | Fog | Blur |
|----------|------|----------|---------------|-----|------|
| Y-R      | 0.974 | 0.972    | 0.971         | 0.967 | 0.969 |
| Y-N      | 0.977 | 0.965    | 0.962         | 0.944 | 0.952 |

Table 5. Final result.

| mAP(0.5)   | mAP(0.5:0.95) | mIoU   |
|------------|---------------|--------|
| 0.999      | 0.956         | 0.966  |

8. CONCLUSION

In this paper we proposed a practical ensemble model to detect parasitic egg in microscope images. The high performance of our solution to this challenge reveals a high potential of deep learning techniques in the application of biological examination. Through implementation, we conclude that data augmentation is a necessary approach to accomplish biological-related tasks. A series of suitable feature extractors with ensemble learning can effectively improve models’ performance. In addition, models’ robustness against noises should be another main concern in practical application, since there exists various interference in the real scenario that may ruin the model’s inference ability. We expect that our work may provide a brand new baseline for future improvement.

7. FINAL RESULT

Final result of our ensemble model on ICIP 2022 challenge of Parasitic Egg Detection and Classification in Microscopic Images is presented in Tab. 5.
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