a) Overview

Figure 1 illustrates the overview of our framework, which consists of a coarse-to-fine segmentation module, a loop control module and a module of parasite life stage classifier. Our coarse-to-fine segmentation method applies deep learning models by three consecutive steps of analysis: 1) a coarse segmentation model which inputs a microscopic image and outputs a mask with delimited contours that delineate individual or grouped) parasites. 2) a shape classification model which allows to input cropped images of parasites that have been detected by previous step and outputs their classes (grouped or individual). 3) a fine segmentation model which inputs only the parasite crop identified as grouped in previous step and isolates them by delimiting each of their contours. Subsequently, a loop control module helps to detect outlier parasites. In addition, a classifier with high discriminatory power is used to distinguish the life stages of the parasites.
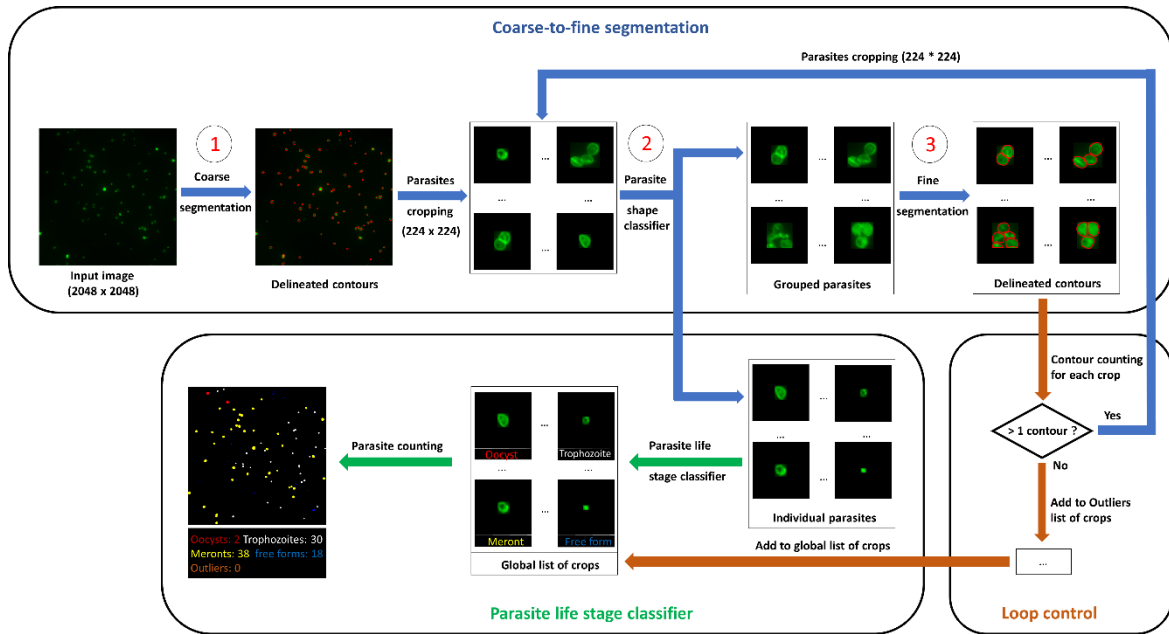

Fig 1: An overview of our proposed framework for Cryptosporidium parasite image analysis.

b) Experimental results for deep learning models
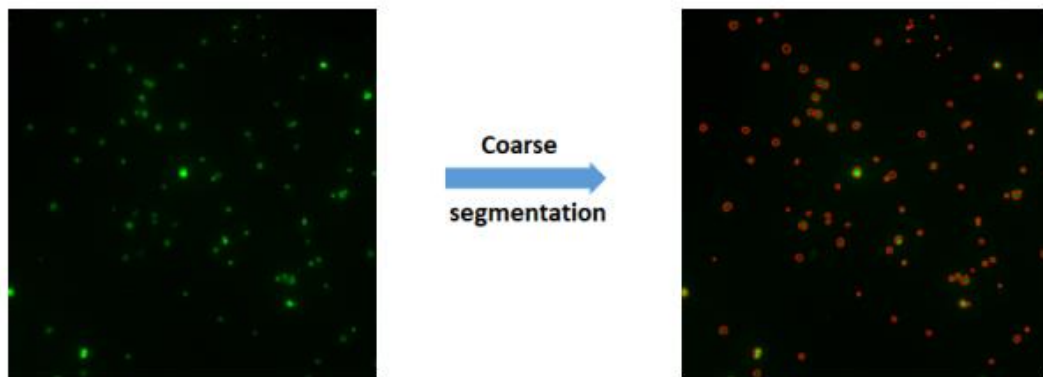- Coarse segmentation

Fig 2: The coarse segmentation step.

As illustrated in Figure 2, the coarse segmentation step that outputs the contours of each parasite, whether it exists in individual or grouped forms. We compared our approach with five other approaches, including three deep learning approaches (U-Net_VGG19, U-

Net_ResNet34 and SwinUnet [1]) and two conventional approaches (watershed algorithm [2] and HSV color filter). Figure 3 illustrates the AP (Average Precision) curves for six architectures computed on the validation set of the coarse segmentation. AP is defined as AP=TP / (TP + FP + FN), where TP is true positive, FP is false positive, FN is false negative in term of parasite object compared to the ground truth.
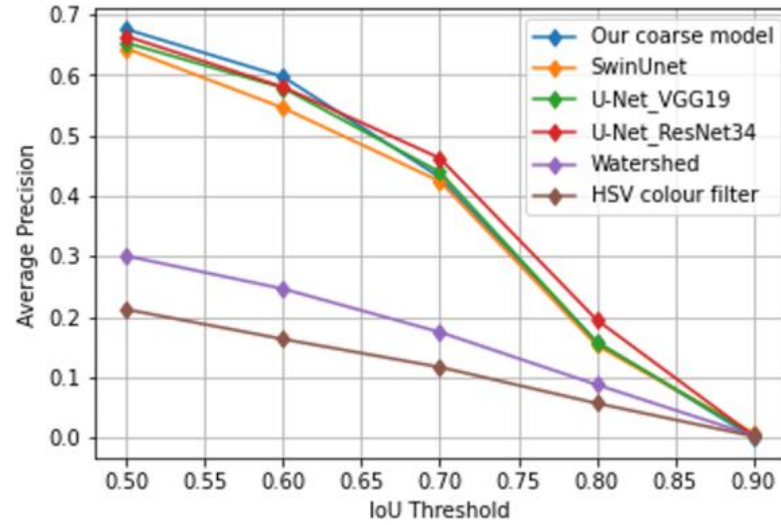

Fig 3: AP curves on the validation set of the coarse segmentation.

They are computed with the IoU (Intersection over Union) metric ranging from a threshold of 0.5 to 1. The curves demonstrate that our model is outperforming the others. In fact, our coarse model achieved 67% AP with an IoU threshold of 0.5. It can also be noted that the performances of conventional segmentation approaches (watershed and color filter) are very low compared to CNN, which clearly shows that use of simple features, such as color, is not sufficient to solve the issue of parasite segmentation.

- Parasite shape classification
  The shape classification step that permits to identify grouped parasites (as displayed in Figure 4).
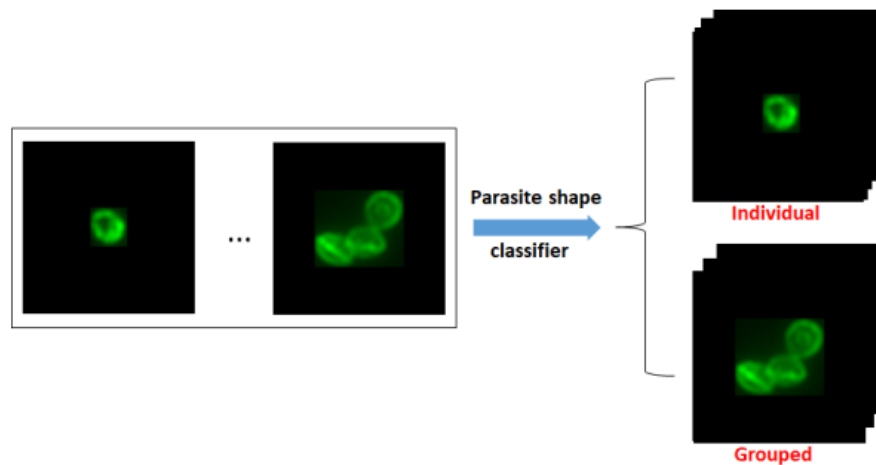

Fig 4: The shape classification step.

The confusion matrix on the validation set illustrates that our model has performed perfectly on the classification of the parasite shape. From the Figure 5, our model succeeds to classify all the validation data.
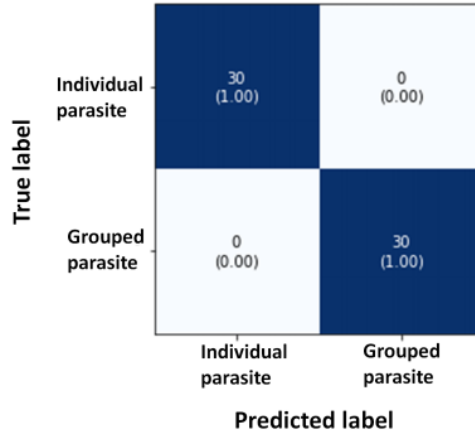
Fig 5: Confusion matrices obtained by our model on the parasite shape validation set.

- Fine segmentation

Figure 6 shows the fine segmentation step that permits to isolate each parasite from the grouped ones.
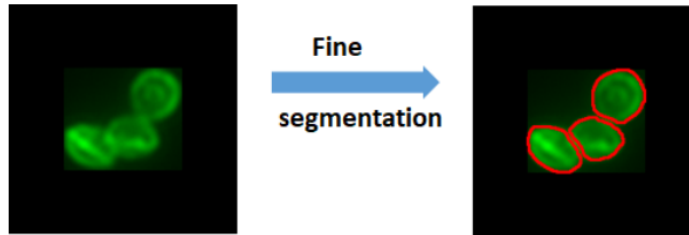

Fig 6: The fine segmentation step.

Like the coarse segmentation, we compared our model with three deep learning approaches. We also followed the same training protocol along with the evaluation metric (Average Precision). Figure 7 demonstrates the AP curves computed on the validation set for our fine segmentation model. The curves indicate that our model gives a better performance than the other models. It is notable that even with a high IoU threshold, the AP value of our model maintains the best AP value amongst the other models, which reveals a high accuracy in parasite separation.
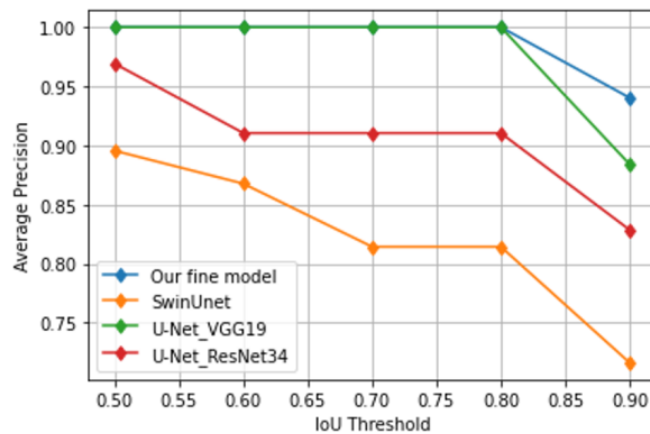

Fig 7: AP curves computed on the validation set of fine segmentation.

- Parasite life stage classification

  Figure 8 shows the parasite life stage classification step that permits to distinguish the Cryptosporidium parvum parasite among 4 asexual stages: oocyst, trophozoite, meront, and free form.
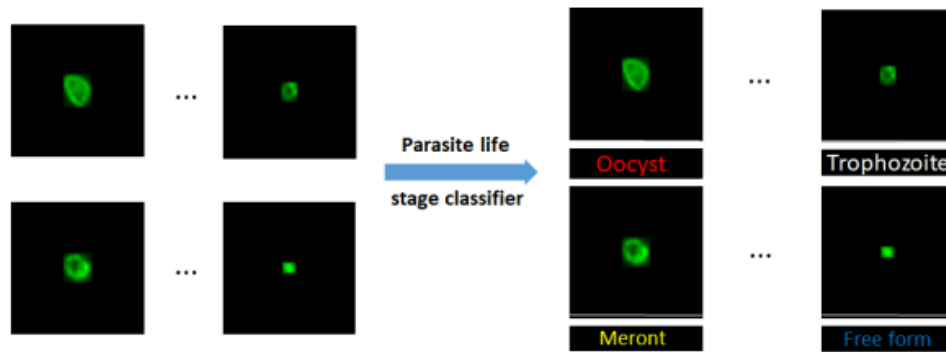

Fig 8: AP curves computed on the validation set of fine segmentation.

The confusion matrix on the validation set illustrates that our model has well performed on all 4 classes (as displayed in Figure 9). For the oocyst and free form, the accuracy is much better than the other two parasite species, which is 97% and 99% respectively. While for the trophozoite and meront, both accuracy are 93%, which shows a little bit of a gap compared to the other two species. This is because a few images may be confused between them.

Fig 9: Confusion matrices obtained by our model on the parasite life stage validation set.

c) Conclusion

This chapter has presented a deep learning-based framework to automatically analyze and diagnose the Cryptosporidium parvum infection. The framework allows to precisely segment a group of parasites from microscopic images by employing a coarse-to-fine segmentation approach, followed by a subsequent classifier with high discriminatory power to distinguish the parasite life stages among 4 asexual stages: oocyst, trophozoite, meront, and free form. Our coarse-to-fine segmentation module has achieved an average precision of 73% on our validation dataset and permits to obtain about 5% of average precision in comparison with the direct segmentation.

Additionally, for the parasite life stage classification module, our model also outperformed better than other state-of-the-art models, with 95.5% of accuracy.

Reference:

[1] Cao, H., Wang, Y., Chen, J., Jiang, D., Zhang, X., Tian, Q., & Wang, M. (2021). Swin-unet: Unet-like pure transformer for medical image segmentation. arXiv preprint arXiv:2105.05537.

[2] Najman, L., & Schmitt, M. (1994). Watershed of a continuous function. Signal Processing, 38(1), 99-112.