Nuclei segmentation and classification in histopathology images with StarDist for the CoNIC Challenge 2022

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Abstract—Segmentation and classification of nuclei in histopathology images is an important task in computational pathology. Here we describe how we used StarDist, a deep learning based approach based on star-convex shape representations, for the Colon Nuclei Identification and Counting (CoNIC) challenge 2022.

I. INTRODUCTION

Reliably identify individual cell nuclei in microscopy images is a ubiquitous task in the life sciences. This task can be challenging when objects are densely packed together and commonly used bounding-box based detection methods struggle. To address this problem, we – together with collaborators – introduced in [6, 7] a deep learning based object detection approach called StarDist. Instead of bounding boxes, StarDist uses star-convex polygons to represent the shape of objects. For roundish objects (such as nuclei) these predicted polygon shapes are typically of high enough fidelity that one can also call this an instance segmentation method.

As a robust and easy-to-use method, StarDist has been well received by the biomedical community, in no small part because we aim to provide and continuously improved high-quality implementations for the tools and languages used by the community. Check out the main repository at https://github.com/stardist/stardist if you’re interested. Being primarily developed for fluorescence microscopy, we were curious to see how StarDist would perform on images from other modalities which is why we participated in the Colon Nuclei Identification and Counting (CoNIC) challenge [2].

II. METHOD

A. Nuclei detection/segmentation

We use the basic detection approach as outlined in [6, 7]: First, a convolutional neural network (CNN) takes a single input image and for each pixel predicts 1) an object probability to know if it is part of an object, and 2) radial distances to the boundary of the object at that location (i.e. a star-convex polygon representation). Second, each pixel with an object probability above a chosen threshold votes for a polygon to represent the shape of the object it belongs to. Since a given object is potentially represented by many pixels which voted for its shape, a non-maximum suppression (NMS) step is performed to get rid of the redundant polygons that likely represent the same object.

B. Nuclei classification

The original approach given in [6, 7] only allowed for the prediction of object shapes. To additionally perform object classification, we simply add a semantic segmentation head to the CNN backbone that is used to predict the object probability/distance vector for every pixel. There are improvements and extensions of StarDist that are part of our public code repository. Additional code developed to create our challenge submissions will be made available after the challenge has ended.

1We used the branch feature for all our challenge submissions.
III. LEARNING

A. Data

We only use the Lizard dataset [1] for training our models, specifically the extracted patches provided by the CoNIC challenge organizers. Of those, we use 90% for training and 10% as validation set. Besides dividing pixels values by 255, we do not perform any image preprocessing or data cleaning.

B. Augmentations

Based on our own augmentation library Augmend, we randomly apply common augmentations to each pair of input and label image on-the-fly during training: flips and 90 degree rotations, elastic deformations, Gaussian blur, adjustments to hue, brightness, and saturation, affine pixel-wise rescaling, spatial image rescaling, and stain augmentation.

C. Model and Training

We use a Stardist model with a U-Net [5] backbone of depth 4. We apply binary cross-entropy loss for the object probabilities, mean absolute error for the radial distances, and the sum of categorical cross-entropy and dice loss for the class probabilities. Training was done from randomly initialized weights for 1000 epochs (256 batches of size 4) using the Adam [3] optimizer starting with learning rate of 0.0003, which was reduced by half if no progress was made for 80 epochs.

IV. PREDICTION

A. Test-time augmentations (TTA)

We use test-time augmentations (TTA) to make results more robust. Concretely, we apply all 90 degree rotations (optionally also with horizontal flip each) to the input image and collect the CNN predictions for object probabilities, radial distances, and class probabilities. Prediction tensors are merged by taking the element-wise median for radial distances and object probabilities, and computing the mean of the class probability vectors.

B. Postprocessing and shape refinement

Non-maximum suppression (NMS) is performed based on a set of polygon candidates (those with object probability above a chosen threshold) obtained from the merged CNN predictions. In each round of NMS, of the remaining polygons that haven’t been suppressed, the one with highest object probability is selected as the “winner” and will suppress all other polygons that sufficiently overlap. Instead of just keeping the winner polygon in each round to yield the final object instances, we group each winner polygon together with all the polygons that it suppressed. For each group, we rasterize all polygons as binary masks and aggregate them by majority vote to obtain the mask of the given object instance (refine). Furthermore, each object instance is assigned a class (i.e., nucleus category) by aggregating the class probabilities from all pixels that are part of the respective object.

C. Ensembling

We additionally aggregate (in the same way as for TTA) the intermediate predictions from a small number of models.

V. RESULTS

A. Task 1: Nuclear segmentation and classification

We evaluated Stardist on the validation set with the metrics used by the CoNIC challenge, in particular PQ, the panoptic quality [4] between ground truth and predicted objects irrespective of the object class, and mPQ, the multi-class panoptic quality as the average of the panoptic quality evaluated for each class independently. Table I shows the results for different prediction modalities, demonstrating the positive effect of adding test-time augmentation, shape refinement, and ensemble prediction on the final results.

B. Task 2: Prediction of cellular composition

We used the same models as for Task 1 and simply reported the number of found objects per class.

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TABLE I

| Prediction mode                                      | PQ     | mPQ     |
|------------------------------------------------------|--------|---------|
| default                                              | 0.6866 | 0.4991  |
| default + TTA                                        | 0.6943 | 0.5200  |
| default + TTA + refinement                           | 0.6992 | 0.5260  |
| default + TTA + refinement + ensemble (2 models)     | 0.7028 | 0.5343  |

2 https://github.com/stardist/augmend