Domain Adaptation for Multi-Organ Nuclei Segmentation

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1. Data Preparation

A total of 209 training images from 46 patients were released for training. The training images were stained using H&E and scanned at 40× optical magnification. Each WSI was provided with four pixel-level ground truth labels (epithelial cells, lymphocytes, neutrophils and macrophages) annotated by pathologists. The original training images at 40× optical magnification are divided into smaller patches (256 × 256) using a sliding window with a stride of 64. When the training image's width or height is smaller than 256, the image is padded with white background. Out of 209 training images, 168 images are used for training and 41 images are set aside for validation.

During training phase, data augmentations (RGBShift, ChannelShuffle, RandomBrightnessContrast, ShiftScaleRotate, ElasticTransform, Horizontal/Vertical flips and Transpose) are applied using albumentation library [1].

On top of four different nuclei types, we have additionally created a nuclei boundary mask and included in the training. The boundary information highlights the boundaries between adjacent nuclei which is import for separating different nuclei.

2. Proposed Model

The model proposed in this task is inspired by U-Net architecture, which has a single encoder and a decoder to convert an image into a segmentation map [2]. As a backbone encoder, our proposed model uses 50 layers ResNet [3] with added Squeeze-and-Excitation (SE) blocks [4].

A noticeable gap between data distributions in train and test domains is observed, which results in severe performance loss at inferencing testing images. To address this challenge, an unsupervised domain adaptation (UDA) method is applied in our proposed model. The UDA method adapted to our model is adversarial entropy minimization [5]. This method utilizes the Shannon Entropy to constrain the model to produce high-confident prediction on testing images while minimizing loss value between prediction from source image and ground truth [5]. In this work, our proposed model utilized direct entropy minimization approach. Once the model is trained, testing

images are inferenced and corresponding entropy values are calculated for all the testing images. The inferenced testing images with entropy values lower than 0.5 and their corresponding predictions are included in the training data for the next model's training (pseudo-labeling) [6].

We used combination of weighted categorical cross-entropy and Lovasz-Softmax loss [7] functions for optimizing the model.

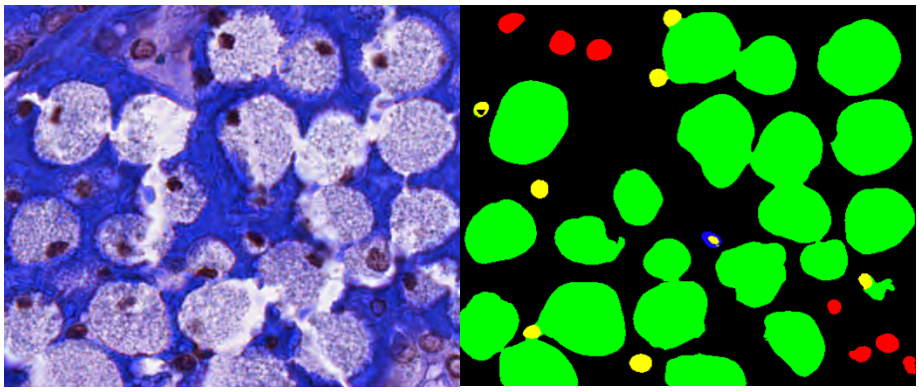

Figure 1. Example of a testing image and corresponding segmentation mask. Color codes correspond to the MoNuSAC2020 website

3. Post-processing

A testing-time-augmentation (TTA) strategy is applied to inference test images. The TTA includes rotations (90, 180 and 270 degrees), vertical/horizontal flips and transpose. Probability maps obtained by different augmentation operations are averaged as the final predictions. Testing images are masked using ambiguous masks provided by the organizer and fed to our model for UDA training.

4. Experimental Results

Five best models are chosen based on panoptic quality (PQ) [8] and final prediction masks are generated by major voting.

	PQ
Model 1	0.5109
Model 2	0.4669
Model 3	0.5517
Model 4	0.4695
Model 5	0.4920

5. References

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