UNSW-AU

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Platform: Windows

Prerequisites: Python 3.7.1 with Pytorch 1.0.0 and Tensorflow 2.1.0

UNSW-AU: SUMMARY

We use neural architecture search (NAS) to automatically generate deep neural networks for the cell segmentation. The network framework (also called macro network) used by the NAS to search for the deep neural network is similar as the one in **BGU-IL (5)**. The detailed micro search space and search strategy are described in [1].

UNSW-AU: PREPROCESSING

The training datasets are enlarged by data augmentation which includes random horizontal and vertical flip, random 90° rotation, random sequence reverse ([*t*, *t-1*, …, *2*, *1*]), and random affine and elastic transformations. The training images are normalized using standard normalization, and for the images in **Fluo-C2DL-Huh7**, the contrast limited adaptive histogram equalization (CLAHE) [2] is also adopted for the preprocessing. Each training sample corresponds to two gold-truth maps for the training, which are the cell segmentation map and cell marker map. They are obtained from the gold-truth cell instance labels provided with the datasets. Especially, the cell segmentation map is a semantic segmentation map with two (*background* and *cell*) or four (*background*, *cell*, *touch*, and *gap*) classes depending on the presence/absence of adjacent/touching cells [1].

UNSW-AU: SEGMENTATION

The searched deep neural network generates two outputs, which are the predicted cell segmentation image and the predicted cell marker image. The segmentation prediction image has two or four channels (detailed in [1]) respectively representing the probability of each pixel belonging to the *background* and *cell* regions (and, in the case of four channels, the *touch* and *gap* regions). The marker prediction is a single channel map representing the probability of each pixel belonging to a cell marker. The searched deep neural network is trained using the classical distance weighted cross-entropy loss function to penalize the segmentation map and binary cross-entropy loss function to penalize the marker map, and the final loss is set to be the sum of the two. The searched deep neural network is trained from scratch

for a maximum 500 epochs (or, if the loss does not drop for 100 epochs, the training will stop early) with Adam optimizer, learning rate of 0.0003, weight decay of 0.0001, batch size of 8, and unroll length of 2 on NVIDIA V100 GPU.

UNSW-AU: POST-PROCESSING

To obtain an instance segmentation from the probability channels of the predicted segmentation map, we first apply the maximum a-posteriori decision rule, which assigns to each pixel a label corresponding to the channel with the highest probability for that pixel. In the case of four channels, *gap* pixels are then relabeled as background, and *touch* pixels are merged with their nearest cell, unless they are not connected to any cell, in which case they too are labeled as background. Also, holes in cells are filled by using the morphological holefilling operation, and then cell instances are obtained by applying the connected components labeling algorithm. Finally, we threshold the predicted marker map to yield cell markers and run a marked-controlled watershed algorithm to separate merged cell instances. This way, the final segmentation mask is generated.

REFERENCES

1. Zhu Y, Meijering E. Automatic improvement of deep learning based cell segmentation in time-lapse microscopy by neural architecture search. *Bioinformatics*, in press, 2021.
2. Pizer SM, Amburn EP, Austin JD, Cromartie R, Geselowitz A, Greer T, Romeny BH, Zimmerman JB, Zuiderveld K. Adaptive histogram equalization and its variations. *Computer Vision, Graphics, and Image Processing* **39**, 355-368 (1987).