

MU-Ra-US

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Platform: Linux

Prerequisites: Python 3.7.6 with PyTorch 1.7 and OpenCV-Python 4.2

MU-Ra-US: SUMMARY

Our cell segmentation pipeline consists of three main modules: image preprocessing, cell segmentation using a custom deep convolutional U-Net [1], named U-SE-ResNet similar to our previous Motion U-Net described in [2] having a deeper backbone with squeeze-and-excitation blocks [3], and post-processing.

MU-Ra-US: PREPROCESSING

We apply standard normalization with 1% intensity clipping after we convert the 16-bit input to 32-bit float. This would remove outlier pixels and improves the contrast of images. This normalization step is the same for all 2D and 3D datasets. As a data augmentation strategy for training our networks, we have applied a random 512×512 crop (translation), random rotation, random flipping, and random gaussian noise.

MU-Ra-US: SEGMENTATION

We used a custom deep convolutional U-Net [1], named U-SE-ResNet similar to our previous Motion U-Net described in [2] to generate segmentation cell masks and cell markers, where cell markers are an erosion of the cells and the erosion size is different for each dataset. U-SE-ResNet is an encoder-decoder type architecture with a ResNet-50 backbone [4] used for feature extraction in the encoder module. Each of the residual blocks in the encoder are equipped with a squeeze-and-excitation blocks [3]. The overall network is similar to the U-Net architecture [1] with skip connections after each block of ResNet-50. Since we want to optimize the overlap score, a combined loss function including Tversky loss [5] and binary cross-entropy loss was used to train the network. We give a weight to each pixel in our final loss map before we aggregate; this weight is higher around edges of a cell and lower away from the cells. This way, we guide our network to learn better cell outlines. Our U-SE-ResNet was trained for 120 epochs with mini-batch size of 4. Adam optimizer was used during training with an initial learning rate of 0.0001 that was reduced by a factor of 2 after every 30 epochs. For all of the datasets analyzed, we used

only the provided silver/gold truth segmentation masks to train the network, with a split of 90% for training and 10% for validation.

MU-Ra-US: POST-PROCESSING

The described network produces two output maps. The first output map is a binary cells mask, the second is a binary mask for cell markers. We use connected components algorithm on the markers to generate the different cell IDs. Then, we use the distance transform of the binary cell mask, and we use that along with the labeled marker map to generate a final labeled cell mask. In order to remove small spurious detections, mathematical morphology operations were used. Spurious detections were eliminated by removing connected components in the cell masks of size smaller than T .

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