UCH-CL

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Platform: Linux

Prerequisites: Python 3.7.3

UCH-CL: SUMMARY

The whole methodology is divided into two parts: 3D nuclei detection and 2D nuclei segmentation. Both modules rely strongly on the inference of fully convolutional CNN models based on the U-Net [1, 2] and require a post-processing step to obtain the detected nuclei centers and segmentation masks. Finally, those partial outputs are used to generate an instance-based segmentation mask containing the identified cell nuclei.

UCH-CL: PREPROCESSING

The input volume is divided into patches that constitute the processing unit of the workflow. For nuclei detection, patch size is equal to 128 × 128 × 25. For nuclei segmentation, patch size equals to 128 × 128. Sampling is done with 50% overlapping between patches. Besides, each patch is normalized by C = 65535 as it is the maximum possible value according to the 16-bit codification.

UCH-CL: DETECTION

CNN inference. The extracted patches pass through the CNN model trained for 3D detection and then a softmax function is applied, generating one output probability map for each input patch. All output patches are then aggregated into a final probability map for the corresponding input volume, keeping the maximum probability values for overlapped output patches.

Blob detection. For 3D nuclei detection, a blob detection step is performed after the CNN inference. Specifically, 3D multiscale Laplacian of Gaussian method was used to identify nuclei centers from the detection probability map. Probability values smaller than T_{det} were considered as background and Gaussian kernels with standard deviations between σ_{min} and σ_{max} voxels were used to find blobs.

UCH-CL: SEGMENTATION

CNN inference. The extracted patches pass through the CNN model trained for 2D segmentation and then a softmax function is applied, generating one output probability map for each input patch. All output patches are then aggregated into a final probability map for the corresponding input volume, keeping the maximum probability values for overlapped output patches.

Thresholding. For 2D nuclei segmentation, a thresholding step is performed after the CNN inference. Otsu's method was used to generate the segmentation mask from the probability volume obtained through the CNN inference. Thresholding was done for 128 × 128 non-overlapped patches and a fixed threshold of T_{seg} was required to correct false positives generated by Otsu's method.

3D seeded Watershed. A 3D Watershed algorithm is applied for labeling the segmentation mask generated after post-processing, using the segmentation probability map as the input topographic map and detected centers as the markers from which flooding is performed. This procedure produces the final segmentation mask, containing the labeled 3D cell nuclei according to the input volume.

REFERENCES

1. Ronneberger O, Fischer P, Brox T. U-net: Convolutional networks for biomedical image segmentation. In *Proceedings of Medical Image Computing and Computer-Assisted Intervention*, 234-241 (2015).
2. Çiçek Ö, Abdulkadir A, Lienkamp SS, Brox T, Ronneberger O. 3D U-Net: Learning dense volumetric segmentation from sparse annotation. In *Proceedings of Medical Image Computing and Computer-Assisted Intervention*, 424-432 (2016).