

# Instance-U-Net and Watershed: Improved Segmentations for breast cancer cells

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Introduction Segmenting single cells from blood/tissue sample is critical to

identify diseased cells to achieve early diagnosis. On the other side, the behaviors of single cells have brought more attention in

biological researches. For example, the lineage tracking of single

embryo cells is vital to understand the mechanisms in early stage

embryo developments; the shape analysis of mammalian cells

during Epithelial-Mesenchymal transition is key to dissect the

transformation of how normal cells become cancer cells. Till now,

identifying cells in images (cell segmentation) has been challenging due to the high density and imbalanced illumination of the sample.

Recently, machine learning and deep learning has became the instrumental tool for computer vision tasks [1] [3]. In this work, we

proposed a highly efficient and effective neural network model that

has accurate predictions on both cell segmentation and cell count.

Fig.1 Training data (a) raw image (b) segmentation mask

Contributions Capture each single cell in cell clusters, we integrated Region Proposal Networks (RPN) to detect cells with bounding boxes

Predict the cell segmentations by integrating U-Net with pre-

Integrate Watershed algorithm with cell centroids (predicted by

RPN) and cell segmentations (predicted by U-Net) as inputs

improve the boundaries predictions of densely touching cells.

Dataset

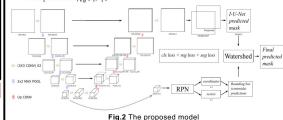
Network Architecture

Feature extraction network and region proposal network (RPN) [2] we build our own end-to-end feature extractor. Here is the training procedure: The input cell images with the size of 448 × 448 are fed into the convolutional

- neutral network (CNN) with the kernel size of 3 × 3. The feature maps with size of 28 × 28 × 512 are fed into RPN, then the region proposals were generated by placing k anchors on each pixel of the feature map. Bounding box and corresponding class scores are introduced to training.
- The cost function of RPN is denoted as:

$$L(p_{i}, t_{i}) = \frac{1}{N_{cls}} \sum_{i} L_{cls}(p_{i}, p_{i}^{*}) + \frac{1}{N_{reg}} \sum_{i} p_{i}^{*} L_{reg}(t_{i}, t_{i}^{*})$$

Where i is the index of the anchor and  $p_i$  is the predicted probability of anchor *i* being an object. The ground-truth label  $p_i^*$  is 1 if the anchor is positive, and 0 if negative.  $t_i$  is a vector that represents coordinates of the predicted bounding box,  $t_i^*$  is the ground-truth box associated with a positive anchor. The classification loss  $L_{cls}$  is log loss over two classes (object vs. non-object). We use  $L_1$  loss for  $L_{reg}(t_i,t_i^*)$ .



#### Instance U-Net

- To improve the cell segmentation performance, we bring the objectiveness
- insights into original U-Net. The abovementioned feature extractor network as encoder of U-Net is integrated
- with deconvolutional layers for extract optimal features.
- Two cost functions are implemented: binary cross-entropy (BCE) loss function for segmentation and dice loss.
- The BCE loss is denoted as:

$$L_{BCE} = \sum w(x) \log(p_{l(x)}(x))$$

- Where w(x) is the weight map.  $\log(p_{l(x)}(x))$  is the pixel-wise cross-entropy sum over all pixels.
- The weight map is computed for each ground-truth segmentation mask to urge the network to learn the small separation borders between touching cells.

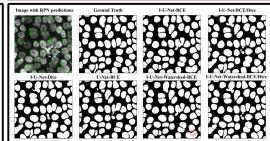
e small separation borders between touching co  

$$w(x) = w_c(x) + w_0 e^{-\frac{(d_1(x) + d_2(x))^2}{2\sigma^2}}$$
ight map to balance the class frequencies,  $d_1(x)$ 

- Where  $w_c$  is the weight map to balance the class frequencies,  $d_1(x)$  and  $d_2(x)$  denote the distance to the border of the nearest cell second nearest cell. In practice we set  $w_0 = 10$  and  $\sigma = 5$ .
- The soft Dice loss is denoted as:

$$L_{Dice} = 1 - 2 \frac{\sum_{i} p_{i}(x) y_{i}(x)}{\sum_{i} p_{i}^{2}(x) + \sum_{i} y_{i}^{2}(x) + }$$

 $L_{Dice} = 1 - 2 \frac{\sum_{i} p_{i}(x) y_{i}(x)}{\sum_{i} p_{i}^{2}(x) + \sum_{i} y_{i}^{2}(x) + \epsilon}$  Where  $p_{i}(x)$  and  $y_{i}(x)$  are the binary labels from prediction and ground truth labels.  $\epsilon$  is a small factor to prevent division by zero, in practice we set  $\epsilon=10^{-\epsilon}$  Results



Sample results. For the inference cycle, test images(top left without bounding boxes are fed into different models and generate: 1. the object predictions(top left bounding boxes) with confidence scores and 2. the predicted masks by different models. Among all them, Instance-U-Net with joint BCE/Dice loss obtains the visually best results, it also has the best Watershed separation boundaries without introducing too many errors. Trained with BCE or Dice loss separately only achieved good shape or touching edge segmentations.

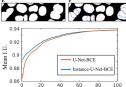
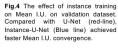


Fig.3 Zoomed-in analysis on the effect of instance training and Watershed algorithm in dense region. effect of instance training and Watershed algorithm in dense region.



# Analysis and Future Directions

- The Instance-U-Net with joint loss achieves a superior segmentation results in microscope images with densely touching cells
- The proposed model achieve fast convergence speed (~7h)
- The implementation of Watershed at the end further improves the
- performance of separating touching cells by 3 folds.

  In the future, we hope to incorporate the adversarial strategy and experiments

### References

[1] Kaiming He, Georgia Gkioxari, Piotr Dollar, and Ross Girshick. Mask r-cnn. 2017 IEEE International Conference on Computer Vision (ICCV), Oct 2017.
[2] Shaoqing Ren, Kaiming He, Ross Girshick, and Jian Sun. Faster r-cnn: towards real-time

object detection with region proposal networks. IEEE Transactions on Pattern Analysis & Machine Intelligence, 2017.
[3]Li Liu, Wanli Ouyang, Xiaogang Wang, Paul Fieguth, Jie Chen, Xinwang Liu, and

MattiPietikäinen. Deep learning for generic object detection: A survey, 2018.

#### Extensive quantitative evaluations illustrated the superiority of the proposed method compared with state-of-the-art segmentation models

computed weight matrices.

#### ZEISS LSM 700 confocal microscope Dataset

- 40X objective on MCF10A human breast cancer cell line The cell nucleus was stained by DAPI and illuminated by laser
- with wavelength 405nm
- Training dataset includes 484 images with ground-truth binary mask, and 8 images with the corresponding masks for validation
- The size of image is of 448 × 448, and each image contains around 100 cells
- The ground truth labels are computed using thresholding and other segmentation methods, segmentation errors are manually corrected image-by-image. The ground truth coordinates for bounding boxes are computed based on the ground truth labels.

# Data augumentation

Augmented data with cropping, adding noise, rotation, mirror