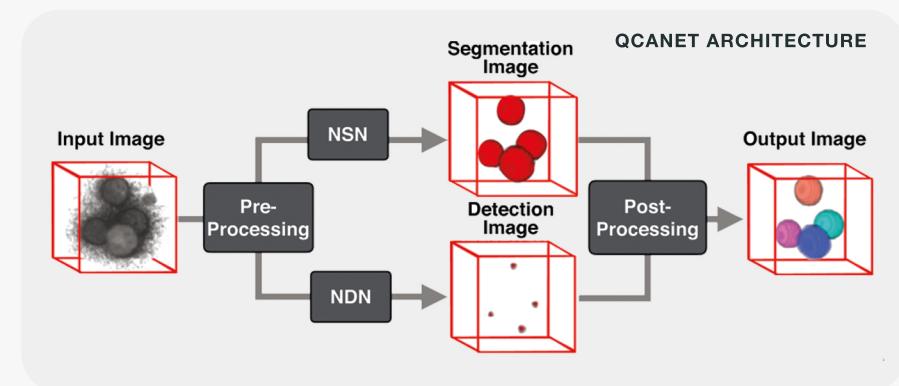


3D Time-Series Cell Segmentation with CNNs

Reproduction of '3D Convolutional Neural Networks-based Segmentation to Acquire Quantitative Criteria of the Nucleus during Mouse Embryogenesis' by Tokuoka et al. [1].

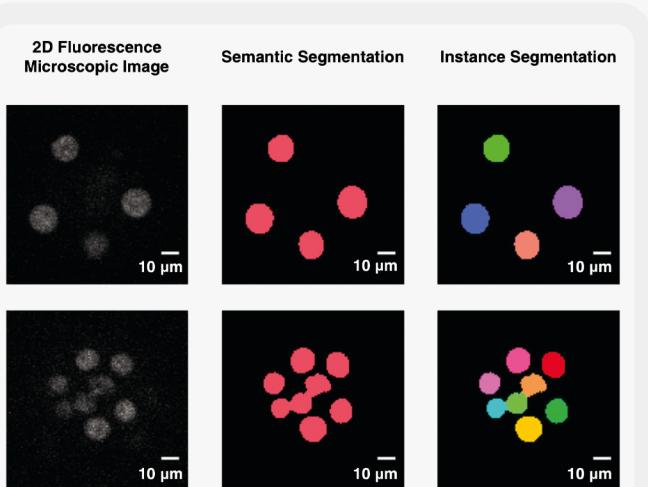
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Tokuoka et al. [1] propose QCANet to generalise and improve segmentation accuracy of 3D fluorescence microscopic images. As shown in the above figure, it consists of two subnetworks: Nuclear Segmentation Network (NSN), and Nuclear Detection Network (NDN); responsible for semantic segmentation and instance segmentation.

As shown below, semantic segmentation refers to labelling each voxel in an image with the correct class, whereas instance segmentation partitions this class into distinct instances.



1. Y. Tokuoka et al., '3D convolutional neural networks-based segmentation to acquire quantitative criteria of the nucleus during mouse embryogenesis', *npj Syst Biol Appl*, vol. 6, no. 1, p. 32, Oct. 2020, doi: 10.1038/s41540-020-00152-8.

2. Ö. Çiçek, A. Abdulkadir, S. S. Lienkamp, T. Brox, and O. Ronneberger, '3D U-Net: Learning Dense Volumetric Segmentation from Sparse Annotation'. *arXiv*, Jun. 21, 2016. Accessed: Apr. 10, 2024. [Online]. Available: <http://arxiv.org/abs/1606.06650>

3. M. Maška et al., 'A benchmark for comparison of cell tracking algorithms', *Bioinformatics*, vol. 30, no. 11, pp. 1609–1617, Jun. 2014, doi: 10.1093/bioinformatics/btu080.

1 Introduction

During embryogenesis, cells repeatedly divide and dynamically change their position in 3D space, resulting in a highly dynamic environment. A number of studies have tried to acquire quantitative criteria such as chromosome numbers, the synchrony of cell division, and the rate of development, using image segmentation.

2 Approach

Models. Both NSN and NDN are based on 3D U-Net [2]. NSN returns whether a given voxel is a cell or not, whereas NDN learns to distinguish different cell centres. Using this information, full cells (and their creation time) can be identified.

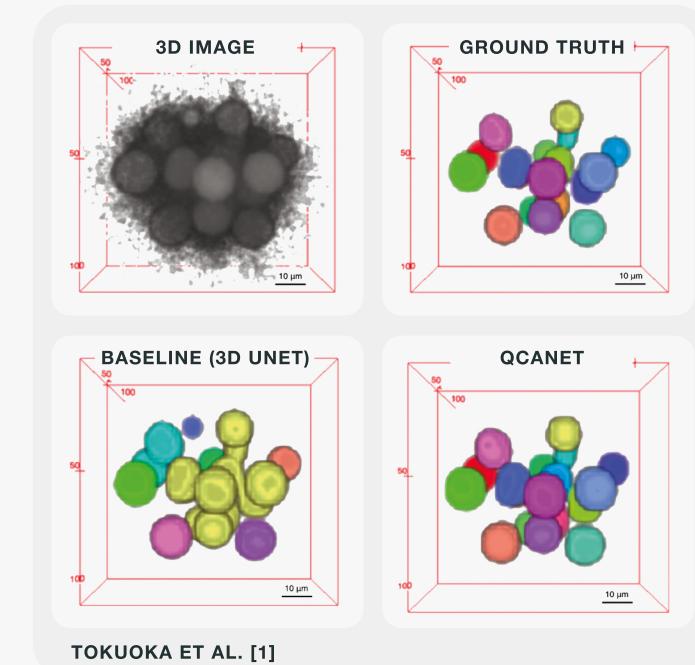
Dataset. Tokuoka et al. [1] prepared a dataset of the early development of 11 mouse embryos with fluorescently identifiable nuclei. The authors manually labelled a ground truth for the training set at 11 time points in 11 mouse embryos.

Pre-Processing. The authors perform mirror padding to fit the patch area within the image, and interpolate along the z-axis by a factor of 2.1875 to remedy warping from the microscope. Lastly, due to the few training samples, each image is flipped on the x and y axes for data augmentation.

Post-Processing. To complete QCANet's cell-instance segmentation, marker-based watershed divides the semantic segmentation region with the centre region of the identified nucleus as a marker.

5 Results & Discussion

QCANet detected nuclei more accurately, whereas 3D U-Net [3] (baseline) and QCANet w/o NDN fused some nuclei to each other, and Mask R-CNN missed several nuclei. Furthermore, it can more easily be generalised to other data, like yeast cells.



Reproduction Comparison. In our reproduction, instance-segmentation NSN seems to work well, but NDN runs in noise issues resulting in false-positives. This could be due to our models being under-trained, as we have to resort to fewer epochs and have skipped the data augmentation step.

3 Setup

The authors train for 150 epochs, reporting that NSN performs better with SGD, and NDN with Adam optimisation.

Evaluation Metrics. IoU (Intersection over Union) is used in image segmentation to evaluate accuracy in terms of false-positive and false-negative rates. To evaluate whether segmentation is accurate over time (i.e. nuclei are not fused), SEG [3] represents the average instance IoU by the sum of the numbers of correct regions. Another metric,

ate individual segmented nuclear regions, and represents the average of the IoU of each instance by the sum of the number of segmentation regions.

$$\text{IoU} = \frac{\text{TP}}{\text{TP} + \text{FP} + \text{FN}}$$

$$\text{MUCov} = \sum_i^N \frac{1}{N_j} \max \text{IoU}(y_i, y_j^*)$$

$$\text{SEG} = \sum_j^N \frac{1}{N_i} \max \text{IoU}(y_i, y_j^*),$$

