PREDICTION OF MULTIPLE 3D TISSUE STRUCTURES BASED ON SINGLE-MARKER IMAGES USING CONVOLUTIONAL NEURAL NETWORKS

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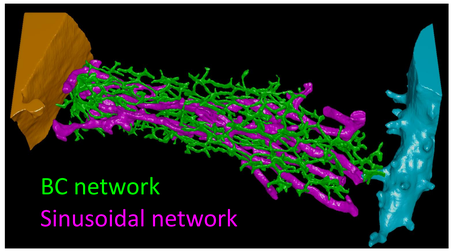
INTRODUCTION

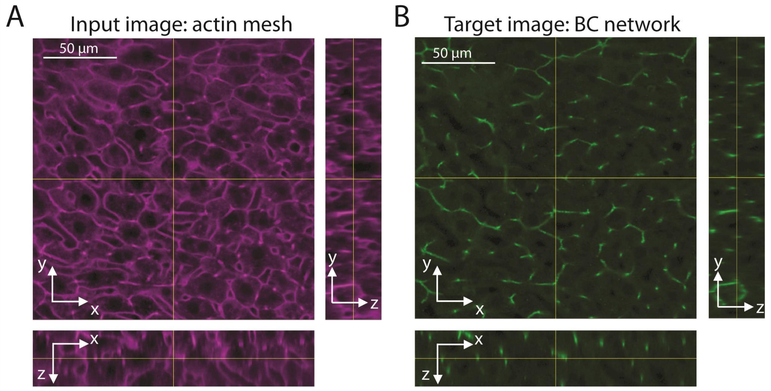
A quantitative understanding of biological tissues requires reconstructing the structure of their different components. Fluorescence microscopy allows visualizing simultaneously several tissue components. However, it can be time consuming and is limited by the number of fluorescent markers that can be used.

We described a toolbox of algorithms based on convolutional neural networks (CNN) for the prediction of 3D tissue structures by learning features embedded within single-marker images. We used it to predict the bile canaliculi (BC) and sinusoidal networks in liver tissue using images of the cortical actin mesh as input.



DATA SET OF 3D TISSUE IMAGES

We used a training set consisting of spatially registered pairs of 3D images of the cortical actin mesh (input image, A) and the BC network (target image, B) for the training, validation and test.

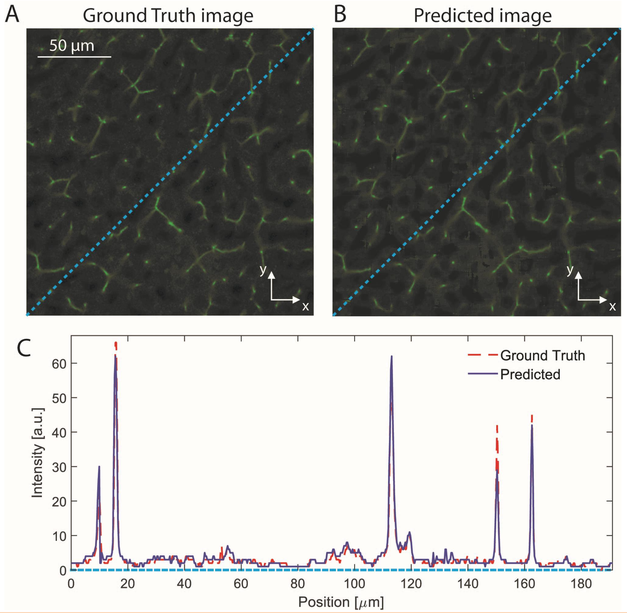


NETWORKS ARCHITECTURES AND TRAINING

We adapted the semantic segmentation approach to predict pixel-wise intensities. Three different network architectures were trained and tested in our data set: 1) A simple CNN (SCNN) consisting of 4 sequentially repeated modules (a convolutional, a batch normalization and a ReLu layers) followed by a final pixel-wise classification layer, 2) a SegNet and 3) a Unet-based with 4 encoder-decoder blocks. For convolution layers, we used 64 filters of size 3x3. To fix the bias due to class imbalance, we used median frequency weighting. Cross-Entropy Loss was used in the classification layer.

PREDICTION OF THE BC NETWORK

SegNet and UNet-based CNNs shows high predictive accuracy as shown by 2D sections of a 3D fluorescent image (ground truth, A) and the corresponding predicted one (B). Intensity values across the dotted line in the images of panels A and B is shown in C.

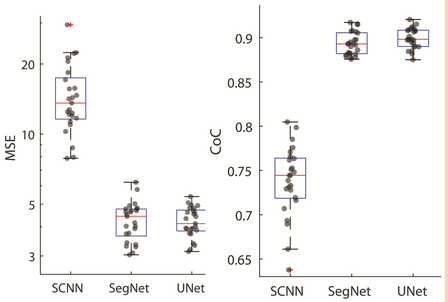


QUANTITATIVE EVALUATION

$$MSE = \frac{\sum_{i\in\Omega}\left(I_i - I_i^*\right)^2}{|\Omega|}$$

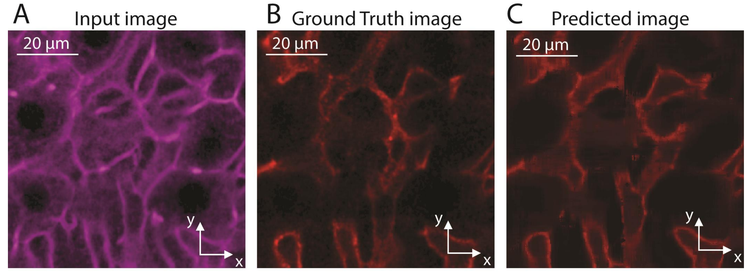
$$CoC = \frac{\sum_{i\in\Omega}\left(I_i - \langle I\rangle\right)\cdot\left(I_i^* - \langle I^*\rangle\right)}{\left(\sum_{i\in\Omega}\left(I_i - \langle I\rangle\right)^2 \cdot \sum_{i\in\Omega}\left(I_i^* - \langle I^*\rangle\right)^2\right)^{1/2}}$$

Ω is the region of interest, I_i and I^*_i are the intensities of the predicted and ground truth images



TRANSFER LEARNING FOR THE PREDICTION OF THE SINUSOIDAL NETWORK

We fine-tuned our pre-trained CNNs (trained for the BC) for the prediction of the sinusoidal network using a small data set of pairs of 3D images of the actin mesh (A) and the extra-cellular matrix lining the sinusoidal network (B). The prediction of the sinusoidal network (C) accurately matches with the image generated experimentally (B) .



CONCLUSION

We present a toolbox of algorithms based on CNNs to generate accurate predictions of 3D tissue structures such as BC and sinusoidal networks, using images of the actin mesh as the sole input.

This approach allows for a complete reconstruction of tissue microarchitecture using a single marker.