IE:5995 Deep Learning Project: Articular Cartilage Segmentation

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Abstract

The gold standard for evaluating articular cartilage tissue relies heavily on human-eye observations. However, this method is not only subjective but also time consuming. In this project, we propose an automated system for evaluating microscopic cartilage tissue using state-of-art deep learning methods. Our approach consists of first segmenting stained cartilage tissue using the fully convolutional neural network, U-Net [1]. We supplement this by developing a method for segmenting the cells within the would-be segmented region. We compare two methods in this regard: (1) U-Net and (2) a Deep Convolutional Aware Network (DCAN) [2]. The resulting binary masks from this step is then used as part of a post processing technique for counting articular cartilage cells. We hope our method will alleviate histology based approaches for the evaluation of the articular cartilage.

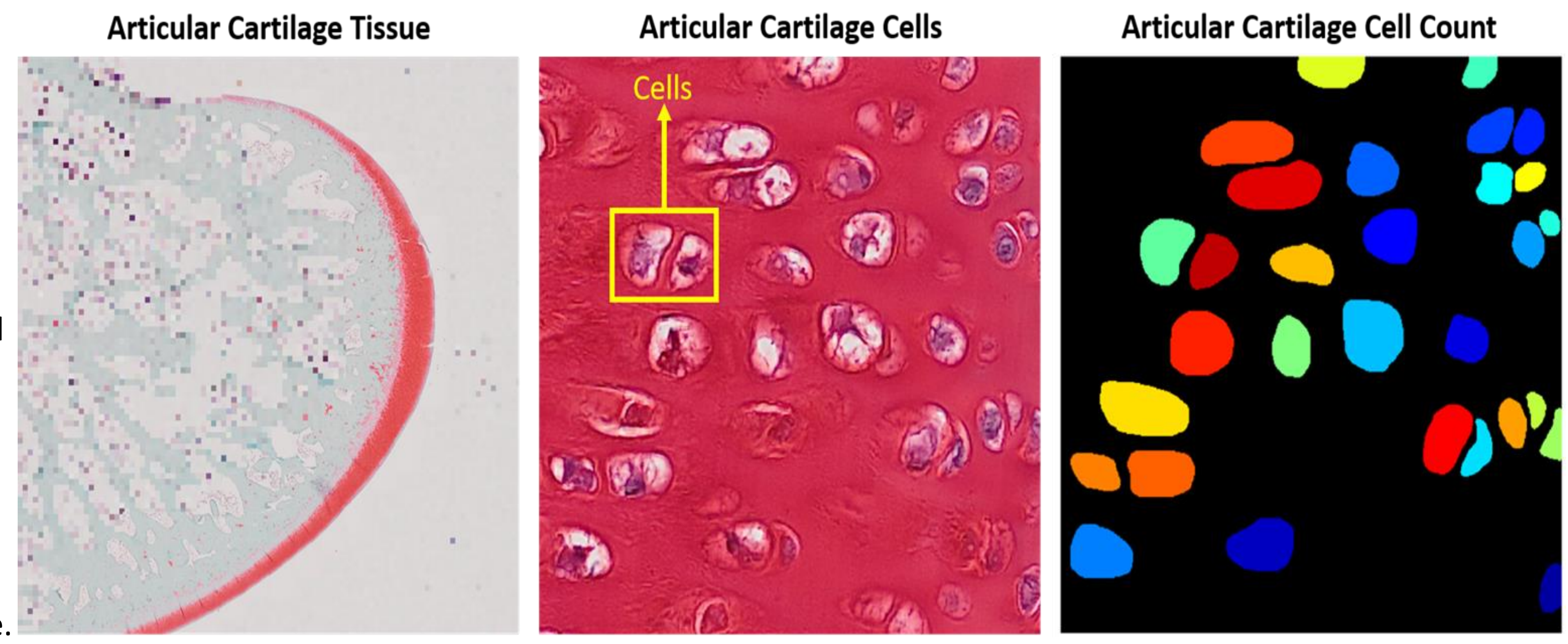


Figure 1. Overview of the main goals of this project. First, a method is required for segmenting the red stained articular cartilage tissue. Within this segmented area, articular cartilage cells are segmented. The resulting binary mask of the segmented cells are then counted. This cell count provides valuable insight in the health of articular cartilage tissue. An automated version of this process will reduce the time and improve the accuracy over human eye cell counting methods.

Setting Up the Architecture

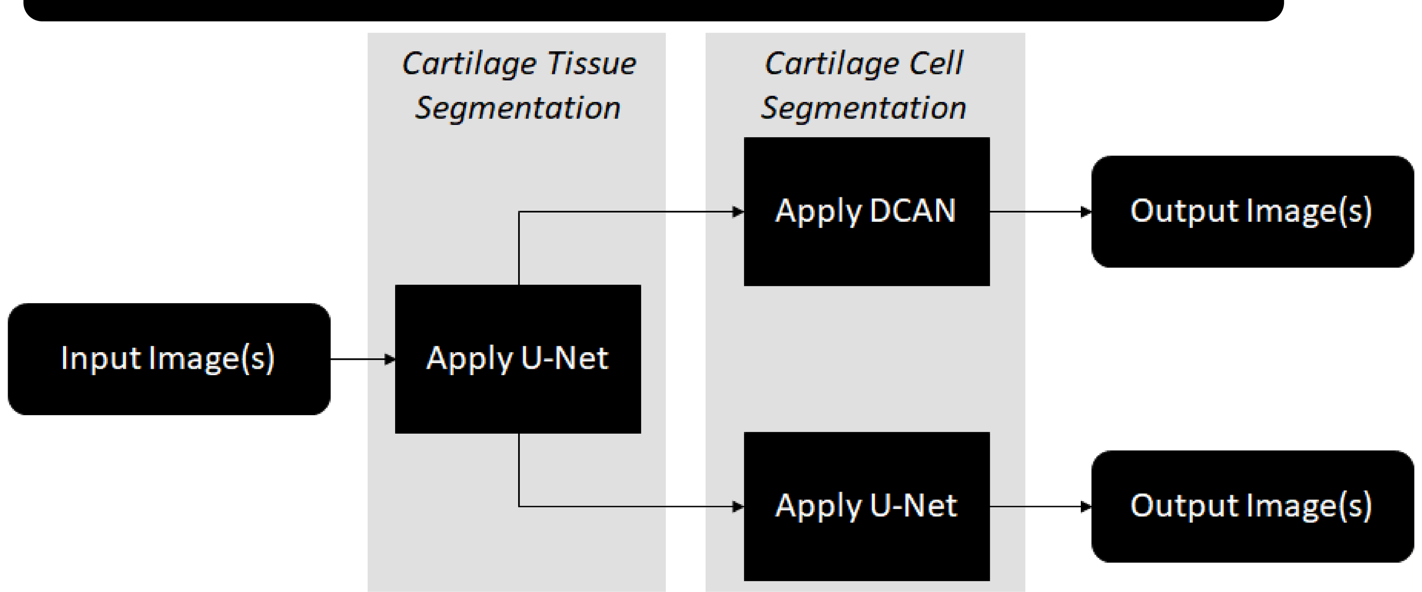


Figure 2. Overview of the processing pipeline developed for instance segmentation of articular cartilage cells. A modified U-Net neural network is trained to first segment cartilage tissue. Two different neural networks, U-Net and DCAN, were compared in order to determine the optimal cell instance segmentation method.

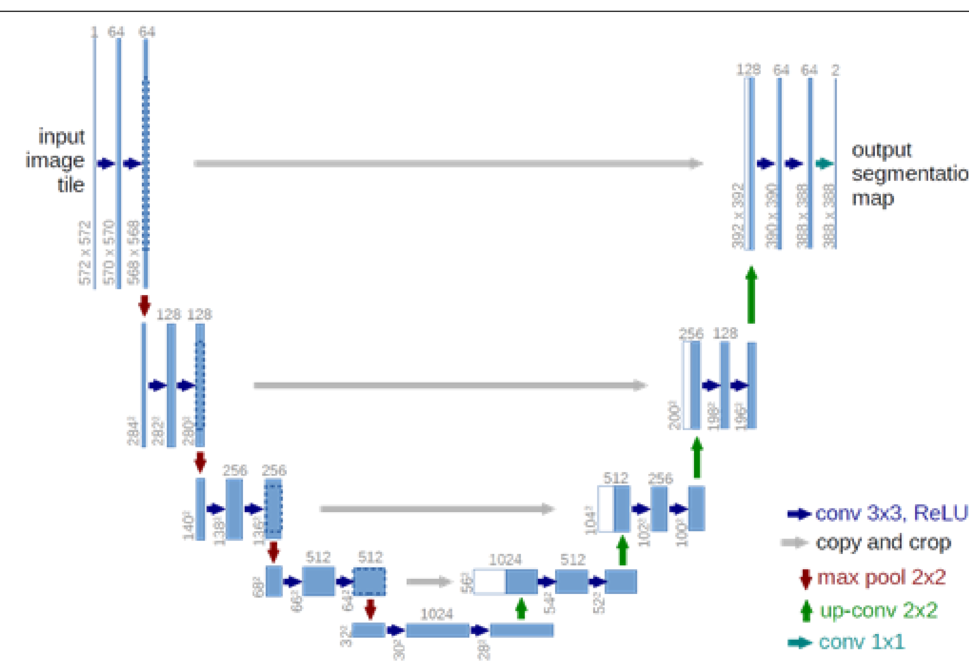
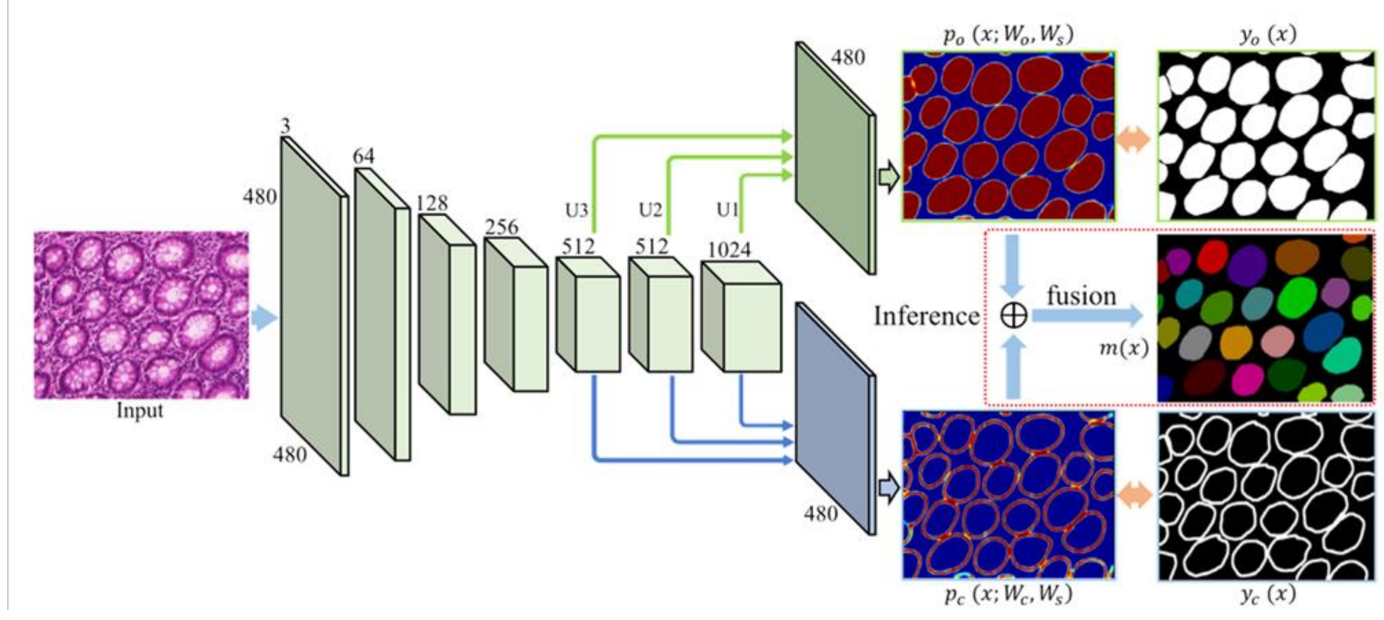


Figure 3. The architecture of the neural network, U-Net, developed by Olaf et al [1]. This network is composed of a fully convolutional neural network. More specifically, an encoding path to capture context and a decoding path that enables precise localization.

Figure 4. Overview of the Deep Contour Aware Network (DCAN) developed by Chen *et al* [2]. This neural network has found success in identifying individual cells in clusters by incorporating both object and contour masks. DCAN uses end-to-end fully convolutional network to deal with variation in input images. In addition, auxiliary supervision is employed to help the network deal with vanishing gradients.



Tissue Segmentation

The original U-Net architecture is retained with a several modifications. Batch normalization layer is added after convolution layer. Padding is applied to keep the image size through each convolution.

Table 1 describes the data augmentation approaches used. These include linear transformation, brightness transformation, elastic deformation as well as hue adjustment . We used a loss function combination of dice loss and cross binary entropy. Table 2 lists how images were partitioned between training, validation and testing. This function is minimized by an Adam optimizer. The final segmentation result is evaluated using the dice metric.

Table 1. Summary of the 7 various data augmentation methods used for both segmentation tasks. Blurring was not used for tissue segmentation.

Augmentation Type	Change
Hue Adjustment	Adjust image hue in range (0.5,1.0)
Brightness Adjustment	Adjust brightness in (0.9,1.0)
Elastic Deformation	Scale images in x and y direction
Image Gaussian Blurring	Convolve image with gaussian function
Image Reflection	Flip image vertically/horizontally
Image Rotation	Rotate image (0,90) degrees

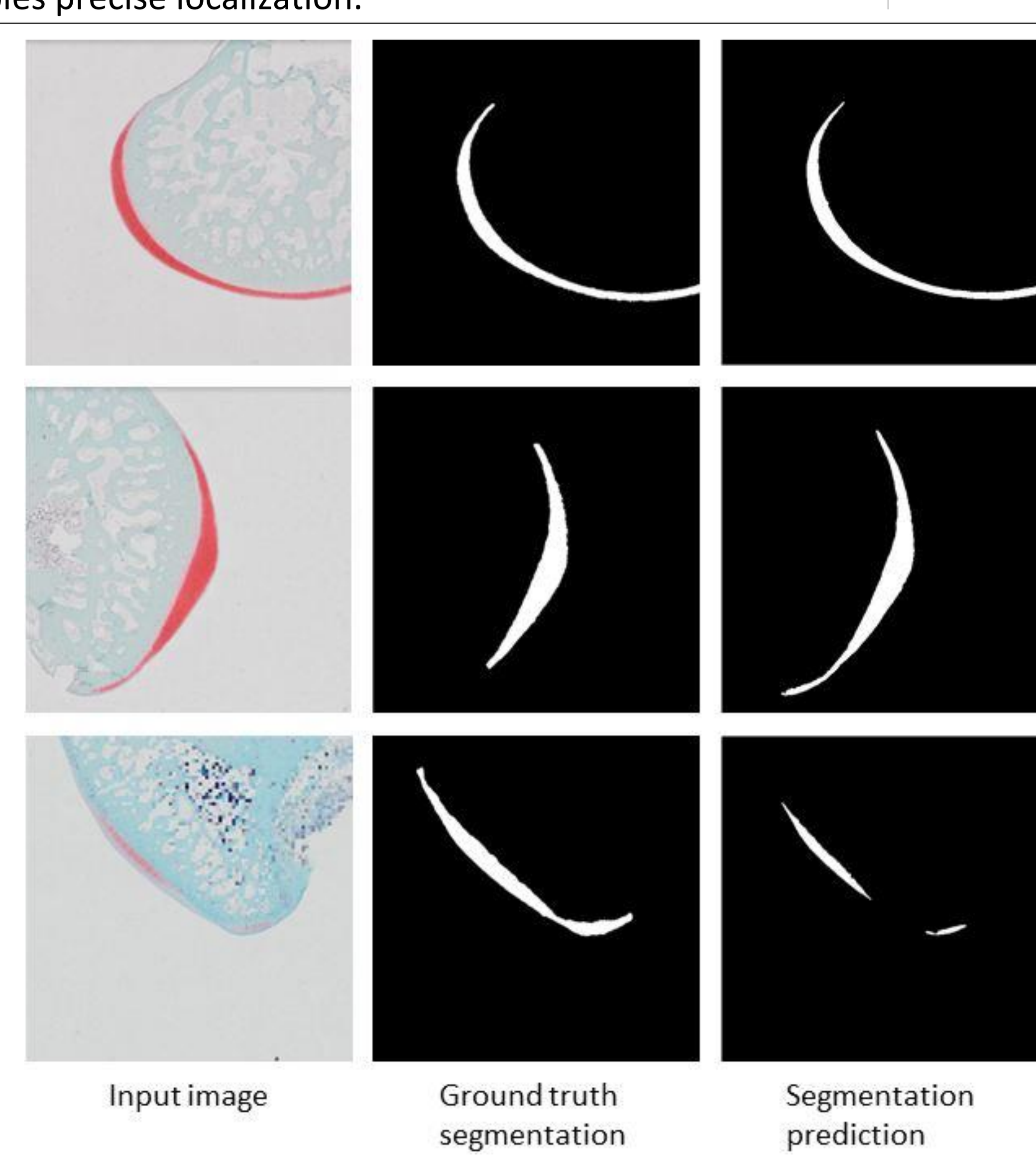


Figure 5. Examples of input images, ground truth segmented images, and predicted segmentations output from the implemented U-Net. The first two rows correspond to successful segmentation predictions. The last row corresponds to a failed segmented prediction which may be attributed to the lack of the red stain in the input image. An average dice coefficient of 0.9032 is achieved. The lowest value of 0.5285 is obtained from the image in the 3rd row in the figure 5. All other (9 images) test predictions had values above 0.9.

Table 2. The number of images input into the processing pipeline for articular cartilage tissue segmentation. A variety of healthy and injurious cartilage cross sectional images were used. More unhealthy images were used as injurious cartilage tissue does not stain as well as healthy. In addition, the average dice coefficient computed for the test images is also given.

	Training Images	Validation Images	Test Images
Count	35	10	10
Dice Coef.	-	-	0.9032

Cell Segmentation

In this task, two methods are applied and compared:

1. U-Net applied with loss weight map to account for class imbalance as well as improving its ability to differentiate adjacent cells.
2. DCAN: Two ground truth masks are used. One for the object (whole cell) and another of the object's contour (edges). The loss function of both are summed.

Table 3. The number of original images input into the processing pipeline. A variety of images were used to reflect the different tissue boundaries and degree of stain. Also shown are the average dice coefficient and F1 scores computed for the test images of both the U-Net and DCAN.

		Training Images	Validation Images	Test Images
	Count	100	20	20
U-Net	Dice Coef.	-	-	0.8846
	F1 Score	-	-	0.8469
DCAN	Dice Coef.	-	-	0.6483
	F1 Score	-	-	0.6749

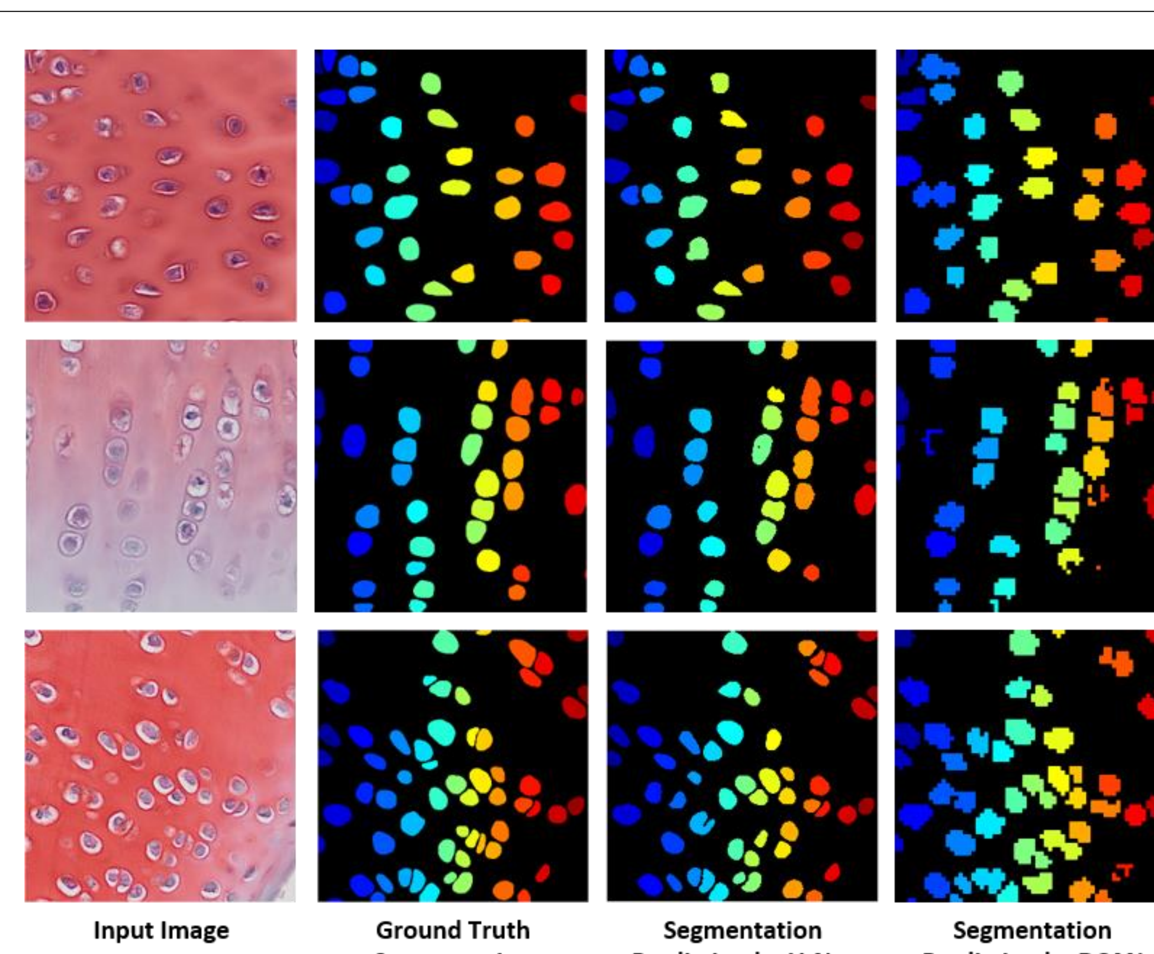


Figure 6. Examples of some test images, their ground truth segmentation masks, as well as the predicted segmentation from U-Net and DCAN. U-Net achieves an average dice coefficient of 0.8846 and a F1 score of 0.8469. Its prediction on some cells with certain appearance is poor and results in low metrics' value (lowest 0.4898 for F1 and 0.4809 for dice, respectively). The segmentation results for DCAN were worse, yielding an average dice loss and F1 scores of 0.6483 and 0.6749, respectively. Maximum and minimum dice loss values were 0.8761 and 0.0772. Similar metric were obtained for the F1 score: 0.9054 and 0.0645. It should be noted that auxiliary supervision was omitted in our implementation of DCAN.

Conclusions

We have shown our method for instance segmentation of articular cartilage cells using a deep learning approach. Using U-Net is sufficient for segmenting both articular cartilage cells and tissues as it yielded high dice coefficient and F1 scores. However, we obtained worse segmentation results from the DCAN model. These results may be attributed to how we combined the results from the auxiliary supervision as well as omitting regularization in the loss function. We anticipate by optimizing these components as well as adding more training images, we may improve the performance of the DCAN model.

Future Work

A number of future works remain to be done. These include the following:

- Improve the DCAN neural network implementation.
- Increase the number of training images used to train the neural networks in order to improve the performance of the segmentations.
- Apply DCAN and U-Net on the entire resulting masks from the articular cartilage tissue segmentation step.
- Incorporate a method for counting the number of cells from the final segmentation task into the processing pipeline.

Acknowledgements

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References

[1] Ronneberger, Olaf *et al*. "U-net: Convolutional networks for biomedical image segmentation." International Conference on Medical image computing and computer-assisted intervention. Springer, Cham, 2015.

[2] Chen, Hao *et al*. "DCAN: Deep contour-aware networks for object instance segmentation from histology images," Medical Image Analysis, vol. 36, pp. 135-146, 2017.