

2D Cell Segmentation in Differential Interference Contrast Microscopy with Convolutional Neural Networks

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Keywords:	Deep Learning, Instance Segmentation, Cell Imaging

1 Task Description

Differential Interference Contrast (DIC) microscopy is a technique to microscope cells. It doesn't require the staining of specimen which makes it faster, avoids dealing with reagents and doesn't damage or even kill the cells. This comes with the cost of not having a very clear visual separation of fore- and background, which is the case for fluorescence microscopy. Not having such a clear visual separation, makes it more complicated to segment cell nuclei and bodies using traditional Computer Vision techniques. Existing methods addressing this problem exist, but struggle to perform.

The goal of this thesis is to train and evaluate a Deep Convolutional Neural Network to segment body and nucleus instances in DIC images. An application should make these models available for non machine learning experts.

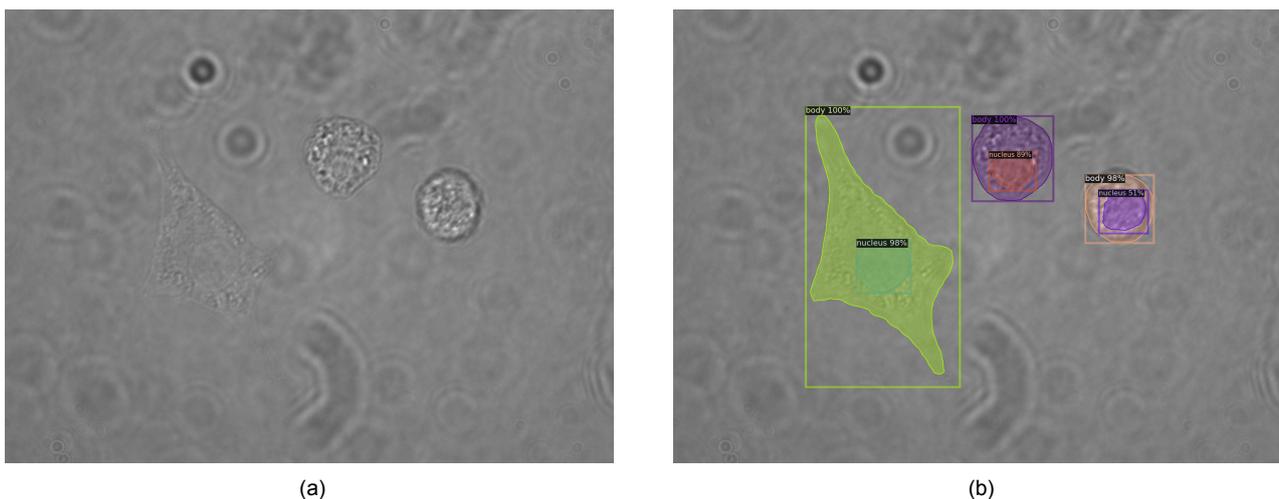


Figure 1: Example DIC images (a) with the segmentation results from our thesis (b)

2 Results

We present a modern web application to analyze batches of DIC images. The application features live analysis updates, clear batch overview statistics, fine-grained image analysis results and rich result export functionalities (figure 2).

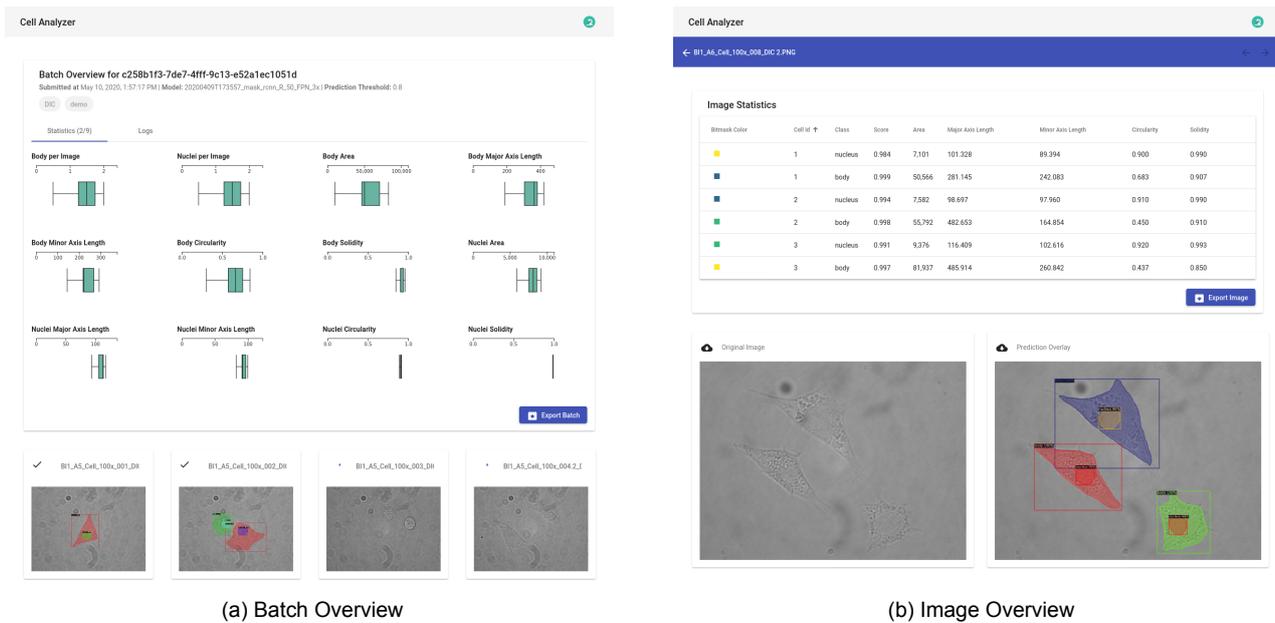


Figure 2: Cell Analyzer batch overview page (a) and detailed image overview (b)

Our trained models, powering the application, produce high-quality instance segmentation results for cell bodies and nuclei.

They achieve an average precision (with an Intersection over Union of 50%) of ~ 93.800 and ~ 85.747 on the *cells0g* dataset from the HSLU Space Biology Research Group for cell bodies and nuclei, respectively. A model using the same configuration, but trained on the *DIC-C2DH-HeLa* dataset ranks in top places in the Cell Tracking Challenge [1] for segmentation.

3 Solution Concept

The web application is powered by a modern Python¹ and Angular stack. The real-time NoSQL database *rethinkdb* persists the analysis results and together with WebSockets produce live events for the web front-end.

Several Deep Convolutional Neural Networks have been evaluated and experimented with. The models were implemented with *detectron2* [2] and are based on the *Mask R-CNN* framework [3]. They use a ResNet-50-FPN backbone and were transfer learned from weights based on the 2017 COCO dataset heavily relying on data augmentation.

¹REST and WebSocket API with *fastapi*

4 Challenges

The provided DIC images were unlabeled and therefore needed to be annotated for training, which is not trivial for non-microbiology experts. We implemented a hybrid method of hand-made and semi-automated annotation techniques to label the images.

Furthermore, creating and optimizing high-quality instance segmentation models is challenging. We've carefully chosen metrics and conditions for the training and evaluation of the models.

The application required an enjoyable user-interface that is easily accessible by non machine learning experts. To achieve this we drafted mock-ups reviewed by our future users and refined them to enable the best possible user experience.

5 Outlook

The Cell Analyzer application allows to reliably segment cell bodies and nuclei on the *cells0g* DIC images and also generalizes to similar datasets, such as *DIC-C2DH-HeLa*. It can be improved in terms of stability and scalability, by distributing the analysis to multiple GPU workers.

We highly recommend to further investigate the potential of our models, to increase their performance even more and base new models on our observations. Adding more DIC datasets to the training and validation will certainly help to further improve and generalize the models. We also suggest to use our models as a basis to compete in the Cell Tracking Challenge.

References

- [1] Cell tracking challenge. <http://celltrackingchallenge.net>, May 2020.
- [2] Yuxin Wu, Alexander Kirillov, Francisco Massa, Wan-Yen Lo, and Ross Girshick. Detectron2. <https://github.com/facebookresearch/detectron2>, 2019.
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