

Introduction

The quantification of the mechanical forces exerted by biological cells on their substrate is fundamental to the comprehension of cell behaviour. Traditionally, fluorescent markers are employed for the identification of cells and the nanopillars they deform [1][2]. However, these markers can introduce complexity and are often unsuitable for a multitude of applications. The objective of this project is to investigate the potential of deep learning models, including convolutional neural networks, for accurately segmenting cell locations in brightfield images, thereby facilitating a more widespread application. This project focuses on implementing various deep learning-based image segmentation models and systematically comparing their performance. The objective is to evaluate the effectiveness of different models in segmenting images, aiming to achieve high precision while keeping computational costs low. Through detailed benchmarking, we aim to identify models that balance simplicity and performance, potentially matching or surpassing the capabilities of more complex, generalized models.

Key points

- The dataset consists of **12,793 brightfield images** captured at different focal points and **1,163 corresponding binary masks**.
- A **baseline U-net model** was the starting point followed by **hyperparameter tuning** to find the best model.
- **Class imbalance** is present where cell only represents 10-20% of the full picture.

U-net architecture

The structure consists of an encoder, that progressively reduces dimensions while extracting feature representations, and a decoder that reconstructs the spatial resolution while concatenating features from corresponding levels in the encoder.

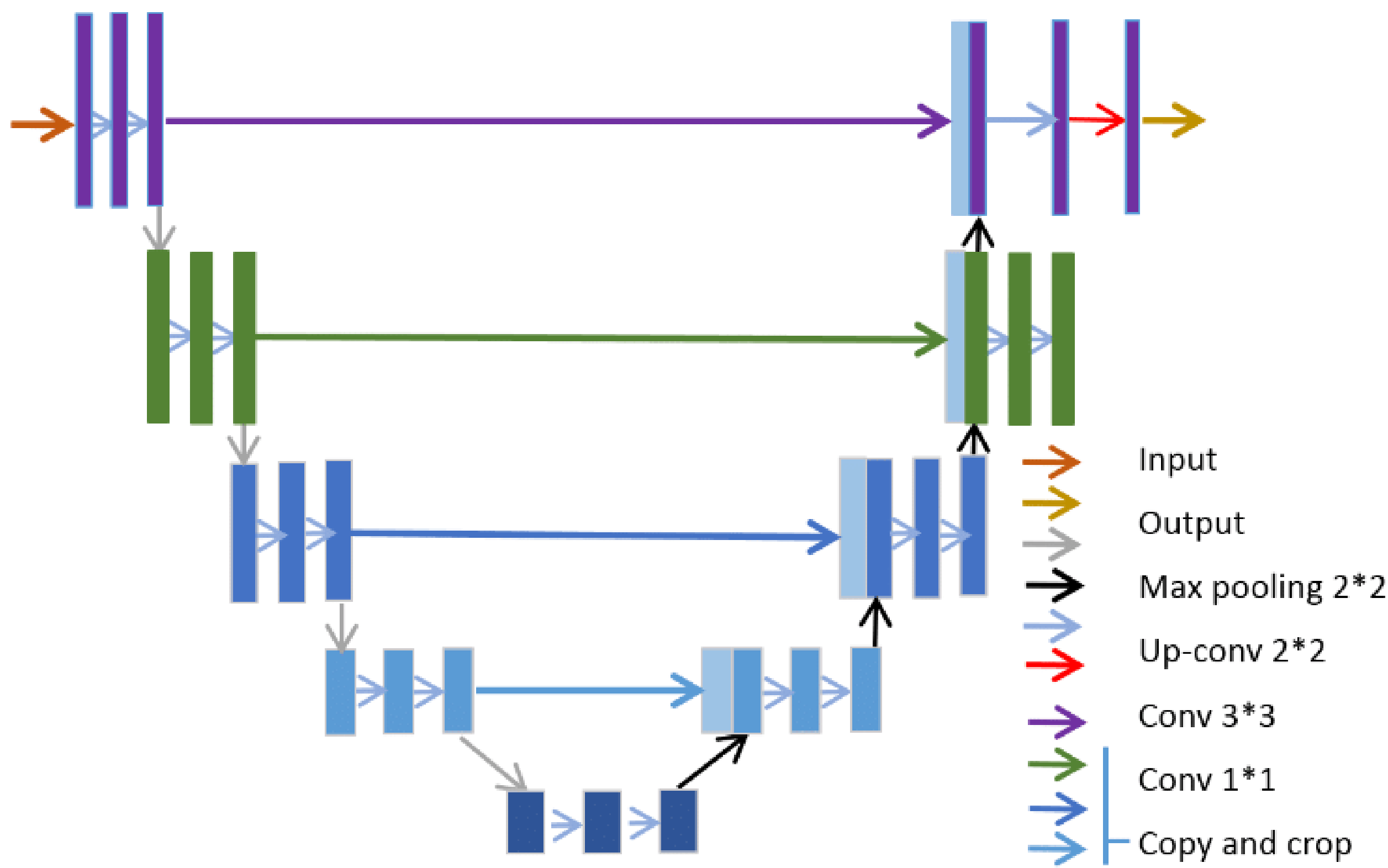


Figure 1: Model architecture representation.

Data visualization

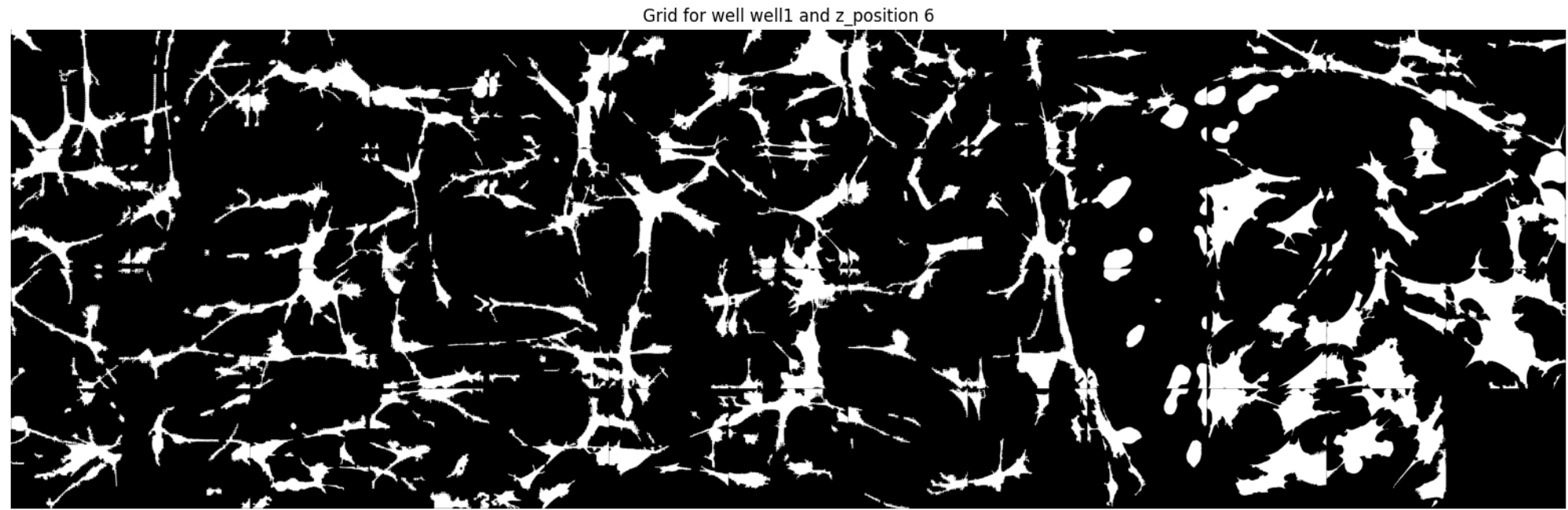


Figure 2: Mask of the brightfield grid for well 1 with the 6th focal point.

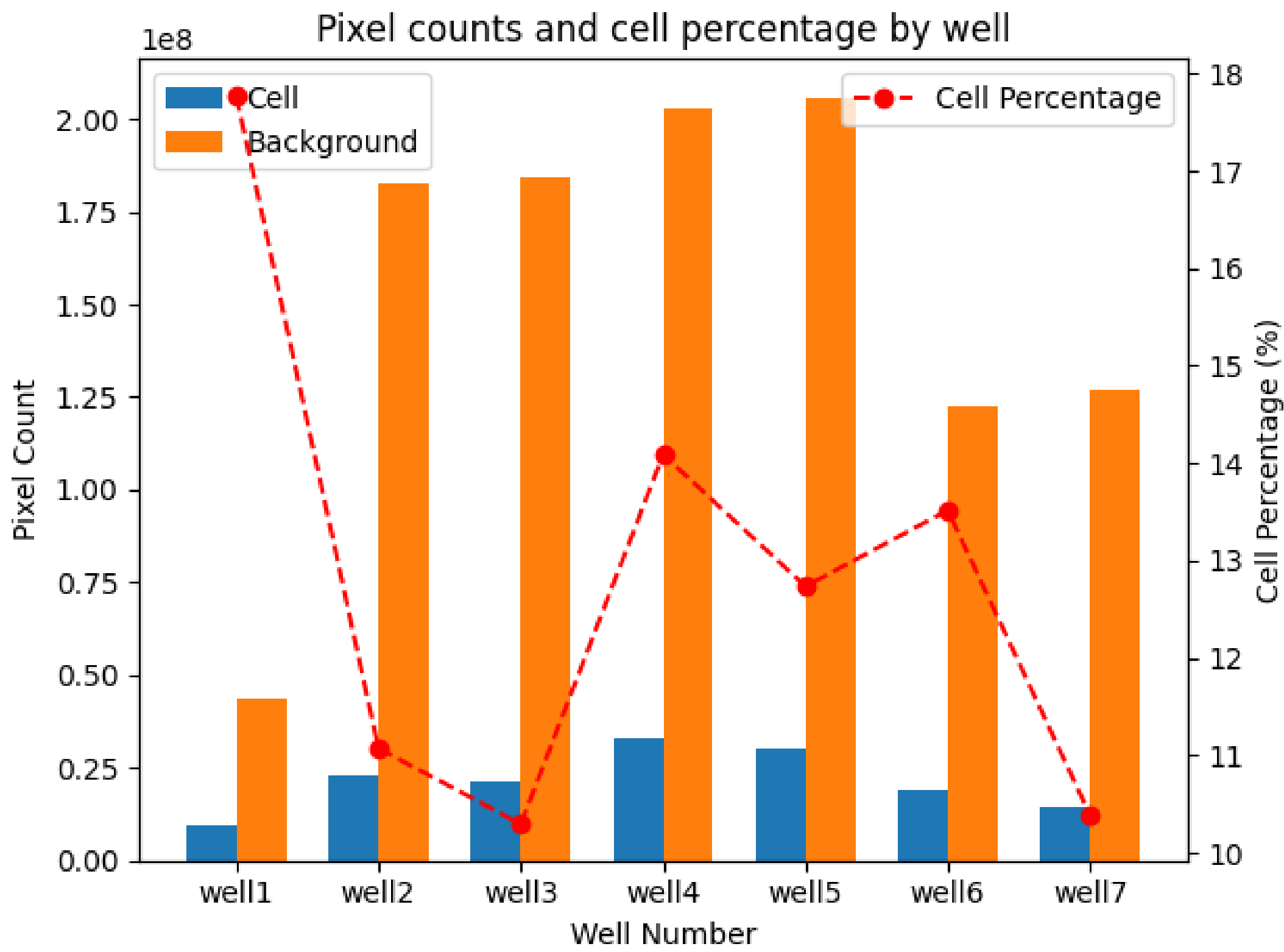


Figure 3: Class distribution showing the imbalance, where cells account for only 10-20% of the full picture.

Both images effectively highlight the significant class imbalance in the dataset. The background occupies a dominant portion of the image, while the cell body accounts for only 10-20% of all pixels across all wells.

Model performance

The results for IoU and Dice are better for Model 1, although the accuracy is 5% better for Model 2.

Table 1: Performance metrics (IoU, Dice, and Accuracy as Rand Index) achieved by all models tested, starting from the Baseline model and incorporating various hyperparameter tuning experiments.

Model	IoU	Dice	Accuracy
Baseline	0.4287	0.5772	0.8519
1	0.5055	0.6669	0.8225
2	0.4893	0.6399	0.8670
3	0.1663	0.2770	0.6791
4	0.4690	0.6215	0.8568
5	0.4224	0.5788	0.8287
6	0.4230	0.5746	0.8325
7	0.4631	0.6158	0.8463
8	0.4456	0.5972	0.8290
9	0.4141	0.5591	0.8498
10	0.4963	0.6433	0.8646

Visualization of Performance

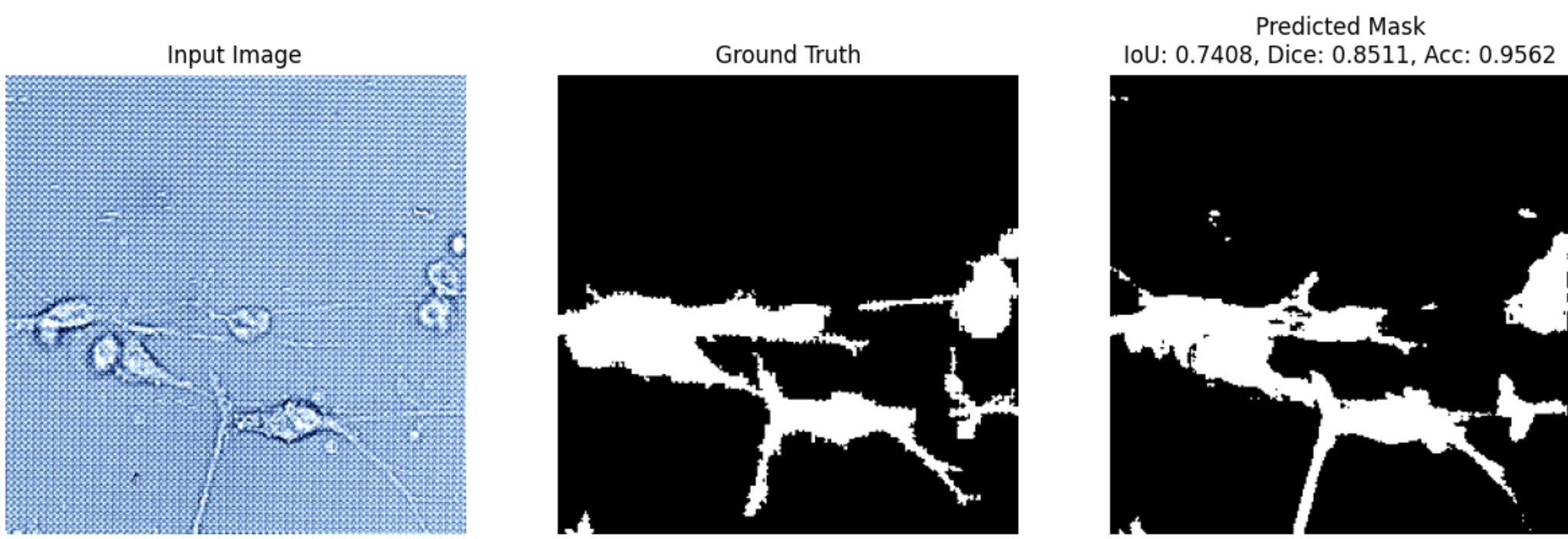


Figure 4: Comparison of Bright Field Picture, Ground Truth Mask, and Predicted Mask of Model 1 for an example sample

The prediction of the model show promising results. Some background noise, that can probably be assimilated as air bubbles, is still visible, but the model was able to effectively segment the cells body and to handle the dataset's class imbalance.

Performance metrics plots



Figure 5: Validation loss plot for Model 1. The green-dotted line indicates the best results (epoch 38).

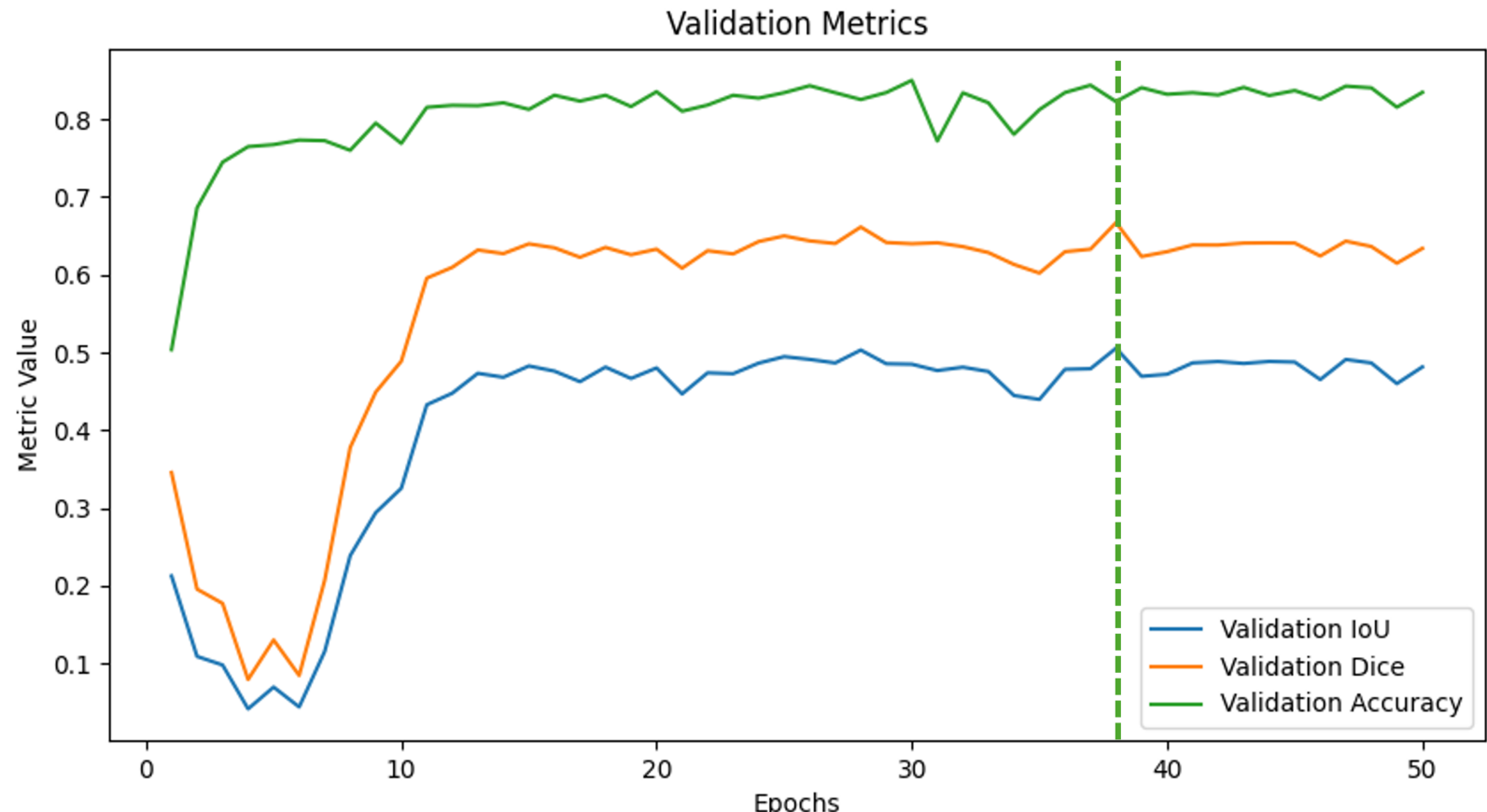


Figure 6: Metrics plot showing IoU, Dice, and accuracy for Model 1 up to epoch 50.

After a slight increase during the first epochs, the evaluation metrics converge and stabilize around epoch 15, indicating successful model training and convergence. The observed fluctuations may be attributed to inherent randomness in optimization process or the impact of batch-level noise during training.

Acknowledgements

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References

- [1] John L Tan, Joe Tien, Dana M Pirone, Darren S Gray, Ki-ran Bhadriraju, and Christopher S Chen, "Cells lying on a bed of microneedles: An approach to isolate mechanical force," Tech. Rep.
- [2] Olivia Du Roure, Alexandre Saez, Axel Buguin, Robert H Austin, Philippe Chavrier, Pascal Silberzan, and Benoît Ladoux, "Force mapping in epithelial cell migration," Tech. Rep., 2005