

Application of U-Net architecture on a cell segmentation problem of nucleus identification

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Abstract—Cell segmentation is a fundamental task in image analysis, which aims to identify and delineate cells and their components in microscopic images. It is a challenging problem due to variations in cell morphology, staining, and imaging conditions. In recent years, deep learning-based methods have shown promising results for cell segmentation tasks. U-Net is a widely used deep learning architecture that has demonstrated excellent performance in various biomedical image segmentation problems.

In this paper, we discuss the application of U-Net for cell segmentation in microscopic images. We first provide a brief overview of U-Net's architecture and its characteristics. We then describe the pre-processing steps used to prepare the data for the training process and discuss the evaluation metrics used to quantify the performance of the segmentation model. For further work we will explore possibilities for new activation functions to improve performance of the U-Net architecture for this task.

Index Terms—Index Terms—Short-Term Load Forecasting, Recurrent Neural Network, Deep Learning, Residential Load Forecasting

I. INTRODUCTION

Cell segmentation is a crucial task in biomedical image analysis, which involves identifying and delineating cells and their components in microscopic images. It is a fundamental step in various applications, including cell counting, cell tracking, and disease diagnosis. Accurate cell segmentation is challenging due to variations in cell morphology, staining, and imaging conditions. Traditional methods for cell segmentation rely on handcrafted features and rule-based algorithms, which often require extensive human intervention and are prone to errors.

In recent years, deep learning-based methods have shown significant progress in various biomedical image segmentation tasks, including cell segmentation. Deep learning-based methods can automatically learn features from data, making them more robust and accurate than traditional methods. Among deep learning architectures, U-Net has gained considerable attention for its outstanding performance in biomedical image segmentation tasks, including cell segmentation.

The U-Net architecture is a convolutional neural network (CNN) that uses a contracting path and an expanding path to capture the spatial information at different scales. The

contracting path is composed of convolutional and pooling layers, which extract high-level features from the input image. The expanding path uses upsampling and concatenation operations to recover the spatial information lost during the contracting path. The skip connections between the contracting and expanding paths enable the model to learn detailed spatial information while maintaining the context of the input image.

In this paper, we show the implementation of U-Net architecture for the cell segmentation task of identifying the nucleus, including the pre-processing steps, training process, evaluation metrics, and the current state-of-the-art results. We also discuss the challenges and future directions for improving cell segmentation using newly proposed activation functions.

II. LITERATURE SURVEY

We looked at the following papers and resources for our literature survey of cell segmentation task and computer vision architectures - 1. "Deep learning for nuclei segmentation: A review" by Bhavika Tekwani et al. (2020): This review paper provides an overview of recent deep learning-based methods for nuclei segmentation. The paper discusses various approaches, including U-Net, Mask R-CNN, and Watershed-based methods. 2. "U-Net: Convolutional Networks for Biomedical Image Segmentation" by Ronneberger et al. (2015). This was the original paper that introduced the U-Net architecture for Biomedical Image Segmentation. 3. "2018 Data Science Bowl" which is a dataset for the task of finding the nuclei in divergent images to advance medical discovery. 4. "Comparison of different convolutional neural network activation functions and methods for building ensembles" by Loris Nanni et al. This paper proposed new activation functions for convolution neural networks which could improve the performance of the U-Net architecture.

III. IMPLEMENTATION

For the report, we have implemented the U-Net architecture on the problem of finding the nuclei of cells from the dataset "2018 Data Science Bowl"

A. U - Net

U-Net gets its name from its U-shaped architecture, which consists of a contracting path and an expanding path.

The contracting path of the U-Net consists of several convolutional and pooling layers, which extract high-level features from the input image. The purpose of this path is to reduce the spatial dimensions of the input image while increasing the number of feature channels. This helps capture the global context of the image and the high-level features that are necessary for accurate segmentation.

At the end of the contracting path, the feature map is compressed into a bottleneck layer. The bottleneck layer acts as a bridge between the contracting path and the expanding path. It has a higher number of channels than the previous layers, which helps maintain the spatial resolution of the image and capture more detailed features.

The expanding path of the U-Net consists of several deconvolutional and upsampling layers, which upsample the feature maps and restore the spatial dimensions of the image. The deconvolutional layers perform a convolution operation, which increases the spatial dimensions of the feature map while decreasing the number of feature channels. The upsampling layers perform a simple operation, such as nearest-neighbor interpolation or bilinear interpolation, to restore the original spatial dimensions of the image.

The expanding path also uses skip connections to combine the high-resolution feature maps from the contracting path with the upsampled feature maps from the expanding path. These skip connections help the network to preserve the spatial information of the input image and capture fine details, such as edges and boundaries.

Finally, the output of the U-Net is obtained using a softmax layer, which produces a probability map for each pixel in the input image. The probability map indicates the likelihood of each pixel belonging to a specific class, such as the cell nucleus or background.

preprocessing, we perform the resizing of training and testing images and masks.

Then we proceed to train our U-Net model created from our class on our selected dataset.

IV. RESULTS

We were able to achieve an accuracy of 92% from our implementation.

V. CONCLUSION

From our implementation of the U-Net architecture, we were able to achieve a reasonably high accuracy for the task of finding nuclei from the dataset "2018 Data Science Bowl". Further we plan to implement newly proposed activation functions to improve performance of the U-Net architecture for this task, as described in the paper "Comparison of different convolutional neural network activation functions and methods for building ensembles" (2021)

REFERENCES

- [1] "Deep learning for nuclei segmentation: A review" by Bhavika Tekwani et al. (2020) :
- [2] "U-Net: Convolutional Networks for Biomedical Image Segmentation" by Ronneberger et al. (2015) <https://arxiv.org/abs/1505.04597>
- [3] "2018 Data Science Bowl" <https://www.kaggle.com/c/data-science-bowl-2018>
- [4] "Comparison of different convolutional neural network activation functions and methods for building ensembles" by Loris Nanni et al. (2021) <https://arxiv.org/abs/2103.15898>

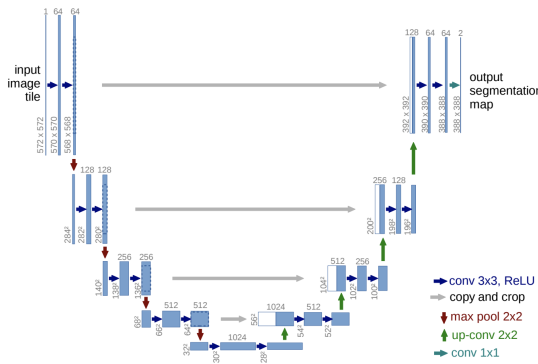


Fig. 1. U-Net architecture (example for 32x32 pixels)

B. Code Implementation

We firstly import the libraries and define our UNet class. The images are firstly imported from the dataset. Then for