School of Engineering and Applied Science (SEAS), Ahmedabad University

ECE501: Digital Image Processing

Group Name: NetraByte

Project: 11. Automated Object Counting

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I. What has been done so far (Progress)

- This week, we quantitatively compared the ground-truth masks (previously converted from JSON to images) and the segmentation results we generated using the adaptive thresholding method.
- We calculated evaluation metrics to quantify the accuracy of the segmentation. The process involved:
  1. Loading the ground truth TIF mask and the predicted segmentation mask.
  2. Binarization of both images, so that their pixel value ranges are identical: foreground = 1, background = 0.
  3. Computing the Confusion Matrix and different performance metrics, which include:
     - Accuracy: It checks for the overall correctness of our predicted mask.
     - Precision: It checks for the fraction of correctly predicted cell pixels among all predicted cells.
  4. Visualizing the ground truth mask and the predicted mask side by side for qualitative assessment.
- We further classified the dataset by cell type for easier analysis:
  - Extracted and copied images corresponding to a given cell type(such as BV2,SkBr3) from the totally converted TIF dataset and placed them in separate folders.
  - This step in organization helps in cell-type–specific evaluation and training of future models.

Results

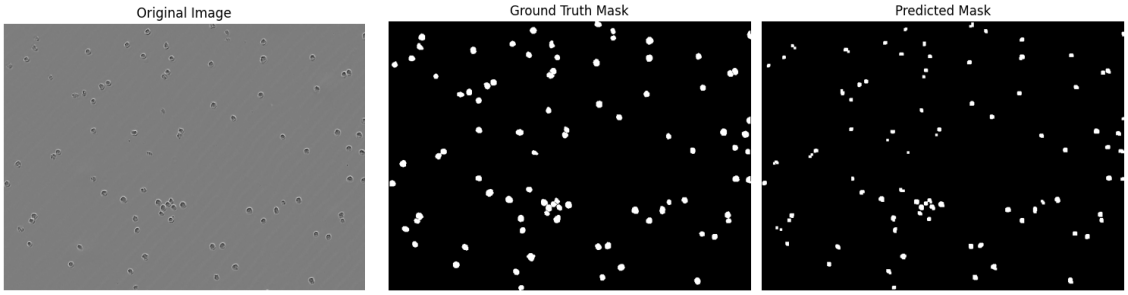

Figure 1: First Image is the original image for the dataset of BV2 and the second image is the Ground Truth for the original image and the third image is the Predicted output for theoriginal image

Performance Metric	**Value (%)**
Accuracy	98.60
Precision	97.20
Recall	53.23

Table 1: Performance Metrics for Fig 1

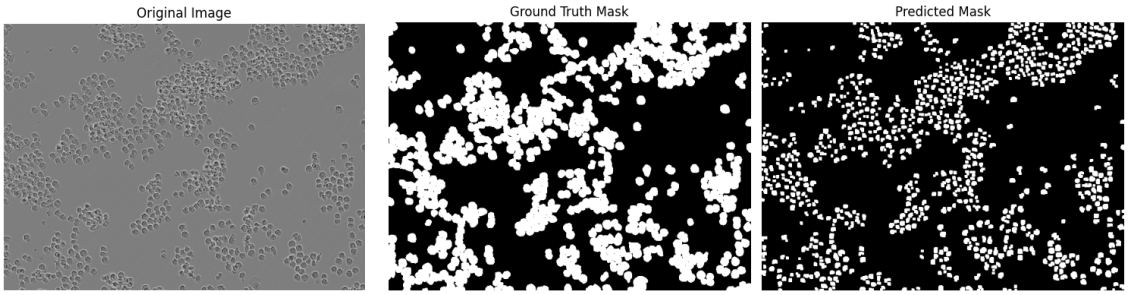

Figure 2: First Image is the original image for the dataset of BV2 and the second image is the Ground Truth for the original image and the third image is the Predicted output for theoriginal image

Performance Metric	**Value (%)**
Accuracy	78.39
Precision	87.27
Recall	42.52

Table 2: Performance Metrics for Fig 2

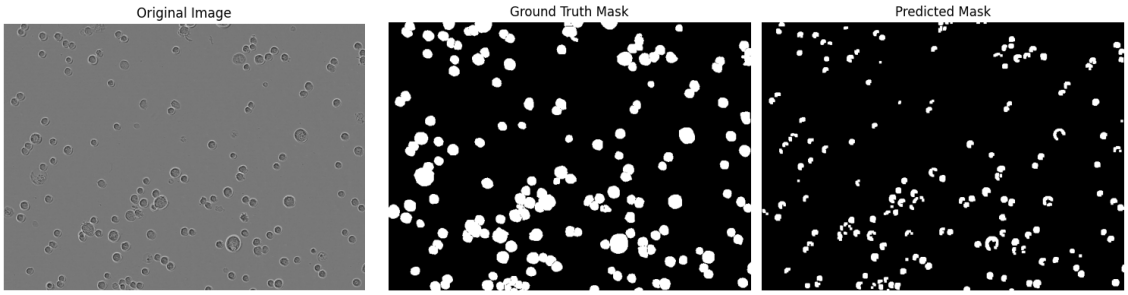

Figure 3: First Image is the original image for the dataset of SkBr3 and the second image is the Ground Truth for the original image and the third image is the Predicted output for the original image

Performance Metric	**Value (%)**
Accuracy	90.62
Precision	99.88
Recall	34.68

Table 3: Performance Metrics for Fig 3

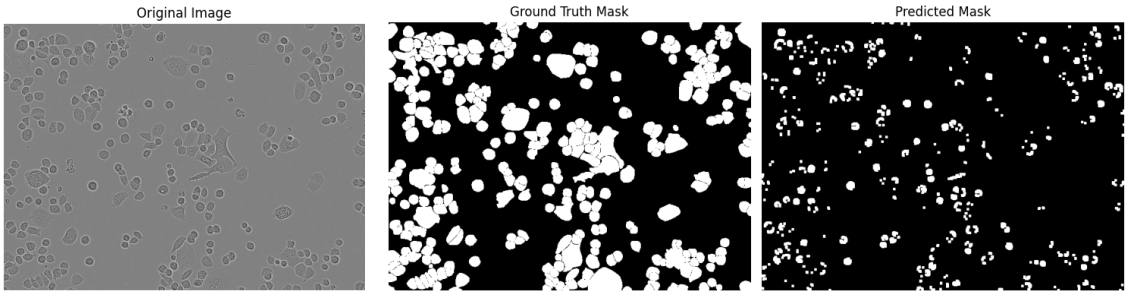

Figure 4: First Image is the original image for the dataset of SkBr3 and the second image is the Ground Truth for the original image and the third image is the Predicted output for the original image

Performance Metric	**Value (%)**
Accuracy	75.81
Precision	99.88
Recall	21.03

Table 4: Performance Metrics for Fig 4

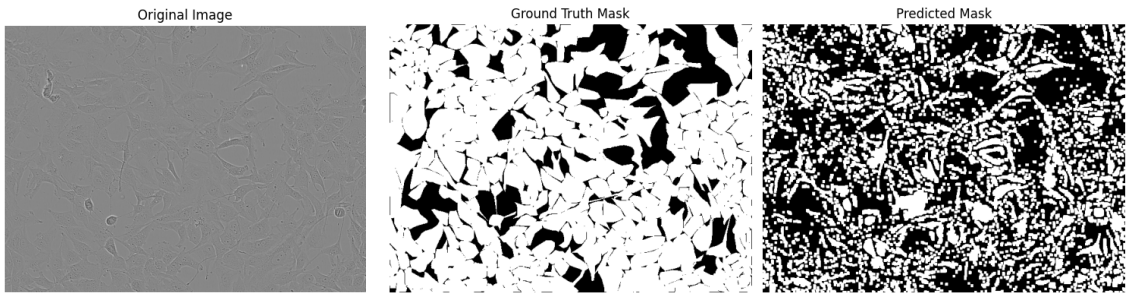

Figure 5: First Image is the original image for the dataset of A172 and the second image is the Ground Truth for the original image and the third image is the Predicted output for the original image

Performance Metric	**Value (%)**
Accuracy	57.03
Precision	89.21
Recall	50.66

Table 5: Performance Metrics for Fig 5

Discussion

- For Fig. 1, the model gave 98.60% accuracy where cells were clearly separated. This indicates that when the image is clean and the cells are not touching/overlapping, it can easily outline and detect the cells.
- However, in Fig. 2, many cells are overlapping, and the accuracy dropped to 78.39%. That is because the model found it more challenging to tell where one cell ended and another began. This shows that overlapping cells are more difficult to segment correctly.
- We then used the same pipeline for a non-rounded cell type and got bizarre result. We observed that the predicted mask produces a large number of fragmented and noisy predictions. This resulted in low accuracy (57.03%). However the precision is high that is 89.21%, suggesting that the cells that are actually present in the image are correctly predicted by the model.

II. What is planned for next week

1. Try to improve the accuracy by training the model with more overlapping examples and changing some hyperparameters of the model.
2. Test on varied cell types as there is very poor performance with non-rounded cells. We will apply the same pipeline to other cell types. Based on the outcomes, we will modify certain settings/parameters of the current pipeline to achieve improved accuracy for each cell type.

3. Try to work with different algorithm that works really well for images containing overlapping cells by studying connected component analysis.

4. To discuss and clarify some doubts with the professor and TAs. We are facing few challenges currently and would benefit from Professor's guidance to move forward effectively. We have some blurry ideas which we would like to discuss first. So that, we could have their feedback and insights to make sure we are on right track.

References

[1] C. Edlund, T. R. Jackson, N. Khalid, N. Bevan, T. Dale, A. Dengel, S. Ahmed, J. Trygg, and R. Sjögren, "LIVECell—A large-scale dataset for label-free live cell segmentation," *Nature Methods*, vol. 18, no. 9, pp. 1038–1045, 2021. [Online]. Available: `https://www.nature.com/articles/s41592-021-01249-6`