Image segmentation using K-Means clustering

Final Presentation

Data Analysis Project, 4. FS MoBi
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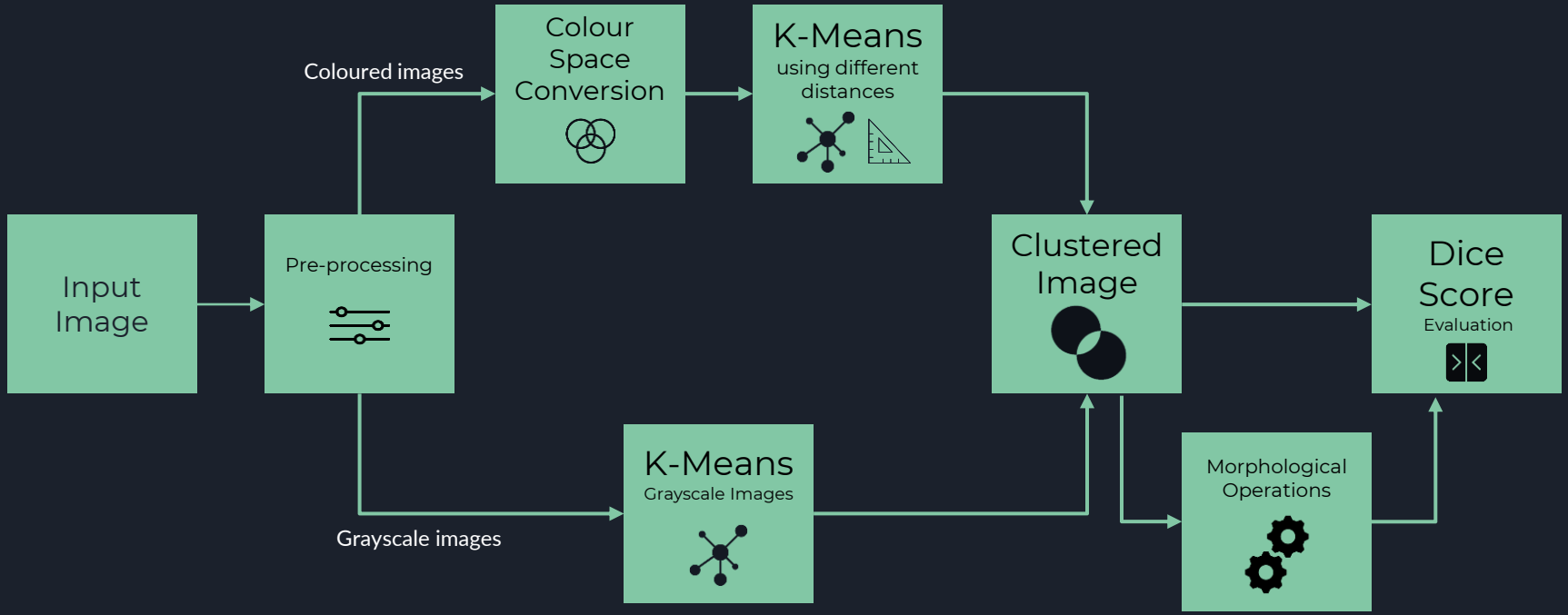
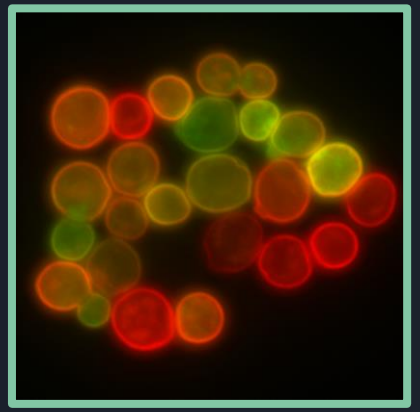
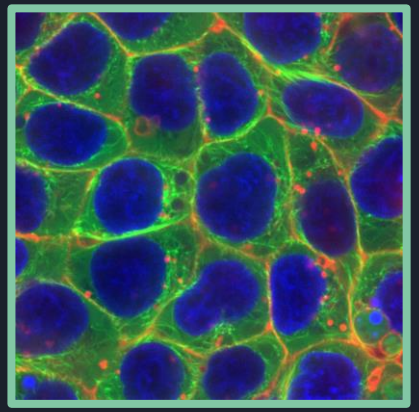
Overview


Input Image
Pre-processing
Coloured images
Colour Space Conversion
K-Means using different distances
Grayscale images
K-Means Grayscale Images
Clustered Image
Morphological Operations
Dice Score Evaluation

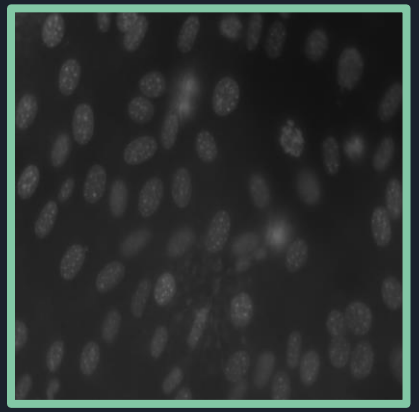
Input data



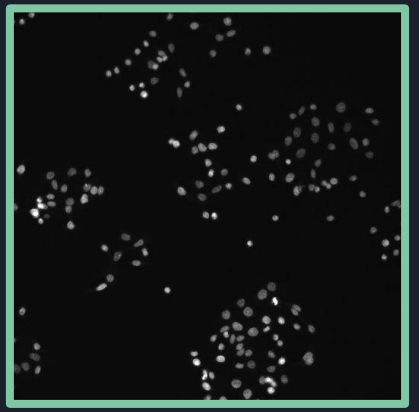
Yeast Cells



Cell Nuclei



NIH3T3



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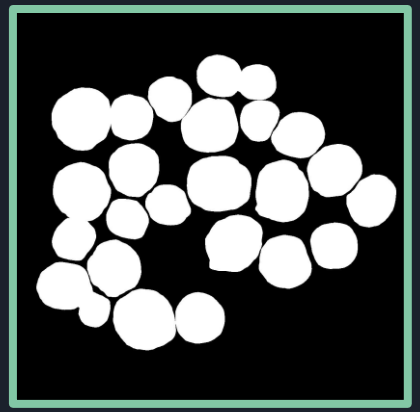
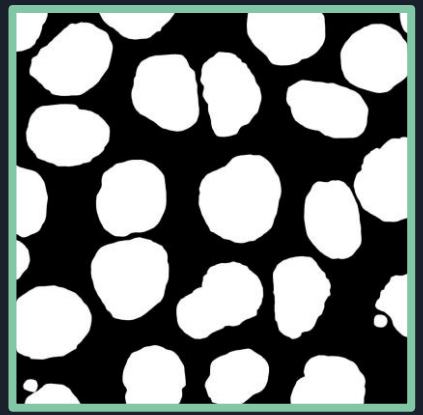
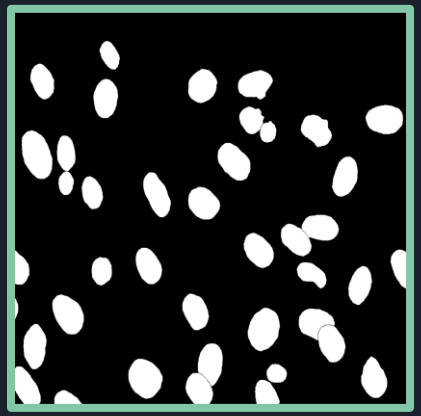
Ground truth images



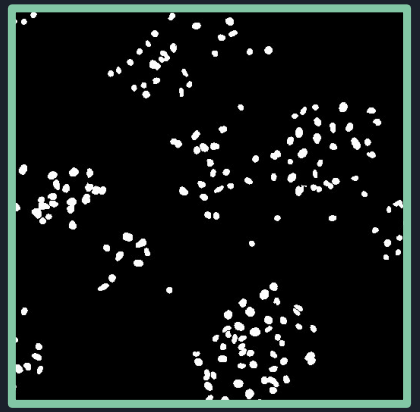
Yeast Cells



Cell Nuclei



NIH3T3



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Methods

Pre-processing	01	Noise Reduction, Bright Spots Removal
Colour Space Conversion	02	RGB, LAB, HSV, YCbCr
K-Means Clustering	03	Image Segmentation
Morphological Operations	04	Retouch and improvement of results
Dice Score	05	Evaluation of segmentation algorithm

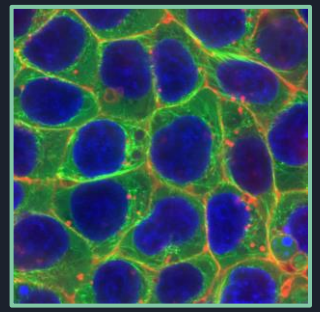
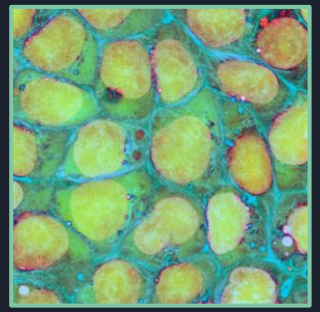
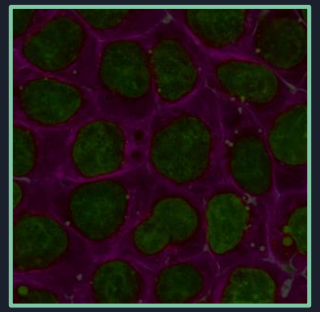
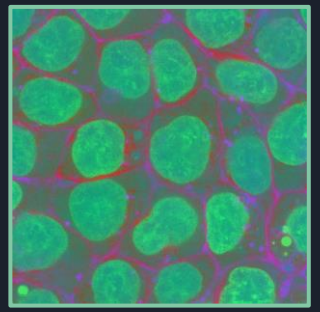
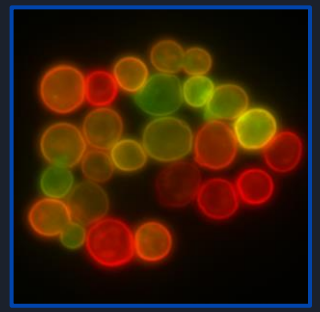
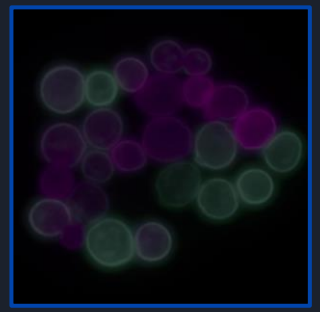
Methods - K-Means

Distances

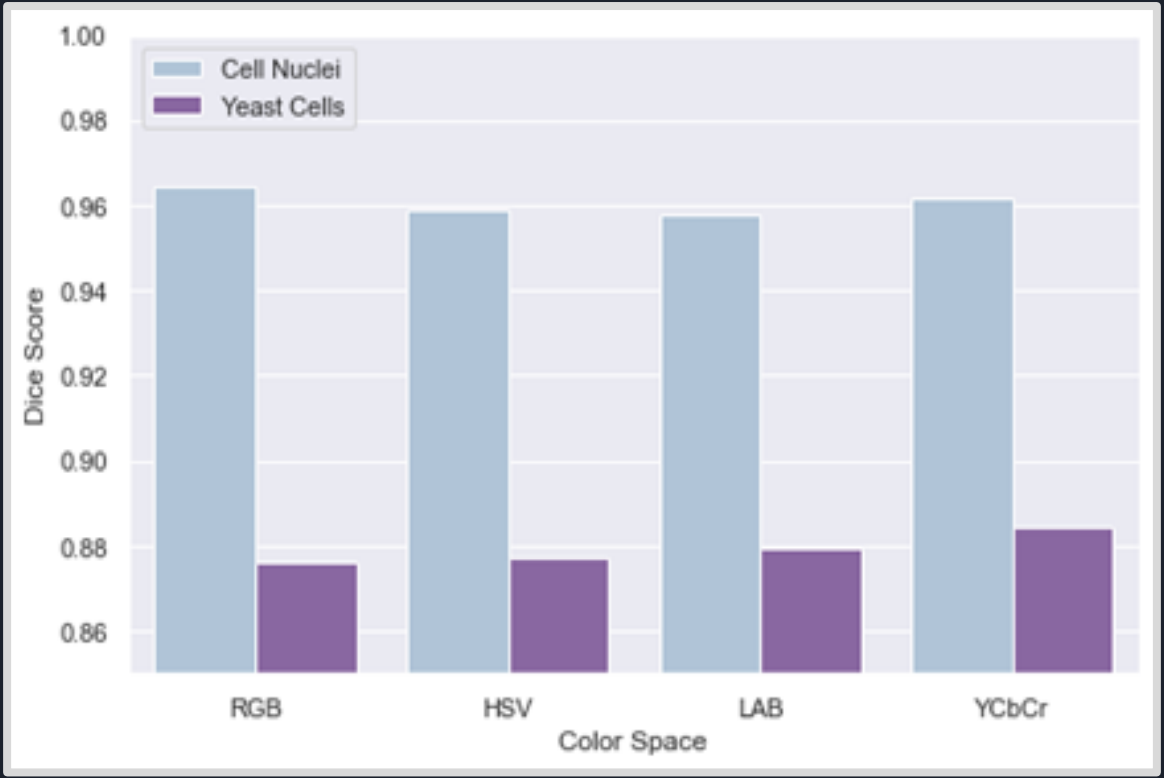
Colour Spaces

Positions

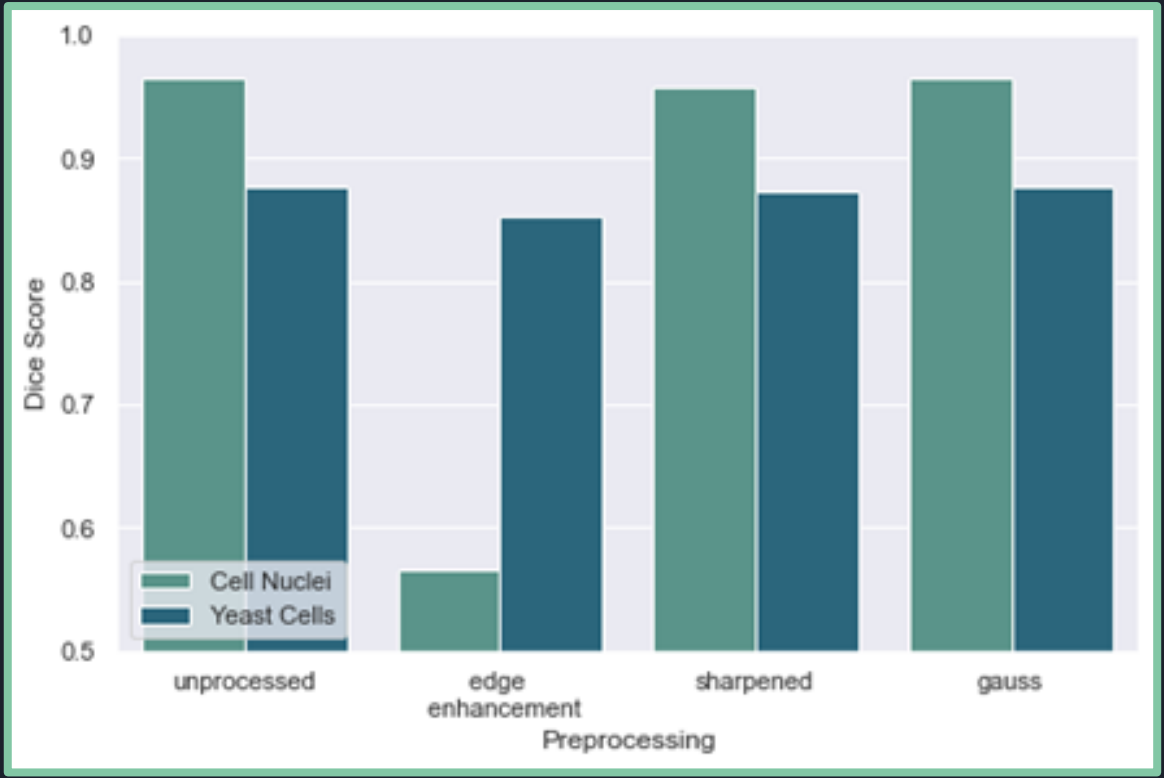
Methods - Colour Space Conversion

	RGB	HSV	LAB	YCbCr
Cell Nuclei				
Yeast Cells				

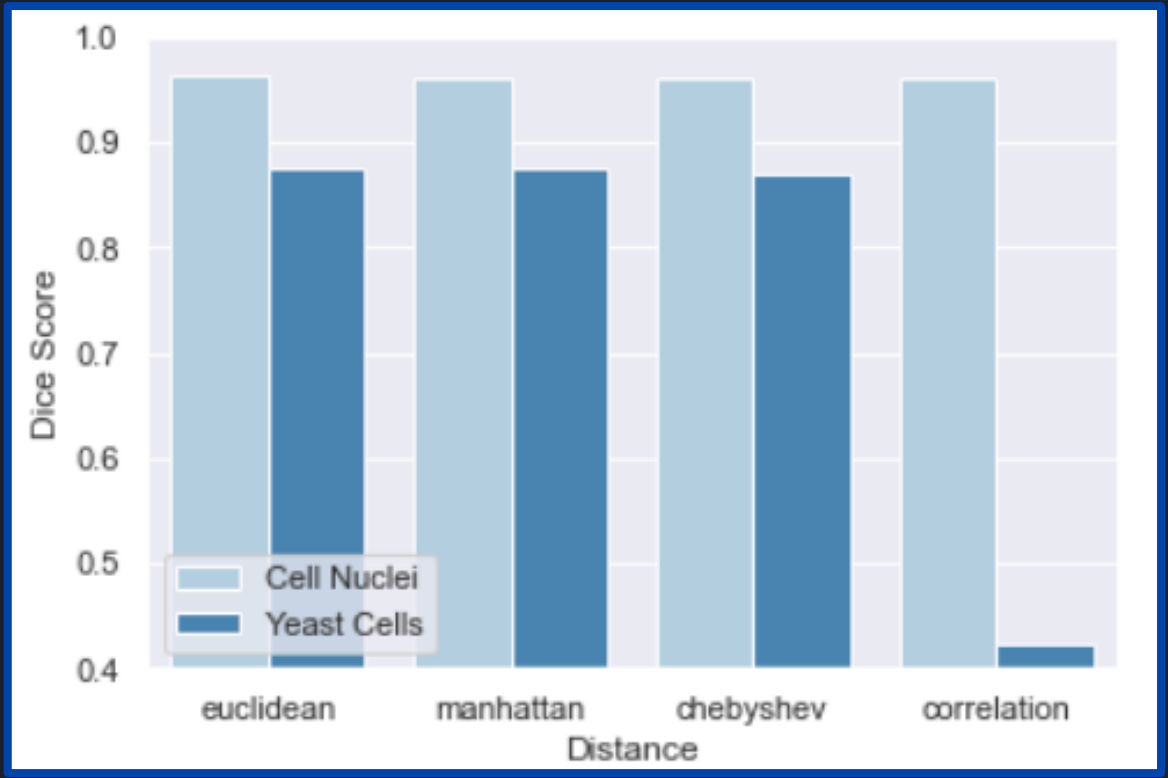
Results - Colour Spaces



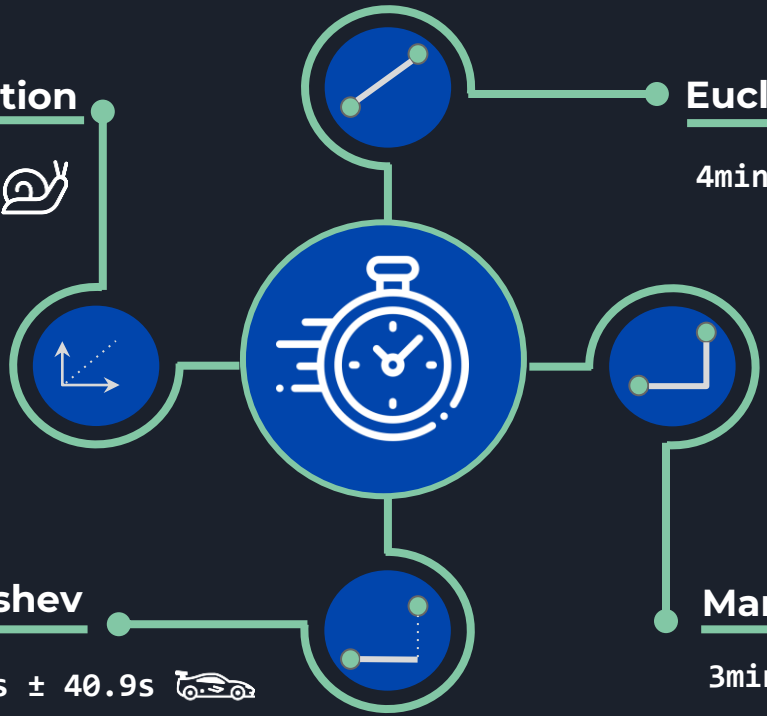
Results - Preprocessing



Results - Distances



Results - Run-time



Correlation

2h 14min 7s ± 4h 28min

Euclidean

4min 27s ± 1min 40s

Chebyshev

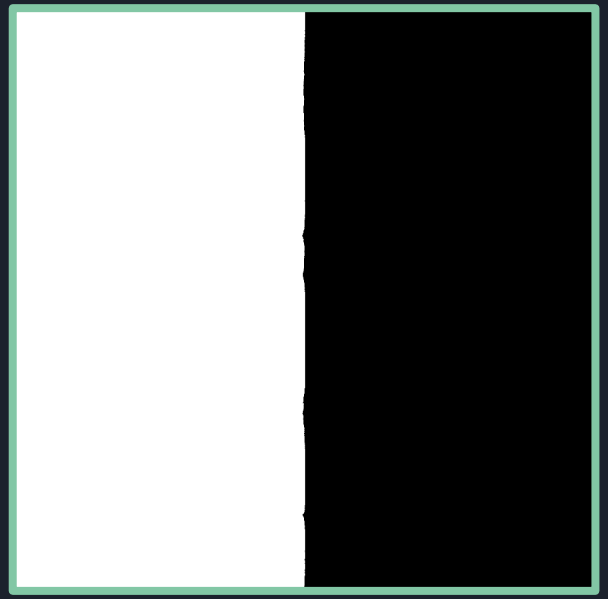
2min 25s ± 40.9s

Manhattan

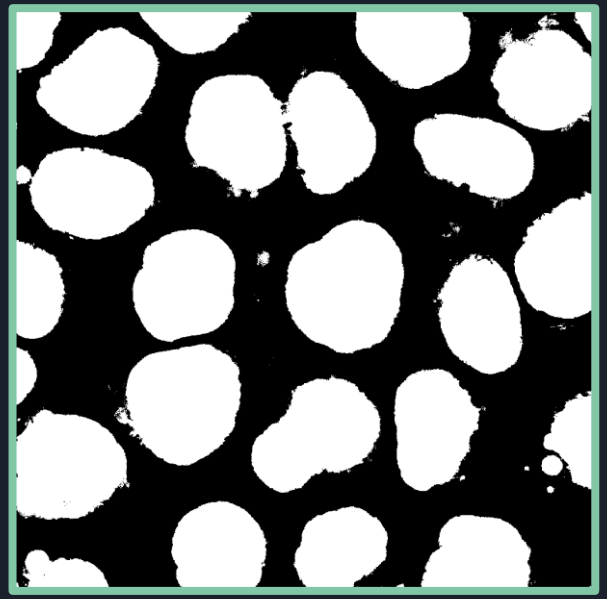
3min ± 42.4s

Results - Position

100 %



10 %

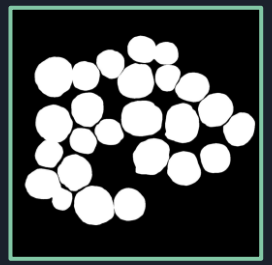


Results - Best Combinations

Yeast Cells: Unprocessed + YCbCr + Manhattan

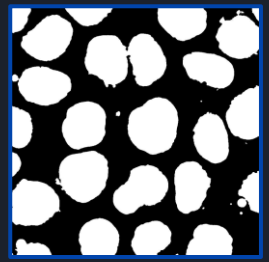
clustered

88,6%



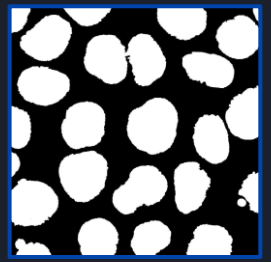
ground truth image

Cell Nuclei: Gauss + RGB + Euclidean



clustered

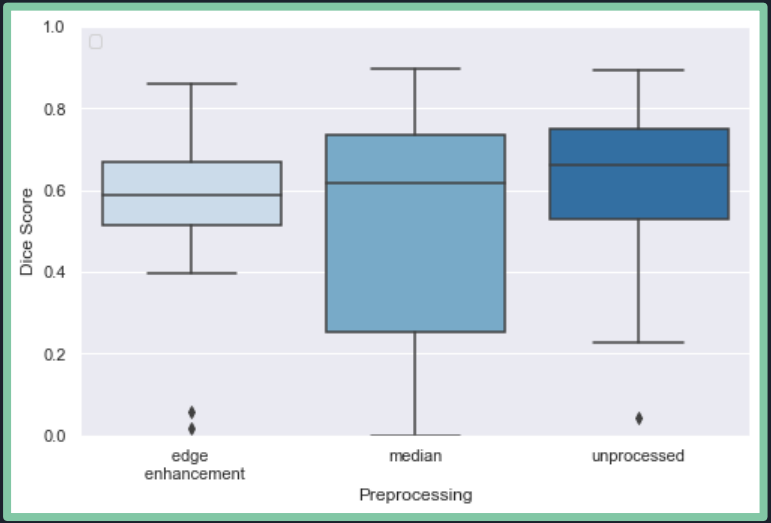
96,4%



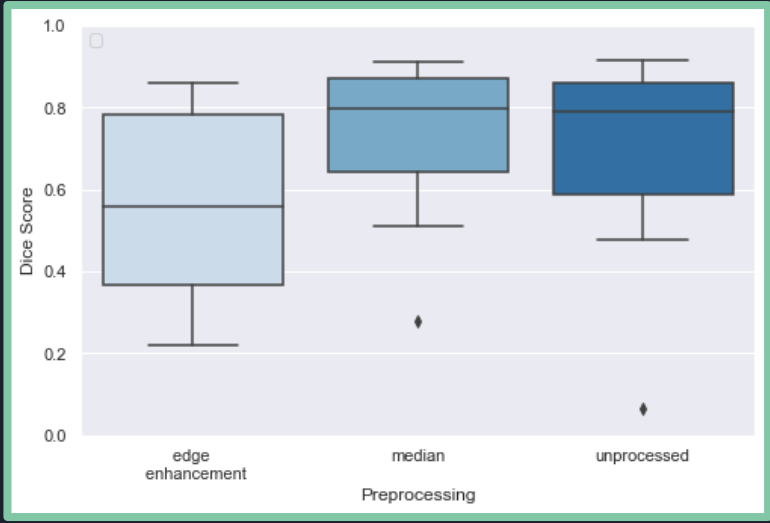
ground truth image

Results - Grayscale images

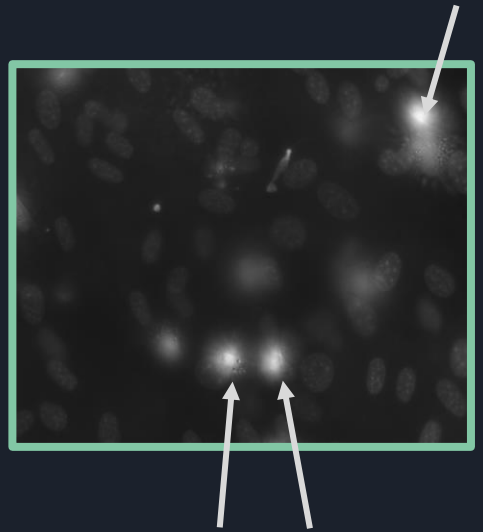
NIH3T3



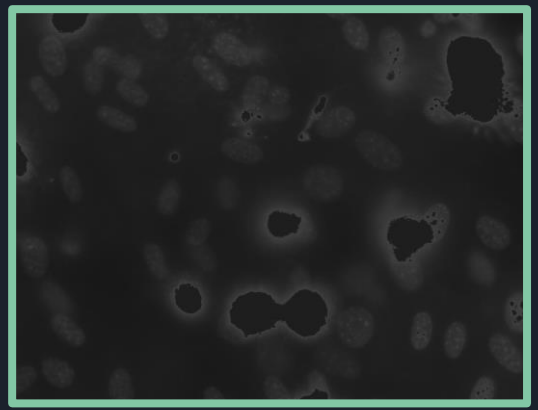
BBBC images



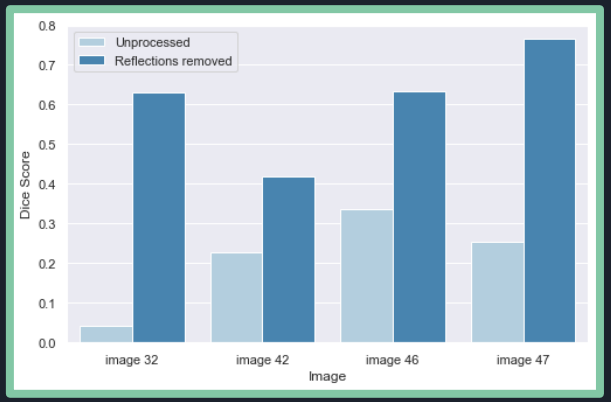
Challenges in grayscale images



Bright spots



Bright spots removal



Improvement of Dice Score

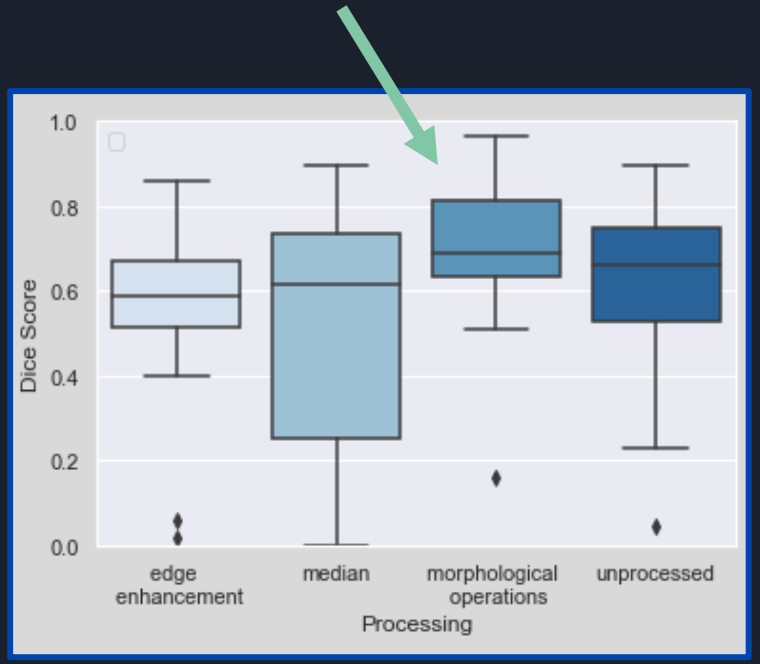
Morphological operations

Erosion **Dilation** **Opening** **Closing**

(only applied on coloured images)

No improvement for coloured images

Dilation increased Dice Score for NIH3T3 grayscale images



NIH3T3 data set

Morphological operations - Example

33,7% Dice Score

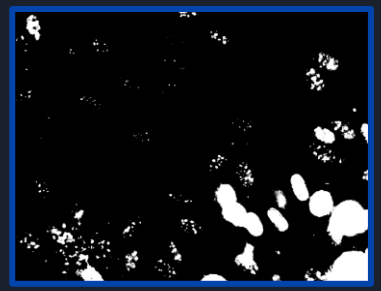


Image 46, clustered

Dilation

63,4% Dice Score

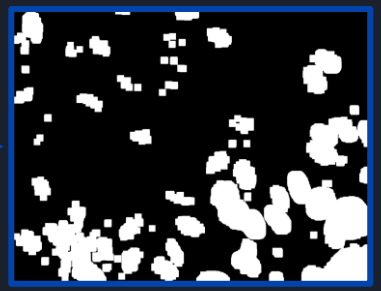


Image 46, clustered and dilated

88% improvement

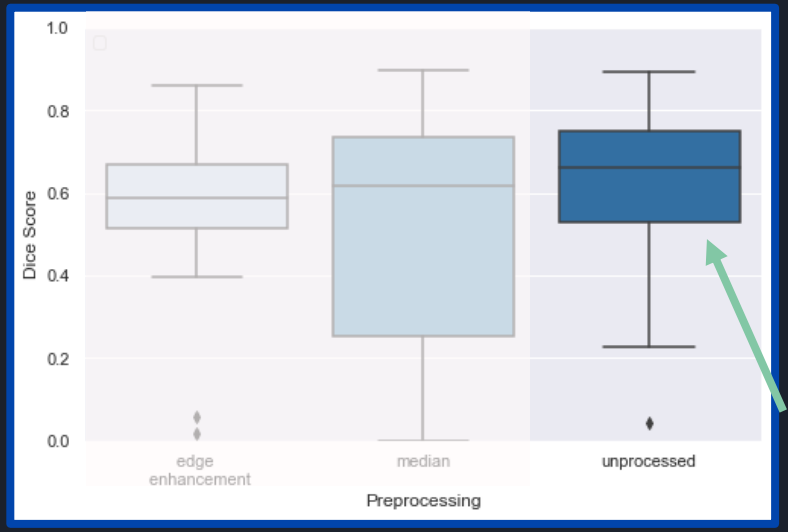
Image 46, ground truth image

Dilation is generally a good method to retouch the clustered images and improve the Dice Scores

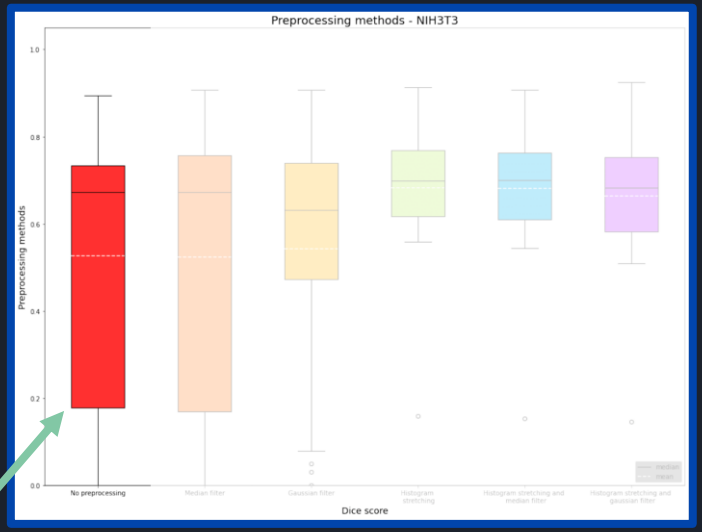
Comparison with OpenCV

	Our algorithm	OpenCV algorithm
Cell Nuclei (unprocessed, RGB, Euclidean)	96,4%	96,4%
Yeast Cells (unprocessed, RGB, Euclidean)	87,6%	87,2%
Dna-0 (NIH3T3)	89,4%	84,8%
Dna-32 (NIH3T3)	4,22%	2,62%

Comparison with Otsu Thresholding



NIH3T3 after applying K-Means clustering



NIH3T3 after applying Otsu Thresholding
(results from Group 04)

Conclusion

Colour Spaces and **Minkowski Distances** had no significant impact on results

Manually created **ground truth images** distort dice score

Morphological operations improved the output more than **Preprocessing**

K-Means clustering led to similar results as **OpenCV** and **Otsu**

Further improvement could be achieved using **Soft K-Means**

No perfect “recipe” could be determined

Thank you for your attention!