

Median filter

Gaussian filter

Histogram stretching

Preprocessing  
Postprocessing

3 datasets

Global Otsu  
thresholding

Two-level Otsu  
thresholding

Local adaptive Otsu  
thresholding average

Two-level Otsu thresholding clip

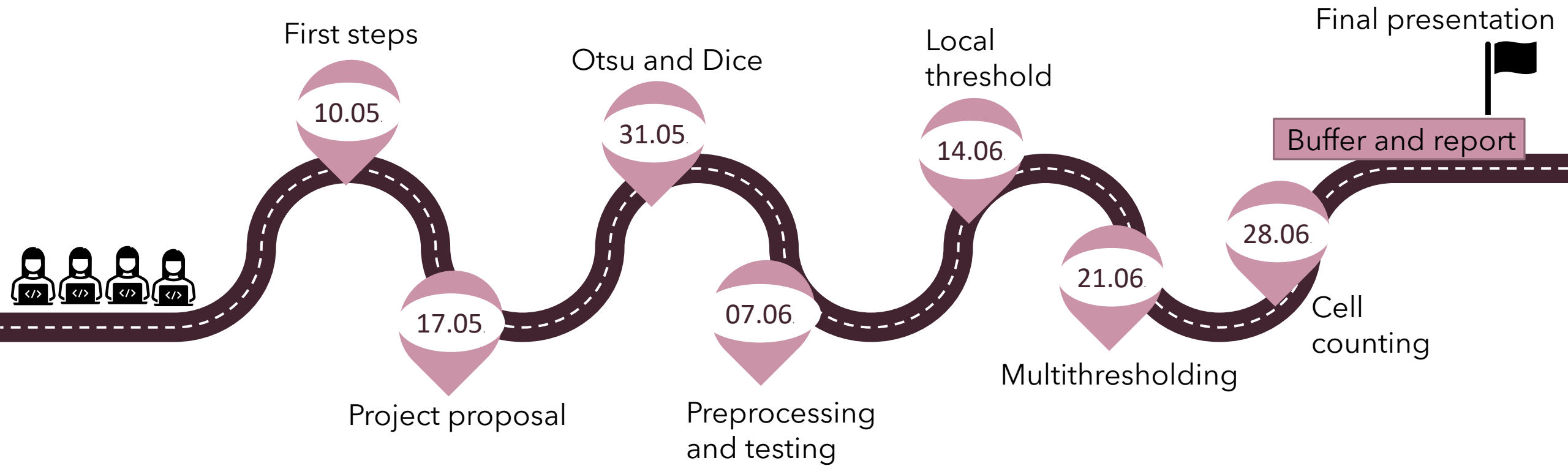


Dice Score

Optimal segmented image

# Timeline recap

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# Cell Nuclei Segmentation

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IMPLEMENTATION AND EVALUATION  
OF OTSU THRESHOLDING

**Final presentation**

**Topic 01: Biomedical Image Analysis**

**Supervisor:** PD Dr. Karl Rohr, Christian Ritter, Tutor: Marie Becker

**Group 01.04:** Marie-Claire Indilewitsch, Helen Jade, Maribel Schneider, Ieva Sorokina-Ozola

**Date:** 20.07.2022



# Overview

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Recap  
datasets  
difficulties

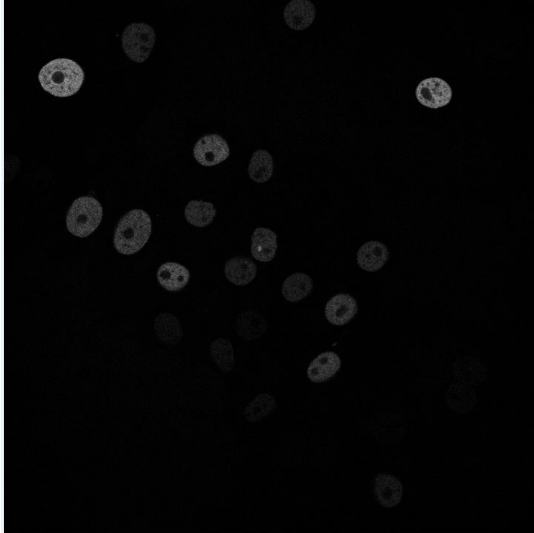
Results  
and  
Discussion

Challenges

Summary-  
the perfect  
recipe

# N2DH-GOWT1

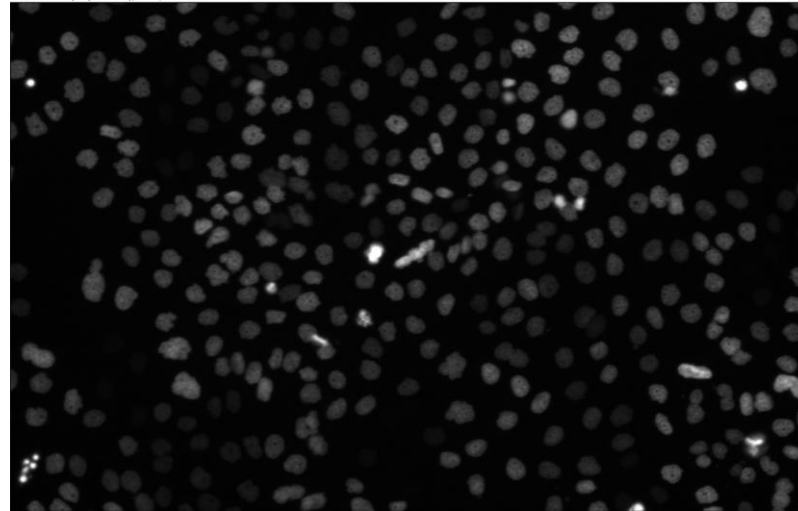
(first dataset)



- Noise
- Low contrast
- Holes

# N2DL-HeLa

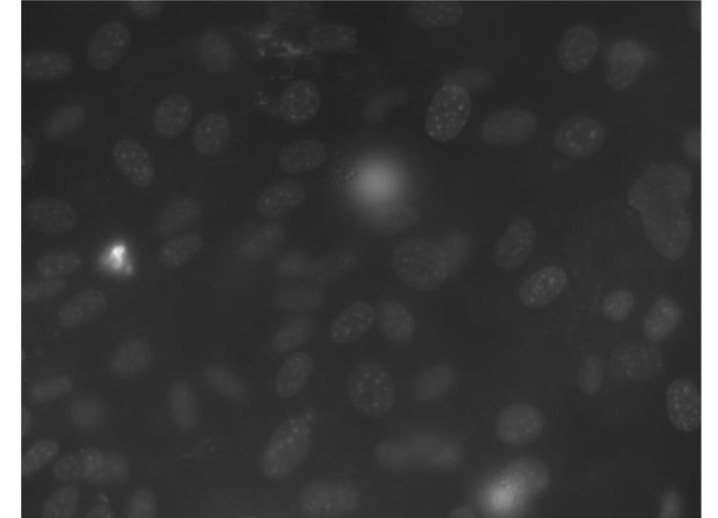
(second dataset)



- Varying brightness of cell nuclei
- Low contrast

# NIH3T3

(third dataset)



- Non-uniform illumination
- Reflections

N: nuclear

2D: two-dimensional

H: high resolution

L: low resolution

# Expectations

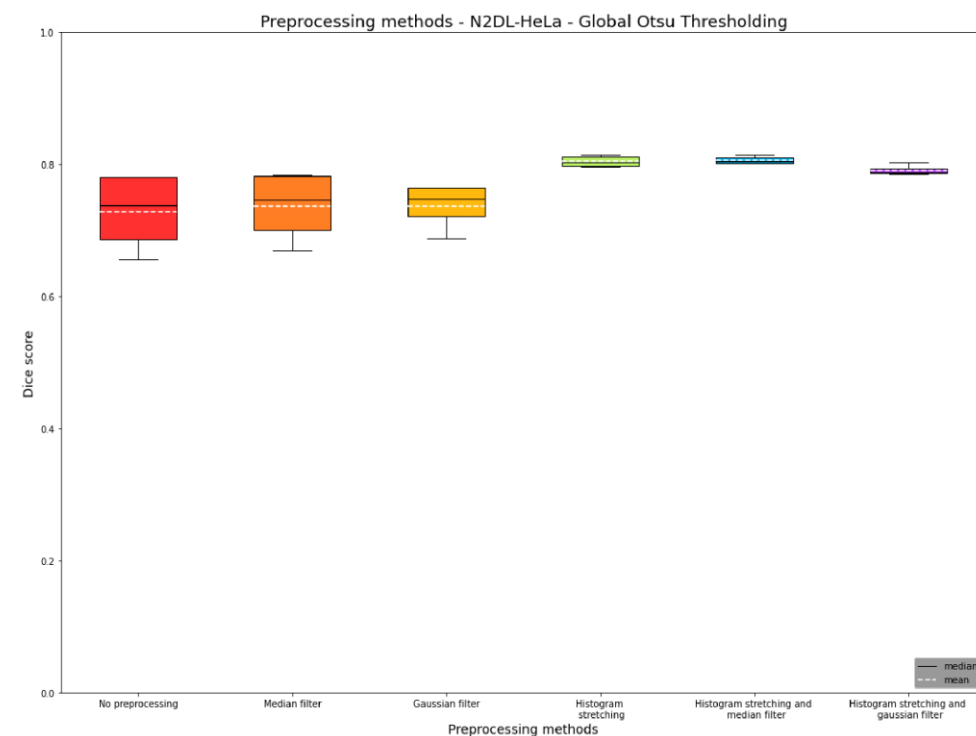
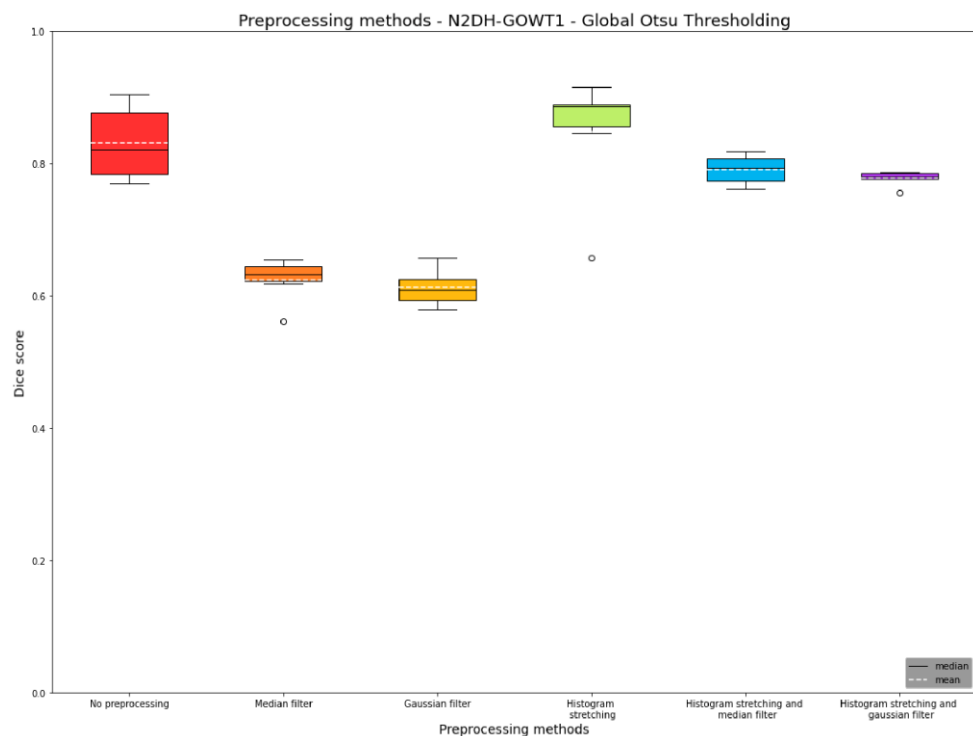
	Challenge	Preprocessing method	Otsu thresholding variation
<b>N2DH-GOWT1</b>	Noise Low contrast Holes	Filters Histogram stretching and combinations +postprocessing	Global Otsu Two-level Otsu
<b>N2DL-HeLa</b>	Varying brightness of cell nuclei Low contrast	Filters Histogram stretching and combinations	Global Otsu Two-level Otsu Local adaptive thresholding
<b>NIH3T3</b>	Non-uniform illumination Reflection	Filters Histogram stretching and combinations	Global Otsu Two-level Otsu Local adaptive thresholding



*Does the combination between preprocessing method and Otsu thresholding variation solve/improve the challenge?*

# Global Otsu thresholding

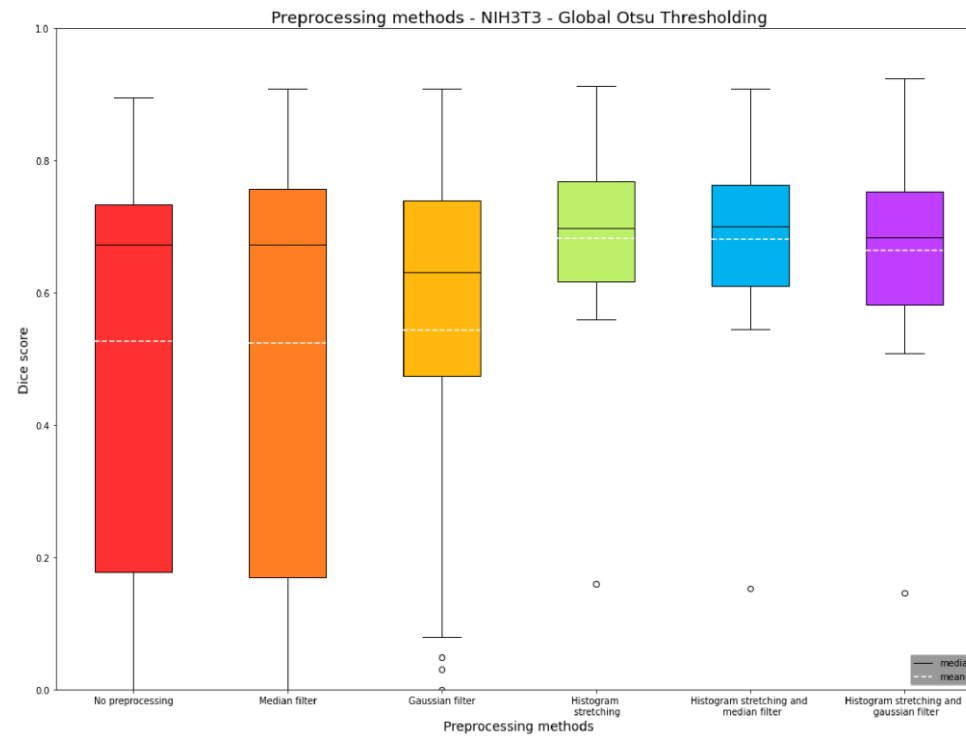
# Preprocessing methods N2DH-GOWT1 and N2DL-HeLa





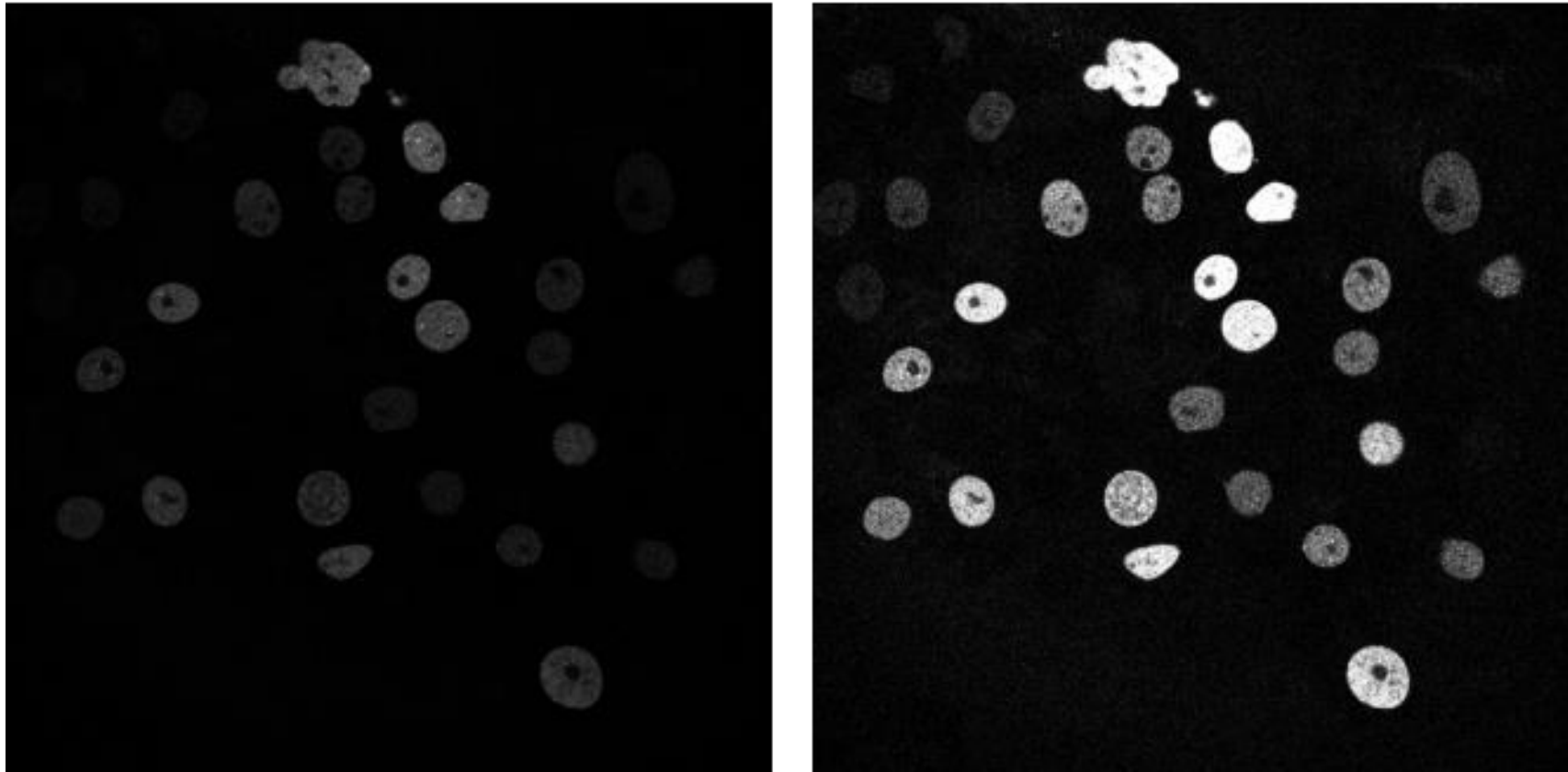
# Preprocessing methods NIH3T3

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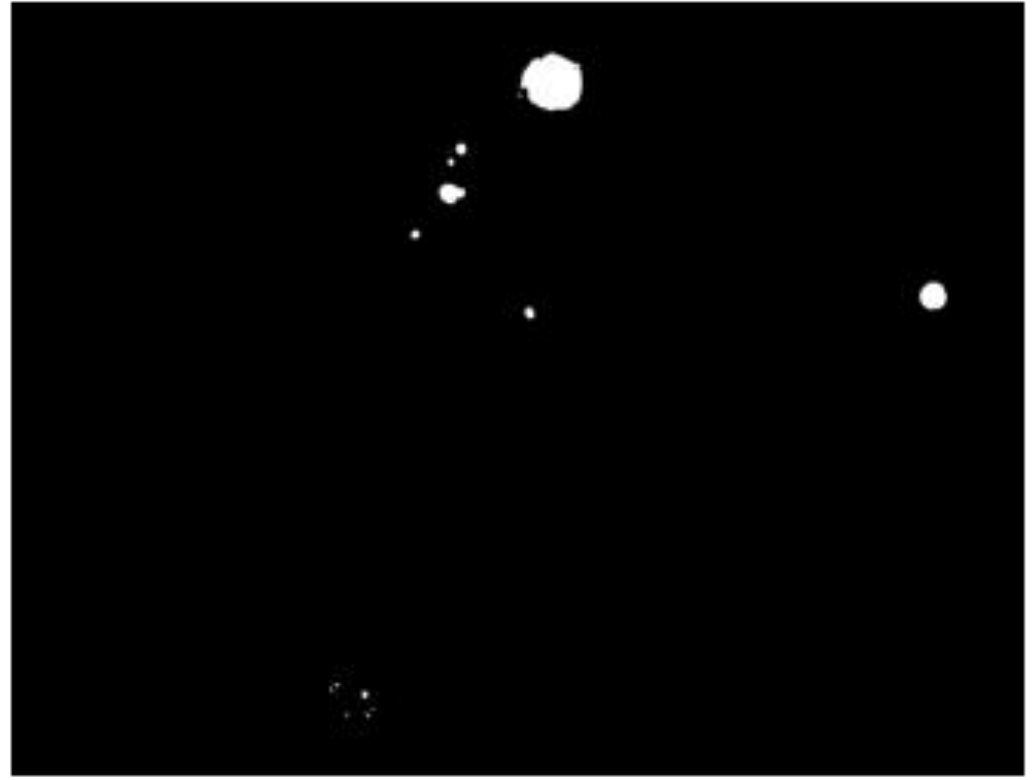
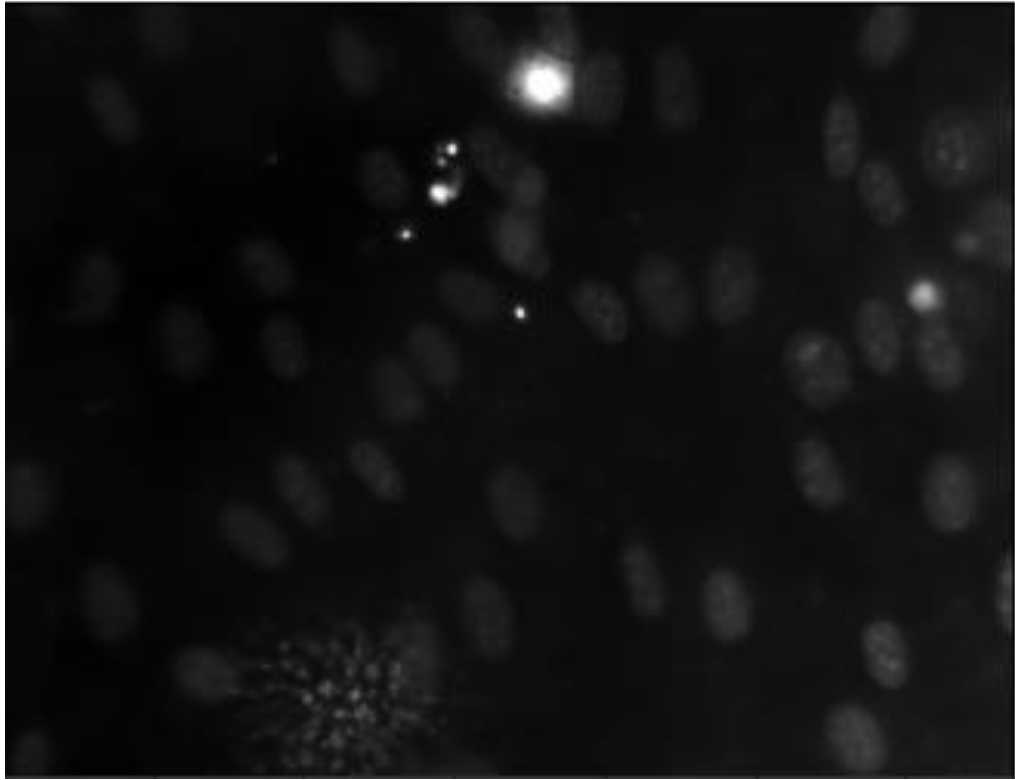
## N2DH-GOWT1: Effects of histogram stretching

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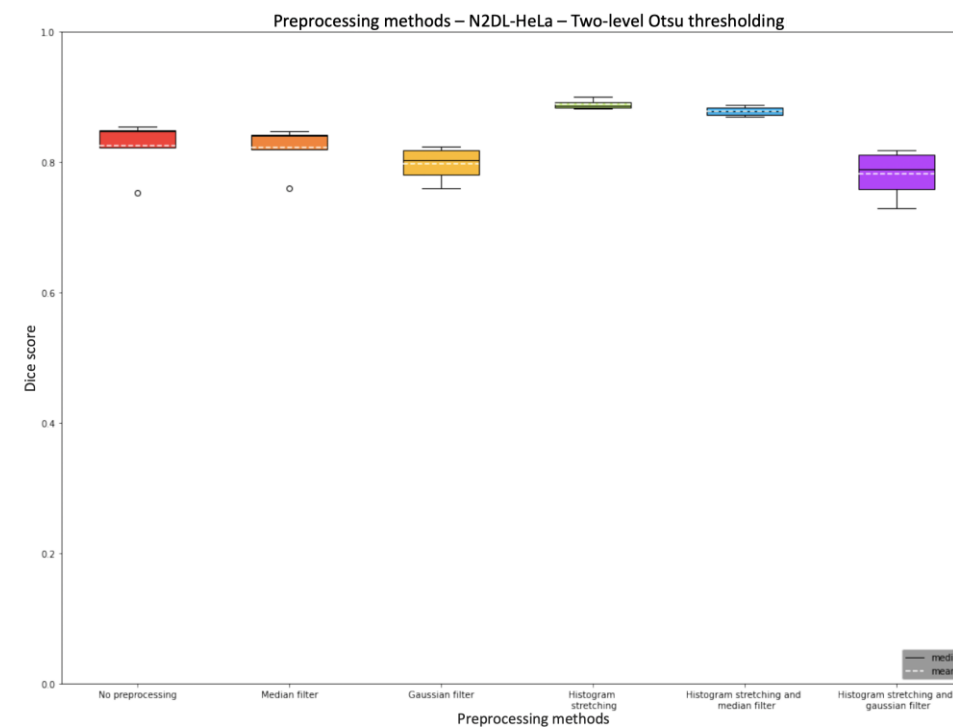
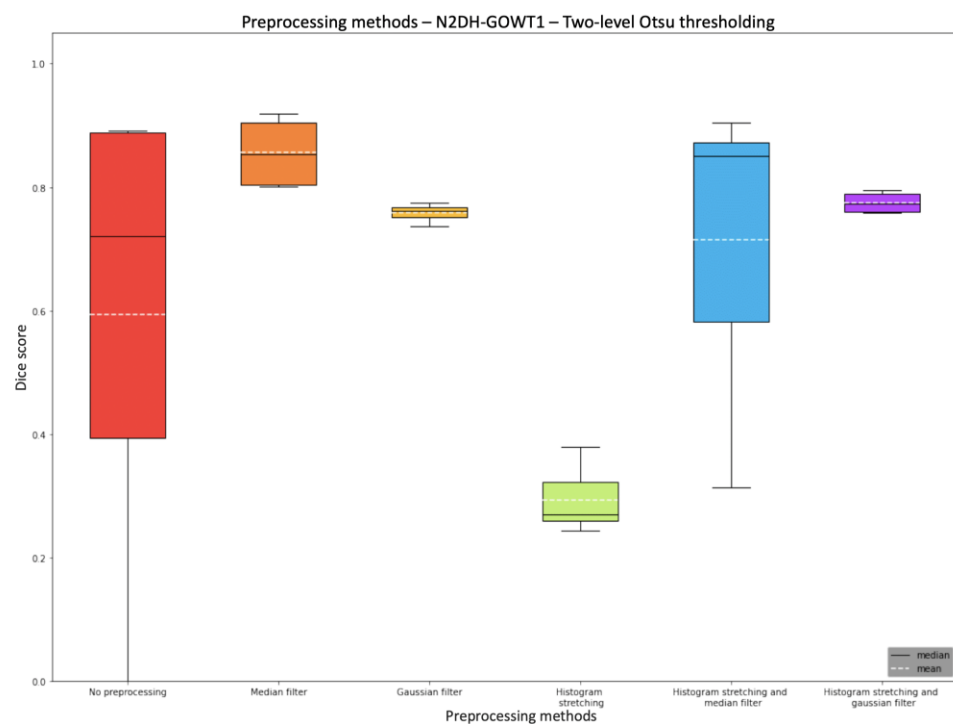
## NIH3T3: Reflections

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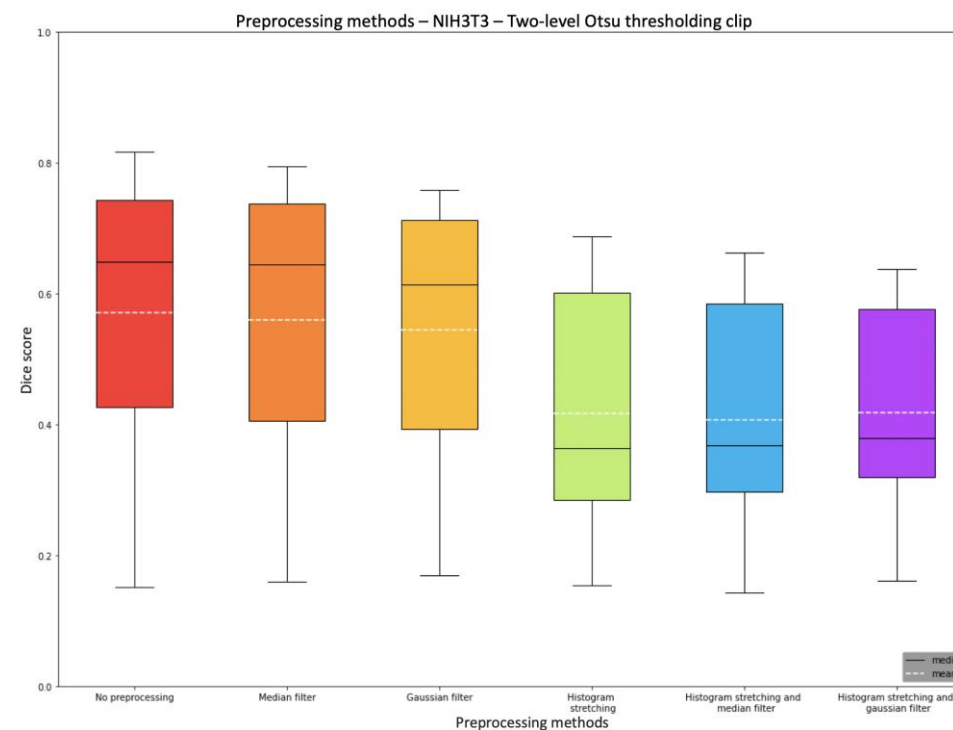
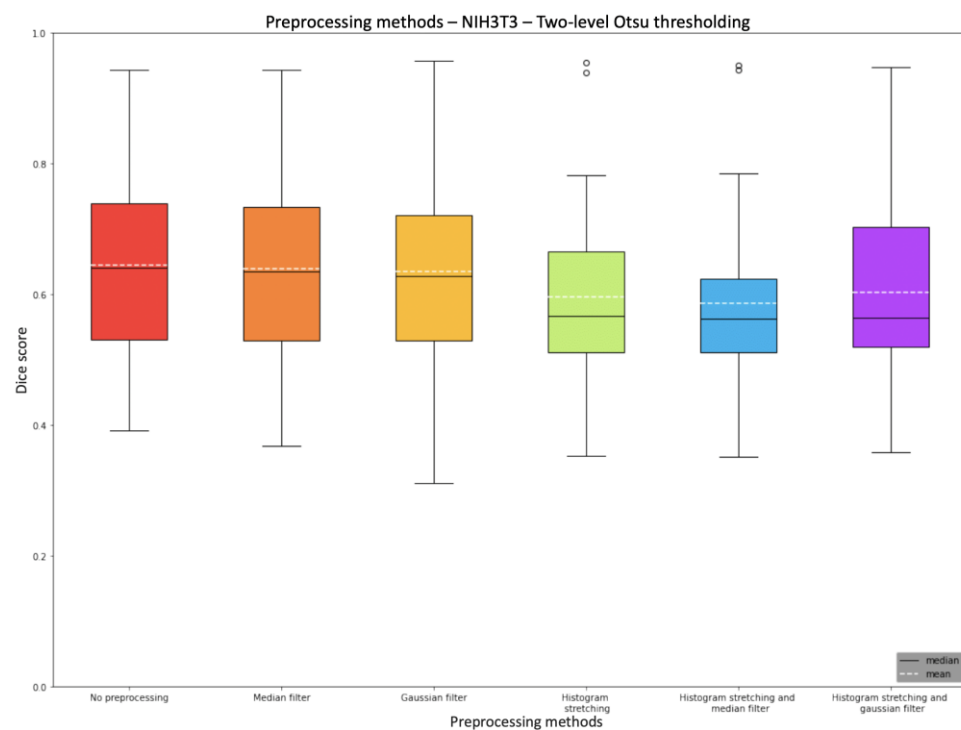


# Two-level Otsu thresholding

# Preprocessing methods N2DH-GOWT1 and N2DL-HeLa



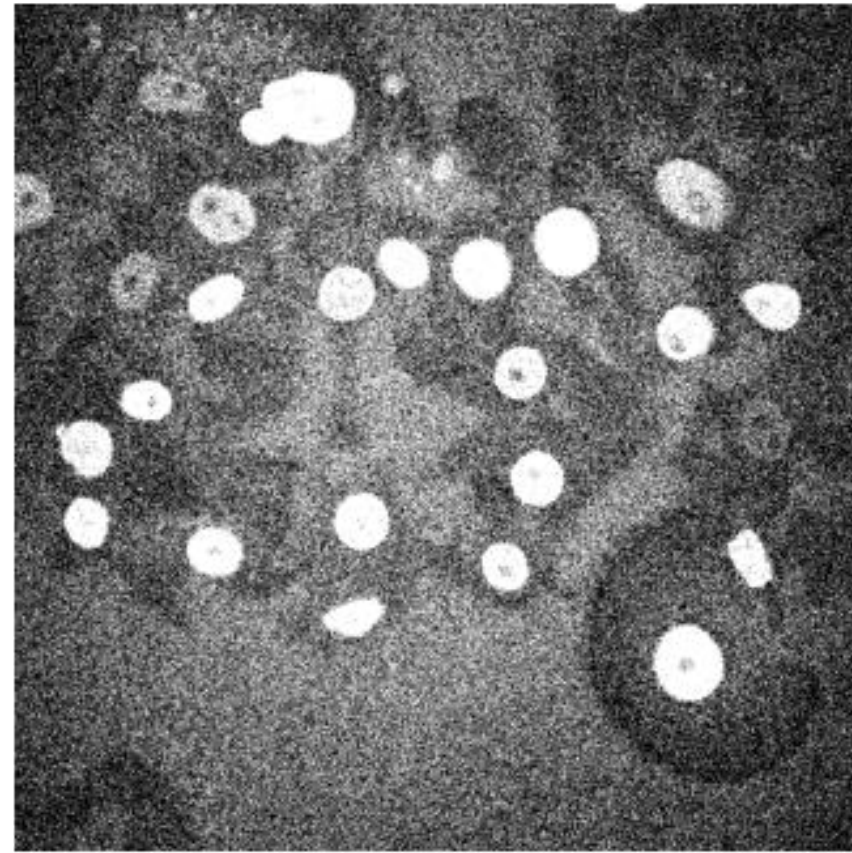
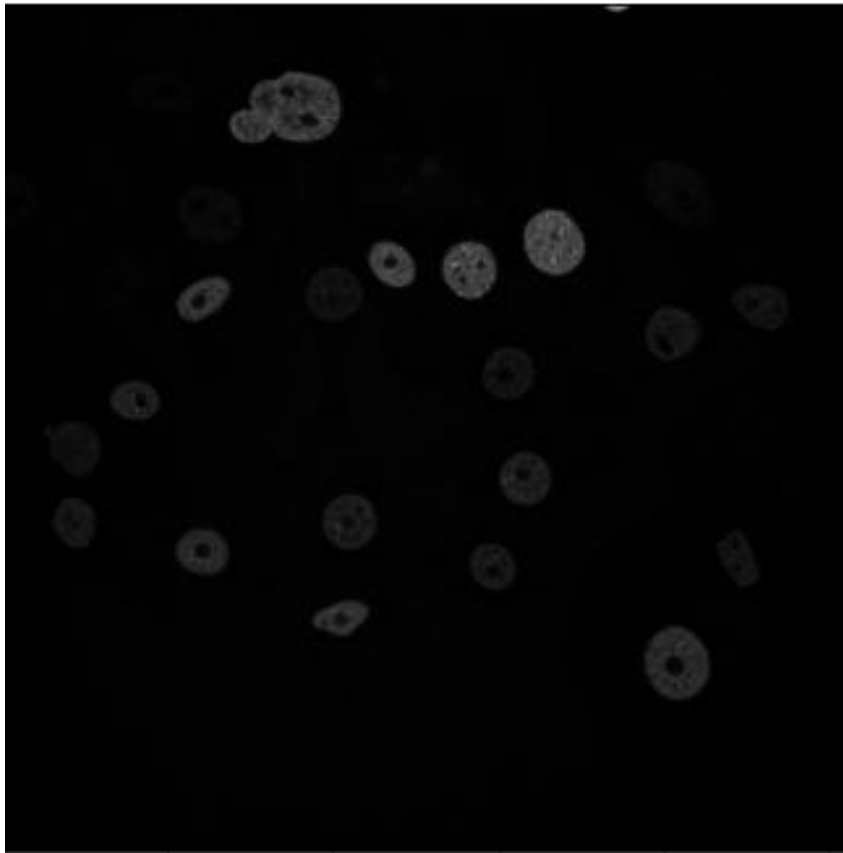
# Preprocessing methods NIH3T3 two-level Otsu and clip





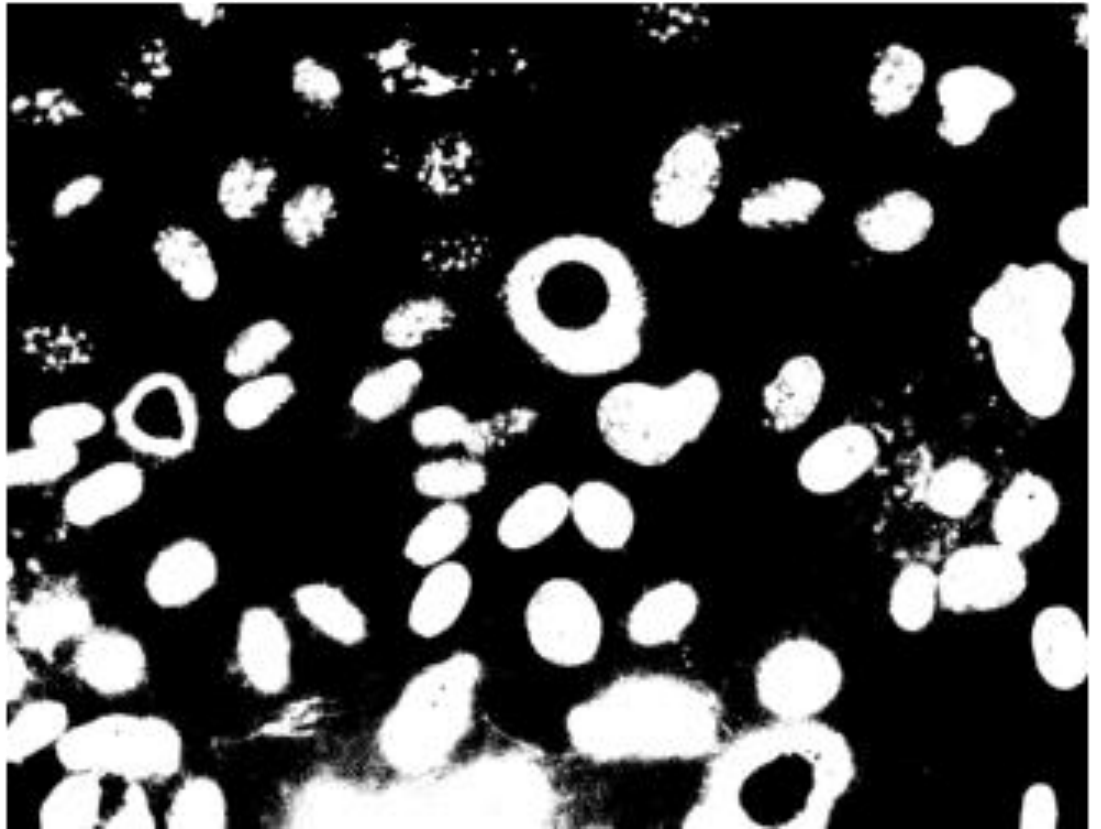
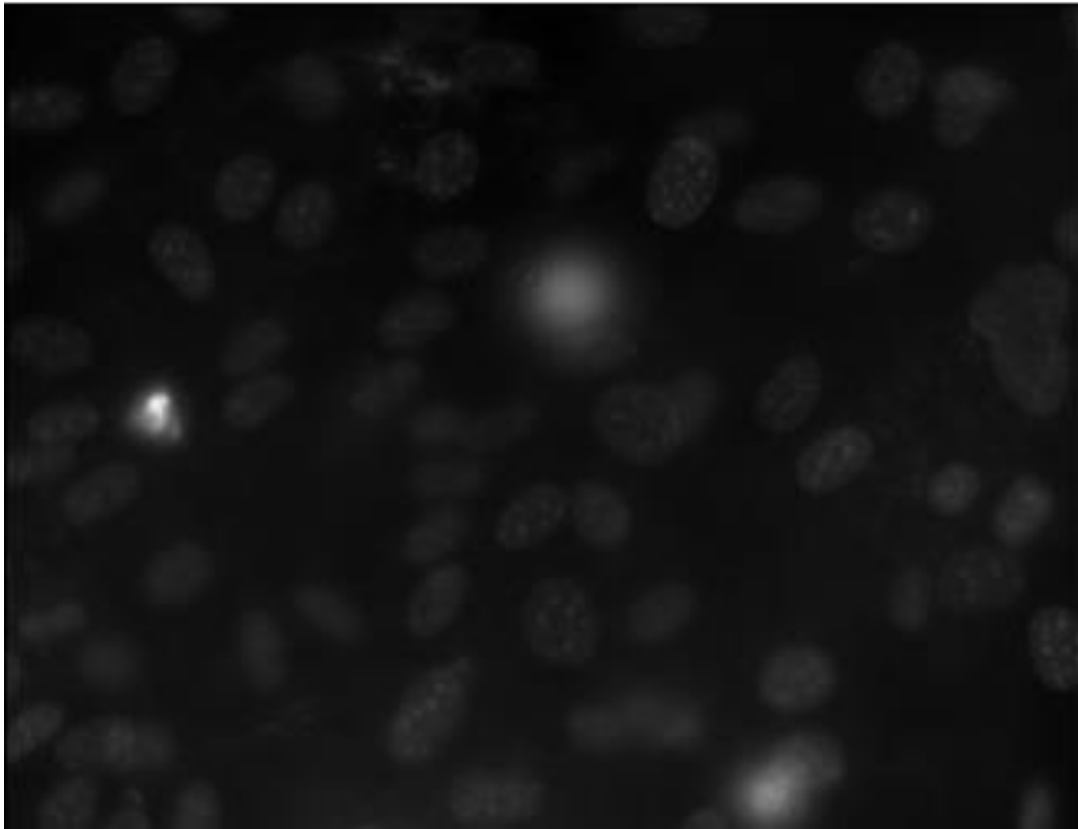
## N2DH-GOWT1: Effects of histogram stretching

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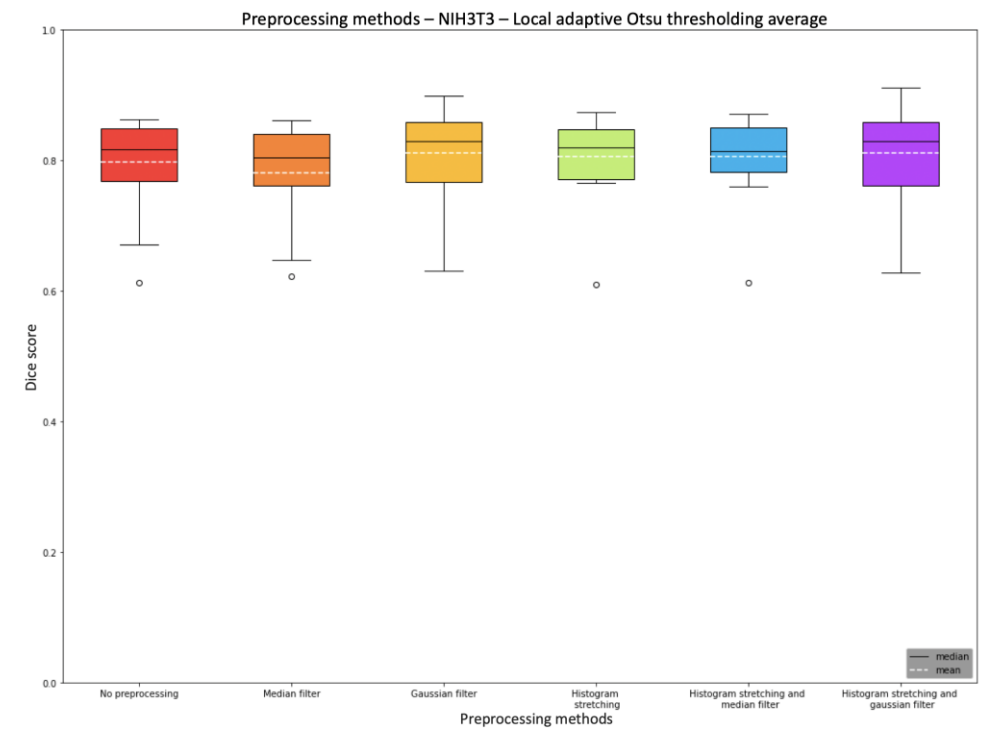
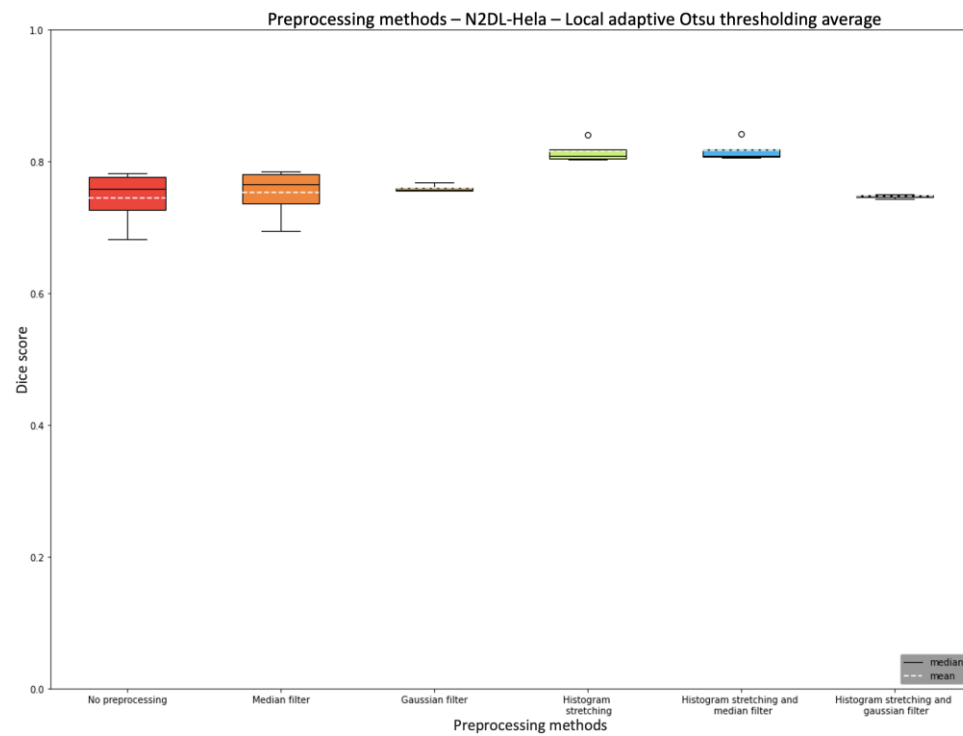
## NIH3T3: Two-level Otsu thresholding clip

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# Local adaptive Otsu thresholding

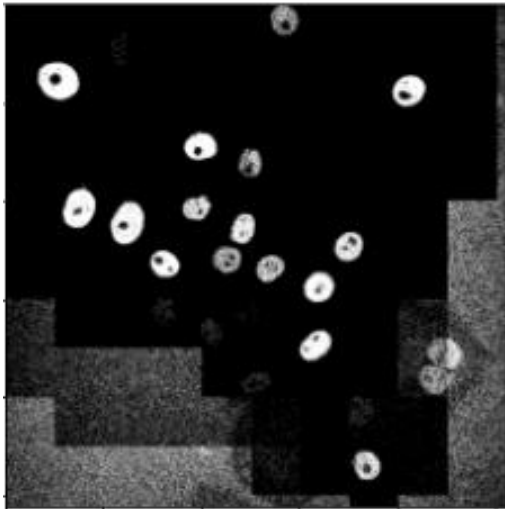
# Preprocessing methods N2DL-HeLa and NIH3T3



# Challenges

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RANDOM NOISE

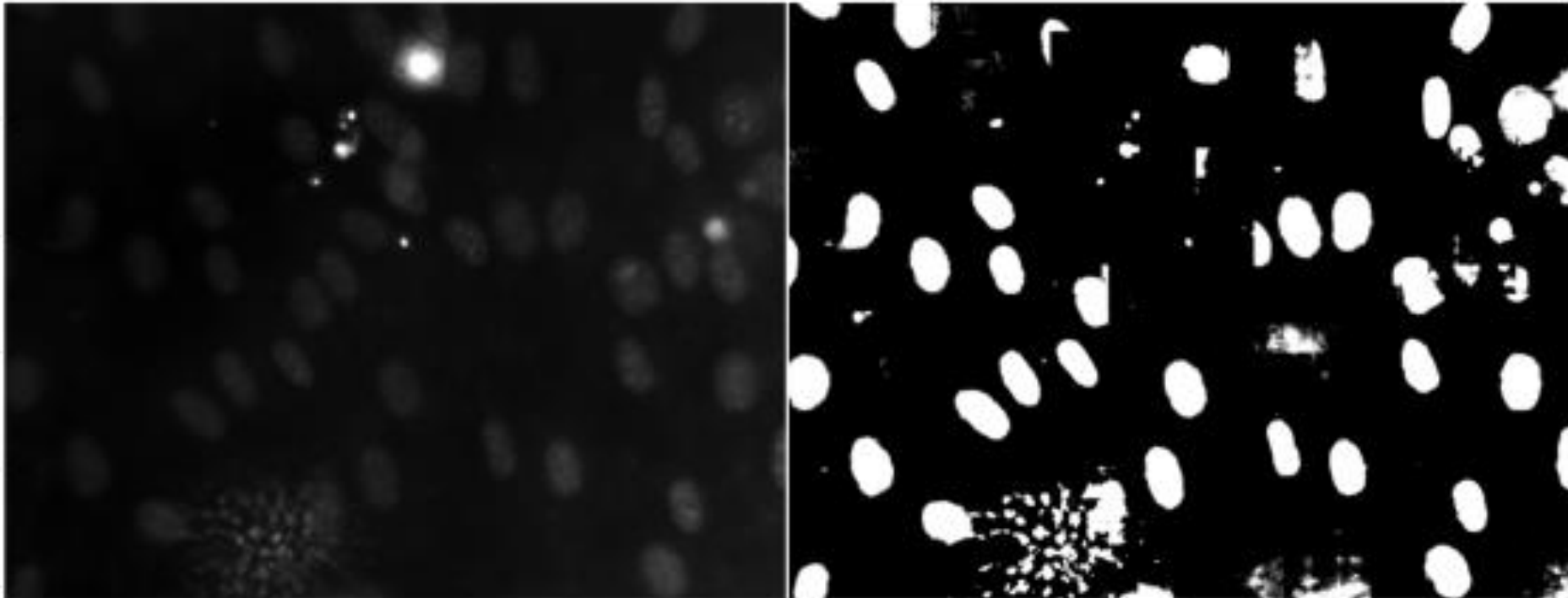


UNSEGMENTED EDGES



## NIH3T3: Effects of local adaptive Otsu thresholding

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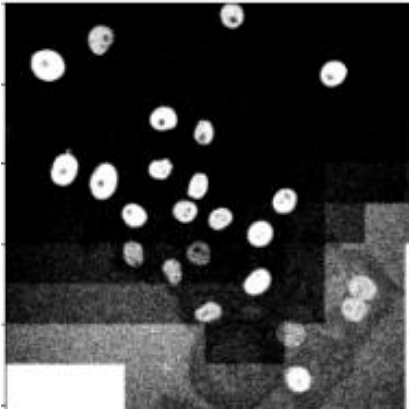




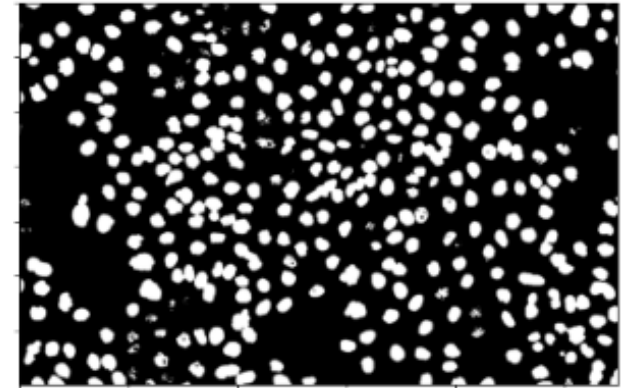
# Local adaptive two-level Otsu thresholding

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Local Two-level Otsu thresholding average - N2DH-GOWT1 - t31



Local Two-level Otsu thresholding average - N2DL-HeLa - t75



Local Two-level Otsu thresholding clip average - NIH3T3 - dna32



# Challenges

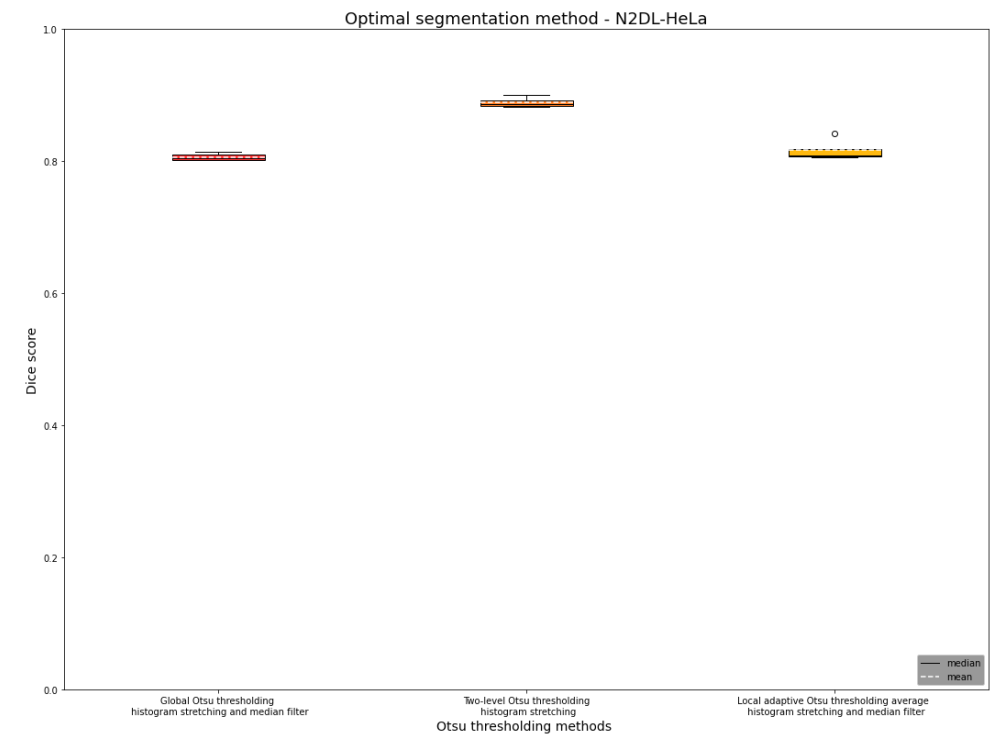
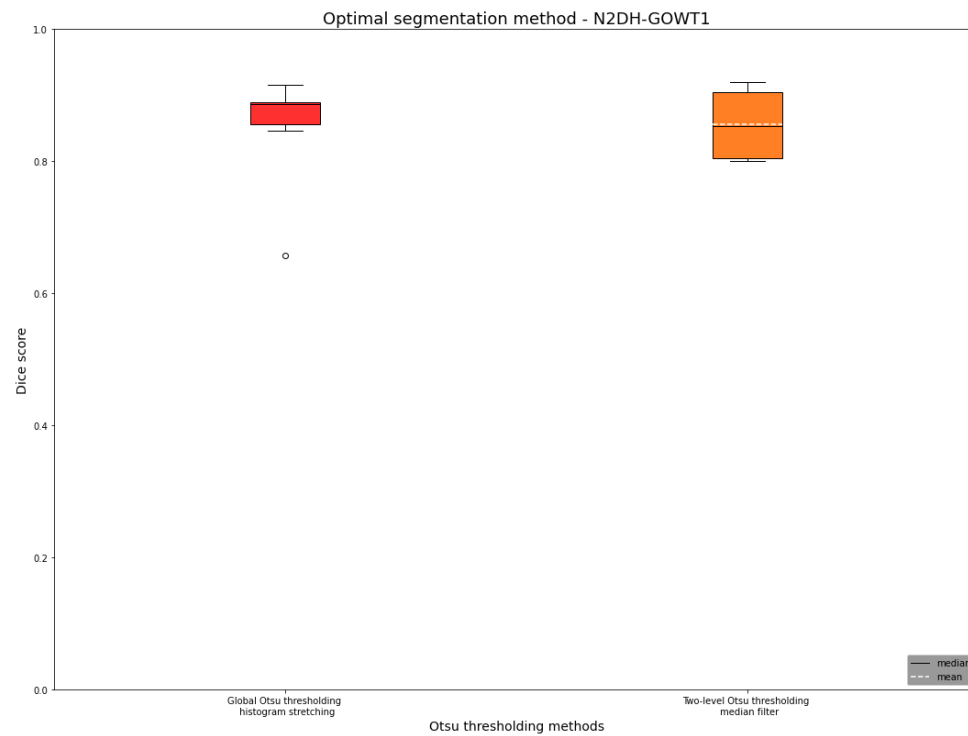
# Challenges

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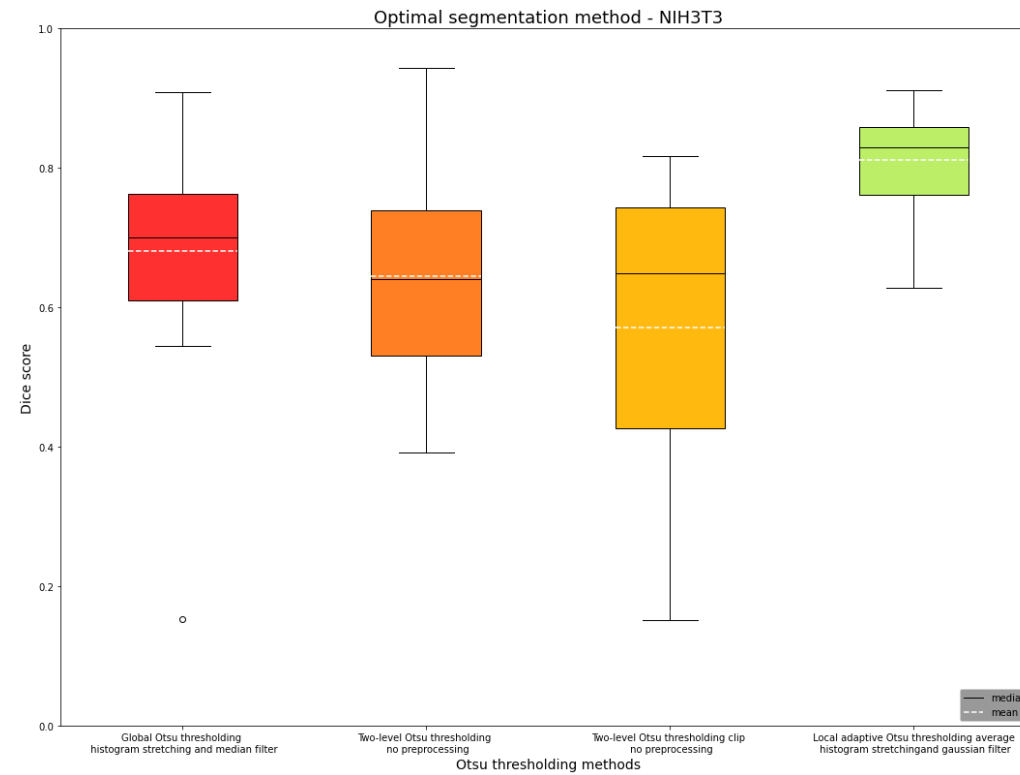
- Runtime
- Optimal bin size
- Optimal filter size
- Edge issue
- Local adaptive Otsu thresholding count vs. average

All challenges solved?

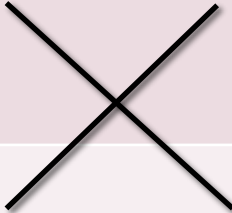
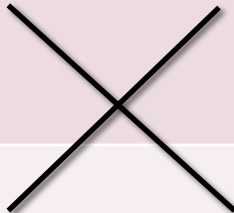
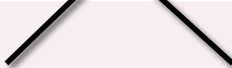
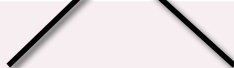
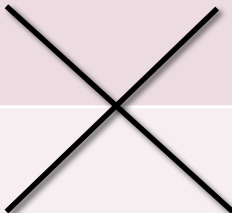

# Optimal segmentation method for N2DH-GOWT1 and N2DL-HeLa



# Optimal segmentation method NIH3T3





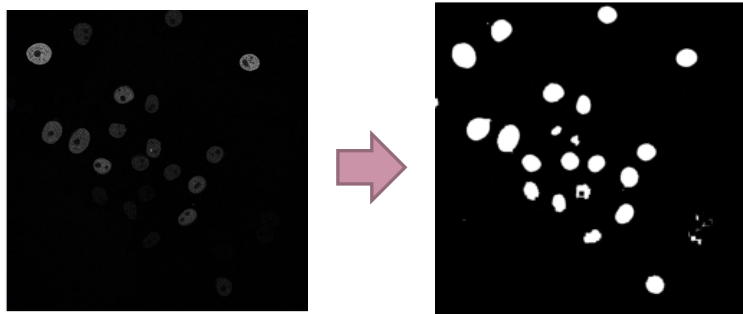
		Global Otsu Thresholding	Two-level Otsu thresholding	Two-level Otsu Clip	Local adaptive thresholding average
<b>N2DH-GOWT1</b>	Preprocessing method	Histogram stretching	Median filter		
	Dice Score	<b>0.89</b>	0.85		
<b>N2DL-HeLa</b>	Preprocessing method	Histogram stretching and median	Histogram stretching		Median filter and histogram stretching
	Dice Score	0.80	<b>0.89</b>		0.81
<b>NIH3T3</b>	Preprocessing method	Histogram stretching and median	No preprocessing	No preprocessing	Gaussian filter and histogram stretching
	Dice Score	0.70	0.64	0.65	<b>0.83</b>

# Conclusion

# The perfect recipe

## N2DH-GOWT1

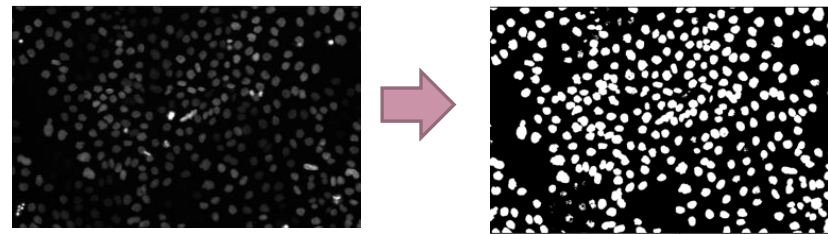
(first dataset)



- **Preprocessing:** histogram stretching
- **Postprocessing:** hole filling
- **Otsu:** global Otsu thresholding
- **Final median Dice Score:** 0.8864

## N2DL-HeLa

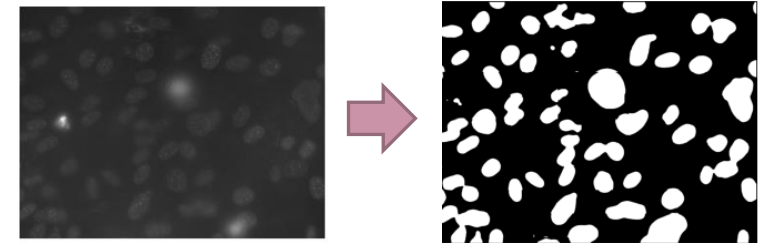
(second dataset)



- **Preprocessing:** histogram stretching
- **Otsu:** two-level Otsu thresholding
- **Final median Dice Score:** 0.8866

## NIH3T3

(third dataset)



- **Preprocessing:** Gaussian filter + histogram stretching
- **Otsu:** local adaptive Otsu thresholding
- **Final median Dice Score:** 0.8293

N: nuclear

2D: two-dimensional

H: high resolution

L: low resolution

# Thank you for your attention!

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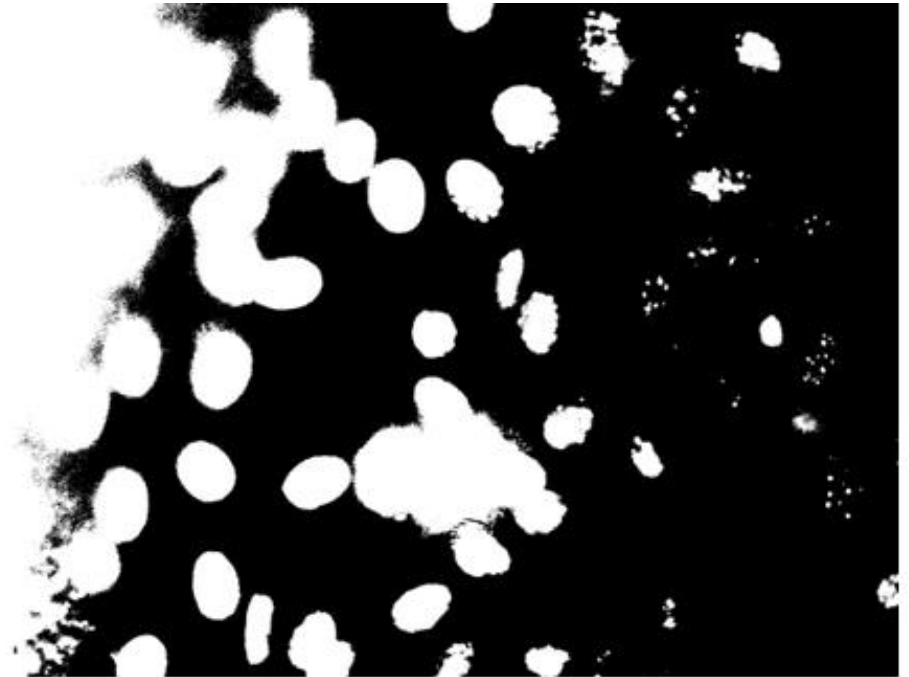
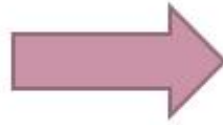
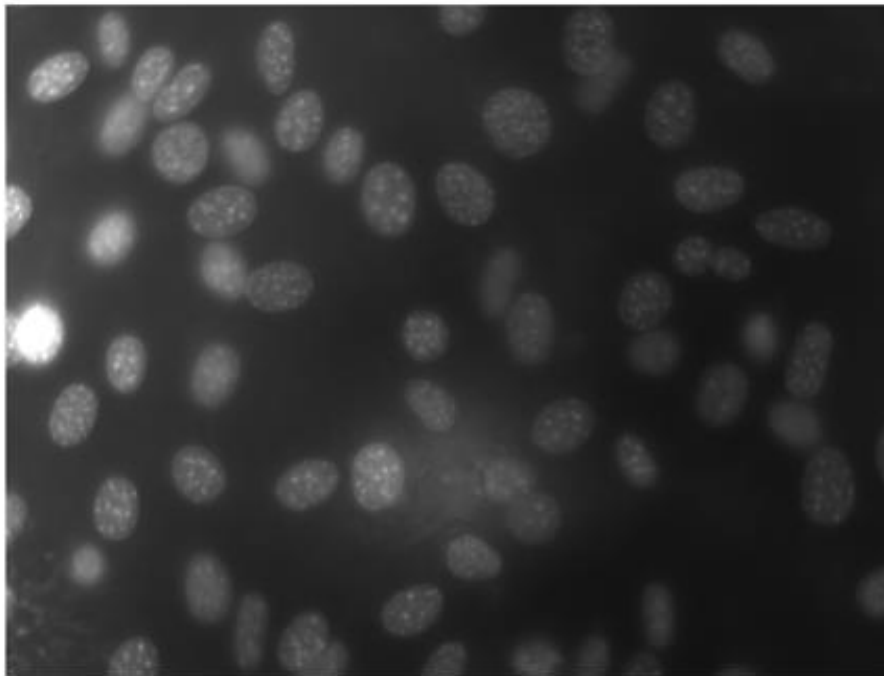


# Extra slides

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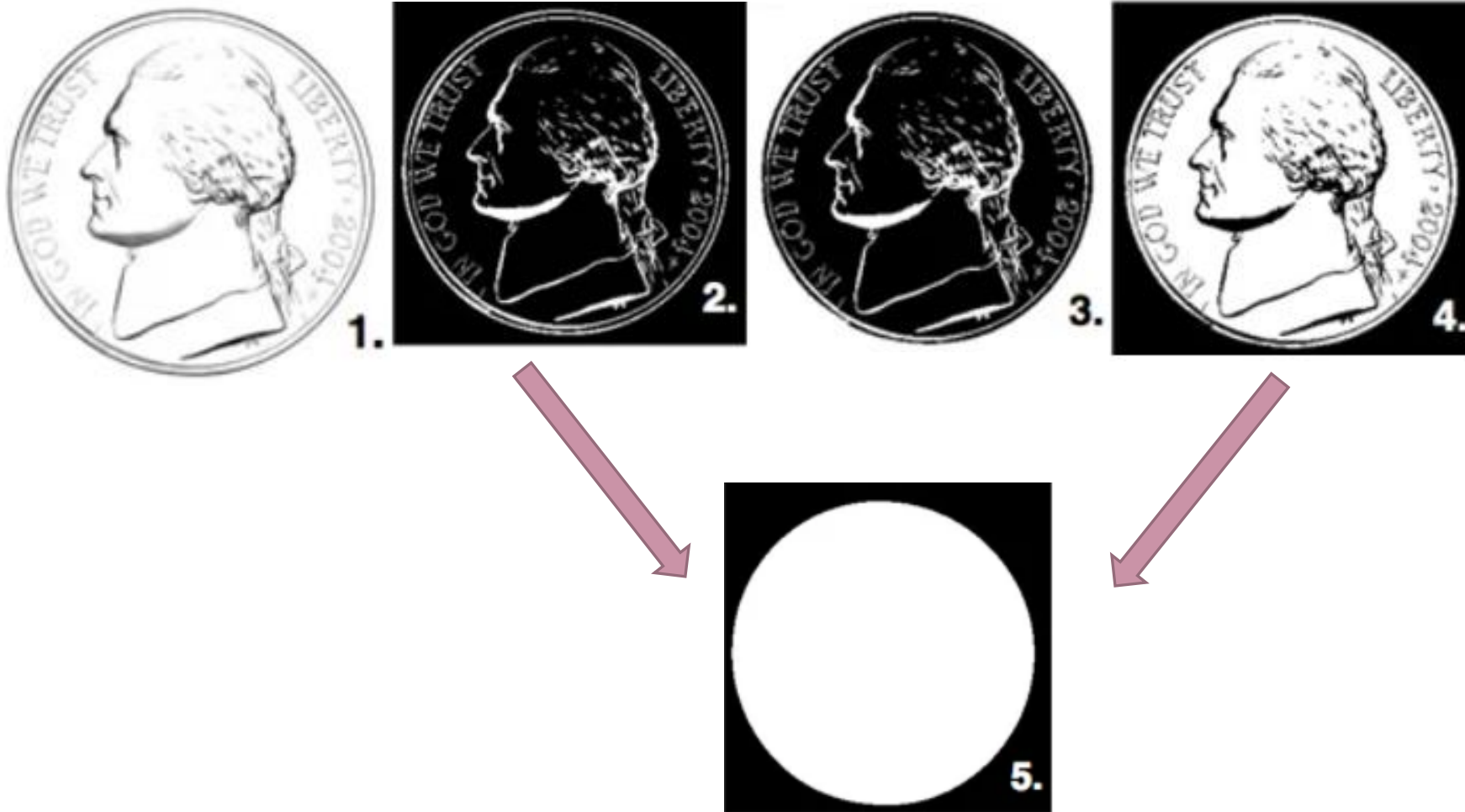
# Why local thresholding?

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# Hole filling



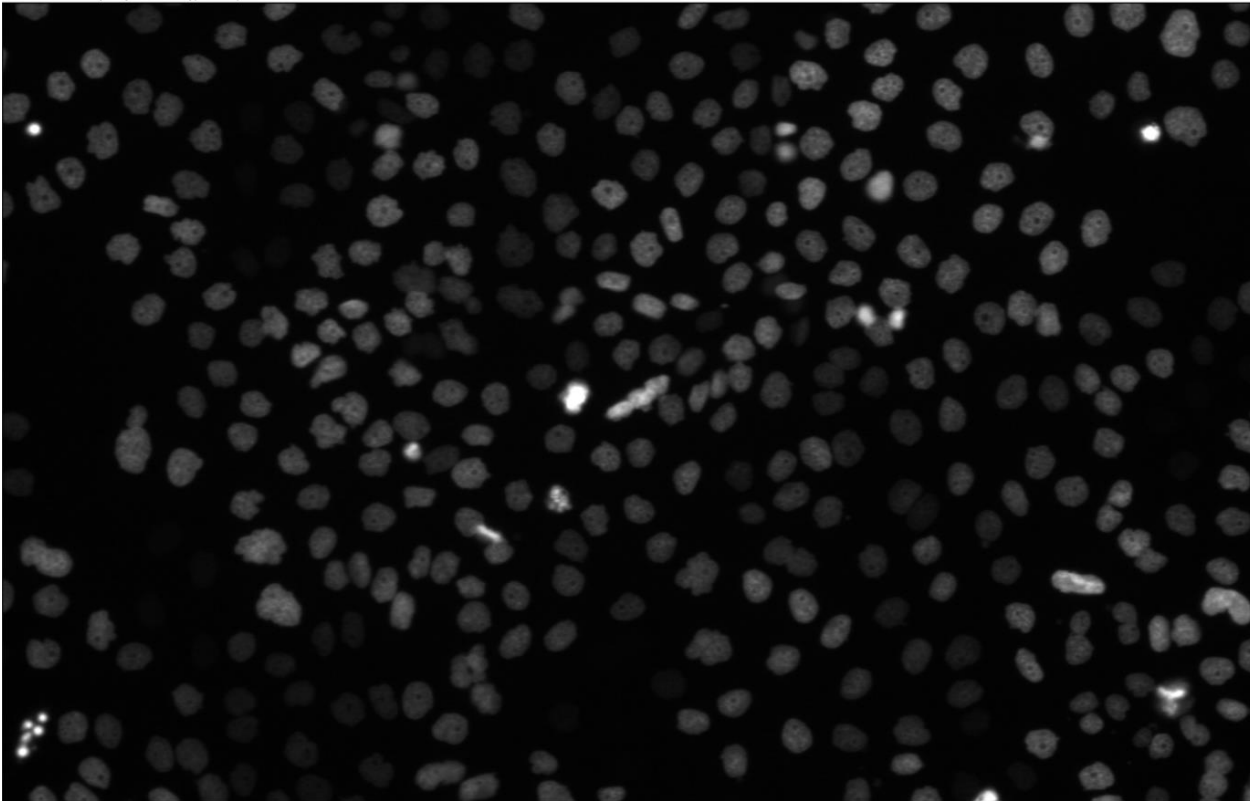
# Solution Ideas

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Challenge	Solution
Random noise	Gaussian filter, median filter
Holes	Median filter
Low contrast	Histogram stretching
Reflections	Intensity clipping, multithresholding
Brightness	Local thresholding

# Challenges: N2DL-HeLa

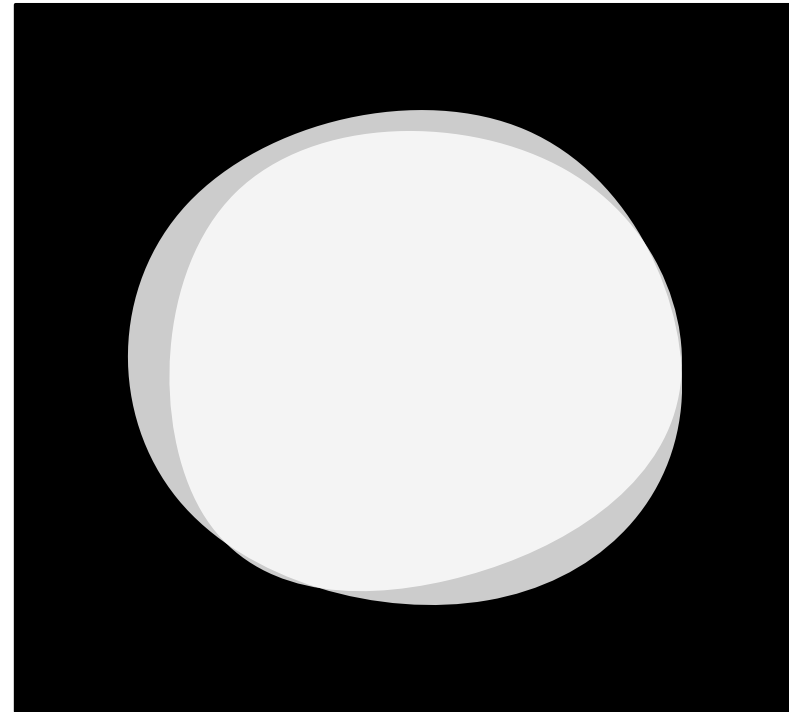
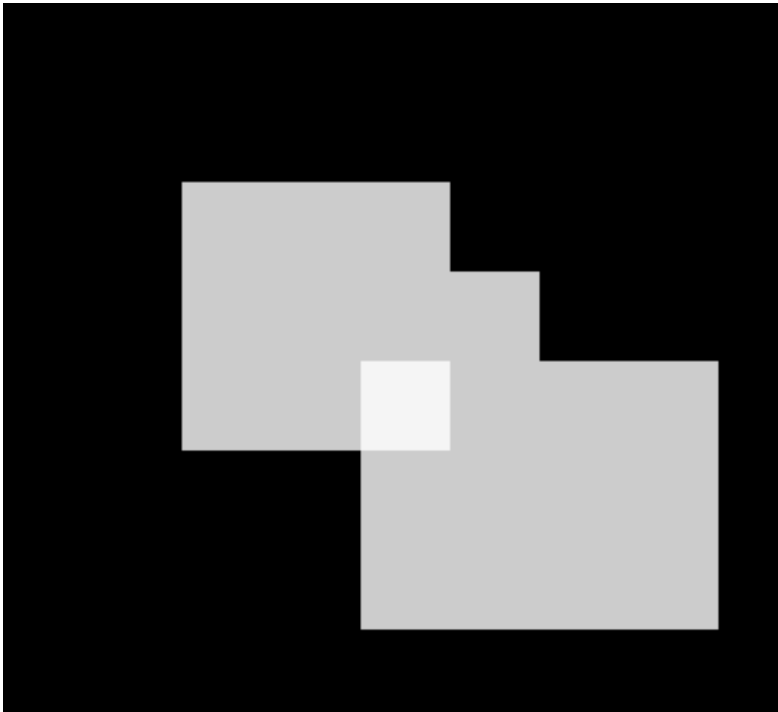
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Reflections

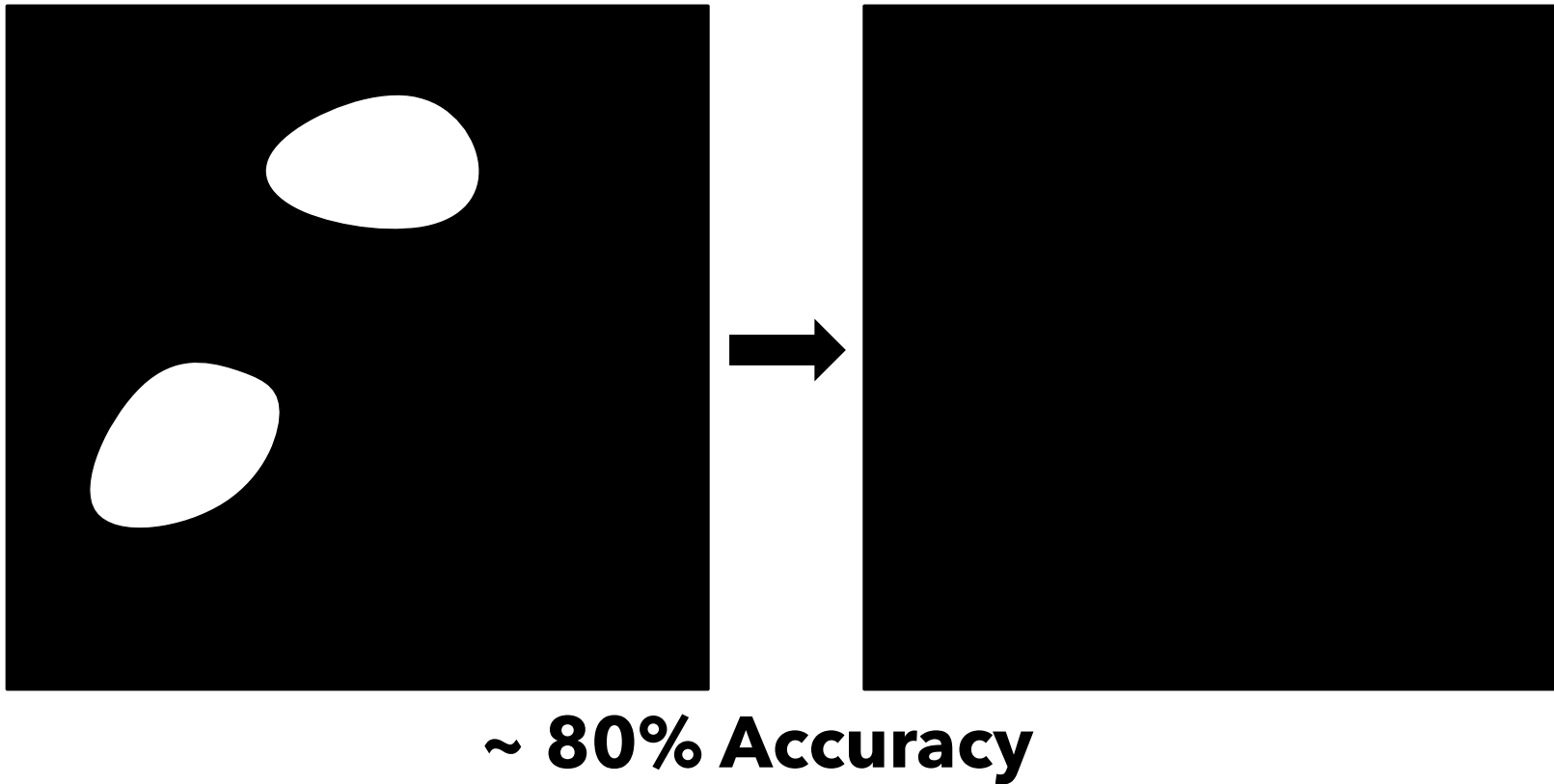
# Dice score - Issues

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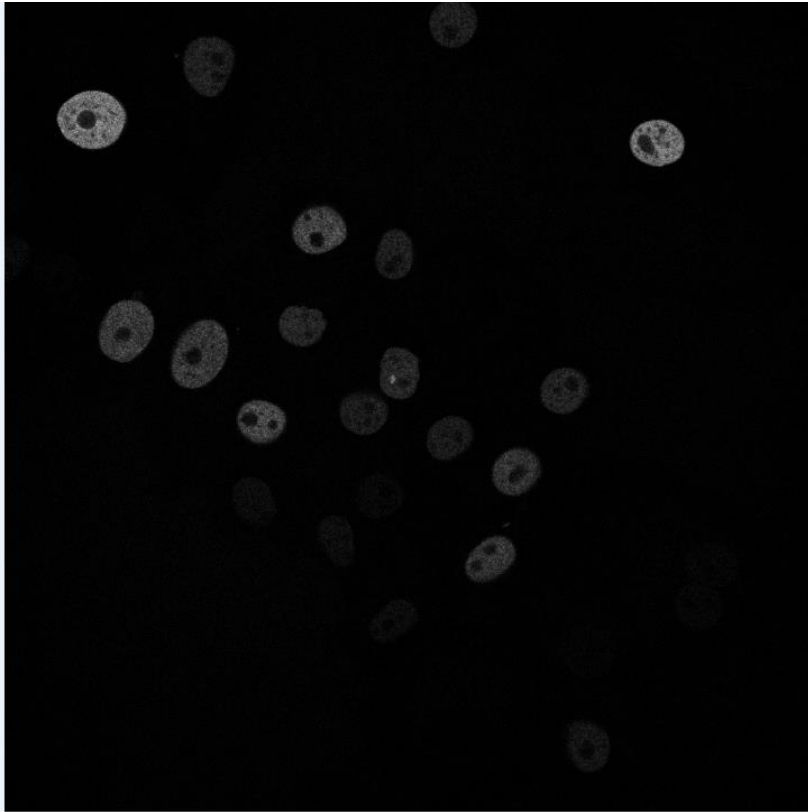
# Evaluation algorithm – Dice score

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# N2DH-GOWT1

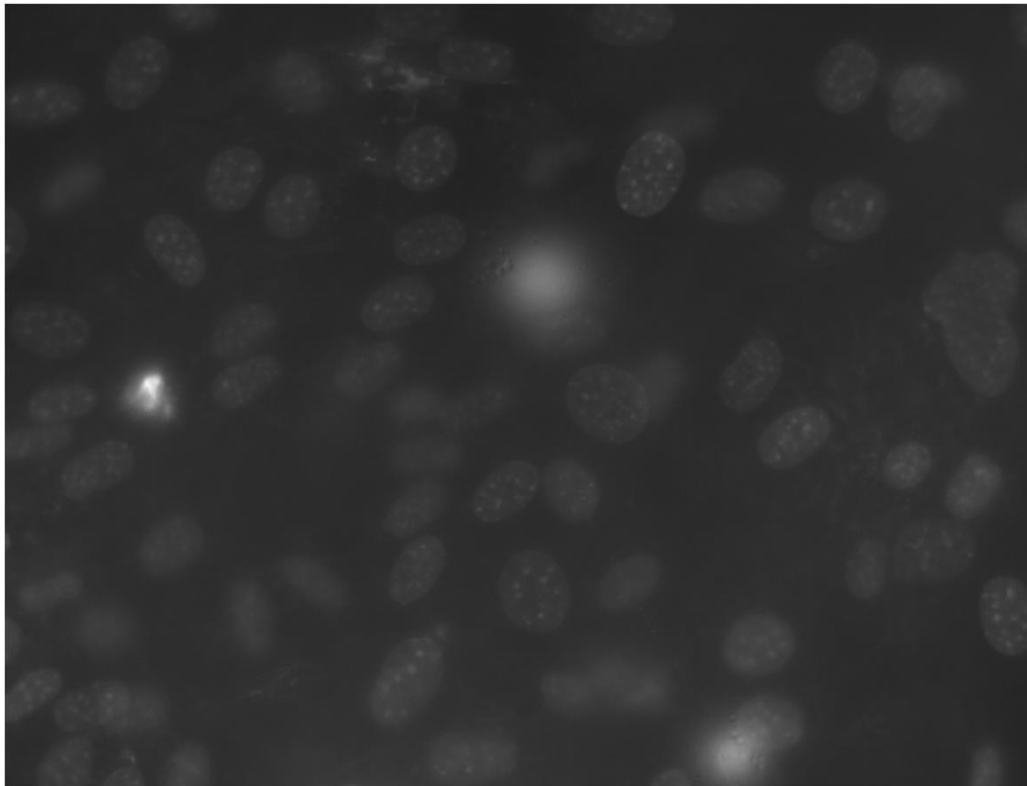
Cell type: embryonic stem cells | Organism: Mouse (*Mus musculus*)



- Express Oct4-GFP
- Leica TGS SP5 (confocal microscope)
- 6 images total
- 1024x1024 pixels
- 10-20 nuclei per image

# NIH3T3

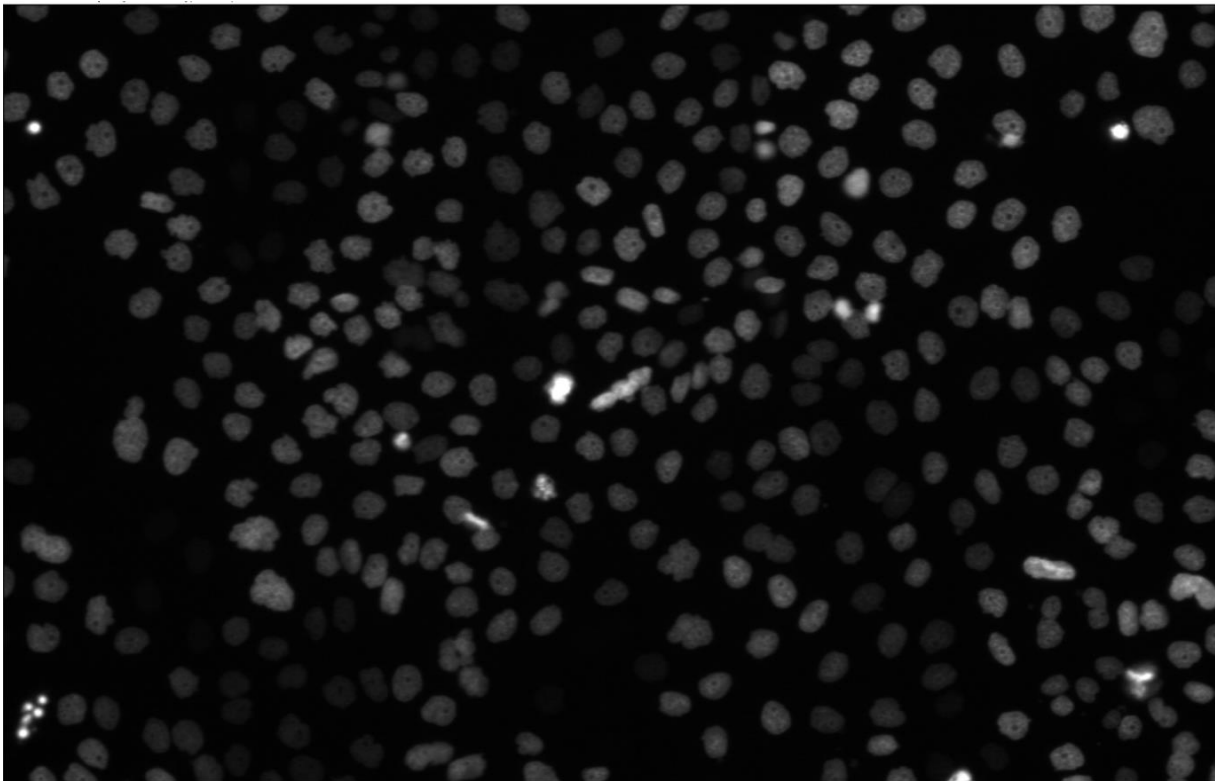
Cell type: Embryonic fibroblast cells | Organism: Mouse (*Mus musculus*)



- Stained with Hoechst (fluorescent dye)
- Fluorescence microscope
- 18 images total
- Size: 1344x1024 pixels
- about 60 nuclei per image

# N2DL-HeLa

Cell type: cervical adenocarcinoma cells | organism: human (*Homo sapiens*)



- Express H2B-GFP
- Olympus IX81 Confocal Microscope
- 4 images total
- Size: 1100x 700 pixels
- 30-50 nuclei per image



# Otus Thresholding usage

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- Locate cell boundaries
- Cell type classification
  - Cell counting
  - Cell phenotype analysis (size, shape,..)
- **But not used for very complex images !**

# Otsu Thresholding

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Class probabilities ( $\omega_{0,1}$ ):

$$\omega_0 = \Pr(C_0) = \sum_{i=1}^k p_i = \omega(k)$$

$$\omega_1 = \Pr(C_1) = \sum_{i=k+1}^L p_i = 1 - \omega(k)$$

Class mean levels ( $\mu_{0,1}$ ) and total mean level ( $\mu_T$ ):

$$\mu_0 = \sum_{i=1}^k i \Pr(i|C_0) = \sum_{i=1}^k ip_i/\omega_0 = \mu(k)/\omega(k)$$

$$\mu_1 = \sum_{i=k+1}^L i \Pr(i|C_1) = \sum_{i=k+1}^L ip_i/\omega_1 = \frac{\mu_T - \mu(k)}{1 - \omega(k)}$$

$$\mu_T = \mu(L) = \sum_{i=1}^L ip_i$$

Class variances ( $\sigma_{0,1}^2$ ) and total variance ( $\sigma_T^2$ ):

$$\sigma_0^2 = \sum_{i=1}^k (i - \mu_0)^2 \Pr(i|C_0) = \sum_{i=1}^k (i - \mu_0)^2 p_i/\omega_0$$

$$\sigma_1^2 = \sum_{i=k+1}^L (i - \mu_1)^2 \Pr(i|C_1) = \sum_{i=k+1}^L (i - \mu_1)^2 p_i/\omega_1$$

$$\sigma_T^2 = \sum_{i=1}^L (i - \mu_T)^2 p_i$$

$L$  = Number of gray levels in the picture

$n_i$  = Number of pixels at level  $i$

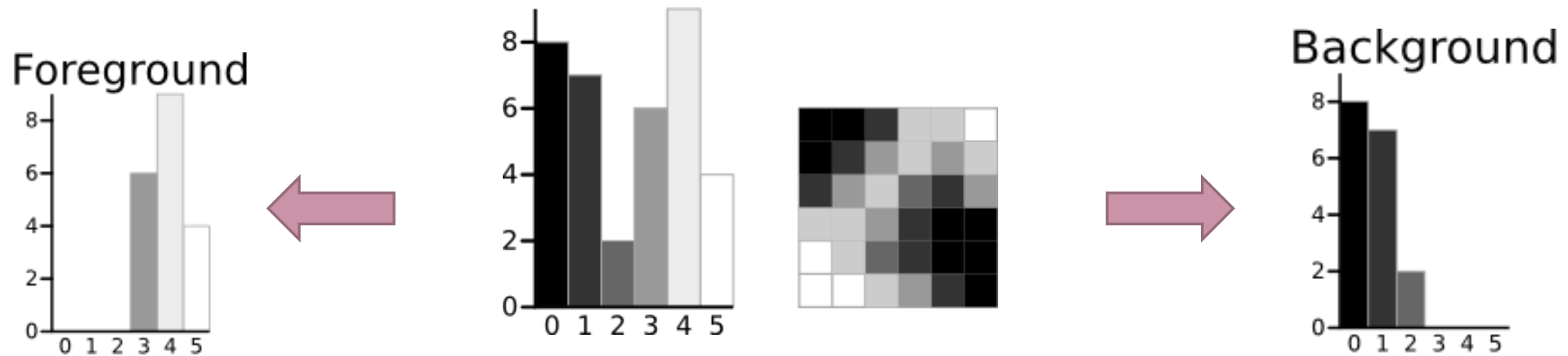
$N$  = Total number of pixels

$p_i$  = Probability of level  $i$

$k$  = Threshold intensity

$$p_i = n_i/N$$

# Otsu Thresholding



$$\begin{aligned}
 \text{Weight } W_f &= \frac{6 + 9 + 4}{36} = 0.5278 \\
 \text{Mean } \mu_f &= \frac{(3 \times 6) + (4 \times 9) + (5 \times 4)}{19} = 3.8947 \\
 \text{Variance } \sigma_f^2 &= \frac{((3 - 3.8947)^2 \times 6) + ((4 - 3.8947)^2 \times 9) + ((5 - 3.8947)^2 \times 4)}{19} \\
 &= \frac{(4.8033 \times 6) + (0.0997 \times 9) + (4.8864 \times 4)}{19} \\
 &= 0.5152
 \end{aligned}$$

$$\begin{aligned}
 \text{Weight } W_b &= \frac{8 + 7 + 2}{36} = 0.4722 \\
 \text{Mean } \mu_b &= \frac{(0 \times 8) + (1 \times 7) + (2 \times 2)}{17} = 0.6471 \\
 \text{Variance } \sigma_b^2 &= \frac{((0 - 0.6471)^2 \times 8) + ((1 - 0.6471)^2 \times 7) + ((2 - 0.6471)^2 \times 2)}{17} \\
 &= \frac{(0.4187 \times 8) + (0.1246 \times 7) + (1.8304 \times 2)}{17} \\
 &= 0.4637
 \end{aligned}$$

# Discriminant Criterion Measure

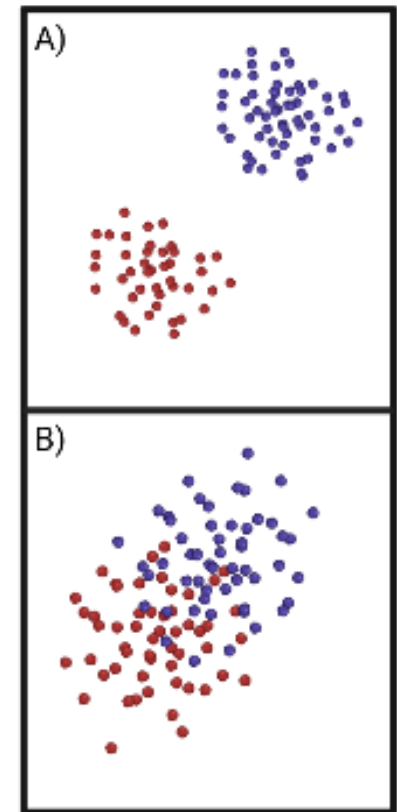
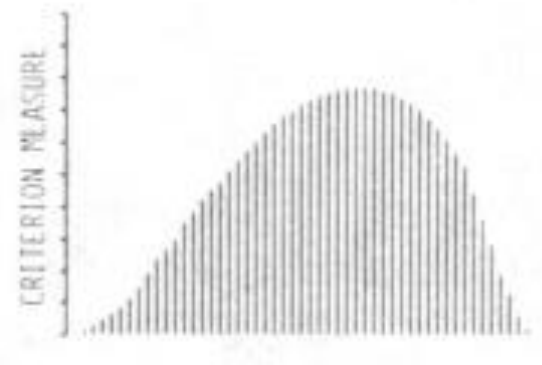
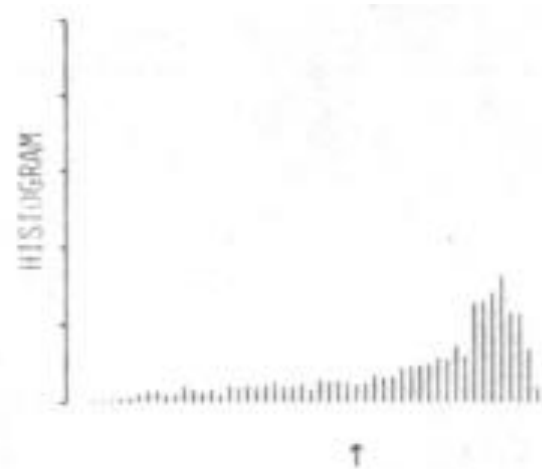
## Criterion measure

$$\eta(T) = \sigma_B^2(T) / \sigma_T^2$$

$\sigma_B^2$  = Between-class variance

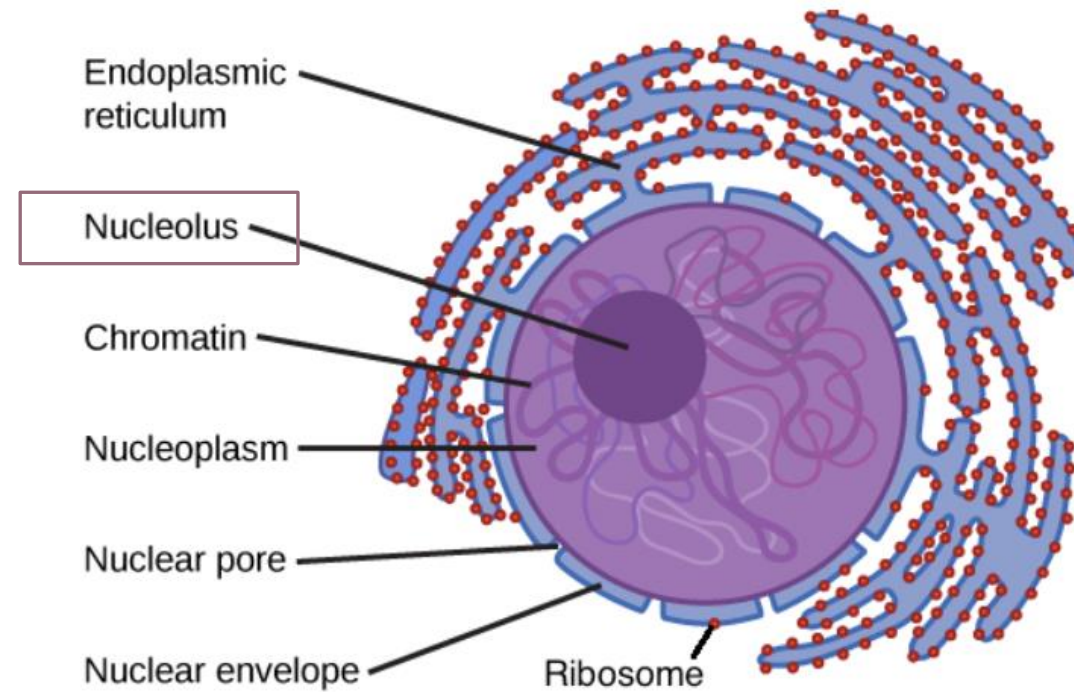
$\sigma_T^2$  = Total variance

$$0 \leq \eta^* \leq 1$$



# Holes

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*Bildquelle: OpenStax Biology.*

# Histogram stretching

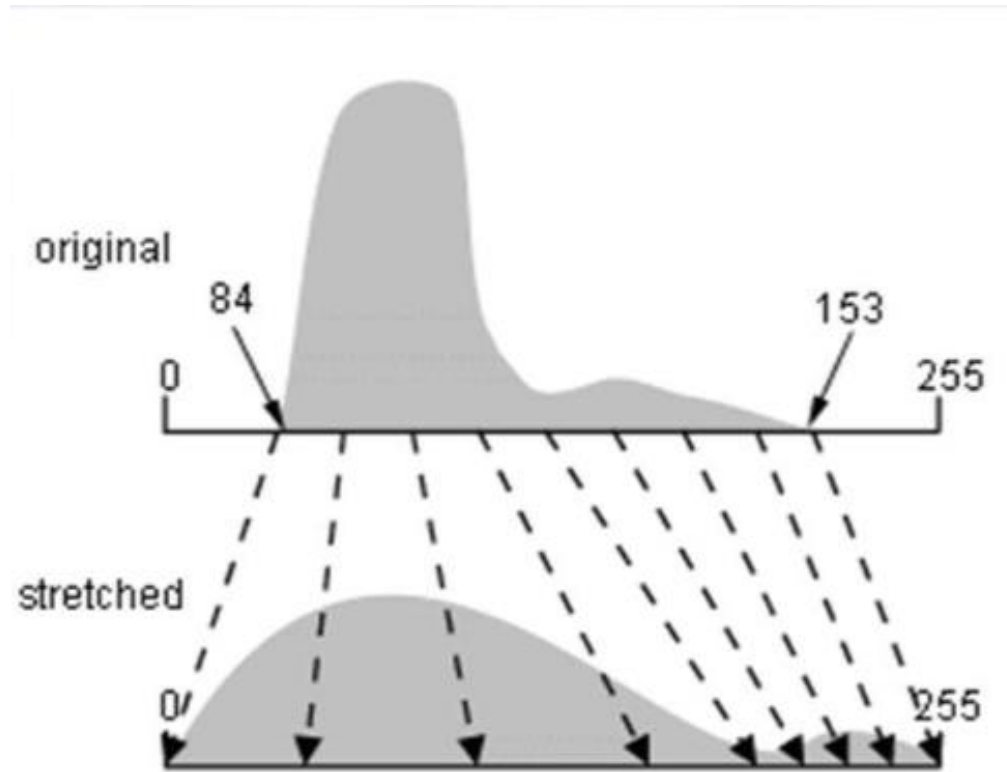
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- stretching range of intensity values to achieve a higher contrast -> linear scaling

$$P_{\text{out}} = (P_{\text{in}} - c) \left( \frac{b-a}{d-c} \right) + a$$

# Example Histogram stretching

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# Two-level Otsu Thresholding

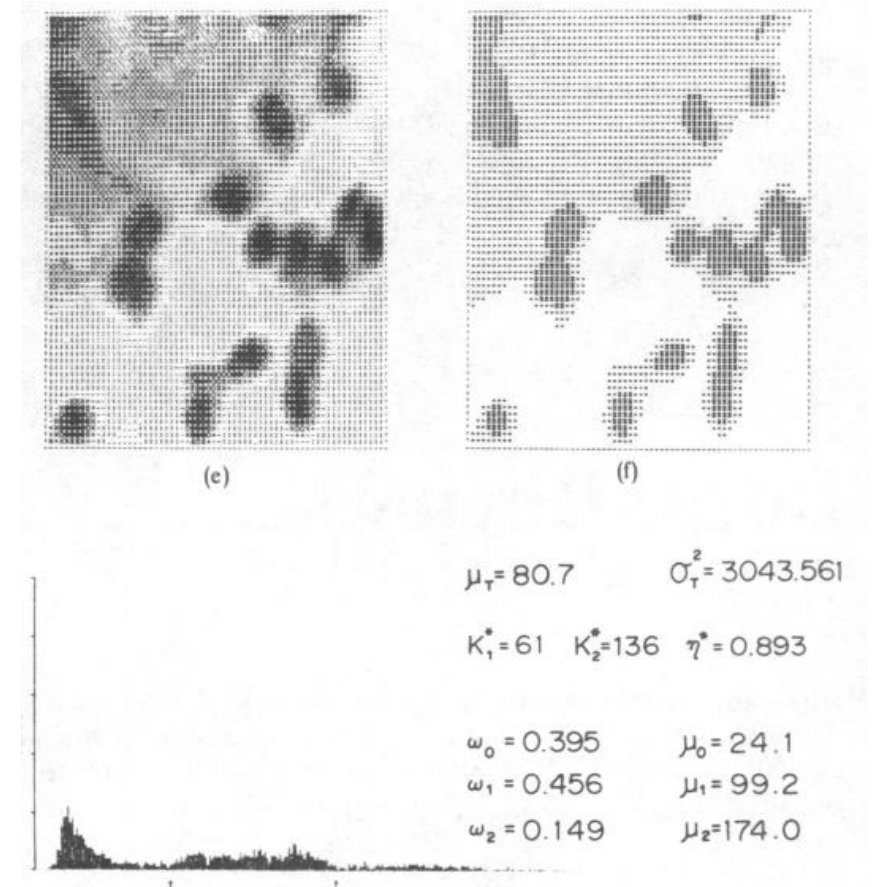
## Two-level Otsu Thresholding

$$\sigma_B^2 = \omega_1(\mu_1 - \mu_T)^2 - \omega_2(\mu_2 - \mu_T)^2 - \omega_3(\mu_3 - \mu_T)^2$$

$\omega_{1,2,3}$  = Probabilities of class occurrence

$\mu_{1,2,3}$  = Class mean levels

$\mu_T$  = Total mean level





# Application of Filter

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- Choose Filtermask
- Convolution
  - Flipping filter
  - Multiplication of filter values with image intensity values
  - Summation of the multiplication results