

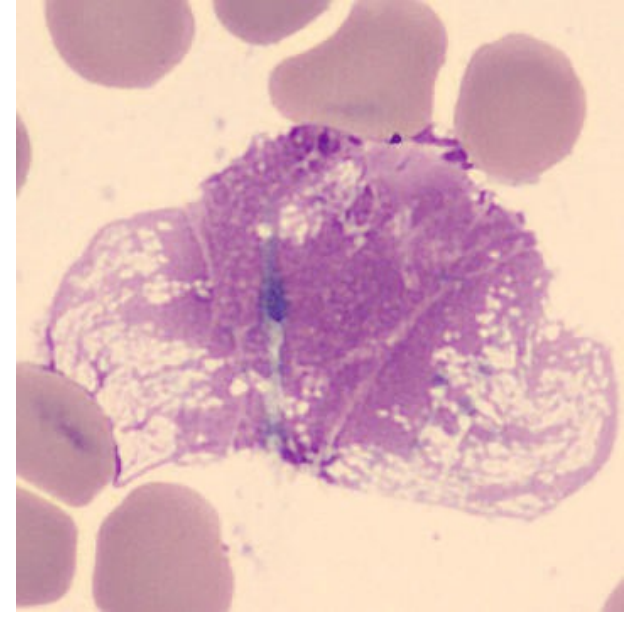
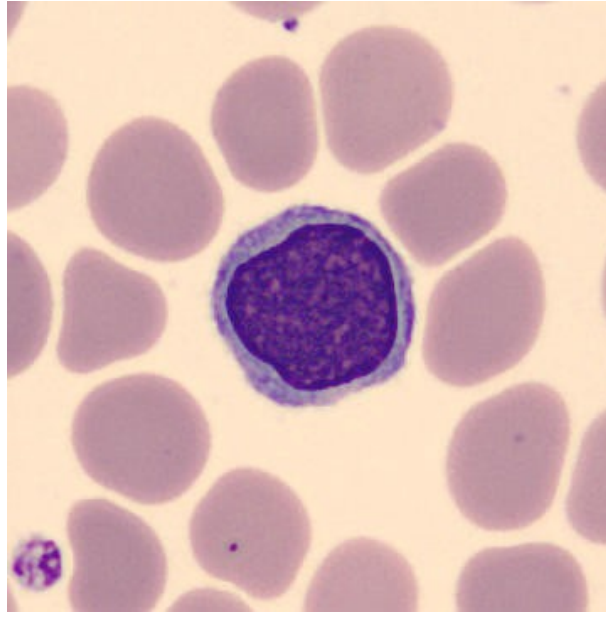
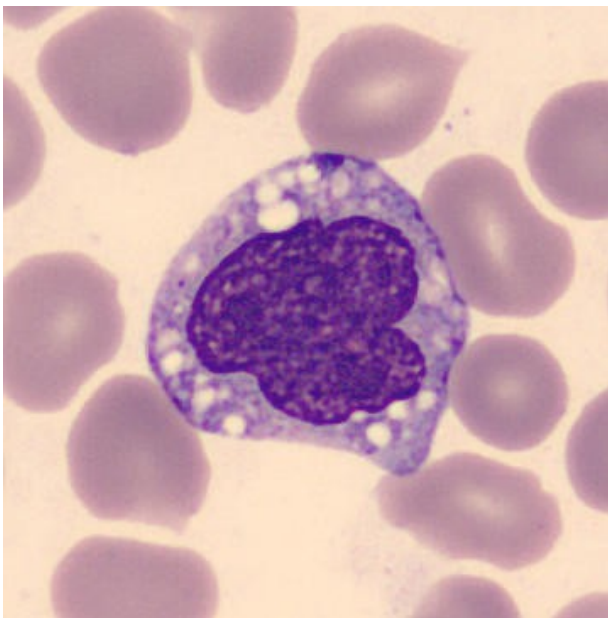
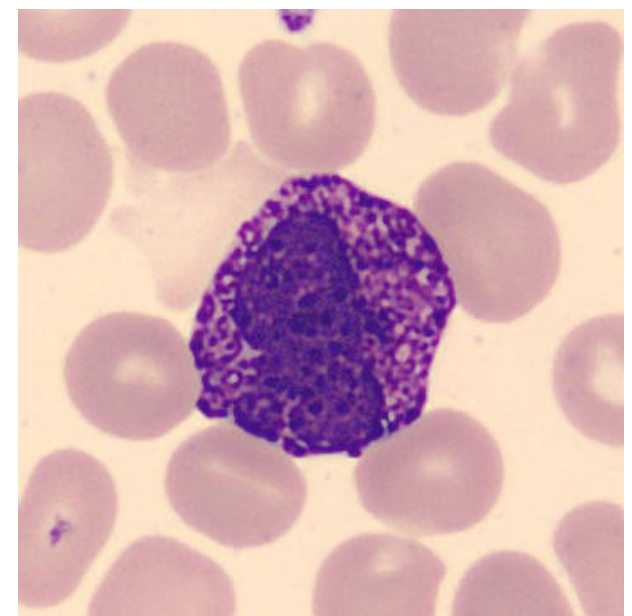
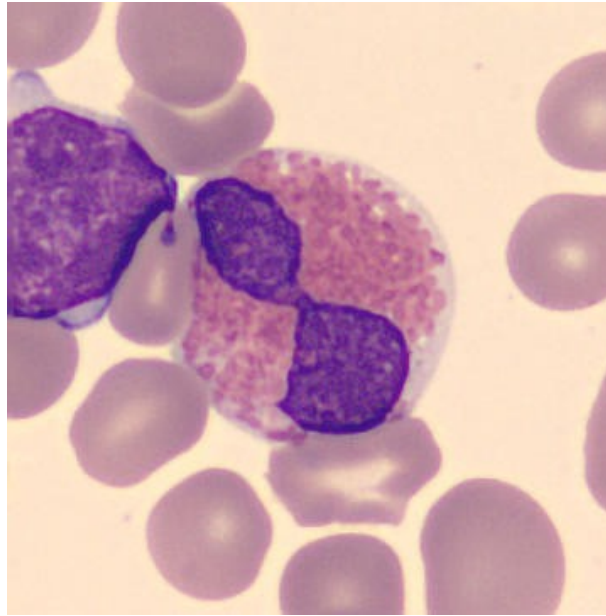
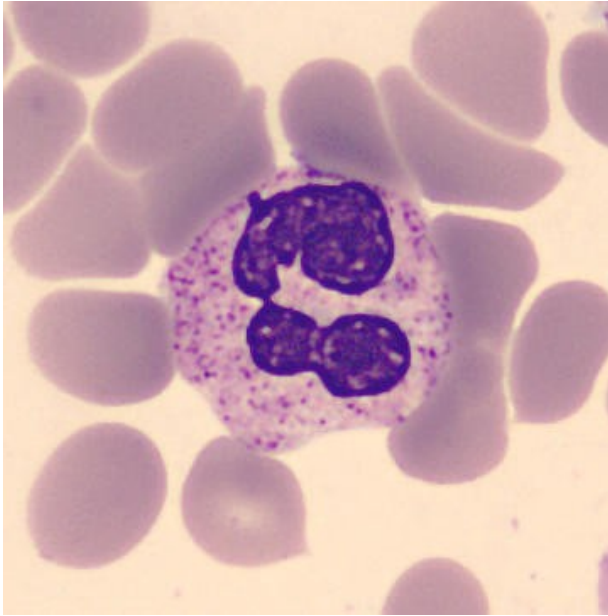
# Leucocyte Segmentation and Classification

Bc. Adam Chromý

# Goals of project

- ▶ Input images are acquired from optical microscope scanning leucocytes in smear blood. Centroids of leucocytes or of its clumps are determined and rectangle around this centroid is saved.
- ▶ First goal is to segment leucocytes from image.
- ▶ Second goal is to create algorithm classifying leucocytes to appropriate group.
- ▶ Then verify reliability of classification algorithm on testing data (different from training data).

# Input Images

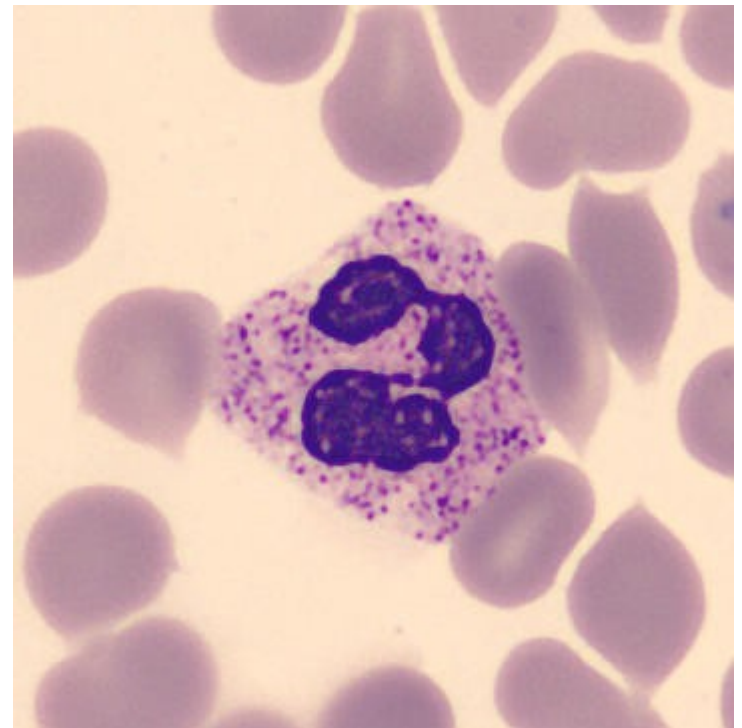


# Results of Project

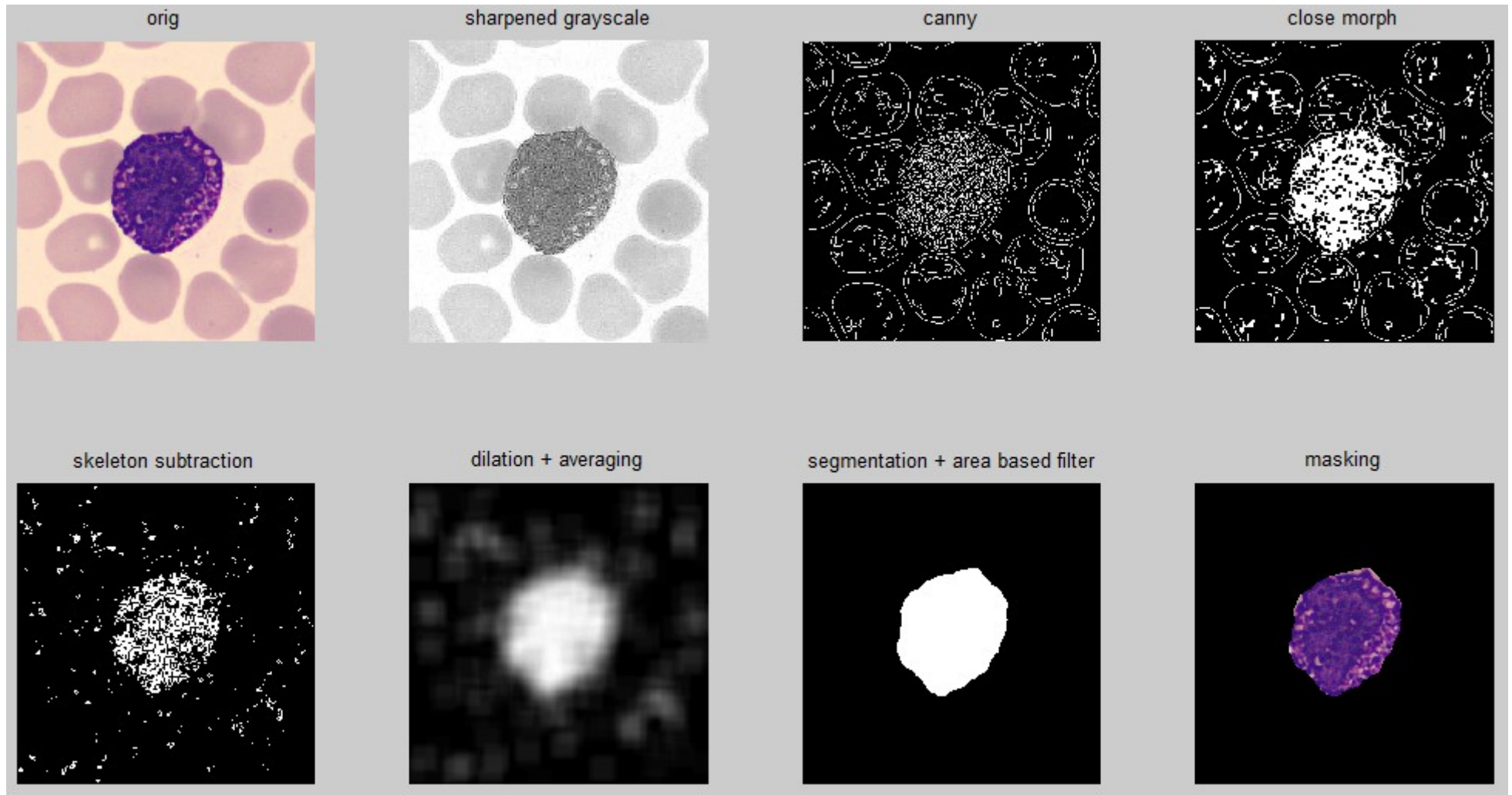
- ▶ **Classification based on extracted features:**
  - ▶ each type has its own characteristic fetures (not unique for just one class)
  - ▶ we are looking for features distinguishing two classes
- ▶ **STEP 1: Segmentation**
  - ▶ to be able to measure characteristic fetures, proper segmantation is neccessary
- ▶ **STEP 2: Classification**
  - ▶ empirically chosen features are computed for each leucocyte
  - ▶ classification based on decision-tree

# Step 1: Segmentation (1/3)

- ▶ surface of leucocyte is covered with texture containing colors of surroundings – thresholding useless
- ▶ erythrocytes are smooth – disadvantage could be taken as advantage
  - ▶ texture could be defined as noise
  - ▶ noisy-area detection defines leucocyte

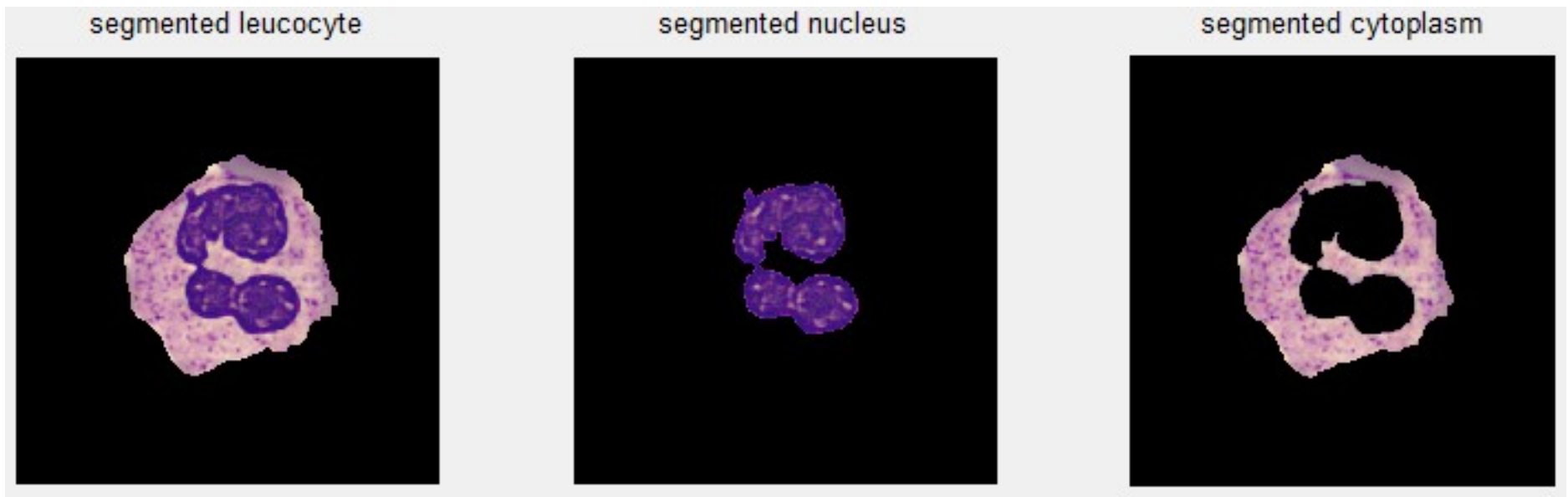


# Step 1: Segmentation (2/3)



# Step 1: Segmentation (3/3)

- ▶ nucleus can be easily distinguished from rest of leucocyte by thresholding



# Step 2: Classification (1/3)

- ▶ totally 1837 samples available
  - ▶ 1377 samples used for training
  - ▶ 460 samples used for verifying (testing of accuracy)
- ▶ in case of each sample, features are extracted:
  - ▶ size of leucocyte and its nucleus → nucleus coverage of cell
  - ▶ average cytoplasm color – various color models
  - ▶ statistical spread of feature values in each class

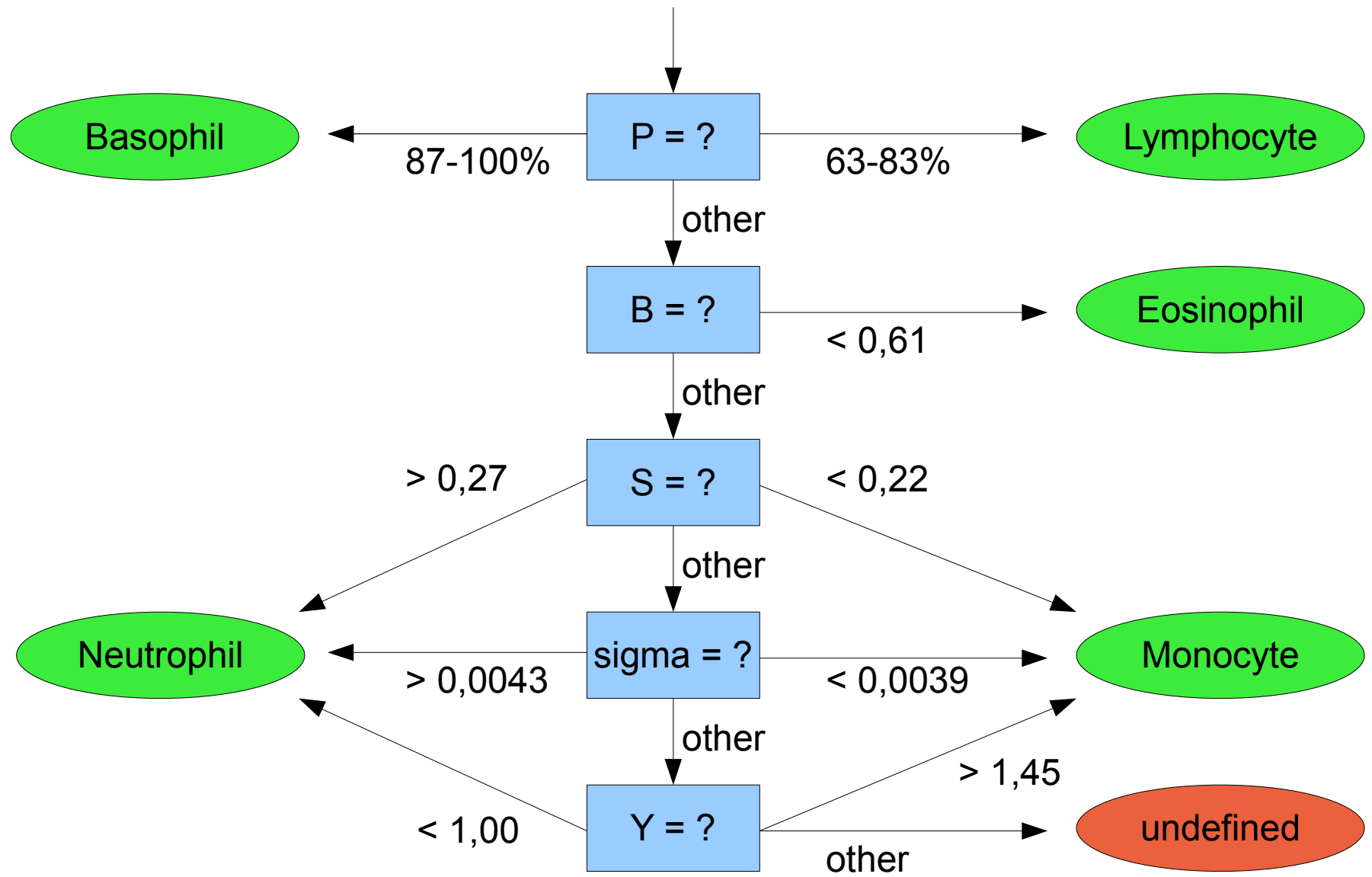


## Step 2: Classification (2/3)

| příznak                | Neutrofil   | Monocyt     | Eosinofil | Bazofil    | Lymfocyt  |
|------------------------|-------------|-------------|-----------|------------|-----------|
| pokrytí buňky jádrem   | 20 – 45 %   | 40 – 63 %   | 20 – 43 % | 87 – 100 % | 63 – 83 % |
| prům. barva cytopl – R | 0,69 – 0,83 | 0,65 – 0,82 | -         | -          | -         |
| prům. barva cytopl – G | 0,45 – 0,66 | 0,51 – 0,70 | -         | -          | -         |
| prům. barva cytopl – B | 0,62 – 0,71 | 0,65 – 0,72 | max. 0,61 | -          | -         |
| prům. barva cytopl – H | 0,65 – 0,85 | 0,43 – 0,88 | -         | -          | -         |
| prům. barva cytopl – S | 0,22 – 0,36 | 0,18 – 0,27 | -         | -          | -         |
| prům. barva cytopl – V | 0,69 – 0,83 | 0,69 – 0,82 | -         | -          | -         |
| prům. barva cytopl – Y | max. 1,45   | min. 1,00   | -         | -          | -         |
| sigma (Cb-Cr)/(Cb+Cr)  | min. 0,0039 | max. 0,0043 | -         | -          | -         |

- ▶ Note: Basophil really covers about 20-33% of cell, but because of high density of dark granulas, it seems to be entirely covered by nucleus.

# Step 2: Classification (3/3)



# Algorithm Reliability

- ▶ 460 testing samples from various smear bloods
- ▶ wrong classification at 46 cases – eg. 90% reliability
  - ▶ dead cells or scattered epithelium – classified to random class (18x)
  - ▶ large lymphocyte and monocyte – difficult to distinguish also for trained human (11x)
  - ▶ very bright neutrophil and monocyte (10x)
  - ▶ lymphocyte segmentation error – wrong features extracted (7x)

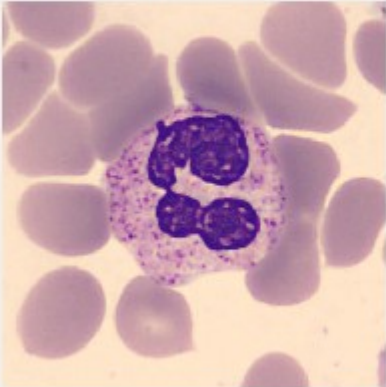
# User Interface Demonstration (1/6)

Leucocyte classification

Computing time: 1.06 s


image 1 / 460

original image




statistics

Total area: 23296  
Nucleus area: 8783 ( 37.70%)  
B: 0.6747  
S: 0.2573  
Y: 1.1258  
sigma: 0.0072

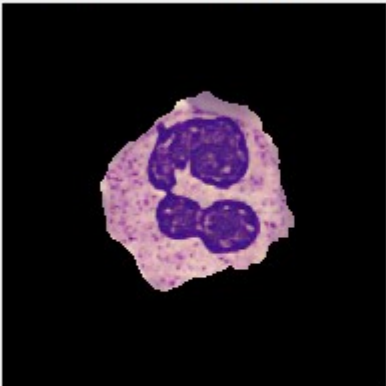


Class: Neutrophil

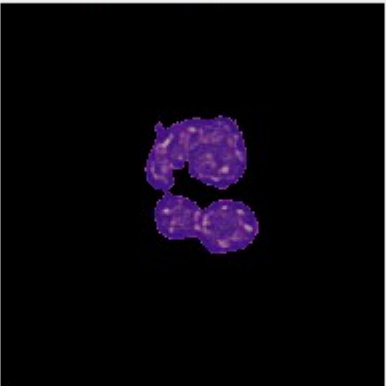
noised-area detection



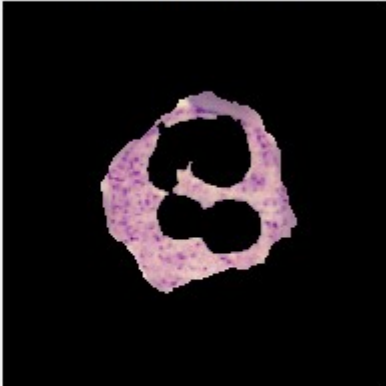
segmented leucocyte



segmented nucleus



segmented cytoplasm



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Next image >>

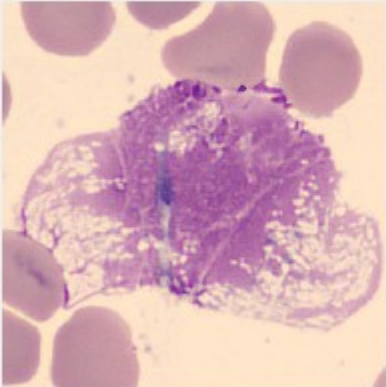
# User Interface Demonstration (2/6)

Leucocyte classification

Computing time: 1.23 s


image 2 / 460

original image



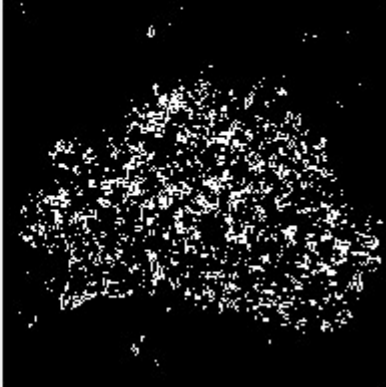
statistics

Total area: 52779  
Nucleus area: 0 ( 0.00%)  
B: 0.6984  
S: 0.2929  
Y: 0.7222  
sigma: 0.0243

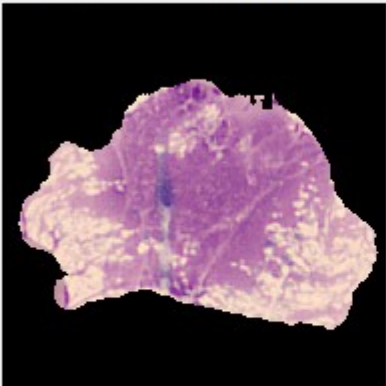


Class: UNKNOWN

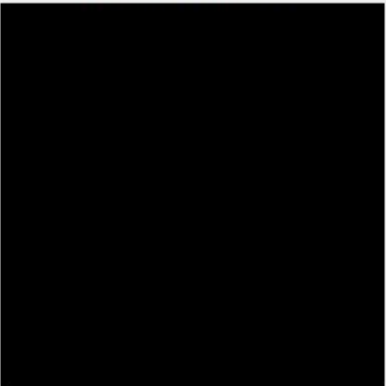
noised-area detection



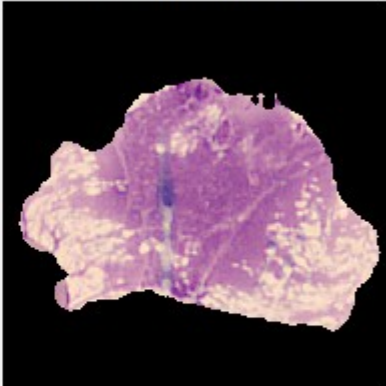
segmented leucocyte



segmented nucleus



segmented cytoplasm



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Next image >>

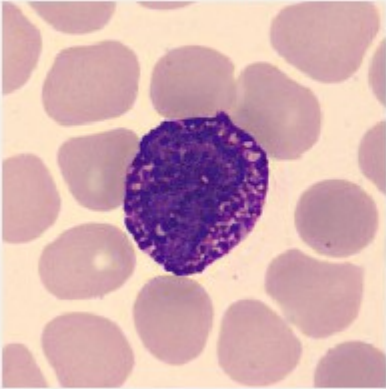
# User Interface Demonstration (3/6)

Leucocyte classification

Computing time: 0.97 s


image 4 / 460

original image




statistics

Total area: 17006  
Nucleus area: 14938 ( 87.84%)  
B: 0.6313  
S: 0.2558  
Y: 4.5016  
sigma: 0.0010

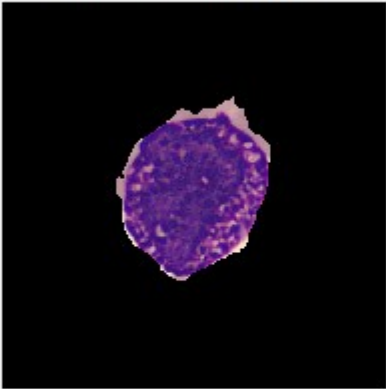


Class: Basophil

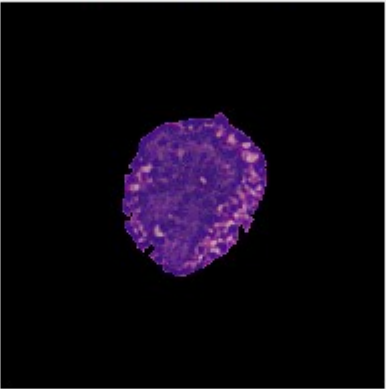
noised-area detection




segmented leucocyte



segmented nucleus



segmented cytoplasm



<< Previous image

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Next image >>

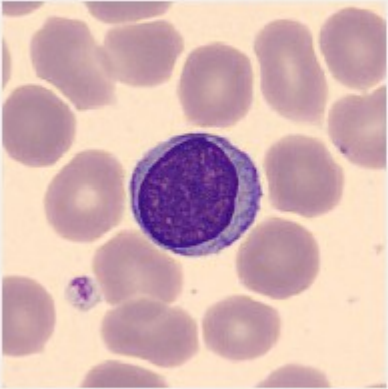
# User Interface Demonstration (4/6)

Leucocyte classification

Computing time: 1.15 s


image 6 / 460

original image



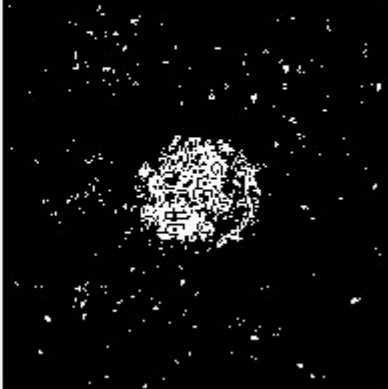
statistics

Total area: 11197  
Nucleus area: 7395 ( 66.04%)  
B: 0.6782  
S: 0.3034  
Y: 2.6365  
sigma: 0.0007

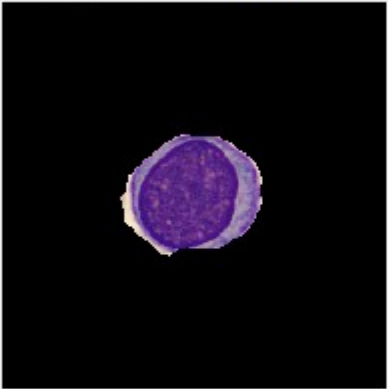


Class: Lymphocyte

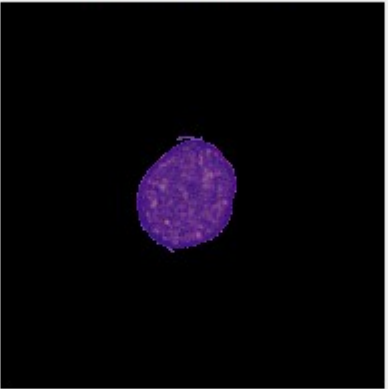
noised-area detection




segmented leucocyte



segmented nucleus



segmented cytoplasm



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Next image >>

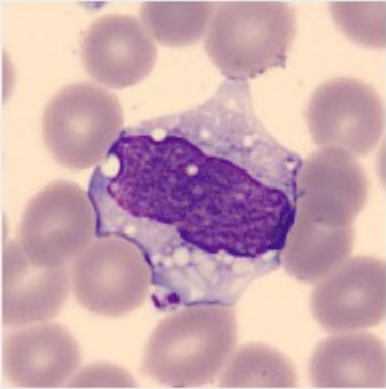
# User Interface Demonstration (5/6)

Leucocyte classification

Computing time: 1.19 s


image 7 / 460

original image



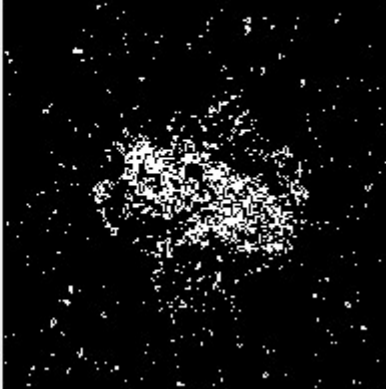
statistics

Total area: 25079  
Nucleus area: 12293 ( 49.02%)  
B: 0.7064  
S: 0.1999  
Y: 1.2122  
sigma: 0.0027

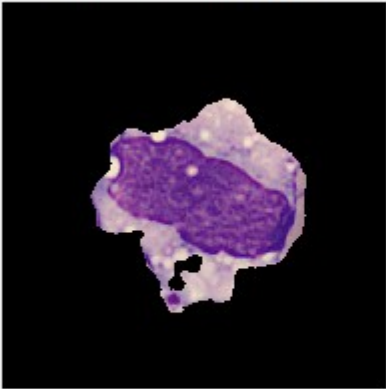


Class: Monocyte

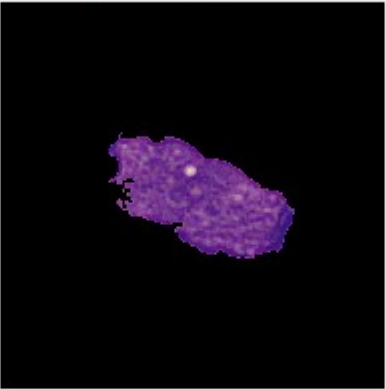
noised-area detection



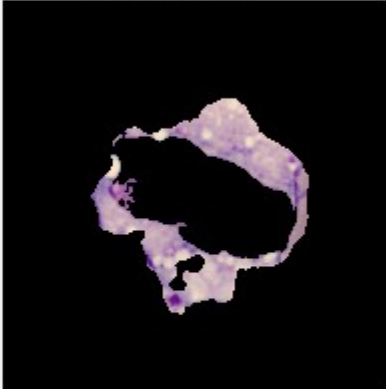
segmented leucocyte



segmented nucleus



segmented cytoplasm



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Next image >>



# User Interface Demonstration (6/6)

Leucocyte classification

Computing time: 1.20 s

image 8 / 460

original image



statistics

Total area: 33675  
Nucleus area: 14946 ( 44.38%)  
B: 0.6086  
S: 0.3423  
Y: 0.9226  
sigma: 0.0102



Class: Eosinophil

noised-area detection



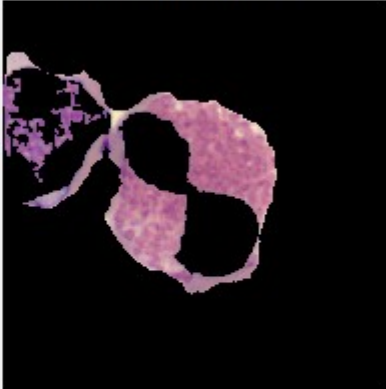
segmented leucocyte



segmented nucleus



segmented cytoplasm



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# Conclusion

- ▶ classifier realized as decision-tree based on extracted features
- ▶ about 90% reliability
- ▶ there is big chance for improvements:
  - ▶ detection of dead cells
  - ▶ probability-based approach to features (fuzzy classification)

Děkuji za pozornost

# Reference

- ▶ <http://old.lf3.cuni.cz/histologie/atlas/demo/73/index.htm>
- ▶ [http://en.wikipedia.org/wiki/White\\_blood\\_cell#Overview\\_table](http://en.wikipedia.org/wiki/White_blood_cell#Overview_table)
- ▶ <http://www.zshk.cz/files/trochahematologie.pdf>