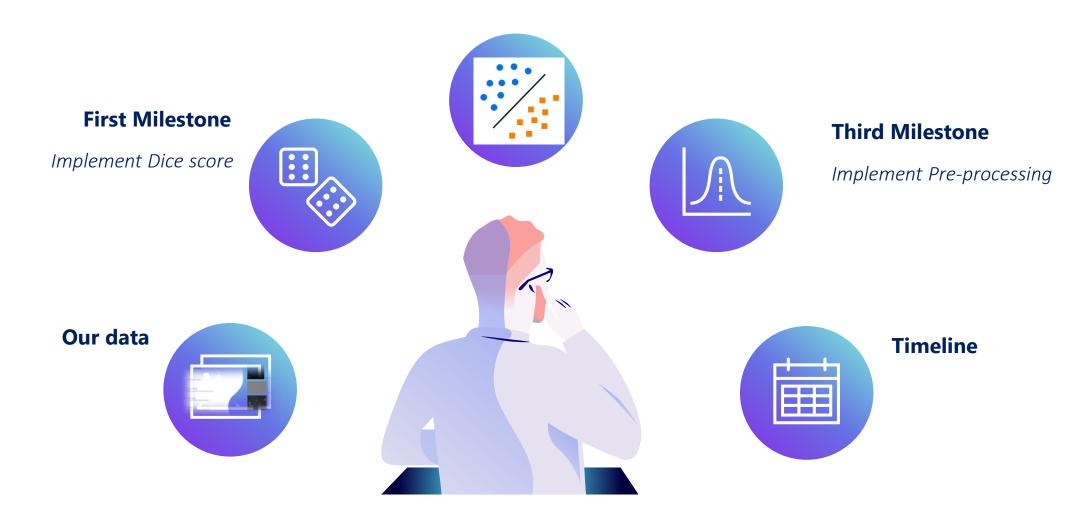
## Cell nuclei segmentation: support vector machine

Project proposal by Michelle Emmert, Juan Hamdan, Laura Sanchis und Gloria Timm



## Our data

28 images of nuclei

N2DH-GOWT1

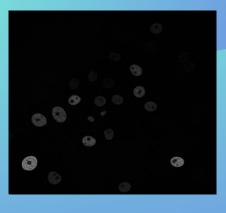
GFP transfected GOWT1 mouse embryonic stem cells

) N2DL-HeLa

Histone 2B (H2B)-GFP expressing HeLa cells

) NIH3T3

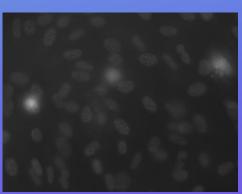
mouse embyonic fibroblast – CD tagged (EGFP)



N2DH-GOWT1



N2DL-HeLa



NIH3T3

## Our data

#### N2DH-GOWT1

- Medium difficulty
- Heterogeneous staining
- Prominent nucleoli + mitoses
- Cells entering and leaving the field of view and frequent cell collisions

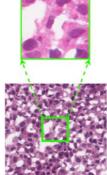
#### N2DL-HeLa

- High difficulty
- High cell density and low resolution
- Frequent mitoses
- Presence of colliding, entering and leaving cells with low fluorescence intensity

#### NIH3D3

- Medium difficulty
- Nuclei far apart + less clustering
- Nuclei homogeneous in shape and size
- But they also vary in brightness between images
- Images often contain visible debris.

## Our goal



PART OF LESS

Input: Microscopic images

Preprocessing & filtering

<u>Segmentation</u>:

Support vector machine

<u>Data mining</u>: Counting nuclei

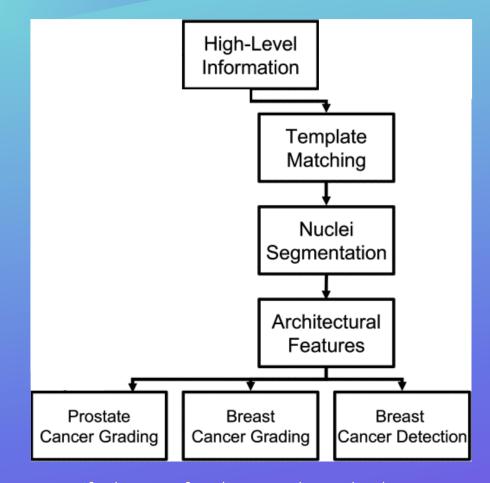


Output: Segmented image & number of nuclei

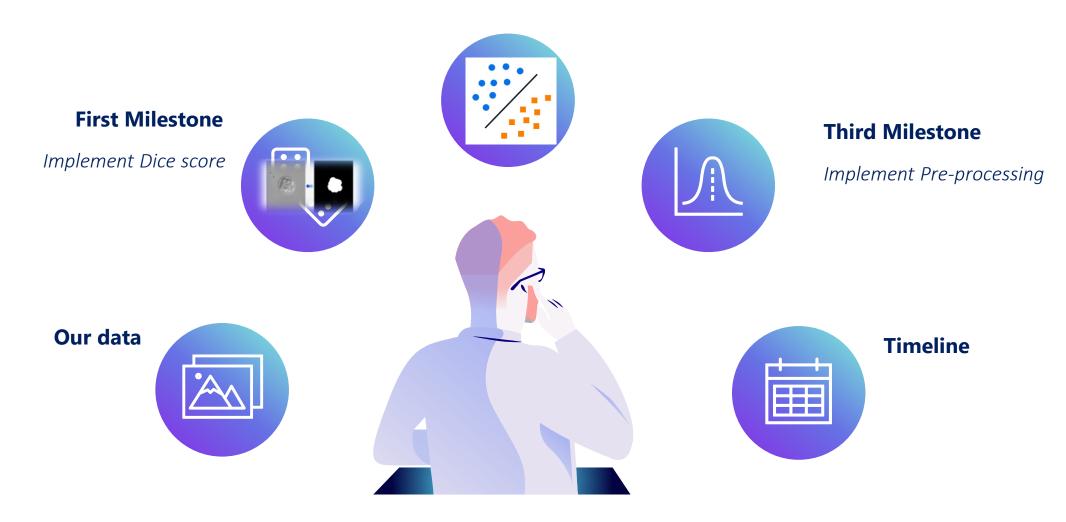
## Our goal

Cell nuclei segmentation using support vector machine

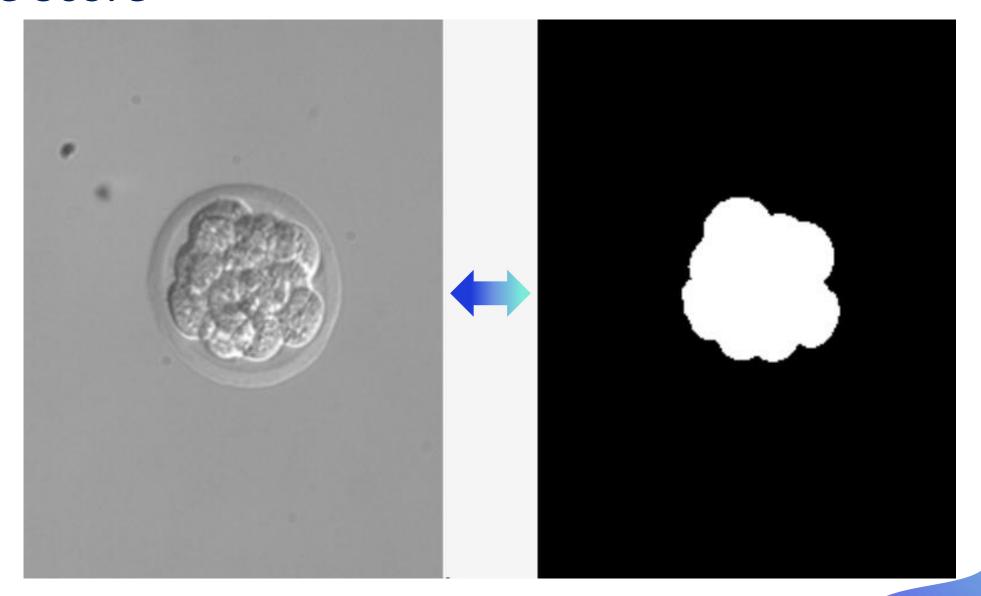
Quantification of cell nuclei



→ key feature to predict patient prognosis
 and decide on treatment options

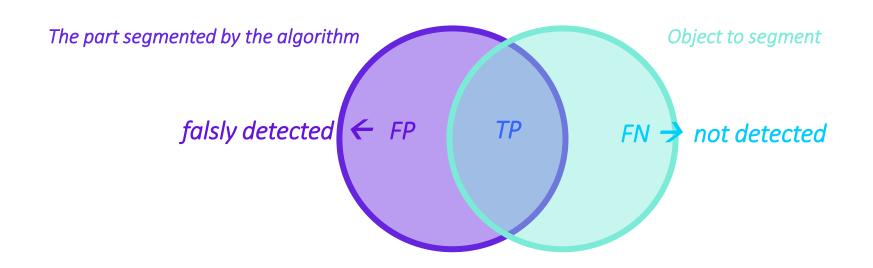


## Dice Score



## Dice Score

Evaluating the quality of the segmentation quantitatively



$$---- Loss = 1 - \frac{2\sum bf}{\sum b+f}$$

## Dice Score

The part segmented by the algorithm 
$$falsly\ detected\ \leftarrow\ FP \qquad TP \qquad FN \ \Rightarrow\ not\ detected$$

IoU = 
$$\frac{Intersection}{Union} = \frac{TP}{TP+FP+FN}$$
  $\leftarrow$  not as well differentiable

Better: Dice = 
$$\frac{2*Intersection}{Union+Intersection} = F_1 = \frac{1}{\frac{1}{Prec} + \frac{1}{Recall}} = \frac{2TP}{2TP+FP+FN}$$

Loss = 
$$1 - Dice \in [0;1]$$

Loss = 
$$1 - \frac{2\sum bf}{\sum b+f}$$

## Planned analysis steps

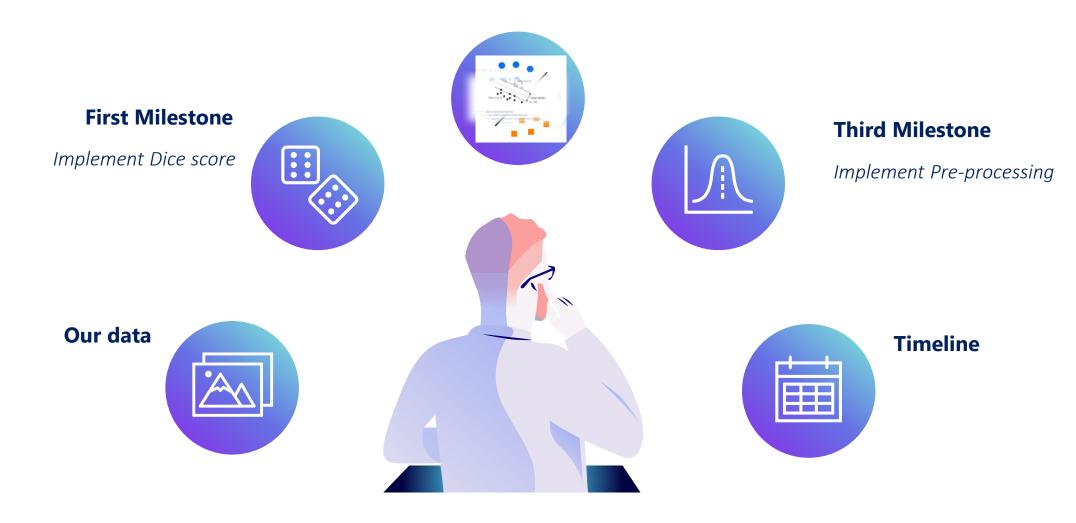
- → Write code for Dice-Score function
- → Unit-testing
- → Write code for synthetic images

#### Characteristics of the first Milestone

→ Measure for evaluating our model

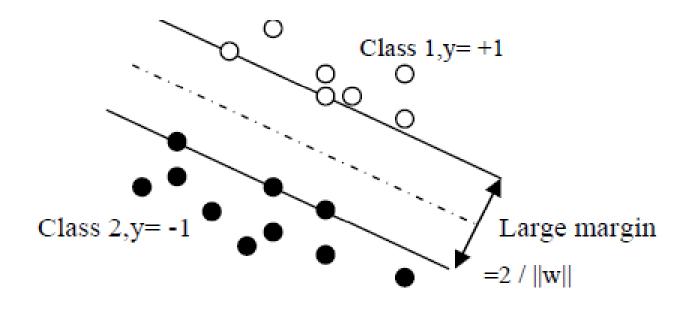
#### The purpose

— Quantify the quality of our model



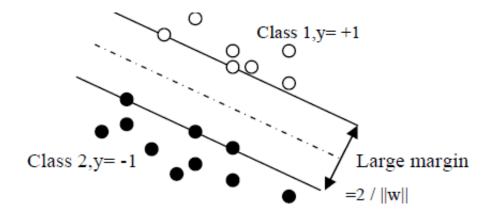
## Mathe – Michelle ©©©

## Support Vector machine



- based on statistical learning theory
  - uses a decision function that defines a hyperplane
    - hyperplane is the classifier, that categorizes data into two groups
      - Phase 1: training phase
        - Phase 2: generalization phase

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## Planned analysis steps

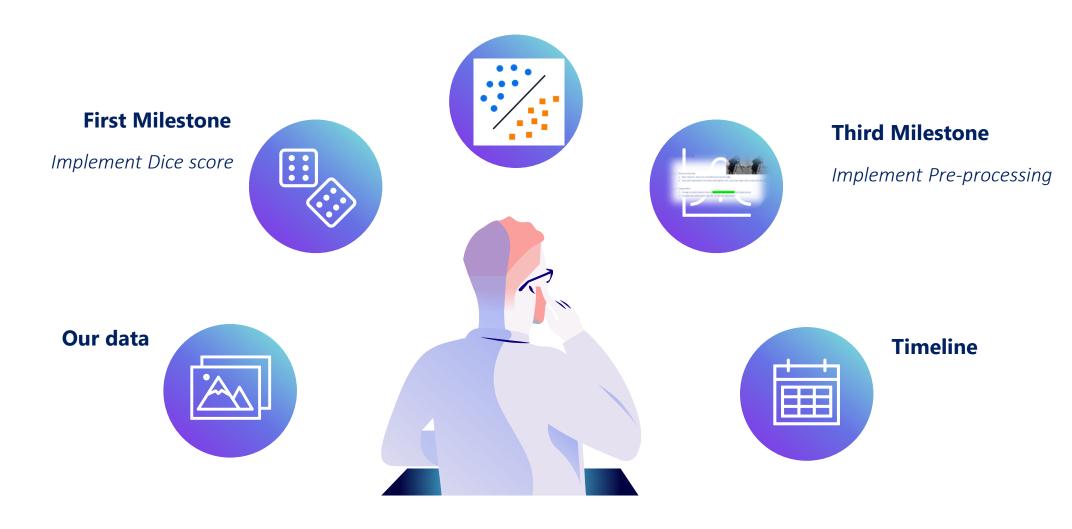
- Implement a support vector machine
- Using the Dice-score-function to evaluate the performance of our SVM

#### Characteristics of the second Milestone

 Support vector machine labels pixels with ,cell nucleus' or ,background'

#### The purpose

- Use trained model to automatically segment cell nuclei images
- Compare the segmented images to the ground truth
  using Dice Score



## Pre-processing



- Pre-processing steps:
- Noise reduction: reduce the noise while preserving the edges
- Super-pixel segmentation: join similar pixels together into a super-pixel region with a similar intensity value
- Desired effect:
  - Average local pixel intensity values to reduce missing information from original picture
  - 2. Separate nuclei which appear fused for an improved segmentation

## Pre-processing



- Pre-processing steps:
  - 1. Noise reduction: reduce the noise
  - 2. Super-pixel segmentation: join pixels into a super-pixel region
- Desired effect:
  - 1. Reduce missing information from picture
  - 2. Separate nuclei which appear fused

#### Planned analysis steps

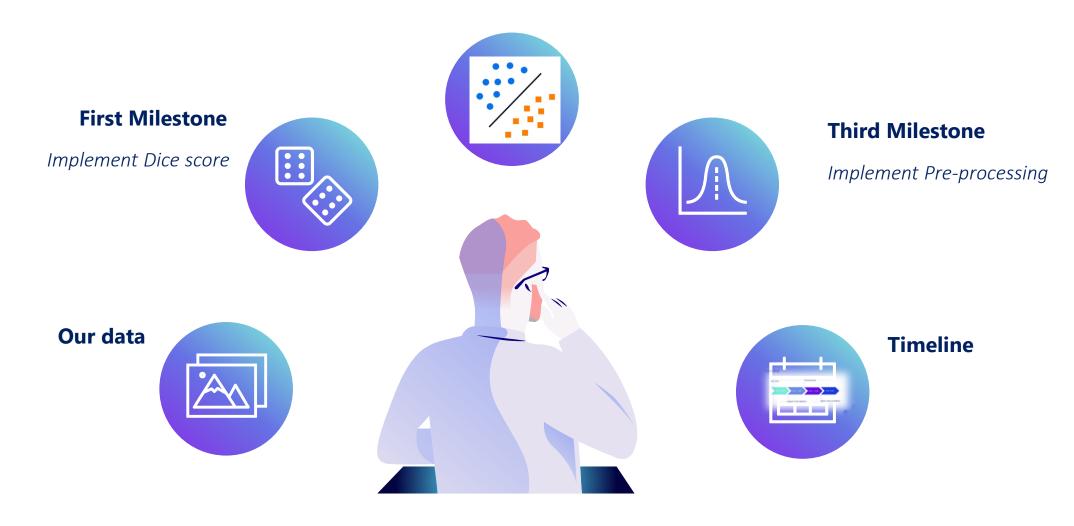
- → *Methods*:
  - 1. Gaussian filter
  - Gradient-ascend-based super pixel algorithms,
    e.g. Watershed

#### Characteristics of the third Milestone

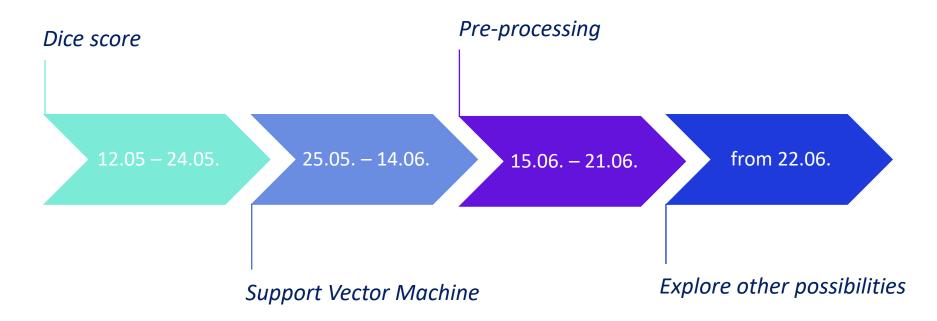
Improve Dice Score of segmentation method through better image quality

### The purpose

- Achieve better registration results



## Timeline

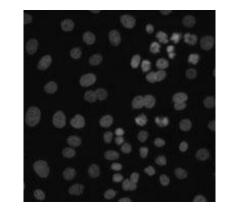




## Other options to be explored

- testing our algorithm **on other data**, on which other algorithms were already tested on **-** compare results

e.g. Broad Bioimage Benchmark Collection 001 which was already used in Nosova SA, Turlapov VE (2019) Detection of Brain Cells in Optical Microscopy Based on Textural Features with Machine Learning Methods. Program Comput Soft 45, 171–179



- try out more advanced pre-processing e.g. anisotropic filtering



# Thank you for listening!