FRIEDRICH-ALEXANDER UNIVERSITÄT ERLANGEN-NÜRNBERG
FACULTY OF ENGINEERING

Mitobunny

--Mitosis detection

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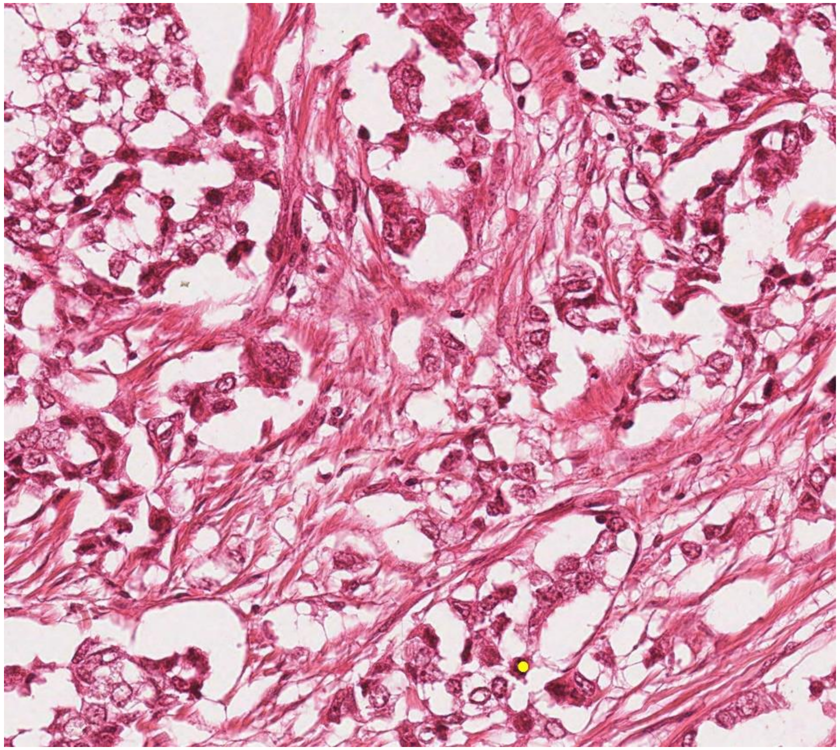
Introduction

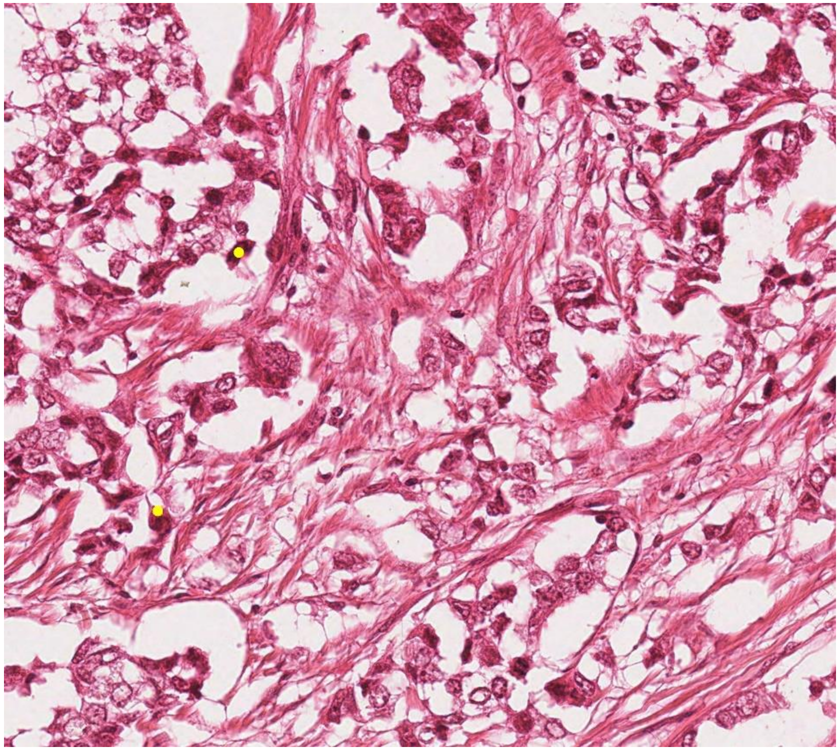
1) Medical use of mitosis(cancer assessment)

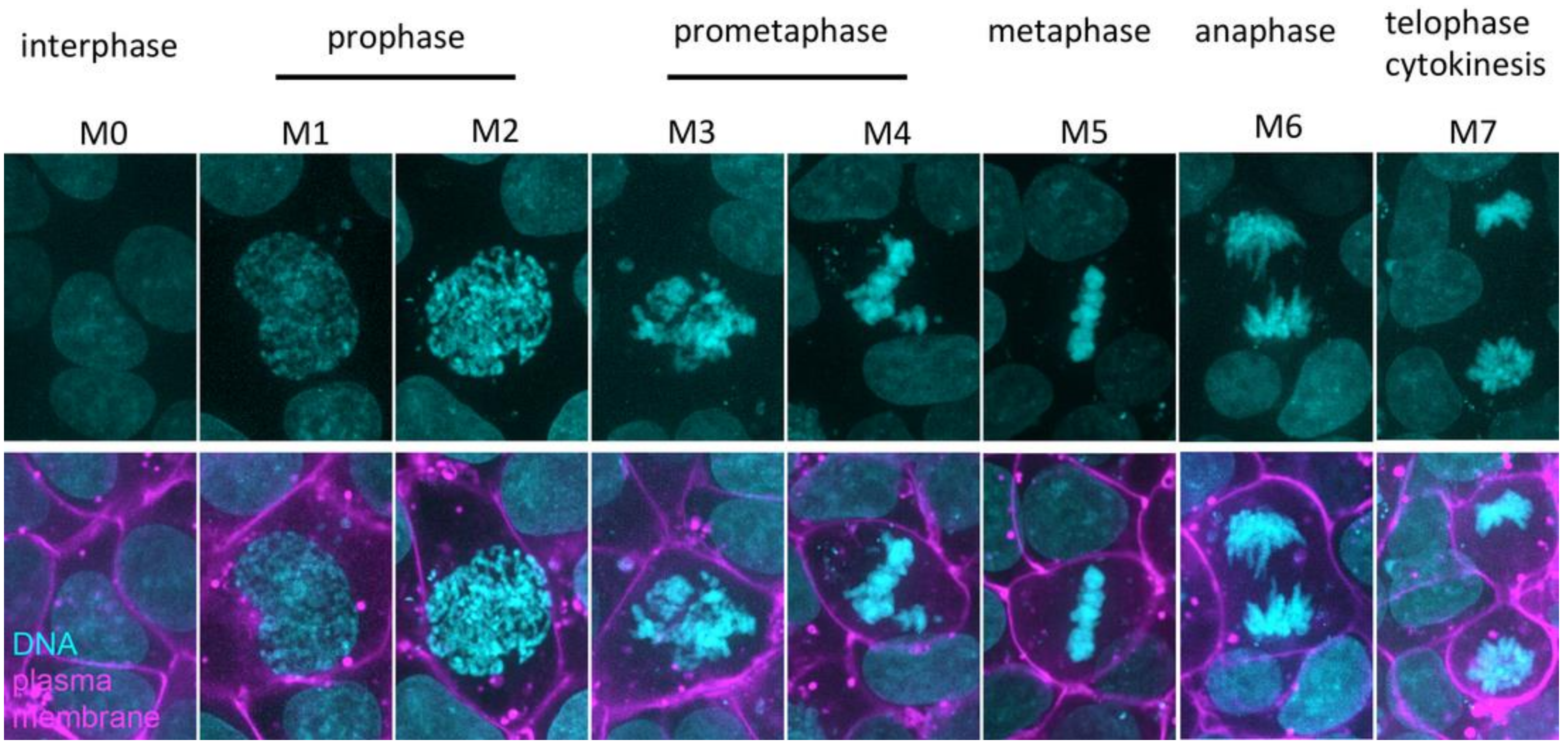
2) Traditional method of mitosis detection and its disadvantages(counting, cumbersome, time, money)

3) Our project

True image of mitosis under microscope



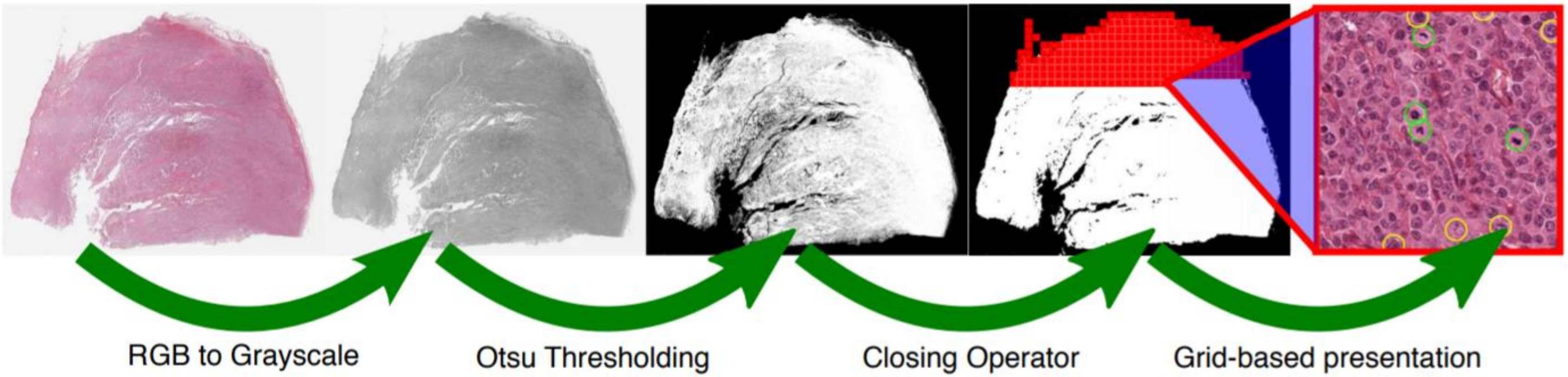


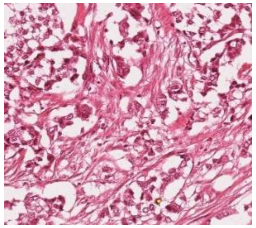


interphase
prophase
prometaphase
metaphase
anaphase
telophase
cytokinesis
M0
M1
M2
M3
M4
M5
M6
M7
DNA
plasma
membrane

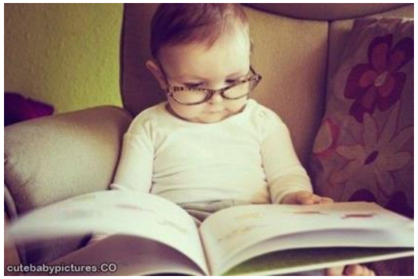
Database

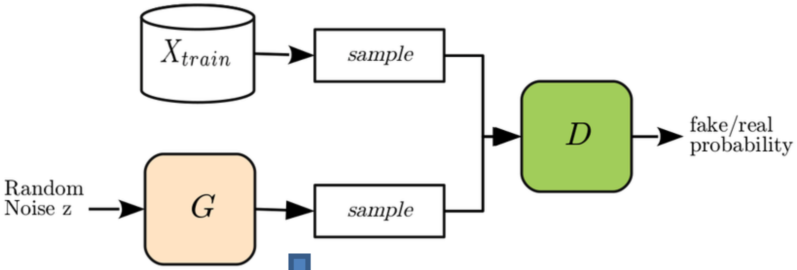
MITOS-ATYPIA-14
TUPAC16

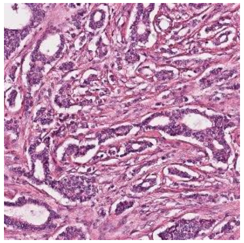




Given data(labeled)

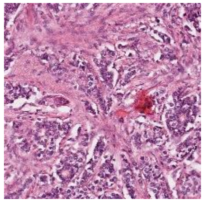


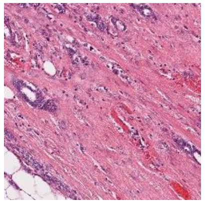


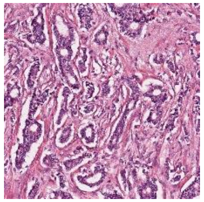


generated data(unlabeled)

generated data(labeled)







Motivation

1) Make mitotic detection more convenient

2) Limited data(GAN)

3) More robust model with more labeled data

Mitosis Detection with Deep Learning

Field Of Interest Proposal for Augmented Mitotic Cell Count: Comparison of two Convolutional Networks

Marc Aubreville[1], Christof A. Bertram[2], Robert Klopfleisch[2] and Andreas Maier[1]
[1] *Pattern Recognition Lab, Computer Sciences, Friedrich-Alexander-Universität Erlangen-Nürnberg*
[2] *Institute of Veterinary Pathology, Freie Universität Berlin, Germany*
marc.aubreville@fau.de

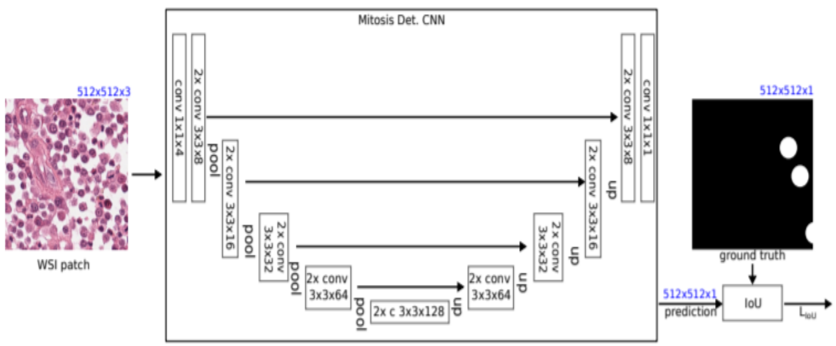


Figure 3: Overview of using U-Net as a mitosis detector. The network predicts a 512×512 full-resolution map, where mitotic figures are represented by filled circles. Intersection-over-Union (IoU) is used for optimization.

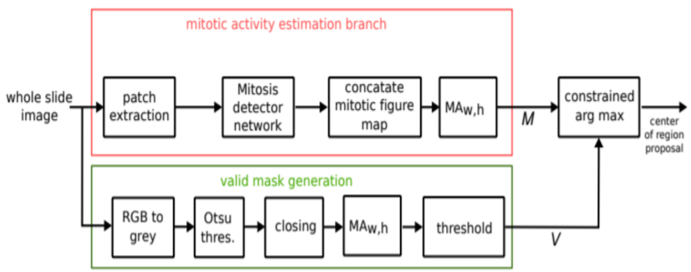
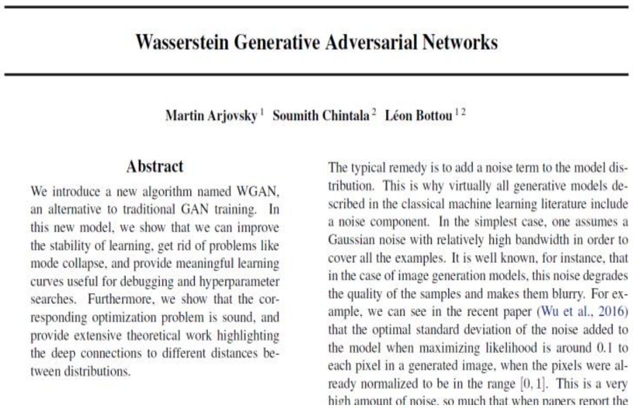


Figure 1: Overview of the proposed approach for mitotic count region proposal (Aubreville et al., 2018b). The upper path will derive singular mitotic annotations, followed by a moving average (MA) filter. The lower path derives an activity map of the image to exclude border regions of the image. This paper compares two mitosis detector CNNs, as further detailed in Fig. 2 and Fig. 3

Literature Review

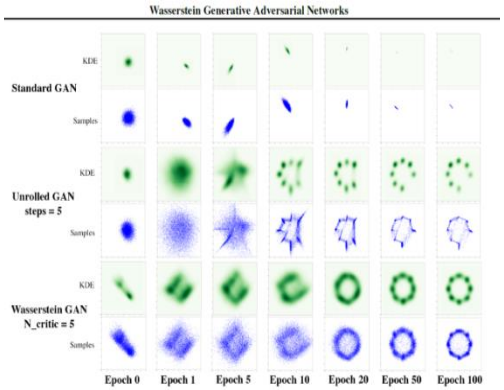

Wasserstein Generative Adversarial Networks

Martin Arjovsky [1] Soumith Chintala [2] Léon Bottou [1 2]

Abstract

We introduce a new algorithm named WGAN, an alternative to traditional GAN training. In this new model, we show that we can improve the stability of learning, get rid of problems like mode collapse, and provide meaningful learning curves useful for debugging and hyperparameter searches. Furthermore, we show that the corresponding optimization problem is sound, and provide extensive theoretical work highlighting the deep connections to different distances between distributions.

The typical remedy is to add a noise term to the model distribution. This is why virtually all generative models described in the classical machine learning literature include a noise component. In the simplest case, one assumes a Gaussian noise with relatively high bandwidth in order to cover all the examples. It is well known, for instance, that in the case of image generation models, this noise degrades the quality of the samples and makes them blurry. For example, we can see in the recent paper (Wu et al., 2016) that the optimal standard deviation of the noise added to the model when maximizing likelihood is around 0.1 to each pixel in a generated image, when the pixels were already normalized to be in the range [0, 1]. This is a very high amount of noise, so much that when papers report the



Key Notes:

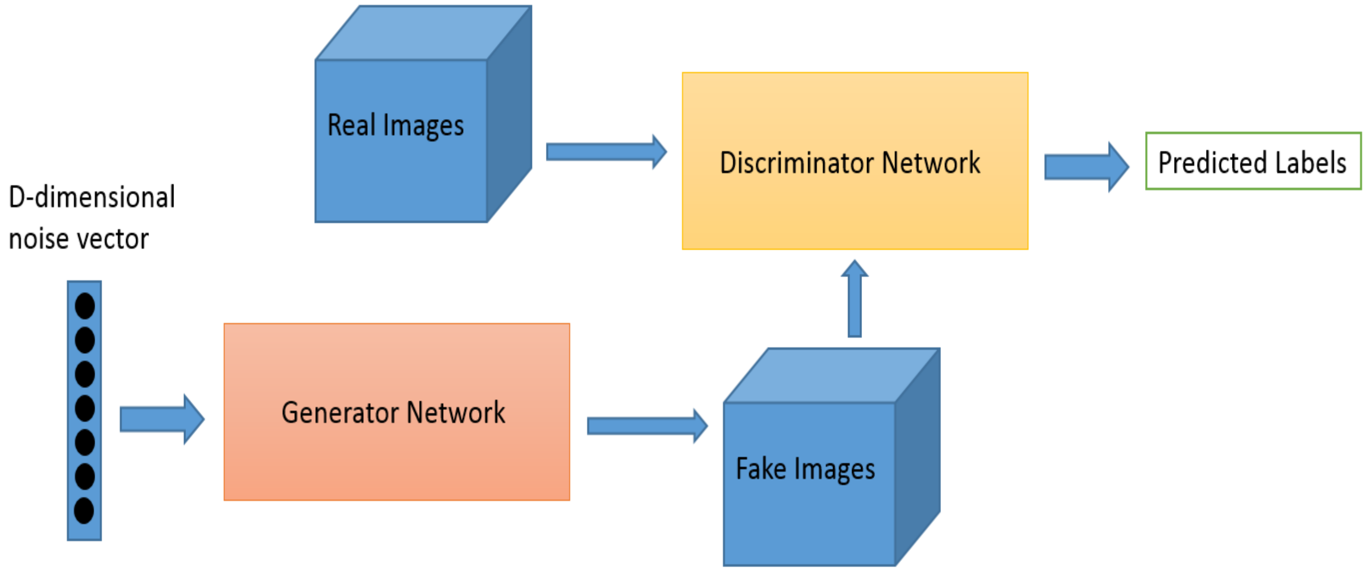
Regular GAN like generator network and discriminator network.

Wasserstein Distance or EM Distance minimisation.(Usable gradient everywhere)

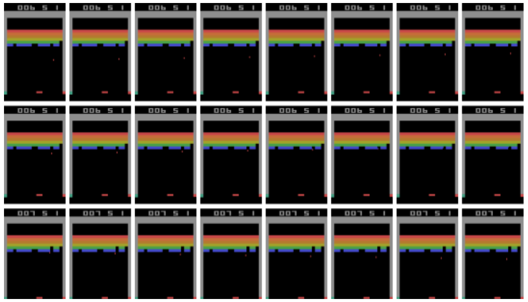
At different Epochs and checkpoints we can save different models with Tensor flow.

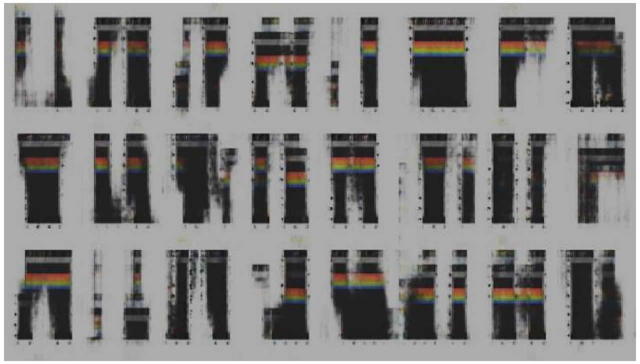
The loss decreases quickly and sample quality increases as well.

Overcomes stability issues of GAN and lack of flexibility of VAE.(No mode collapse)

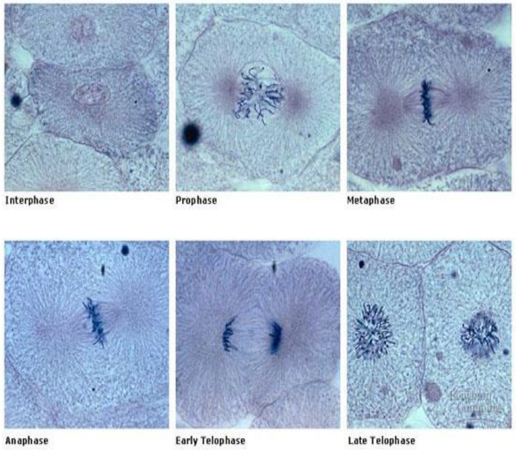


https://skymind.ai/wiki/generative-adversarial-network-gan

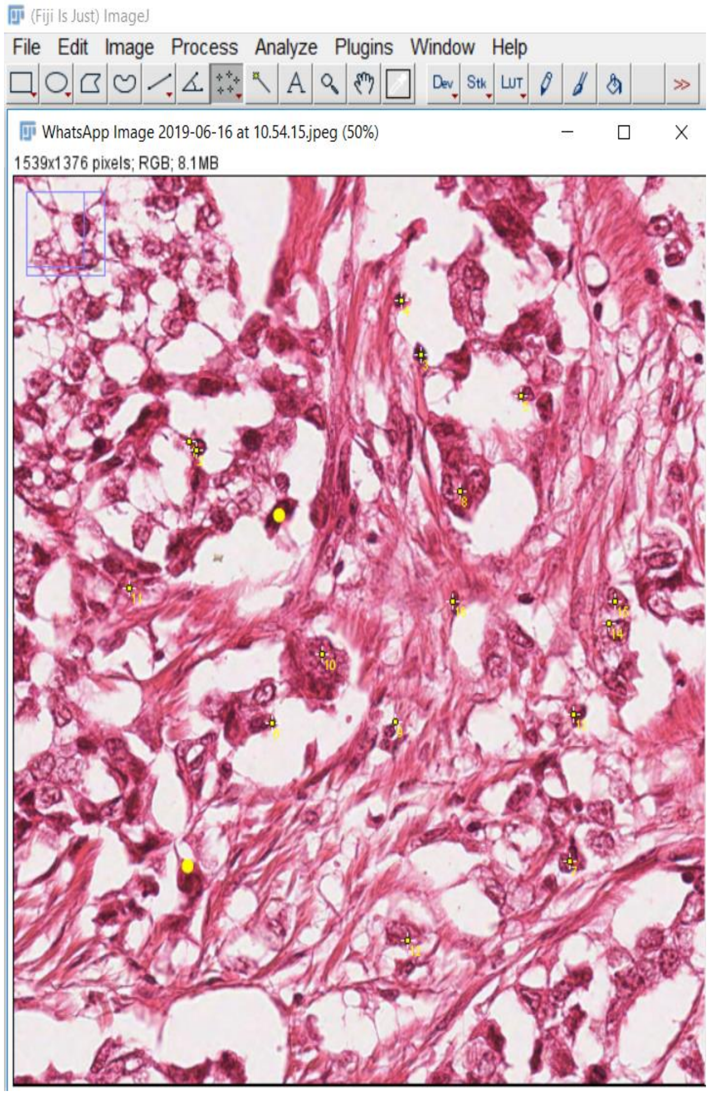




Epoch:3200-CPU



http://fig.cox.miami.edu/~cmallery/150/mitosis/mitosis.htm
https://danieltakeshi.github.io/2016/11/25/frame-skipping-and-preprocessing-for-deep-q-networks-on-atari-2600-games/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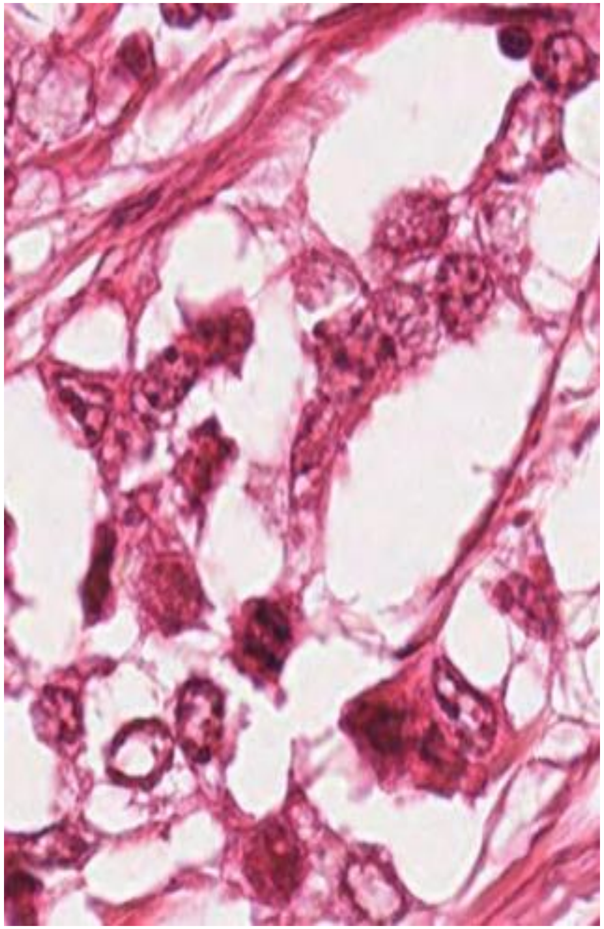
File Edit Image Process Analyze Plugins Window Help
WhatsApp Image 2019-06-16 at 10.54.15.jpeg (50%)
1539x1376 pixels; RGB; 8.1MB

Level 1

“Tinder”Swipe
Training the players to learn about Mitotic Images

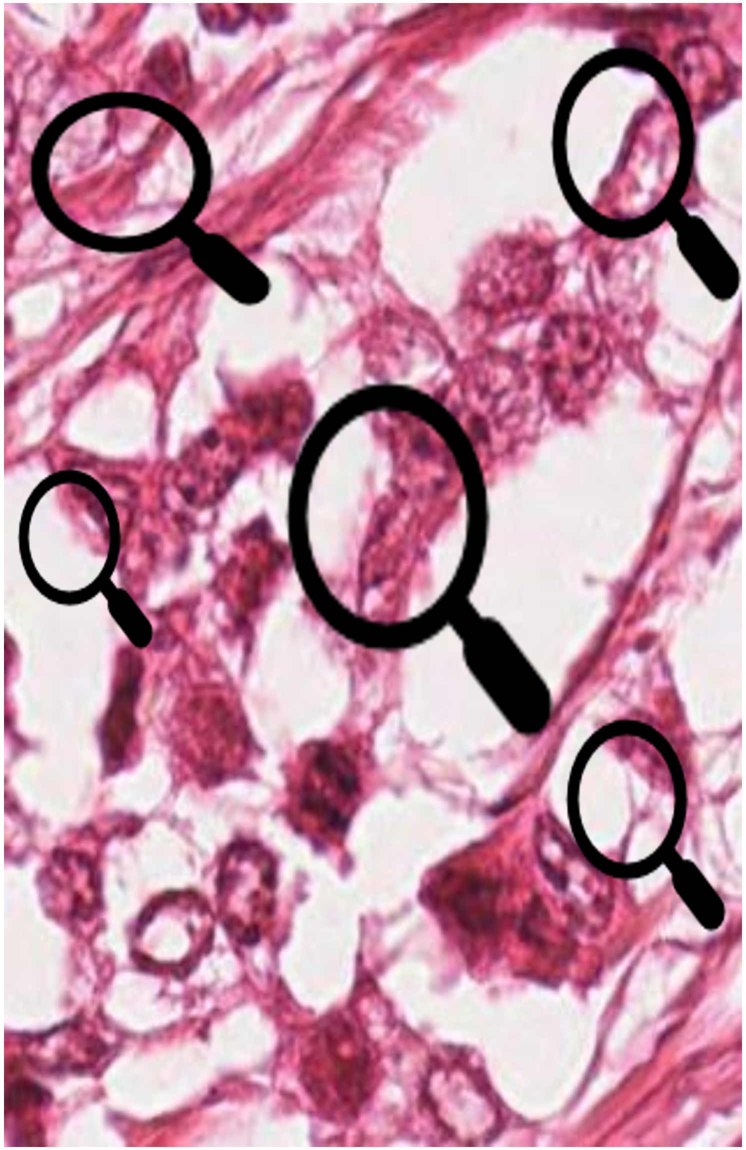


Annotated images. Accuracy should be greater than k to go the next level.

Level 2

Annotate each cell in the image by a simple tap.

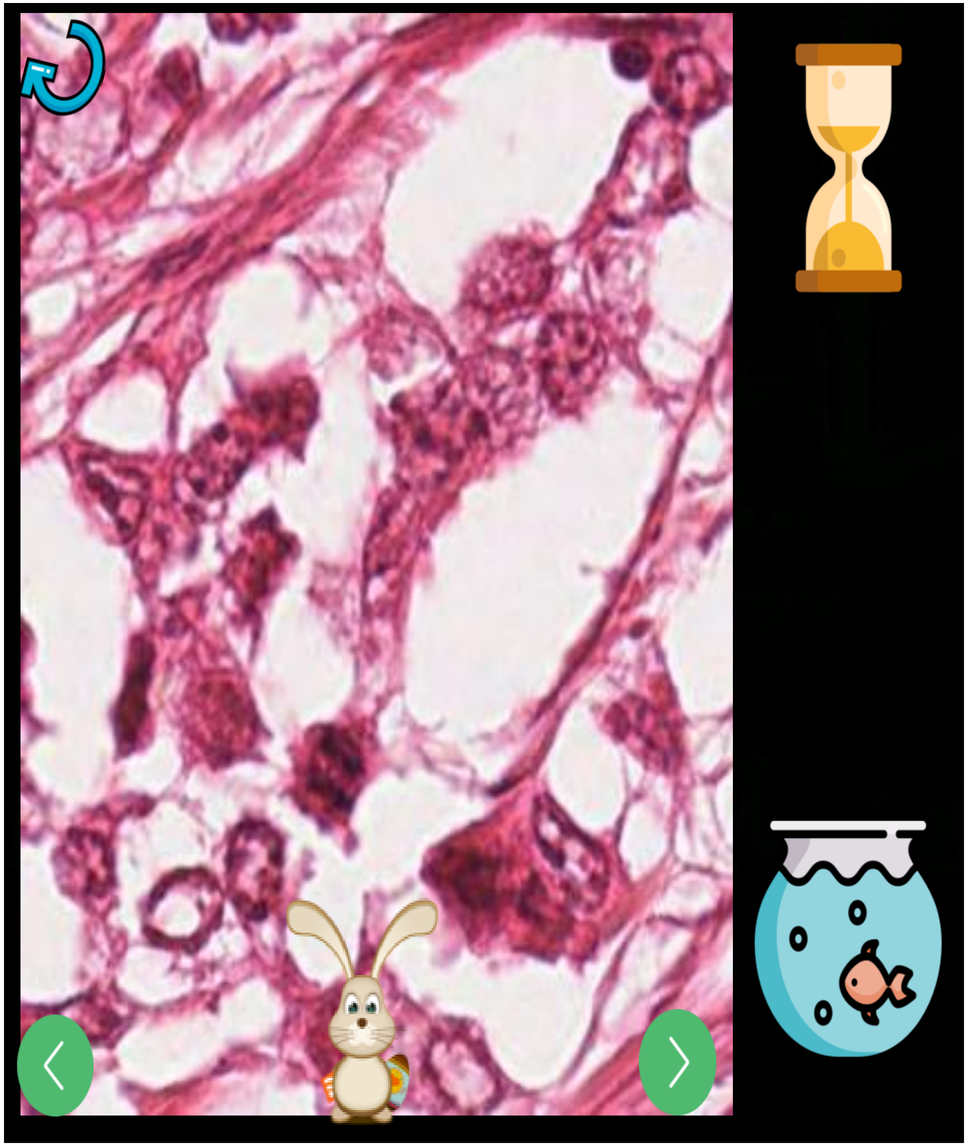
Annotated images. Accuracy should be greater than k to go the next level.



Level 3

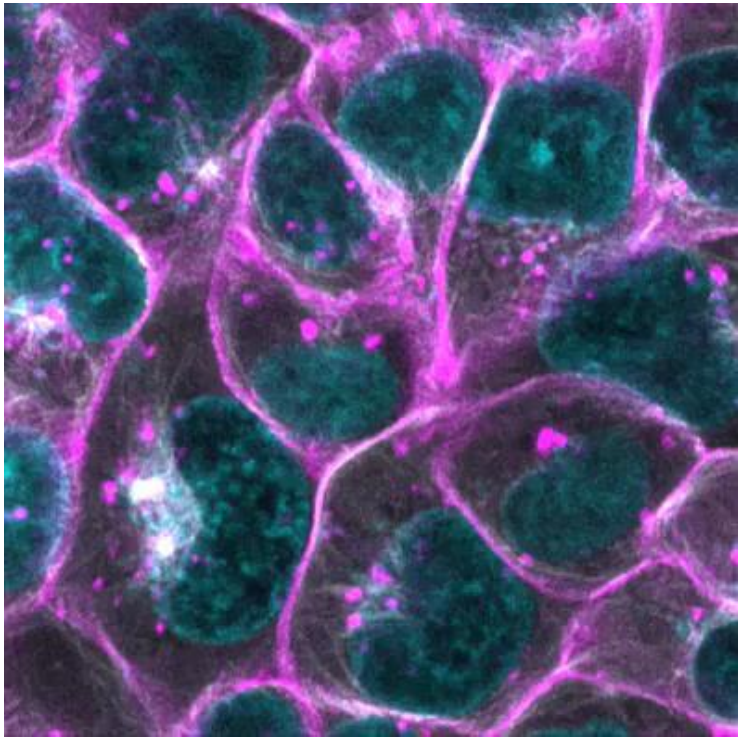
Make the rabbit jump on the mitotic cell.

Then the rabbit burrows and gets a carrot or drowns if it jumps in the black area.



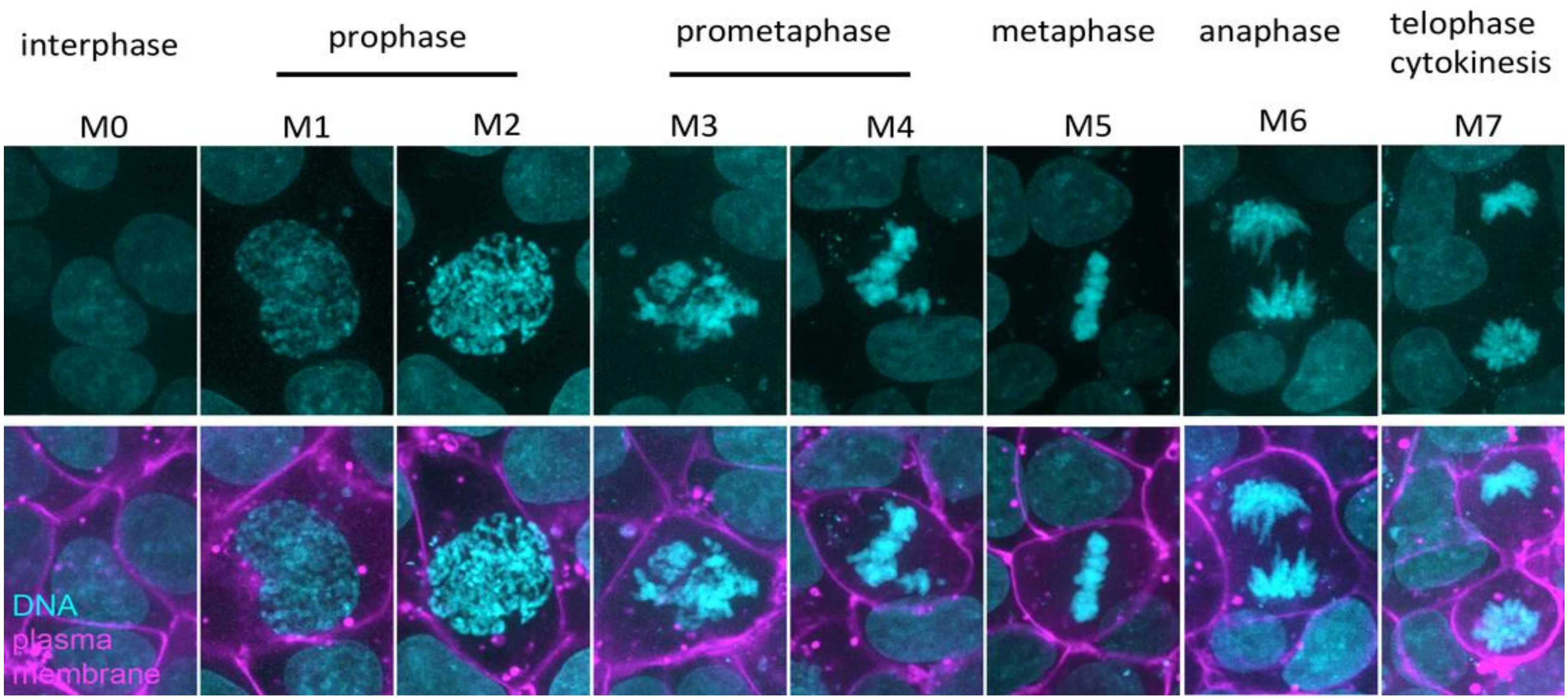
Scoring System

——Stage1. Introduction



Scoring System

——Stage1. Introduction

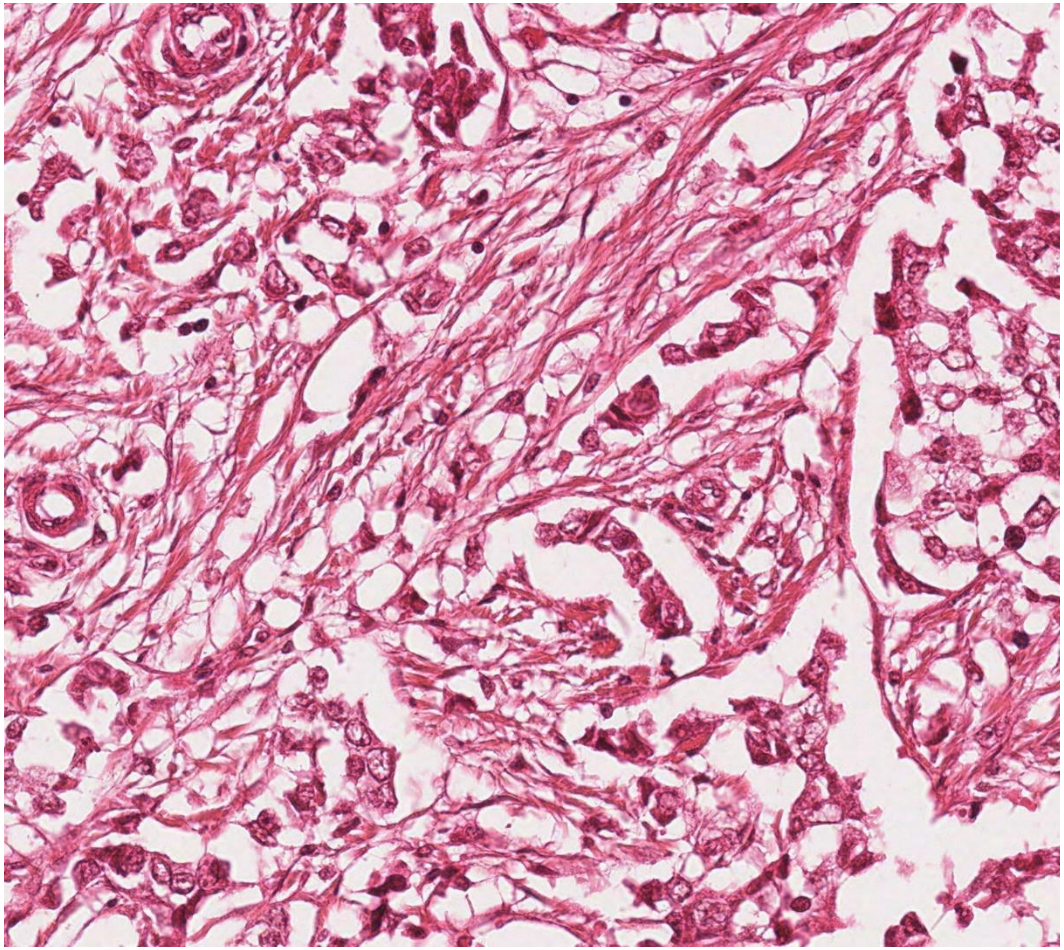


Scoring System

——Stage2. Primary Stage

Scoring System

——Stage3. Intermediate Stage



Scoring System

——Stage3. Intermediate Stage

$$= \text{Foundation Reward} \times (1+\text{Accuracy})$$

$$* \ \text{Accuracy} = \frac{\text{right clicks}}{\text{number of clicks}}$$

Scoring System

——Stage4. Advanced Stage

Players get certain number of unannotated data during the season

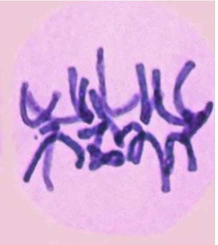
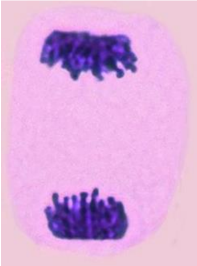
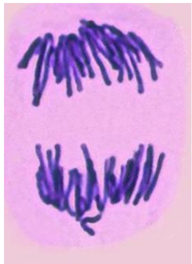
Players get stable rewards after completing annotation of an image

After the season, compute the labeling result by majority voting and user ranking

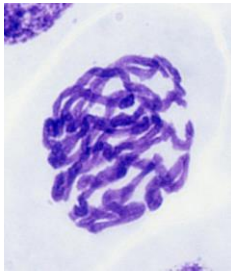
Users get additional reward based on their ranking

Labeling

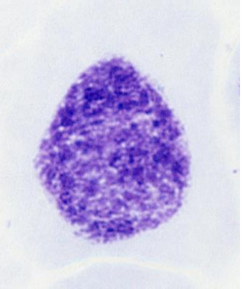
- **Positive**

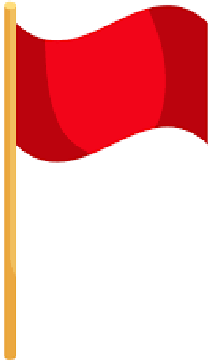




- **(Low Positive)**



- **Negative**

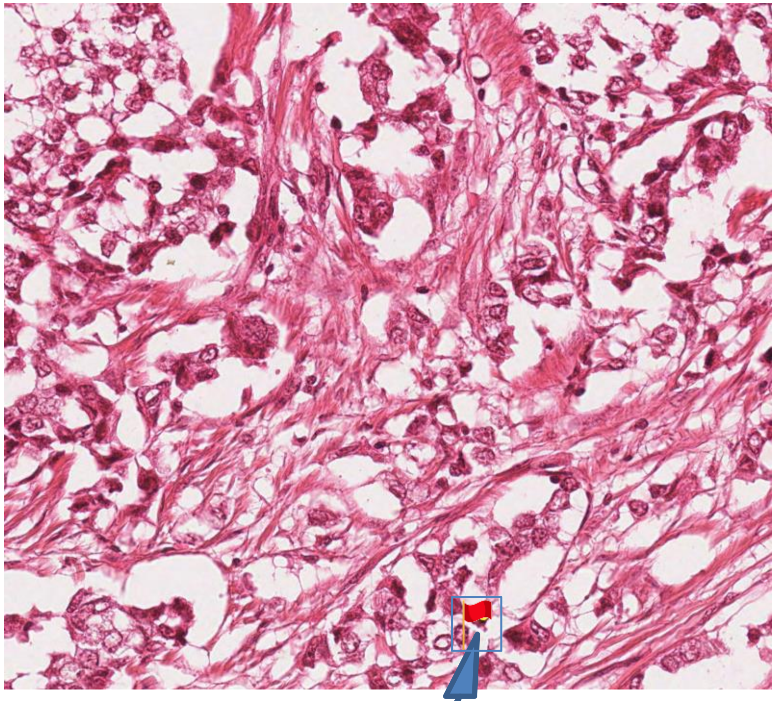




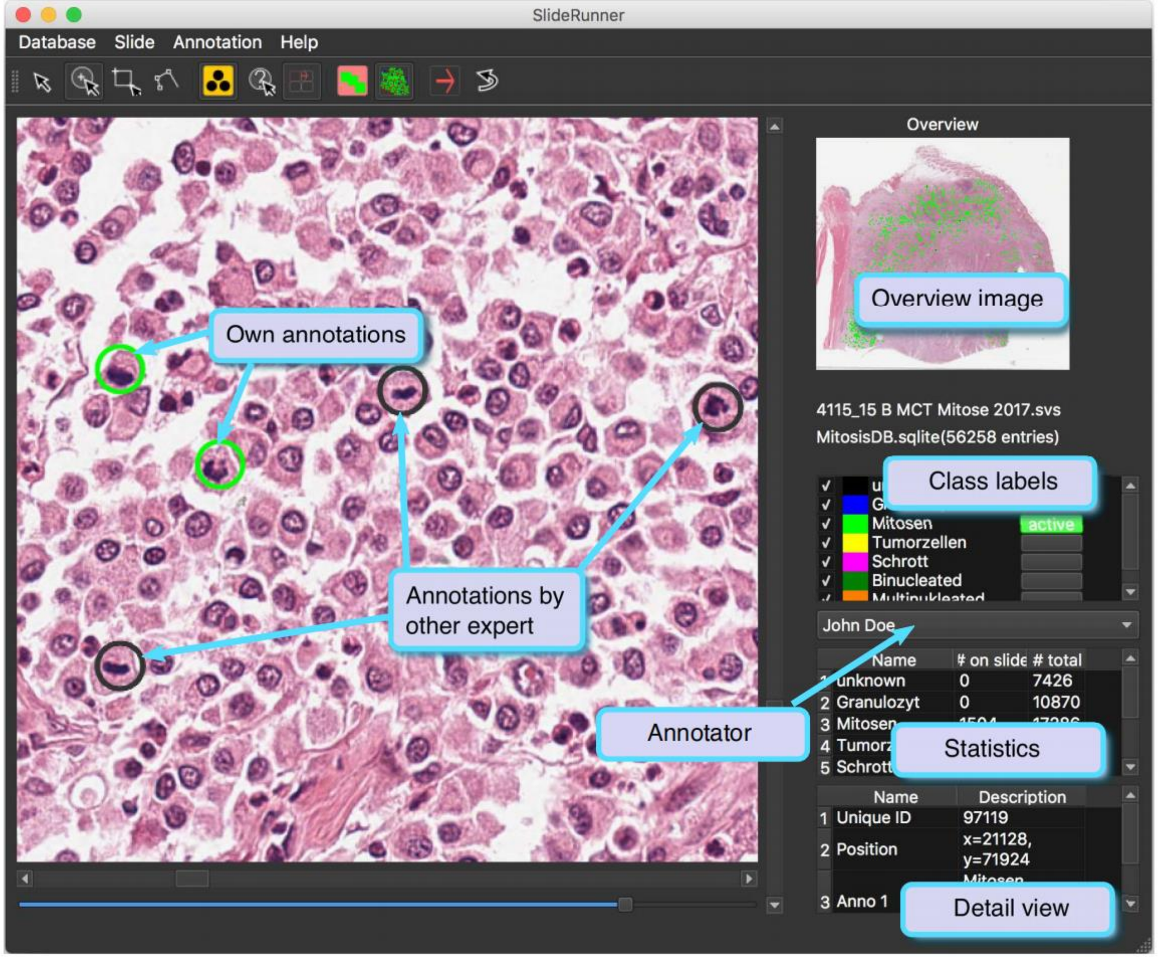
Labeling

Name	X	Y	Hight	Width
1.jpg	1200	960	1500	1800

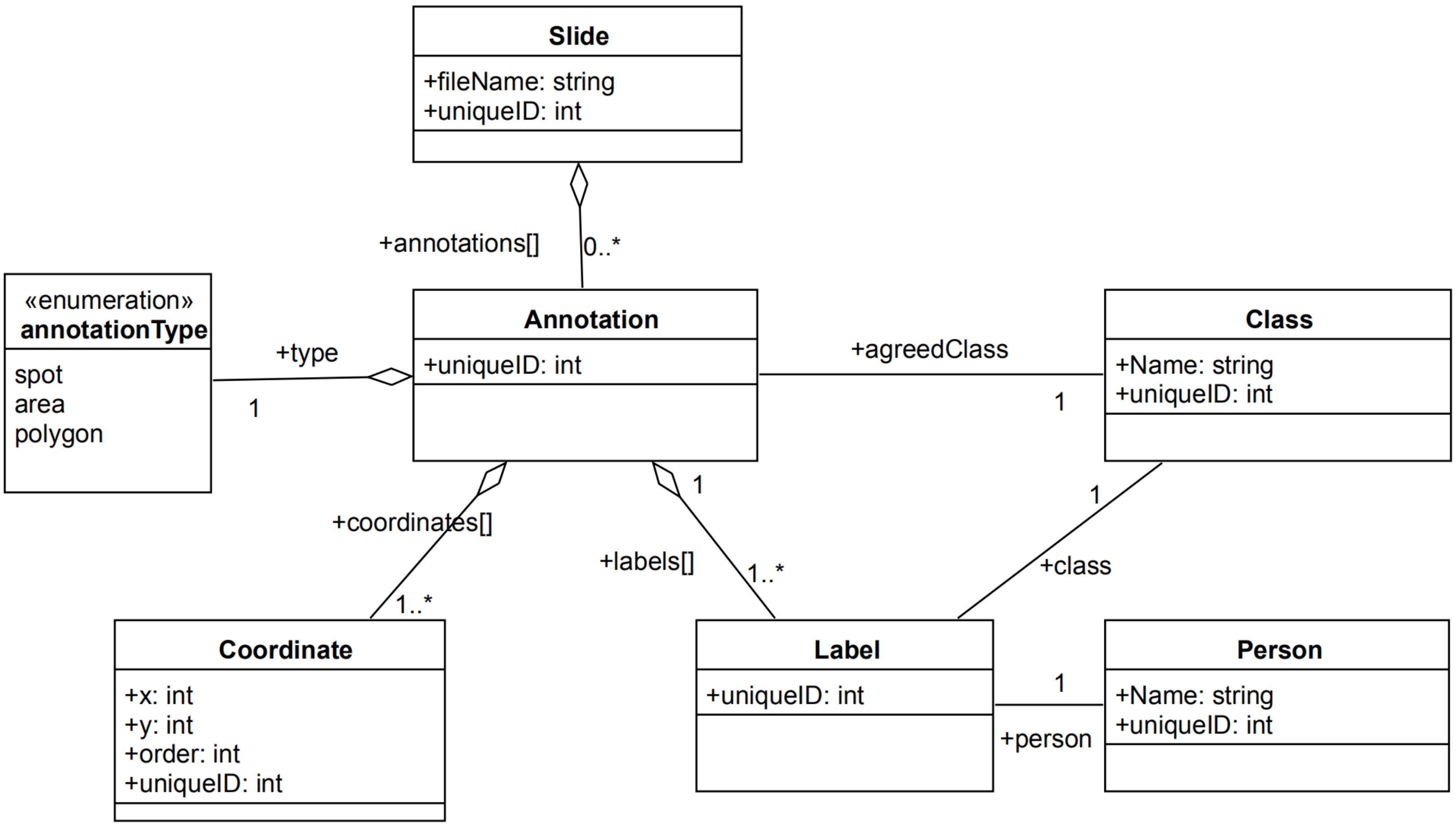
position of the cell



Labeling


SlideRunner
Database Slide Annotation Help
Own annotations
Annotations by other expert
Overview
Overview image
4115_15 B MCT Mitose 2017.svs
MitosisDB.sqlite(56258 entries)
Class labels
Mitosen
active
Tumorzellen
Schrott
Binucleated
John Doe
Name # on slide # total
1 unknown 0 7426
2 Granulozyt 0 10870
3 Mitosen
4 Tumorz
5 Schrott
Statistics
Annotator
Name Description
1 Unique ID 97119
2 Position x=21128, y=71924
3 Anno 1
Detail view

Labeling



Slide
+fileName: string
+uniqueID: int
+annotations[]
0..*
«enumeration»
annotationType
spot
area
polygon
+type
1
Annotation
+uniqueID: int
+agreedClass
1
Class
+Name: string
+uniqueID: int
+coordinates[]
1..*
+labels[]
1
1..*
1
+class
Coordinate
+x: int
+y: int
+order: int
+uniqueID: int
Label
+uniqueID: int
1
+person
Person
+Name: string
+uniqueID: int

Important Parameters

- **minimum accuracy**: ensures each contributor must maintain minimum 80%(or higher) accuracy on test questions throughout the job completion.
- **minimum or average time per task**: ensures each contributor must spend a minimum of 10 seconds to complete one task.
- **maximum number of judgments per contributor**: enable more contributors to participate in the job.
- **trust score**: minimum number of images (20) for the contributor to review in work mode prior to computing a trust score for each contributor and prior to filtering contributors based on their trust score.
- **labels to collect per image**(not sure if segmentation is better)

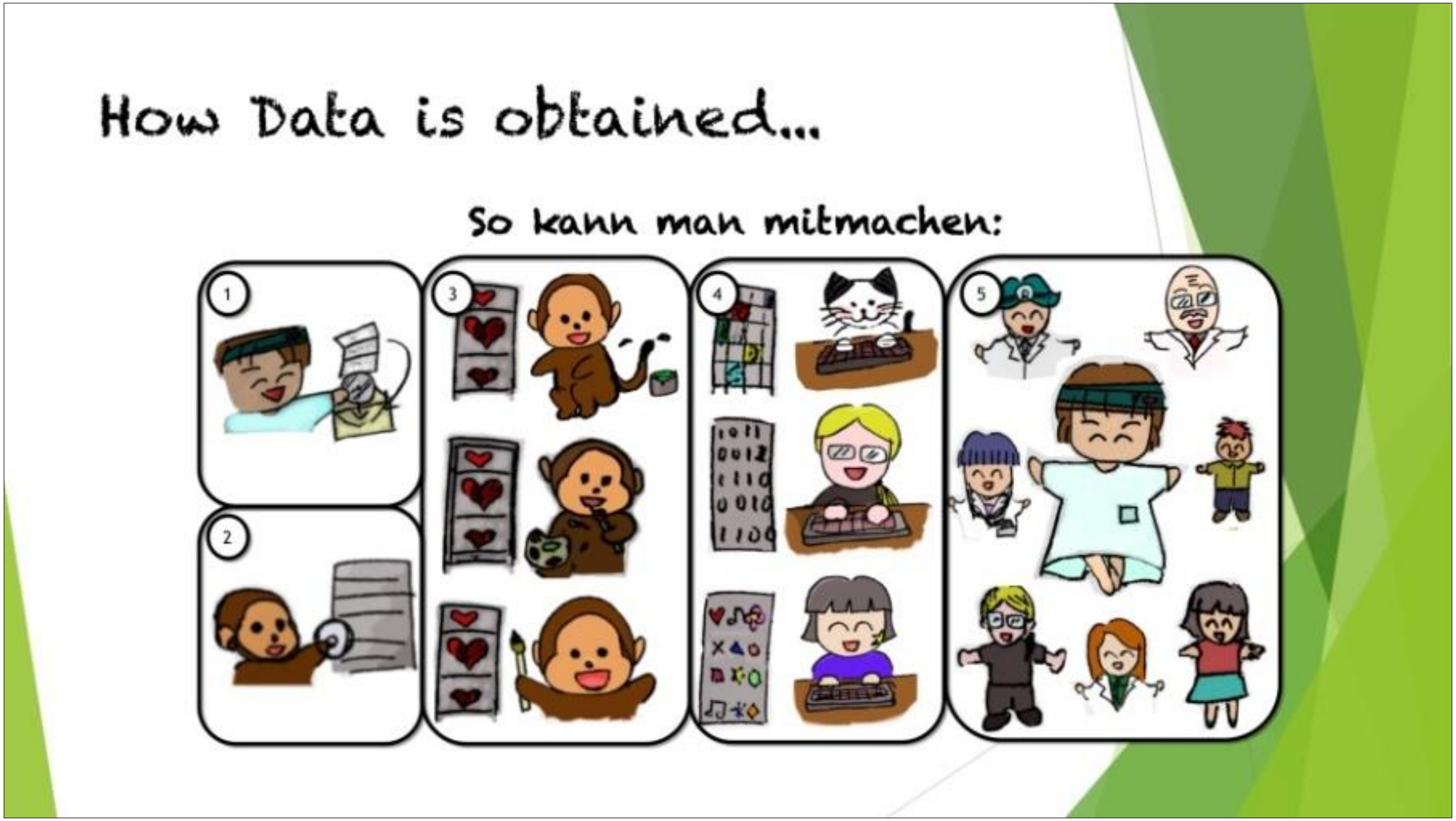
Aggregation Methods

- **maximum crowd votes (CV)**: computed by summing the votes for each label and selecting the label with the maximum number of votes as the aggregated label.
- **maximum crowd trust scores (CT)**: computed by summing the contributor trust score (CT) for each label and selecting the label with the maximum trust score as the aggregated label.
- **maximumweighted crowd votes (ωCV)**
- **maximum weighted crowd trust scores (ωCT)**

$$\omega CV = \frac{\omega_A V_A + \omega_B V_B + \omega_C V_C + \omega_D V_D}{V_A + V_B + V_C + V_D}$$

$$\omega CT = \frac{\omega_A T_A + \omega_B T_B + \omega_C T_C + \omega_D T_D}{T_A + T_B + T_C + T_D}$$

Conclusion:



Q&A and Feedback

THANK YOU!!!