

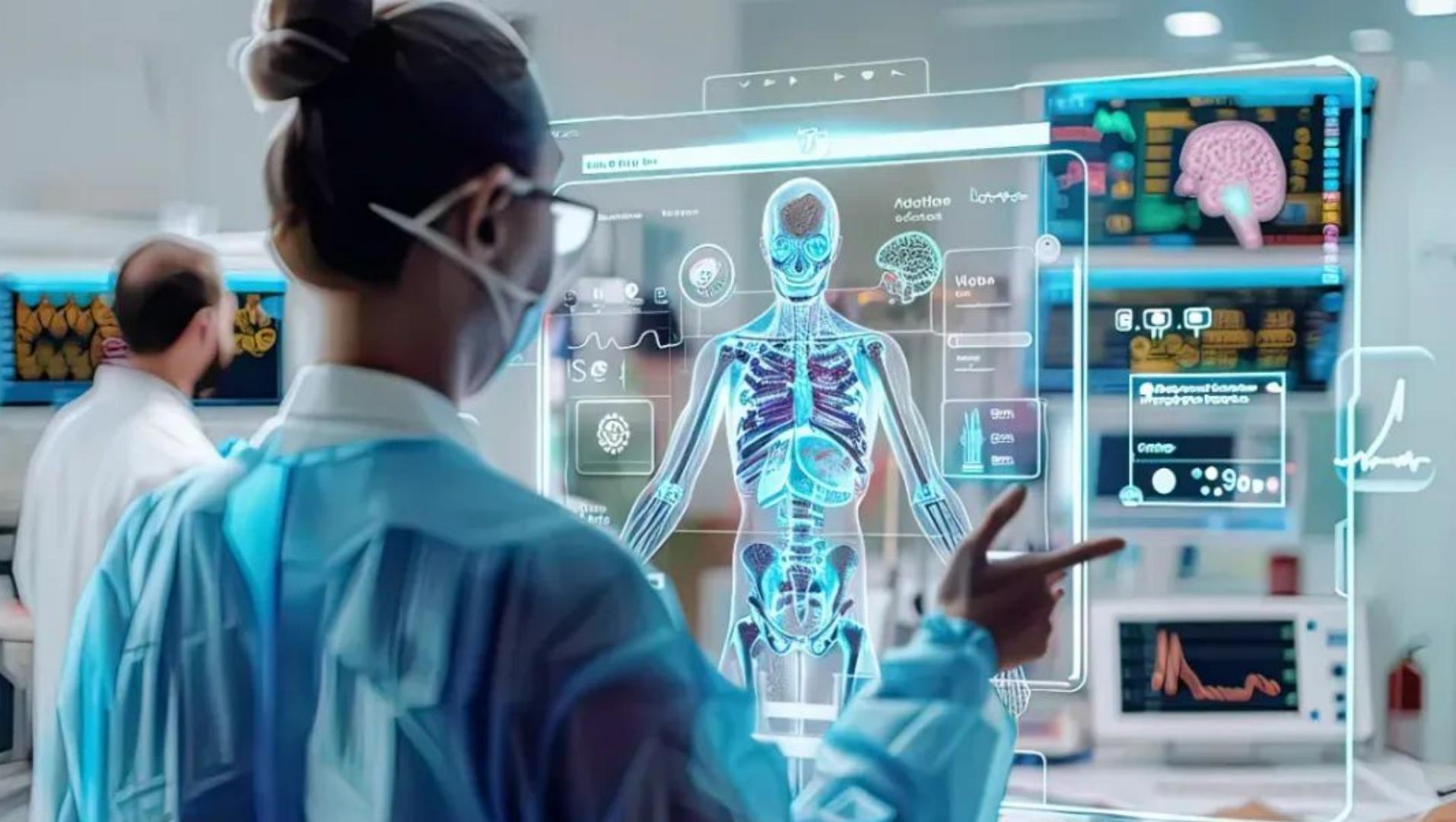
# AI in Medicine

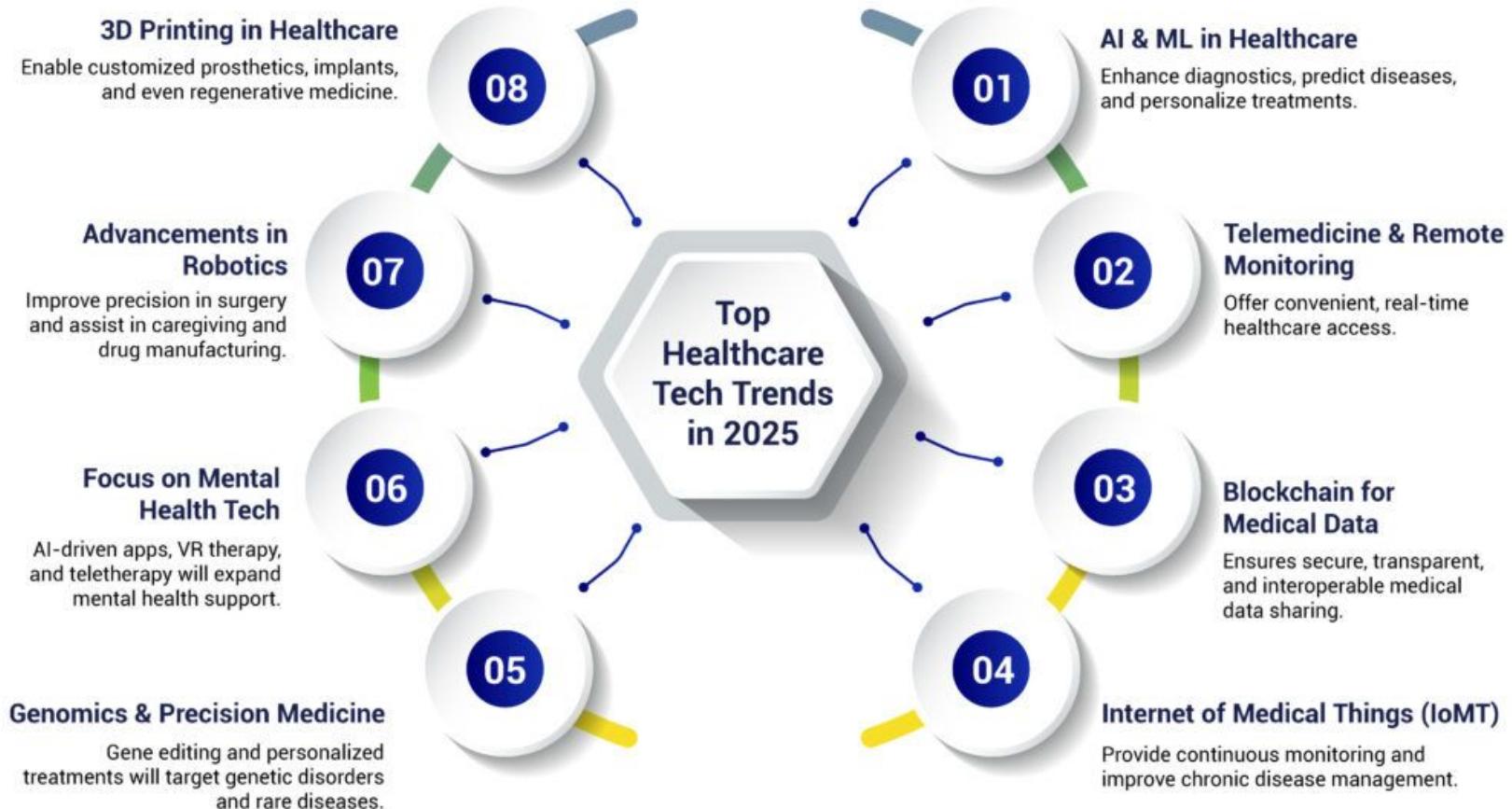
## Point of view

## & use cases

**Natthakorn Kasamsumran, Ph.D. candidate**

Embedded System and IC Design Research Laboratory  
Electrical engineering department, Faculty of engineering,  
Chulalongkorn University, Thailand.





## Last decade

### Medical Products

Equipment, Hardware, Consumables



Differentiation is solely through product innovation. Focused on historic and evidence based-care.

## Current decade

### Medical Platforms

Wearable, Big Data, Health Analytics

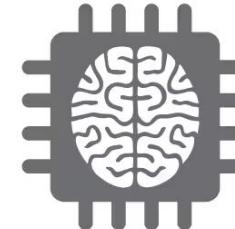


Differentiation by providing services to key stakeholders. Focused on real time outcome based-care.

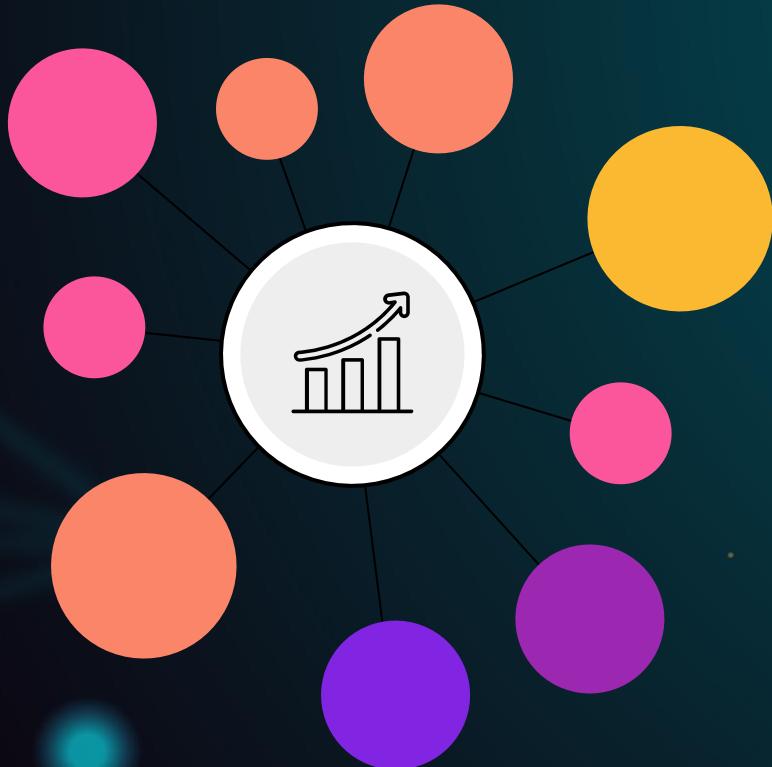
## Next decade

### Medical Solutions

Robotics, AI, Augmented Reality

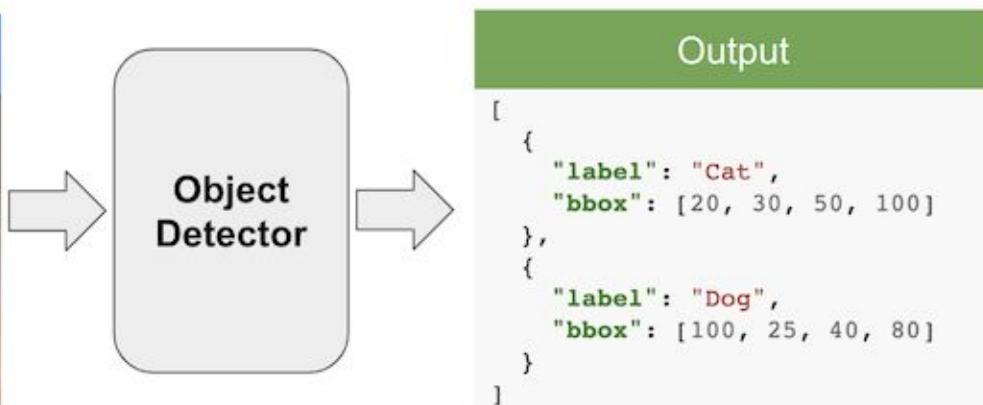
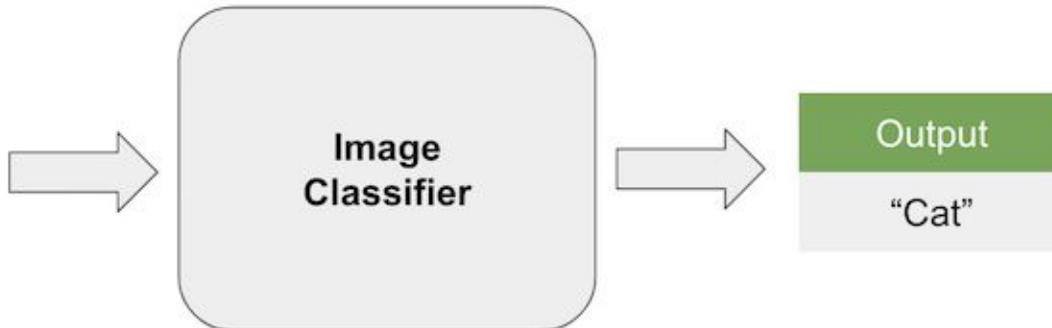
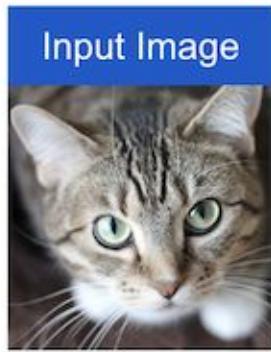


Differentiation via intelligent solutions for evidence/outcome based health. Focused on preventive care.



# How to get good data split with cross-validation

Natthakorn Kasamsumran, Ph.D. candidate  
Embedded System and IC Design Research Laboratory  
Electrical engineering department, Faculty of engineering,  
Chulalongkorn University, Thailand.



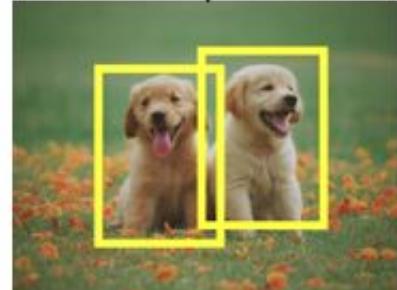
Input Image



Image Classification



Object Detection



Instance Segmentation



Available Data

Training

Testing

(holdout  
sample)

New Available Data

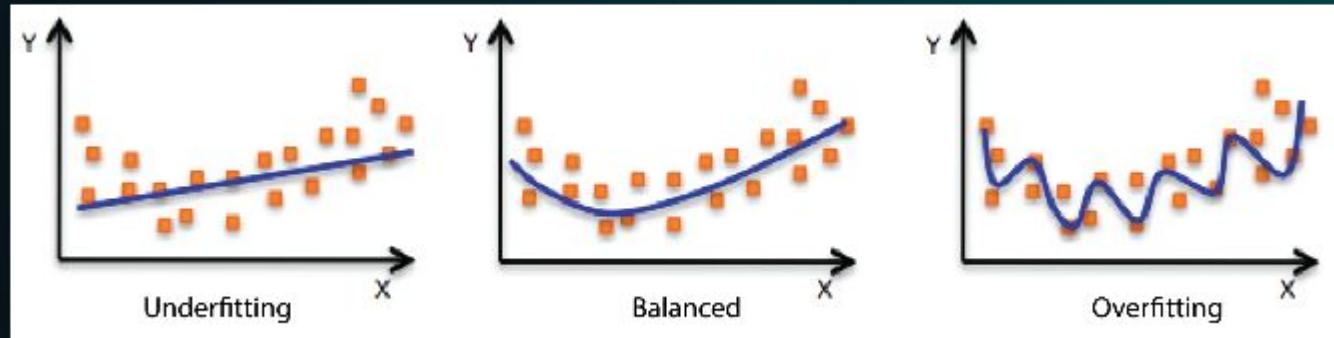
Training

Validation

Testing

(validation  
holdout sample)

(testing  
holdout sample)



When your model does badly on the training data, it is underfitting the data. This is because the relation between the input examples (often referred to as X) and the predicted values cannot be captured by the model (often referred to as Y).

If your model works well on your training data but poorly on your evaluation data, your model is overfitting your training data. This is because the model can't generalize to instances it hasn't seen because it is memorizing the data it has already seen.

Summarize:

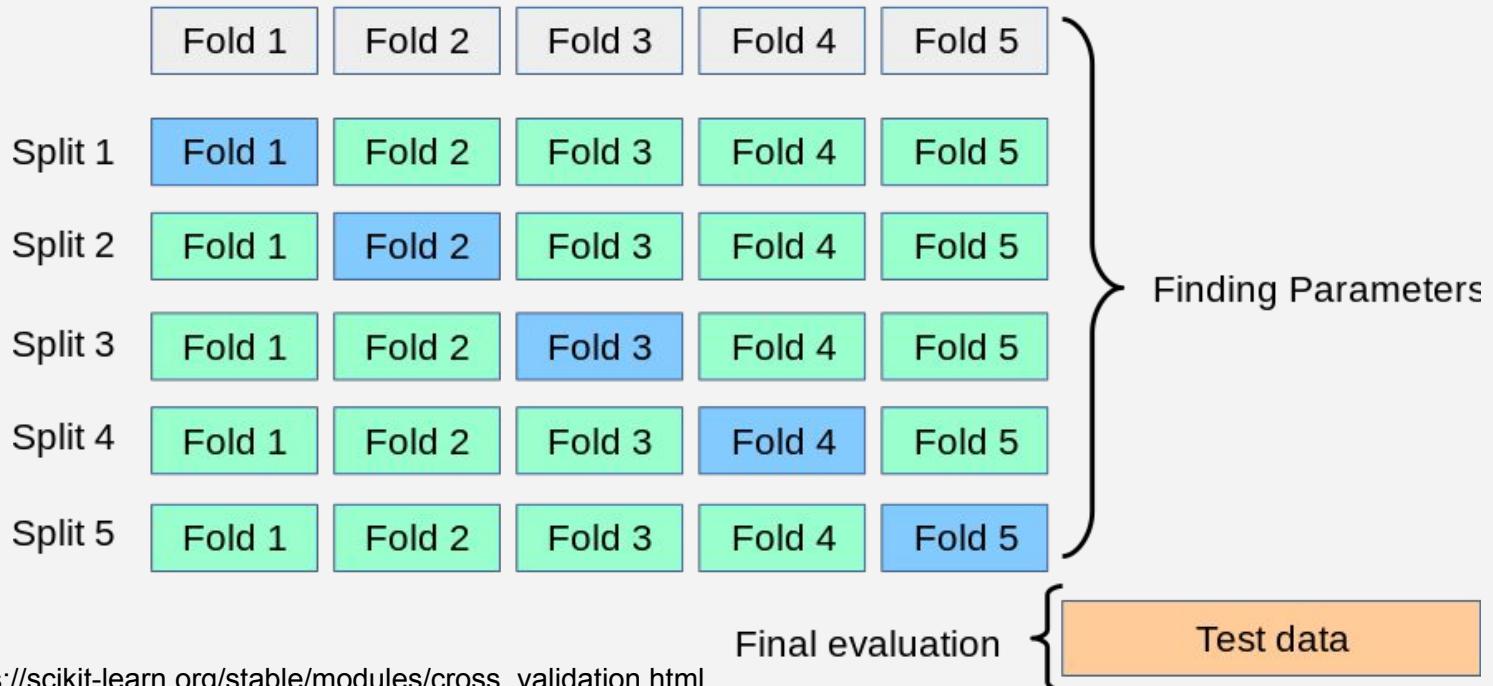
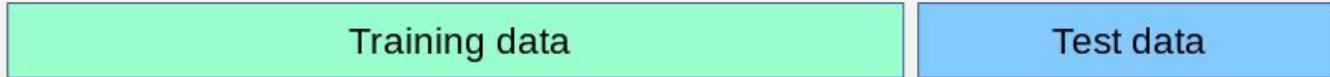
- **Underfitting** is when your model cannot predict everything.
- **Overfitting** means your model can only predict what it has seen. Unseen data cannot be predicted (not a generalization).
- **Balance, or good fit**, as your model is called, can predict unseen data as well (generalization).

# Manual Random Split vs K-Fold Split

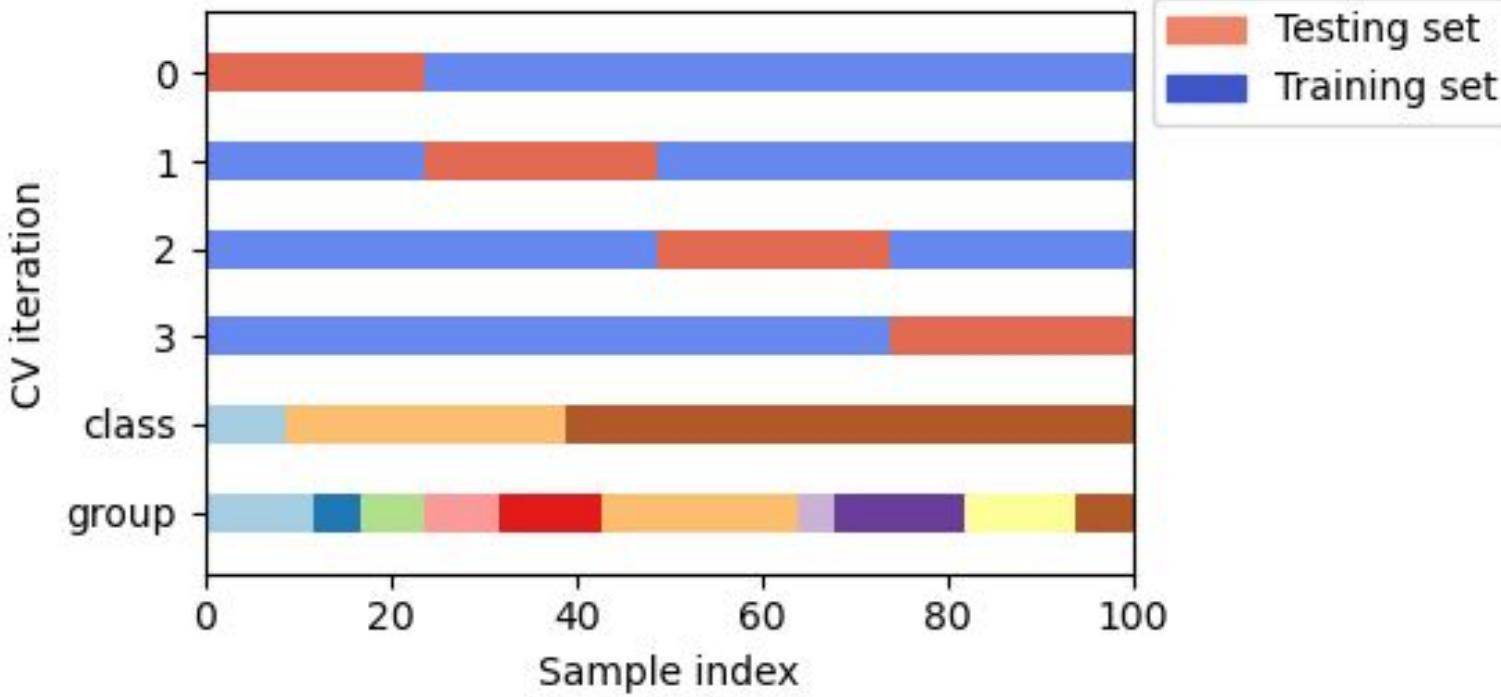


<https://food-hacks.wonderhowto.com/how-to/slice-cake-for-long-lived-freshness-according-science-0155795/>

<https://amycakesbakes.com/cake-cutting-guide/>



## KFold



**KFold** divides all the samples in  $k$  groups of samples, called folds (if  $k=n$ , this is equivalent to the Leave One Out strategy), of equal sizes (if possible). The prediction function is learned using  $k-1$  folds, and the fold left out is used for test.

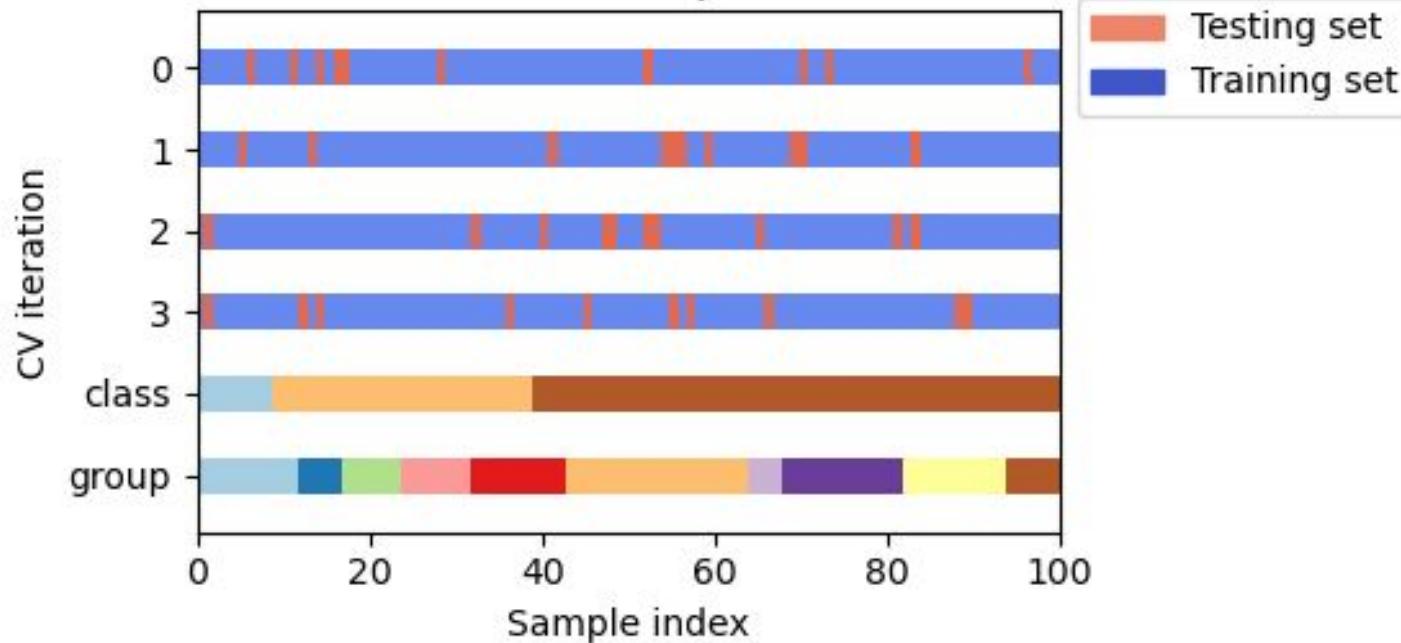


## Shuffle = random data selection.

The shuffle is like randomly asking students to take different sets of exams, in order to prevent memorization of a particular set of exams and can only do that one set

Your model should prevent underfitting and overfitting based on training data.

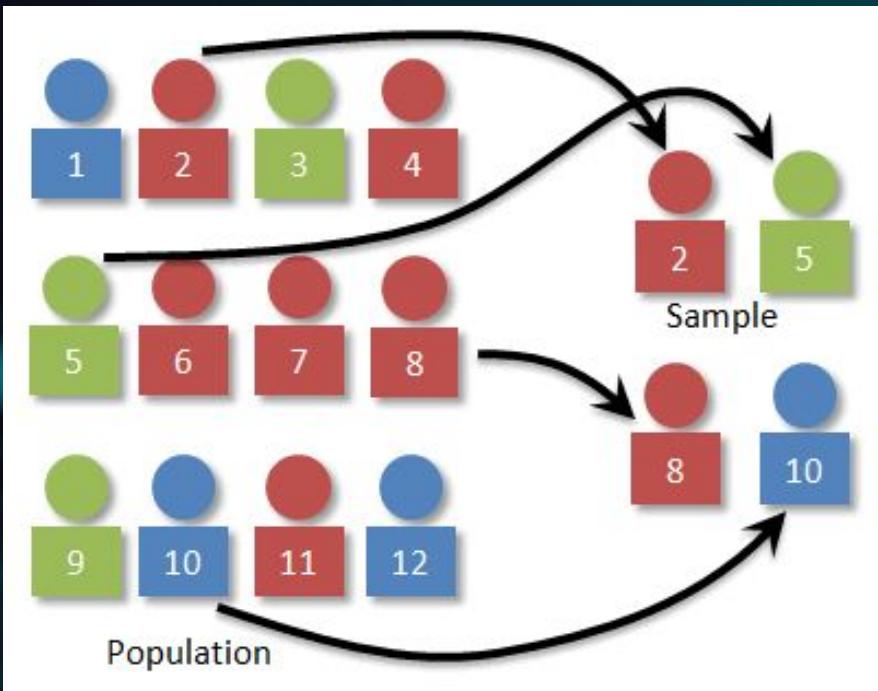
## ShuffleSplit



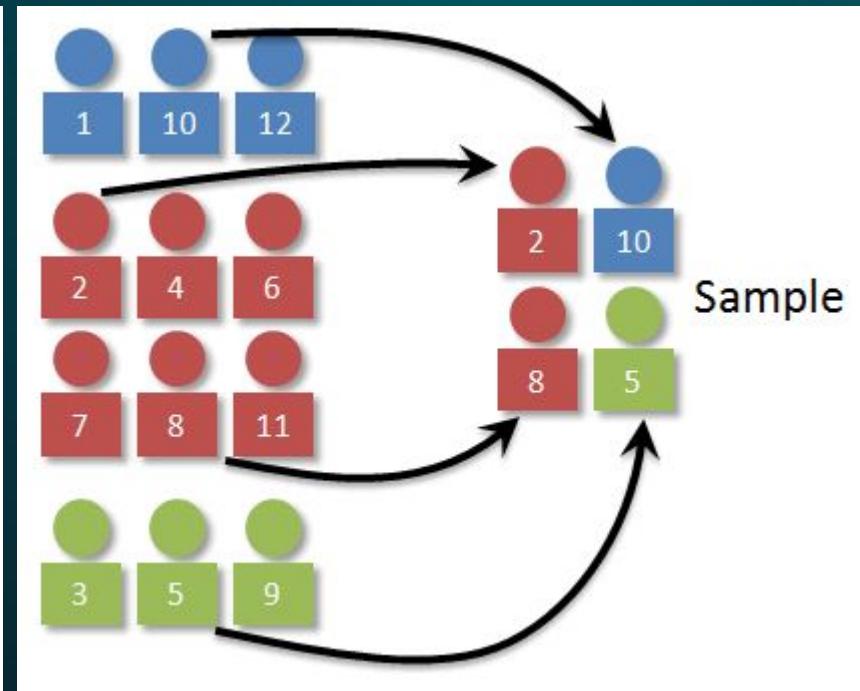
The ShuffleSplit iterator will generate a user defined number of independent train / test dataset splits. Samples are first shuffled and then split into a pair of train and test sets.

ShuffleSplit is thus a good alternative to K-Fold cross validation that allows a finer control on the number of iterations and the proportion of samples on each side of the train / test split.

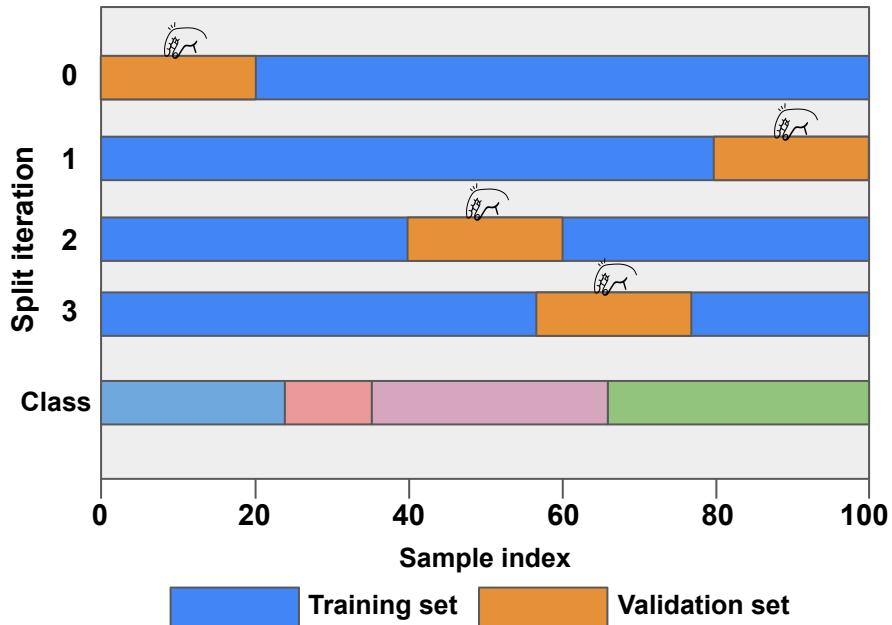
# Random sampling vs Stratified sampling



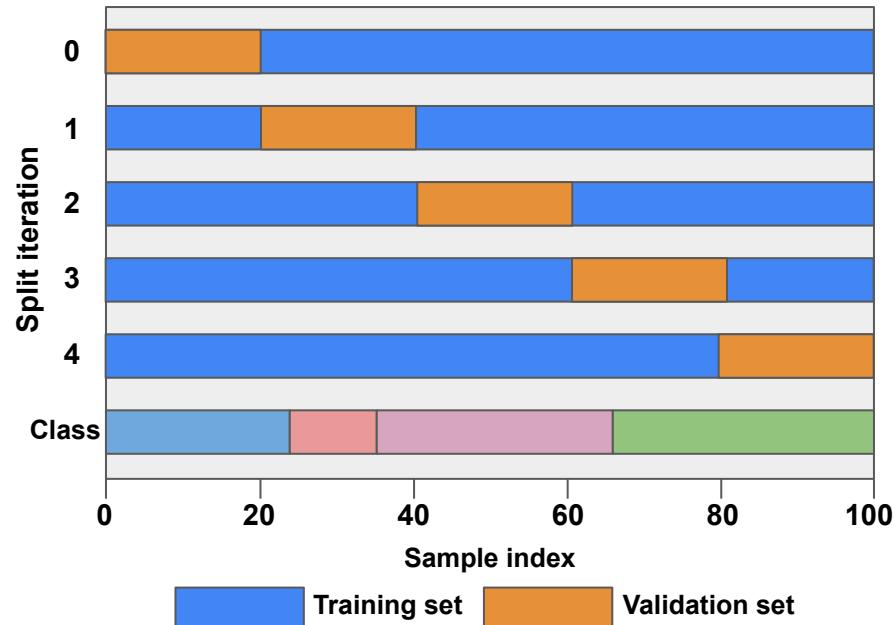
Shuffle? Yes.



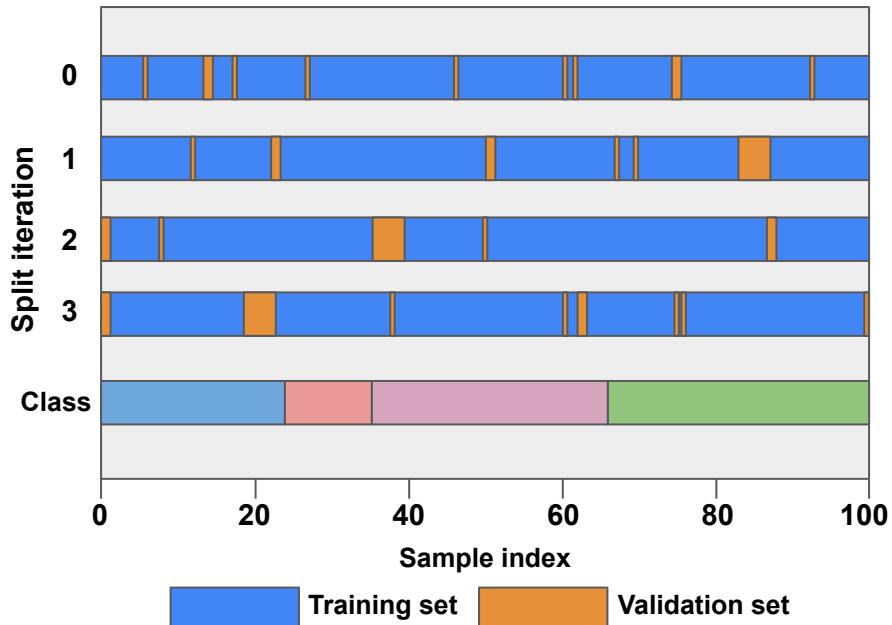
**Manual Split**



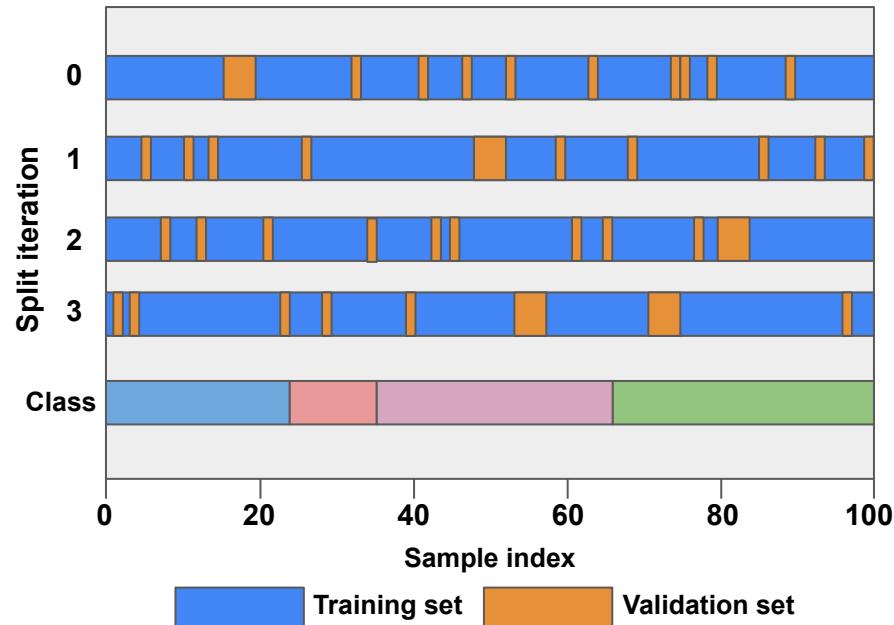
**K Fold Split**



Shuffle Split



Stratified Shuffle Split



The model may be too simple (the input features are not expressive enough to describe the goal well) to perform well on the training data. Flexibility of the model can be increased to enhance performance. Try these to improve model flexibility:

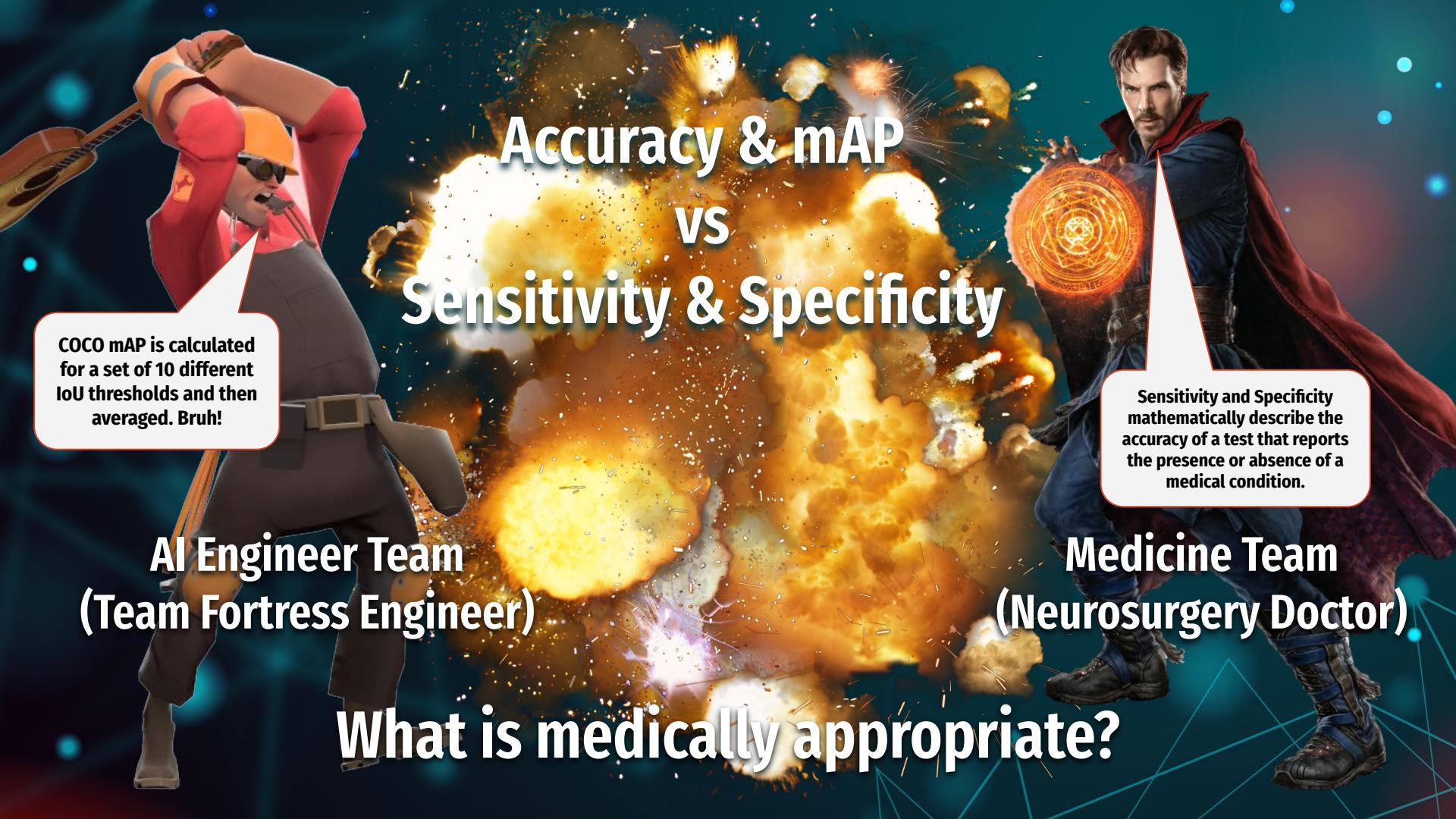
- Add new domain-specific features and increase more sample, and change the types of feature processing used
- Decrease the amount of regularization used (Augmentation, Batch Normalization or Dropout)

If your model is overfitting the training data, it makes sense to take actions that reduce model flexibility. To reduce model flexibility, try the following:

- Feature selection: consider using fewer feature combinations, decreasing similar data, and decreasing the number of numeric attributes (hyperparameters).
- Increase the amount of regularization used. (Augmentation, Batch Normalization or Dropout)

Accuracy on training and test data could be poor because the learning algorithm did not have enough data to learn from. You could improve performance by doing the following:

- Increase the amount of training data examples. (Add more N sample)
- Increase the number of passes on the existing training data. (Increase epoch and iteration)



# Accuracy & mAP vs Sensitivity & Specificity

COCO mAP is calculated for a set of 10 different IoU thresholds and then averaged. Bruh!

AI Engineer Team  
(Team Fortress Engineer)

Medicine Team  
(Neurosurgery Doctor)

What is medically appropriate?

Sensitivity and Specificity mathematically describe the accuracy of a test that reports the presence or absence of a medical condition.

		Positive	Negative
Negative	Positive	TP	FN (Type II Error)
	Negative	FP (Type I Error)	TN
		TRUE POSITIVE	SENSITIVITY

FALSE POSITIVE

$TPR = \frac{TP}{TN + FP}$

f1-score ( $y_{\text{test}}$ ,  $y_{\text{pred}}$ )

RECALL

$FPR = \frac{FP}{TN + FP}$

TRUE NEGATIVE

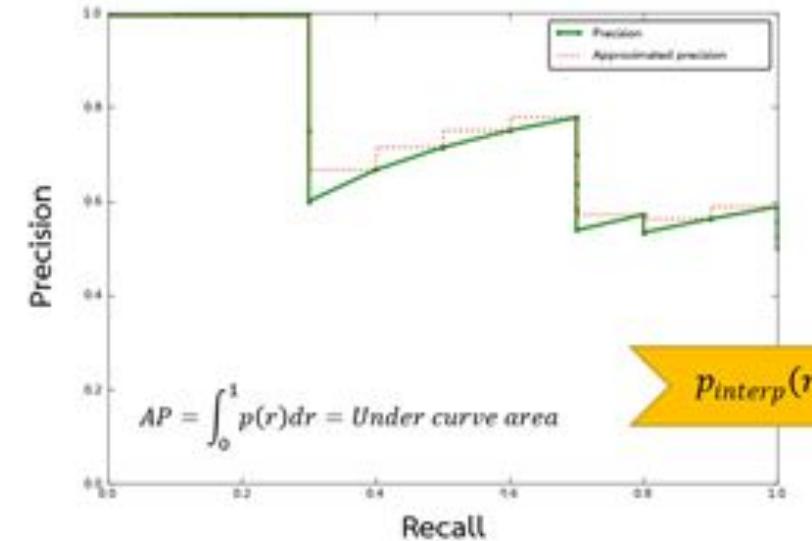
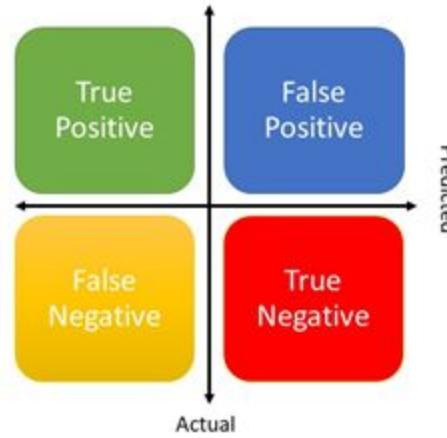
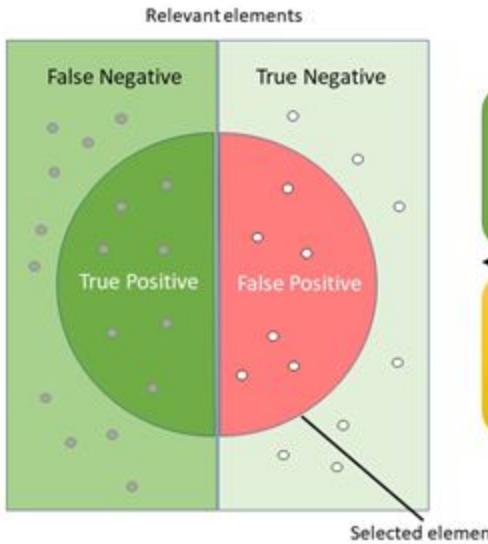
$FNR = \frac{FN}{TP + FN}$

Accuracy =  $\frac{TP + TN}{TP + FN + FP + TN}$

$TNR = \frac{TN}{TN + FP}$

from sklearn.metrics import f1\_score

FALSE NEGATIVE



$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN}$$

### Average precision (AP) vs mean Average Precision (mAP)

$$\text{Precision} = \frac{TP}{TP+FP}$$

$$AP = \sum_{i=1}^n \text{Precision}_i (\text{Recall}_i - \text{Recall}_{i-1})$$

$$\text{Recall} = \frac{TP}{TP+FN}$$

$$mAP = \frac{1}{n_{\text{classes}}} \sum AP_{\text{classes}}$$

## “Gold standard”

	+	-
+	TP	FP
-	FN	TN

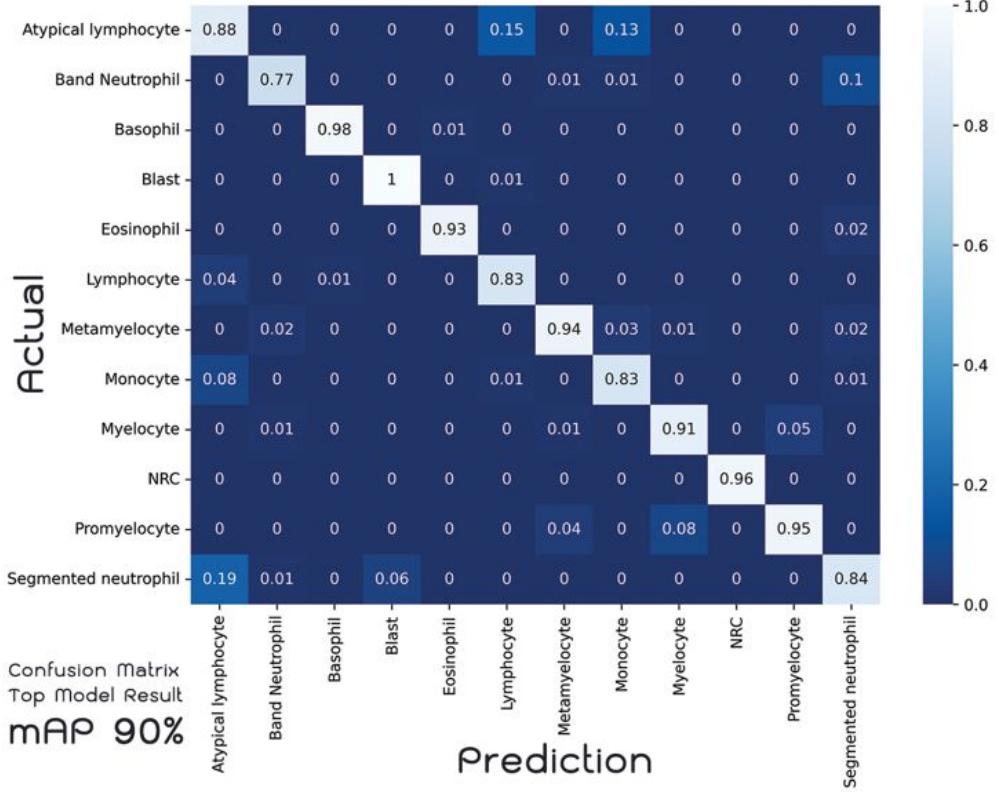
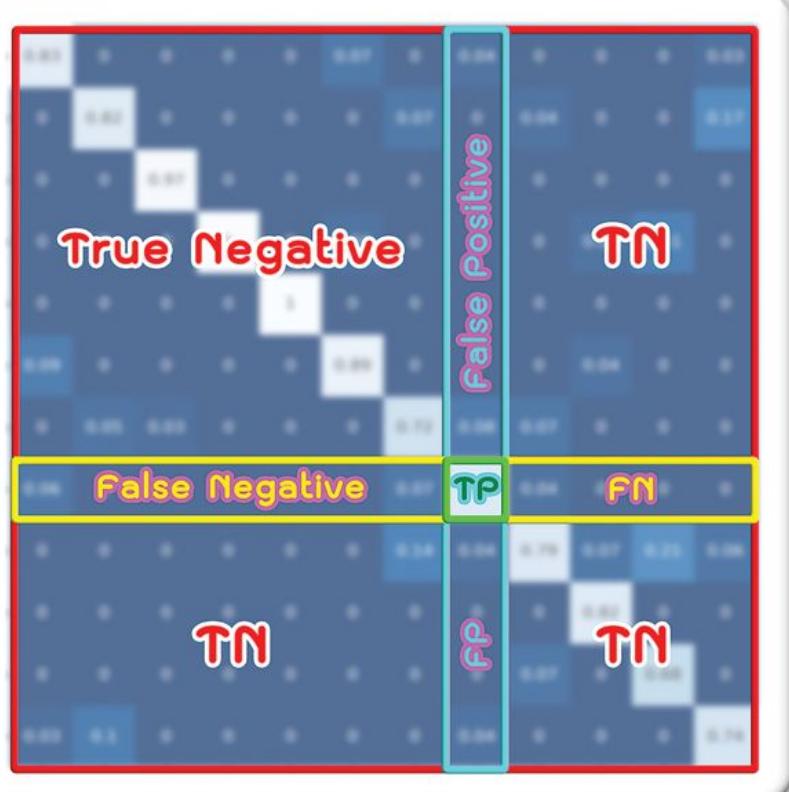
$$\text{Sensitivity} = (\text{TP} / (\text{TP} + \text{FN}))$$

$$\text{Specificity} = (\text{TN} / (\text{TN} + \text{FP}))$$

$$\text{PPV} = (\text{TP} / (\text{TP} + \text{FP}))$$

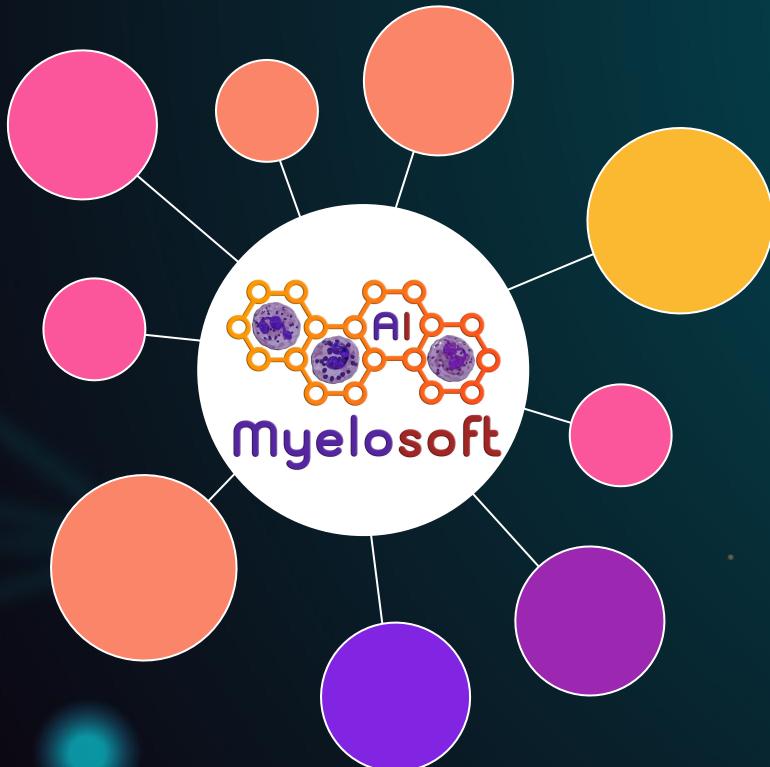
$$\text{NPV} = (\text{TN} / (\text{TN} + \text{FN}))$$

$$\text{Diagnostic Accuracy} = ((\text{TP} + \text{TN}) / (\text{TN} + \text{FP} + \text{FN} + \text{TN}))$$



# Confusion Matrix for Multi-Class. How to calculate?

# Artificial intelligence (AI) for microscopic

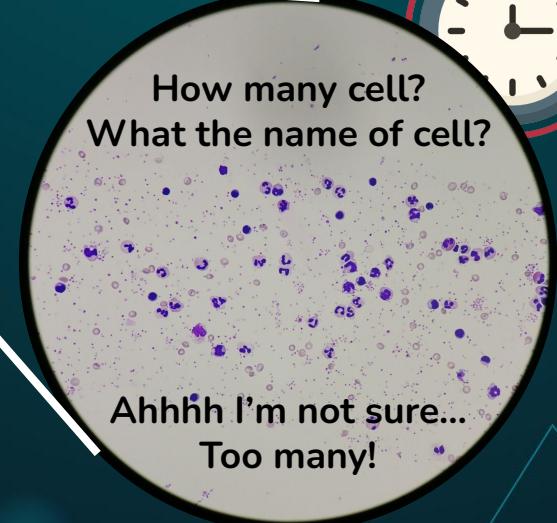
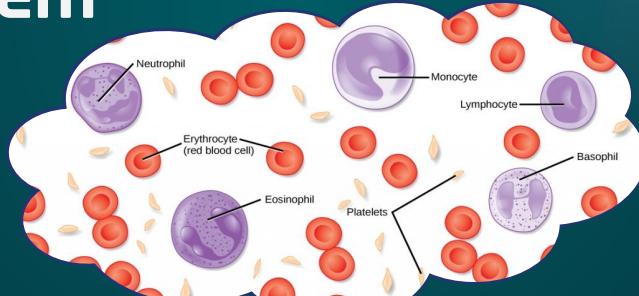
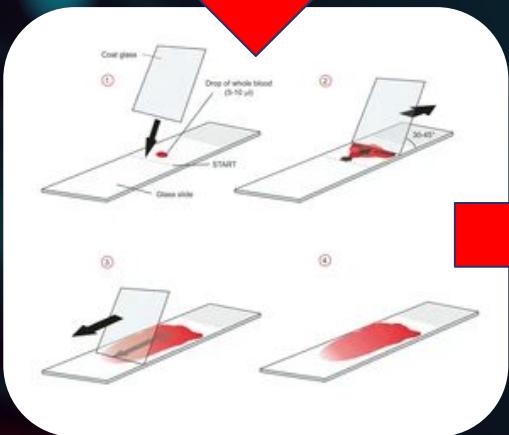
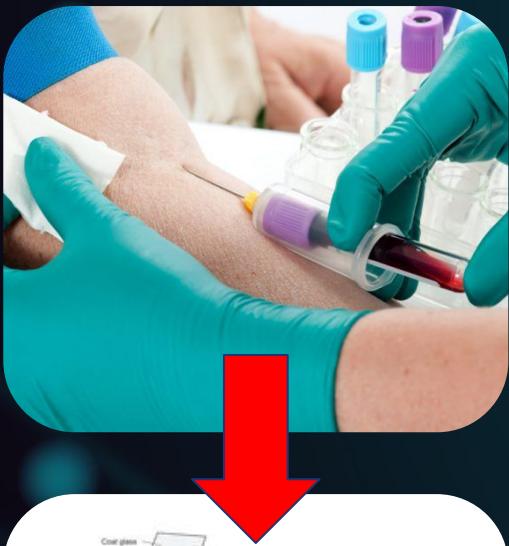


**Myelosoft : Development of  
Abnormal Leukocyte Counting  
System via Smartphone using  
Convolutional Neural Network.**

Natthakorn Kasamsumran, Ph.D. candidate  
Embedded System and IC Design Research Laboratory  
Electrical engineering department, Faculty of engineering,  
Chulalongkorn University, Thailand.

Collaborate with Siriraj Informatics and Data Innovation  
Center (SiData+) and Faculty of Medicine Siriraj Hospital,  
Mahidol University.

# Pain point & Problem

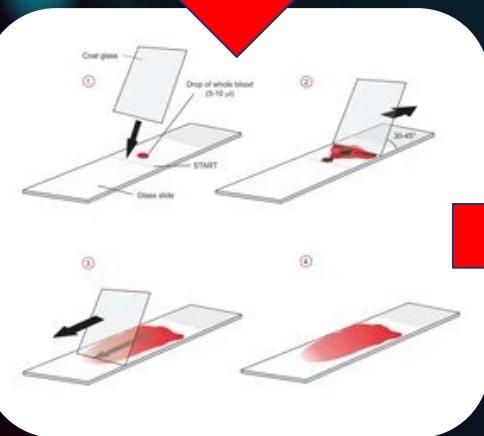


# Pain point & Problem



- In the traditional method, doctors would perform a peripheral blood smear (PBS) microscopic examination, which was a formal standard, but that process takes a waste of time.
- The automated cell counters were developed to make rapid CBC examine, but the cost is 4,310,550 - 5,576,025 Baht per unit, thus becoming available only in medical schools and large hospitals in Thailand.
- There are some disadvantages to an automated machine in cases of PBS containing rare abnormal cells in general conditions. As a result, the device gives inaccurate counting.
- Therefore, the criteria for re-examination by microscopy were established rates increase to 20.20%.

# If an automated machine can't identify abnormal



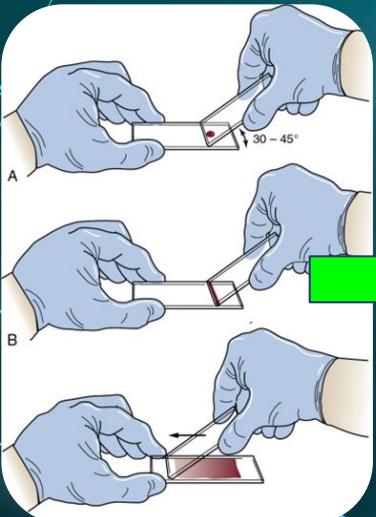
**Staff :** I have lots to do.  
I will reply later.

(wait for few hours/days)



**Intern :** Staff, I need advice.  
This cell is myeloblast  
or not? Please reply.

# 4 Step of Myelosoft

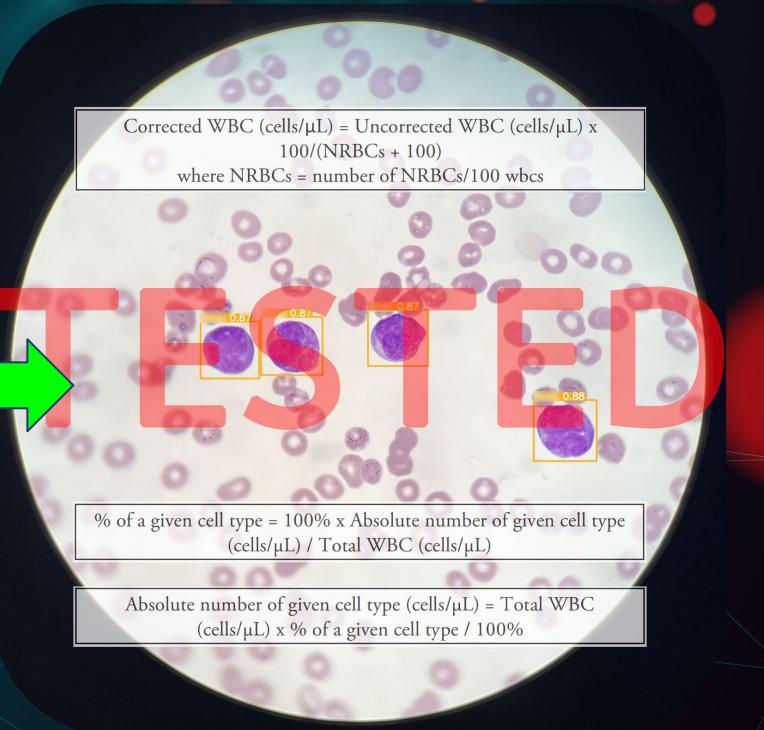


Smear

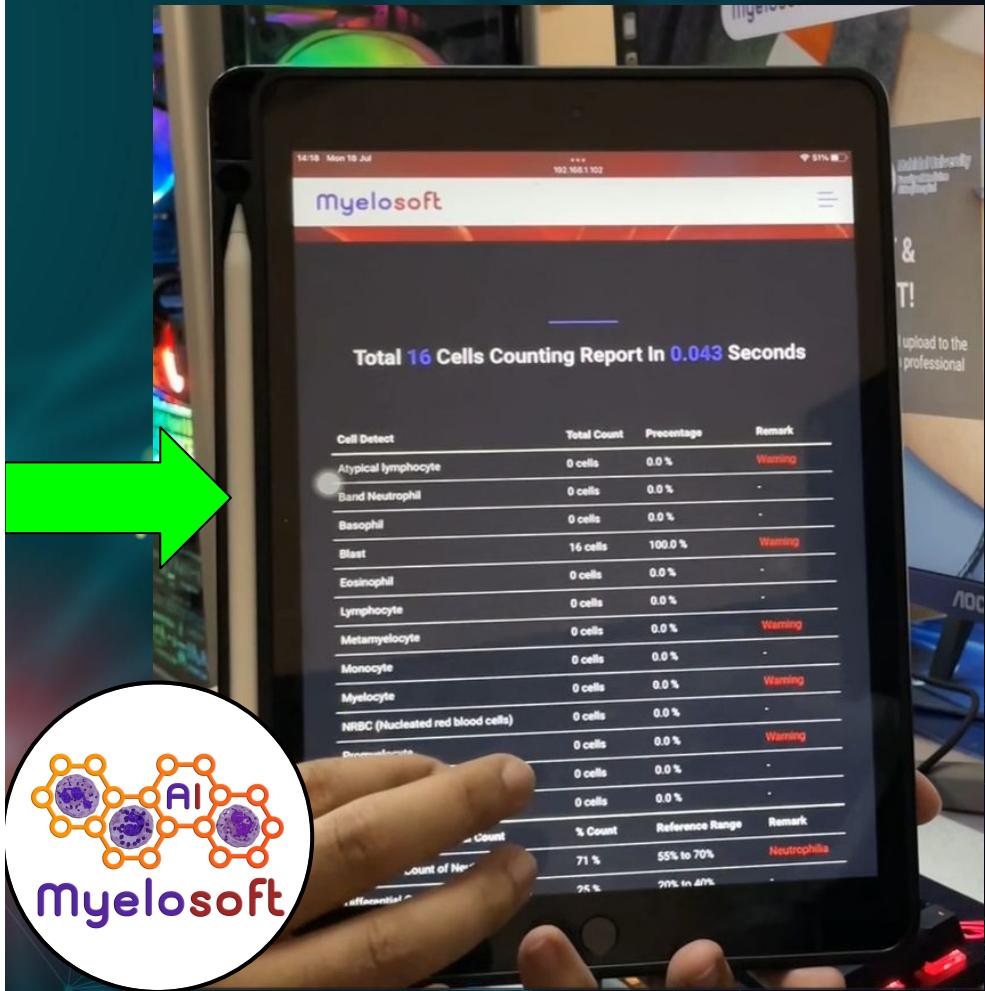
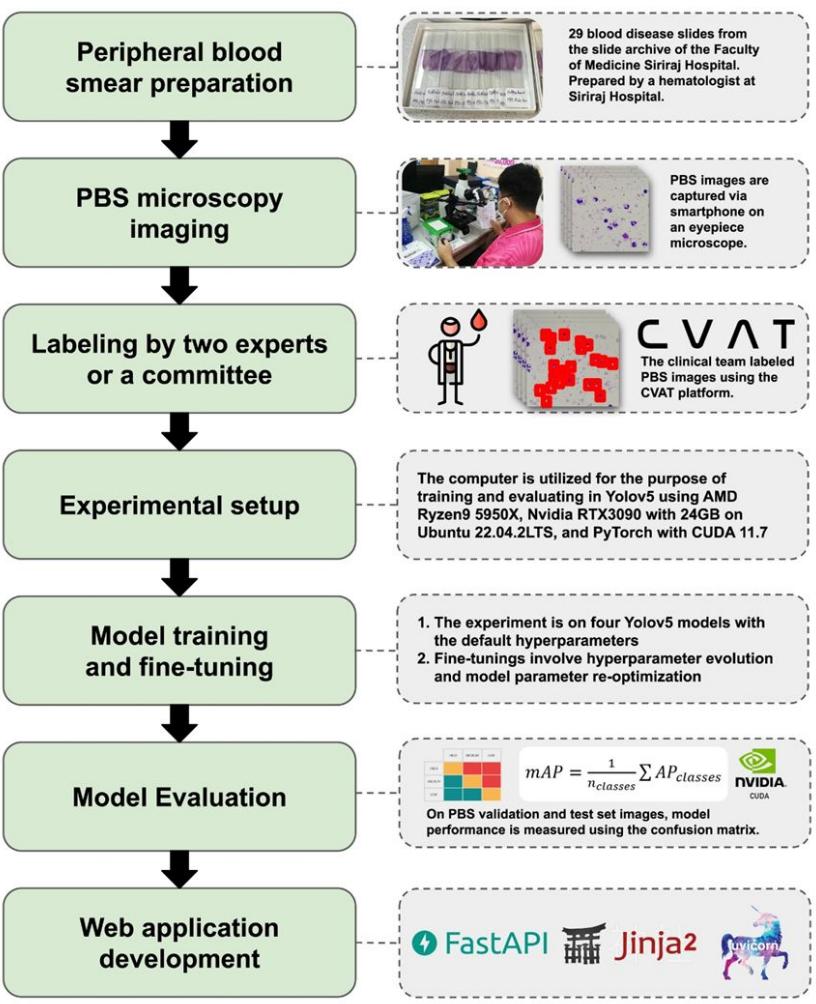
Snapshot



Sent to  
server



See a predicted result

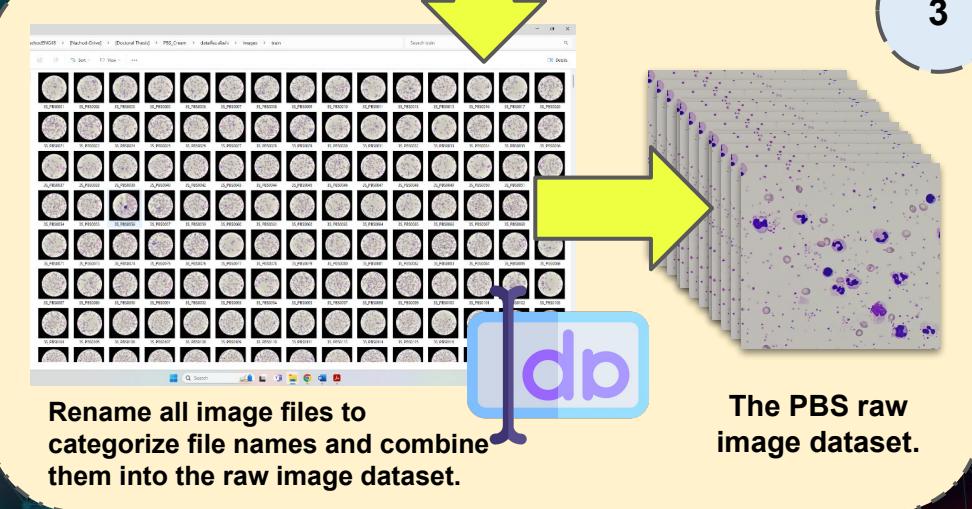
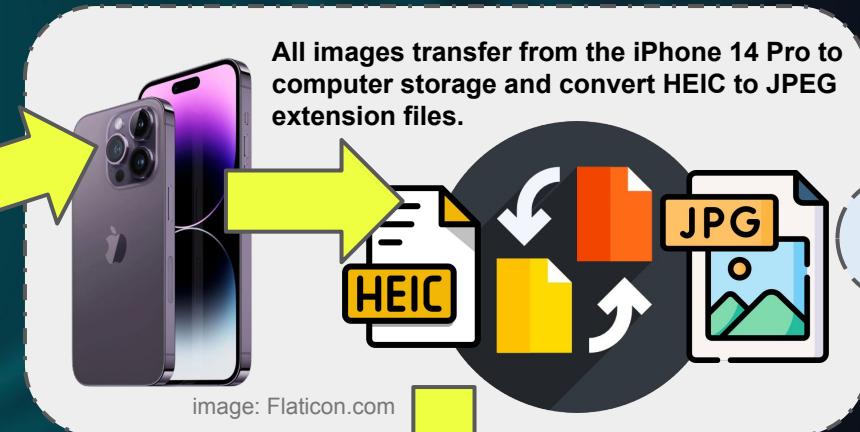




Collect blood slides and snap images with a smartphone controlled by a Bluetooth remote control.

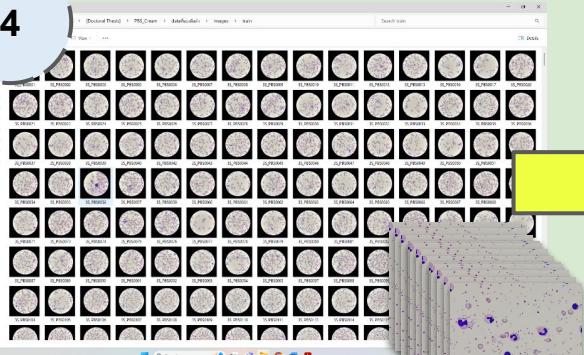


1



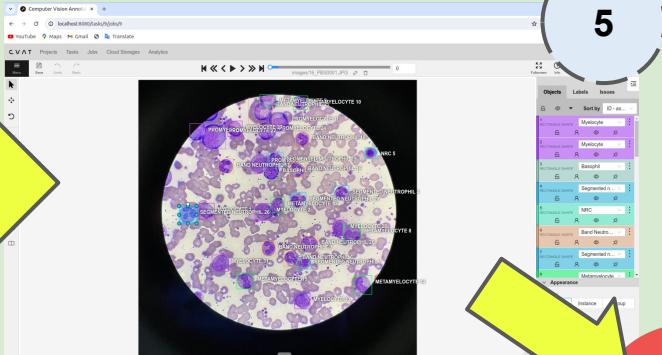
# ESID Lab computer

4



The PBS raw image dataset into CVAT as a PBS project.

5



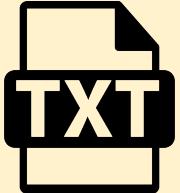
Do labeling with bounding boxes without class names.

8

Images folder.

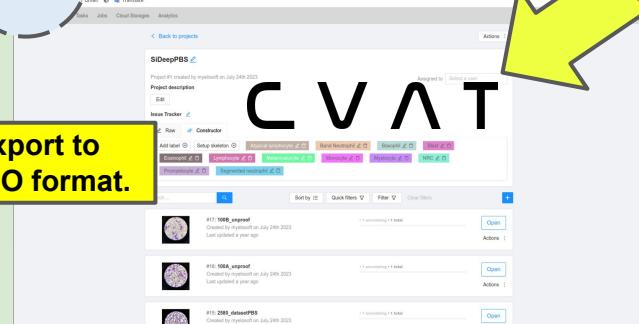


Labels folder.



Export to YOLO format.

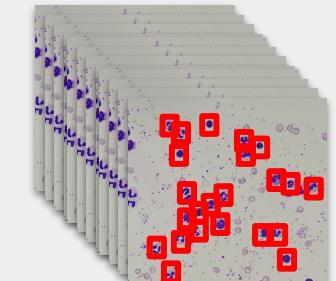
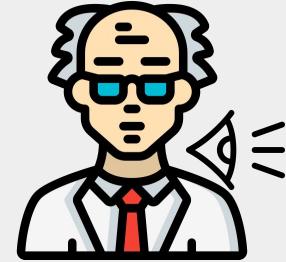
7



Combine the labeled image dataset, export it in Yolo format, and get a YAML file specifying the order of class names.

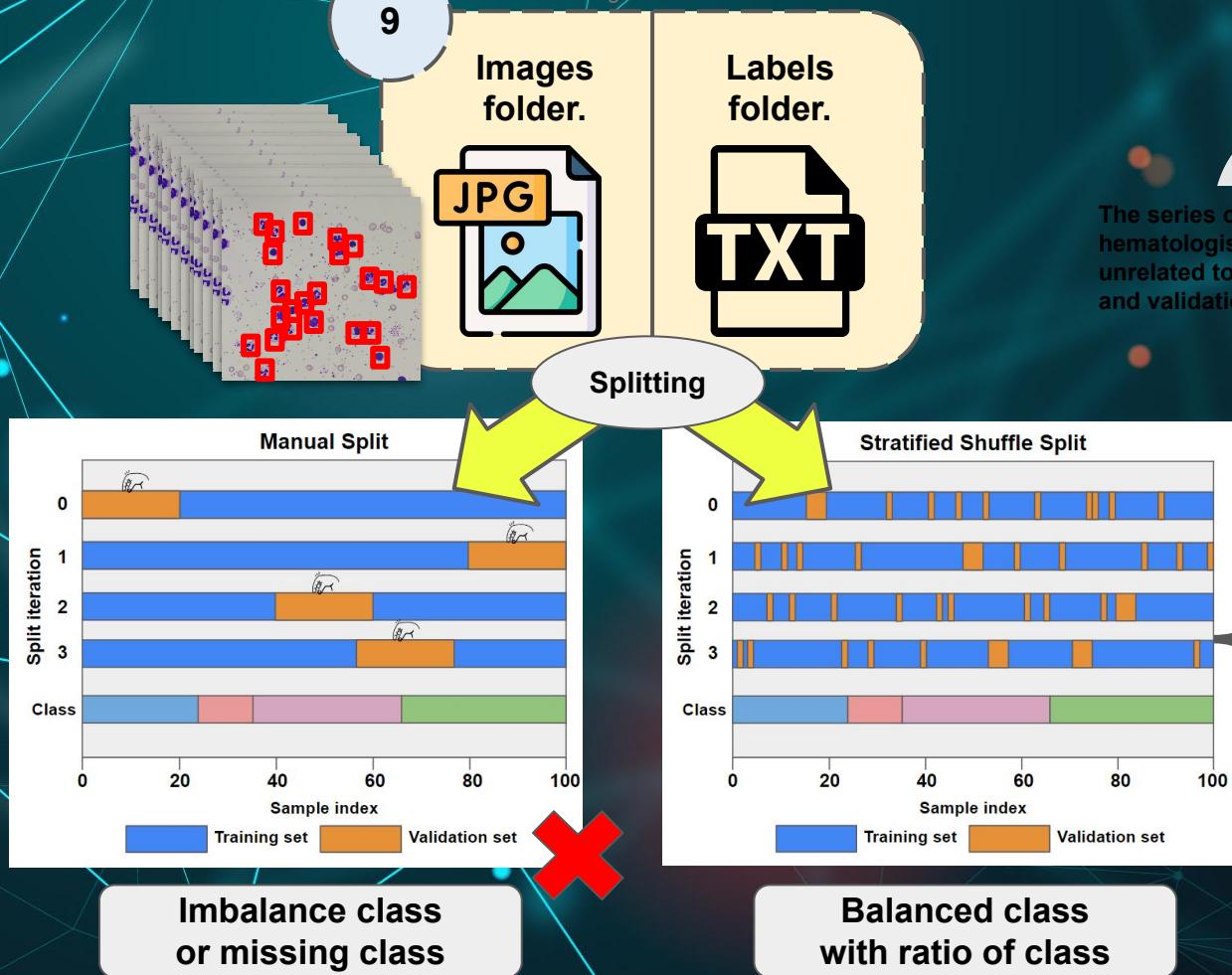
Hospital computer

CVAT



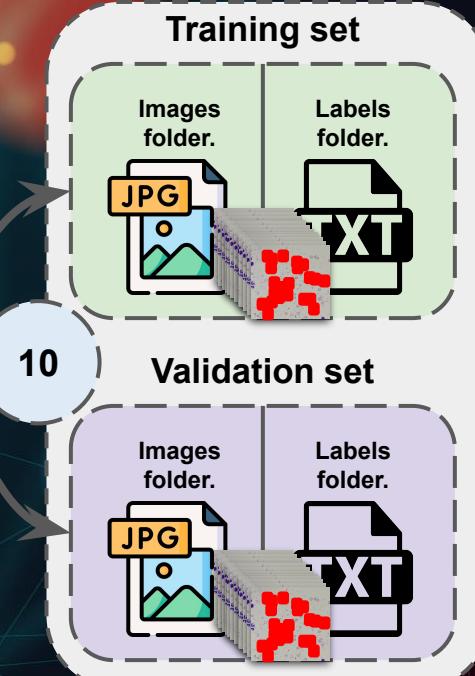
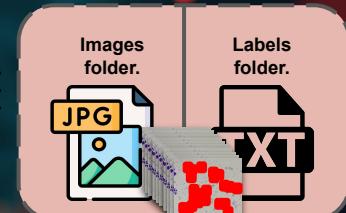
The team of hematologists specifies the class name of each cell.

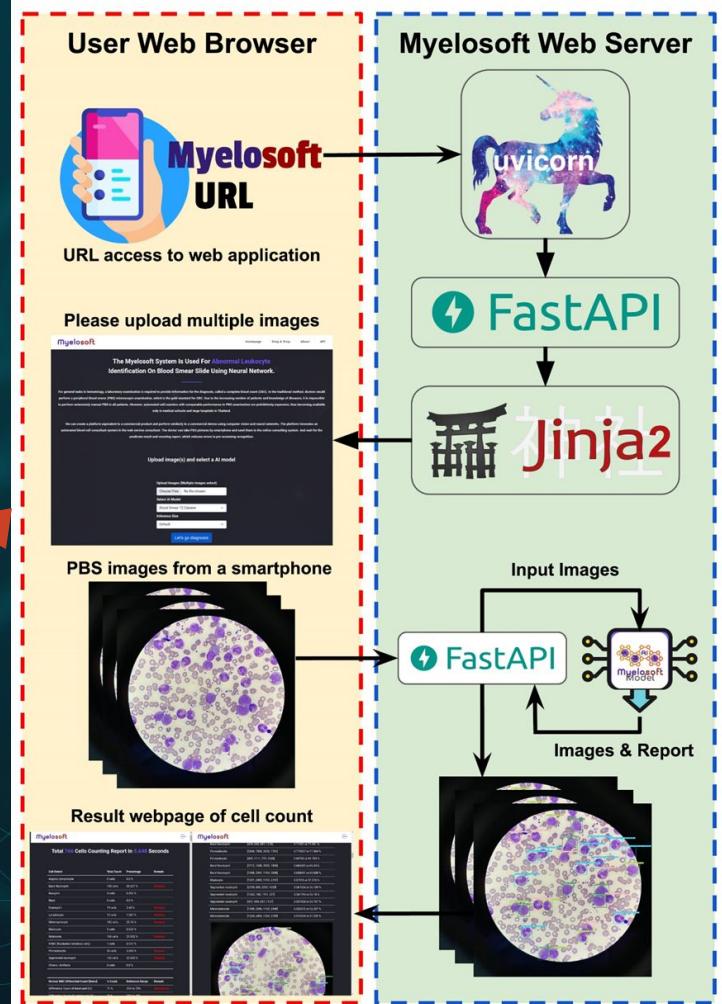
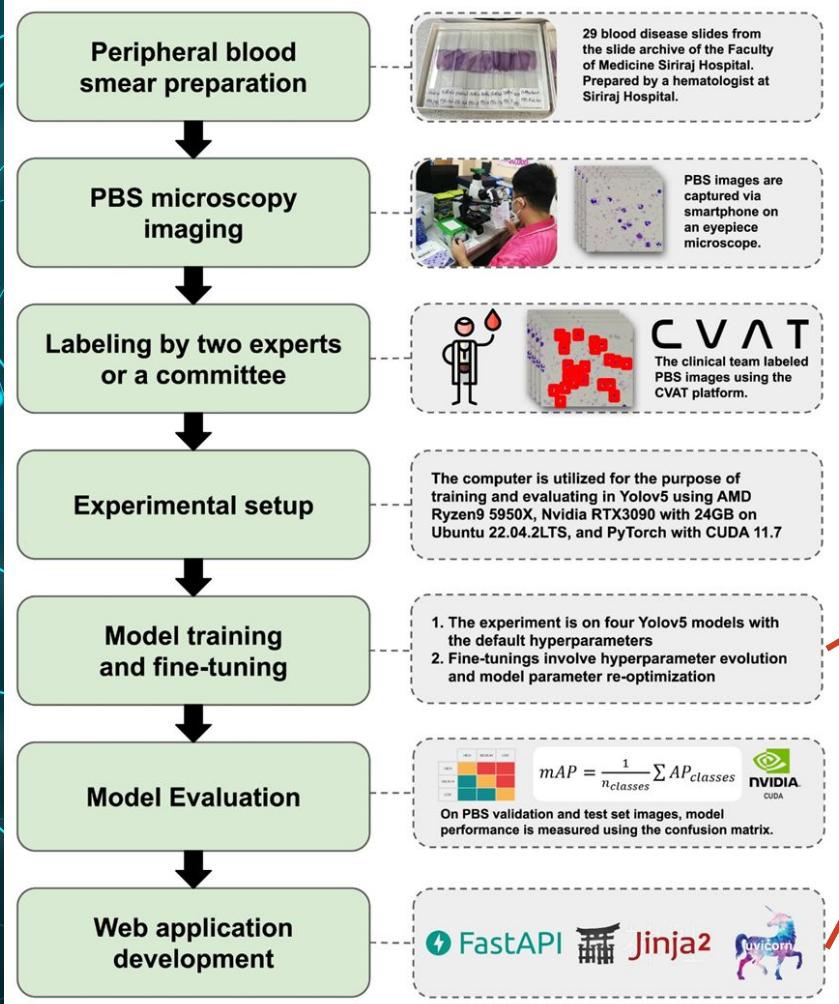
9

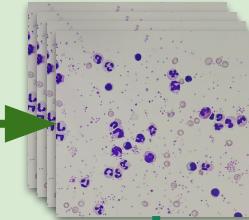
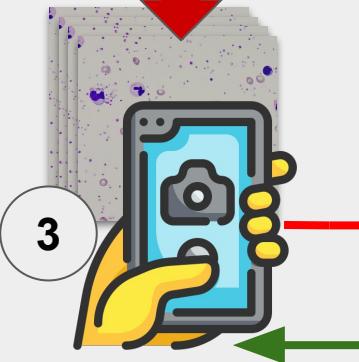


The series of test sets is a hematologist key that is unrelated to the training and validation sets.

Test set A &amp; B

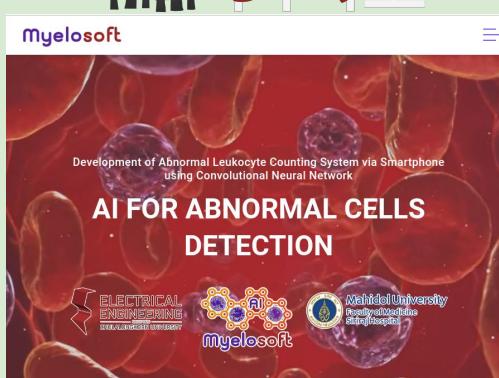






1. Images upload handler.
2. Call PyTorch to make PBS images prediction.
3. Cell counting calculation.
4. Call Jinja2 to generate a result on HTML page.

Web  
Template  
Generator

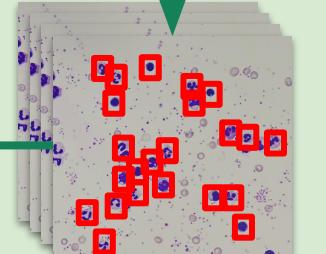
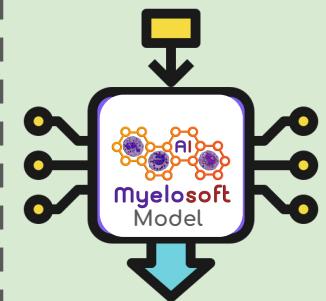


myelosoft  
AI FOR ABNORMAL CELLS  
DETECTION

FastAPI

PyTorch

YOLOv5



Predicted Images



Myelosoft - SiDeepPBS W...

Not secure | 0.0.0.0:8000

YouTube Maps Gmail Translate

# Myelosoft

## Total 766 Cells Counting Report In 5.648 Seconds

Cell Detect	Total Count	Percentage	Remark
Atypical lymphocyte	0 cells	0.0 %	
Band Neutrophil	158 cells	20.627 %	Warning
Basophil	3 cells	0.392 %	
Blast	0 cells	0.0 %	
Eosinophil	19 cells	2.48 %	Warning
Lymphocyte	12 cells	1.567 %	Warning
Metamyelocyte	182 cells	23.76 %	Warning
Monocyte	5 cells	0.653 %	
Myelocyte	168 cells	21.932 %	Warning
NRBC (Nucleated red blood cells)	1 cells	0.131 %	
Promyelocyte	26 cells	3.394 %	Warning
Segmented neutrophil	192 cells	25.065 %	Warning
Others / Artifacts	0 cells	0.0 %	

Normal WBC Differential Count [Demo]	% Count	Reference Range	Remark
Differential Count of Neutrophil (%)	71 %	55% to 70%	Neutrophilia
Differential Count of Lymphocyte (%)	25 %	20% to 40%	

Myelosoft - SiDeepPBS W...

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# Myelosoft

Band Neutrophil	[435, 940, 657, 1138]	0.71681 or 71.681 %
Promyelocyte	[2606, 1508, 2836, 1761]	0.715637 or 71.564 %
Promyelocyte	[469, 1111, 729, 1348]	0.69783 or 69.783 %
Band Neutrophil	[2712, 1348, 2853, 1549]	0.663402 or 66.34 %
Band Neutrophil	[1588, 2347, 1764, 2548]	0.638081 or 63.808 %
Myelocyte	[1291, 2492, 1510, 2747]	0.57516 or 57.516 %
Segmented neutrophil	[2109, 839, 2310, 1029]	0.567036 or 56.704 %
Segmented neutrophil	[1563, 148, 1761, 337]	0.561795 or 56.18 %
Segmented neutrophil	[437, 940, 657, 1137]	0.527668 or 52.767 %
Metamyelocyte	[1588, 2346, 1765, 2548]	0.522072 or 52.207 %
Metamyelocyte	[1294, 2496, 1509, 2749]	0.510334 or 51.033 %

Myelosoft - SiDeepPBS < +

Not secure 0.0.0.0:8000

YouTube Maps Gmail Translate

Dimensions: iPhone 14 Pro Max 430 x 932 90% ▾

Myelosoft

Development of Abnormal Leukocyte Counting System via Smartphone using Convolutional Neural Network

# AI FOR ABNORMAL LEUKOCYTE DETECTION

ELECTRICAL ENGINEERING  
SCHOOL OF ENGINEERING  
Myelosoft

Mahidol University  
Mahidol University  
Medical Engineering  
Development Project

Network >

Preserve log

Disable cache No throttling

Filter

Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

50 ms 100 ms

Name	Status	Type	Initiator	Size	Time
swiper-bundle....	200	sty... (index):22	(d...)	1 ms	
heading-bg.jpg	200	jpeg	template(...)	10 ...	
banner-blood.jpg	200	jpeg	template(...)	10 ...	
data:image/svg...	200	sv...	bootstrap(...)	0 ms	
dark-bg.jpg	200	jpeg	template(...)	5 ms	
data:image/svg...	200	sv...	bootstrap(...)	0 ms	
category-collect...	200	png	template(...)	7 ms	
main-bg.jpg	200	jpeg	template(...)	8 ms	
KFOmCnqEu92F...	200	Font	css2	(d...)	6 ms
KFOlCnqEu92Fr...	200	Font	css2	(d...)	6 ms
blast.png	200	png	isotope.mir	(d...)	2 ms
cf.png	200	png	isotope.mir	(d...)	2 ms
favicon.ico	200	vn...	inpage.js:1	(d...)	1 ms
dom.build.min.js	200	scr...	content_by	3.1...	2 ms
favicon.ico	200	vn...	Other	(d...)	1 ms

16 requests 3.1 kB transferred 2.0 MB resources

Console What's new

Highlights from the Chrome 126 update

Move tracks around with updated UI in Performance panel

Change the order of tracks and hide them with an improved configuration mode in the Performance panel.

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Myelosoft

## Identification On Blood Smear Slide Using Neural Network.

For general tasks in hematology, a laboratory examination is required to provide information for the diagnosis, called a complete blood count (CBC). In the traditional method, doctors would perform a peripheral blood smear (PBS) microscopic examination, which is the gold standard for CBC. Due to the increasing number of patients and knowledge of diseases, it is impossible to perform extensively manual PBS in all patients. However, automated cell counters with comparable performance to PBS examination are prohibitively expensive, thus becoming available only in medical schools and large hospitals in Thailand.

We can create a platform equivalent to a commercial product and perform similarly to a commercial device using computer vision and neural networks. The platform innovates an automated blood cell consultant system in the web service consultant. The doctor can take PBS pictures by smartphone and send them to the online consulting system. And wait for the predicate result and counting report, which reduces errors in pre-screening recognition.

Network >

Preserve log

Disable cache No throttling

Filter

Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

50 ms 100 ms

Name	Status	Type	Initiator	Size	Time
swiper-bundle....	200	sty... (index):22	(d...)	1 ms	
heading-bg.jpg	200	jpeg	template(...)	10 ...	
banner-blood.jpg	200	jpeg	template(...)	10 ...	
data:image/svg...	200	sv...	bootstrap(...)	0 ms	
dark-bg.jpg	200	jpeg	template(...)	5 ms	
data:image/svg...	200	sv...	bootstrap(...)	0 ms	
category-collect...	200	png	template(...)	7 ms	
main-bg.jpg	200	jpeg	template(...)	8 ms	
KFOmCnqEu92F...	200	Font	css2	(d...)	6 ms
KFOlCnqEu92Fr...	200	Font	css2	(d...)	6 ms
blast.png	200	png	isotope.mir	(d...)	2 ms
cf.png	200	png	isotope.mir	(d...)	2 ms
favicon.ico	200	vn...	inpage.js:1	(d...)	1 ms
dom.build.min.js	200	scr...	content_by	3.1...	2 ms
favicon.ico	200	vn...	Other	(d...)	1 ms

16 requests 3.1 kB transferred 2.0 MB resources

Console What's new

Highlights from the Chrome 126 update

Move tracks around with updated UI in Performance panel

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Dimensions: iPhone 14 Pro Max 430 x 932 90% ▾

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University.



Dataset by Physician.

We have a team of doctor, Assoc.Prof.Ekaphun Karpopongse, M.D., Dr.Piyalitt Ittchalitwong, Dr.Kanyakorn Veerakanjan and Medical Students in Faculty of Medicine Siriraj Hospital.



Power Drive by GPU.

The platform innovates an automated blood cell consultant system in the web service consultant. All Images process in high-performance GPU.

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System designed by Nathakorn Kasamsumran, Ph.D. candidate @ Electrical engineering, Chulalongkorn University.

Network >> 521 1 50 ms 100 ms

Filter Preserve log

Disable cache No throttling

Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

Name	Status	Type	Initiator	Size	Time
swiper-bundle....	200	sty... (index):22	(d...)	1 ms	
heading-bg.jpg	200	jpeg	template	10 ...	
banner-blood.jpg	200	jpeg	template	10 ...	
data:image/svg...	200	sv...	bootstrap	0 ms	
dark-bg.jpg	200	jpeg	template	5 ms	
data:image/svg...	200	sv...	bootstrap	0 ms	
category-collect...	200	png	template	7 ms	
main-bg.jpg	200	jpeg	template	8 ms	
KFOmCnqEu92Fr...	200	Font	css2	6 ms	
KFOlCnqEu92Fr...	200	Font	css2	6 ms	
blast.png	200	png	isotope.mir	2 ms	
cfc.png	200	png	isotope.mir	2 ms	
favicon.ico	200	vn...	inpage.js:1	1 ms	
dom.build.min.js	200	scr...	content.bu	3 ms	
favicon.ico	200	vn...	Other	1 ms	

16 requests 3.1 kB transferred 2.0 MB resources

Console What's new X

Highlights from the Chrome 126 update

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result and counting report, which reduces errors in pre-screening recognition.

Upload image(s) and select a AI model

Upload Images (Multiple images select)

Choose Files No file chosen

Select AI Model

Blood Smear 12 Classes

Inference Size

Default

Let's go diagnosis

Confidence range (Default 0.5)

Intersection over Union (Default 0.45)

Advance configuration

NMS class-agnostic

NMS multiple labels

Automatic mixed precision

Network >> 640 1 50 ms 100 ms

Filter Preserve log

Disable cache No throttling

Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

Name	Status	Type	Initiator	Size	Time
swiper-bundle....	200	sty... (index):22	(d...)	1 ms	
heading-bg.jpg	200	jpeg	template	10 ...	
banner-blood.jpg	200	jpeg	template	10 ...	
data:image/svg...	200	sv...	bootstrap	0 ms	
dark-bg.jpg	200	jpeg	template	5 ms	
data:image/svg...	200	sv...	bootstrap	0 ms	
category-collect...	200	png	template	7 ms	
main-bg.jpg	200	jpeg	template	8 ms	
KFOmCnqEu92Fr...	200	Font	css2	6 ms	
KFOlCnqEu92Fr...	200	Font	css2	6 ms	
blast.png	200	png	isotope.mir	2 ms	
cfc.png	200	png	isotope.mir	2 ms	
favicon.ico	200	vn...	inpage.js:1	1 ms	
dom.build.min.js	200	scr...	content.bu	3 ms	
favicon.ico	200	vn...	Other	1 ms	

16 requests 3.1 kB transferred 2.0 MB resources

Console What's new X

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Dimensions: iPhone 14 Pro Max 430 x 932 90% Network Preset log

Disable cache No throttling

Filter Invert Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

Cancel Open Files Open

nachodeng48 NRTC\_Image

Recent Home Desktop Documents Downloads Music Pictures Videos Open files read-only

Name	Type	Modified	Time
16_PBS0235.JPG	Image	26 n.o. 2023	1 ms
16_PBS0238.JPG	Image	26 n.o. 2023	10 ms
16_PBS0239.JPG	Image	26 n.o. 2023	10 ms
16_PBS0248.JPG	Image	26 n.o. 2023	5 ms
21_PBS0023.JPG	Image	26 n.o. 2023	0 ms
21_PBS0024.JPG	Image	26 n.o. 2023	7 ms
21_PBS0025.JPG	Image	26 n.o. 2023	8 ms
21_PBS0026.JPG	Image	26 n.o. 2023	6 ms

(None)

Confidence range (Default 0.5)  
Intersection over Union (Default 0.45)

Advance configuration  
NMS class-agnostic  
NMS multiple labels  
Automatic mixed precision

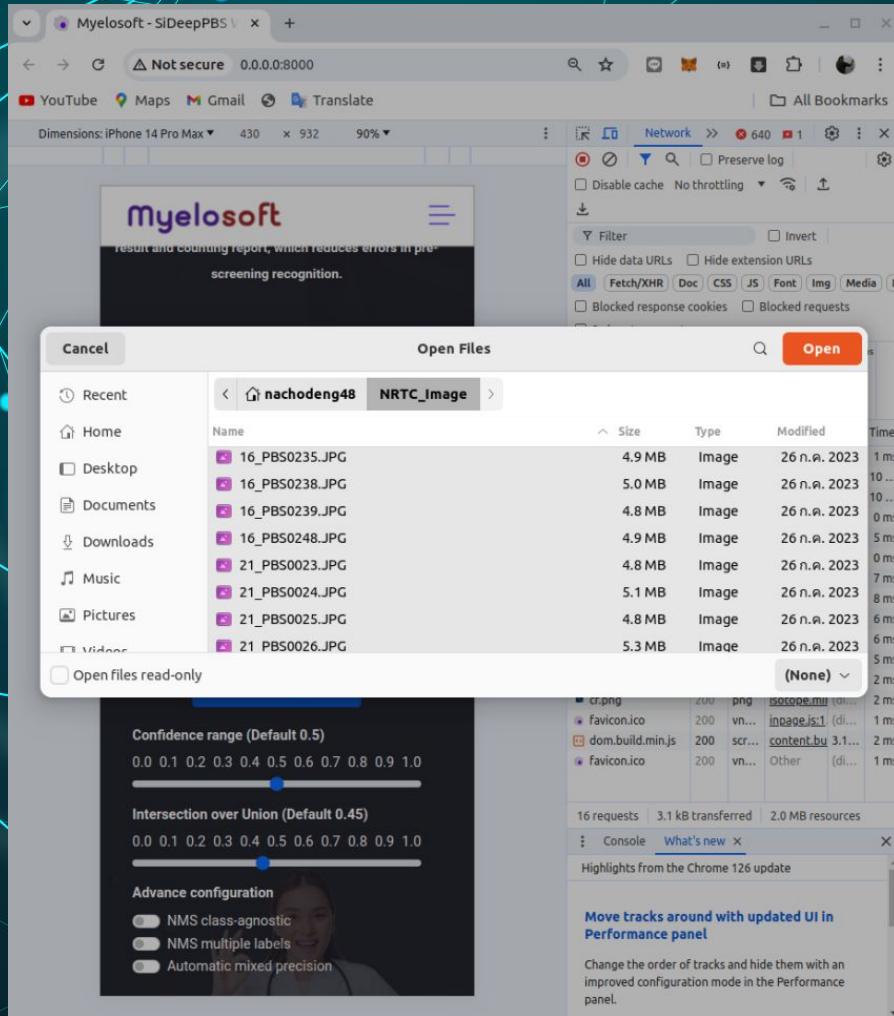
16 requests 3.1 kB transferred 2.0 MB resources

Console What's new X

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Not secure 0.0.0:8000

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Disable cache No throttling

Filter Invert Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

50 ms 100 ms

Name	Sta...	Type	Initiator	Size	Time
swiper-bundle....	200	sty...	(index):22	(di...	1 ms
heading-bg.jpg	200	jpeg	template	(di...	10 ms
banner-blood.jpg	200	jpeg	template	(di...	10 ms
dataimage/svg...	200	sv...	bootstrap	(m...	0 ms
dark-bg.jpg	200	jpeg	template	(di...	5 ms
dataimage/svg...	200	sv...	bootstrap	(m...	0 ms
category-collect...	200	png	template	(di...	7 ms
main-bg.jpg	200	jpeg	template	(di...	8 ms
KFOICnqEu92Fr...	200	font	css2	(di...	6 ms
KFOICnqEu92Fr...	200	font	css2	(di...	5 ms
blast.png	200	png	isotope.mii	(di...	2 ms
cfpng	200	png	isotope.mii	(di...	2 ms
favicon.ico	200	vn...	image.js:1	(di...	1 ms
dom.build.min.js	200	scr...	content.bu	3.1...	2 ms
favicon.ico	200	vn...	Other	(di...	1 ms

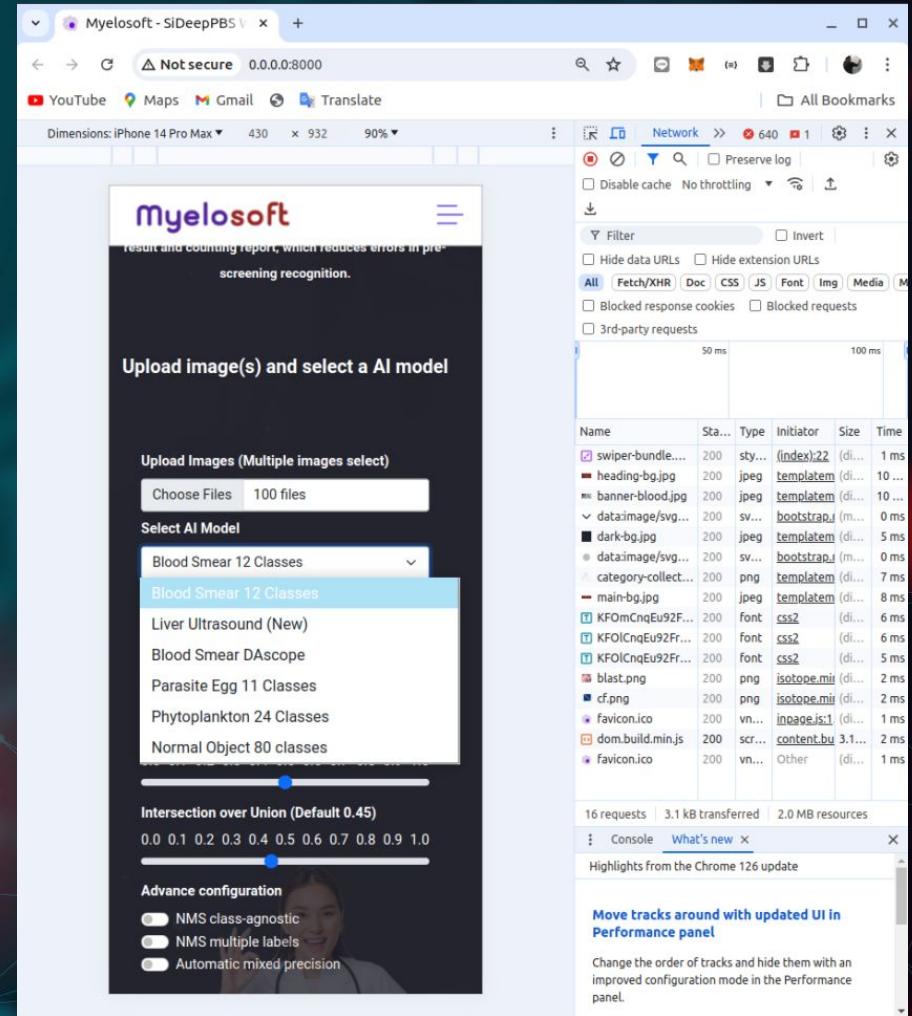
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Dimensions: iPhone 14 Pro Max 430 x 932 90% ▾

# Myelosoft

## Total 728 Cells Counting Report In 35.546 Seconds

Cell Detect	Total Count	Percentage	Remark
Atypical lymphocyte	15	2.06 %	<span style="color: red;">Warning</span>
Band Neutrophil	67	9.203 %	<span style="color: red;">Warning</span>
Basophil	36	4.945 %	<span style="color: red;">Warning</span>
Blast	266	36.538 %	<span style="color: red;">Warning</span>
Eosinophil	26	3.571 %	<span style="color: red;">Warning</span>
Lymphocyte	12	1.648 %	<span style="color: red;">Warning</span>
Metamyelocyte	34	4.67 %	<span style="color: red;">Warning</span>
Monocyte	16	2.198 %	<span style="color: red;">Warning</span>
Myelocyte	77	10.577 %	<span style="color: red;">Warning</span>

Name St... Type Initiator Size Time

- data:image/jpe... zvu jpeg www.myelosoft... 16...
- data:image/jpe... 200 jpeg (index):59 (m... 16...
- data:image/jpe... 200 jpeg (index):59 (m... 16...
- icon-eng.png 200 png (index):59 (di... 4 ms
- icon-doc.png 200 png (index):59 (di... 4 ms
- icon-ai.png 200 png (index):59 (di... 4 ms
- jquery.min.js 200 scr... (index):59 (di... 5 ms
- bootstrap.min.js 200 scr... (index):59 (di... 6 ms
- isotope.min.js 200 scr... (index):59 (di... 6 ms
- owl-carousel.js 200 scr... (index):59 (di... 6 ms
- wow.js 200 scr... (index):59 (di... 6 ms
- tabs.js 200 scr... (index):59 (di... 7 ms
- popup.js 200 scr... (index):59 (di... 6 ms
- custom.js 200 scr... (index):60 (di... 1 ms
- main-bg.jpg 200 jpeg templaten... 2 ms
- favicon.ico 200 vnm... inpage.js:1 (di... 2 ms
- dom.build.min.js 200 scr... content\_bu... 3 ms
- favicon.ico 200 vnm... Other (di... 1 ms

135 requests 272 MB transferred 478 MB resources

Console What's new X

Highlights from the Chrome 126 update

Move tracks around with updated UI in Performance panel

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Dimensions: iPhone 14 Pro Max 430 x 932 90% ▾

# Myelosoft

## cells

Cell Type	Total Count	Percentage	Remark
Monocyte	16	2.198 %	<span style="color: red;">Warning</span>
Myelocyte	77	10.577 %	<span style="color: red;">Warning</span>
NRBC (Nucleated red blood cells)	67	9.203 %	<span style="color: red;">Warning</span>
Promyelocyte	33	4.533 %	<span style="color: red;">Warning</span>
Segmented neutrophil	79	10.852 %	<span style="color: red;">Warning</span>
Others / Artifacts	0	0.0 %	

Name St... Type Initiator Size Time

- data:image/jpe... zvu jpeg www.myelosoft... 16...
- data:image/jpe... 200 jpeg (index):59 (m... 16...
- data:image/jpe... 200 jpeg (index):59 (m... 16...
- icon-eng.png 200 png (index):59 (di... 4 ms
- icon-doc.png 200 png (index):59 (di... 4 ms
- icon-ai.png 200 png (index):59 (di... 4 ms
- jquery.min.js 200 scr... (index):59 (di... 5 ms
- bootstrap.min.js 200 scr... (index):59 (di... 6 ms
- isotope.min.js 200 scr... (index):59 (di... 6 ms
- owl-carousel.js 200 scr... (index):59 (di... 6 ms
- wow.js 200 scr... (index):59 (di... 6 ms
- tabs.js 200 scr... (index):59 (di... 7 ms
- popup.js 200 scr... (index):59 (di... 6 ms
- custom.js 200 scr... (index):60 (di... 1 ms
- main-bg.jpg 200 jpeg templaten... 2 ms
- favicon.ico 200 vnm... inpage.js:1 (di... 2 ms
- dom.build.min.js 200 scr... content\_bu... 3 ms
- favicon.ico 200 vnm... Other (di... 1 ms

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Console What's new X

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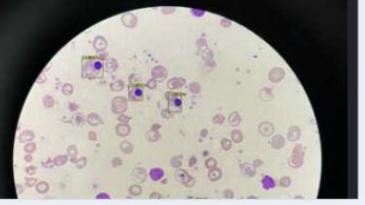
YouTube Maps Gmail Translate

Dimensions: iPhone 14 Pro Max 430 x 932 90% ▾

# Myelosoft

## Prediction Result

Cell Detect	Cell Location [x1, y1, x2, y2]	Confidence (0% to 100%)
NRC	[1621, 2409, 1759, 2573]	0.890633 or 89.063%
NRC	[2241, 1788, 2374, 1943]	0.873299 or 87.33 %
NRC	[1156, 801, 1271, 918]	0.833931 or 83.393 %
NRC	[754, 563, 931, 721]	0.832809 or 83.281 %
NRC	[1673, 1776, 1790, 1892]	0.812723 or 81.272 %
NRC	[1491, 876, 1604, 1017]	0.573643 or 57.364 %



Move tracks around with updated UI in Performance panel

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Network >> 315 1 1

Filter Invert

Disable cache No throttling

Preserve log

Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

20000 ms 40000 ms 60000 ms

Name	St...	Type	Initiator	Size	Time
dataimage/jpe...	200	jpeg	(index):59	(index):10...	10...
dataimage/jpe...	200	jpeg	(index):59	(index):16...	16...
dataimage/jpe...	200	jpeg	(index):59	(index):16...	16...
icon-eng.png	200	png	(index):59	(index):4	4 ms
icon-doc.png	200	png	(index):59	(index):4	4 ms
icon-ai.png	200	png	(index):59	(index):4	4 ms
jquery.min.js	200	scr...	(index):59	(index):5	5 ms
bootstrap.min.js	200	scr...	(index):59	(index):6	6 ms
isotope.min.js	200	scr...	(index):59	(index):6	6 ms
owl-carousel.js	200	scr...	(index):59	(index):6	6 ms
wow.js	200	scr...	(index):59	(index):6	6 ms
tabs.js	200	scr...	(index):59	(index):7	7 ms
popup.js	200	scr...	(index):59	(index):6	6 ms
custom.js	200	scr...	(index):60	(index):1	1 ms
main-bg.jpg	200	jpeg	template	(index):2	2 ms
favicon.ico	200	vn...	image/1	(index):1	2 ms
dom.build.min.js	200	scr...	content_bu	(index):3	3 ms
favicon.ico	200	vn...	Other	(index):1	1 ms

135 requests 272 MB transferred 478 MB resources

Console What's new

Highlights from the Chrome 126 update

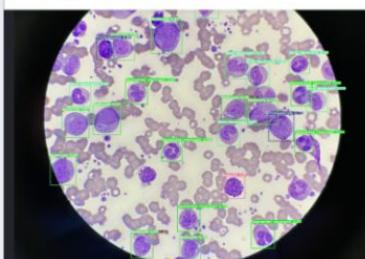
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# Myelosoft



Cell Detect	Cell Location [x1, y1, x2, y2]	Confidence (0% to 100%)
Promyelocyte	[902, 584, 1155, 865]	0.893055 or 89.305 %
Myelocyte	[2280, 579, 2515, 806]	0.89161 or 89.161 %
Band Neutrophil	[2414, 1432, 2628, 1630]	0.887363 or 88.736 %
Metamyelocyte	[1970, 1103, 2167, 1305]	0.882069 or 88.207 %
Segmented neutrophil	[2075, 1621, 2239, 1790]	0.877641 or 87.764 %
Myelocyte	[1791, 2155, 1961, 2333]	0.837607 or 83.761 %
Myelocyte	[763, 747, 1000, 988]	0.830965 or 83.097 %

Network >> 769 1 1

Filter Invert

Disable cache No throttling

Preserve log

Hide data URLs Hide extension URLs

All Fetch/XHR Doc CSS JS Font Img Media

Blocked response cookies Blocked requests

3rd-party requests

20000 ms 40000 ms 60000 ms

Name	St...	Type	Initiator	Size	Time
dataimage/jpe...	200	jpeg	(index):59	(index):10...	10...
dataimage/jpe...	200	jpeg	(index):59	(index):16...	16...
dataimage/jpe...	200	jpeg	(index):59	(index):16...	16...
icon-eng.png	200	png	(index):59	(index):4	4 ms
icon-doc.png	200	png	(index):59	(index):4	4 ms
icon-ai.png	200	png	(index):59	(index):4	4 ms
jquery.min.js	200	scr...	(index):59	(index):5	5 ms
bootstrap.min.js	200	scr...	(index):59	(index):6	6 ms
isotope.min.js	200	scr...	(index):59	(index):6	6 ms
owl-carousel.js	200	scr...	(index):59	(index):6	6 ms
wow.js	200	scr...	(index):59	(index):6	6 ms
tabs.js	200	scr...	(index):59	(index):7	7 ms
popup.js	200	scr...	(index):59	(index):6	6 ms
custom.js	200	scr...	(index):60	(index):1	1 ms
main-bg.jpg	200	jpeg	template	(index):2	2 ms
favicon.ico	200	vn...	image/1	(index):1	2 ms
dom.build.min.js	200	scr...	content_bu	(index):3	3 ms
favicon.ico	200	vn...	Other	(index):1	1 ms

135 requests 272 MB transferred 478 MB resources

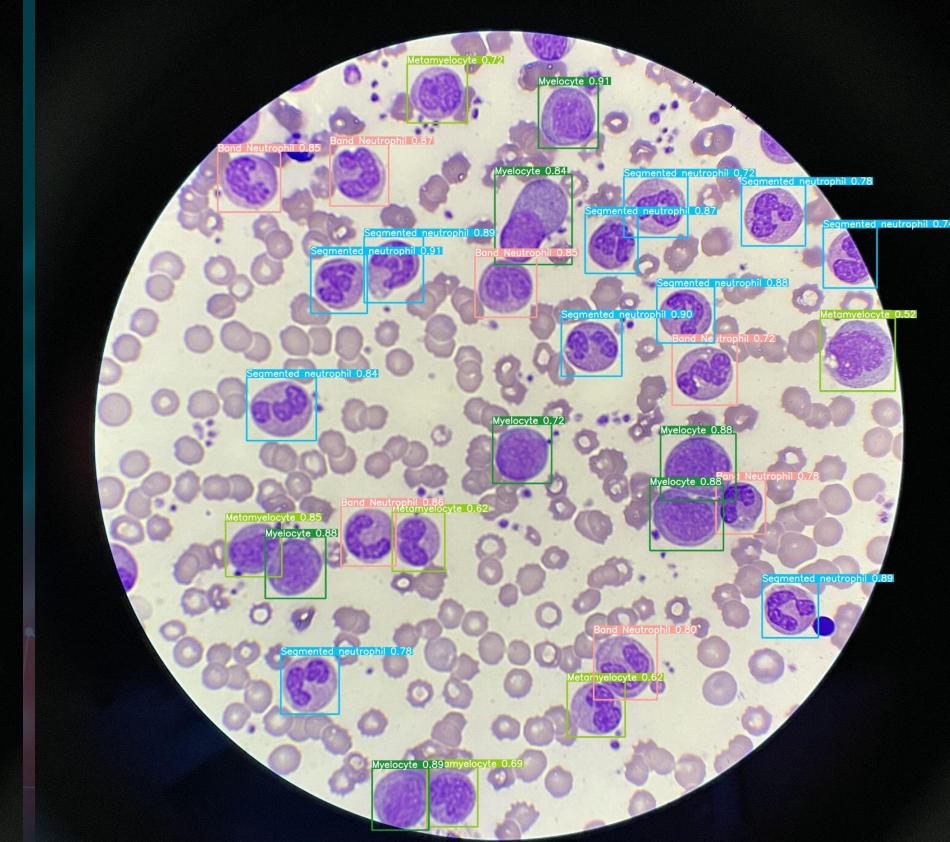
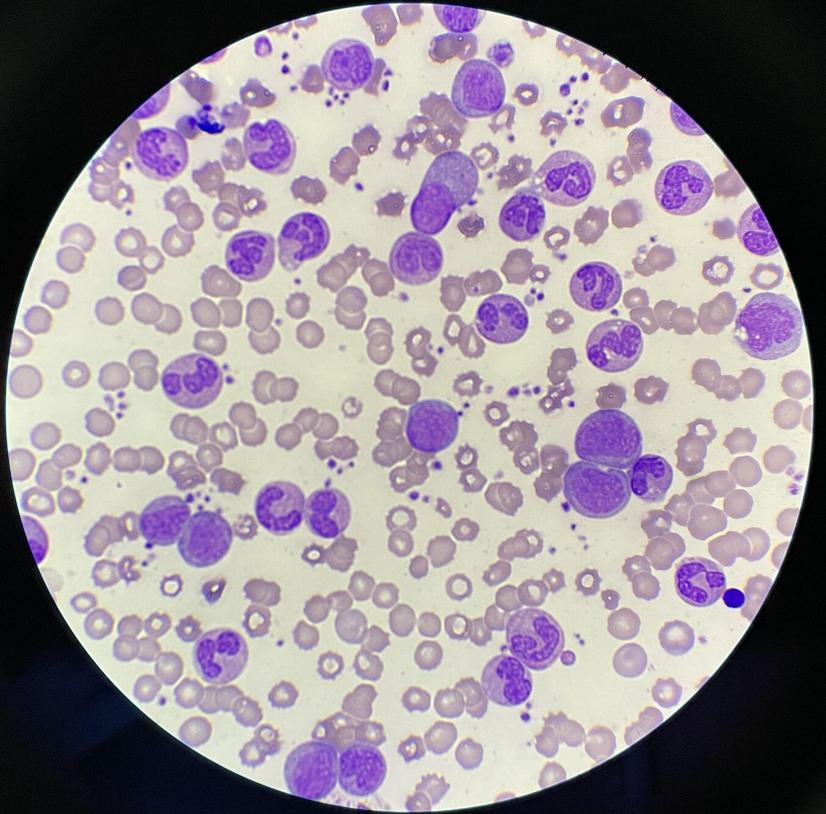
Console What's new

Highlights from the Chrome 126 update

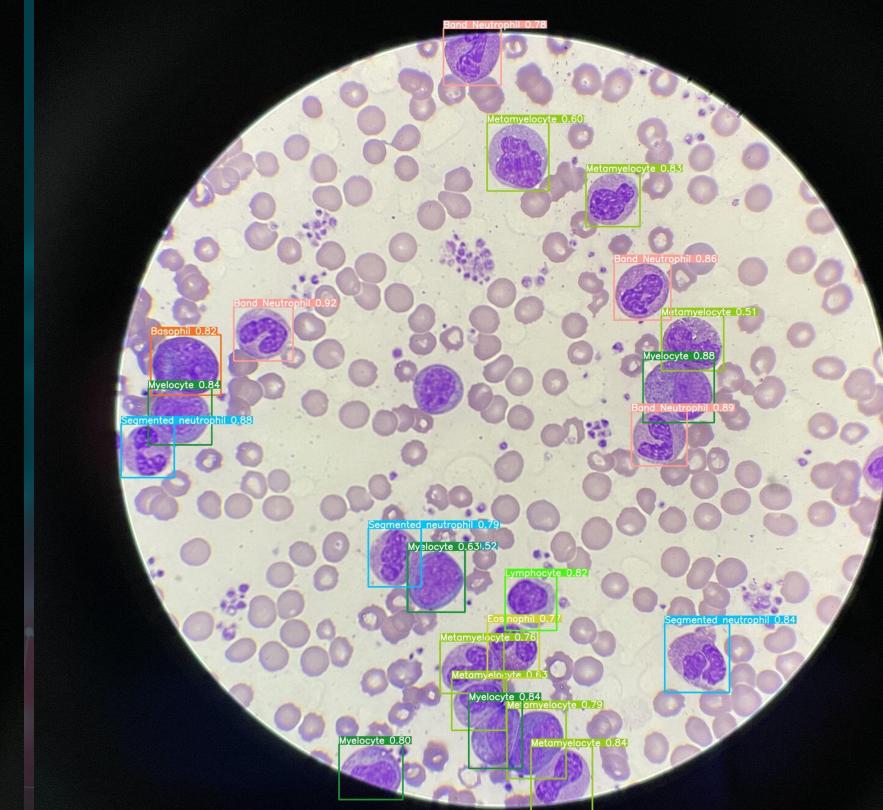
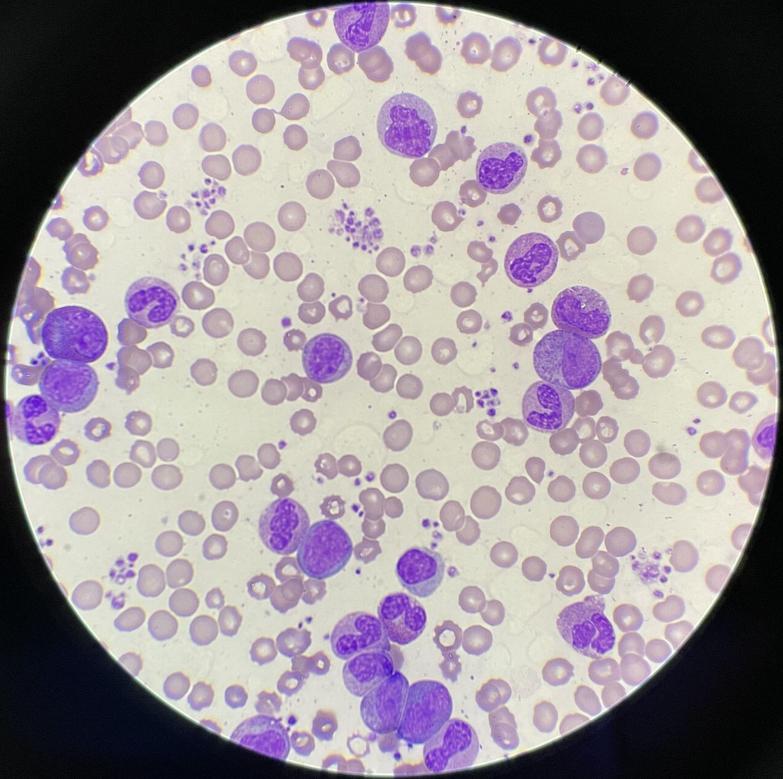
Move tracks around with updated UI in Performance panel

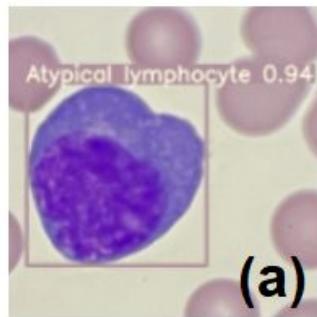
Change the order of tracks and hide them with an improved configuration mode in the Performance panel.

# Microscopic image (Left) vs Predicted image (Right)

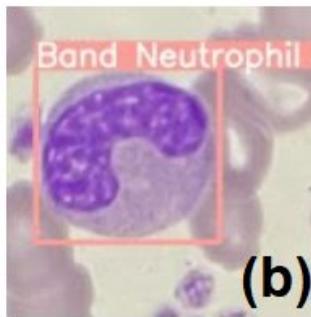


# Microscopic image (Left) vs Predicted image (Right)

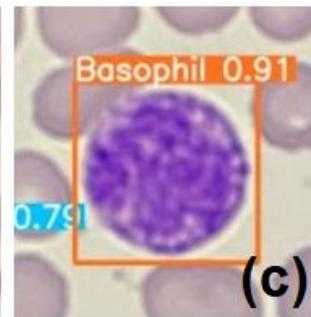




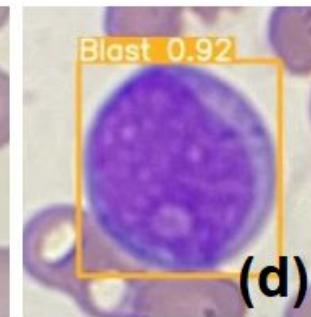
(a)



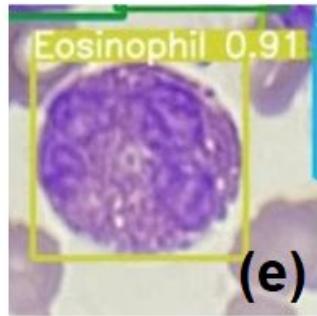
(b)



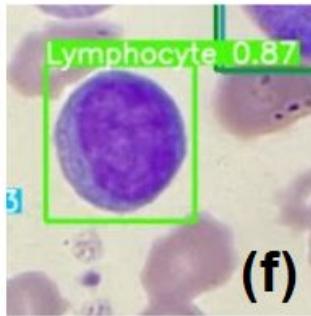
(c)



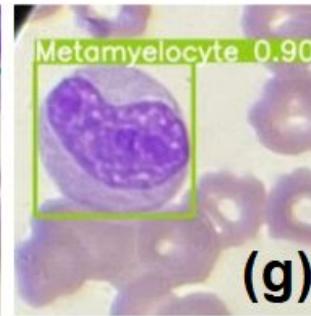
(d)



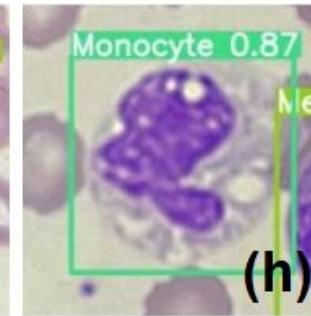
(e)



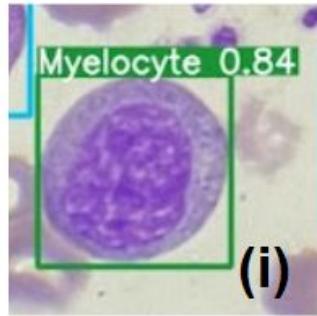
(f)



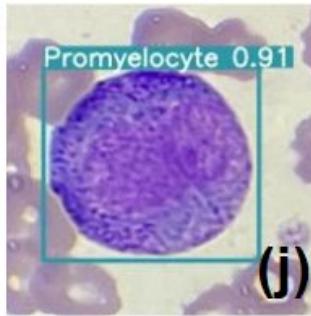
(g)



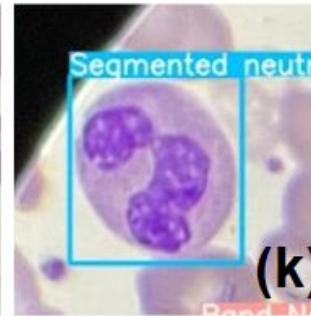
(h)



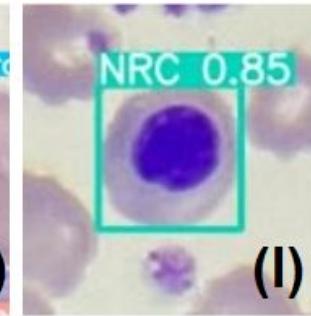
(i)



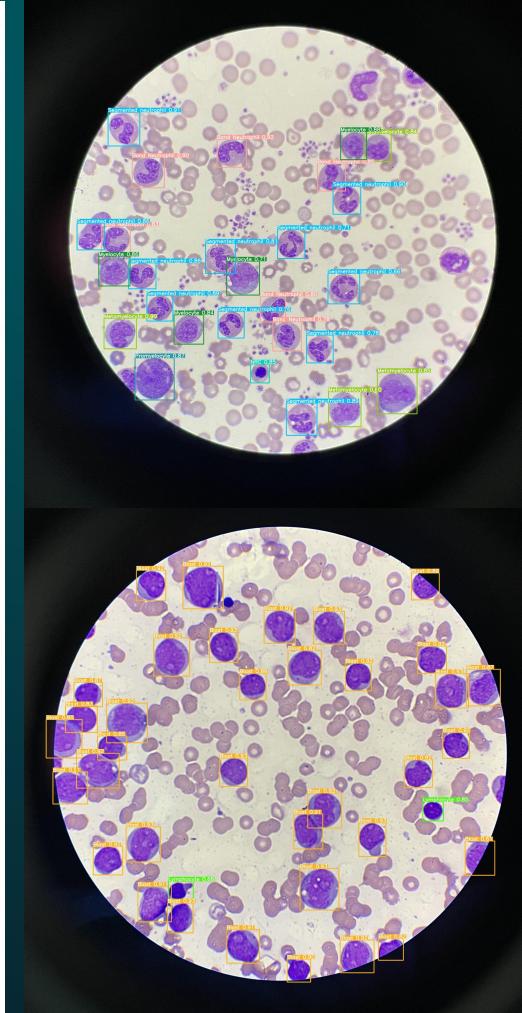
(j)

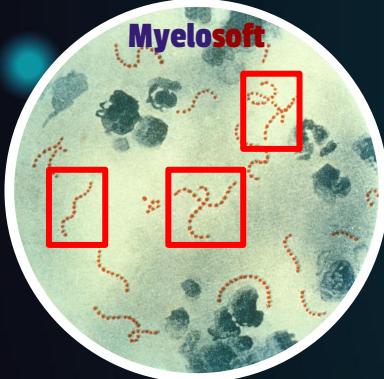


(k)



(l)





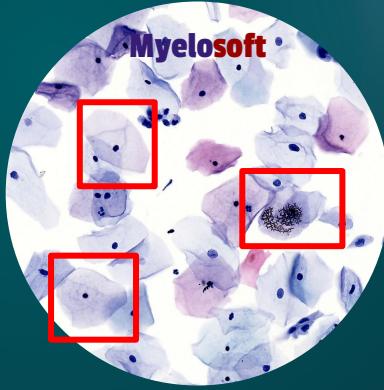
AI for Microbiology



AI for Parasitology



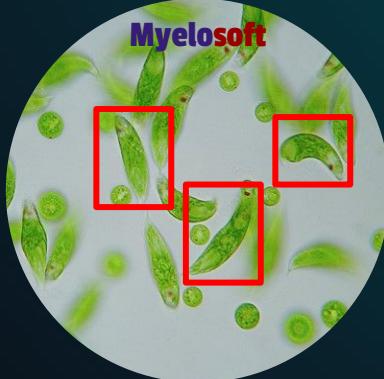
AI for Pathology



AI for Cytology



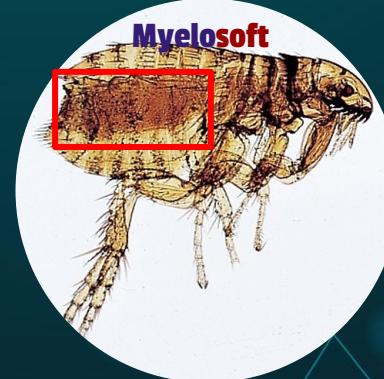
AI for Fishery



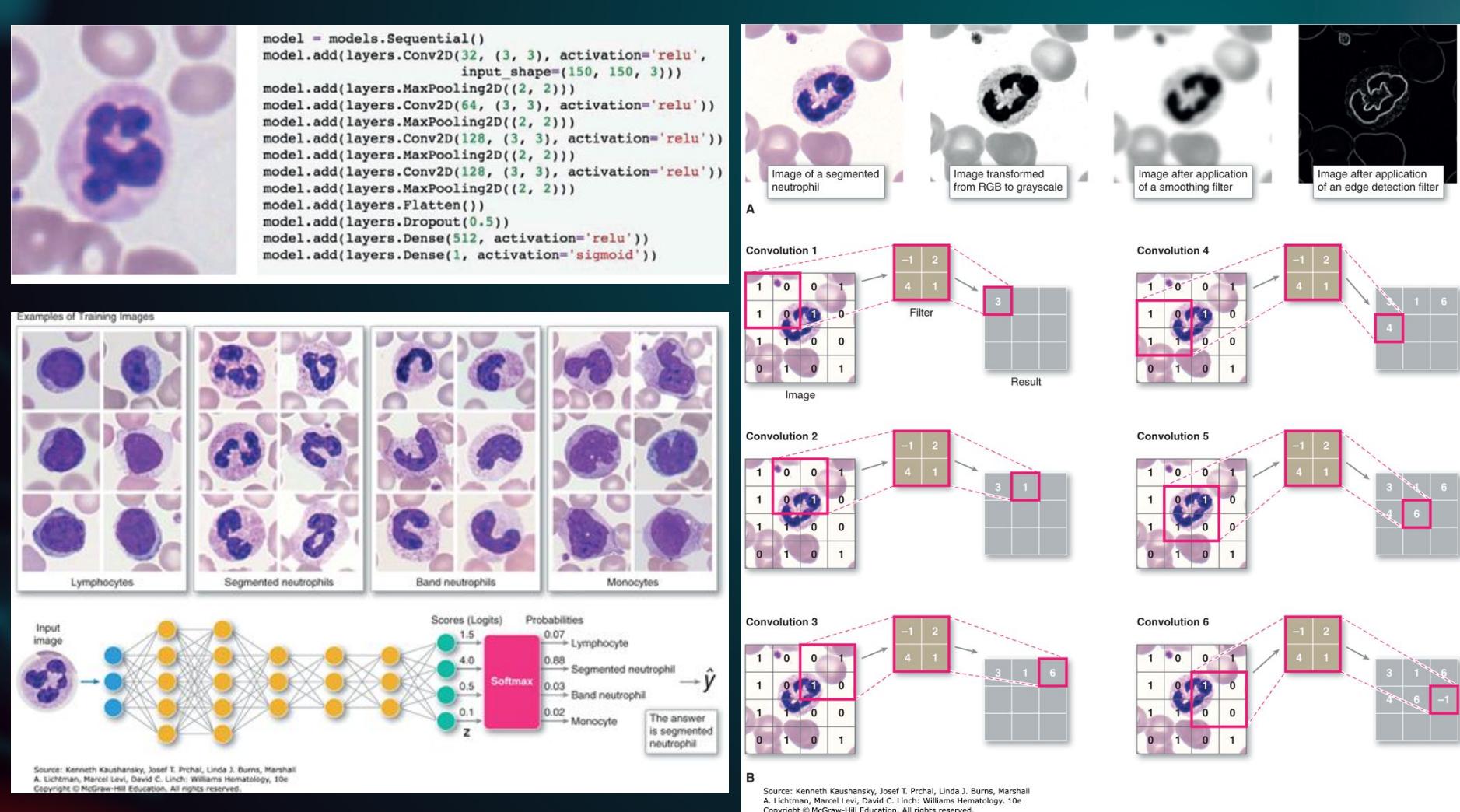
AI for Phycology

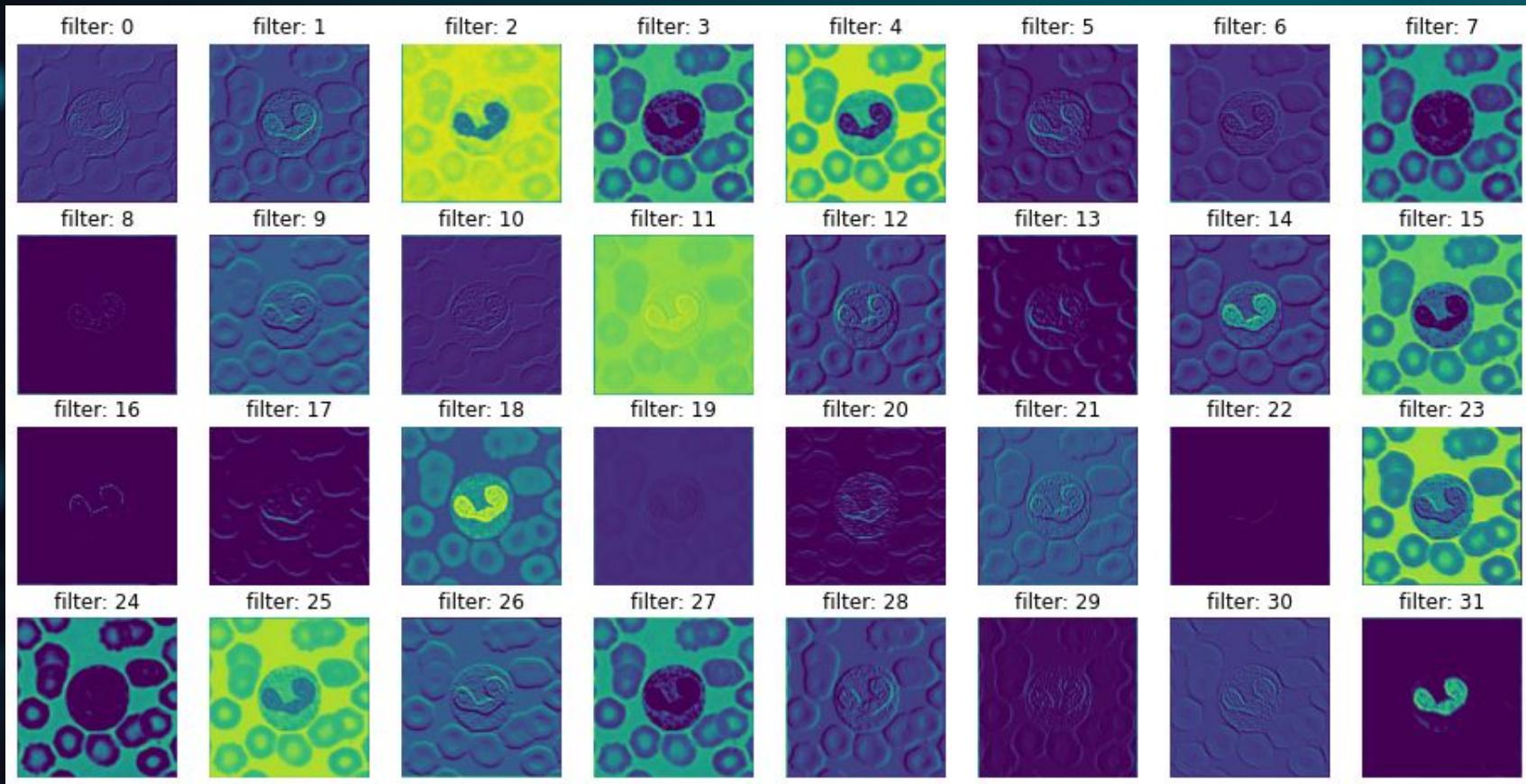


AI for Phytoplankton

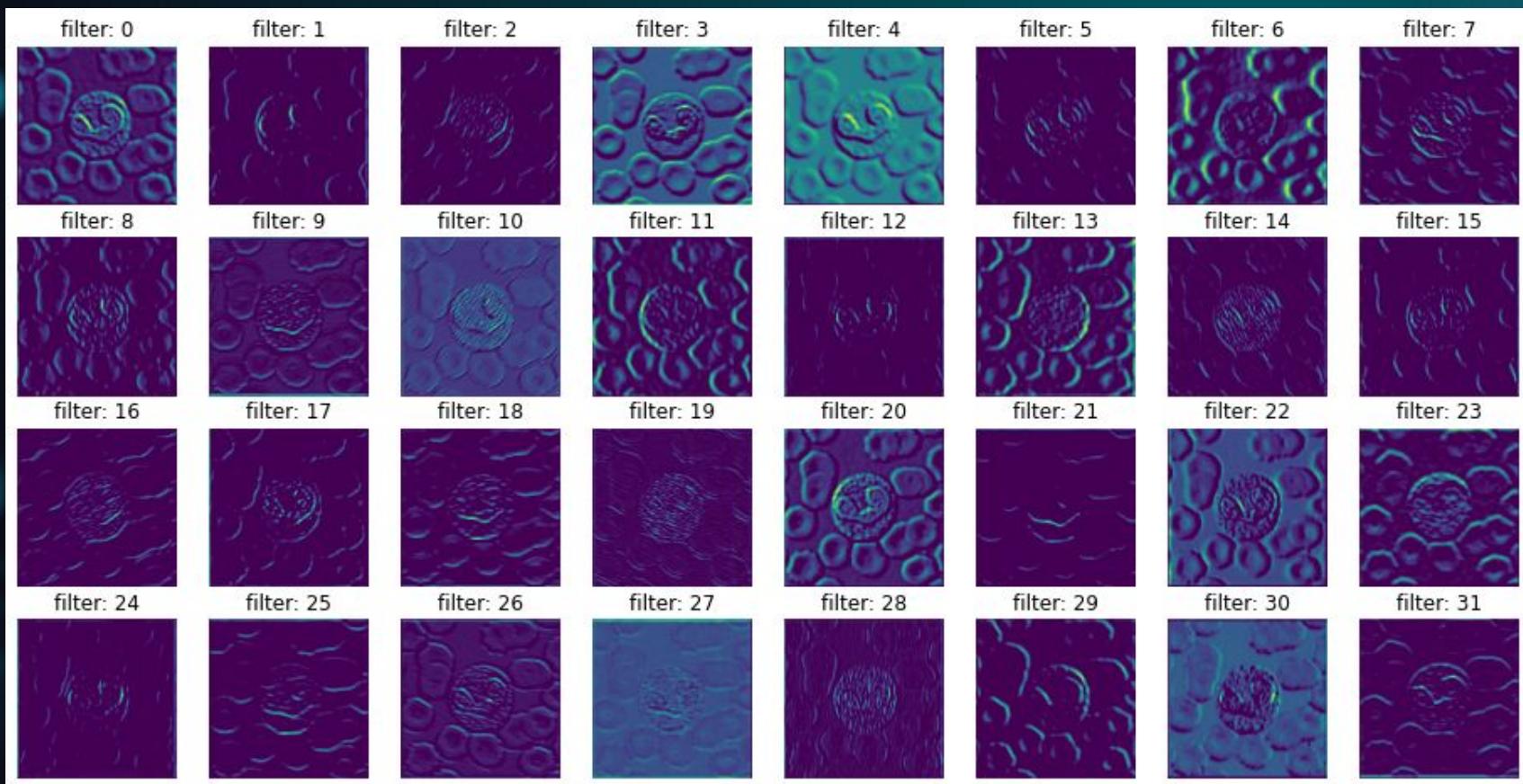


AI for Entomology

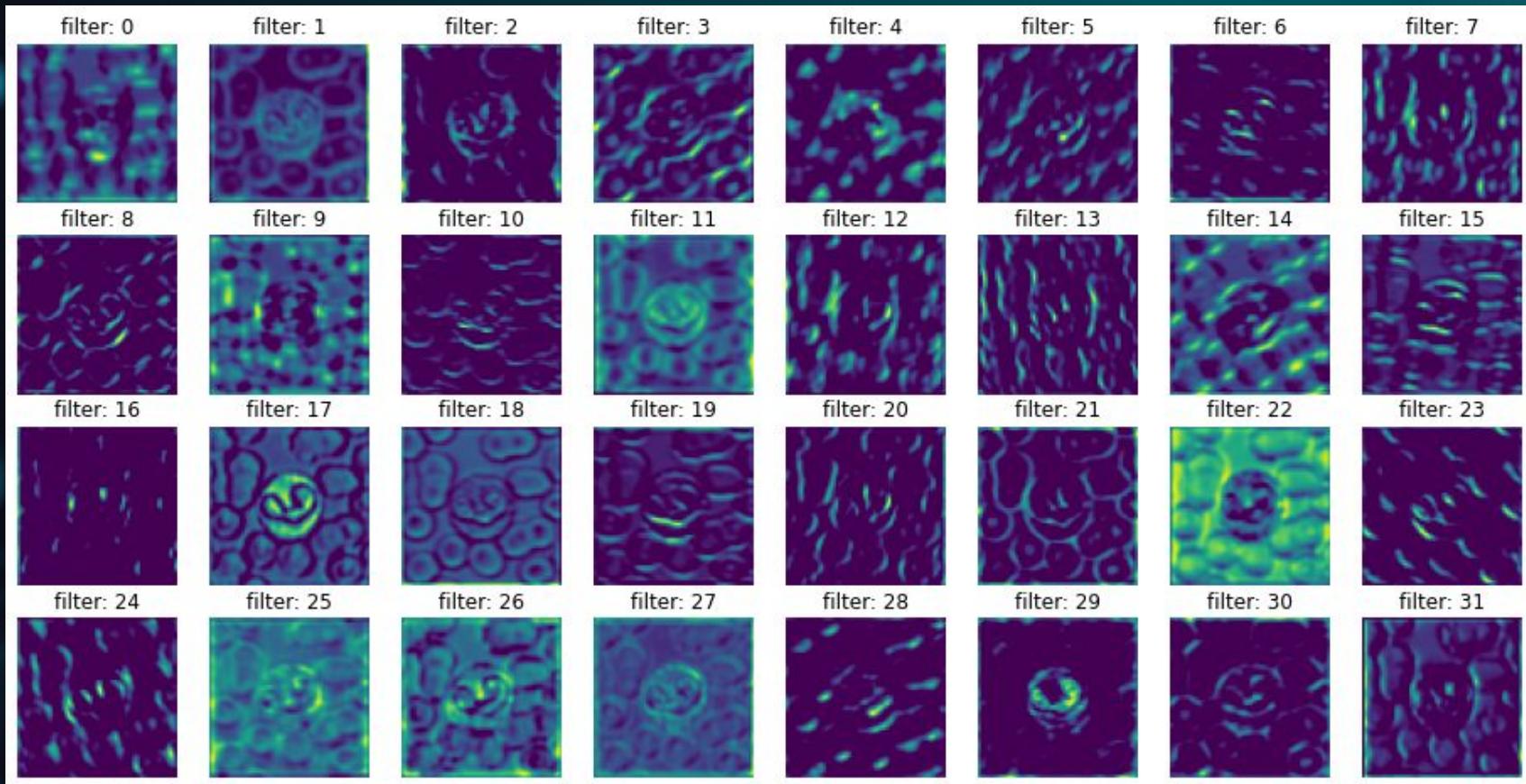




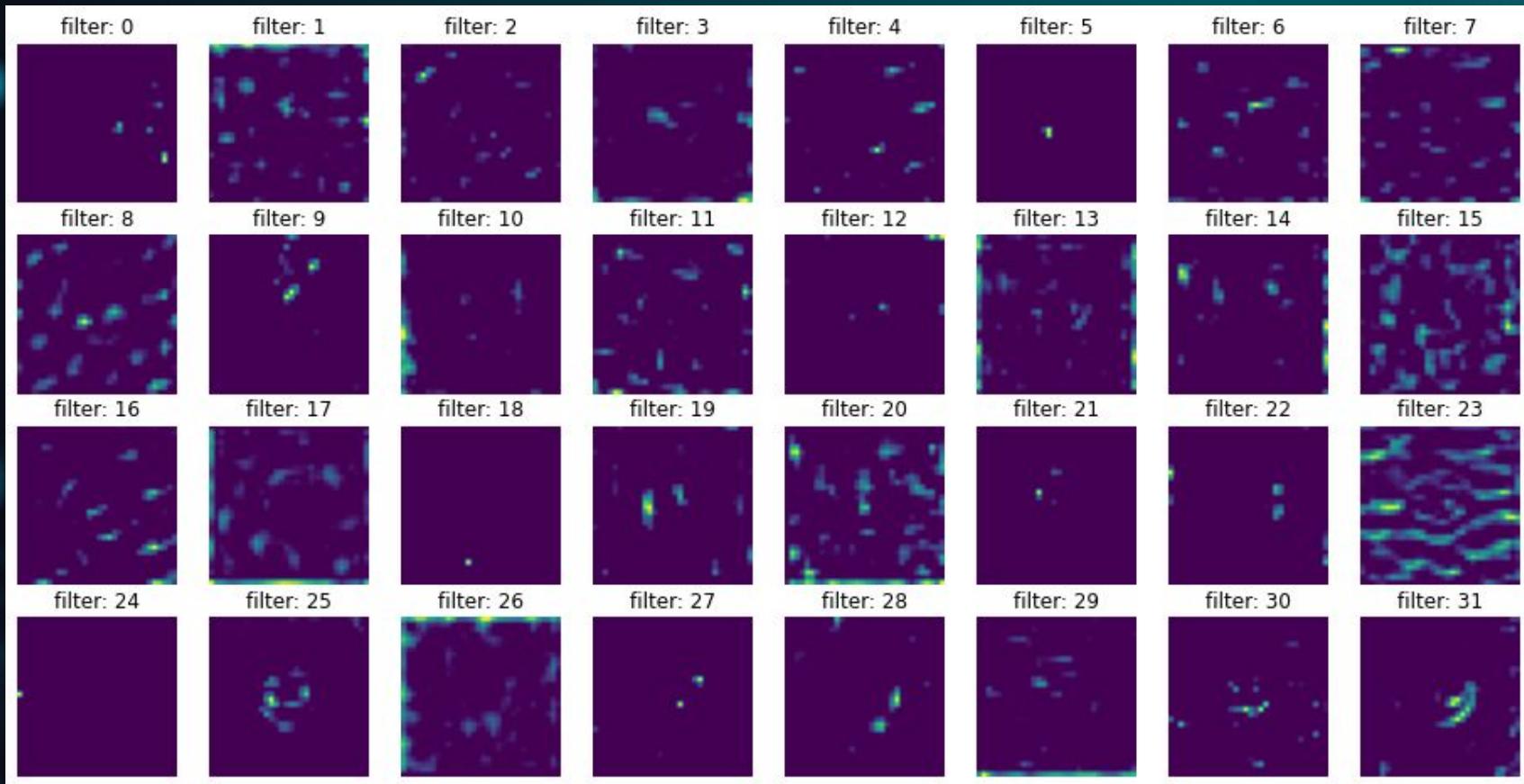
Neutrophil VGG19 block1\_conv2 visualize



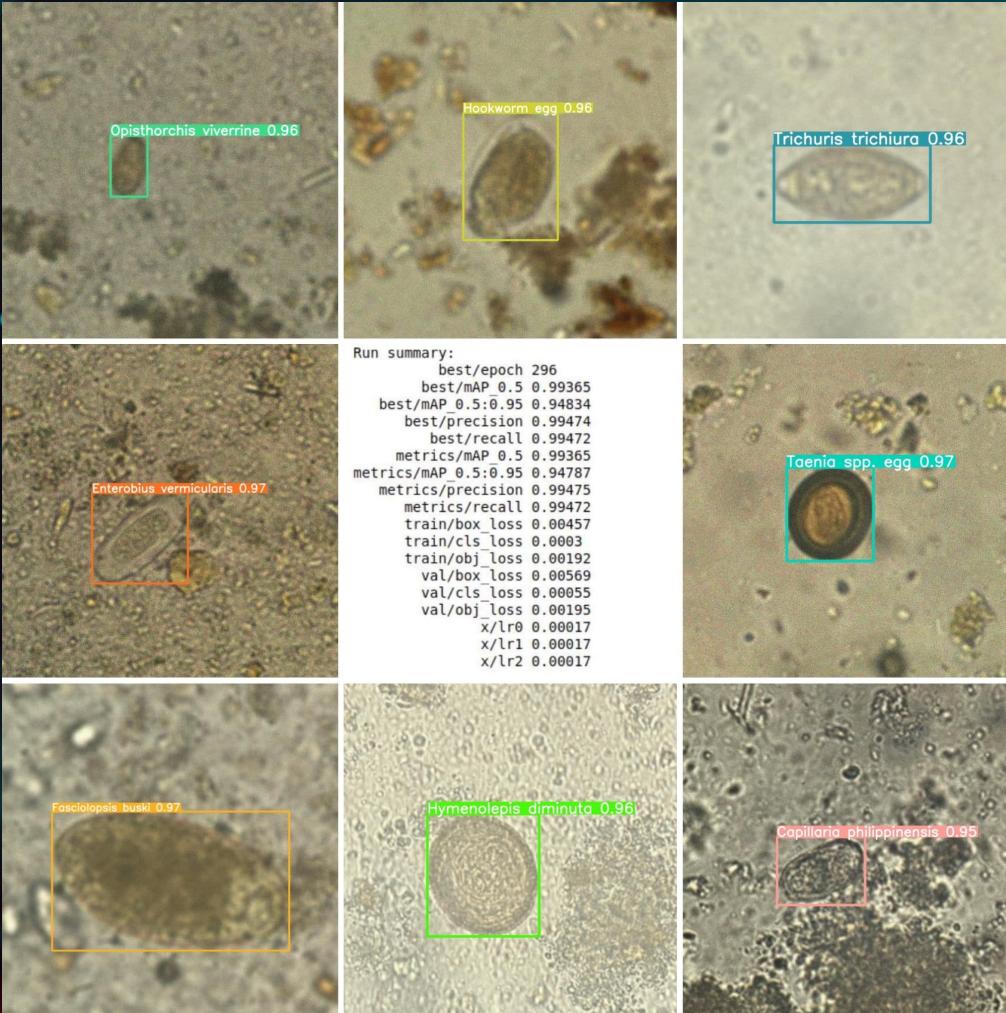
Neutrophil VGG19 block2\_conv2 visualize



Neutrophil VGG19 block3\_conv4 visualize



Neutrophil VGG19 block4\_conv4 visualize



Run summary:

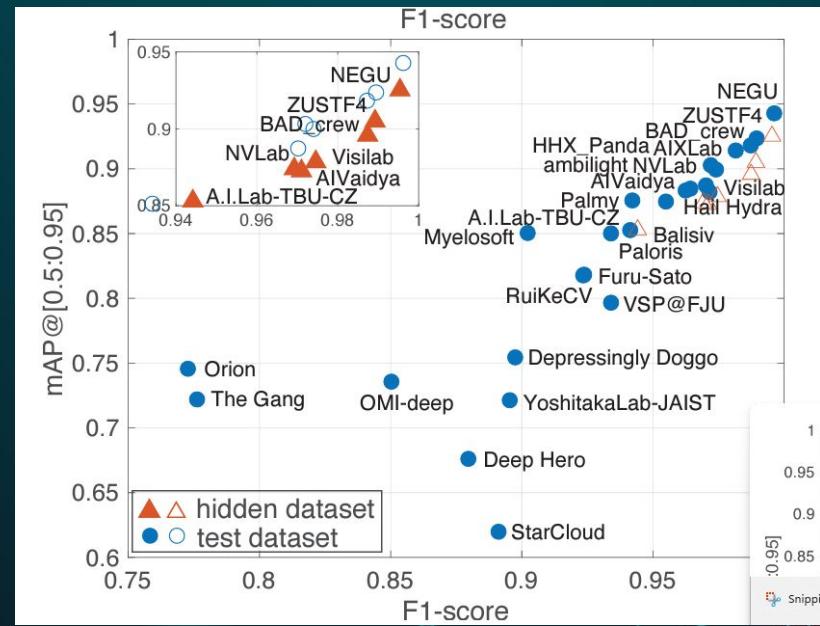
```

best/epoch 296
best/mAP_0.5 0.99365
best/mAP_0.5:0.95 0.94834
best/precision 0.99474
best/recall 0.99472
metrics/mAP_0.5 0.99365
metrics/mAP_0.5:0.95 0.94787
metrics/precision 0.99475
metrics/recall 0.99472
train/box_loss 0.00457
train/cls_loss 0.0003
train/obj_loss 0.00192
val/box_loss 0.00569
val/cls_loss 0.00055
val/obj_loss 0.00195
x/lr0 0.00017
x/lr1 0.00017
x/lr2 0.00017

```

**Our object detection algorithm result with unseen data (2200 test set images) Best test mIoU = 0.915  
Best validation mAP.05 = 0.993, Best validation mAP.95 = 0.984 Train on Nvidia RTX3090 (Local server)**

**Images dataset (11 classes of parasite eggs 11,000 images) by ICIPI 2022 Challenge : Parasitic Egg Detection and Classification in Microscopic Images <https://ictp2022challenge.piclab.ai>**  
University of Bristol, UK

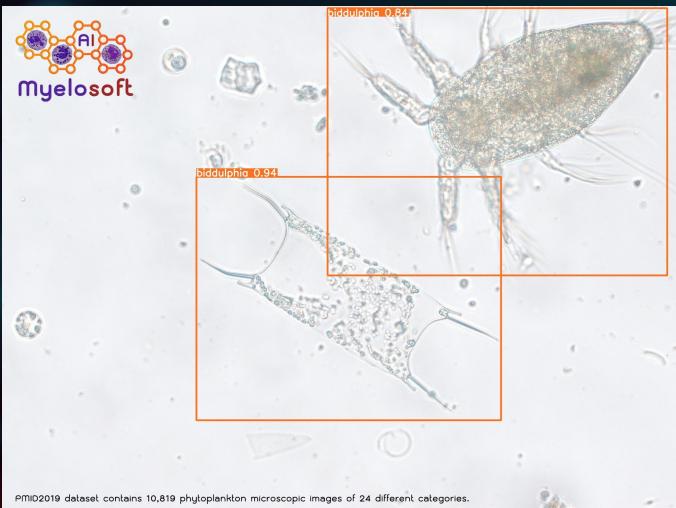




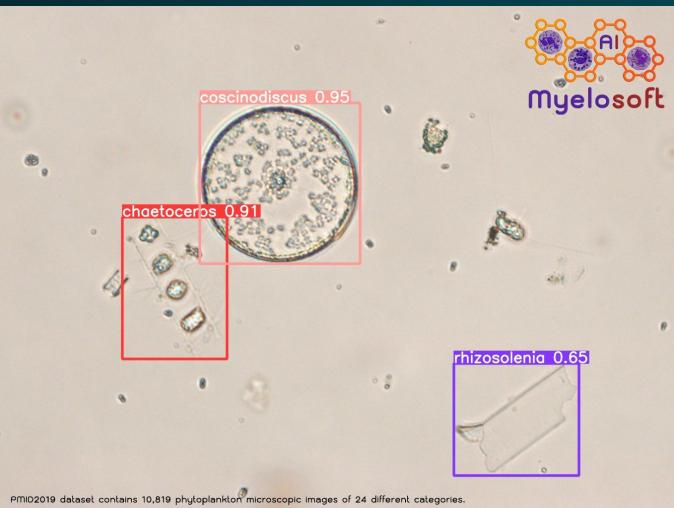
PMIO2019 dataset contains 10,819 phytoplankton microscopic images of 24 different categories.



PMIO2019 dataset contains 10,819 phytoplankton microscopic images of 24 different categories.



PMIO2019 dataset contains 10,819 phytoplankton microscopic images of 24 different categories.



**Our object detection algorithm result with unseen data (Train 80% Validate 10% Test 10% with random sampling) Best validation mAP.05 = 0.961, Best validation mAP.95 = 0.859 Train on Nvidia RTX3090 (Local server) take time 2 day 1 hours 39 minutes 50 seconds**

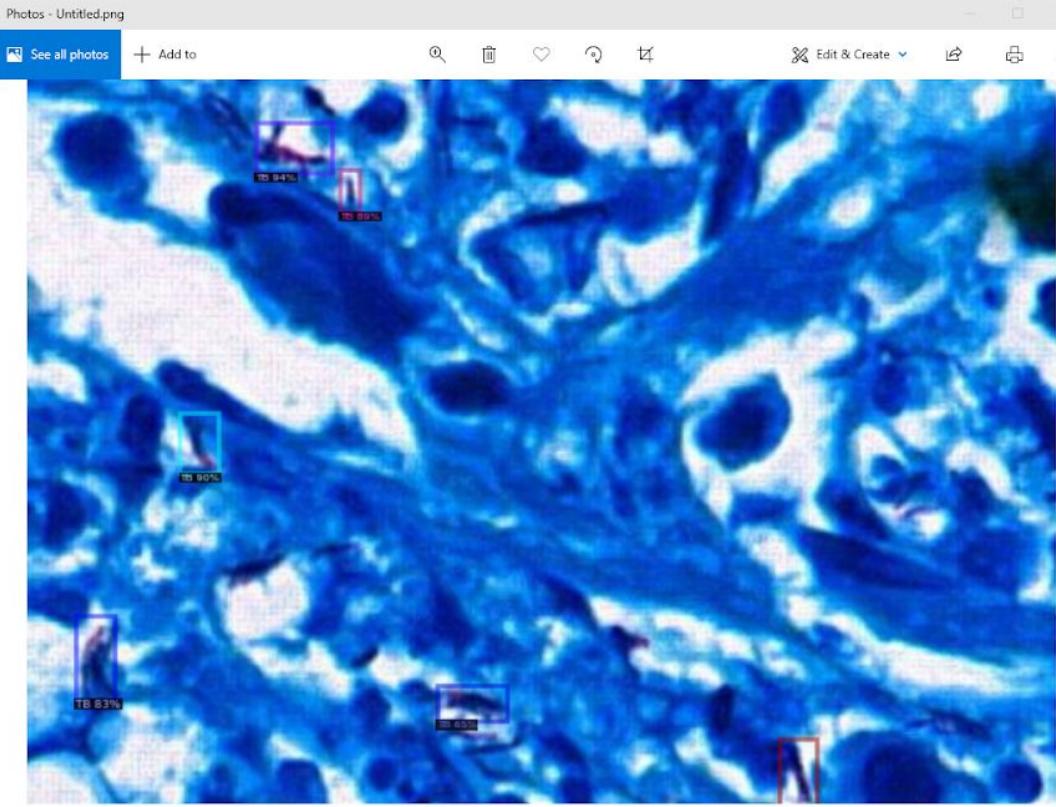
**Images dataset (24 classes of phytoplankton 10,819 images) by Phytoplankton Microscopic Image Dataset for Intelligent Marine Agriculture <https://doi.org/10.1093/icesjms/fsz171>**

**24 classes of phytoplankton:**  
**Bacteriastrum, Biddulphia, Ceratium carriense, Ceratium furca, Ceratium fusus, Ceratium trichoceros, Ceratium tripos, Chaetoceros, Corethron, Coscinodiscus, Coscinodiscus flank, Detonula pumila, Dinophysis caudata, Ditylum, Eucampia, Guinardia flaccida, Helicotheca, Navicula, Pleurosigma pelagicum, Protoperidinium, Rhizosolenia, Skeletonema, Thalassionema frauenfeldii and Thalassionema nitzschiooides**

# AI for Acid-Fast Bacillus (AFB) Mycobacterium tuberculosis detection

```
[05/07 12:26:34 d2.data.common]: Serializing 99 elements to byte tensors and concatenating
[05/07 12:26:34 d2.data.common]: Serialized dataset takes 0.04 MiB
[05/07 12:26:34 d2.evaluation.evaluator]: Start inference on 99 images
[05/07 12:26:36 d2.evaluation.evaluator]: Inference done 11/99. 0.1450 s / img. ETA=0:00:00
[05/07 12:26:41 d2.evaluation.evaluator]: Inference done 46/99. 0.1450 s / img. ETA=0:00:00
[05/07 12:26:46 d2.evaluation.evaluator]: Inference done 81/99. 0.1448 s / img. ETA=0:00:00
[05/07 12:26:49 d2.evaluation.evaluator]: Total inference time: 0:00:13 (0.147300)
[05/07 12:26:49 d2.evaluation.evaluator]: Total inference pure compute time: 0:00:13 (0.147300)
[05/07 12:26:49 d2.evaluation.coco_evaluation]: Preparing results for COCO format ...
[05/07 12:26:49 d2.evaluation.coco_evaluation]: Saving results to ./output/coco_instances_results.json
[05/07 12:26:49 d2.evaluation.coco_evaluation]: Evaluating predictions ...
Loading and preparing results...
DONE (t=0.00s)
creating index...
index created!
Running per image evaluation...
Evaluate annotation type *bbox*
DONE (t=0.56s).
Accumulating evaluation results...
DONE (t=0.03s).
Average Precision (AP) @[ IoU=0.50:0.95 | area= all | maxDets=100 ] = 0.256
Average Precision (AP) @[ IoU=0.50 | area= all | maxDets=100 ] = 0.627
Average Precision (AP) @[ IoU=0.75 | area= all | maxDets=100 ] = 0.147
Average Precision (AP) @[ IoU=0.50:0.95 | area= small | maxDets=100 ] = 0.252
Average Precision (AP) @[ IoU=0.50:0.95 | area=medium | maxDets=100 ] = 0.316
Average Precision (AP) @[ IoU=0.50:0.95 | area= large | maxDets=100 ] = -1.000
Average Recall (AR) @[ IoU=0.50:0.95 | area= all | maxDets= 1 ] = 0.090
Average Recall (AR) @[ IoU=0.50:0.95 | area= all | maxDets= 10 ] = 0.370
Average Recall (AR) @[ IoU=0.50:0.95 | area= all | maxDets=100 ] = 0.446
Average Recall (AR) @[ IoU=0.50:0.95 | area= small | maxDets=100 ] = 0.442
Average Recall (AR) @[ IoU=0.50:0.95 | area=medium | maxDets=100 ] = 0.470
Average Recall (AR) @[ IoU=0.50:0.95 | area= large | maxDets=100 ] = -1.000
[05/07 12:26:49 d2.evaluation.coco_evaluation]: Evaluation results for bbox:
| AP   | AP50  | AP75  | APs  | APM  | API  |
| :--- | :---: | :---: | :---: | :---: | :---: |
| 25.615 | 62.690 | 14.710 | 25.152 | 31.554 | nan  |
[05/07 12:26:49 d2.evaluation.coco_evaluation]: Note that some categories may be missing from this analysis as no ground truth or predicted boxes were found.
[05/07 12:26:49 d2.evaluation.coco_evaluation]: Per-category AP:
| category | AP   |
| :---: | :---: |
| AFB    | nan  |
OrderedDict([('bbox', {'AP': 25.614951256404716,
                      'AP-AFB': nan,
                      'AP-TB': 25.614951256404716,
                      'AP50': 62.69012443271566,
                      'AP75': 14.709953888981017,
                      'API': nan,

```



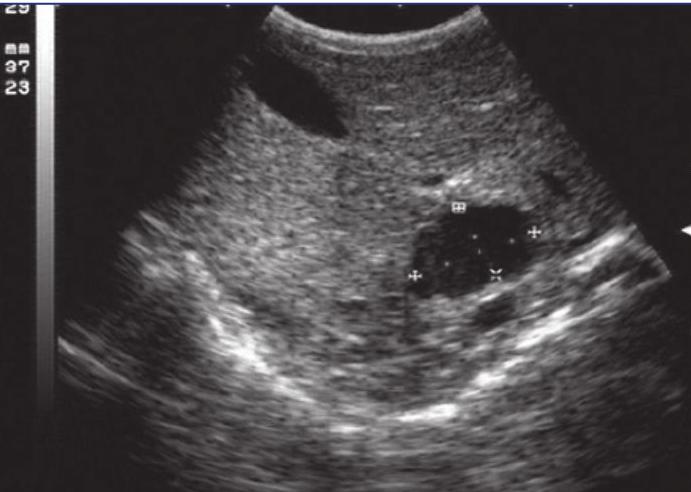
Activities Google Chrome 16 n.o. 17:50

Liver ultrasound in Case 2 x + researchgate.net/Liver-ultrasound-in-Case-2-revealed-a... YouTube Maps Gmail Translate Other bookmarks

Myelosoft - SiDeepPBS W x Not secure | 0.0.0:8000 YouTube Maps Gmail Translate Other bookmarks

ResearchGate Recruit researchers Join for free Login

## AI for Liver Lesions Detection Based on Ultrasound Image



Liver ultrasound in Case 2 revealed a transsonic cyst (3.7/2.3 cm) with acoustic enhancement.

[https://www.researchgate.net/figure/Liver-ultrasound-in-Case-2-revealed-a-transsonic-cyst-37-23-cm-with-acoustic\\_fig3\\_49732432](https://www.researchgate.net/figure/Liver-ultrasound-in-Case-2-revealed-a-transsonic-cyst-37-23-cm-with-acoustic_fig3_49732432)

Source publication ↗



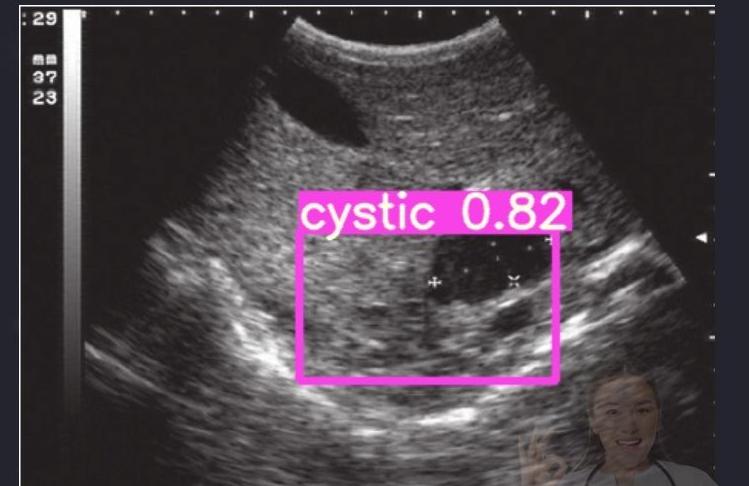
The role of ultrasonography in Albendazole treatment of hydatid liver cyst monitoring in children--

Myelosoft

Results Download

### Prediction Result

Cell Detect	Cell Location [x1, y1, x2, y2]	Confidence (0% to 100%)
cystic	[182, 146, 349, 244]	0.817765 or 81.777 %



cystic 0.82



Activities Google Chrome en

Focal fatty sparing | Radiopaedia.org +  
radiopaedia.org/cases/focal-fatty-sparing  
YouTube Maps Gmail Translate Other bookmarks

## Focal fatty sparing

### AI for Liver Lesions Detection Based on Ultrasound Image

**Presentation**  
Known case of psoriasis on corticosteroids having elevated liver function test.

**Patient Data**  
**Age:** 25 years  
**Gender:** Male

**Note:** This case has been tagged as "legacy" as it no longer meets image preparation and/or other case publication guidelines.  
<https://radiopaedia.org/cases/focal-fatty-sparing>

**ULTRASOUND**



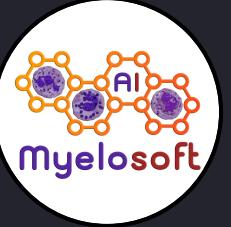
2D 35% C 55 P Low Gen  
Liver  
Ultrasound  
FFS  
Dist 1.29 cm  
Dist 1.81 cm

Myelosoft - SiDeepPBS Web +  
Not secure | 0.0.0.0:8000  
YouTube Maps Gmail Translate Other bookmarks

## Myelosoft

**Results** [Download](#)

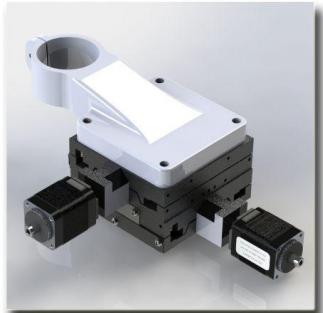
### Prediction Result



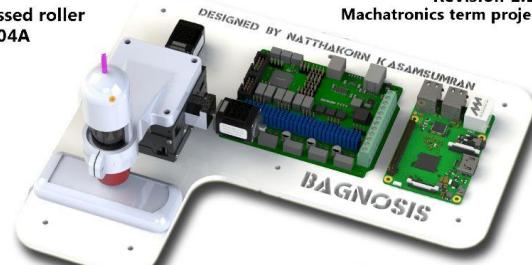
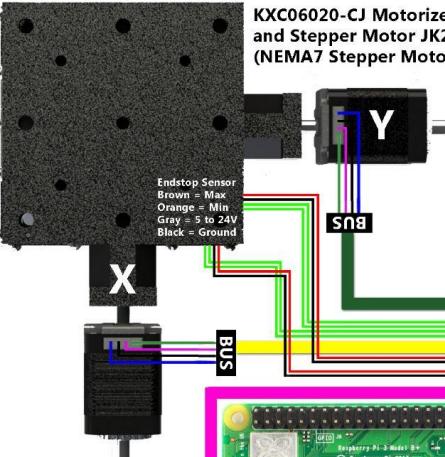
Cell Detect	Cell Location [x1, y1, x2, y2]	Confidence (0% to 100%)
FFS	[234, 126, 296, 162]	0.749246 or 74.925 %

2D 35% C 55 P Low Gen  
Liver  
FFS 0.75  
Dist 1.29 cm  
Dist 1.81 cm





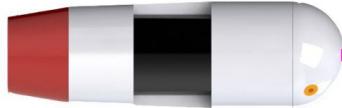
Isometric view of clamp 3D print part  
installed on motorized crossed roller



**Warning!**  
Read instruction before wiring

# BAGNOSIS

USB Digital Microscope 1000X



USB Cable



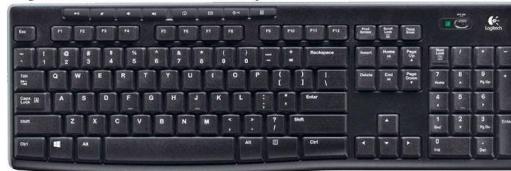
LCD Panel with HDMI Cable



HDMI Cable

Raspberry Pi 3 Model B  
and Raspbian OS on SD card  
- Repetier Host Program  
- sudo apt-get install motion

Logitech MK270R wireless keyboard & mouse

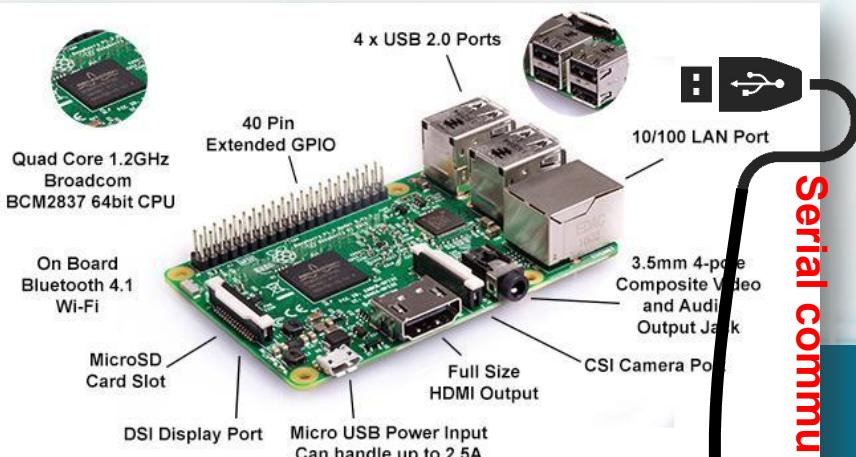


5V 2.1A RPi Adaptor

2019 Mechanical & Electrical engineering department, Faculty of engineering, Chulalongkorn university. 12V 5A DC Adaptor

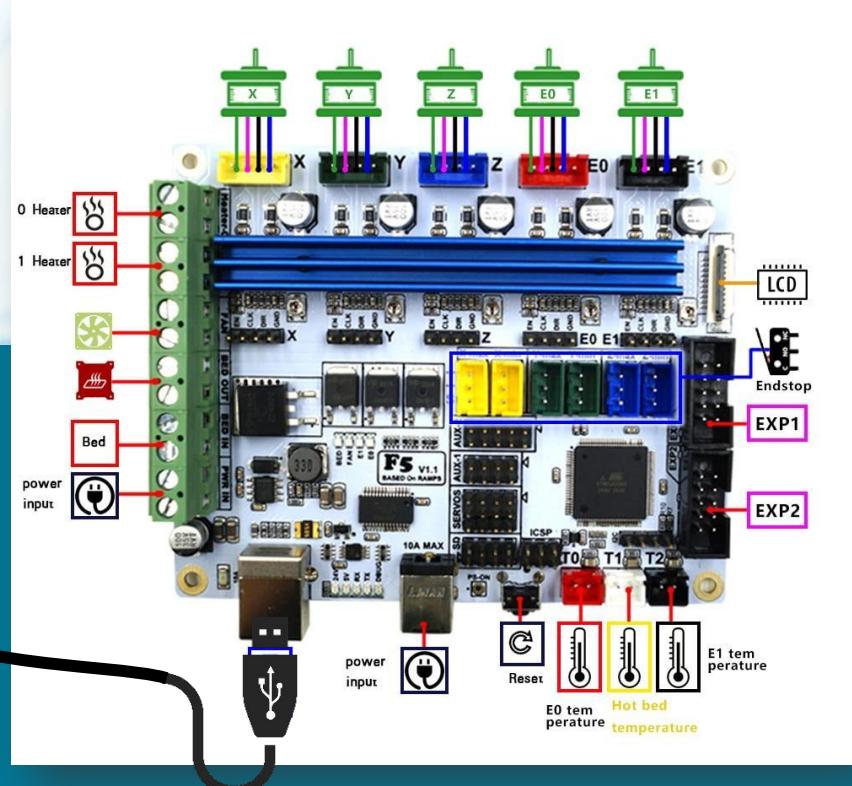
# Microcontroller in System

## Raspberry Pi 3 Model B



Serial communication

## F5 V1.2 RAMPS 1.4 Arduino MEGA

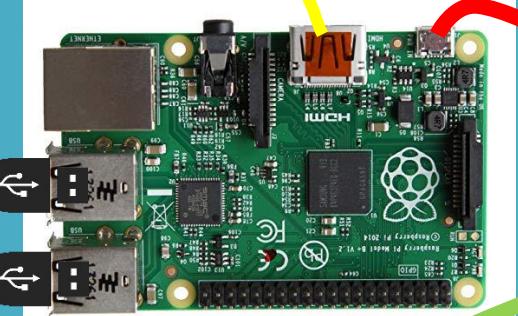


## Raspberry Pi 3 Model B

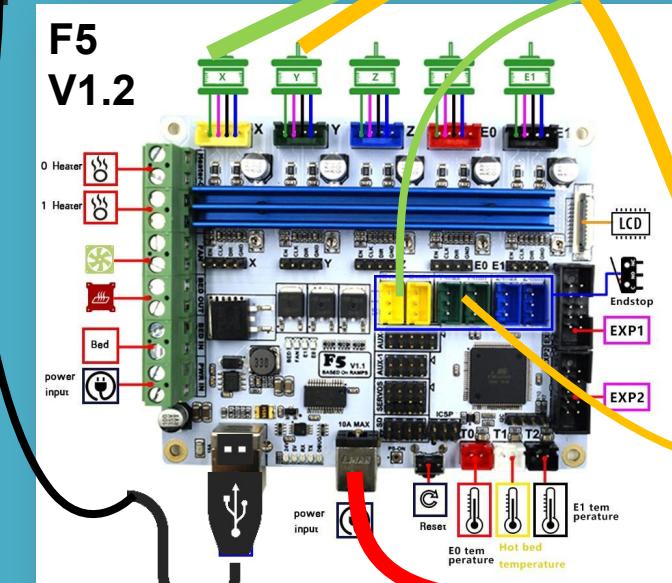
- Python 3.7 and Repetier Host on Linux

## F5 V1.2 RAMPS 1.4

- C/C++ on Arduino IDE with Marlin firmware



5VDC  
2.1A



X stepper

X endstop

Y stepper

**Electronics Diagram & Overall Diagram**



Y endstop



# Logic Diagram

Linux system boot and hardware USB pairing

Turn on camera and Repetier host program

Home positioning to zero x and y axis of cross roller

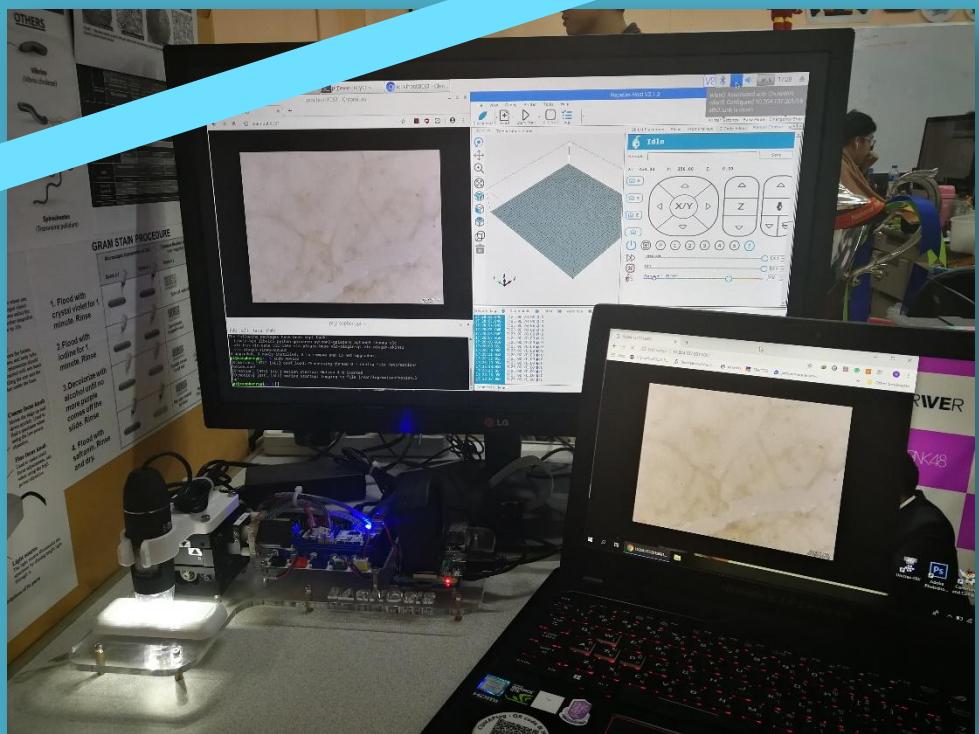
Video broadcast on browser and IP address

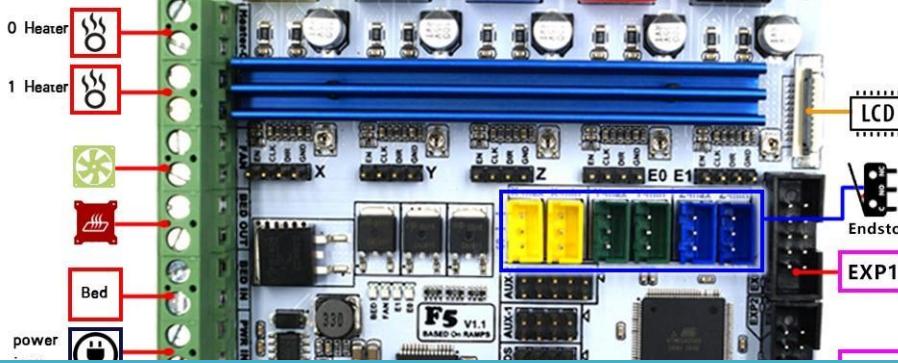
Send G-Code from Raspberry Pi to F5 V1.2 board to stepper moving

G-Code sent by Repetier

Serial link on USB

RAMPS stepper moving





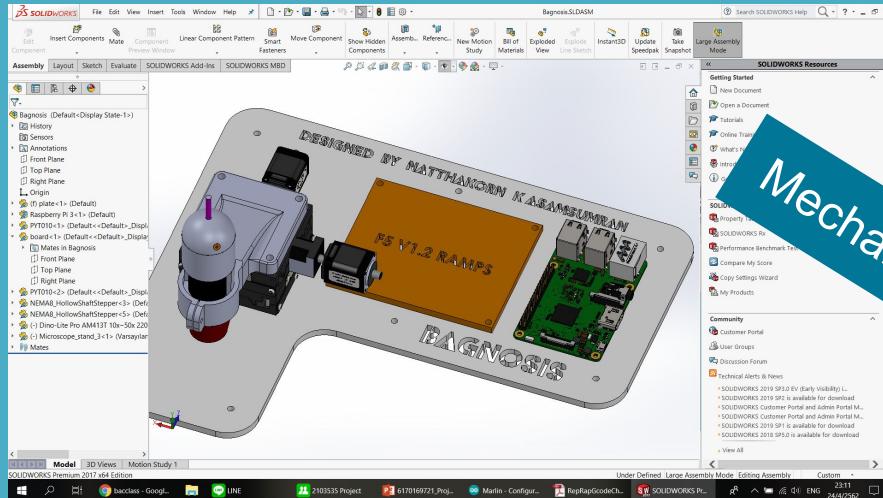
- ✓ *USB Digital Microscope*
- ✓ *F5 V1.2 RAMPS 3D Printer Board*
- ✓ *Marlin 3D Printer Board Firmware*
- ✓ *Repetier Host for G-Code program*
- ✓ *5VDC and 12VDC Adaptor*



- ## The Part lists
- ✓ *Raspberry Pi 3 Model B*
  - ✓ *SD Card + Raspbian Image*
  - ✓ *Keyboard Mouse & HDMI Panel*



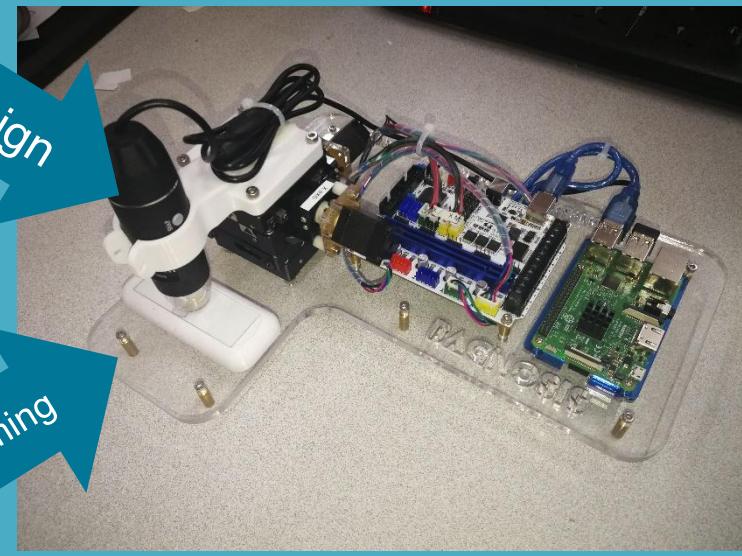
- ✓ *Acrylic laser cutting & 3D print part*
- ✓ *Stepper Motor JK20HS30-0604A*
- ✓ *KXC06020-CJ Motorized X Axis Crossed Roller*



```
513 #define USE_XMAX_PLUG
514 #define USE_YMAX_PLUG
515 #define USE_ZMAX_PLUG
516
517 // Enable pulles for all endstops to prevent a floating state
518 #define ENDSTOPPULLUPS
519 #if DISABLED(ENDSTOPPULLUPS)
520 // Disable ENDSTOPPULLUPS to set pullups individually
521 #define ENDSTOPPULLUP_XMAX
522 #define ENDSTOPPULLUP_YMAX
523 // #define ENDSTOPPULLUP_ZMAX
524 #define ENDSTOPPULLUP_XMIN
525 #define ENDSTOPPULLUP_YMIN
526 // #define ENDSTOPPULLUP_ZMIN
527 // #define ENDSTOPPULLUP_ZMIN_PROBE
528#endif
529
530 // Mechanical endstop with COM to ground and NC to Signal uses "fall"
531 #define X_MIN_ENDSTOP_INVERTING false // set to true to invert the
532 #define Y_MIN_ENDSTOP_INVERTING false // set to true to invert the
533 #define Z_MIN_ENDSTOP_INVERTING false // set to true to invert the
534 #define X_MAX_ENDSTOP_INVERTING false // set to true to invert the
535 #define Y_MAX_ENDSTOP_INVERTING false // set to true to invert the
536
537 // #define Y_MOTOR_PWM_TMR0PORTM2 false
```

- No datasheet of components
- No sensor wiring details (find yourself)
- Original firmware not support NEMA8

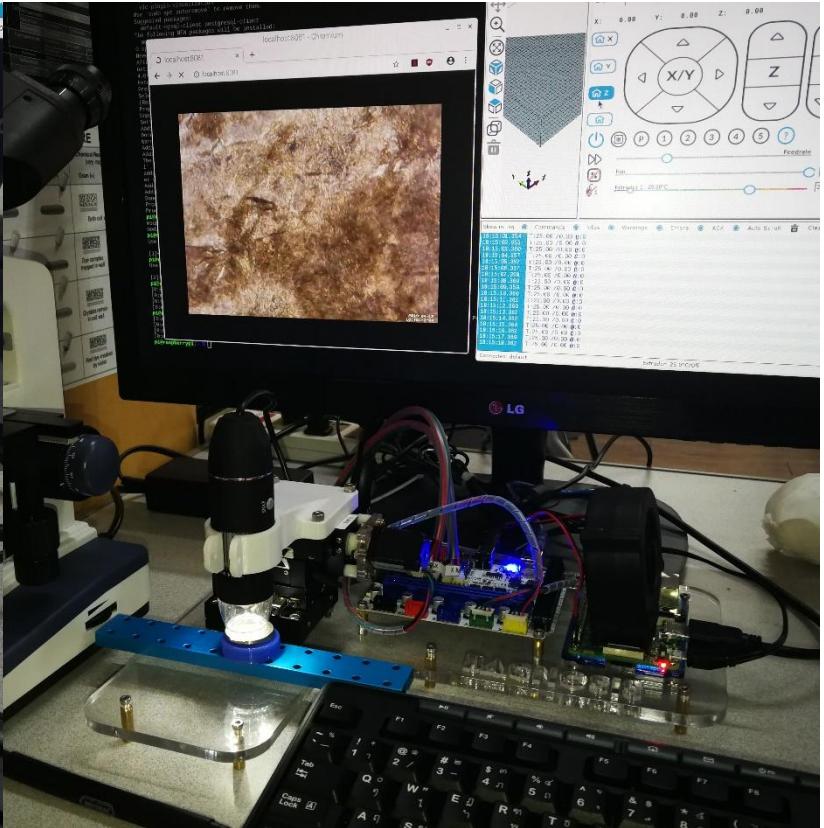
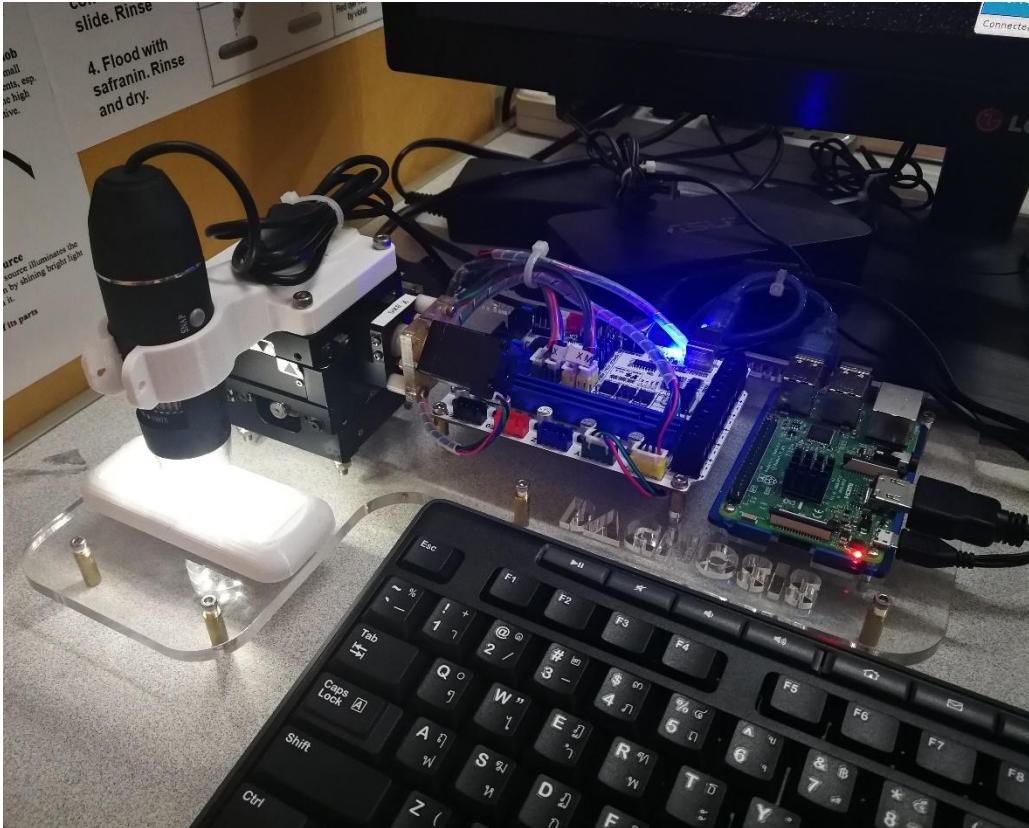
Mechanics Design

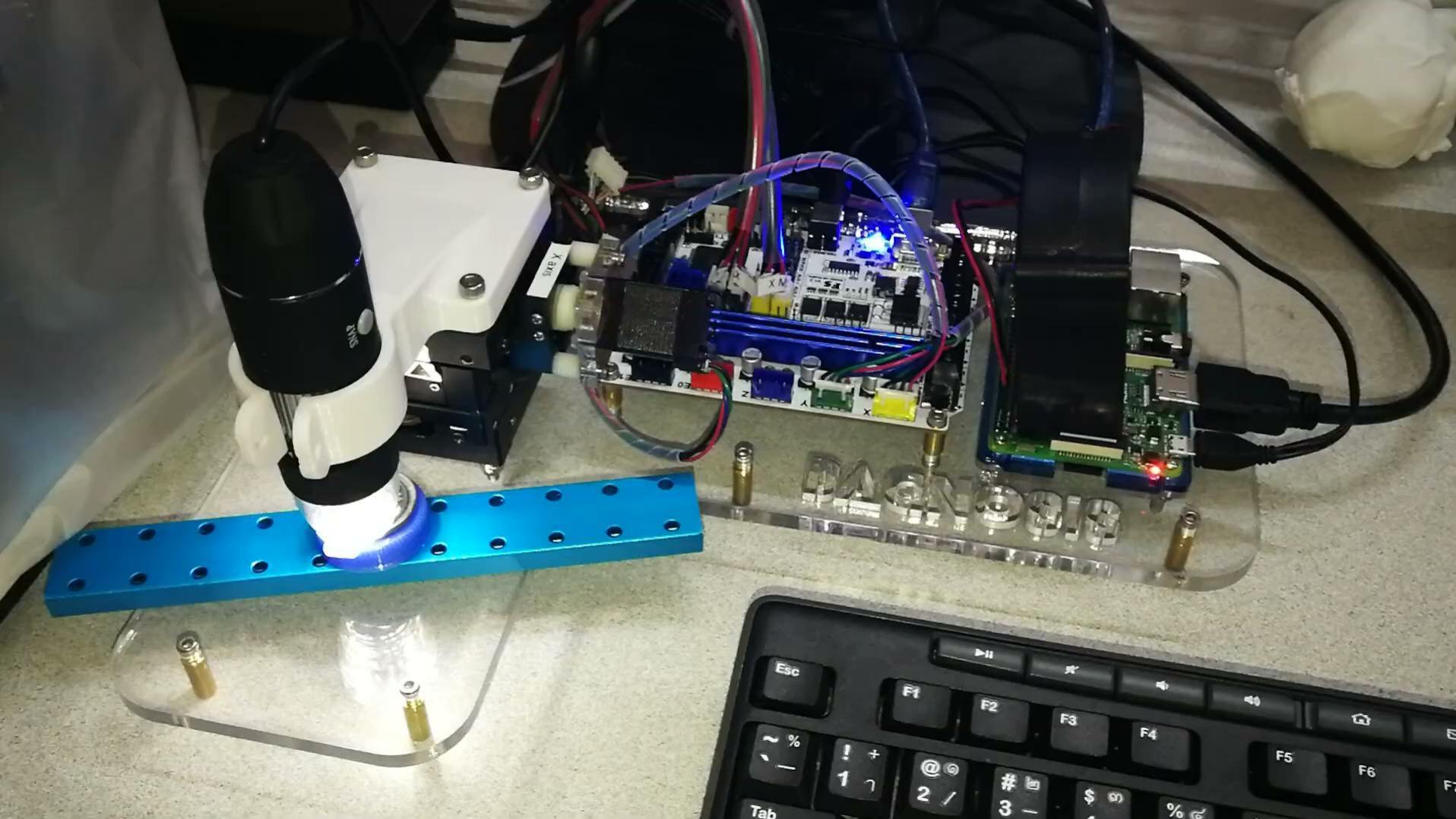


Firmware Programming

- Config and install Marlin firmware on F5 V1.2 with 115200bps serial baud rate.
- Wiring stepper motor and opto-endstop to board. Testing and analysis (increments)

# Current work of project





# Thank you

## Dr.Piyalitt Ittichaiwong

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School of Biomedical Engineering & Imaging Sciences,  
Faculty of Life Sciences & Medicine, King's College London, UK.  
And Siriraj Informatics and Data Innovation Center, Siriraj Hospital.**



## Mr.Natthakorn Kasamsumran

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Embedded System and IC Design Research Laboratory (ESID)  
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Chulalongkorn University, Thailand.**