

# Detecting Brain tumors in Magnetic Resonance Imaging (MRI)

GWU

Machine Learning  
Group 5

Maliha Aziz, Zongzhu Li



# Outline

- Introduction
- Overview of Dataset for Different Types of Brain Tumors
- Data Preprocessing
- Modeling, Prediction and Evaluation
  - SVM, KNN and Naïve Bayes
  - ANN with Parameters Exploratory
- Summary and Discussion

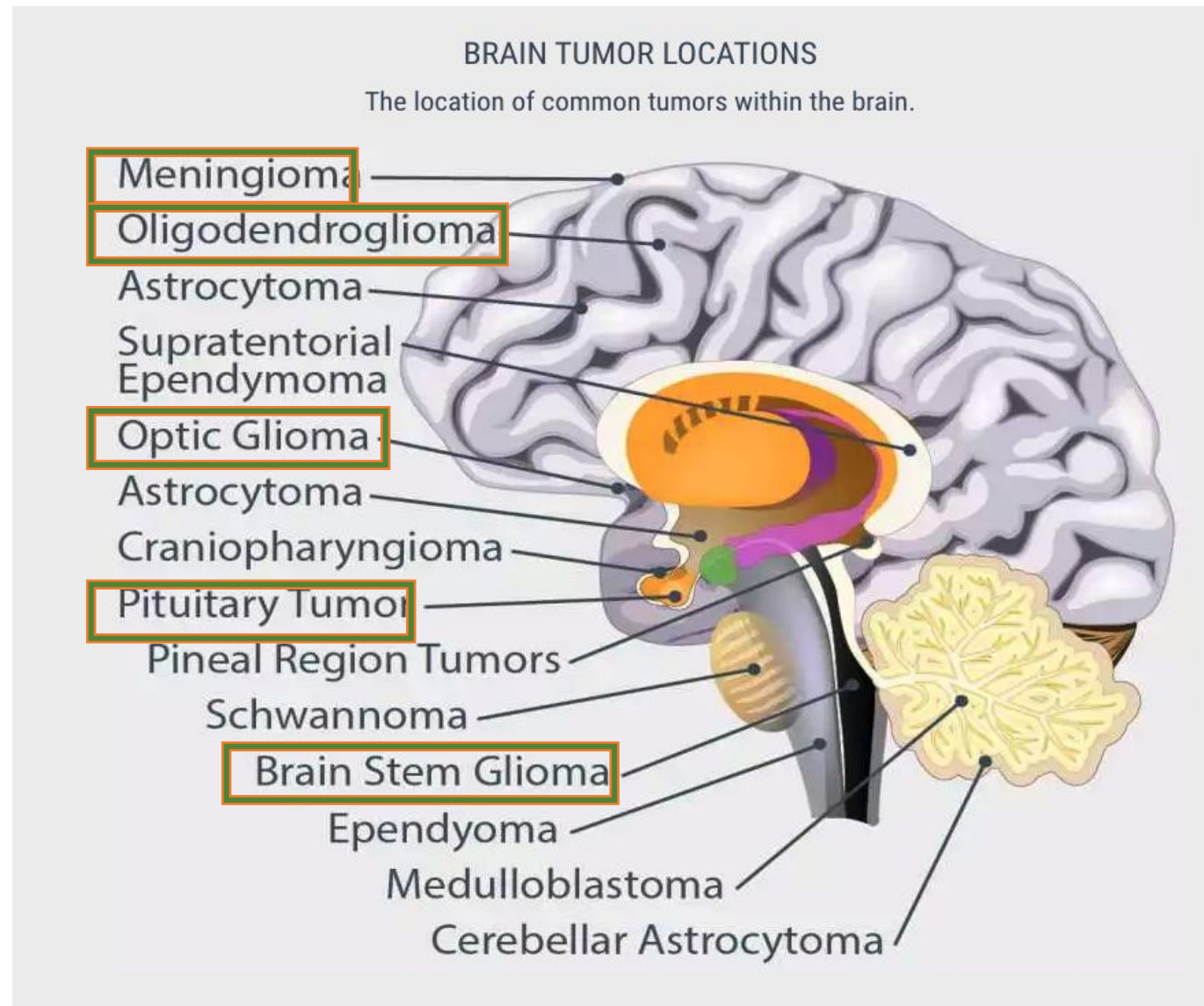


# Introduction

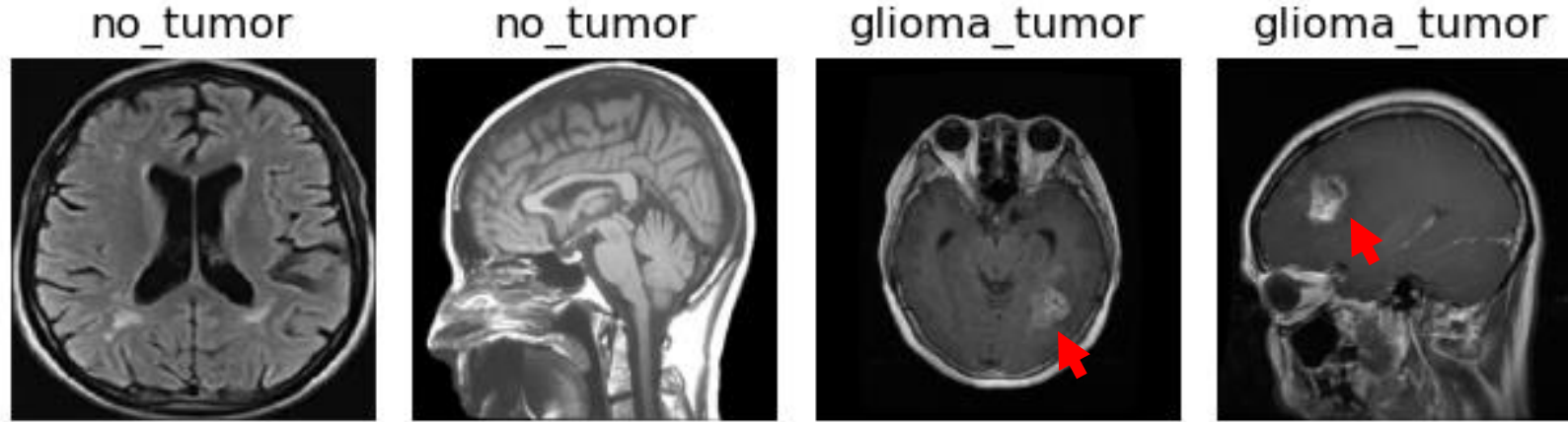
- Challenge in Brain Cancer Diagnosis
  - Breaking through the blood-brain barrier
  - The challenges of surgical removal
  - The efficiency and accuracy of brain cancer diagnosis by doctors
- Application of Machine Learning in Brain Cancer Diagnosis
  - Assist a neuro-oncologist in diagnosing brain tumors
  - Increase the efficiency and accuracy of brain cancer diagnosis



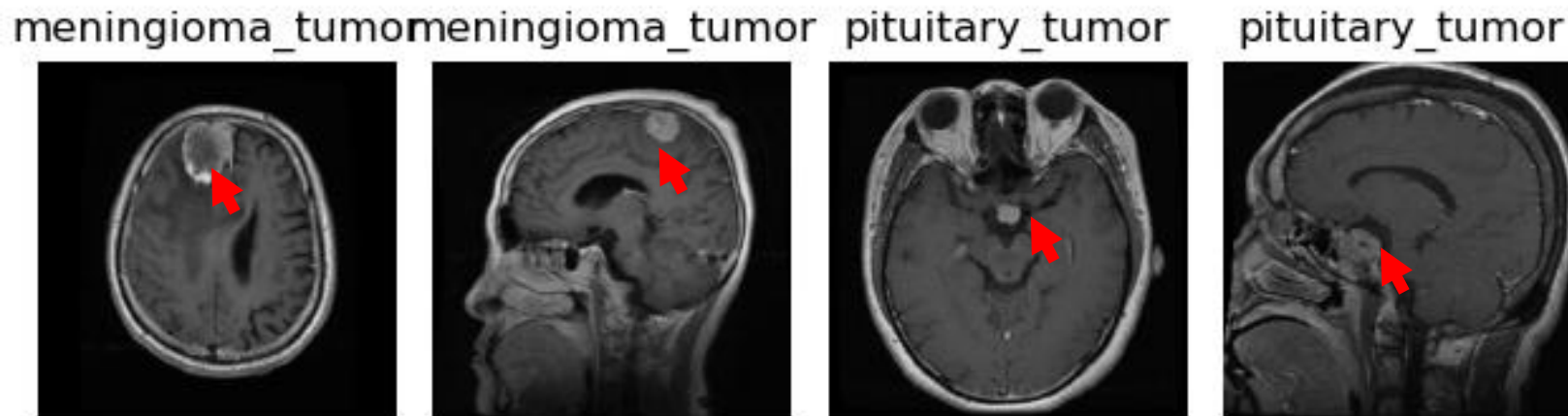
# Brain Cancer Types



# Overview of Dataset for 3 Types of Brain Tumors



{'glioma\_tumor': 826,  
'meningioma\_tumor': 822,  
'no\_tumor': 395,  
'pituitary\_tumor': 827}

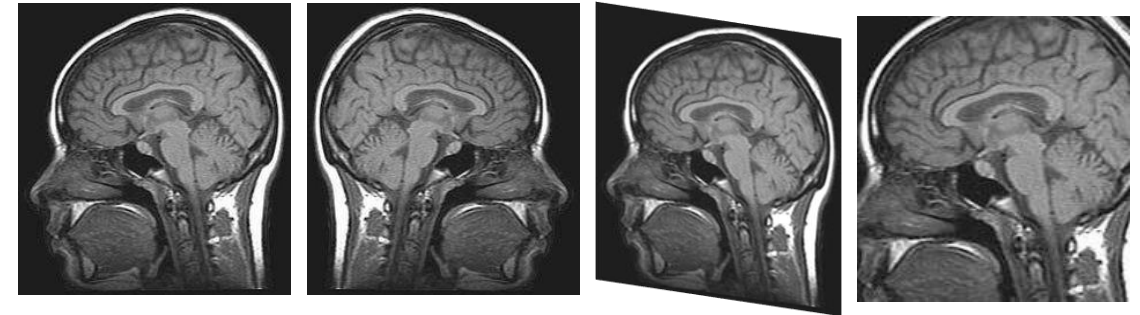


512 X 512 JPG file

<https://www.kaggle.com/sartajbhuvaji/brain-tumor-classification-mri>

# Data Preprocessing

- Resize --- (128 X 128)
- Transform to array from image
- Normalization---(/255.0)
- Data Augmentation---(ImageDataGenerator)
  - rotation\_range=20,
  - width\_shift\_range=0.2,
  - height\_shift\_range=0.2,
  - zoom\_range=0.2,
  - horizontal\_flip=True
- Data reshape from 3D to 2D



pixel image

imread



3-channel matrix

Blue					
Green					
Red					
255	231	42	22	4	30
123	94	83	2	92	124
34	44	187	92	4	142
34	76	232	124	4	
67	83	194	202		

im2vector  
(or flatten)



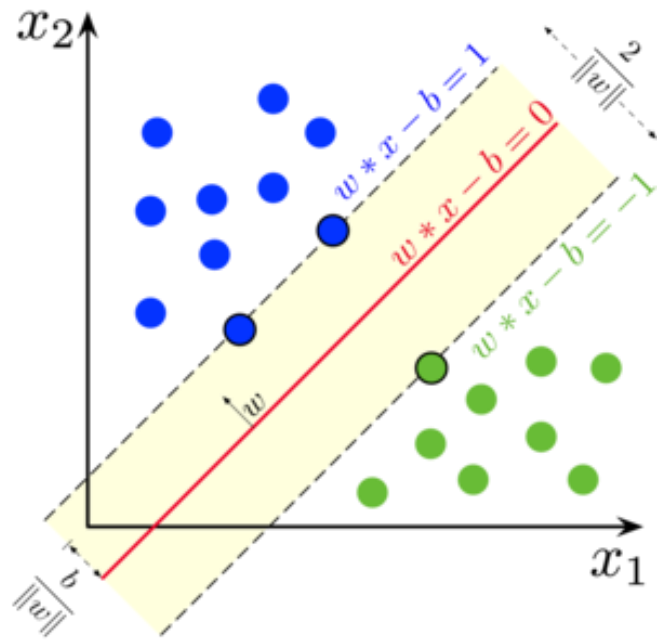
reshaped image vector

$\begin{pmatrix} 255 \\ 231 \\ 42 \\ 22 \\ 123 \\ 94 \\ \vdots \\ \vdots \\ 92 \\ 142 \end{pmatrix}$

# **Modeling, Prediction and Evaluation**

# Modeling, Prediction and Evaluation -- SVM

```
clf = SVC(kernel="poly")
```



True label	Predicted label				
	no_t	pituitary_t	meningioma_t	glioma_t	
	no_t	51	4	13	3
	pituitary_t	0	171	2	1
	meningioma_t	11	12	105	25
glioma_t	1	2	37	136	

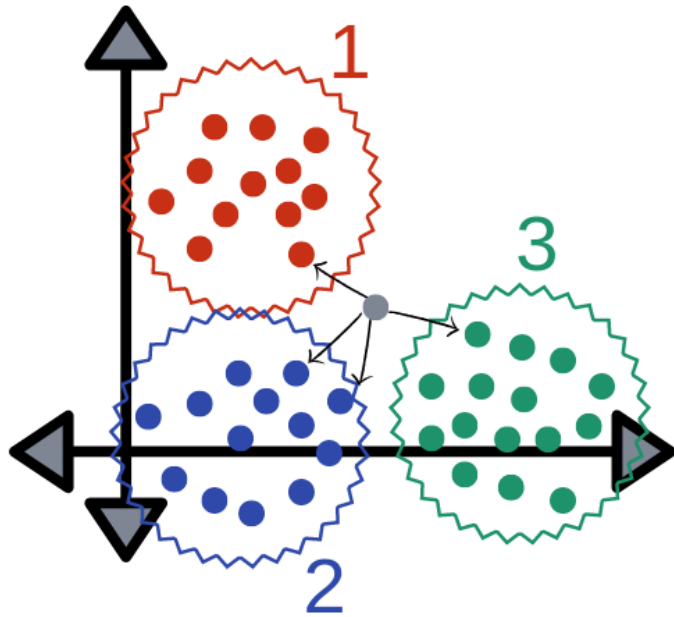
Classification Report:

	precision	recall	f1-score	support
0	0.81	0.72	0.76	71
1	0.90	0.98	0.94	174
2	0.67	0.69	0.68	153
3	0.82	0.77	0.80	176
accuracy				0.81
macro avg				0.80
weighted avg				0.81



# Modeling, Prediction and Evaluation -- KNN

```
clf = KNeighborsClassifier(n_neighbors=4)
```



True label	Predicted label				
	no_t	pituitary_t	meningioma_t	glioma_t	
	no_t	55	8	4	4
	pituitary_t	2	168	1	3
	meningioma_t	15	16	102	20
glioma_t	1	5	18	152	

Classification Report:

	precision	recall	f1-score	support
0	0.75	0.77	0.76	71
1	0.85	0.97	0.91	174
2	0.82	0.67	0.73	153
3	0.85	0.86	0.86	176
accuracy				0.83
macro avg				0.82
weighted avg				0.83

# Modeling, Prediction and Evaluation -- Naïve Bayes

```
clf = GaussianNB()
```

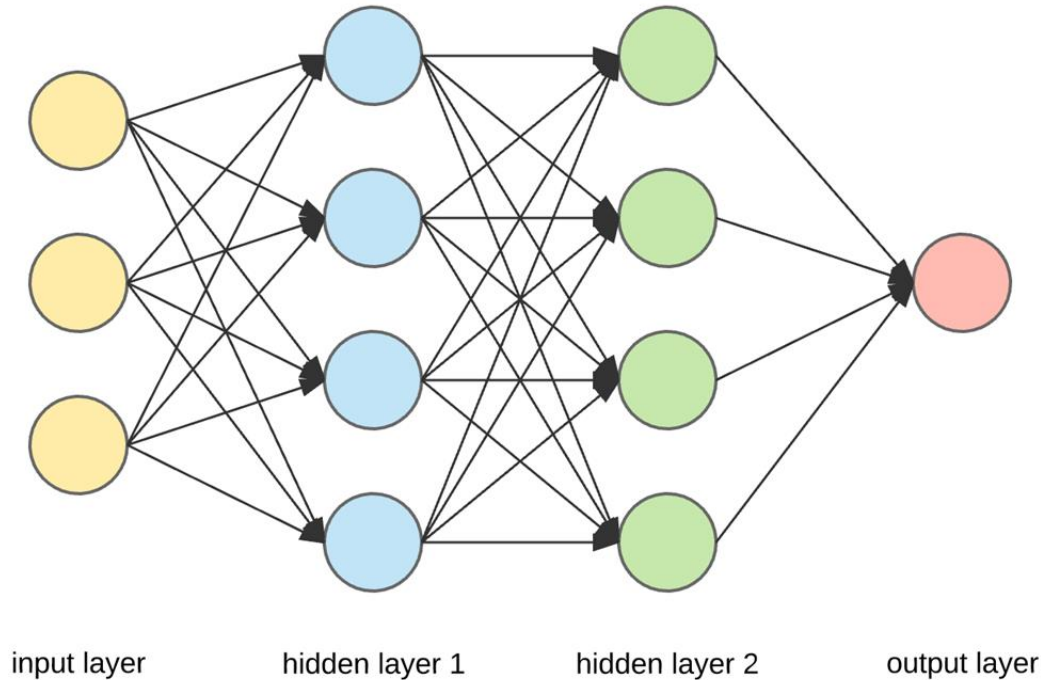
$$P(A|B) = \frac{P(B|A) P(A)}{P(B)}$$

True label		no_t	pituitary_t	meningioma_t	glioma_t
	no_t	35	6	26	4
	pituitary_t	2	145	4	23
	meningioma_t	24	21	17	91
	glioma_t	0	11	1	164
		Predicted label			
		no_t	pituitary_t	meningioma_t	glioma_t

Classification Report:

	precision	recall	f1-score	support
0	0.57	0.49	0.53	71
1	0.79	0.83	0.81	174
2	0.35	0.11	0.17	153
3	0.58	0.93	0.72	176
accuracy			0.63	574
macro avg	0.58	0.59	0.56	574
weighted avg	0.58	0.63	0.58	574

# Modeling, Prediction and Evaluation -- ANN



ANN optimum model discovery

1. Hidden layers and nodes

$(20,20) / (500,500) / (20,20,20,20)$

2. Iteration numbers

500 / 2000

3. Activation

“sigmoid” / “relu”

4. Early-stopping

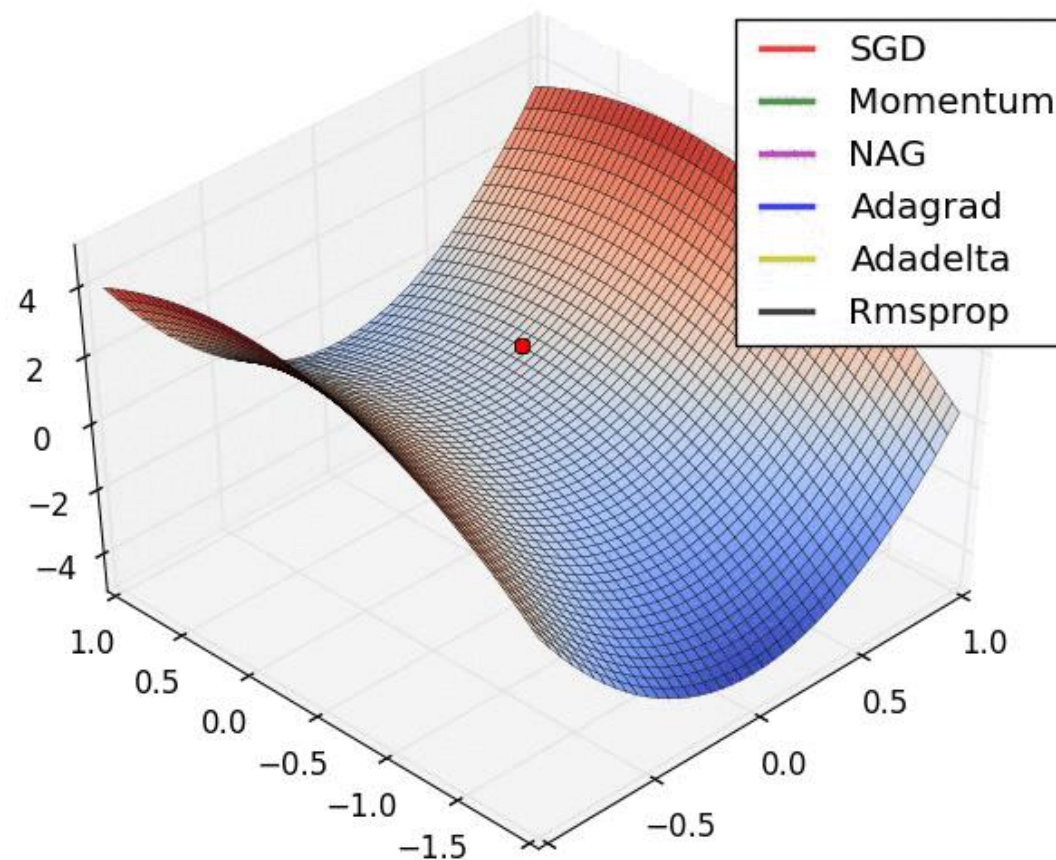
5. Solver

Adam/SGD/RMSprop/Adagrad/Adadelata/Adamax

# Optimizers

Method	Update equation
SGD	$\begin{aligned}g_t &= \nabla_{\theta_t} J(\theta_t) \\ \Delta\theta_t &= -\eta \cdot g_t \\ \theta_t &= \theta_t + \Delta\theta_t\end{aligned}$
Momentum	$\Delta\theta_t = -\gamma v_{t-1} - \eta g_t$
NAG	$\Delta\theta_t = -\gamma v_{t-1} - \eta \nabla_{\theta} J(\theta - \gamma v_{t-1})$
Adagrad	$\Delta\theta_t = -\frac{\eta}{\sqrt{G_t + \epsilon}} \odot g_t$
Adadelata	$\Delta\theta_t = -\frac{RMS[\Delta\theta]_{t-1}}{RMS[g]_t} g_t$
RMSprop	$\Delta\theta_t = -\frac{\eta}{\sqrt{E[g^2]_t + \epsilon}} g_t$
Adam	$\Delta\theta_t = -\frac{\eta}{\sqrt{\hat{v}_t + \epsilon}} \hat{m}_t$

Source: Sebastian Ruder



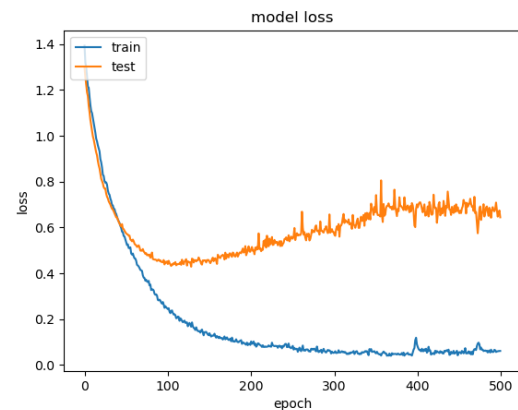
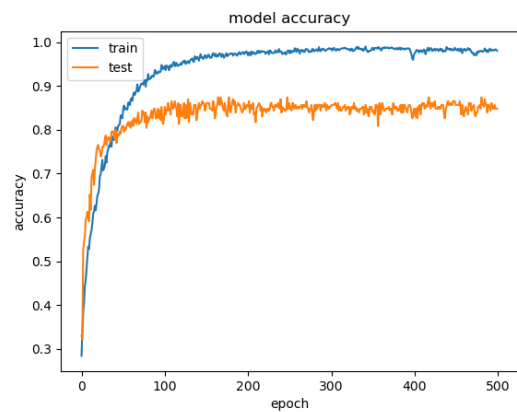
Source: Alec Radford



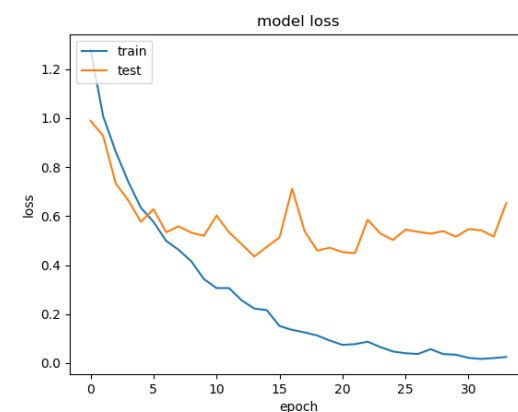
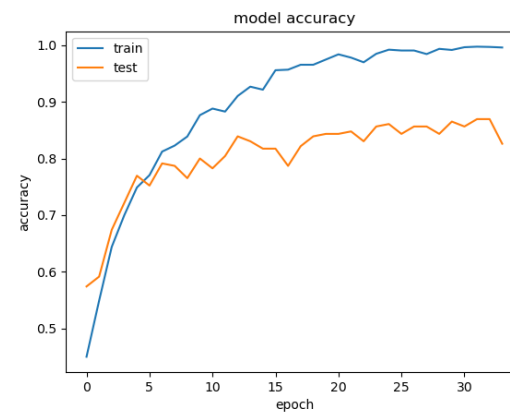
# Experiments Design and Results for ANN with Different Parameters

ANN	Layers & Nodes	Iteration	Activation	Early-stopping	Solver	Accuracy (%)
01	(20, 20)	500	"sigmoid"	False	Adam	84.5
02	(20, 20)	500	"relu"	False	Adam	79.4
03	(20, 20)	500	"sigmoid", "relu"	False	Adam	82.1
04	(500, 500)	500	"sigmoid"	True	Adam	85.2
05	(20, 20, 20,20)	500	"sigmoid"	False	Adam	80.8
06	(20, 20)	2000	"sigmoid"	False	Adam	82.2
07	(20,20)	500	"sigmoid"	False	SGD	81.2
08	(20, 20)	500	"sigmoid"	False	RMSprop	84.8
09	(20, 20)	500	"sigmoid"	False	Adagrad	81.0
10	(20, 20)	500	"sigmoid"	False	Adadelta	78.6
11	(20,20)	500	"sigmoid"	False	Adamax	73.3
ANN	(500, 500, 20)	500	"sigmoid"	False	RMSprop	87.5

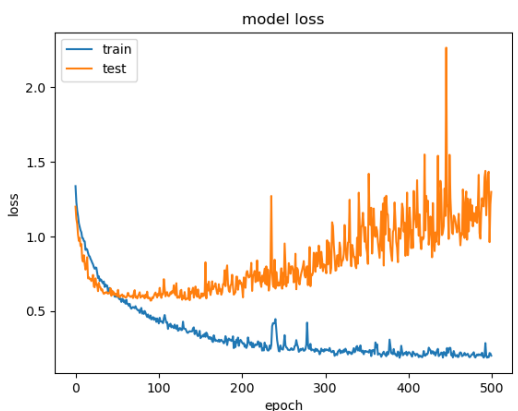
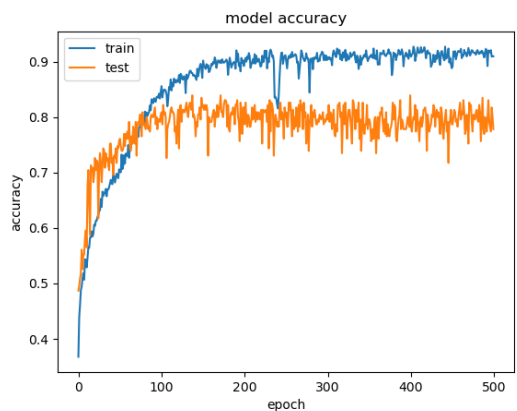
**ANN  
01**



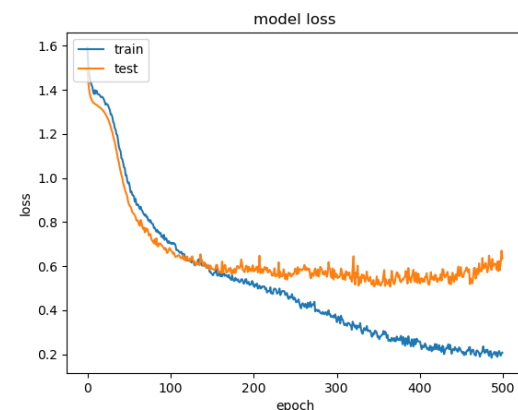
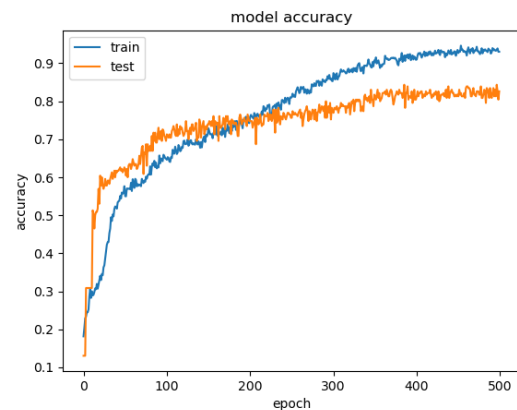
**ANN  
04**



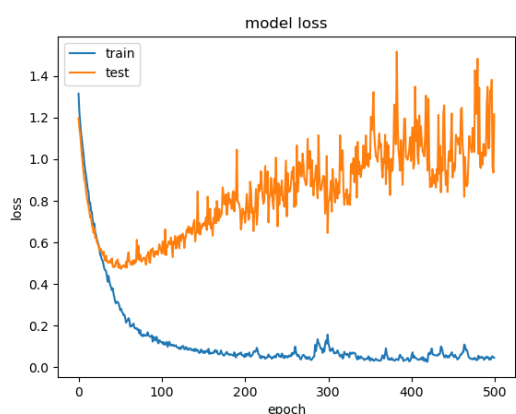
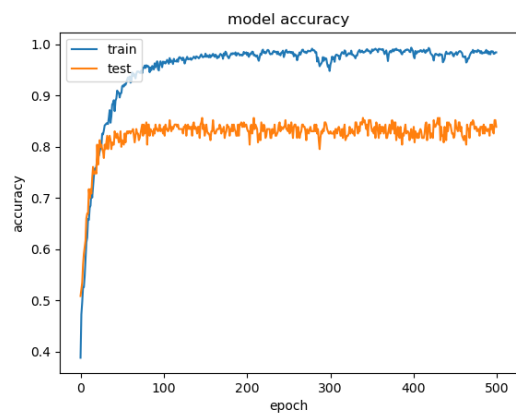
**ANN  
02**



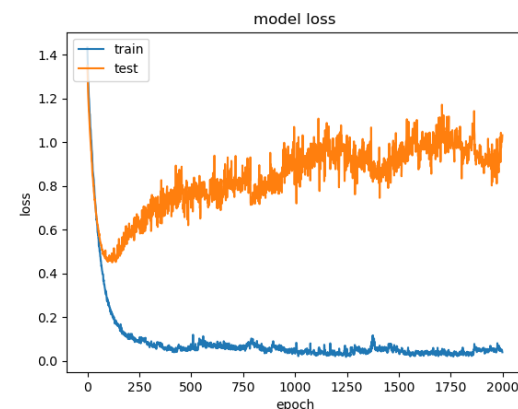
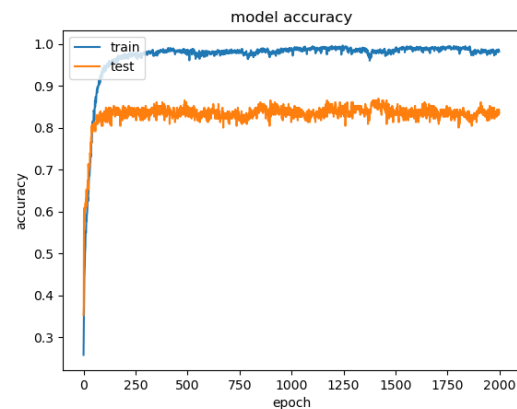
**ANN  
05**



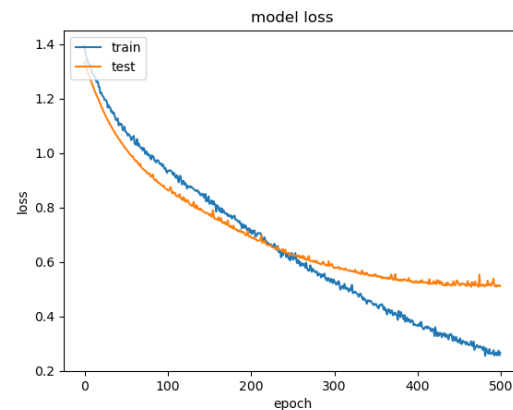
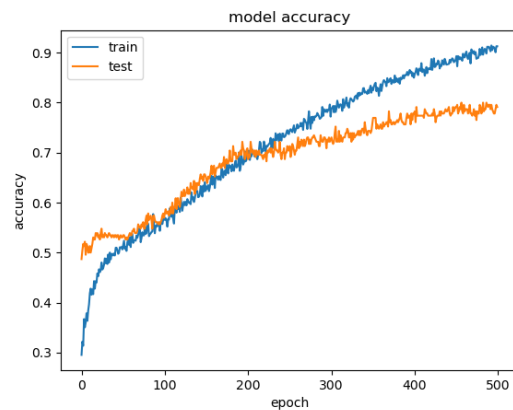
**ANN  
03**



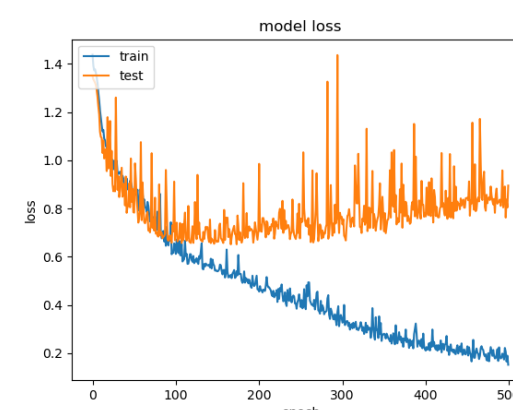
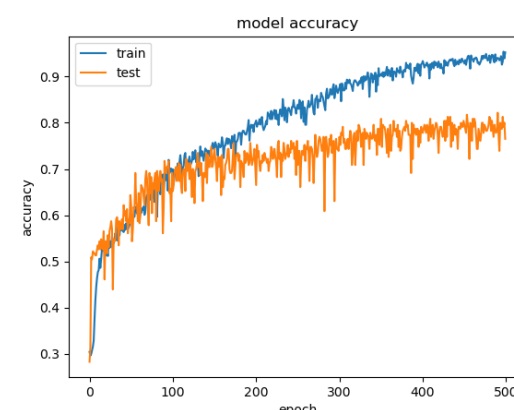
**ANN  
06**



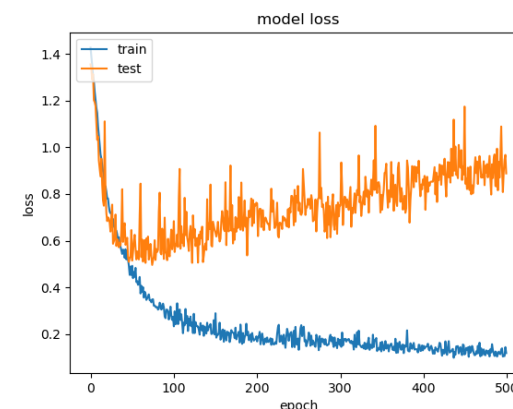
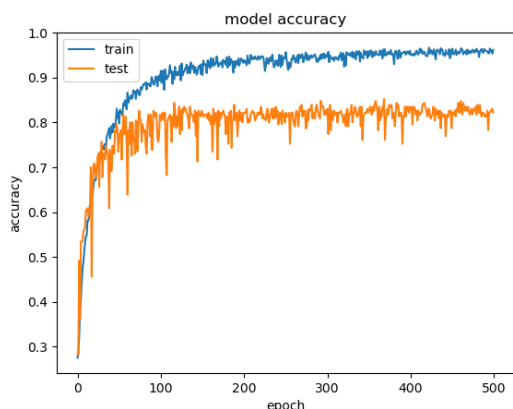
**ANN  
07**



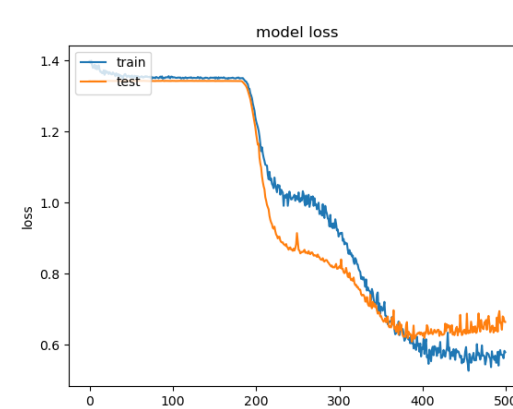
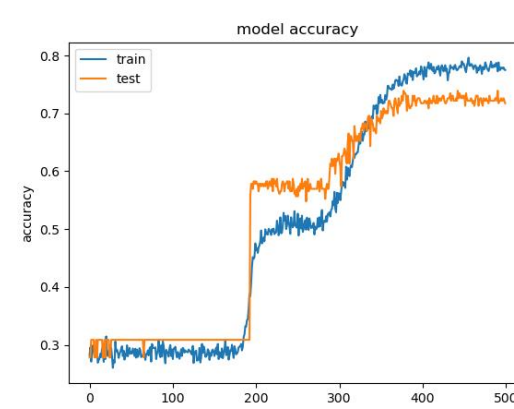
**ANN  
10**



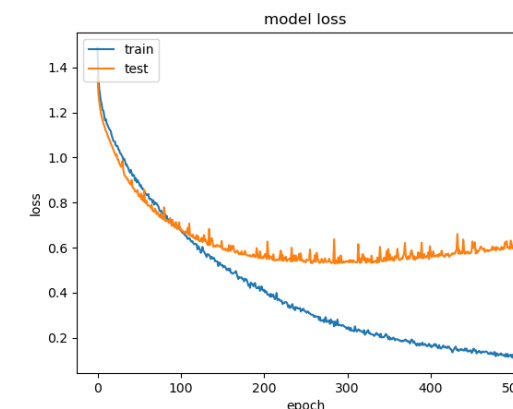
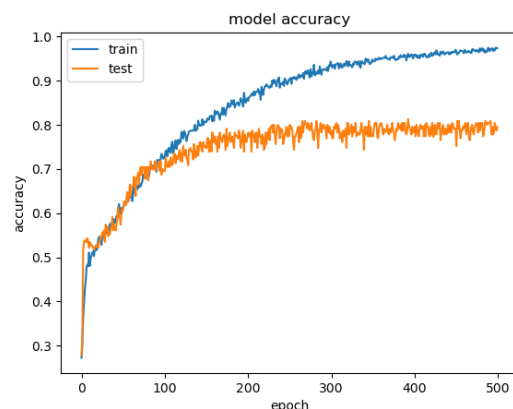
**ANN  
08**



**ANN  
11**



**ANN  
09**



# Modeling, Prediction and Evaluation - ANN

Hidden layers and Nodes: (500,500,20)/ Iteration: 500/ Activation: "sigmoid"/ Solver: RMSpro (lr=0.001)

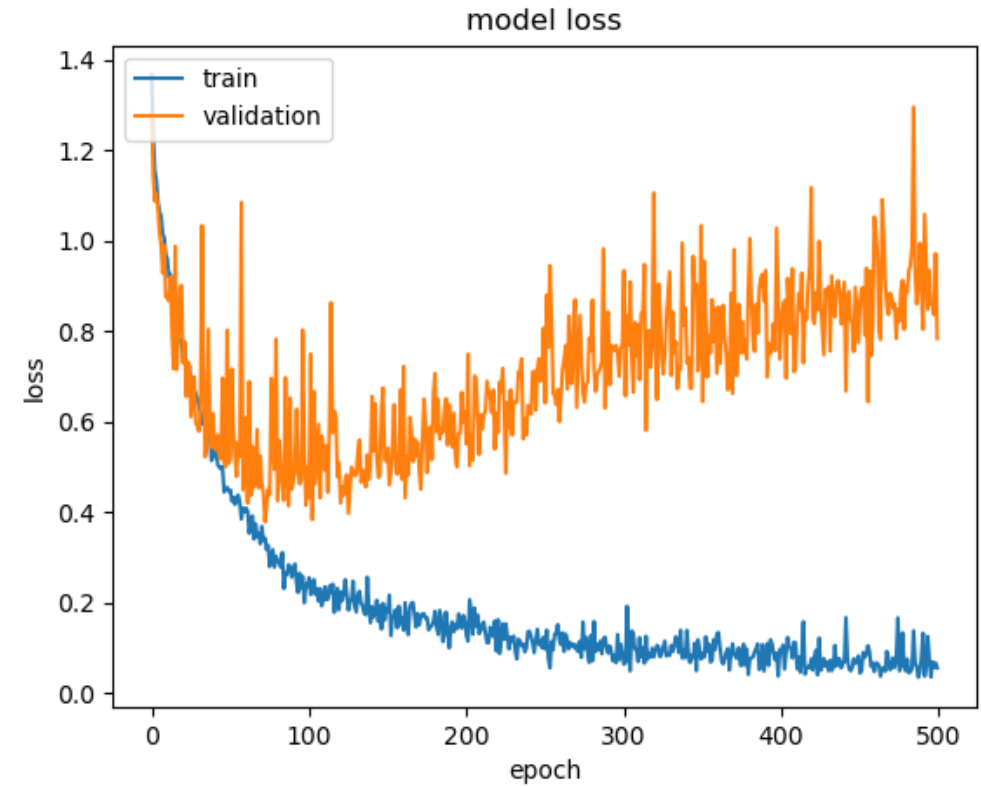
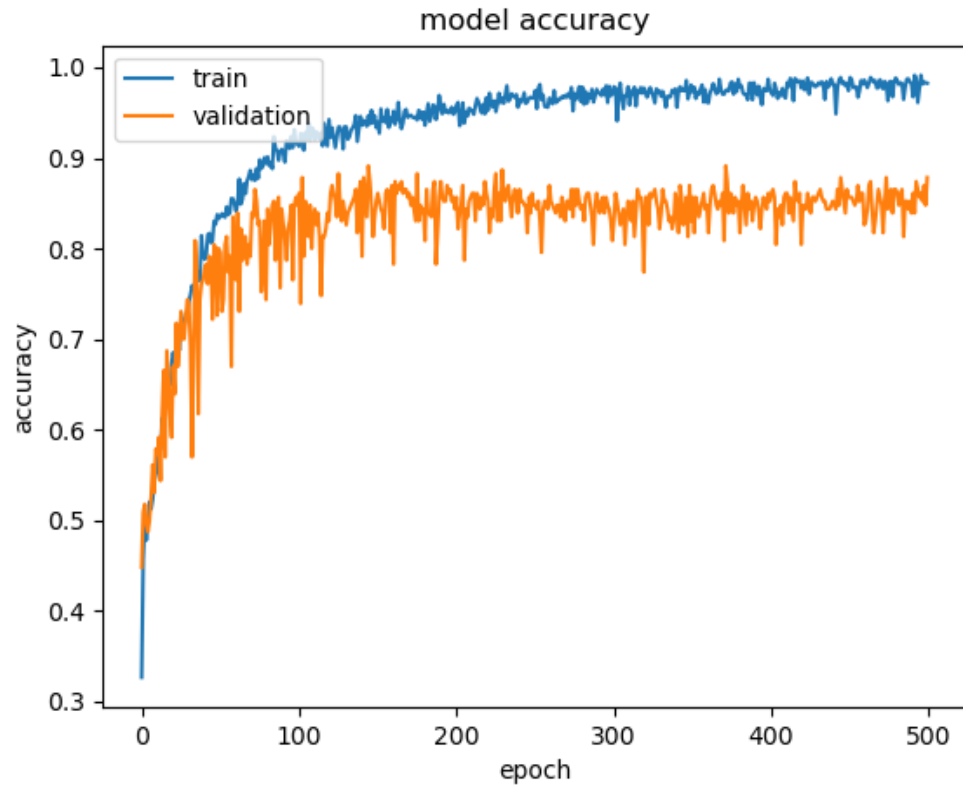
True label	Predicted label				
	no_t	pituitary_t	meningioma_t	glioma_t	
	no_t	62	1	8	4
	pituitary_t	0	146	6	2
	meningioma_t	12	6	137	13
glioma_t	2	1	17	157	

## Classification Report:

	precision	recall	f1-score	support
0	0.82	0.83	0.82	75
1	0.95	0.95	0.95	154
2	0.82	0.82	0.82	168
3	0.89	0.89	0.89	177
accuracy			0.87	574
macro avg	0.87	0.87	0.87	574
weighted avg	0.87	0.87	0.87	574



# Modeling, Prediction and Evaluation - ANN



# Summary and Discussion

1. Activation with “sigmoid” shows better performance and higher accuracy than activation with “relu” and “tanh”.
2. Solver with RMSprop shows higher prediction accuracy with the brain cancer dataset.
3. With ANN model, the accuracy for prediction can reach to 87%, which is better than other models including KNN, SVM and Naïve Bayes.

Deep learning with skills of convolution and maxpool need to be tried to get the accuracy higher.....

# References

1. Aldape, K., Brindle, K.M., Chesler, L. et al. Challenges to curing primary brain tumours. *Nat Rev Clin Oncol* 16, 509–520 (2019). <https://doi.org/10.1038/s41571-019-0177-5>
2. Cao, H., Erson-Omay, E.Z., Li, X. et al. A quantitative model based on clinically relevant MRI features differentiates lower grade gliomas and glioblastoma. *Eur Radiol* 30, 3073–3082 (2020). <https://doi.org/10.1007/s00330-019-06632-8>
3. Nadeem, M. W., Ghamdi, M., Hussain, M., Khan, M. A., Khan, K. M., Almotiri, S. H., & Butt, S. A. (2020). Brain Tumor Analysis Empowered with Deep Learning: A Review, Taxonomy, and Future Challenges. *Brain sciences*, 10(2), 118. <https://doi.org/10.3390/brainsci10020118>
4. Hollon, T.C., Pandian, B., Adapa, A.R. *et al.* Near real-time intraoperative brain tumor diagnosis using stimulated Raman histology and deep neural networks. *Nat Med* **26**, 52–58 (2020). <https://doi.org/10.1038/s41591-019-0715-9>
5. Kingma, D.P., & Ba, J. (2015). Adam: A Method for Stochastic Optimization. CoRR, abs/1412.6980.
6. <https://ml-cheatsheet.readthedocs.io/en/latest/index.html>
7. <https://runder.io/optimizing-gradient-descent/index.html#adamax>
8. <https://miamineurosciencecenter.com/en/conditions/brain-tumors/types/>
9. <https://mlfromscratch.com/optimizers-explained/#/>

# Shameless Plug

Help us save the world (by improving public health)

## The Lab Behind GW's COVID Testing Program

*A team of Milken Institute School of Public Health researchers, led by Professor Cindy Liu, ensure GW's COVID-19 testing provides rapid, consistent and accurate results.*

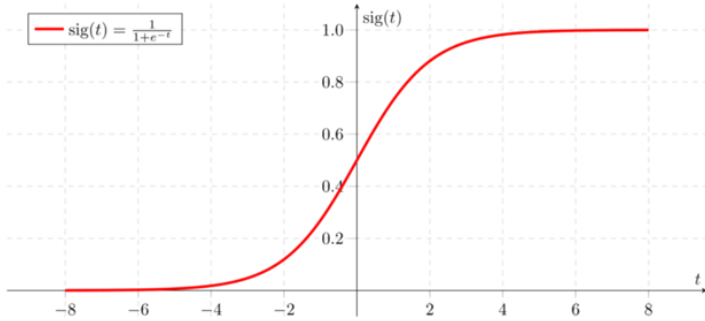


A team of GW researchers process thousands of COVID-19 tests a week as part of a new public health laboratory, led by Associate



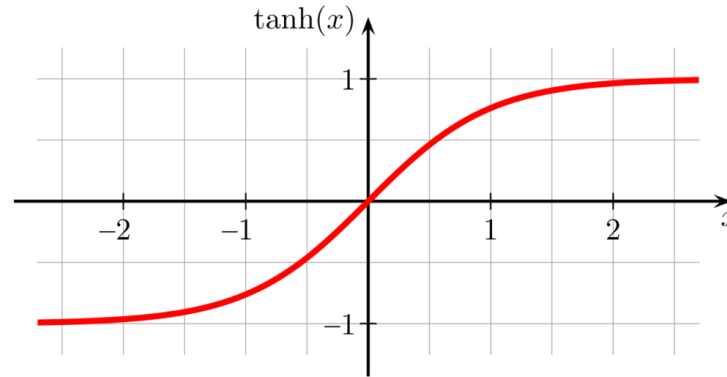
Thank You

sigmoid



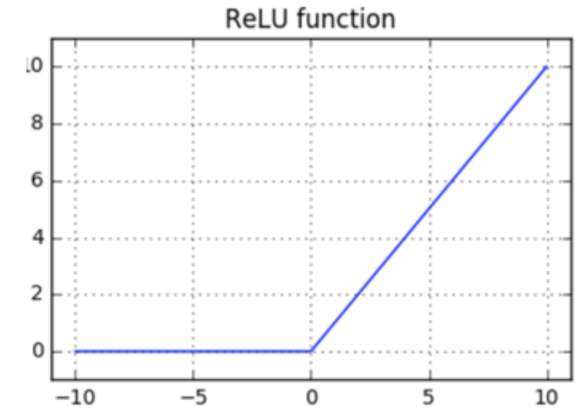
$$y = 1/(1+e^{(-x)})$$

tanh



$$y = \tanh(x)$$

relu



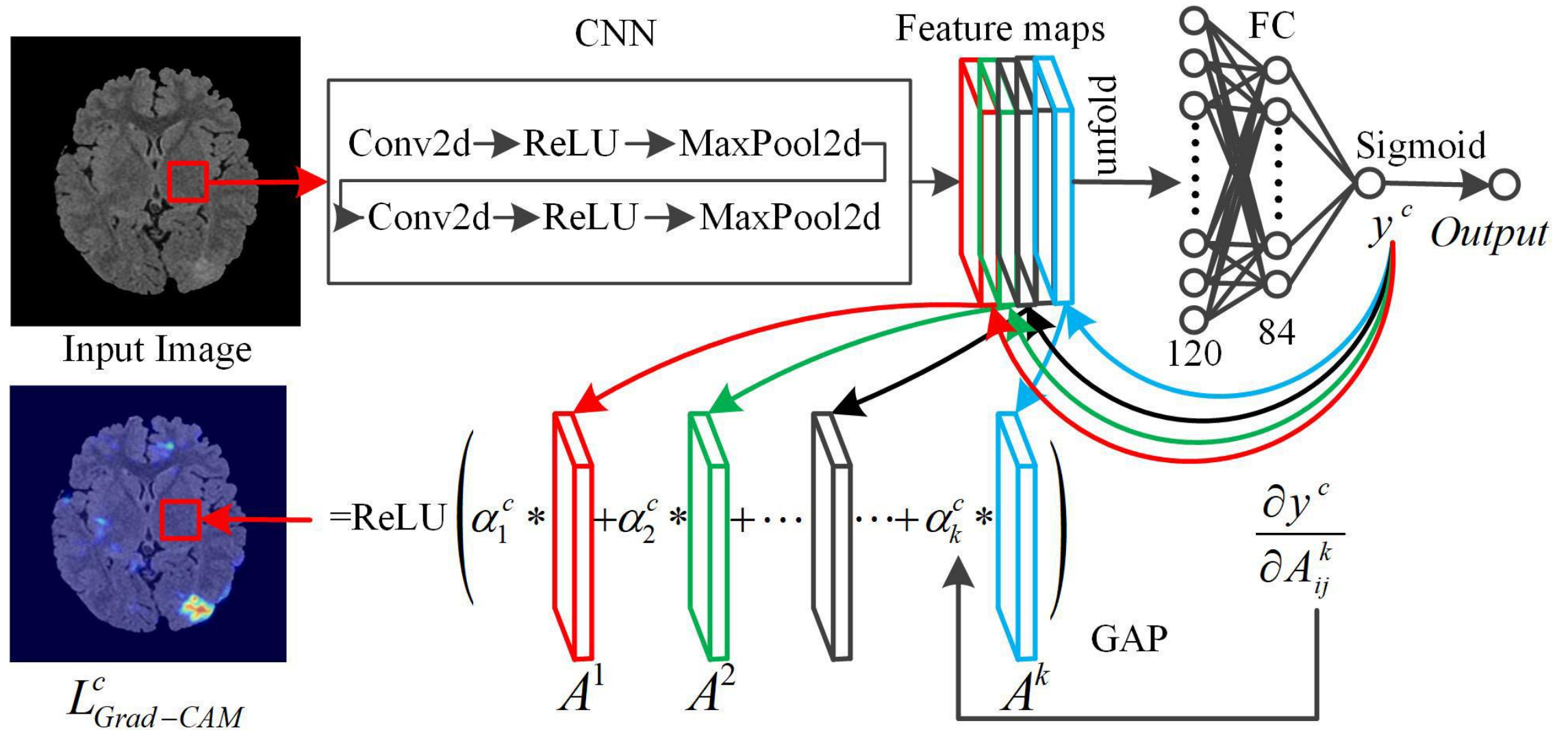
$$\begin{cases} x & \text{if } x \geq 0 \\ 0 & \text{if } x < 0 \end{cases}$$

<https://www.aitude.com/comparison-of-sigmoid-tanh-and-relu-activation-functions/>

Sigmoid: not blowing up activation

Relu : not vanishing gradient

# Modeling, Prediction and Evaluation - CNN



# Modeling, Prediction and Evaluation - CNN

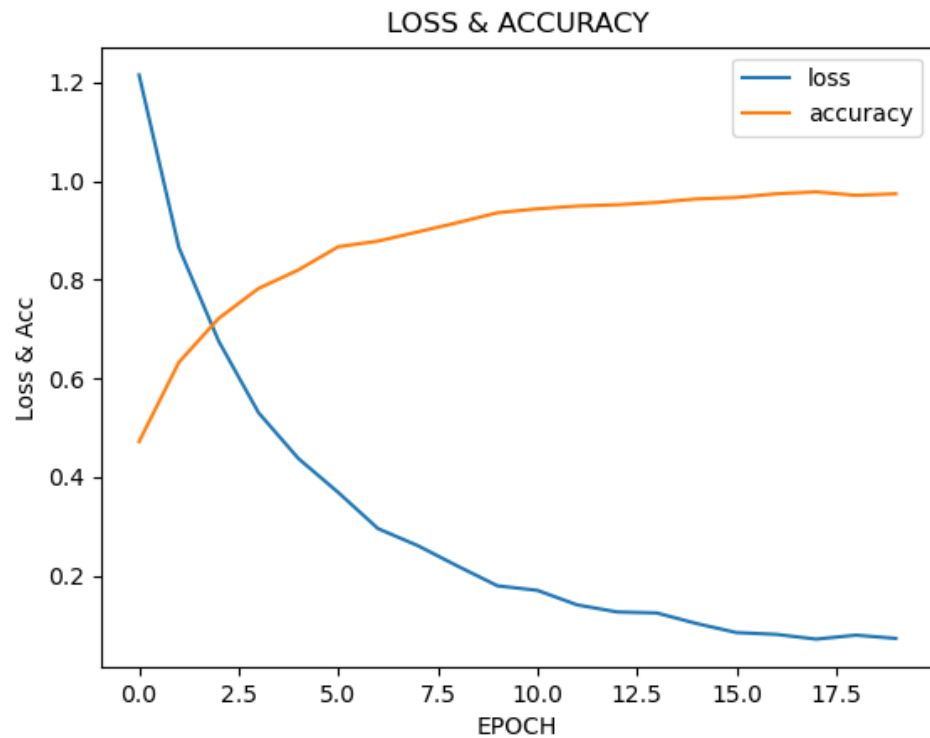
True label	no_t	pituitary_t	meningioma_t	glioma_t	
	no_t	63	0	5	3
	pituitary_t	0	169	2	3
	meningioma_t	2	3	144	4
	glioma_t	0	1	6	169
		Predicted label			
		no_t	pituitary_t	meningioma_t	glioma_t

## Classification Report:

	precision	recall	f1-score	support
0	0.97	0.89	0.93	71
1	0.98	0.97	0.97	174
2	0.92	0.94	0.93	153
3	0.94	0.96	0.95	176
accuracy			0.95	574
macro avg	0.95	0.94	0.95	574
weighted avg	0.95	0.95	0.95	574



# Modeling, Prediction and Evaluation - CNN



```
Epoch 9/50
72/72 [=====] - 339s 5s/step - loss: 0.2201 - accuracy: 0.9155
Epoch 10/50
72/72 [=====] - 315s 4s/step - loss: 0.1801 - accuracy: 0.9355
Epoch 11/50
72/72 [=====] - 310s 4s/step - loss: 0.1710 - accuracy: 0.9434
Epoch 12/50
72/72 [=====] - 312s 4s/step - loss: 0.1416 - accuracy: 0.9490
Epoch 13/50
72/72 [=====] - 318s 4s/step - loss: 0.1273 - accuracy: 0.9517
Epoch 14/50
72/72 [=====] - 315s 4s/step - loss: 0.1252 - accuracy: 0.9564
Epoch 15/50
72/72 [=====] - 306s 4s/step - loss: 0.1038 - accuracy: 0.9634
Epoch 16/50
72/72 [=====] - 305s 4s/step - loss: 0.0855 - accuracy: 0.9665
Epoch 17/50
72/72 [=====] - 323s 4s/step - loss: 0.0819 - accuracy: 0.9739
Epoch 18/50
72/72 [=====] - 317s 4s/step - loss: 0.0722 - accuracy: 0.9778
Epoch 19/50
72/72 [=====] - 455s 6s/step - loss: 0.0803 - accuracy: 0.9708
Epoch 20/50
72/72 [=====] - 391s 5s/step - loss: 0.0737 - accuracy: 0.9739
```