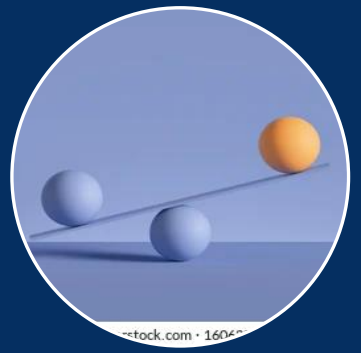
ACCELERATING BRAIN TUMOR DIAGNOSTICS WITH MACHINE LEARNING

AGENDA

Project overview

Data

Modelling



Model comparison

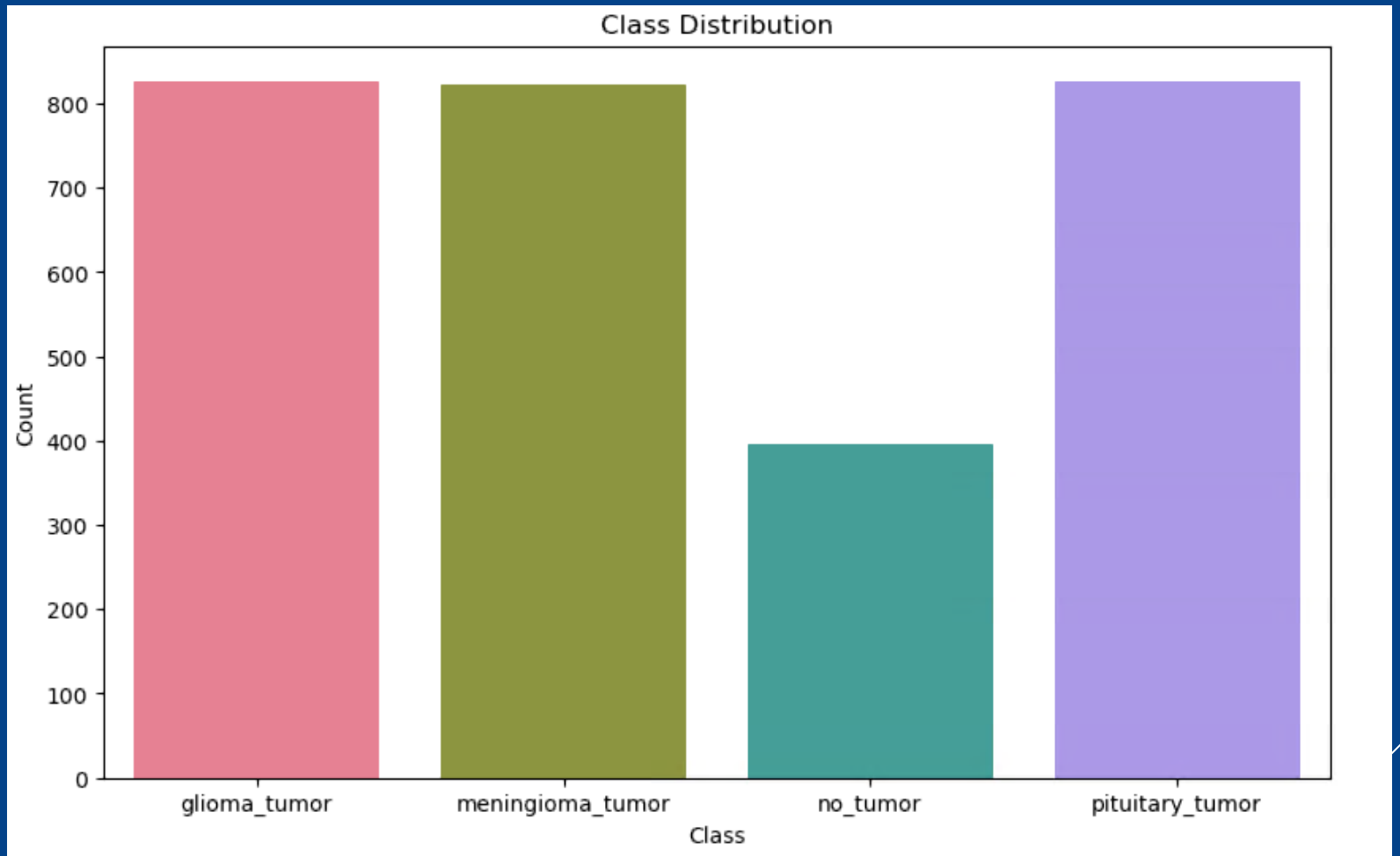
Model deployment & Future work

Comments and Feedback

PROJECT OVERVIEW

- Epidemiology & need
- Diagnostic challenges
- Machine learning advantages
- Operational efficiency
- Impact on global healthcare

DATA

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Total sample size: 2870
Class glioma_tumor: 826 samples
Class meningioma_tumor: 822 samples
Class no_tumor: 395 samples
Class pituitary_tumor: 827 samples
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ML MODEL - CNN

Model Architecture

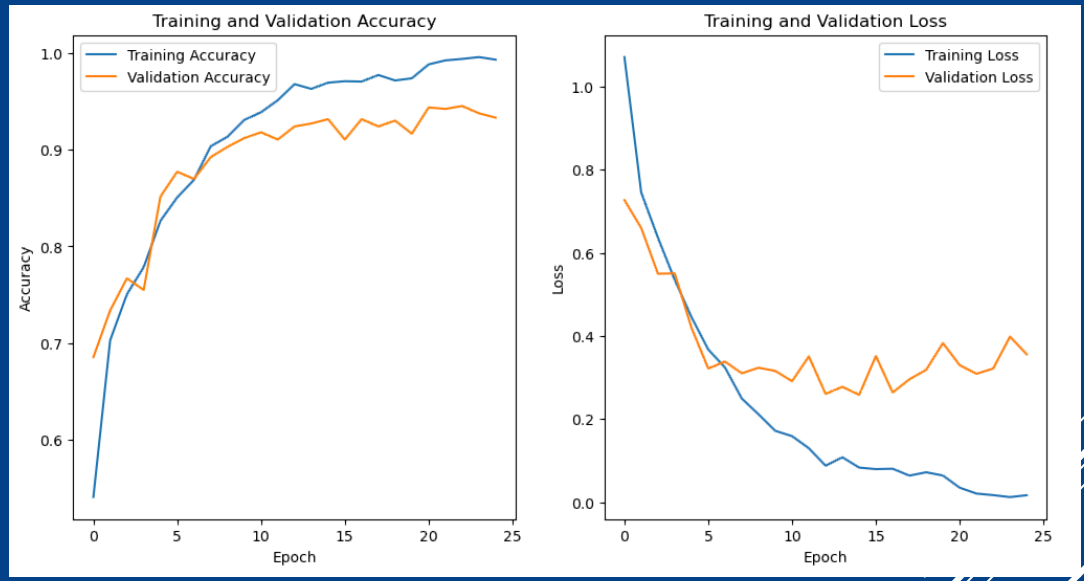
Layer Composition - 4 Conv2D Layers, 4MaxPooling2D Layers

Dense Layers – Flatten Layer, Dense Layer with 128 Neurons

Output Layer

Optimization and Loss

Epochs - 25



Classification Report:

	precision	recall	f1-score	support
glioma_tumor	0.93	0.96	0.94	191
meningioma_tumor	0.89	0.87	0.88	156
no_tumor	0.94	0.91	0.93	163
pituitary_tumor	0.97	0.99	0.98	151
accuracy			0.93	661
macro avg	0.93	0.93	0.93	661
weighted avg	0.93	0.93	0.93	661

Model training time: 669.41 seconds

ML MODEL – RESNET50

Model Architecture

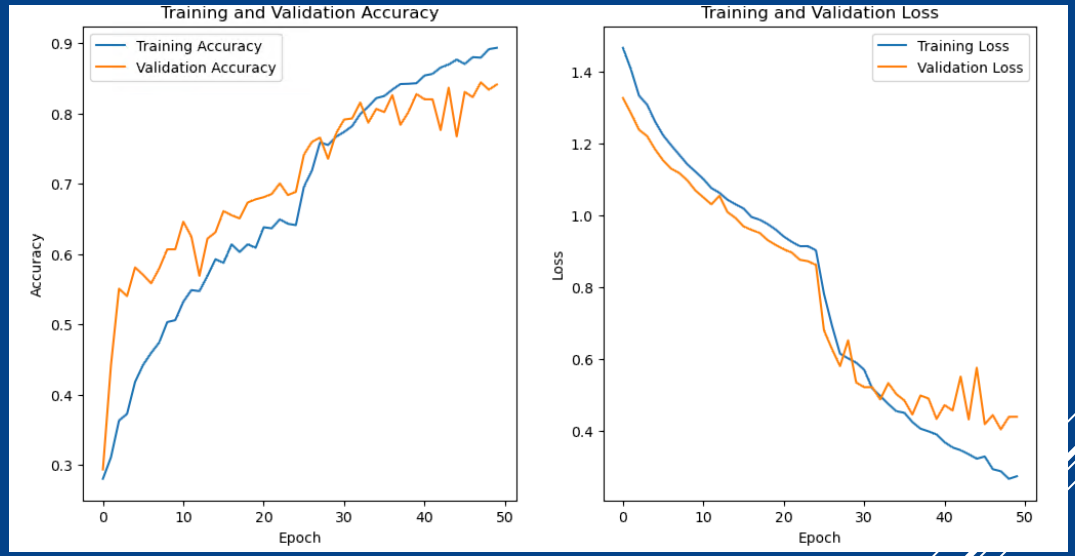
Base Model – ResNet, excluding the top layer, Input shape 128x 128 RGB images

Layers – Global average pooling, Dense Layer (1024 neurons), Relu Activation

Output Layer- Softmax activation

Optimization – Adam Optimizer with learning rate adjustment

Epochs -80



Classification Report:

	precision	recall	f1-score	support
glioma_tumor	0.88	0.78	0.83	191
meningioma_tumor	0.68	0.81	0.74	156
no_tumor	0.95	0.83	0.89	163
pituitary_tumor	0.90	0.95	0.93	151
accuracy			0.84	661
macro avg	0.85	0.85	0.84	661
weighted avg	0.85	0.84	0.84	661

ML MODEL – VGG16

Model Architecture

Base Model – VGG16, excluding the top layer, Input shape 128x 128 RGB images

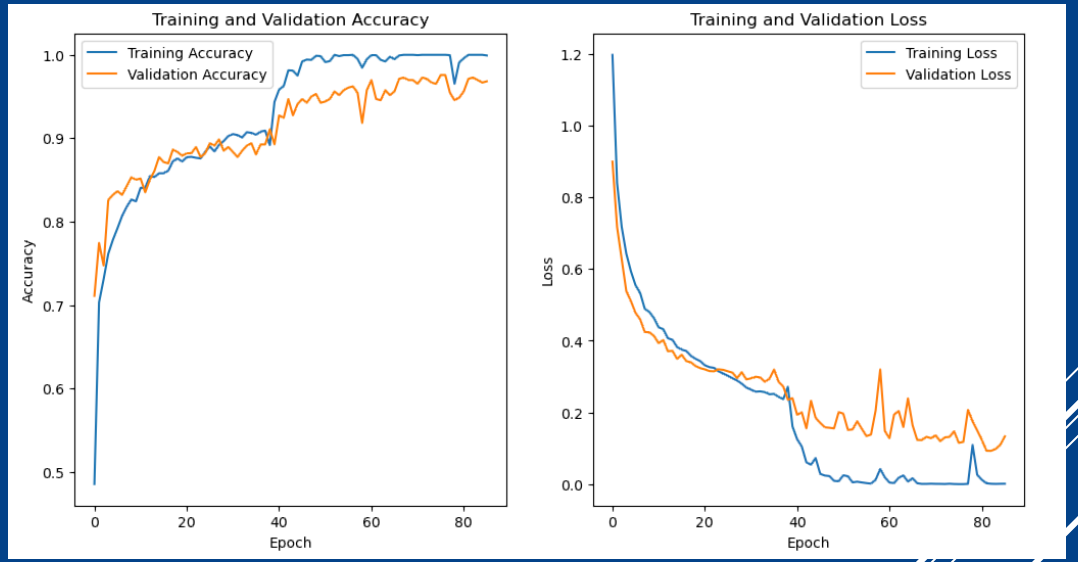
Layers – Global average pooling, Dense Layer (1024 neurons), Relu Activation

Output Layer- Softmax activation

Training – All VGG16 layers are froze initially and unfreezing with reduced learning rate

Optimization – Adam Optimizer with learning rate adjustment

Epochs-50

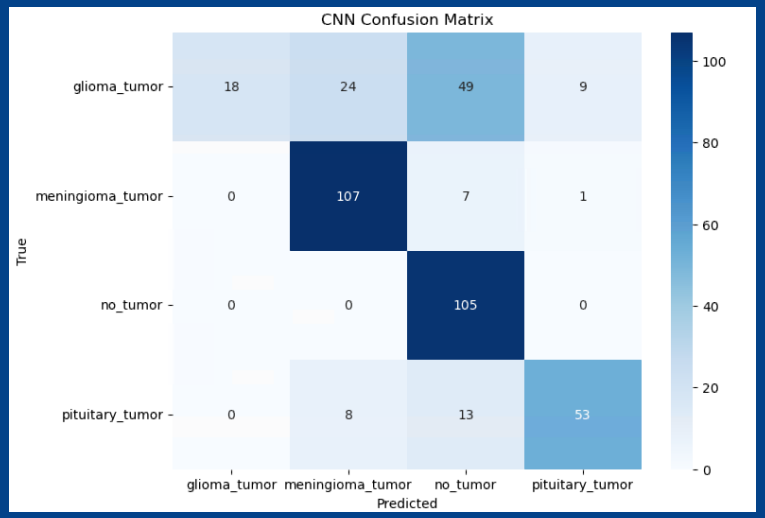


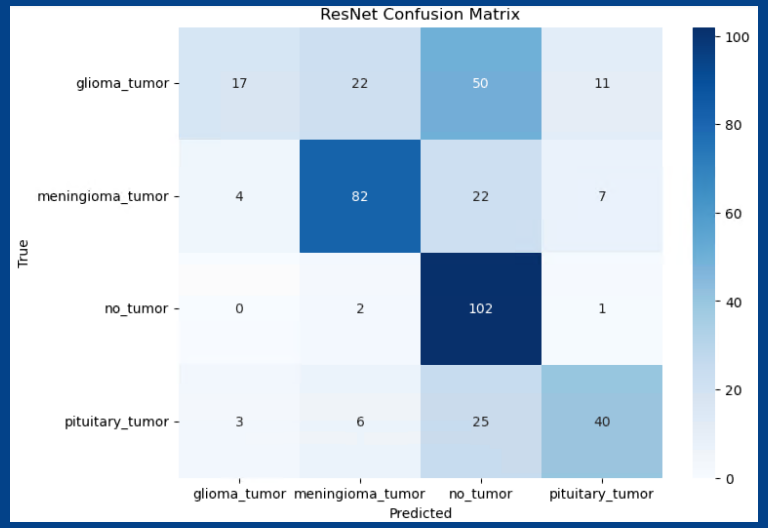
Classification Report:

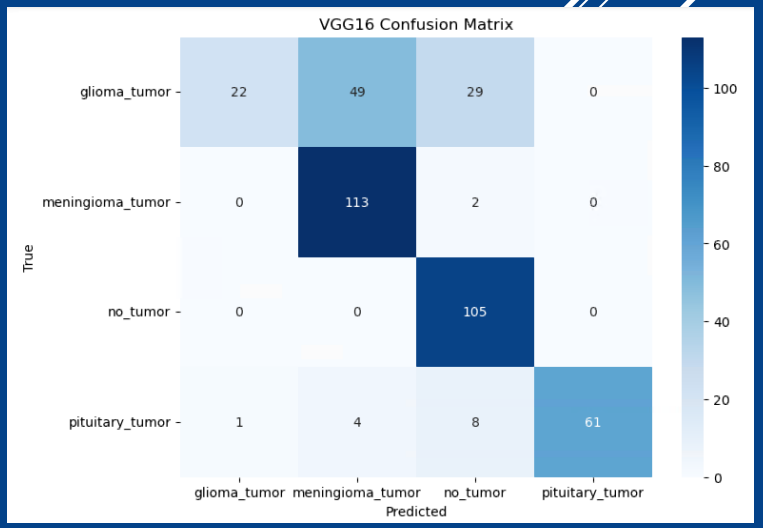
	precision	recall	f1-score	support
glioma_tumor	0.98	0.97	0.98	191
meningioma_tumor	0.93	0.97	0.95	156
no_tumor	0.99	0.98	0.99	163
pituitary_tumor	1.00	0.98	0.99	151
accuracy			0.98	661
macro avg	0.98	0.98	0.98	661
weighted avg	0.98	0.98	0.98	661

ML MODEL COMPARISON

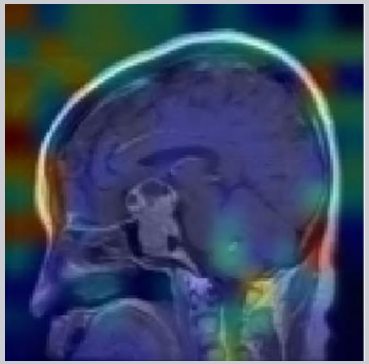
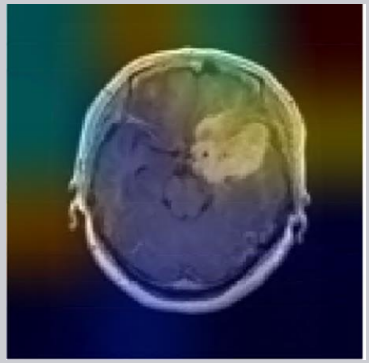
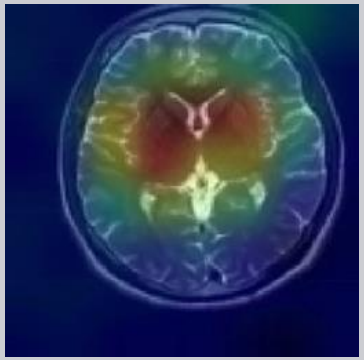
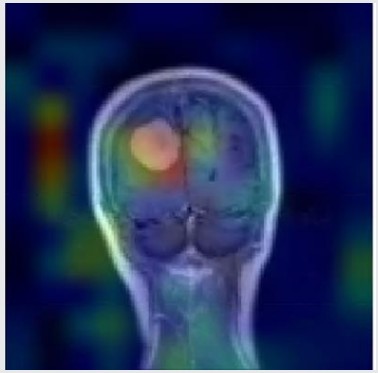
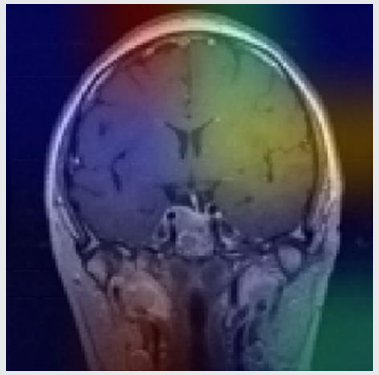
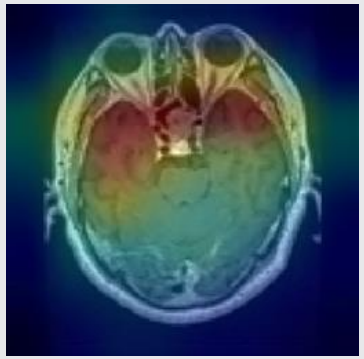
Model	Accuracy	Loss	Precision	Recall	F1-Score	Test Time (seconds)	ROC-AUC
ResNet	0.611675	2.441717	0.657751	0.598753	0.567304	8.316759	0.815211
CNN	0.718274	6.226991	0.821016	0.703375	0.672665	1.414741	0.887187
VGG16	0.763959	3.874465	0.841603	0.756733	0.727268	14.097608	0.933722



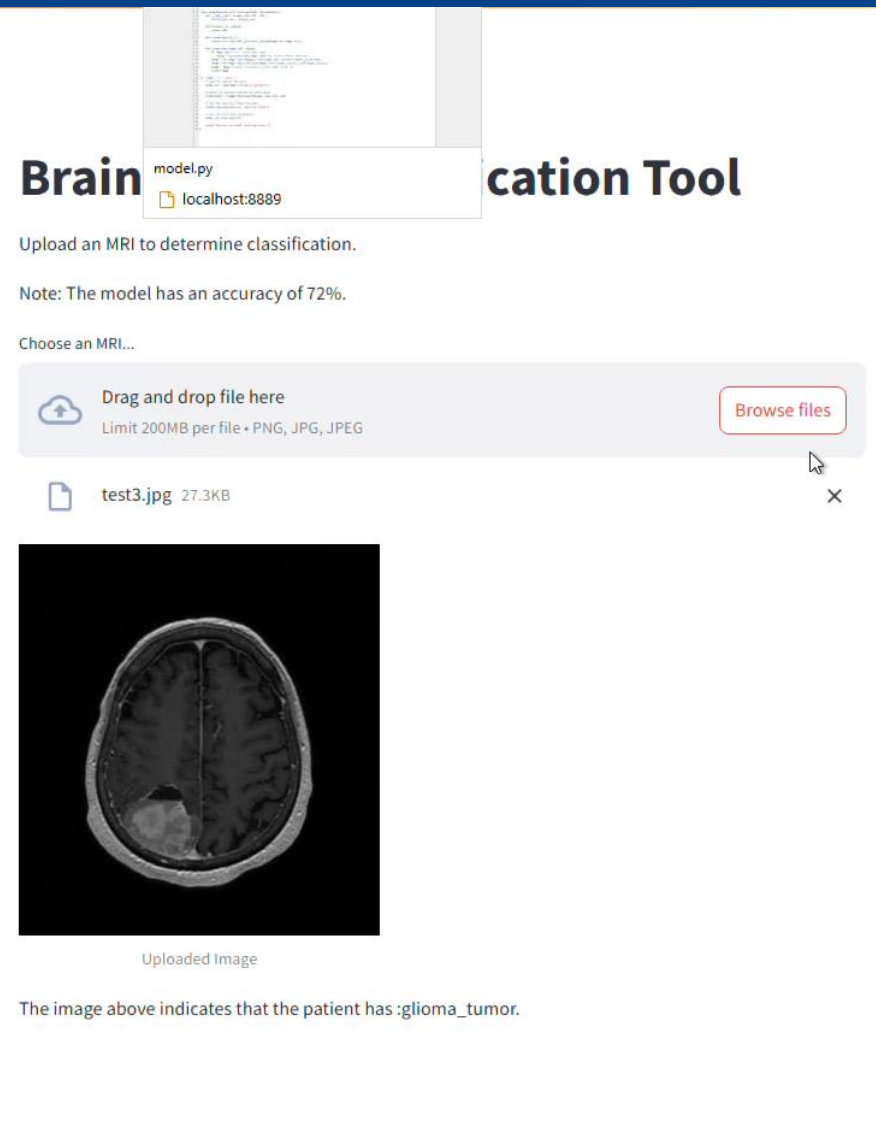




ML MODEL COMPARISON

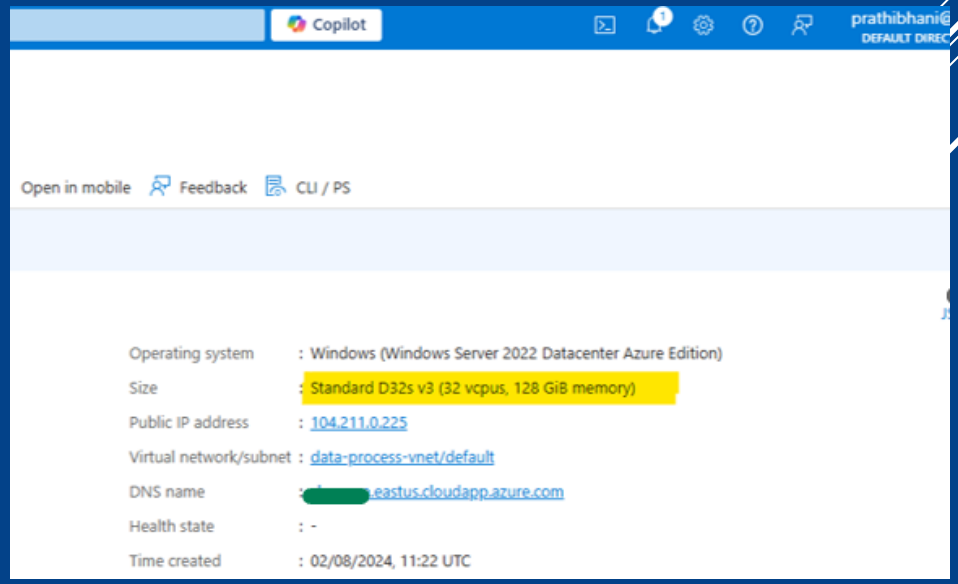
CNN	Restnet	VGG16
		
		

MODEL DEPLOYMENT &FUTURE WORK



MODEL DEPLOYMENT &FUTURE WORK

- Data quality Improvement
- Model improvement
- Improve efficiency



THANK YOU

COMMENTS & FEEDBACK