Brain Tumor

Nature Inspired computation

Presentation by **Bosy / Rofida**

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Dataset Overview

Statistics

- **Total Images:** 7,025 MRI Scans
- **Classes:** Glioma, Meningioma, Pituitary, No Tumor
- **Source:** Kaggle Brain Tumor MRI Dataset
- **Split:** 80% Training / 20% Validation

Preprocessing

- **Resizing:** Uniform 224x224 pixels
- **Normalization:** Rescaled to [0, 1] range
- **Augmentation:**
  - Random Rotations (±15°)
  - Zooming (±10%)
  - Horizontal Flipping

Baseline Model & Search Space

Architecture

MobileNetV2

Selected for efficiency and strong performance on image classification via transfer learning.

Search Space

Learning Rate: [1e-3, 1e-4, 5e-5]

Dense Units: [128, 256, 512]

Dropout: [0.3, 0.4, 0.5]

Constraints

Epochs: 3

Iterations: 7

Limited computational resources required efficient search strategies.

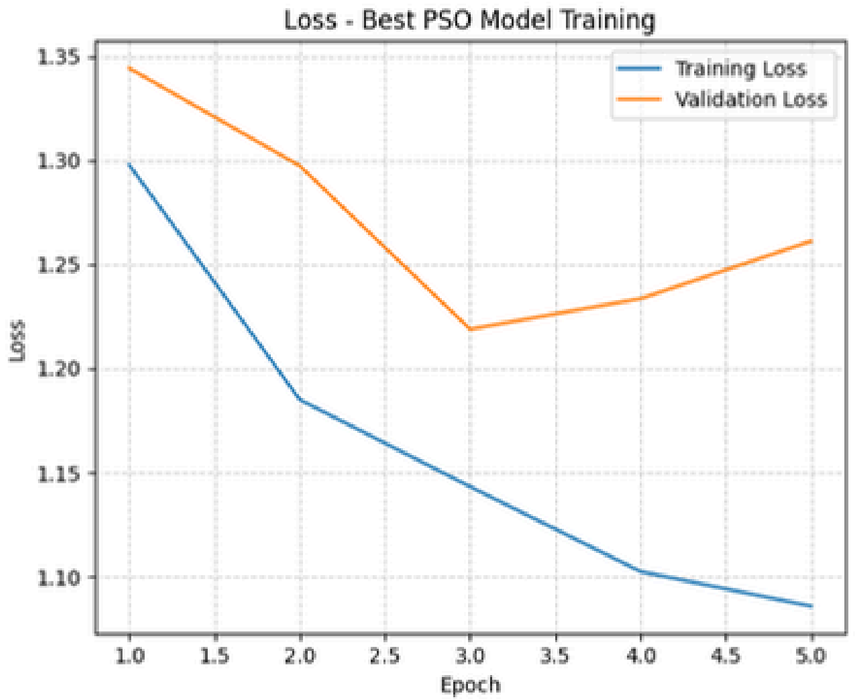
1.Particle Swarm

Best Configurations:
lr=0.000346
dropout=0.190
'dense_units': 256

Validation Accuracy:0.5478

Computation Cost: 4842.00 sec

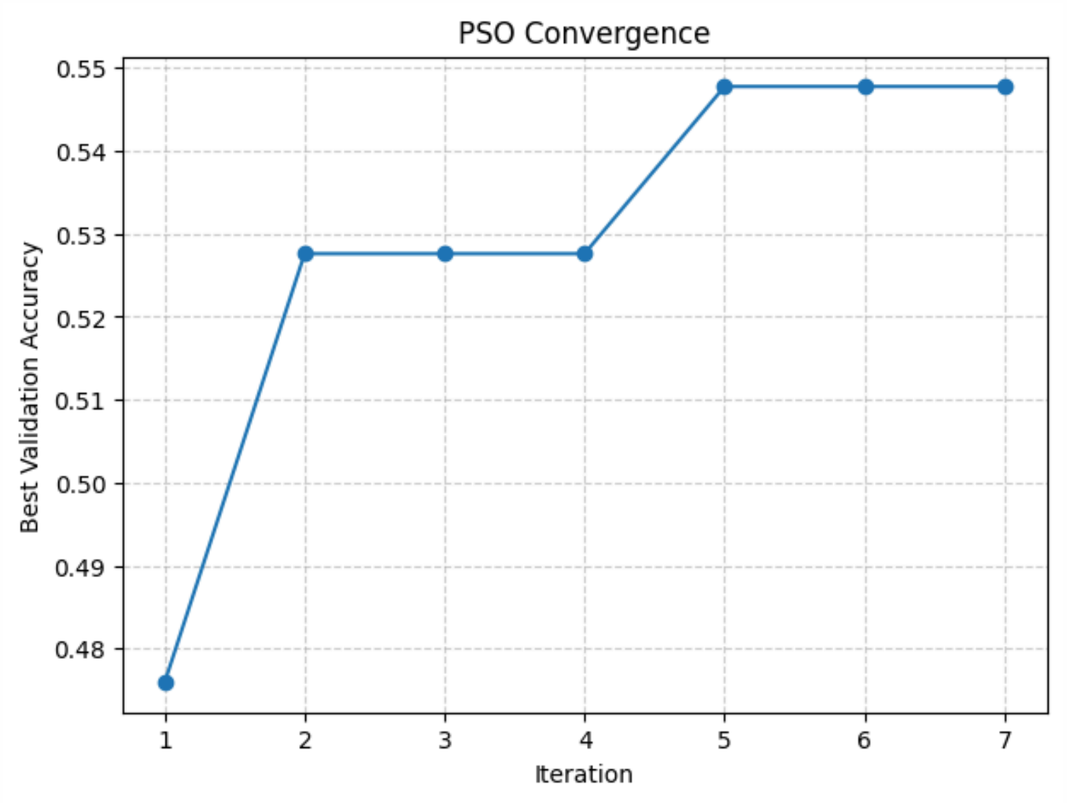
1.Particle Swarm

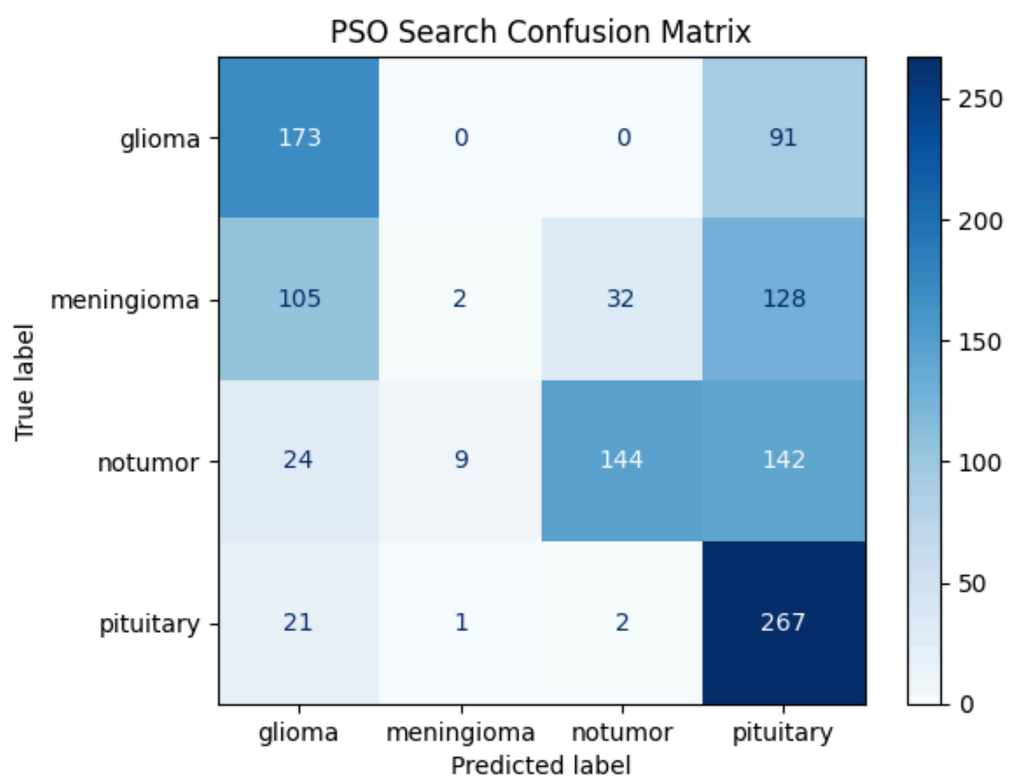


Max Validation Accuracy: 0.4320771396160126

Min Validation Loss: 1.252106189727832

1.Particle Swarm



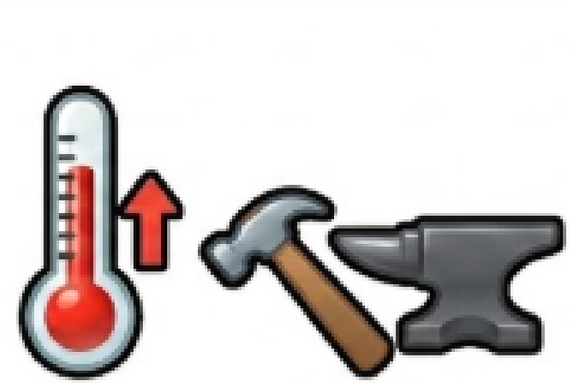


2.Simulated Annealing (SA)

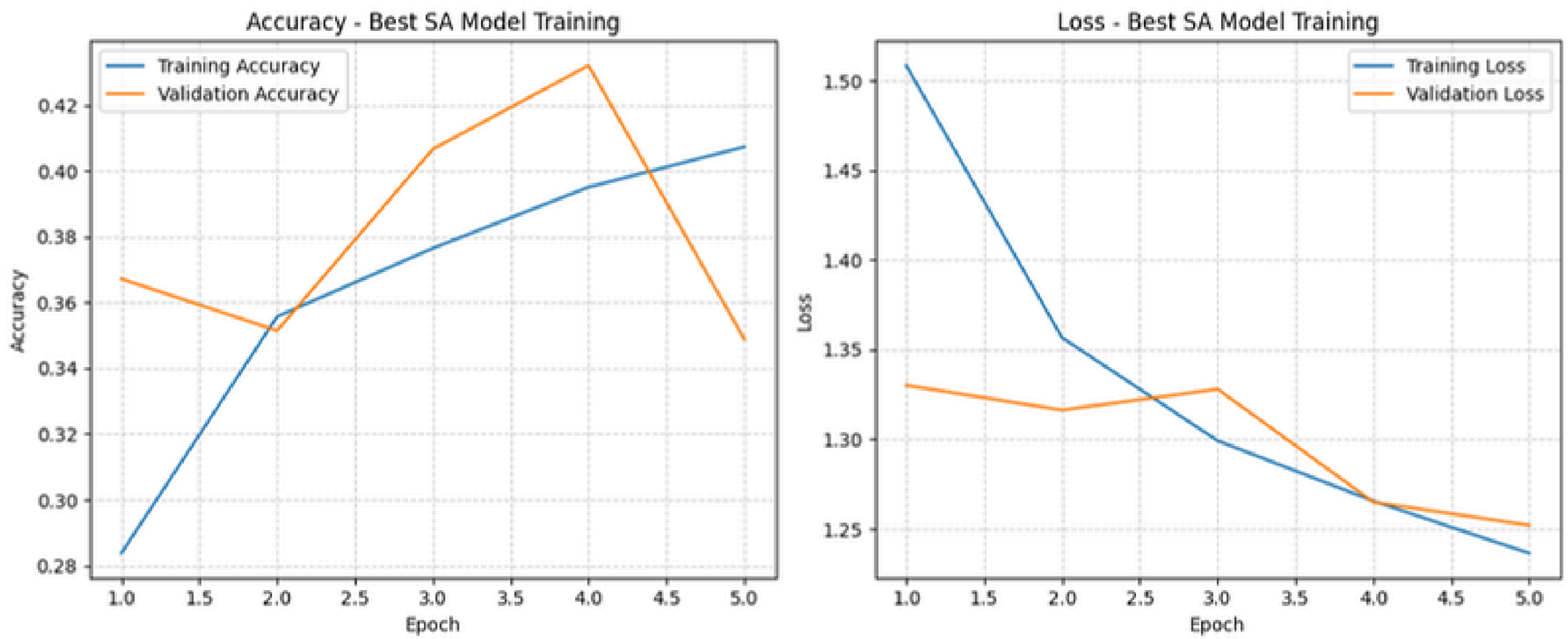
Best Configurations:
'lr': 5e-05
'dense_units': 512
'dropout': 0.3

Validation Accuracy: 0.5346

Computation Cost: 1884.11 sec

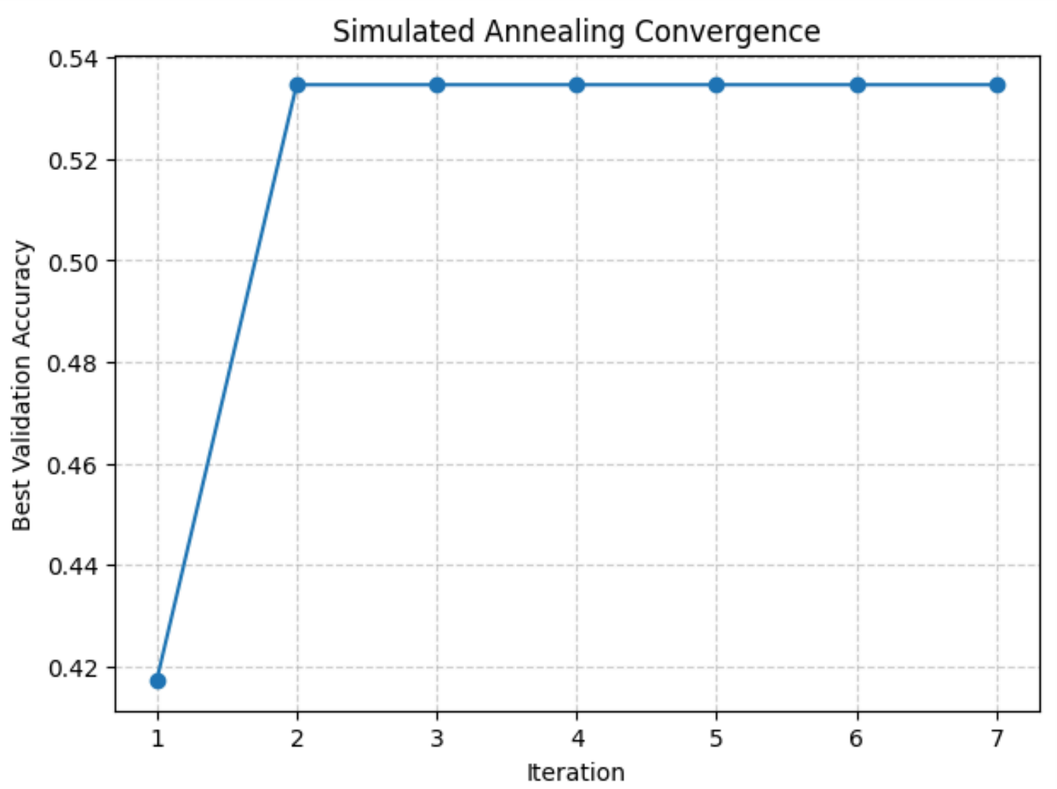


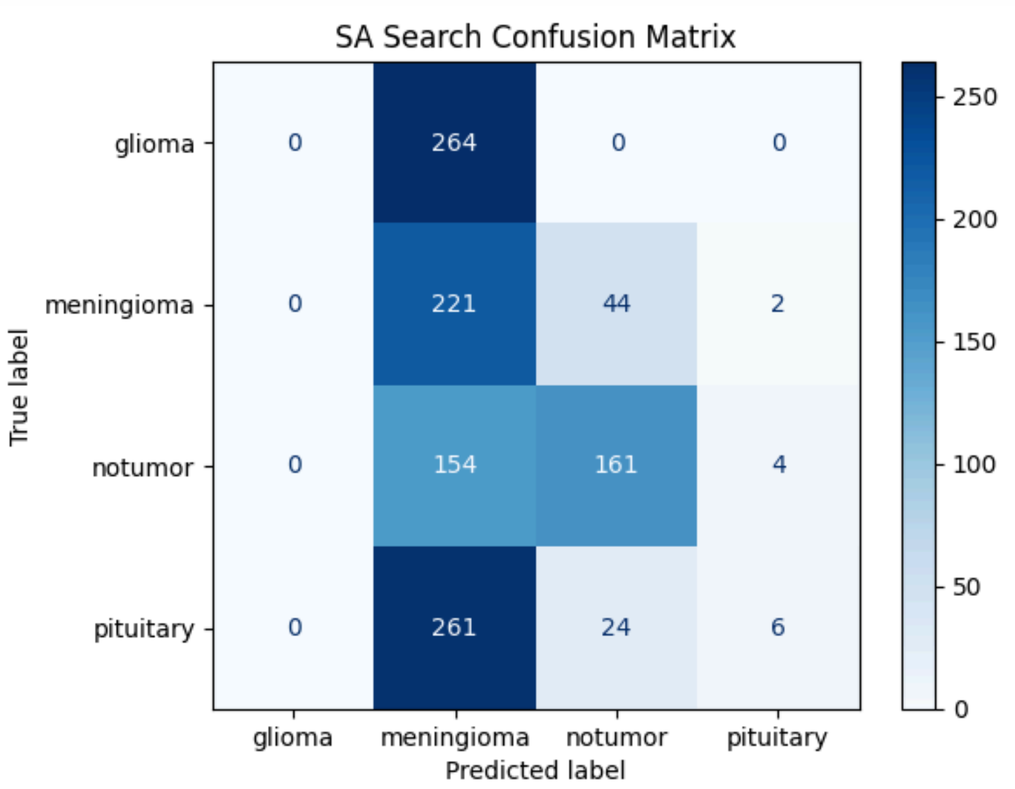
2.Simulated Annealing (SA)



Max Validation Accuracy: 0.4320771396160126
Min Validation Loss: 1.2521061897277832

2.Simulated Annealing (SA)



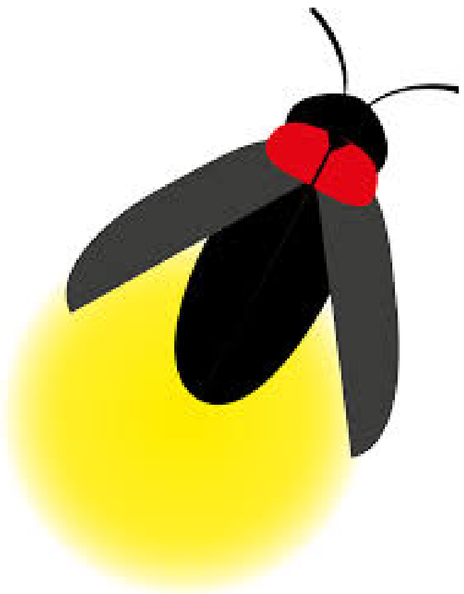


3. FireFly

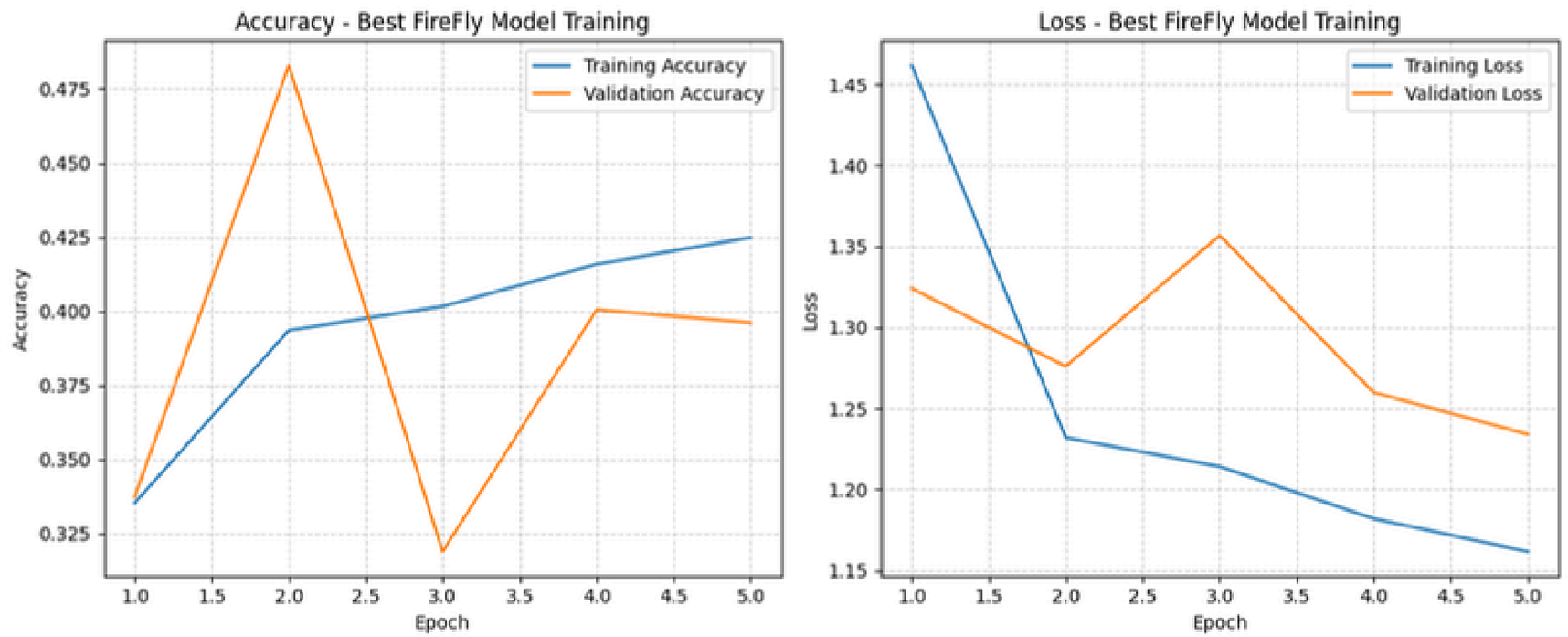
Best Configurations:
'lr': 0.001
'dense_units': 512
'dropout': 0.5

Validation Accuracy: 0.5284838080406189

Computation Cost: 8747.93 sec



3. FireFly



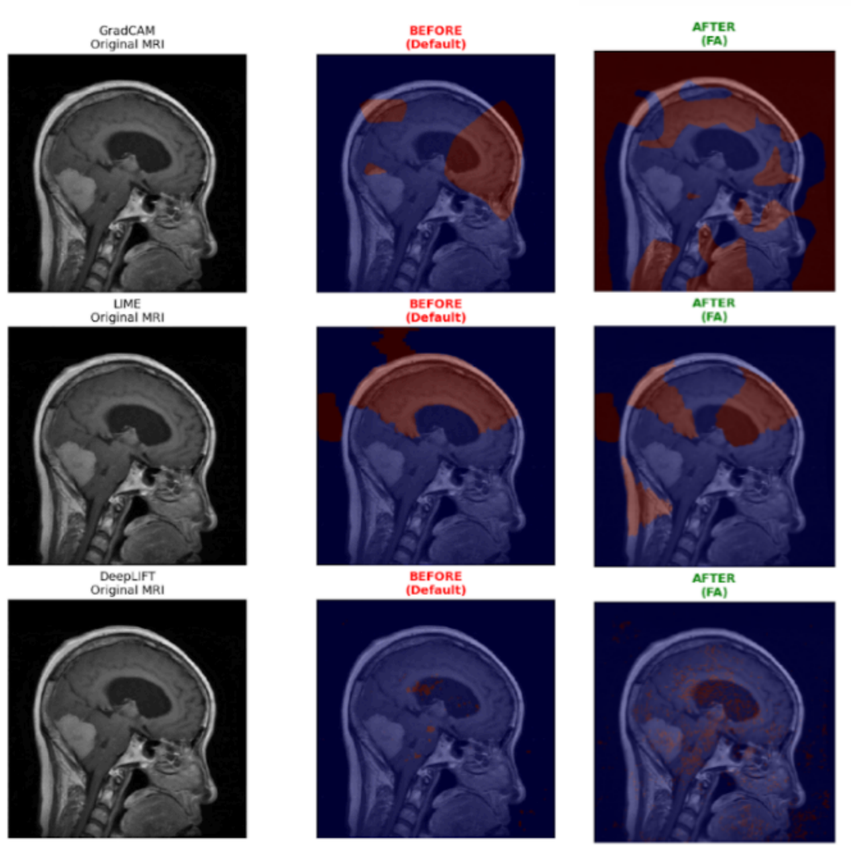
Max Validation Accuracy: 0.4829097390174866

Min Validation Loss: 1.233982801437378

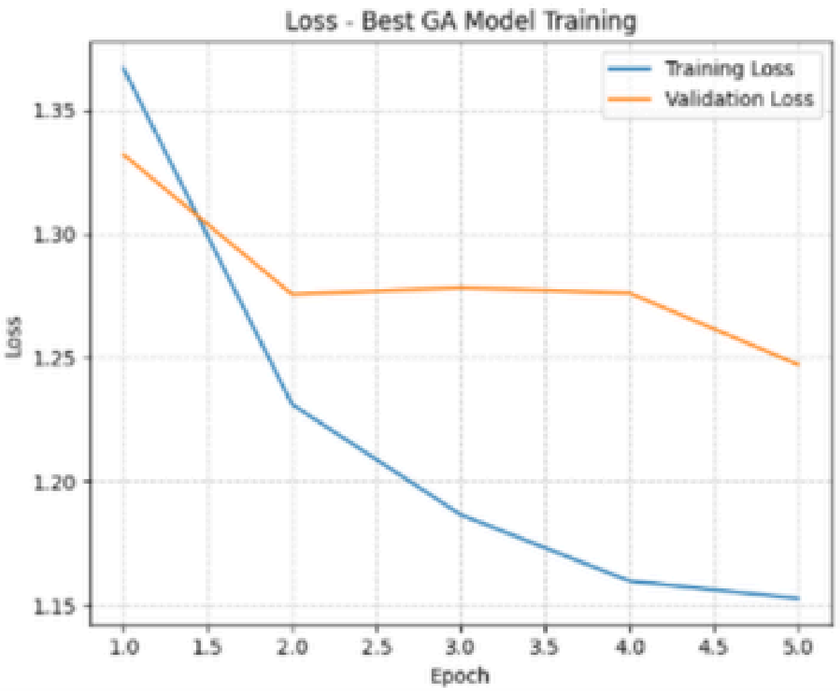
3. FireFly - XAI

Effect of The Optimization Algorithm

- **FA (Firefly)** Often sharpens or intensifies certain tumor regions, making the saliency more focused.

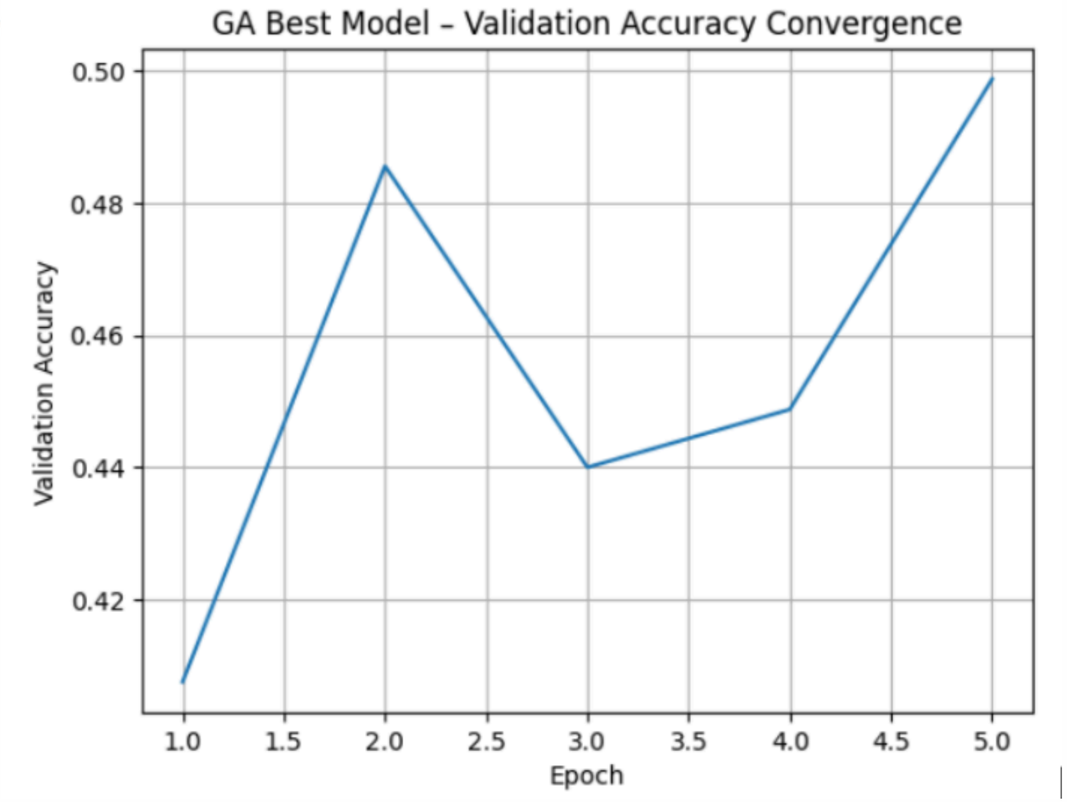


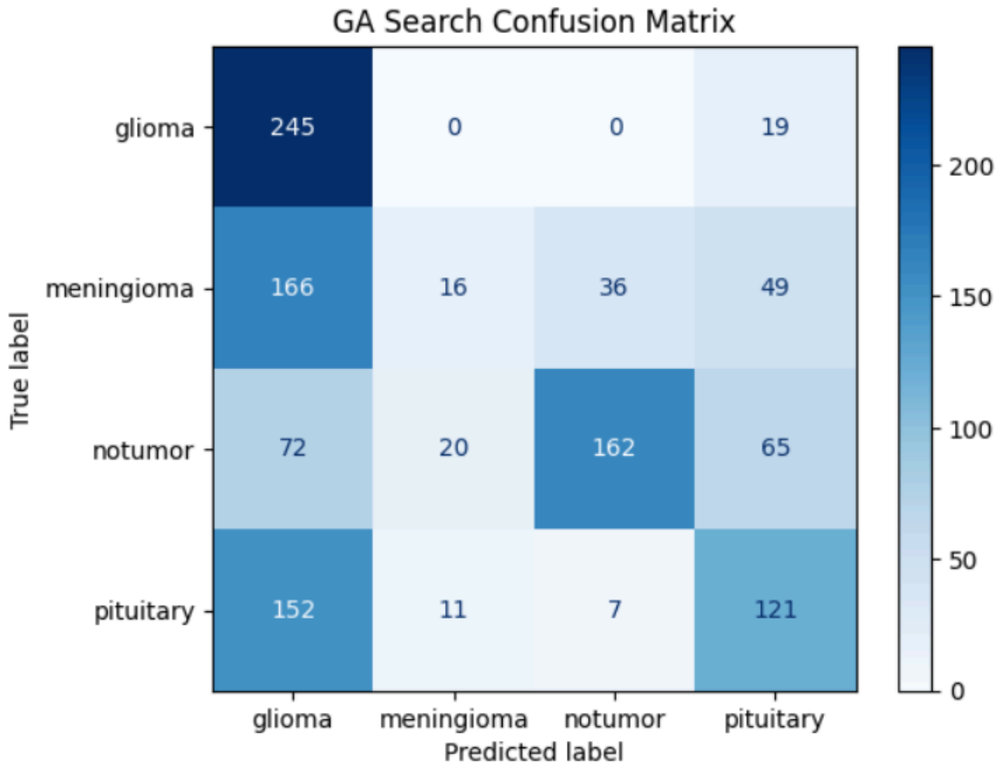
4-Genetic Algorithm



- Max Validation Accuracy: 0.419
- Min Validation Loss: 1.247

4-Genetic Algorithm



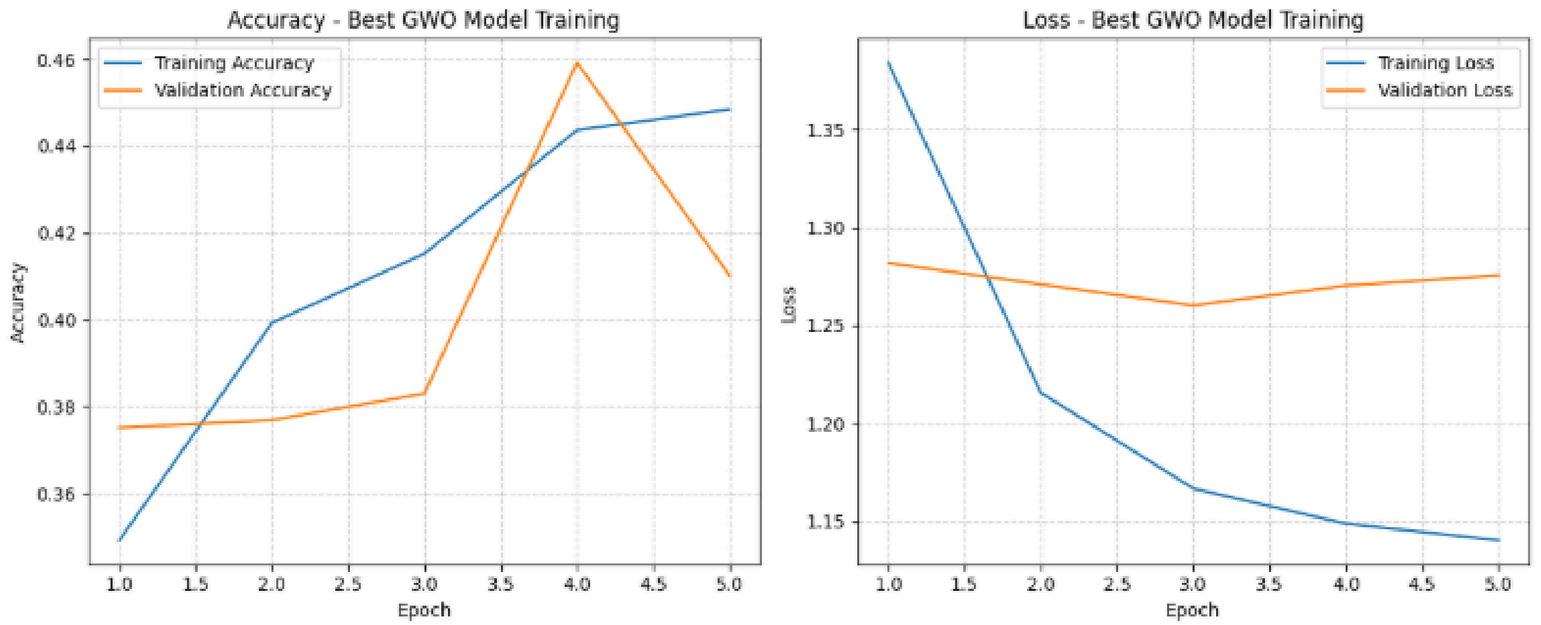


5-Grey Wolf

Best Configurations:
'lr': 0.001
'dense_units': 256
'dropout': 0.4
Validation Accuracy: 0.546012282371521

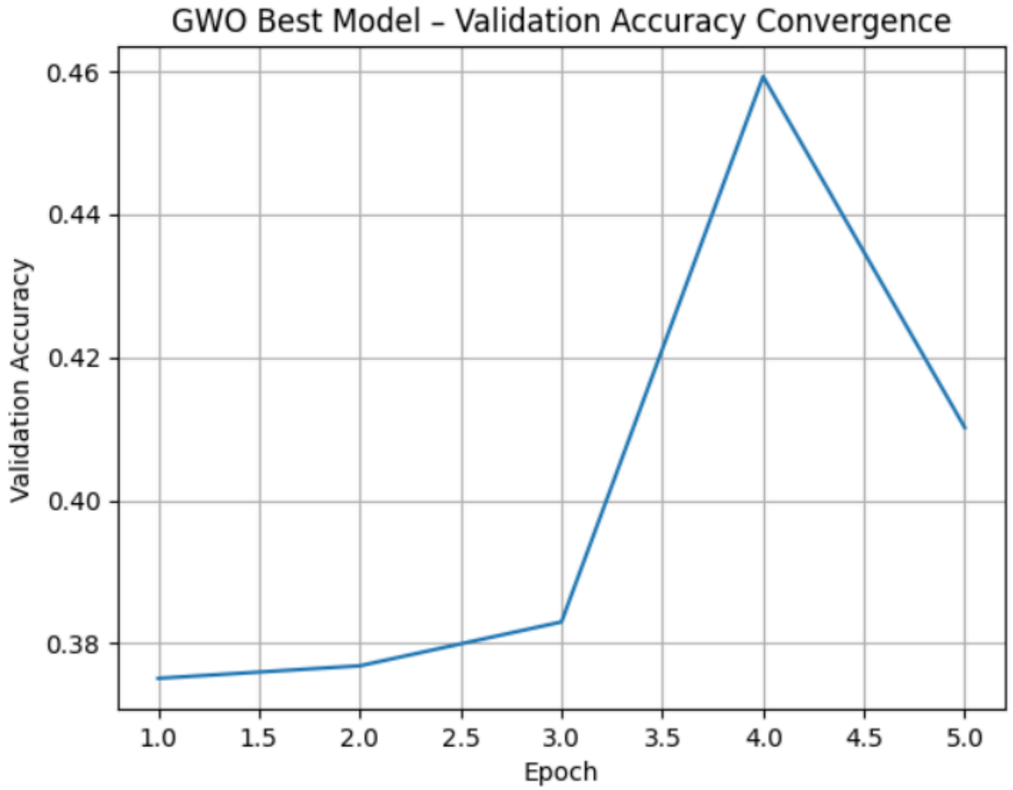
Computation Cost: 9124.43 sec

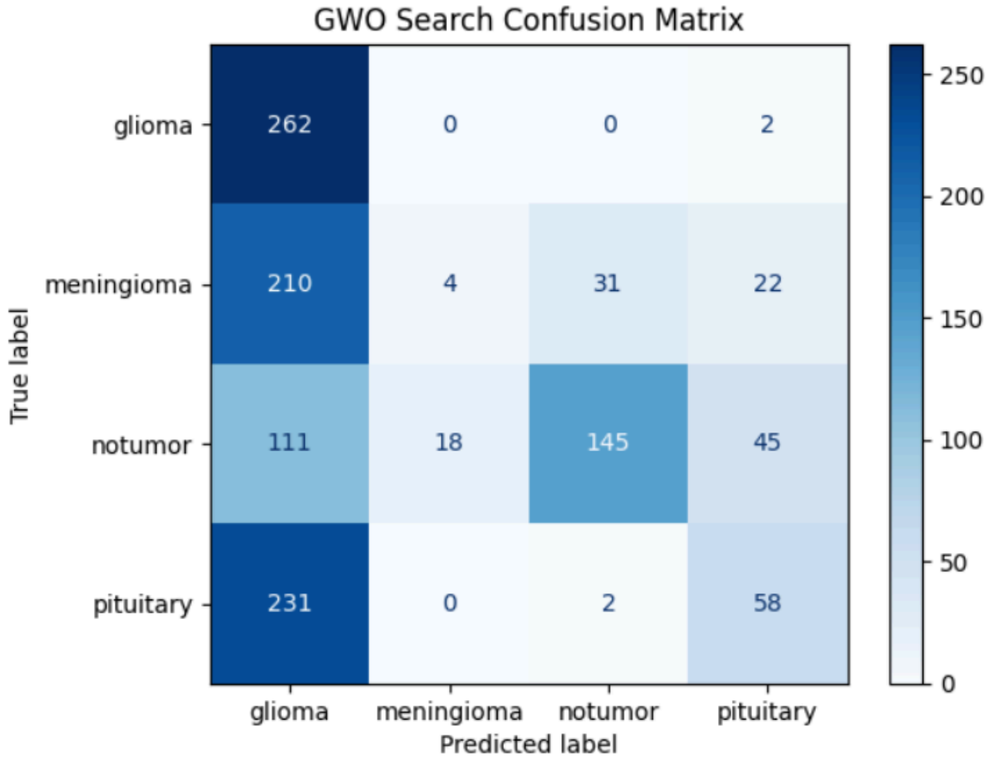
5-Grey Wolf



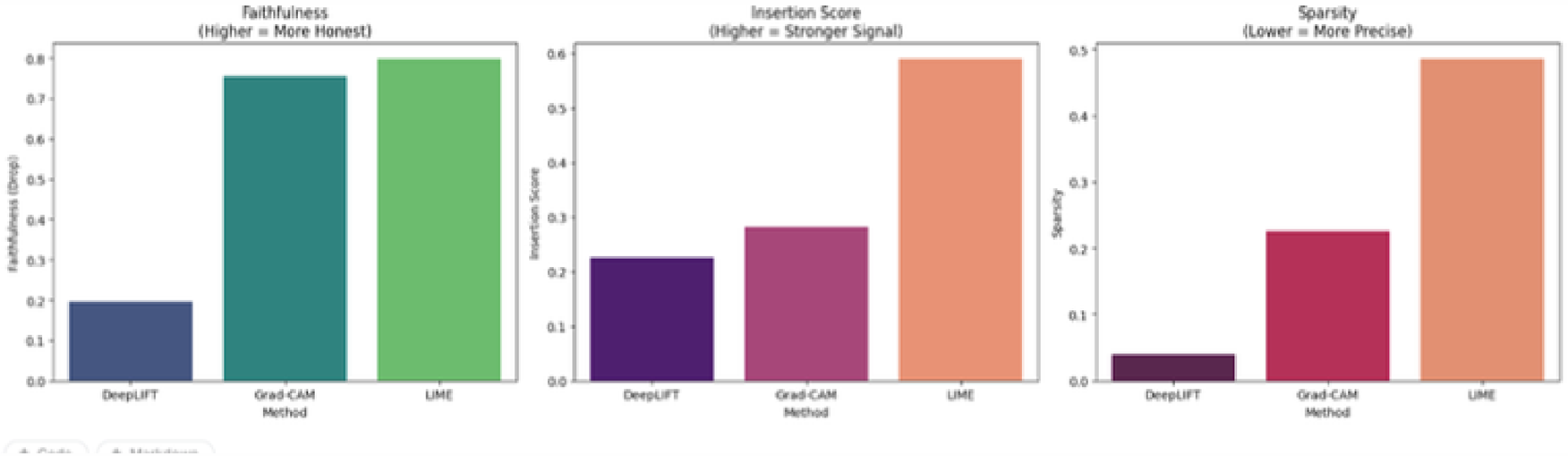
Max Validation Accuracy: 0.45924627780914307
Min Validation Loss: 1.2601633071899414

5-Grey Wolf


GWO Best Model – Validation Accuracy Convergence
Validation Accuracy
0.46
0.44
0.42
0.40
0.38
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
Epoch


GWO Search Confusion Matrix
True label
glioma
meningioma
notumor
pituitary
262
0
0
2
210
4
31
22
111
18
145
45
231
0
2
58
glioma
meningioma
notumor
pituitary
Predicted label
250
200
150
100
50
0

5-Grey Wolf - XAI



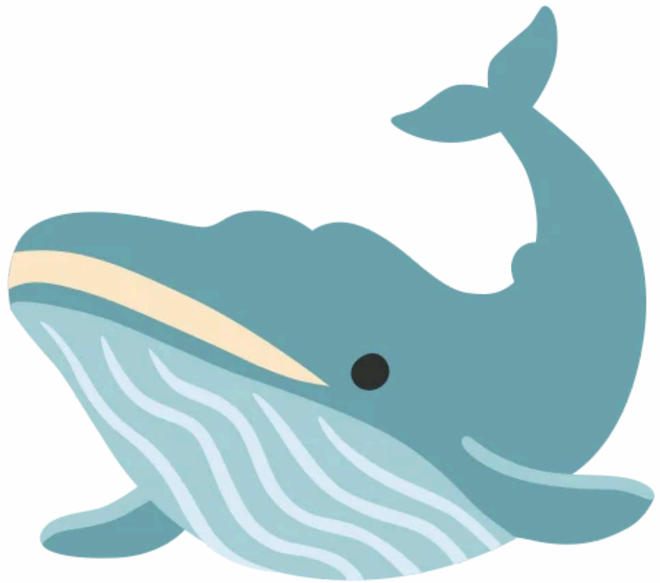
Method	Faithfulness (Drop)	Insertion Score	Sparsity
DeepLIFT	0.196078	0.225534	0.039021
Grad-CAM	0.754962	0.281332	0.225161
LIME	0.797095	0.588902	0.485280

6. Whale

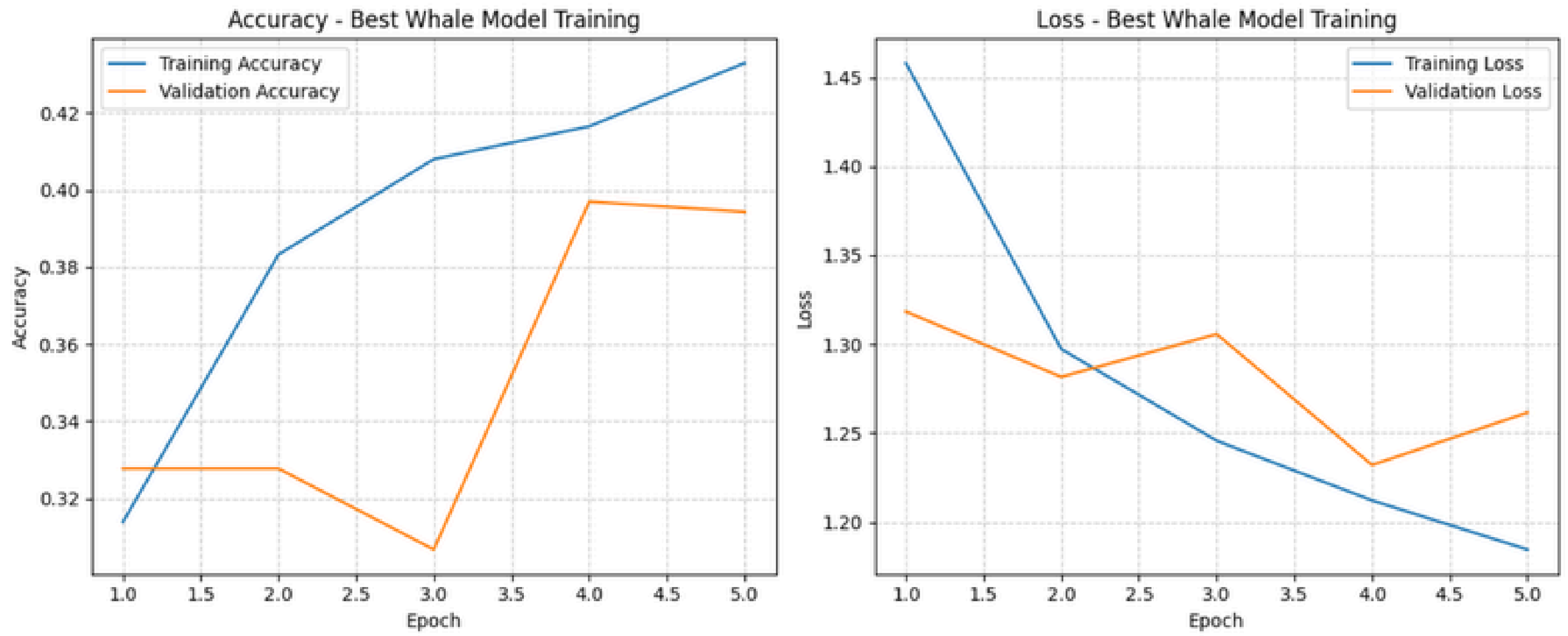
Best Configurations:
'lr': 0.0001
'dense_units': 512
'dropout': 0.3

Validation Accuracy:0.5478

Computation Cost:9397.30 sec

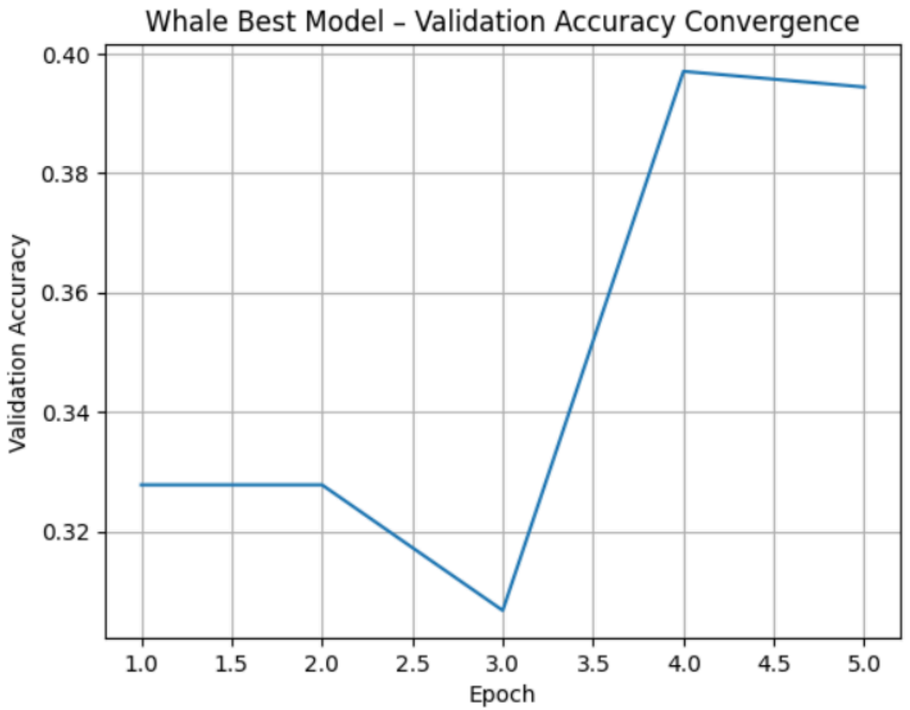


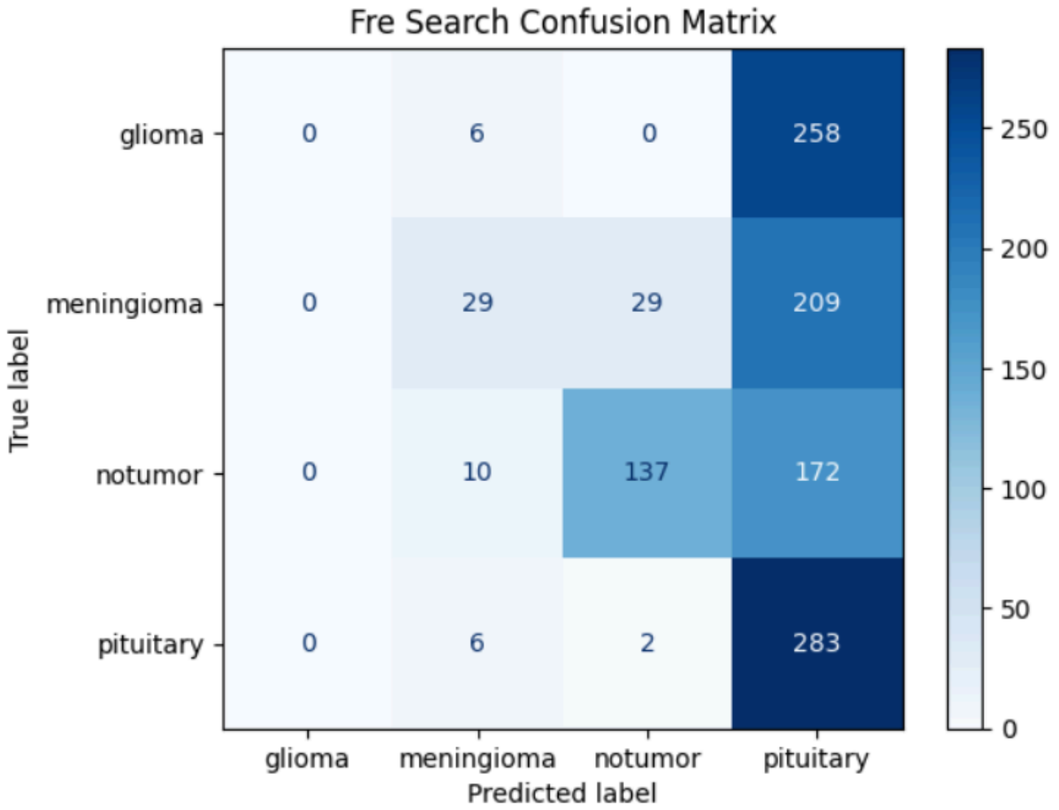
6. Whale



Max Validation Accuracy: 0.397020161151886
Min Validation Loss: 1.2320746183395386

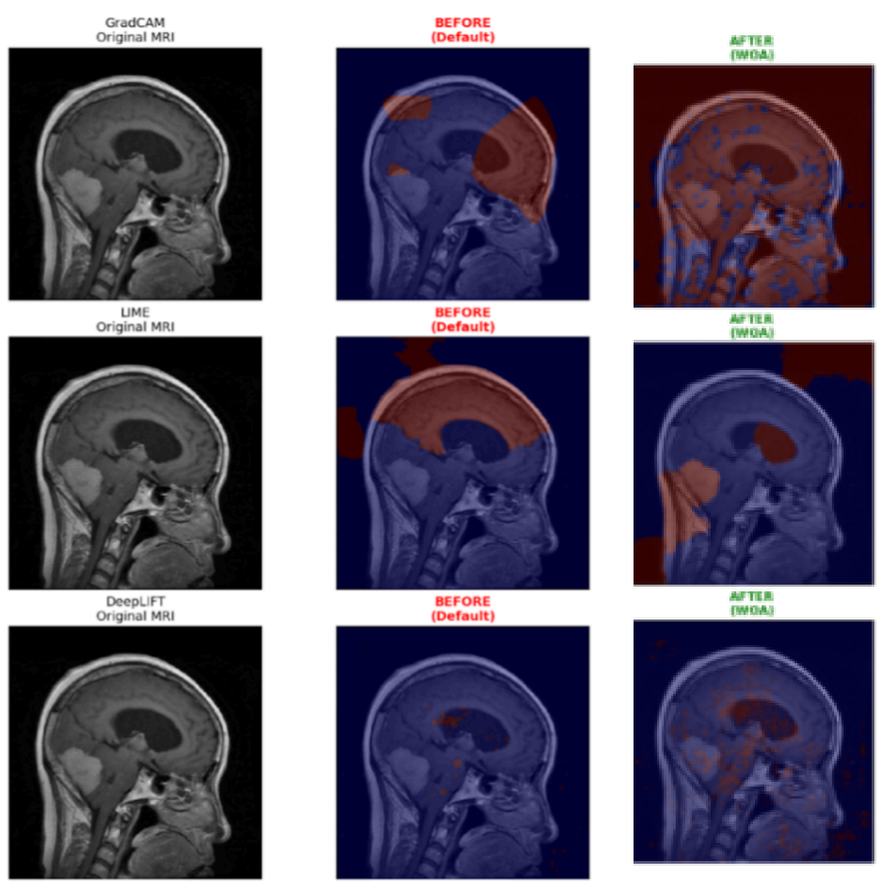
6. Whale


Whale Best Model – Validation Accuracy Convergence
Validation Accuracy
Epoch
0.40
0.38
0.36
0.34
0.32
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0


Fre Search Confusion Matrix
True label
Predicted label
glioma
meningioma
notumor
pituitary
0
6
0
258
0
29
29
209
0
10
137
172
0
6
2
283
250
200
150
100
50
0

6. Whale - XAI

- **WOA (Whale):** Tends to smooth and balance the highlighted areas, reducing noise.



FireFly &WOA Parameters

GradCAM

Optimizer	Faithfulness	Layer Index (P1)	Intensity Threshold (P2)	Sigma (Blur) (P3)	Num Samples (P1)
Firefly (FA)	0.0447	30.0	0.4248	—	1.9169
Whale (WOA)	0.0732	33.0	0.5679	—	1.3199

LIME

Optimizer	Faithfulness	Num Samples (P1)	Compactness (P2)	N-Segments (P3)
Firefly (FA)	−0.0372	54.7043	18.9573	29.5472
Whale (WOA)	−0.0441	100.0000	20.0000	30.0000

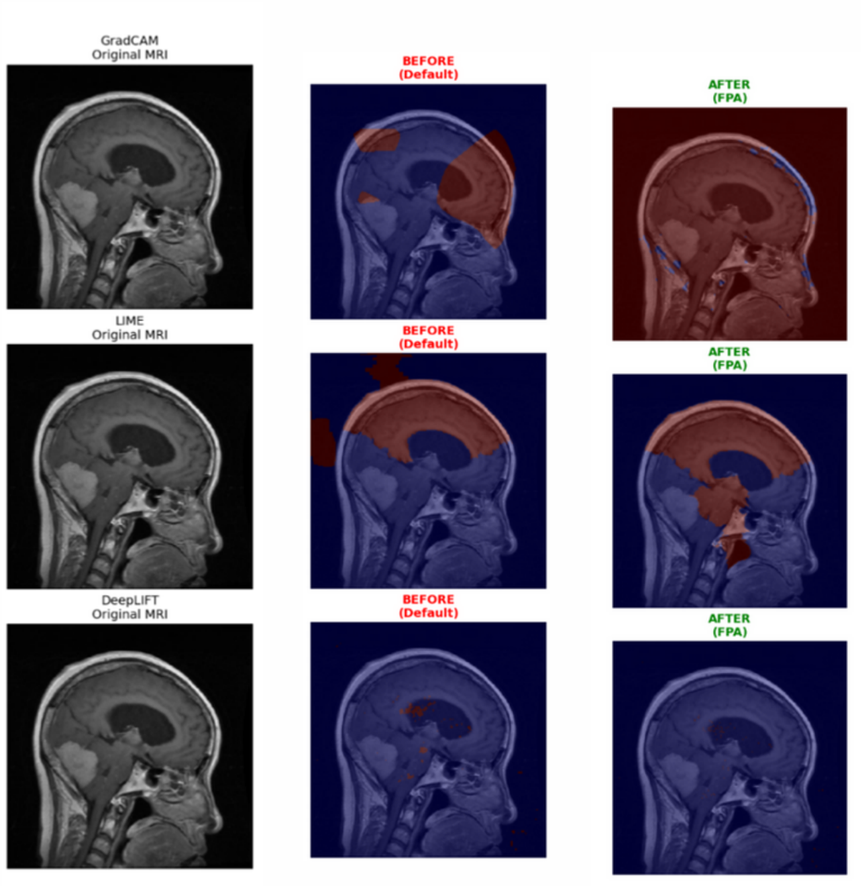
FireFly &WOA Parameters

DeepLIFT

Optimizer	Faithfulness	Threshold (P1)	Sigma (Blur) (P2)	N/A (P3)
Firefly (FA)	0.0325	—	0.5701	0.3704
Whale (WOA)	0.0323	—	0.5968	0.1000

Layer Index, Threshold, Sigma → control how focused and smooth the saliency maps are. **Num Samples, Compactness, N-Segments** → affect how LIME segments and explains the image.

8.FLOWER POLLINATION (FPA)



FPA (Flower): Can expand or redistribute the highlighted regions, sometimes capturing broader tumor boundaries.

Best Parameters :

GRAD-CAM: [Layer Index: 38, Threshold: 0.6105, Sigma: 1.54]

LIME : [Samples: 20, Compactness: 20.0, Segments: 28]

DeepLIFT: [Threshold: 0.3031, Sigma: 0.1]

Comparative Evaluation (5 Iterations)

FPA for GradCAM: Score = 0.2381

7. TABU

Applied on SA and PSO to Optimize Their parameters

```
FINAL RESULTS
TABU → PSO: {'c1': 1.0, 'c2': 1.0, 'w': 0.4} 0.48466256260871887
TABU → SA : {'initial_temp': 5.0, 'cooling_rate': 0.9} 0.46888694167137146
```

Conclusion

Model Optimization Phase

- **Best Performers:** Whale Optimization (WOA) and Particle Swarm (PSO) achieved the highest validation accuracy (~54.7%).
- **Challenges:** Simulated Annealing and Genetic Algorithm failed due to mode collapse (predicting a single class instead of learning features).

Explainable AI (XAI) Tuning

- **Best Performer:** The FA Algorithm outperformed all others in optimizing interpretability parameters.
- **Impact:** Produced the highest scores ensuring accurate and focused visual explanations.