# Regularization Report

- **Twice batch normalization that overfitted on pituitary class I think images are so dark or light .**

	precision	recall	f1-score	support
glioma	0.00	0.00	0.00	64
meningioma	0.18	0.05	0.08	61
notumor	0.75	0.65	0.69	77
pituitary	0.34	0.98	0.50	61
accuracy			0.43	263
macro avg	0.31	0.42	0.32	263
weighted avg	0.34	0.43	0.34	263

Loss (Lower Means Better)


Accuracy (Higher Means Better)
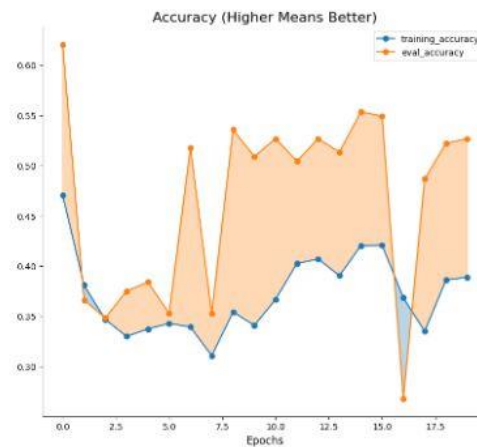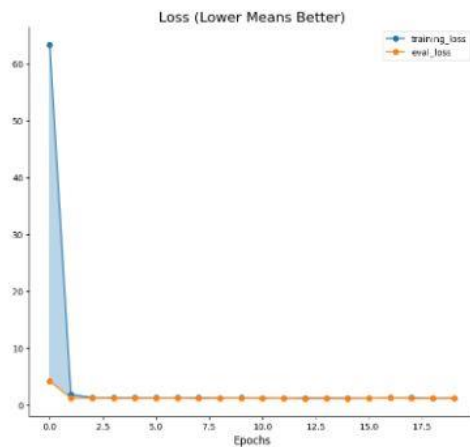
- **Just one batch normalization layer for second convolotion overfitting dosen't occuers but accuracy is less.**

	precision	recall	f1-score	support
glioma	0.68	0.78	0.72	64
meningioma	0.51	0.43	0.46	61
notumor	0.86	0.87	0.86	77
pituitary	0.90	0.89	0.89	61
accuracy			0.75	263
macro avg	0.74	0.74	0.74	263
weighted avg	0.74	0.75	0.74	263
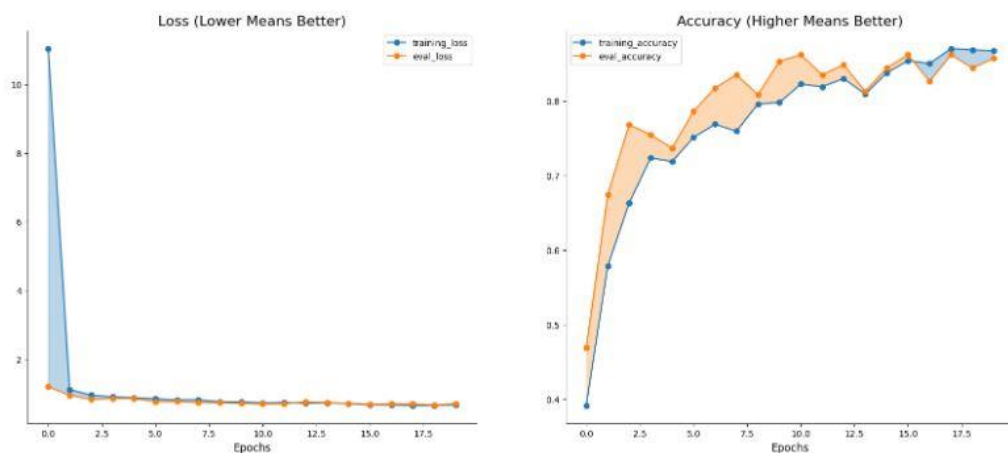
- **Also by without drpout and batch normalization is not good enough .**

	precision	recall	f1-score	support
glioma	0.90	0.56	0.69	64
meningioma	0.49	0.79	0.61	61
notumor	0.85	0.90	0.87	77
pituitary	0.89	0.66	0.75	61
accuracy			0.73	263
macro avg	0.78	0.73	0.73	263
weighted avg	0.79	0.73	0.74	263
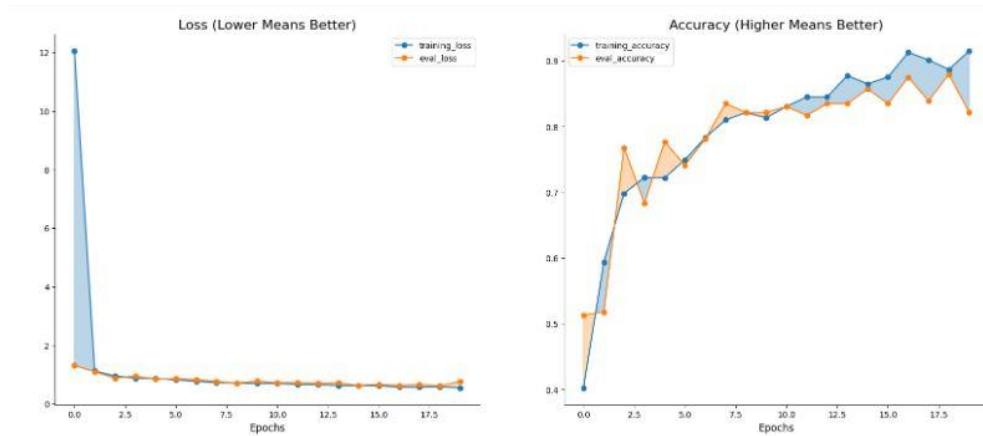
- **By use one dropout with probability 0.5 I got the best result**

	precision	recall	f1-score	support
glioma	0.82	0.70	0.76	64
meningioma	0.72	0.75	0.74	61
notumor	0.96	0.87	0.91	77
pituitary	0.80	0.97	0.87	61
accuracy			0.83	263
macro avg	0.82	0.82	0.82	263
weighted avg	0.83	0.83	0.82	263
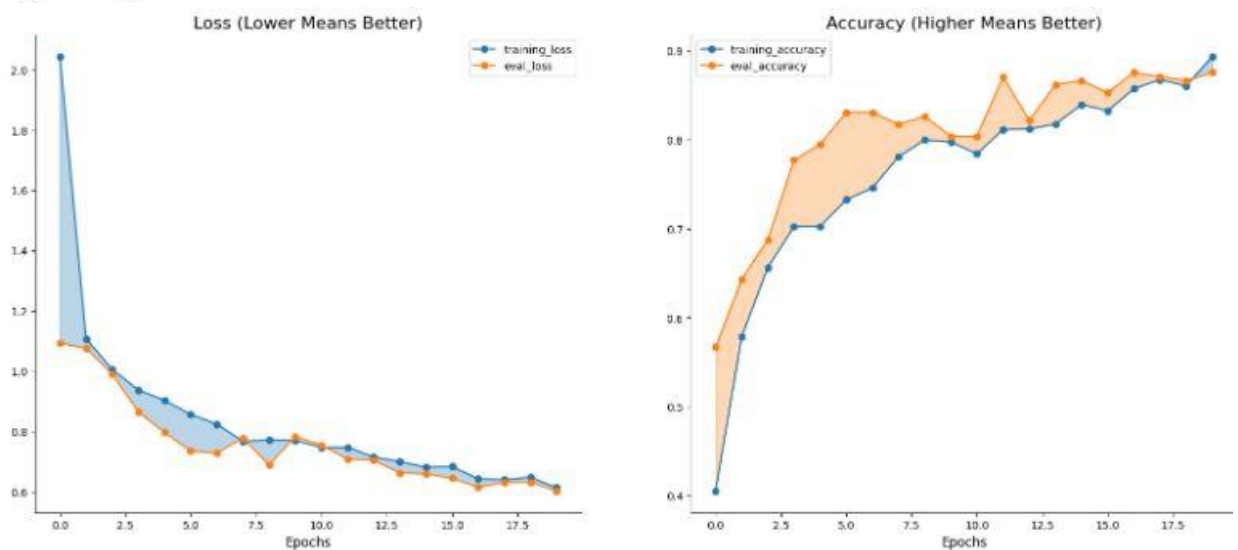
Final analysis

	precision	recall	f1-score	support
glioma	0.79	0.80	0.79	60
meningioma	0.73	0.62	0.67	64
notumor	0.91	0.93	0.92	72
pituitary	0.86	0.94	0.90	67
accuracy			0.83	263
macro avg	0.82	0.82	0.82	263
weighted avg	0.82	0.83	0.83	263
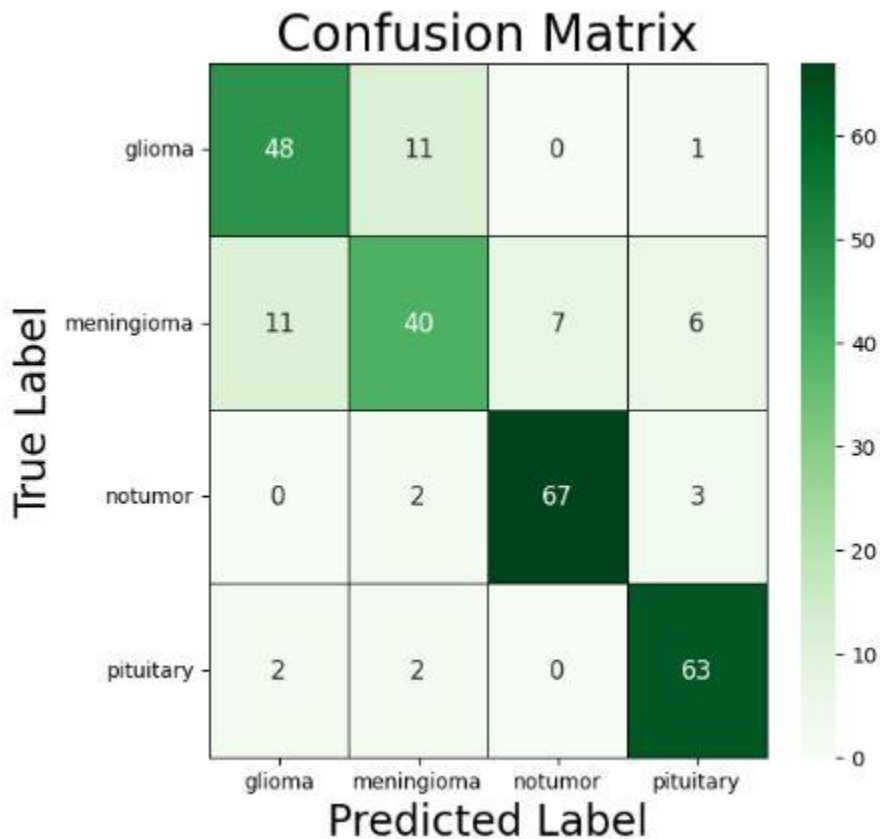
As we see final accuracy by f1-score is 0.83 .

Resaon of lower aaccuracy is meningioma class that confused by gioma class because simmilarity between some samples.

Notumur is so good because data of this part is so visible and ditectable.
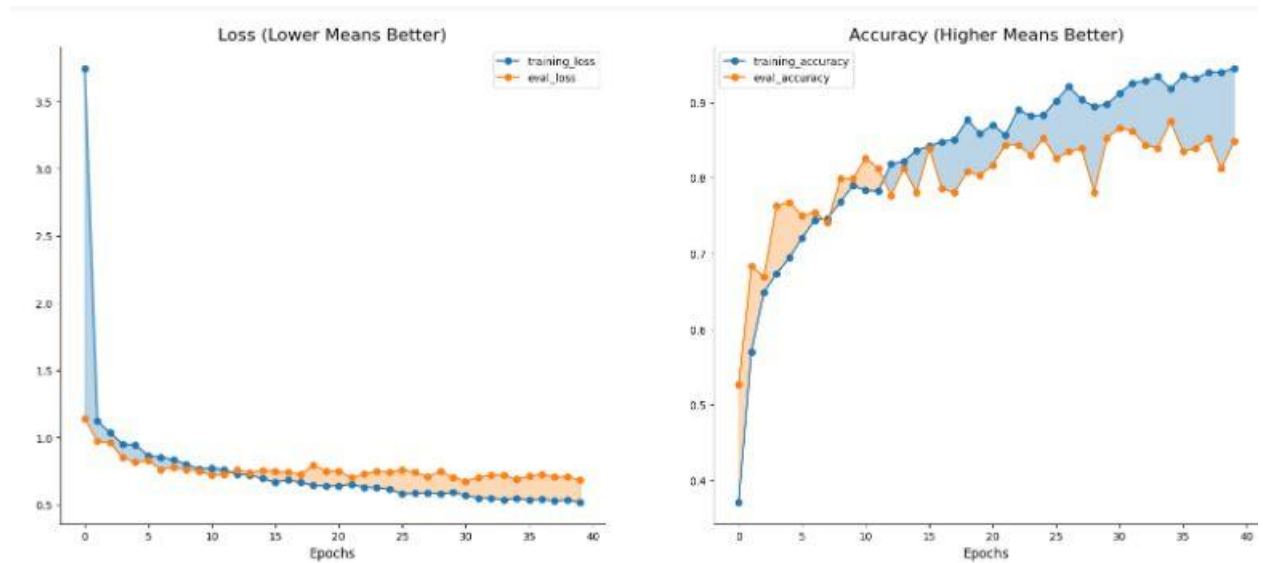
Loss curves shows validation is a little worse than train because it use for check performance , not for learning.

Curves for train and validation are near and loss for train and validation is low s we can say we have no bias and variance so we don't have overfitting and underfitting.