

Raport

In cadrul urmatoarei parti a proiectului am realizat urmatoarele:

La cerinta 2.1, am realizat impartirea setului de date de antrenare folosind StratifiedKFold, unde am selectat parametrul de shuffle sa fie True pentru a putea realiza cross-entropy. Functia StratifiedKFold, mi-a impartit atat train_x cat si train_y in cate 5 folduri egal distribuite, dupa care am selectat toate combinatiile posibile printre-un for in asa fel incat sa am un fold de validare iar restul k-1 sa fie pentru antrenare. Prima oara am antrenat modelul classic, fara sa mai impart in 5 folduri egale, si am observat o imbunatatire a invatarii modelului in momentul in care am trecut de la antrenarea clasica la cea impartita pe folduri, in sensul ca Loss-ul incepea sa scada din ce in ce in ce mai mult pentru fiecare fold in parte. Am generat plot-uri pentru fiecare fold:

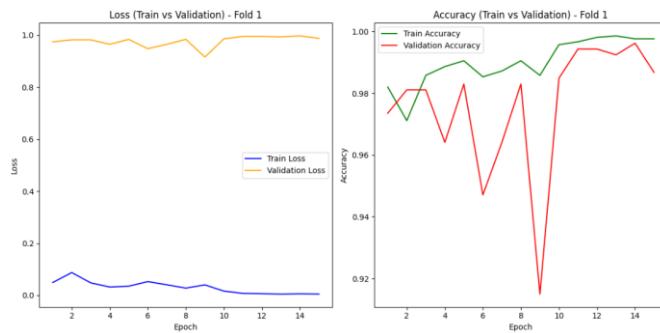
Aceasta este media si deviatia standard metricilor foldurilor :

```
Precision: Mean = 0.9992, Std = 0.0010
Recall: Mean = 0.9992, Std = 0.0010
F1-score: Mean = 0.9992, Std = 0.0010
Accuracy: Mean = 0.9992, Std = 0.0010
```

Am evaluat performanta pe setul de testare(Am avut Adam cu learning_rate=0.001 si CrossEntropyLoss() de la laboratorul 4):

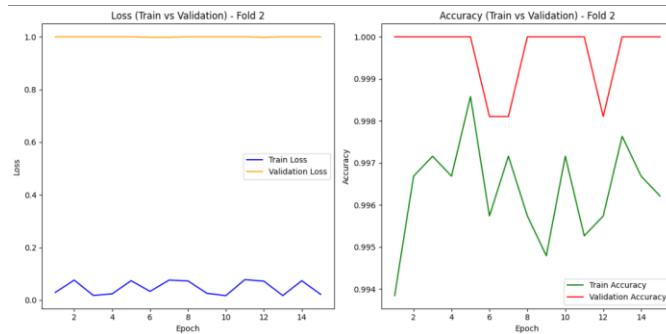
Pentru fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9583	0.2300	0.3710	100
meningioma_tumor	0.7852	0.9217	0.8480	115
no_tumor	0.5330	1.0000	0.6954	105
pituitary_tumor	0.9130	0.6000	0.7241	105
accuracy			0.6988	425
macro avg	0.7974	0.6879	0.6596	425
weighted avg	0.7952	0.6988	0.6674	425



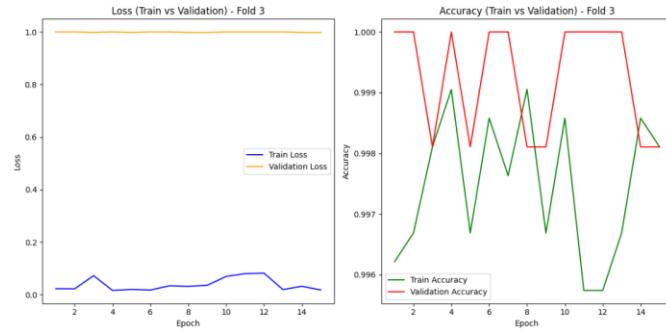
Pentru fold2

	precision	recall	f1-score	support
glioma_tumor	0.8696	0.2000	0.3252	100
meningioma_tumor	0.8000	0.9043	0.8490	115
no_tumor	0.5097	1.0000	0.6752	105
pituitary_tumor	0.9242	0.5810	0.7135	105
accuracy			0.6824	425
macro avg	0.7759	0.6713	0.6407	425
weighted avg	0.7753	0.6824	0.6493	425



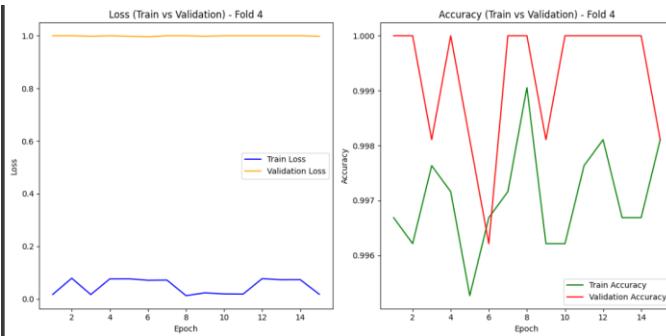
Pentru fold3

	precision	recall	f1-score	support
glioma_tumor	0.9545	0.2100	0.3443	100
meningioma_tumor	0.8455	0.9043	0.8739	115
no_tumor	0.4976	1.0000	0.6646	105
pituitary_tumor	0.9275	0.6095	0.7356	105
accuracy			0.6918	425
macro avg	0.8063	0.6810	0.6546	425
weighted avg	0.8055	0.6918	0.6634	425



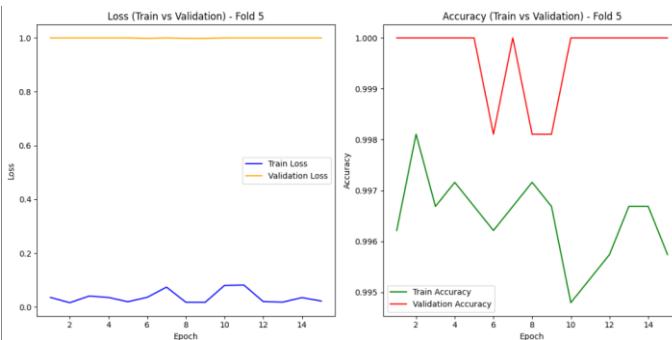
Pentru fold4

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.7681	0.9217	0.8379	115
no_tumor	0.5330	1.0000	0.6954	105
pituitary_tumor	0.9155	0.6190	0.7386	105
accuracy			0.6918	425
macro avg	0.7910	0.6802	0.6436	425
weighted avg	0.7886	0.6918	0.6522	425



Pentru fold5

	precision	recall	f1-score	support
glioma_tumor	0.9231	0.2400	0.3810	100
meningioma_tumor	0.8077	0.9130	0.8571	115
no_tumor	0.5417	0.9905	0.7003	105
pituitary_tumor	0.8831	0.6476	0.7473	105
accuracy			0.7082	425
macro avg	0.7889	0.6978	0.6714	425
weighted avg	0.7878	0.7082	0.6792	425



Nr fold	Acuratete	Metrici		
		precision	recall	f1-score
1	69.88	0.9583 0.7852 0.5330 0.9130	0.2300 0.9217 1.0000 0.6000	0.3710 0.8480 0.6954 0.7241
2	68.24	0.8696 0.8000 0.5097 0.9242	0.2000 0.9043 1.0000 0.5810	0.3252 0.8490 0.6752 0.7135
3	69.18	0.9545 0.8455 0.4976 0.9275	0.2100 0.9043 1.0000 0.6095	0.3443 0.8739 0.6646 0.7356

4	69.18	precision recall f1-score
		glioma_tumor 0.9474 0.1800 0.3025
		meningioma_tumor 0.7681 0.9217 0.8379
		no_tumor 0.5330 1.0000 0.6954
		pituitary_tumor 0.9155 0.6190 0.7386
5	70.82	precision recall f1-score
		glioma_tumor 0.9231 0.2480 0.3810
		meningioma_tumor 0.8077 0.9130 0.8571
		no_tumor 0.5417 0.9905 0.7003
		pituitary_tumor 0.8831 0.6476 0.7473

Pentru cerinta 2.2 mai intai am testat cu metodele de balansare a claselor si rezultatele sunt urmatoarele:

Fara penalizarea de ponderi dar fara augmentari pentru antrenarea clasica fara folduri:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7171	0.9478	0.8165	115
no_tumor	0.6319	0.9810	0.7687	105
pituitary_tumor	0.8814	0.7027	0.7820	74
accuracy			0.7183	394
macro avg	0.7951	0.7054	0.6709	394
weighted avg	0.7844	0.7183	0.6704	394

Iar pentru rularea cu k-folduri am obtinut media metricilor:

```
Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

Evaluarea pe setul de testare

Pentru fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9545	0.2100	0.3443	100
meningioma_tumor	0.7171	0.9478	0.8165	115
no_tumor	0.6442	1.0000	0.7836	105
pituitary_tumor	0.9123	0.7027	0.7939	74
accuracy			0.7284	394
macro avg	0.8070	0.7151	0.6846	394
weighted avg	0.7946	0.7284	0.6836	394

Pentru fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9545	0.2100	0.3443	100
meningioma_tumor	0.7171	0.9478	0.8165	115
no_tumor	0.6478	0.9810	0.7803	105
pituitary_tumor	0.8852	0.7297	0.8000	74
accuracy			0.7284	394
macro avg	0.8012	0.7171	0.6853	394
weighted avg	0.7905	0.7284	0.6839	394

Pentru fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9545	0.2100	0.3443	100
meningioma_tumor	0.7124	0.9478	0.8134	115
no_tumor	0.6603	0.9810	0.7893	105
pituitary_tumor	0.8571	0.7297	0.7883	74
accuracy			0.7284	394
macro avg	0.7961	0.7171	0.6838	394
weighted avg	0.7872	0.7284	0.6832	394

Pentru fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9545	0.2100	0.3443	100
meningioma_tumor	0.7466	0.9478	0.8352	115
no_tumor	0.6398	0.9810	0.7744	105
pituitary_tumor	0.8615	0.7568	0.8058	74
accuracy			0.7335	394
macro avg	0.8006	0.7239	0.6899	394
weighted avg	0.7925	0.7335	0.6889	394

Pentru fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9545	0.2100	0.3443	100
meningioma_tumor	0.7365	0.9478	0.8289	115
no_tumor	0.6364	1.0000	0.7778	105
pituitary_tumor	0.9153	0.7297	0.8120	74
accuracy			0.7335	394
macro avg	0.8107	0.7219	0.6907	394
weighted avg	0.7987	0.7335	0.6891	394

Iar pentru antrenarea clasica fara k-folduri cu augmentari cu penalizari de ponderi:

	precision	recall	f1-score	support
glioma_tumor	0.8261	0.1900	0.3089	100
meningioma_tumor	0.6346	0.8689	0.7306	115
no_tumor	0.6346	0.9429	0.7586	105
pituitary_tumor	0.9153	0.7297	0.8120	74
accuracy			0.6878	394
macro avg	0.7526	0.6809	0.6526	394
weighted avg	0.7359	0.6878	0.6463	394

Un motiv pentru care ar putea fi putin mai mare este faptul ca este posibil ca, clasele majoritare sa fie favorizate ca o consecinta a functiei de pierdere cu penalizari pe weights. Aceasta este media metricilor foldurilor cu penalizare si augmentari dar cu clasele nebalansate

```
Precision: Mean = 0.9914, Std = 0.0169
Recall: Mean = 0.9913, Std = 0.0170
F1-score: Mean = 0.9913, Std = 0.0171
Accuracy: Mean = 0.9913, Std = 0.0170
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9130	0.2100	0.3415	100
meningioma_tumor	0.6755	0.8870	0.7669	115
no_tumor	0.6012	0.9619	0.7399	105
pituitary_tumor	0.9231	0.6486	0.7619	74
accuracy			0.6904	394
macro avg	0.7782	0.6769	0.6526	394
weighted avg	0.7625	0.6904	0.6508	394

Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9048	0.1900	0.3140	100
meningioma_tumor	0.7095	0.9130	0.7985	115
no_tumor	0.6061	0.9524	0.7407	105
pituitary_tumor	0.8500	0.6892	0.7612	74
accuracy			0.6980	394
macro avg	0.7676	0.6862	0.6536	394
weighted avg	0.7579	0.6980	0.6531	394

Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9130	0.2100	0.3415	100
meningioma_tumor	0.7241	0.9130	0.8077	115
no_tumor	0.6098	0.9524	0.7435	105
pituitary_tumor	0.8871	0.7432	0.8088	74
accuracy			0.7132	394
macro avg	0.7835	0.7047	0.6754	394
weighted avg	0.7722	0.7132	0.6725	394

Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9167	0.2200	0.3548	100
meningioma_tumor	0.7664	0.9130	0.8333	115
no_tumor	0.6410	0.9524	0.7663	105
pituitary_tumor	0.8312	0.8649	0.8477	74
accuracy			0.7386	394
macro avg	0.7888	0.7376	0.7005	394
weighted avg	0.7833	0.7386	0.6967	394

Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8800	0.2200	0.3520	100
meningioma_tumor	0.7464	0.8957	0.8142	115
no_tumor	0.6159	0.9619	0.7509	105
pituitary_tumor	0.8657	0.7838	0.8227	74
accuracy			0.7208	394
macro avg	0.7770	0.7153	0.6850	394
weighted avg	0.7679	0.7208	0.6816	394

Observam aici un efect asemănător comparativ cu modelul clasic ca mai devreme, în sensul că acurătatea a crescut, acest efect se datorează funcției de pierdere cu penalizare pe weights.

Iar pentru antrenarea clasica fara k-folduri fara augmentari si cu penalizari de ponderi:

Mentionez că am aplicat transformări cum ar fi conversia imaginii la tipul PIL pentru a putea efectua antrenarea, dar transformări precum: rotație, filtru CLAHE, GAUSSIAN sau SOBEL sau rotație de imagine sau alte augmentări de genul acesta nu au fost aplicate.

	precision	recall	f1-score	support
glioma_tumor	0.9600	0.2400	0.3840	100
meningioma_tumor	0.6962	0.9565	0.8059	115
no_tumor	0.6140	1.0000	0.7609	105
pituitary_tumor	0.9296	0.6286	0.7500	105
accuracy			0.7176	425
macro avg	0.8000	0.7063	0.6752	425
weighted avg	0.7956	0.7176	0.6817	425

Faptul că am obținut o acurătate de 71.76%, mai mare decât atunci când aveam transformările aplicate înseamnă că transformările în sine pe care le aplicam, îi creau modelului dificultate în învățare.

Pentru folduri media obținuta este urmatoarea :

```
⤵ Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

Evaluarea foldurilor în raport cu setul de testare:

Pentru fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9583	0.2300	0.3710	100
meningioma_tumor	0.7143	0.9565	0.8178	115
no_tumor	0.6069	1.0000	0.7554	105
pituitary_tumor	0.9054	0.6381	0.7486	105
accuracy			0.7176	425
macro avg	0.7962	0.7062	0.6732	425
weighted avg	0.7924	0.7176	0.6802	425

Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9583	0.2300	0.3710	100
meningioma_tumor	0.7237	0.9565	0.8240	115
no_tumor	0.5966	1.0000	0.7473	105
pituitary_tumor	0.9041	0.6286	0.7416	105
accuracy			0.7153	425
macro avg	0.7957	0.7038	0.6710	425
weighted avg	0.7921	0.7153	0.6781	425

Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2400	0.3871	100
meningioma_tumor	0.7285	0.9565	0.8271	115
no_tumor	0.6034	1.0000	0.7527	105
pituitary_tumor	0.9211	0.6667	0.7735	105
accuracy			0.7271	425
macro avg	0.8132	0.7158	0.6851	425
weighted avg	0.8091	0.7271	0.6919	425

Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2400	0.3871	100
meningioma_tumor	0.7534	0.9565	0.8429	115
no_tumor	0.6000	1.0000	0.7500	105
pituitary_tumor	0.9250	0.7048	0.8000	105
accuracy			0.7365	425
macro avg	0.8196	0.7253	0.6950	425
weighted avg	0.8159	0.7365	0.7021	425

Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2400	0.3871	100
meningioma_tumor	0.7097	0.9565	0.8148	115
no_tumor	0.5833	1.0000	0.7368	105
pituitary_tumor	0.9848	0.6190	0.7602	105
accuracy			0.7153	425
macro avg	0.8195	0.7039	0.6747	425
weighted avg	0.8148	0.7153	0.6814	425

Fara penalizari, cu augmentari:

Pentru antrenarea clasica fara k-folduri:

	precision	recall	f1-score	support
glioma_tumor	0.9048	0.1900	0.3140	100
meningioma_tumor	0.7724	0.8261	0.7983	115
no_tumor	0.5538	0.9810	0.7079	105
pituitary_tumor	0.8438	0.7297	0.7826	74
accuracy			0.6878	394
macro avg	0.7687	0.6817	0.6507	394
weighted avg	0.7611	0.6878	0.6484	394

Cu k-folduri:

Media Foldurilor:

```
Precision: Mean = 0.9987, Std = 0.0012
Recall: Mean = 0.9987, Std = 0.0012
F1-score: Mean = 0.9987, Std = 0.0012
Accuracy: Mean = 0.9987, Std = 0.0012
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9444	0.1700	0.2881	100
meningioma_tumor	0.6603	0.8957	0.7601	115
no_tumor	0.6319	0.9810	0.7687	105
pituitary_tumor	0.9298	0.7162	0.8092	74
accuracy			0.7005	394
macro avg	0.7916	0.6907	0.6565	394
weighted avg	0.7755	0.7005	0.6518	394

Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9412	0.1600	0.2735	100
meningioma_tumor	0.6711	0.8870	0.7640	115
no_tumor	0.6265	0.9905	0.7675	105
pituitary_tumor	0.8983	0.7162	0.7970	74
accuracy			0.6980	394
macro avg	0.7843	0.6884	0.6505	394
weighted avg	0.7704	0.6980	0.6467	394

Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.8947	0.1700	0.2857	100
meningioma_tumor	0.6667	0.8870	0.7612	115
no_tumor	0.6303	0.9905	0.7704	105
pituitary_tumor	0.9298	0.7162	0.8092	74
accuracy			0.7005	394
macro avg	0.7804	0.6909	0.6566	394
weighted avg	0.7643	0.7005	0.6520	394

Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.6871	0.8783	0.7710	115
no_tumor	0.6265	0.9905	0.7675	105
pituitary_tumor	0.9032	0.7568	0.8235	74
accuracy			0.7081	394
macro avg	0.7910	0.7014	0.6661	394
weighted avg	0.7776	0.7081	0.6610	394

Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9444	0.1700	0.2881	100
meningioma_tumor	0.6731	0.9130	0.7749	115
no_tumor	0.6420	0.9905	0.7790	105
pituitary_tumor	0.9310	0.7297	0.8182	74
accuracy			0.7107	394
macro avg	0.7976	0.7008	0.6651	394
weighted avg	0.7821	0.7107	0.6606	394

Concluziile care se pot trage de aici sunt urmatoarele: modelul avea dificultati in a invata in urma transformarilor aplicate, deoarece transformarile in sine nu reflectau imaginile, sau mai bine zis nu au generat modificari neaparat relevante pentru clasificarea in sine.

Cerinta 2.3

Pentru primul set de transformari am folosit:

```

train_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        Lambda(func=lambda x: custom_image_processing(x, False)), # aplic transformarile de CLAHE, Sobel descrise in functia custom_image_processing
        RandZoom(min_zoom=0.9, max_zoom=1.1, prob=0.5), # aplic o augmentare de Zoom de probabilitate 50% intre o micșorare usoara de 0.9 si o mare usoara de 1.1
        Resize(spatial_size=(128, 128)), # dau resize la imagine
    ]
)

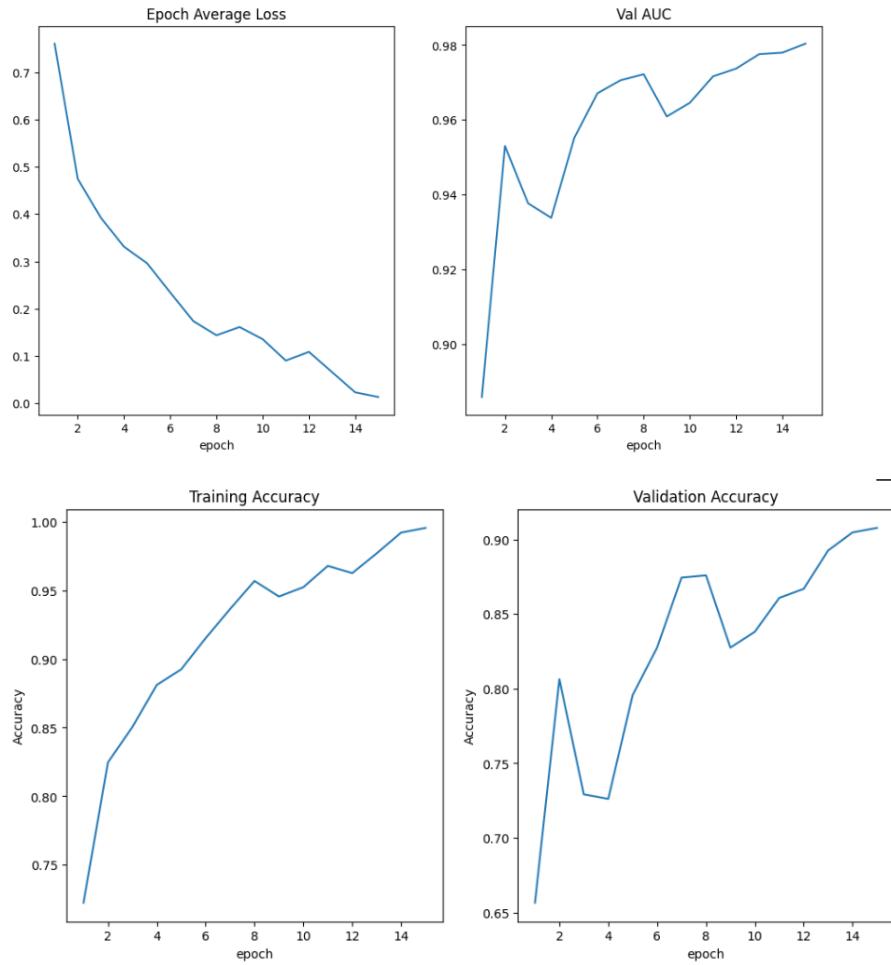
val_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        Lambda(func=lambda x: custom_image_processing(x, False)), # aplic transformarile de CLAHE, Sobel descrise in functia custom_image_processing
        RandZoom(min_zoom=0.9, max_zoom=1.1, prob=0.5), # aplic o augmentare de Zoom de probabilitate 50% intre o micșorare usoara de 0.9 si o mare usoara de 1.1
        Resize(spatial_size=(128, 128)), # dau resize la imagine
    ]
)

y_pred_trans = Compose([Activations(softmax=True)]) # aplic functia de activare Softmax
y_trans = Compose([AsDiscrete(to_onehot=num_class_train)]) # folosesc one hot encoder pentru encoding

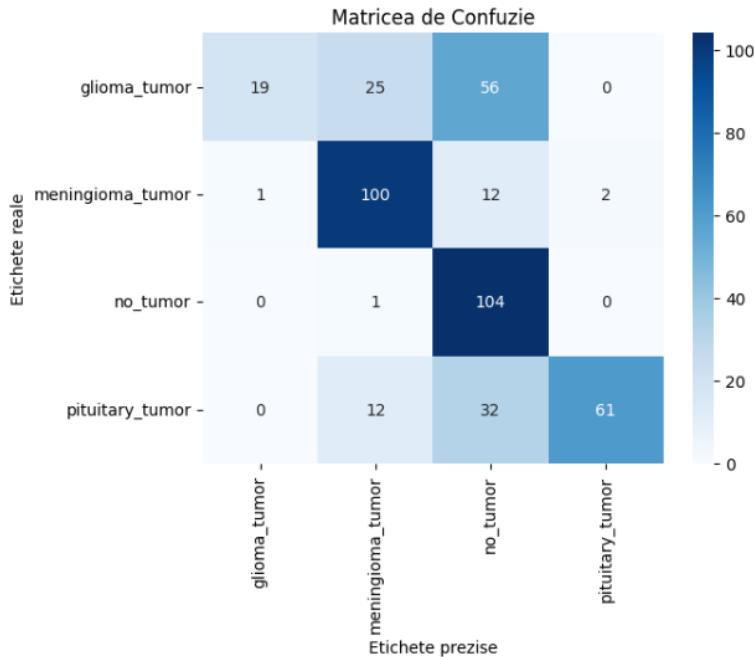
```

In custom image processing am pus transformarile precum: GAUSSIAN FILTER, SOBEL, CLAHE si EDGE DETECTION, din laboratoarele trecute. Am aplicat un RandZoom si un Resize la 128 x 128. Imaginele sunt Grayscale inainte si dupa transformari. Pentru acest set de transformari rezultatele sunt urmatoarele :

Pentru antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7246	0.8696	0.7905	115
no_tumor	0.5098	0.9905	0.6731	105
pituitary_tumor	0.9683	0.5810	0.7262	105
accuracy			0.6682	425
macro avg	0.7882	0.6577	0.6266	425
weighted avg	0.7848	0.6682	0.6341	425



Observam ca avem o acuratete scazuta comparativ cu acuratetea cazului in care nu aveam transformari aplicate, deoarece cel mai probabil sunt transformari care creeaza dificultati modelului in invatare.

Pentru folduri:

```
Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

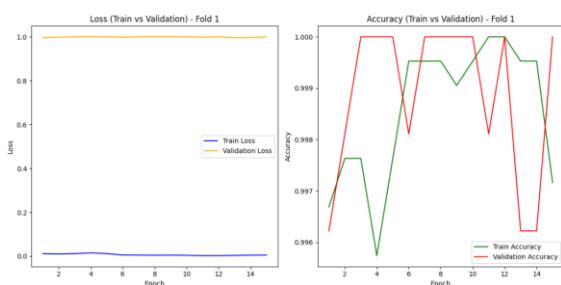
Aceasta este media rularilor

Evaluarea in functie de setul de testare pentru fiecare fold in parte:

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7874	0.8696	0.8264	115
no_tumor	0.4976	0.9905	0.6624	105
pituitary_tumor	0.9420	0.6190	0.7471	105
accuracy			0.6776	425
macro avg	0.7943	0.6673	0.6382	425
weighted avg	0.7923	0.6776	0.6464	425

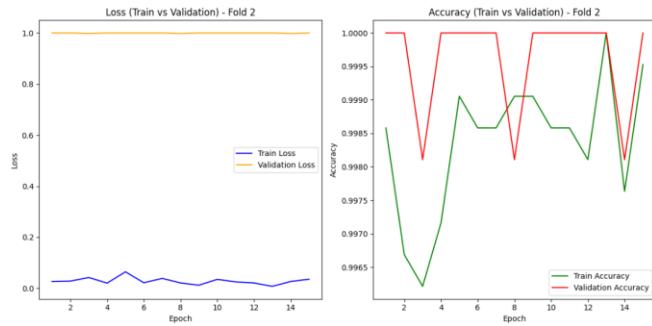
AUC for Fold 1: 0.8609



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9091	0.2000	0.3279	100
meningioma_tumor	0.7857	0.8609	0.8216	115
no_tumor	0.4791	0.9810	0.6438	105
pituitary_tumor	0.9677	0.5714	0.7186	105
accuracy			0.6635	425
macro avg	0.7854	0.6533	0.6279	425
weighted avg	0.7840	0.6635	0.6360	425

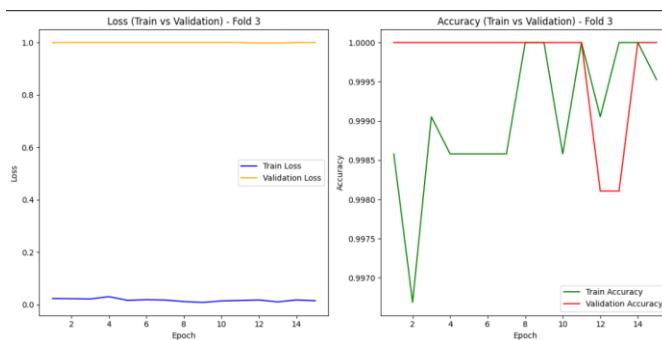
AUC for Fold 2: 0.8601



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9167	0.2200	0.3548	100
meningioma_tumor	0.7286	0.8870	0.8000	115
no_tumor	0.5306	0.9905	0.6910	105
pituitary_tumor	0.9385	0.5810	0.7176	105
accuracy			0.6800	425
macro avg	0.7786	0.6696	0.6409	425
weighted avg	0.7758	0.6800	0.6480	425

AUC for Fold 3: 0.8752

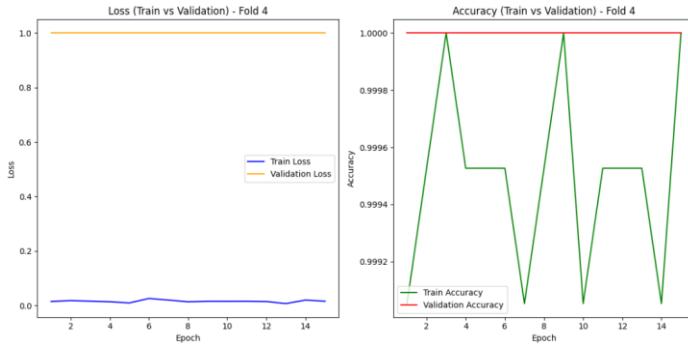


Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9048	0.1900	0.3140	100
meningioma_tumor	0.7786	0.8870	0.8293	115
no_tumor	0.4883	0.9905	0.6541	105
pituitary_tumor	0.9833	0.5619	0.7152	105
accuracy			0.6682	425
macro avg	0.7887	0.6573	0.6281	425
weighted avg	0.7871	0.6682	0.6366	425

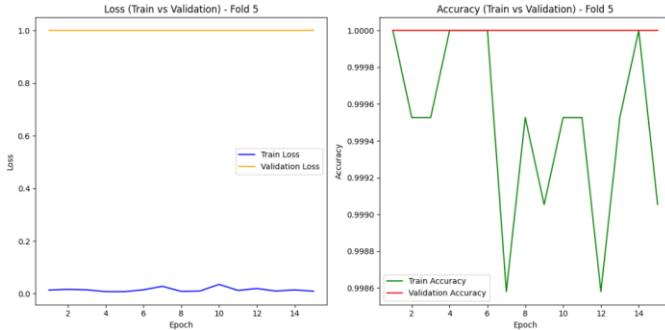
AUC for Fold 4: 0.8764

----- Evaluating Fold 5 -----



Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7710	0.8783	0.8211	115
no_tumor	0.4976	0.9905	0.6624	105
pituitary_tumor	0.9846	0.6095	0.7529	105
accuracy			0.6776	425
macro avg	0.8008	0.6671	0.6383	425
weighted avg	0.7983	0.6776	0.6464	425
AUC for Fold 5:	0.8751			



```
===== Overall AUC on Test Set =====
Average AUC: 0.8695
```

Observam spike-uri in cadrul foldurilor ceea ce indica faptul ca transformarile din acest set creeaza dificultati in invatarea modelului, posibil crearea de overfitting la invatarea pe date.

Observatie: Se poate observa ca am lasat expusi pasii din acest set de transformare mai jos, acest lucru a ramas din cadrul primei etape si am decis sa las separat pasii expusi deoarece nu am avut mereu la dispozitie GPU-ul si am avut dificultati la timpii de antrenare deoarece erau ingreunati semnificativ, deci pentru eficientizare i-am lasat separate.

Pentru setul 2 de transformari am folosit:

```

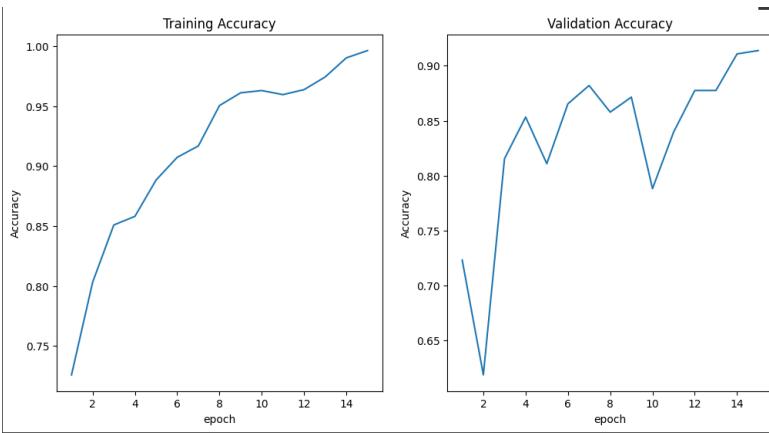
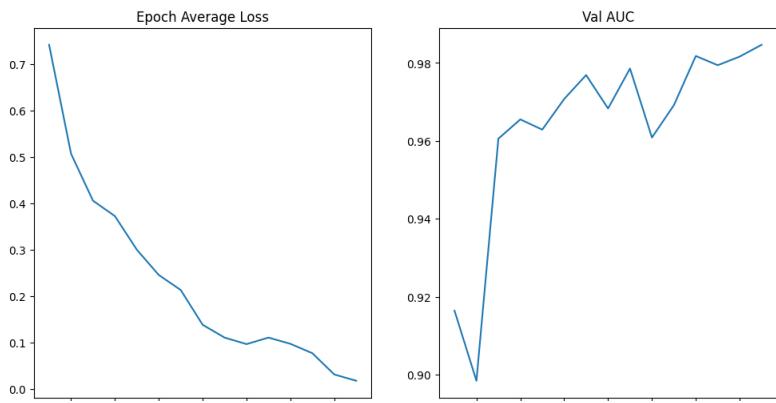
train_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        Lambda(func=lambda x: custom_image_processing(x, False)), # aplic transformarile de CLAHE, Sobel descrise in functia custom_image_processing
        RandZoom(min_zoom=0.9, max_zoom=1.1, prob=0.5), # aplic o augmentare de Zoom de probabilitate 50% intre o micsorare usoara de 0.9 si o marire usoara de 1.1
    ]
)

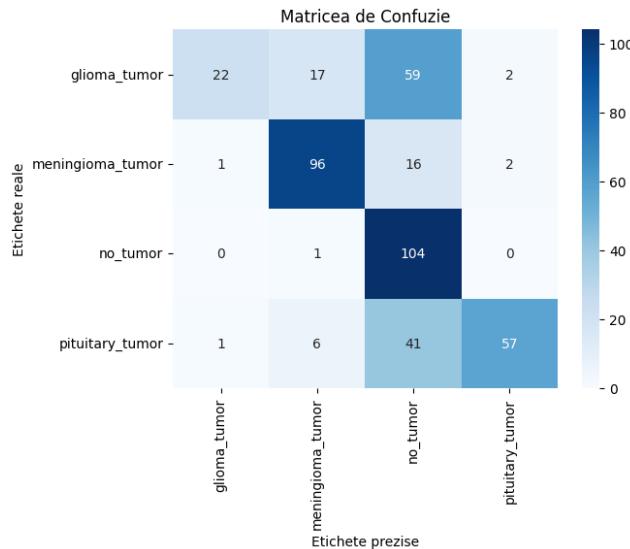
val_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        Lambda(func=lambda x: custom_image_processing(x, False)), # aplic transformarile de CLAHE, Sobel descrise in functia custom_image_processing
        RandZoom(min_zoom=0.9, max_zoom=1.1, prob=0.5), # aplic o augmentare de Zoom de probabilitate 50% intre o micsorare usoara de 0.9 si o marire usoara de 1.1
    ]
)

y_pred_trans = Compose([Activations(softmax=True)]) # aplic functia de activare Softmax
y_trans = Compose([AsDiscrete(to_onehot=num_class_train)]) # folosesc one hot encoder pentru encoding

```

Am eliminat acel resize de 128 x 128 in scopul de a pastra imaginea in formatul sau original, iar in rest, transformarile sunt la fel. Acestea sunt metricile evaluate in raport cu setul de testare.





	precision	recall	f1-score	support
glioma_tumor	0.9167	0.2200	0.3548	100
meningioma_tumor	0.8000	0.8348	0.8170	115
no_tumor	0.4727	0.9905	0.6400	105
pituitary_tumor	0.9344	0.5429	0.6867	105
accuracy			0.6565	425
macro avg	0.7810	0.6470	0.6247	425
weighted avg	0.7798	0.6565	0.6324	425

Observam o crestere atat la acuratete cat si la precision, deci acea transformare de resize la dimensiunea 128 x 128 a creat dificultati in invatare pentru model.

Pentru folduri:

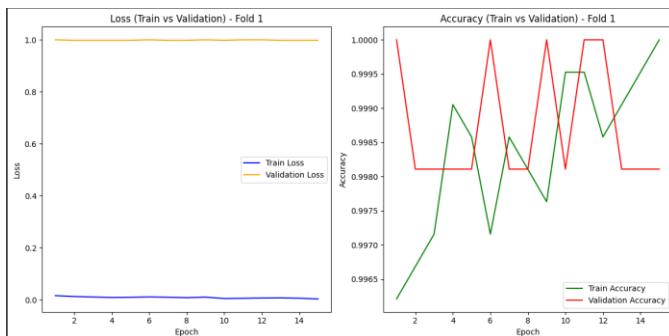
```
Precision: Mean = 0.9989, Std = 0.0010
Recall: Mean = 0.9989, Std = 0.0010
F1-score: Mean = 0.9989, Std = 0.0010
Accuracy: Mean = 0.9989, Std = 0.0010
```

Aceasta este media metricilor foldurilor

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9130	0.2100	0.3415	100
meningioma_tumor	0.8883	0.8435	0.8255	115
no_tumor	0.4771	0.9905	0.6440	105
pituitary_tumor	0.9688	0.5905	0.7337	105
accuracy			0.6682	425
macro avg	0.7918	0.6586	0.6362	425
weighted avg	0.7908	0.6682	0.6441	425

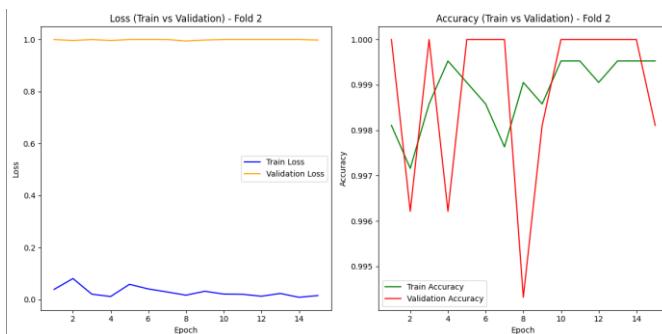
AUC for Fold 1: 0.8502



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2000	0.3333	100
meningioma_tumor	0.7840	0.8522	0.8167	115
no_tumor	0.5000	0.9905	0.6645	105
pituitary_tumor	0.9167	0.6286	0.7458	105
accuracy			0.6776	425
macro avg	0.8002	0.6678	0.6401	425
weighted avg	0.7974	0.6776	0.6478	425

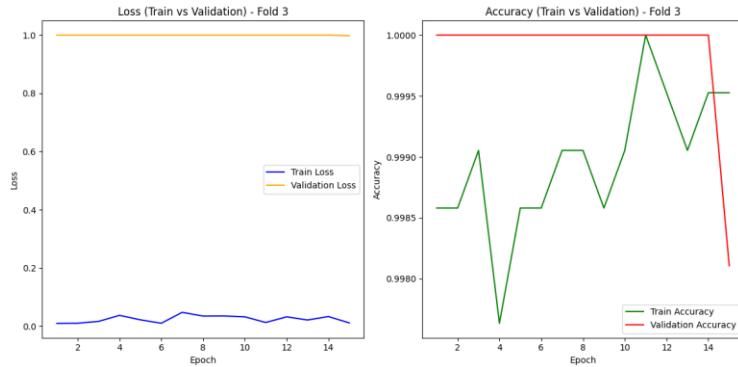
AUC for Fold 2: 0.8472



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.8750	0.2100	0.3387	100
meningioma_tumor	0.8051	0.8261	0.8155	115
no_tumor	0.4727	0.9905	0.6400	105
pituitary_tumor	0.9524	0.5714	0.7143	105
accuracy			0.6588	425
macro avg	0.7763	0.6495	0.6271	425
weighted avg	0.7758	0.6588	0.6349	425

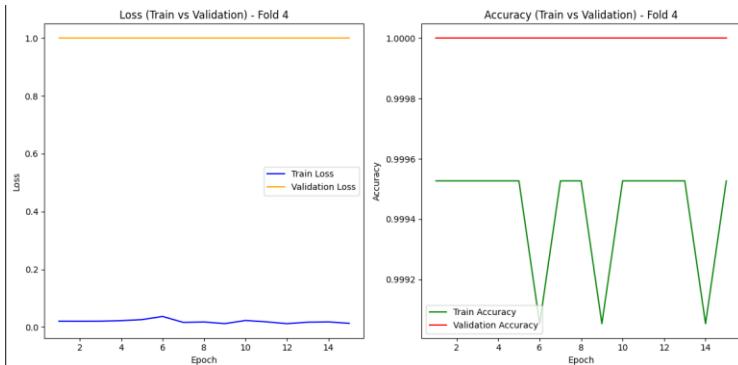
AUC for Fold 3: 0.8580



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9231	0.2400	0.3810	100
meningioma_tumor	0.8220	0.8435	0.8326	115
no_tumor	0.4839	1.0000	0.6522	105
pituitary_tumor	0.9531	0.5810	0.7219	105
accuracy			0.6753	425
macro avg	0.7955	0.6661	0.6469	425
weighted avg	0.7946	0.6753	0.6544	425

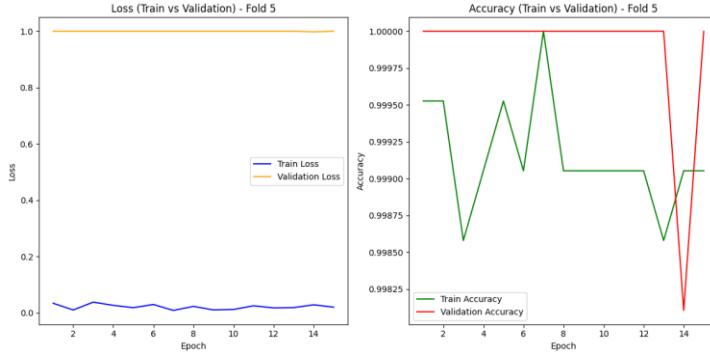
AUC for Fold 4: 0.8648



Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.7742	0.2400	0.3664	100
meningioma_tumor	0.8407	0.8261	0.8333	115
no_tumor	0.4861	1.0000	0.6542	105
pituitary_tumor	0.9538	0.5905	0.7294	105
accuracy			0.6729	425
macro avg	0.7637	0.6641	0.6458	425
weighted avg	0.7654	0.6729	0.6535	425

AUC for Fold 5: 0.8593



```
===== Overall AUC on Test Set =====
Average AUC: 0.8559
```

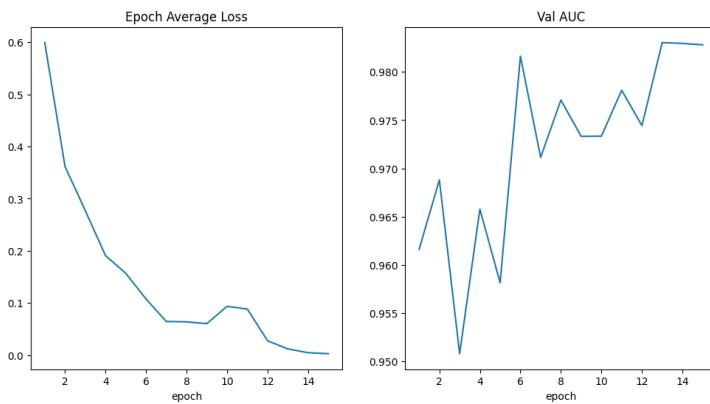
Pentru cel de-al treilea set de transformari avem:

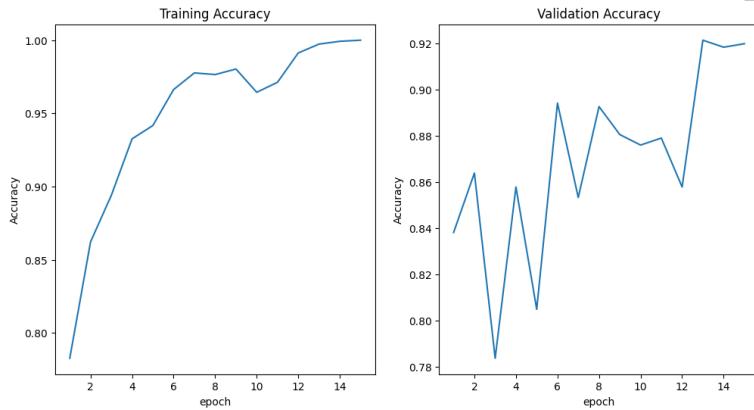
```
train_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        Lambda(func=lambda x: custom_image_processing(x, False)), # aplic transformarile de CLAHE, Sobel descrise in functia custom_image_processing
        Lambda(func=lambda x: x.float()) # convertesc imaginile la tensor de tip float32
    ]
)

val_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        Lambda(func=lambda x: custom_image_processing(x, False)), # aplic transformarile de CLAHE, Sobel descrise in functia custom_image_processing
        Lambda(func=lambda x: x.float()) # convertesc imaginile la tensor de tip float32
    ]
)

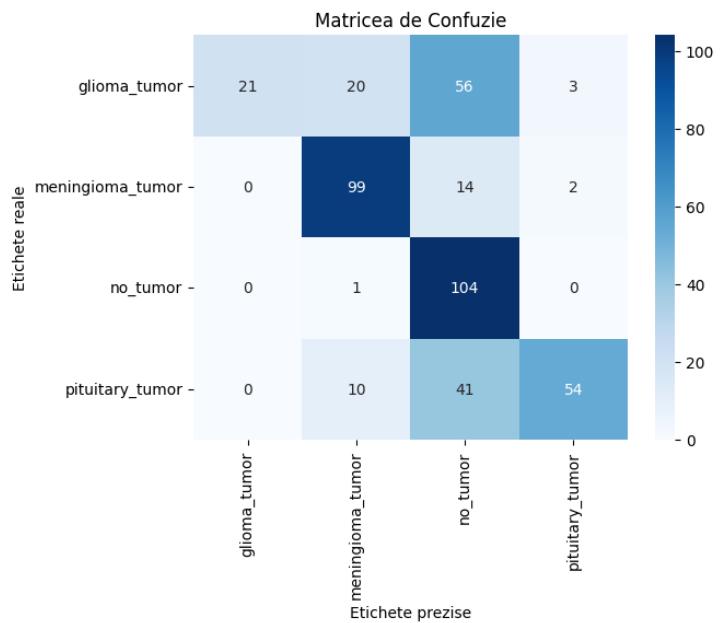
y_pred_trans = Compose([Activations(softmax=True)]) # aplic functia de activare Softmax
y_trans = Compose([AsDiscrete(to_onehot=num_class_train)]) # folosesc one hot encoder pentru encoding
```

Am scos si acel RandZoom fata de setul precedent, in schimb am mai adaugat o transformare de conversie a tensorilor la tipul float pentru a corespunde tipurilor primite ca parametrii la antrenare.





	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.7615	0.8609	0.8082	115
no_tumor	0.4837	0.9905	0.6500	105
pituitary_tumor	0.9153	0.5143	0.6585	105
accuracy			0.6541	425
macro avg	0.7901	0.6439	0.6160	425
weighted avg	0.7870	0.6541	0.6236	425



Acesta sunt metrice evaluate in raport cu setul de testare, tot sunt mai bune comparativ cu daca am fi avut acel resize.

Pentru folduri:

```
Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

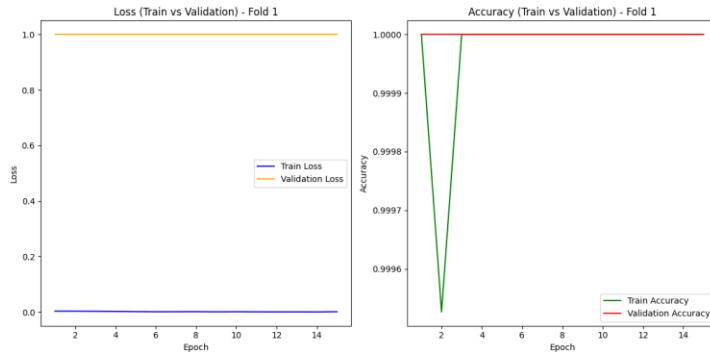
Aceasta este media metricilor din timpul antrenarii

Evaluarea in raport cu setul de testare

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2000	0.3333	100
meningioma_tumor	0.7656	0.8522	0.8066	115
no_tumor	0.4664	0.9905	0.6341	105
pituitary_tumor	0.9630	0.4952	0.6541	105
accuracy			0.6447	425
macro avg	0.7987	0.6345	0.6670	425
weighted avg	0.7956	0.6447	0.6150	425

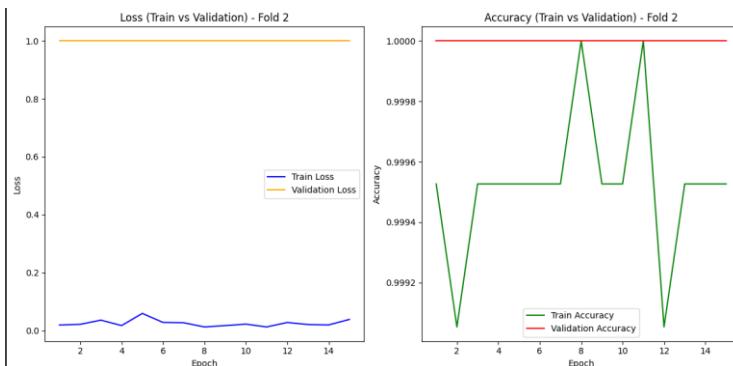
AUC for Fold 1: 0.8597



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.7481	0.8522	0.7967	115
no_tumor	0.4706	0.9905	0.6380	105
pituitary_tumor	0.9615	0.4762	0.6369	105
accuracy			0.6424	425
macro avg	0.7951	0.6322	0.6847	425
weighted avg	0.7915	0.6424	0.6123	425

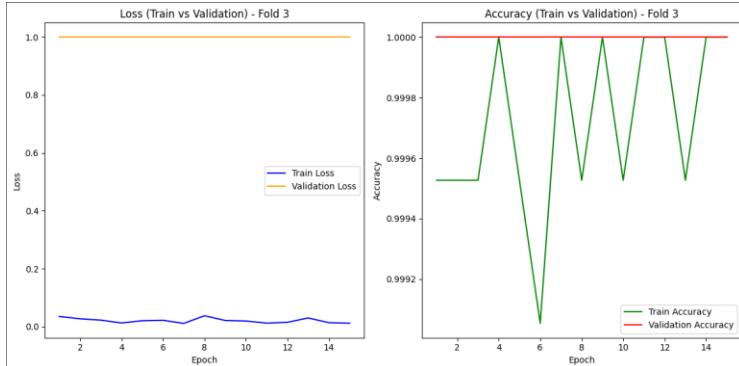
AUC for Fold 2: 0.8687



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2400	0.3871	100
meningioma_tumor	0.8099	0.8522	0.8305	115
no_tumor	0.4706	0.9905	0.6380	105
pituitary_tumor	0.9661	0.5429	0.6951	105
accuracy			0.6659	425
macro avg	0.8117	0.6564	0.6377	425
weighted avg	0.8094	0.6659	0.6452	425

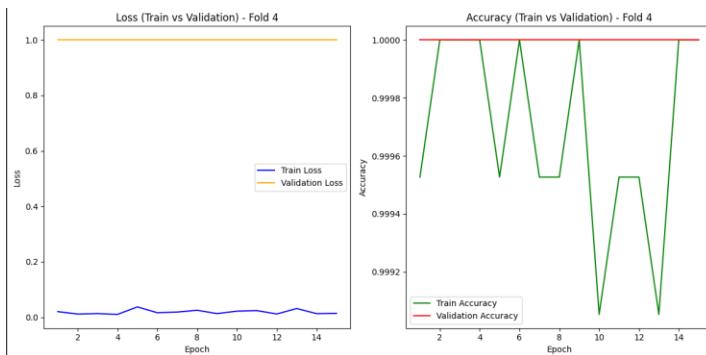
AUC for Fold 3: 0.8733



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2000	0.3333	100
meningioma_tumor	0.8000	0.8000	0.8000	115
no_tumor	0.4333	0.9905	0.6029	105
pituitary_tumor	0.9800	0.4667	0.6323	105
accuracy			0.6235	425
macro avg	0.8033	0.6143	0.5921	425
weighted avg	0.8009	0.6235	0.6001	425

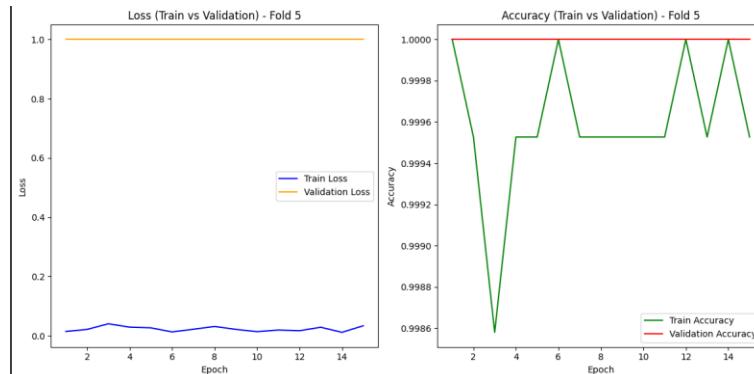
AUC for Fold 4: 0.8736



Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.8070	0.8000	0.8035	115
no_tumor	0.4351	0.9905	0.6047	105
pituitary_tumor	0.9815	0.5048	0.6667	105
accuracy			0.6282	425
macro avg	0.8059	0.6188	0.5950	425
weighted avg	0.8037	0.6282	0.6033	425

AUC for Fold 5: 0.8736



===== Overall AUC on Test Set =====
Average AUC: 0.8698

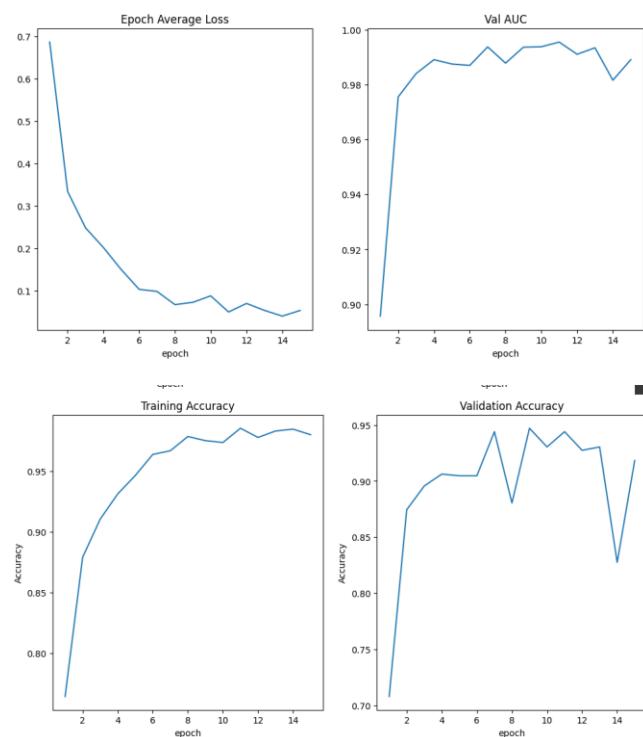
Pentru cel de-al patrulea set de transformari avem :

```
train_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        ToTensor(), # convertesc imaginile la tensor
        RandZoom(min_zoom=0.9, max_zoom=1.1, prob=0.5), # aplic o augmentare de Zoom de probabilitate 50% intre o micsorare usoara de 0.9 si o mareire usoara de 1.1
        Resize(spatial_size=(128, 128)) # dau resize la imagine
    ]
)

val_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        ToTensor(), # convertesc imaginile la tensor
        RandZoom(min_zoom=0.9, max_zoom=1.1, prob=0.5), # aplic o augmentare de Zoom de probabilitate 50% intre o micsorare usoara de 0.9 si o mareire usoara de 1.1
        Resize(spatial_size=(128, 128)) # dau resize la imagine
    ]
)

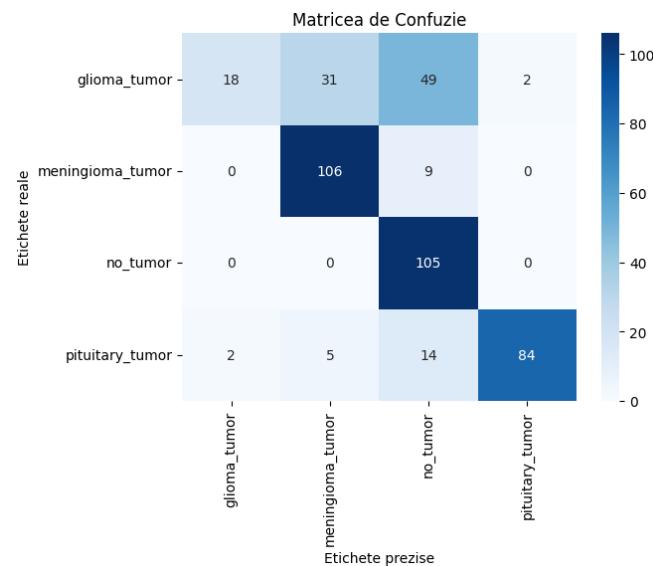
y_pred_trans = Compose([Activations(softmax=True)]) # aplic functia de activare Softmax
y_trans = Compose([AsDiscrete(to_onehot=num_class_train)]) # folosesc one hot encoder pentru encoding
```

Am scos acele transforme pentru filtrele CLAHE, GAUSSIAN, SOBEL, EDGE DETECTION si am readus RandZoom si Resize si am adaugat conversia la Tensor pentru a putea aplica transformarile de RandZoom si Resize.



	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.7465	0.9217	0.8249	115
no_tumor	0.5932	1.0000	0.7447	105
pituitary_tumor	0.9767	0.8000	0.8796	105
accuracy			0.7365	425
macro avg	0.8041	0.7254	0.6873	425
weighted avg	0.8016	0.7365	0.6951	425

Acstea sunt rezultatele in comparatie cu setul de testare, observam ca eliminarea acelor filtre gaussiene, sobel si chiar clahe au ajutat la invatarea modelului intrucat metricile sunt imbunatatite.



Pentru folduri:

```
Precision: Mean = 0.9985, Std = 0.0034
Recall: Mean = 0.9985, Std = 0.0034
F1-score: Mean = 0.9985, Std = 0.0034
Accuracy: Mean = 0.9985, Std = 0.0034
```

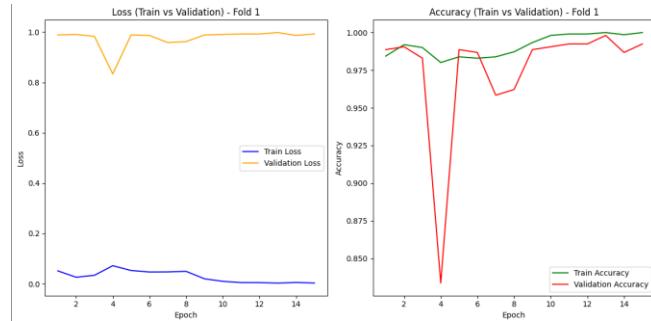
Aceasta este media metricilor foldurilor din timpul antrenarii

In comparatie cu setul de testare

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7292	0.9130	0.8108	115
no_tumor	0.5497	1.0000	0.7895	105
pituitary_tumor	0.9722	0.6667	0.7910	105
accuracy			0.7012	425
macro avg	0.8128	0.6899	0.6541	425
weighted avg	0.8086	0.7012	0.6619	425

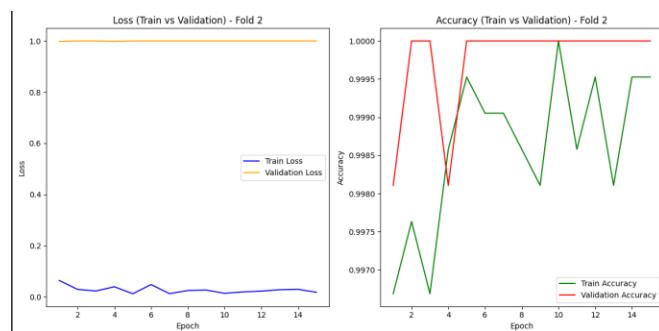
AUC for Fold 1: 0.8883



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7055	0.8957	0.7893	115
no_tumor	0.5707	1.0000	0.7266	105
pituitary_tumor	0.9333	0.6667	0.7778	105
accuracy			0.6988	425
macro avg	0.7899	0.6881	0.6526	425
weighted avg	0.7860	0.6988	0.6598	425

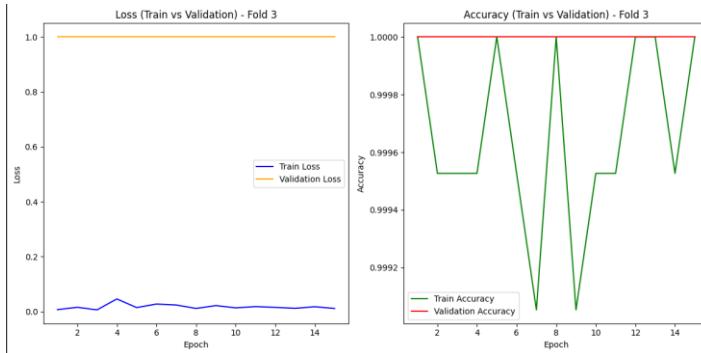
AUC for Fold 2: 0.8859



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.7162	0.9217	0.8061	115
no_tumor	0.5676	1.0000	0.7241	105
pituitary_tumor	0.9583	0.6571	0.7797	105
accuracy			0.7012	425
macro avg	0.7855	0.6897	0.6525	425
weighted avg	0.7826	0.7012	0.6602	425

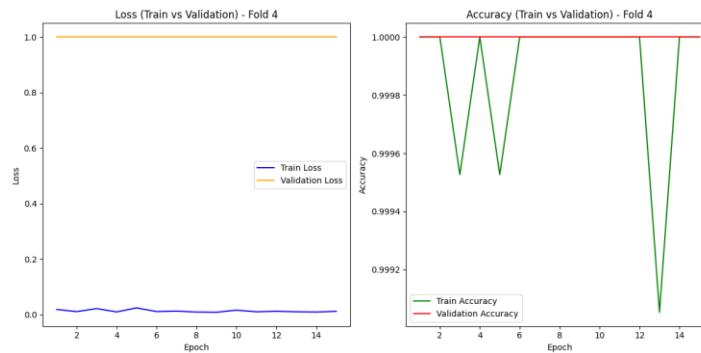
AUC for Fold 3: 0.9085



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7571	0.9217	0.8314	115
no_tumor	0.5276	1.0000	0.6908	105
pituitary_tumor	0.9706	0.6286	0.7630	105
accuracy			0.6941	425
macro avg	0.8138	0.6826	0.6476	425
weighted avg	0.8103	0.6941	0.6559	425

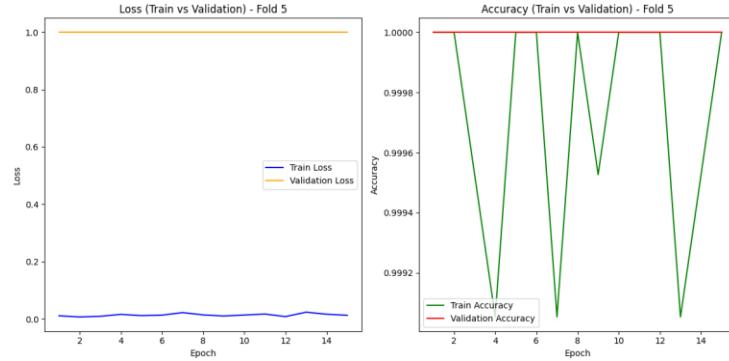
AUC for Fold 4: 0.8945



Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7413	0.9217	0.8217	115
no_tumor	0.5385	1.0000	0.7000	105
pituitary_tumor	0.9710	0.6381	0.7701	105
accuracy			0.6965	425
macro avg	0.8127	0.6850	0.6492	425
weighted avg	0.8088	0.6965	0.6573	425

AUC for Fold 5: 0.9018



===== Overall AUC on Test Set =====
Average AUC: 0.8958

Observam metrii mai bune in mare parte peste tot nu ca pentru setul trecut de transformari. Eliminarea Filtrelor CLAHE, SOBEL GAUSSIAN FILTER si EDGE DETECTION a ajutat la invatarea mai precisa si concreta a modelului.

Setul 5 de transformari:

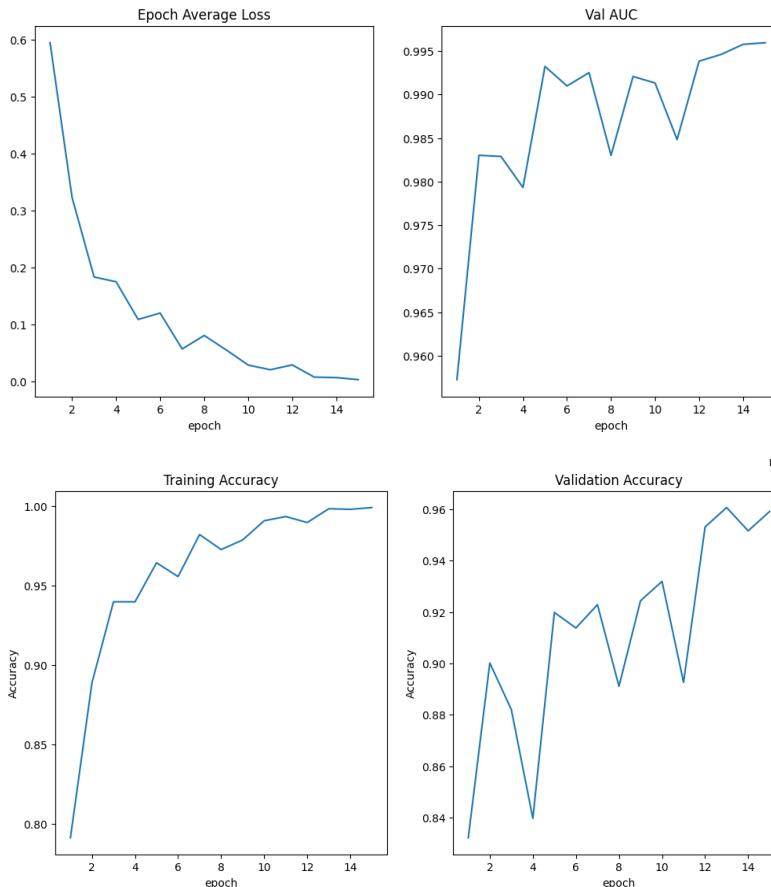
```
train_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        ToTensor(), # convertesc imaginile la tensor
        Resize(spatial_size=(128, 128)), # dau resize la imagine
    ]
)

val_transforms = Compose(
    [
        LoadImage(image_only=True), # incarc imaginea dar pastrez doar datele de imagine
        Lambda(func=convert_to_pil), # aplic functia de convertire la PIL pentru fiecare imagine
        Lambda(func=lambda x: Image.fromarray(x.numpy()) if isinstance(x, MetaTensor) else x), # convertire de la MetaTensor la Tensor pentru fiecare imagine
        ToTensor(), # convertesc imaginile la tensor
        Resize(spatial_size=(128, 128)), # dau resize la imagine
    ]
)

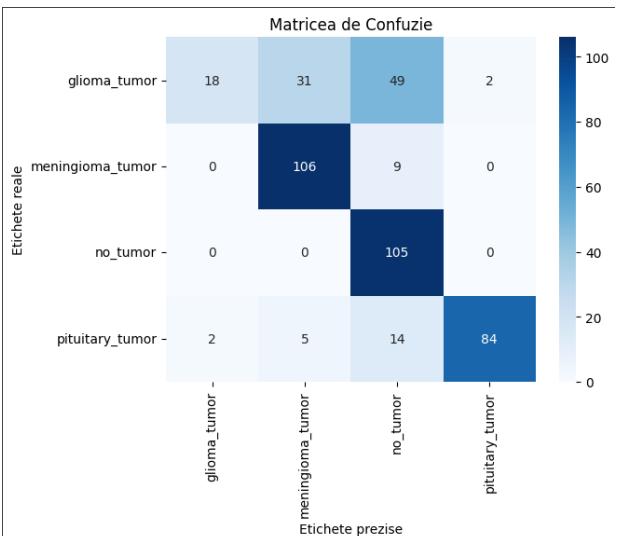
y_pred_trans = Compose([Activations(softmax=True)]) # aplic functia de activare Softmax
y_trans = Compose([AsDiscrete(to_onehot=num_class_train)]) # folosesc one hot encoder pentru encoding
```

Am lasat doar Resize-ul de 128 x 128 pentru a vedea daca va contribui negativ la invatarea modelului.

Pentru antrenarea clasica fara k-folduri in comparative cu setul de testare:



	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7941	0.9391	0.8606	115
no_tumor	0.5000	1.0000	0.6667	105
pituitary_tumor	1.0000	0.5810	0.7349	105
accuracy			0.6871	425
macro avg	0.8235	0.6750	0.6418	425
weighted avg	0.8208	0.6871	0.6509	425



Observam o scadere a metricilor atat la acuratete, cat si pentru clasa no_tumor, deci Resize-ul in cazul antrenarii clasice fara k-folduri intr-adevar ingreuneaza invatarea.

Pentru folduri:

```
Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

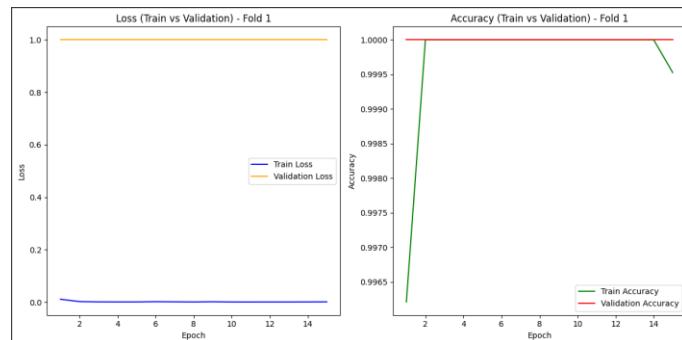
Aceasta este media metricilor din timpul antrenarii.

In raport cu setul de testare:

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7643	0.9304	0.8392	115
no_tumor	0.5172	1.0000	0.6818	105
pituitary_tumor	0.9844	0.6000	0.7456	105
accuracy			0.6894	425
macro avg	0.8165	0.6776	0.6429	425
weighted avg	0.8131	0.6894	0.6515	425

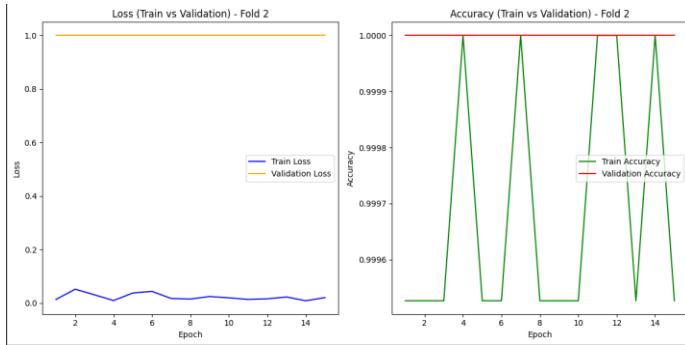
AUC for Fold 1: 0.8874



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.8092	0.9217	0.8618	115
no_tumor	0.4953	1.0000	0.6625	105
pituitary_tumor	1.0000	0.6095	0.7574	105
accuracy			0.6894	425
macro avg	0.8261	0.6778	0.6467	425
weighted avg	0.8237	0.6894	0.6558	425

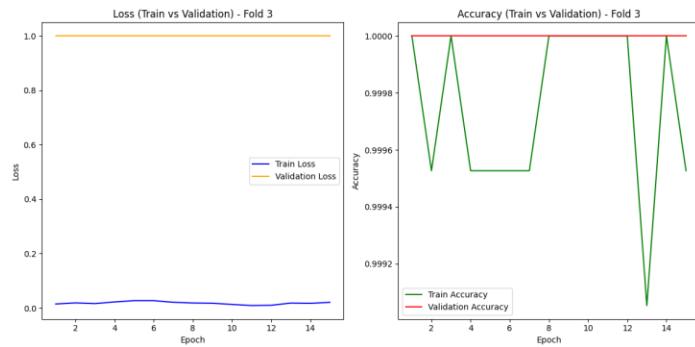
AUC for Fold 2: 0.8874



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.8281	0.9217	0.8724	115
no_tumor	0.4930	1.0000	0.6604	105
pituitary_tumor	0.9848	0.6190	0.7602	105
accuracy			0.6918	425
macro avg	0.8265	0.6802	0.6495	425
weighted avg	0.8245	0.6918	0.6588	425

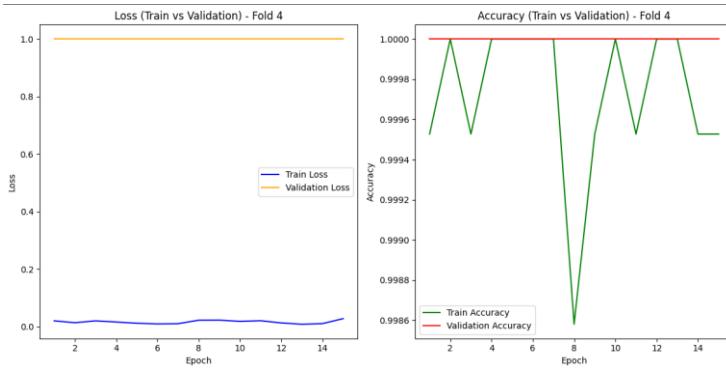
AUC for Fold 3: 0.8907



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.8217	0.9217	0.8689	115
no_tumor	0.4953	1.0000	0.6625	105
pituitary_tumor	0.9848	0.6190	0.7602	105
accuracy			0.6918	425
macro avg	0.8255	0.6802	0.6492	425
weighted avg	0.8233	0.6918	0.6584	425

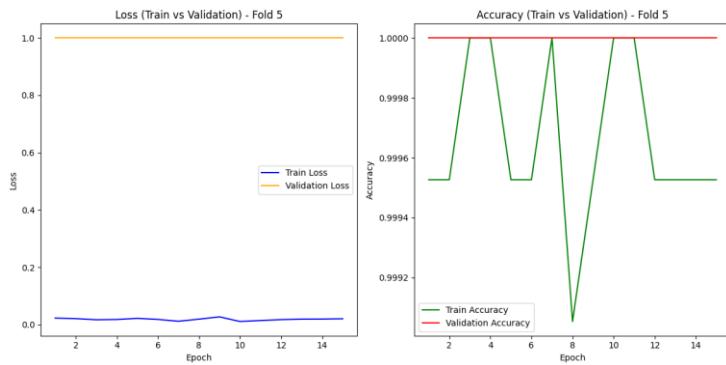
AUC for Fold 4: 0.8906



Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.8015	0.9478	0.8685	115
no_tumor	0.5048	1.0000	0.6709	105
pituitary_tumor	1.0000	0.6000	0.7500	105
accuracy			0.6941	425
macro avg	0.8266	0.6820	0.6486	425
weighted avg	0.8239	0.6941	0.6578	425

AUC for Fold 5: 0.8878



===== Overall AUC on Test Set =====
 Average AUC: 0.8888

Observam o scadere predominantă în acuratețe de la ultimele 3 folduri, aici presupun că depinde de datele în sine cum sunt vazute și interpretate, iar din grafice la acuratețea train vs test observăm spike-uri ceea ce indică faptul că depinde de cum influențează acest resize imaginea, în sensul că unele imagini cu resize-ul de 128 x 128 ajută la învățare și altele nu, dimpotrivă creează mai multă dificultate.

Set de transformări	Fold	Acurateți	AUC	Alte metrii

1	1	67.76	0.8609	precision	recall	f1-score	
				glioma_tumor	0.9500	0.1900	0.3167
				meningioma_tumor	0.7874	0.8696	0.8264
				no_tumor	0.4976	0.9905	0.6624
				pituitary_tumor	0.9420	0.6190	0.7471
1	2	66.35	0.8601	precision	recall	f1-score	
				glioma_tumor	0.9091	0.2000	0.3279
				meningioma_tumor	0.7857	0.8609	0.8216
				no_tumor	0.4791	0.9810	0.6438
				pituitary_tumor	0.9677	0.5714	0.7186
1	3	68	0.8752	precision	recall	f1-score	
				glioma_tumor	0.9167	0.2200	0.3548
				meningioma_tumor	0.7286	0.8870	0.8000
				no_tumor	0.5306	0.9905	0.6910
				pituitary_tumor	0.9385	0.5810	0.7176
1	4	66.82	0.8764	precision	recall	f1-score	
				glioma_tumor	0.9048	0.1900	0.3140
				meningioma_tumor	0.7786	0.8870	0.8293
				no_tumor	0.4883	0.9905	0.6541
				pituitary_tumor	0.9833	0.5619	0.7152
1	5	67.76	0.8751	precision	recall	f1-score	
				glioma_tumor	0.9500	0.1900	0.3167
				meningioma_tumor	0.7710	0.8783	0.8211
				no_tumor	0.4976	0.9905	0.6624
				pituitary_tumor	0.9846	0.6095	0.7529
2	1	66.82	0.8502	precision	recall	f1-score	
				glioma_tumor	0.9130	0.2100	0.3415
				meningioma_tumor	0.8083	0.8435	0.8255
				no_tumor	0.4771	0.9905	0.6440
				pituitary_tumor	0.9688	0.5905	0.7337
2	2	67.76	0.8472	precision	recall	f1-score	
				glioma_tumor	1.0000	0.2000	0.3333
				meningioma_tumor	0.7840	0.8522	0.8167
				no_tumor	0.5000	0.9905	0.6645
				pituitary_tumor	0.9167	0.6286	0.7458
2	3	65.88	0.8580	precision	recall	f1-score	
				glioma_tumor	0.8750	0.2100	0.3387
				meningioma_tumor	0.8051	0.8261	0.8155
				no_tumor	0.4727	0.9905	0.6400
				pituitary_tumor	0.9524	0.5714	0.7143

2	4	67.53	0.8648	precision	recall	f1-score	
				glioma_tumor	0.9231	0.2400	0.3810
				meningioma_tumor	0.8220	0.8435	0.8326
				no_tumor	0.4839	1.0000	0.6522
				pituitary_tumor	0.9531	0.5810	0.7219
2	5	67.29	0.8593	precision	recall	f1-score	
				glioma_tumor	0.7742	0.2400	0.3664
				meningioma_tumor	0.8407	0.8261	0.8333
				no_tumor	0.4861	1.0000	0.6542
				pituitary_tumor	0.9538	0.5905	0.7294
3	1	64.47	0.8597	precision	recall	f1-score	
				glioma_tumor	1.0000	0.2000	0.3333
				meningioma_tumor	0.7656	0.8522	0.8066
				no_tumor	0.4664	0.9905	0.6341
				pituitary_tumor	0.9630	0.4952	0.6541
3	2	64.24	0.8687	precision	recall	f1-score	
				glioma_tumor	1.0000	0.2100	0.3471
				meningioma_tumor	0.7481	0.8522	0.7967
				no_tumor	0.4706	0.9905	0.6380
				pituitary_tumor	0.9615	0.4762	0.6369
3	3	66.59	0.8733	precision	recall	f1-score	
				glioma_tumor	1.0000	0.2400	0.3871
				meningioma_tumor	0.8099	0.8522	0.8305
				no_tumor	0.4706	0.9905	0.6380
				pituitary_tumor	0.9661	0.5429	0.6951
3	4	62.35	0.8736	precision	recall	f1-score	
				glioma_tumor	1.0000	0.2000	0.3333
				meningioma_tumor	0.8000	0.8000	0.8000
				no_tumor	0.4333	0.9905	0.6029
				pituitary_tumor	0.9800	0.4667	0.6323
3	5	62.82	0.8736	precision	recall	f1-score	
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.8070	0.8000	0.8035
				no_tumor	0.4351	0.9905	0.6047
				pituitary_tumor	0.9815	0.5048	0.6667
4	1	70.12	0.8883	precision	recall	f1-score	
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.7292	0.9130	0.8108
				no_tumor	0.5497	1.0000	0.7095
				pituitary_tumor	0.9722	0.6667	0.7910

4	2	69.88	0.8859		precision	recall	f1-score
				glioma_tumor	0.9500	0.1900	0.3167
				meningioma_tumor	0.7055	0.8957	0.7893
				no_tumor	0.5707	1.0000	0.7266
				pituitary_tumor	0.9333	0.6667	0.7778
4	3	70.12	0.9085		precision	recall	f1-score
				glioma_tumor	0.9000	0.1800	0.3000
				meningioma_tumor	0.7162	0.9217	0.8061
				no_tumor	0.5676	1.0000	0.7241
				pituitary_tumor	0.9583	0.6571	0.7797
4	4	69.41	0.8945		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.7571	0.9217	0.8314
				no_tumor	0.5276	1.0000	0.6908
				pituitary_tumor	0.9706	0.6286	0.7630
4	5	69.95	0.9018		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.7413	0.9217	0.8217
				no_tumor	0.5385	1.0000	0.7000
				pituitary_tumor	0.9710	0.6381	0.7701
5	1	68.94	0.8874		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.7643	0.9304	0.8392
				no_tumor	0.5172	1.0000	0.6818
				pituitary_tumor	0.9844	0.6000	0.7456
5	2	68.94	0.8874		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.8092	0.9217	0.8618
				no_tumor	0.4953	1.0000	0.6625
				pituitary_tumor	1.0000	0.6095	0.7574
5	3	69.18	0.8907		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.8281	0.9217	0.8724
				no_tumor	0.4930	1.0000	0.6604
				pituitary_tumor	0.9848	0.6190	0.7602
5	4	69.18	0.8906		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.8217	0.9217	0.8689
				no_tumor	0.4953	1.0000	0.6625
				pituitary_tumor	0.9848	0.6190	0.7602

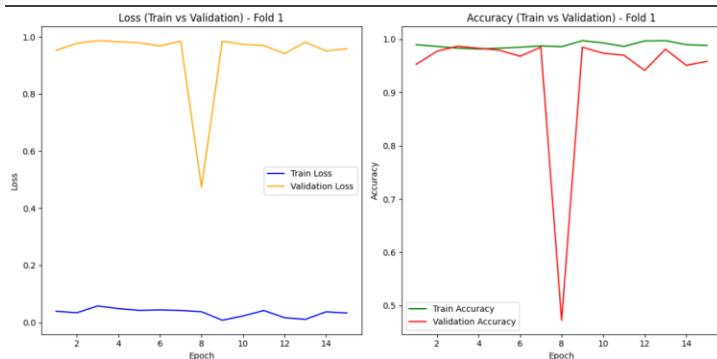
5	5	69.41	0.8878		precision	recall	f1-score
				glioma_tumor	1.0000	0.1800	0.3051
				meningioma_tumor	0.8015	0.9478	0.8685
				no_tumor	0.5048	1.0000	0.6709
				pituitary_tumor	1.0000	0.6000	0.7500

Observam ca cea mai buna acuratete a fost obtinuta la setul 4, acest set nu contineau filtrele CLAHE, SOBEL, GAUSSIAN si nici EDGE DETECTION. Filtrul Gaussian adauga zgomot in poza, aceasta transformare fiind efectuata in functia custom_image_processing. Sobel in combinatie cu edge detection incercau sa ofere o claritate imaginii prin a evidenta mai bine contururile, deci incercau sa imbunatateasca aceasta calitate a imaginii. Clahen incerca sa contrasteze mai bine zonele luminoase si intunecate din imagine. Consider ca filtrul gaussian aducea o mare dificultate in invatarea modelului. Alta transformare care a introdus dificultate ridicata in invatare a fost resize la 128 x 128. Schimbarea rezolutiei imaginii, schimba natura pixelilor si creeaza ca sim ai devreme, dificultati in invatarea modelului.

CERINTA 2.4

Aici trebuie sa fac o precizare: eu am folosit pana acum un scheduler de tipul ReduceLROnPlateau atat la antrenarea clasica fara k-folduri cat si la cea cu k-folduri. Pentru aceasta cerinta am scos schedulerul la partea de folduri si am folosit setul de transformari pe care eu am avut cele mai bune rezultate. Prima data am rulat fara scheduler si dupa aceea l-am pus la loc, dupa acea rulat, foldul cu cele mai slabe rezultate a fost primul fold cu urmatoarele rezultate:

	precision	recall	f1-score	support
glioma_tumor	0.9200	0.2300	0.3680	100
meningioma_tumor	0.7153	0.8957	0.7954	115
no_tumor	0.5412	1.0000	0.7023	105
pituitary_tumor	0.9677	0.5714	0.7186	105
accuracy			0.6847	425
macro avg	0.7861	0.6743	0.6461	425
weighted avg	0.7828	0.6847	0.6529	425
AUC for Fold 1:	0.8731			



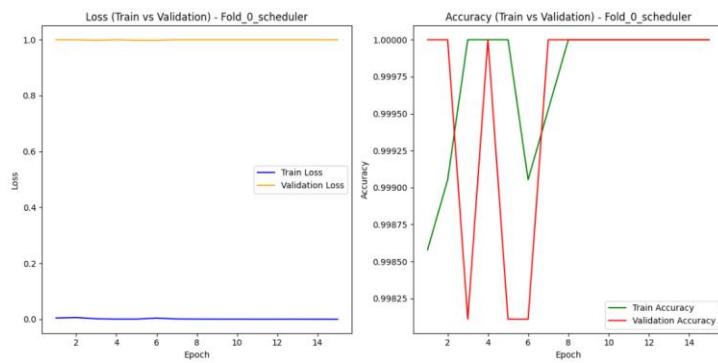
Dupa ce am rulat cu scheduler-ul am obtinut :

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7006	0.9565	0.8088	115
no_tumor	0.5833	1.0000	0.7368	105
pituitary_tumor	0.9853	0.6381	0.7746	105
accuracy			0.7082	425
macro avg	0.8048	0.6962	0.6592	425
weighted avg	0.8007	0.7082	0.6668	425

AUC for Fold 0 scheduler: 0.8958

===== Overall AUC on Test Set =====

Average AUC: 0.8958



Pentru antrenarea acestui fold cu aceasta metoda a durat undeva la 1m 9s.

Pentru Early_Stopping am realizat o clasa care imi salveaza un checkpoint in cazul in care se imbunatateste performanta si in caz de nu va opri antrenarea.

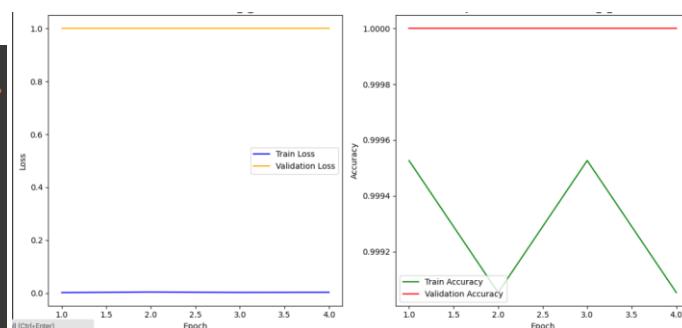
Cu Early_Stopping, antrenarea s-a oprit la epoca 3 pentru primul fold, rezultatele fiind:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7208	0.9652	0.8253	115
no_tumor	0.5801	1.0000	0.7343	105
pituitary_tumor	0.9583	0.6571	0.7797	105
accuracy			0.7129	425
macro avg	0.8148	0.7006	0.6611	425
weighted avg	0.8104	0.7129	0.6691	425

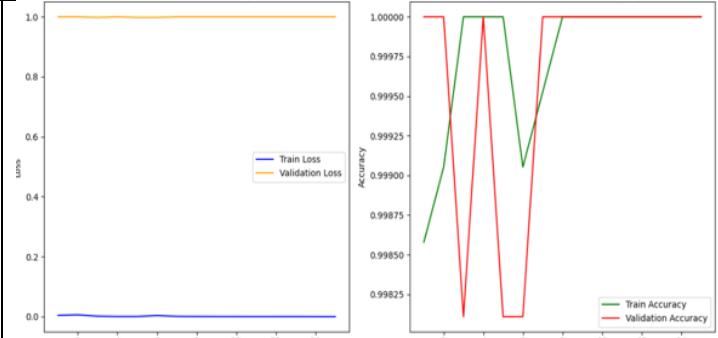
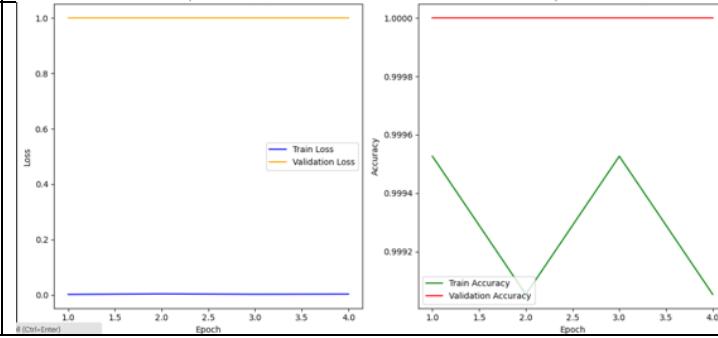
AUC for Fold 0 scheduler: 0.8910

===== Overall AUC on Test Set =====

Average AUC: 0.8910



Timpul a fost mult mai scurt aici, durata fiind undeva pe la 5 secunde. Acest lucru indica faptul ca dupa epoca, cu numarul 3 performanta nu se mai imbunatatesta.

Fold	Timp	Metoda	Acc(train vs validate)	AUC	Acc & Loss(train vs validate)
0	1m 30s	ReduceLROnPlateau	70.82	0.8959	
0	5s	EarlyStopping	71.29	0.8910	

In acest tabel am comparat acuratetea AUC si evolutia pe epoci a acuratetei si a Pierderii atat pentru Train cat si pentru Validate cat si durata de rulare, pentru fiecare metoda in parte.

CERINTA 2.5

Selectarea celui mai slab fold am realizat-o uitandu-ma la acuratete, f1-score, precision, recall.

Observatie: la aceasta cerinta am facut si antrenarea fara k-folduri ca sa se poata observa o comparative intre antrenarea cu k-folduri si fara k-folduri. Cand am experimentat cu weight_Decay, m-am aexprimat: "cu scheduler cu weight_decay", pentru ca am vrut sa pastrez scheduler-ul de la cerinta 2.4 si am combinat cu weight_decay la optimizatorul curent folosit.

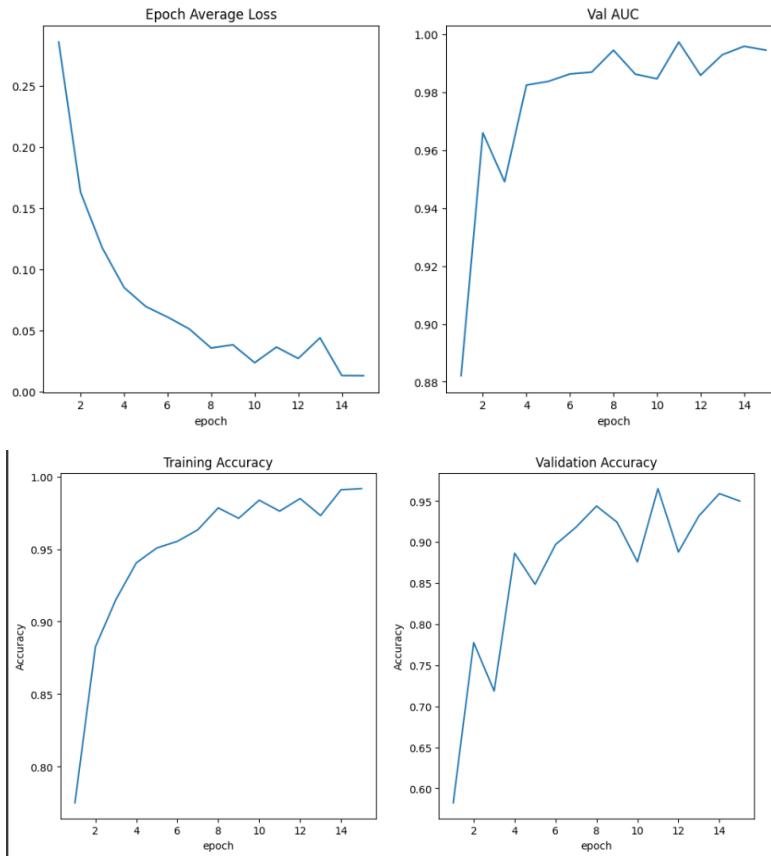
In realizarea experimentelor am tinut cont de urmatorii parametrii: optimizator (Adam si SGD), learning_rate (0.01 si 0.001), batch_size(32 si 64), dropout (cu si fara), Early_Stopping, weight_decay si functia de pierdere.

Majoritatea rezultatelor slabe au fost obtinute in cadrul experimentelor rulate cu optimizatorului SGD, cu cateva exceptii.

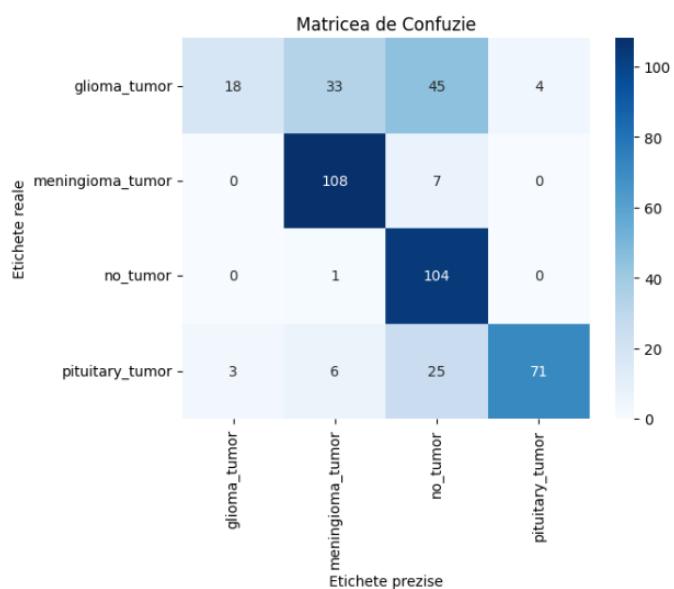
BCEWithLogitsLoss:

Am inceput aceasta cerinta prin a schimbat functia de loss cu BCEWithLogitsLoss batch_size = 32 si optimizatorul Adam cu learning_rate = 0.001 fara dropout.

Pentru antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1800	0.2975	100
meningioma_tumor	0.7297	0.9391	0.8213	115
no_tumor	0.5746	0.9905	0.7273	105
pituitary_tumor	0.9467	0.6762	0.7889	105
accuracy			0.7082	425
macro avg	0.7770	0.6964	0.6587	425
weighted avg	0.7750	0.7082	0.6668	425



Pentru k-folduri:

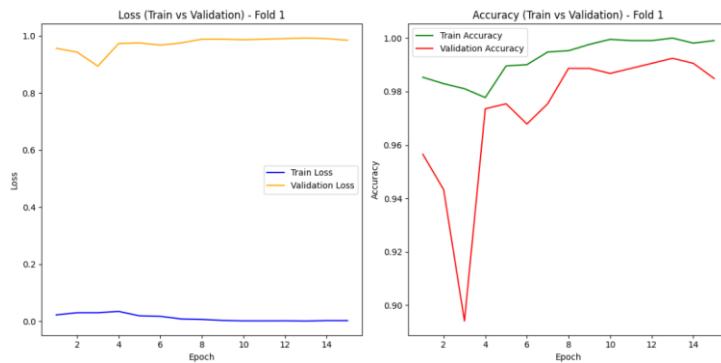
```
Precision: Mean = 0.9970, Std = 0.0067
Recall: Mean = 0.9970, Std = 0.0068
F1-score: Mean = 0.9970, Std = 0.0068
Accuracy: Mean = 0.9970, Std = 0.0068
```

Media metricilor dupa antrenarea pe k-folduri

Pentru fold1:

	precision	recall	f1-score	support
glioma_tumor	0.8421	0.1600	0.2689	100
meningioma_tumor	0.7051	0.9565	0.8118	115
no_tumor	0.5954	0.9810	0.7410	105
pituitary_tumor	0.9610	0.7048	0.8132	105
accuracy			0.7129	425
macro avg	0.7759	0.7006	0.6587	425
weighted avg	0.7735	0.7129	0.6669	425

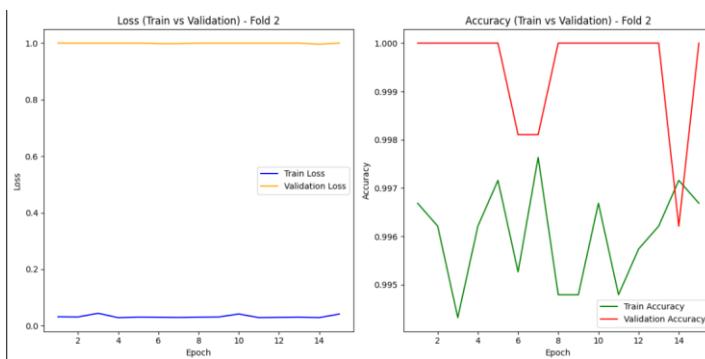
AUC for Fold 1: 0.9164



Pentru fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.7143	0.9565	0.8178	115
no_tumor	0.5722	0.9810	0.7228	105
pituitary_tumor	0.9722	0.6667	0.7910	105
accuracy			0.7082	425
macro avg	0.8015	0.6960	0.6585	425
weighted avg	0.7978	0.7082	0.6665	425

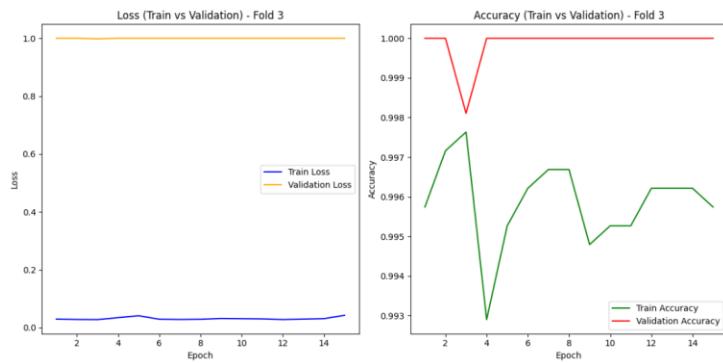
AUC for Fold 2: 0.9081



Pentru fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9444	0.1700	0.2881	100
meningioma_tumor	0.7255	0.9652	0.8284	115
no_tumor	0.5920	0.9810	0.7384	105
pituitary_tumor	0.9750	0.7429	0.8432	105
accuracy			0.7271	425
macro avg	0.8092	0.7148	0.6745	425
weighted avg	0.8057	0.7271	0.6827	425

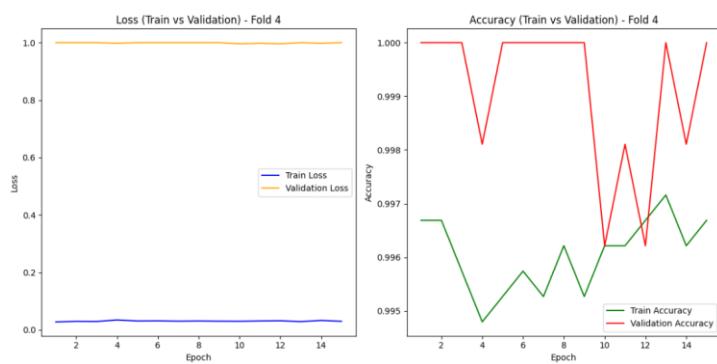
AUC for Fold 3: 0.9178



Pentru fold4:

	precision	recall	f1-score	support
glioma_tumor	0.8889	0.1600	0.2712	100
meningioma_tumor	0.7219	0.9478	0.8195	115
no_tumor	0.5691	0.9810	0.7203	105
pituitary_tumor	0.9867	0.7048	0.8222	105
accuracy			0.7106	425
macro avg	0.7916	0.6984	0.6583	425
weighted avg	0.7888	0.7106	0.6667	425

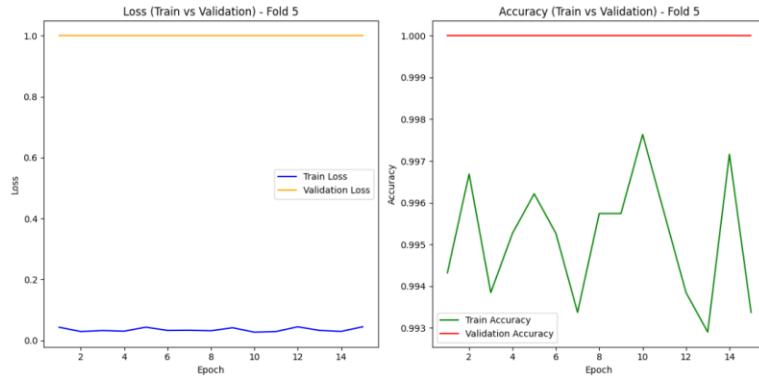
AUC for Fold 4: 0.9165



Pentru fold5:

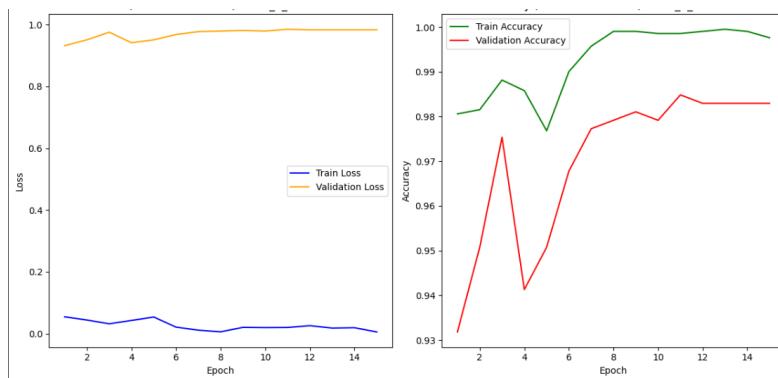
	precision	recall	f1-score	support
glioma_tumor	0.9565	0.2200	0.3577	100
meningioma_tumor	0.6957	0.9739	0.8116	115
no_tumor	0.6242	0.9810	0.7630	105
pituitary_tumor	0.9737	0.7048	0.8177	105
accuracy			0.7318	425
macro avg	0.8125	0.7199	0.6875	425
weighted avg	0.8081	0.7318	0.6943	425

AUC for Fold 5: 0.9224



Cel mai slab fold este foldul 2 in acest caz

Am introdus weight_decay cu valoarea 1e-4 si cu schedulerul ReduceLROnPlateau cu patience=3



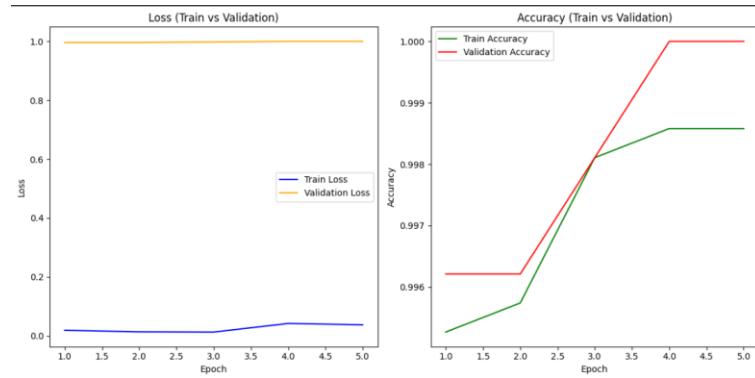
	precision	recall	f1-score	support
glioma_tumor	0.9565	0.2200	0.3577	100
meningioma_tumor	0.6974	0.9217	0.7940	115
no_tumor	0.5722	0.9810	0.7228	105
pituitary_tumor	0.9429	0.6286	0.7543	105
accuracy			0.6988	425
macro avg	0.7922	0.6878	0.6572	425
weighted avg	0.7881	0.6988	0.6639	425

AUC for Fold 1 scheduler: 0.9094

===== Overall AUC on Test Set =====

Average AUC: 0.9094

Iar pentru early_stopping:



	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7432	0.9565	0.8365	115
no_tumor	0.5361	0.9905	0.6957	105
pituitary_tumor	0.9692	0.6000	0.7412	105
accuracy			0.6941	425
macro avg	0.8121	0.6817	0.6446	425
weighted avg	0.8083	0.6941	0.6531	425

AUC early_stopping: 0.8850

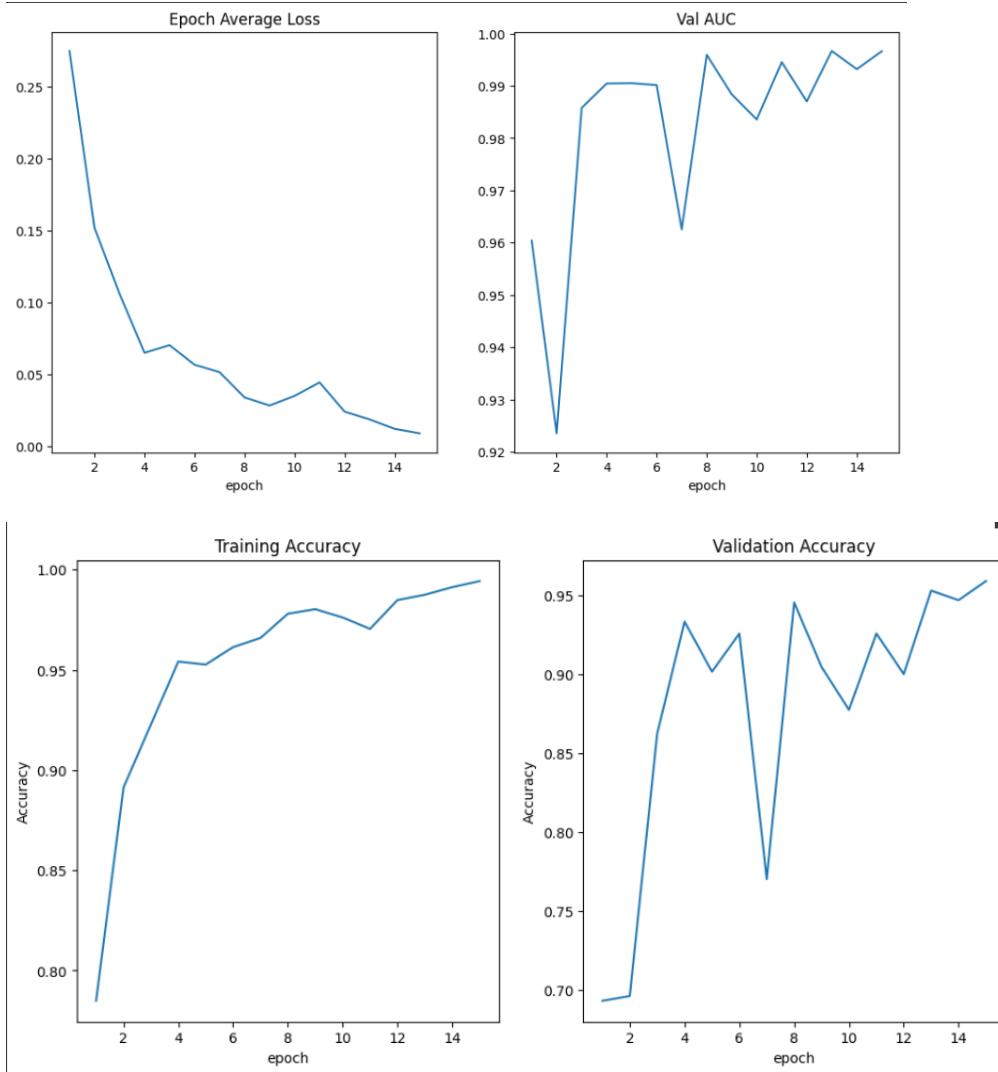
===== Overall AUC on Test Set =====

Average AUC: 0.8850

Fata de cerinta 2.4 cand la early_stopping se opreste la cea de-a treia epoca, acum s-a oprit la epoca 5.

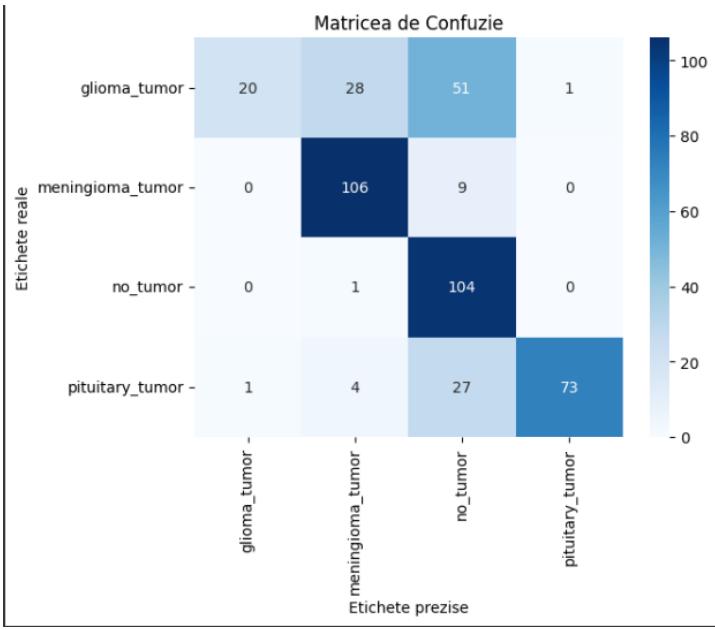
Acum am introdus dropout la modelul meu si am testat tot pentru batch_size = 32 cu optimizatorul Adam cu learning_rate de 0.001 si cu dropout.

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.9524	0.2000	0.3306	100
meningioma_tumor	0.7626	0.9217	0.8346	115
no_tumor	0.5445	0.9905	0.7027	105
pituitary_tumor	0.9865	0.6952	0.8156	105
accuracy			0.7129	425
macro avg	0.8115	0.7019	0.6709	425
weighted avg	0.8087	0.7129	0.6787	425

Observam ca a crescut acuratetea fata de mai devreme pana sa introduc dropout



Antrenarea cu k-folduri dar cu dropout inclus:

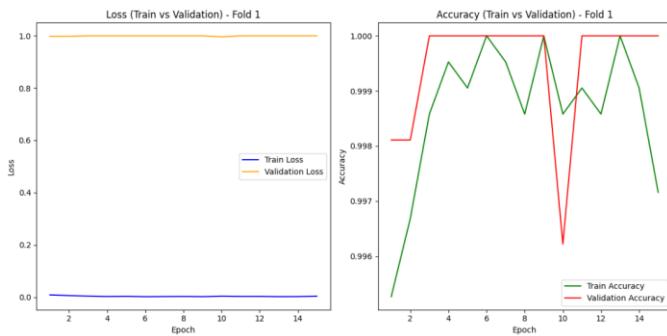
```
Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

Media metricilor la rulare

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.6962	0.9565	0.8059	115
no_tumor	0.5886	0.9810	0.7357	105
pituitary_tumor	0.9589	0.6667	0.7865	105
accuracy			0.7106	425
macro avg	0.8109	0.6985	0.6619	425
weighted avg	0.8060	0.7106	0.6693	425

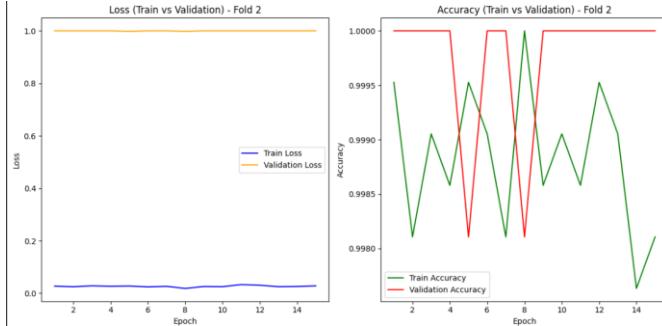
AUC for Fold 1: 0.9105



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.6981	0.9652	0.8102	115
no_tumor	0.5691	0.9810	0.7203	105
pituitary_tumor	0.9701	0.6190	0.7558	105
accuracy			0.6988	425
macro avg	0.8093	0.6863	0.6478	425
weighted avg	0.8045	0.6988	0.6557	425

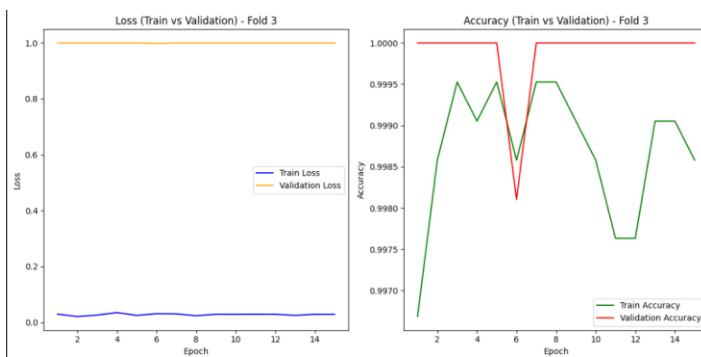
AUC for Fold 2: 0.9041



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.7552	0.9391	0.8372	115
no_tumor	0.5683	0.9905	0.7222	105
pituitary_tumor	0.9750	0.7429	0.8432	105
accuracy			0.7271	425
macro avg	0.8246	0.7156	0.6805	425
weighted avg	0.8209	0.7271	0.6884	425

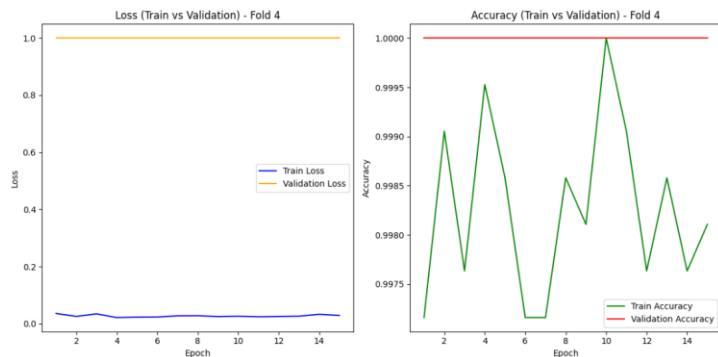
AUC for Fold 3: 0.9158



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2000	0.3333	100
meningioma_tumor	0.7208	0.9652	0.8253	115
no_tumor	0.5754	0.9810	0.7254	105
pituitary_tumor	0.9722	0.6667	0.7910	105
accuracy			0.7153	425
macro avg	0.8171	0.7032	0.6687	425
weighted avg	0.8127	0.7153	0.6764	425

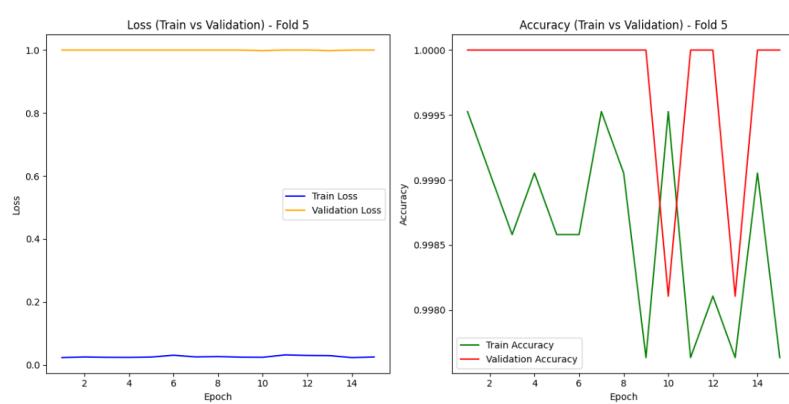
AUC for Fold 4: 0.9168



Fold5:

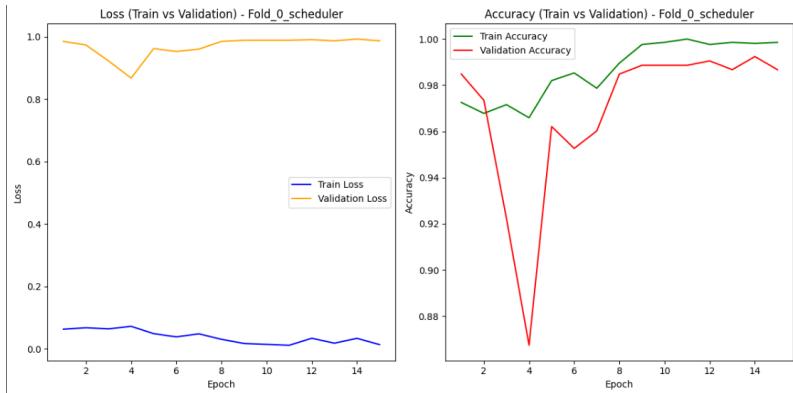
	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2000	0.3333	100
meningioma_tumor	0.7152	0.9391	0.8120	115
no_tumor	0.5659	0.9810	0.7178	105
pituitary_tumor	0.9722	0.6667	0.7910	105
accuracy			0.7082	425
macro avg	0.8133	0.6967	0.6635	425
weighted avg	0.8088	0.7082	0.6709	425

AUC for Fold 5: 0.9107



Foldul cel mai slab ramane si in acest caz foldul 2

Scheduler cu weight_decay

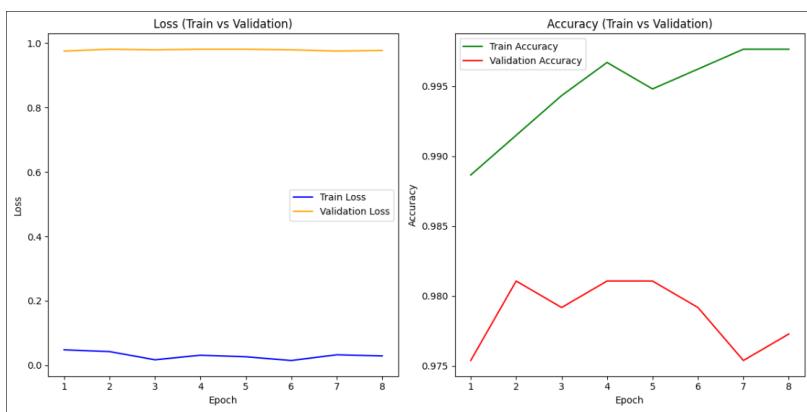


	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.7376	0.9043	0.8125	115
no_tumor	0.5445	0.9905	0.7027	105
pituitary_tumor	0.9459	0.6667	0.7821	105
accuracy			0.6988	425
macro avg	0.8070	0.6879	0.6542	425
weighted avg	0.8031	0.6988	0.6618	425

AUC for Fold 1 scheduler: 0.9072
===== Overall AUC on Test Set =====
verage AUC: 0.9072

Fata de cazul anterior, acuratetea este la fel in schimb valori mai bune la precision

Cu early_stopping :



```

precision    recall   f1-score  support
glioma_tumor 1.0000  0.1900  0.3193    100
meningioma_tumor 0.7086  0.9304  0.8045    115
no_tumor      0.5417  0.9905  0.7003    105
pituitary_tumor 0.9683  0.5810  0.7262    105

accuracy          0.6847    425
macro avg       0.8046  0.6730  0.6376    425
weighted avg    0.8001  0.6847  0.6453    425

AUC early_stopping: 0.8967

===== Overall AUC on Test Set ======
Average AUC: 0.8967

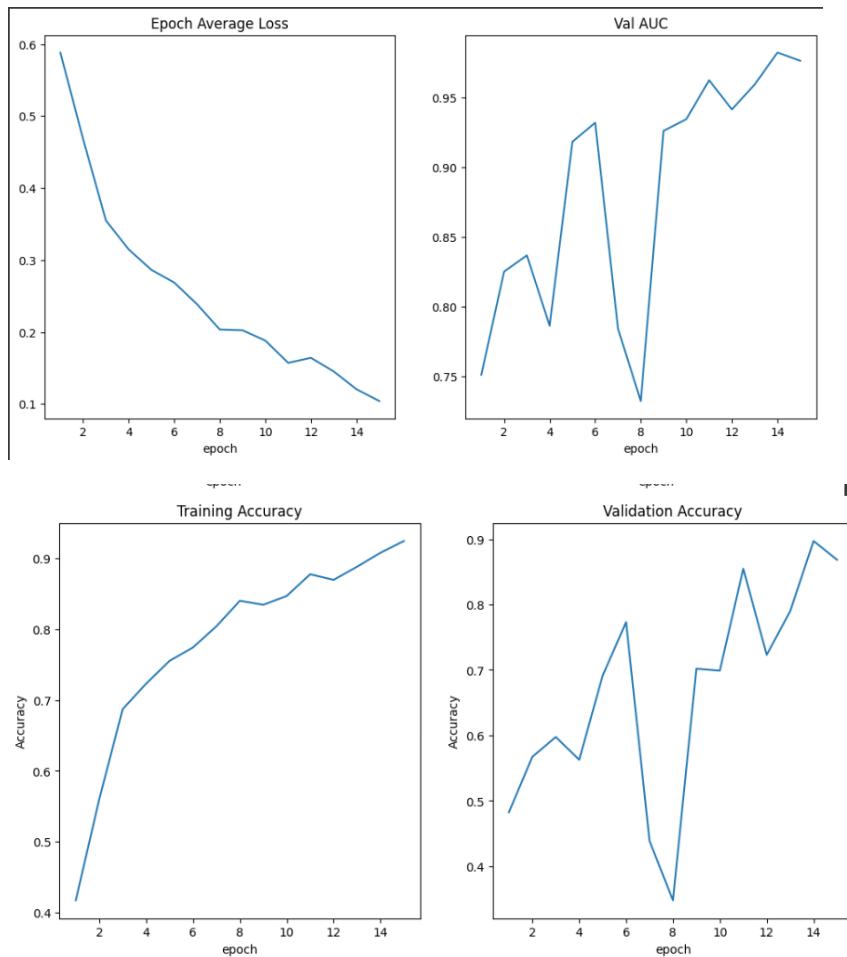
```

Antrenarea s-a oprit la epoca 8.

Nu a crescut acuratetea fata de scheduler iar restul metrictilor sunt asemanatoare cum ar fi la precision pentru glanda pituitara precizia a crescut, dar la recall a scazut.

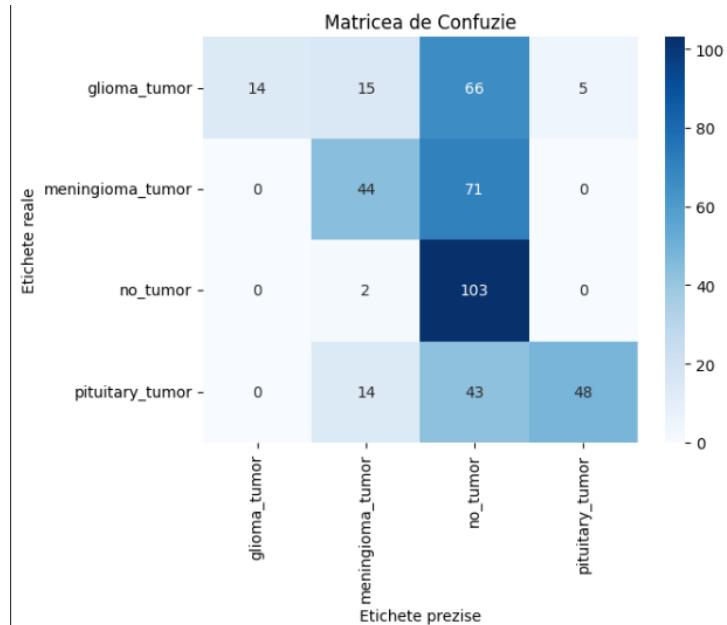
Acum am urcat larning_rate la 0.01 pentru optimizatorul Adam, batch_size=32, mai intai fara dropout

O mica mentionare : AUC pe evaluarea cu setul de testare a fost inclus in screenshot-ul cu fold-ul 5



	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1400	0.2456	100
meningioma_tumor	0.5867	0.3826	0.4632	115
no_tumor	0.3640	0.9810	0.5309	105
pituitary_tumor	0.9057	0.4571	0.6076	105
accuracy			0.4918	425
macro avg	0.7141	0.4902	0.4618	425
weighted avg	0.7077	0.4918	0.4644	425

Observam ca a scazut acuratetea drastic.



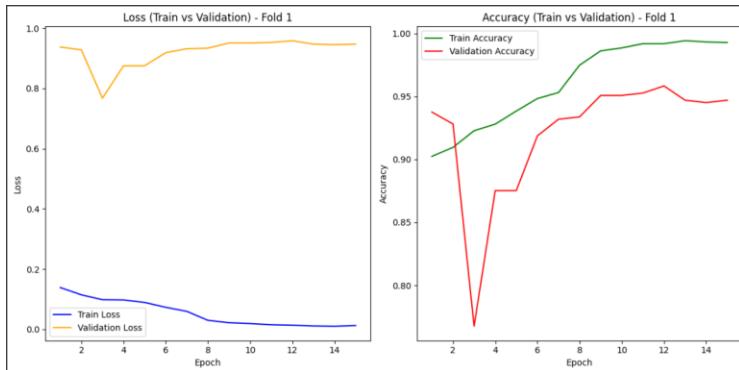
Pentru fold-uri, media metricilor este:

```
Precision: Mean = 0.9865, Std = 0.0220
Recall: Mean = 0.9864, Std = 0.0222
F1-score: Mean = 0.9864, Std = 0.0222
Accuracy: Mean = 0.9864, Std = 0.0222
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.6855	0.9478	0.7956	115
no_tumor	0.5372	0.9619	0.6894	105
pituitary_tumor	0.9322	0.5238	0.6707	105
accuracy			0.6659	425
macro avg	0.7756	0.6534	0.6146	425
weighted avg	0.7714	0.6659	0.6225	425

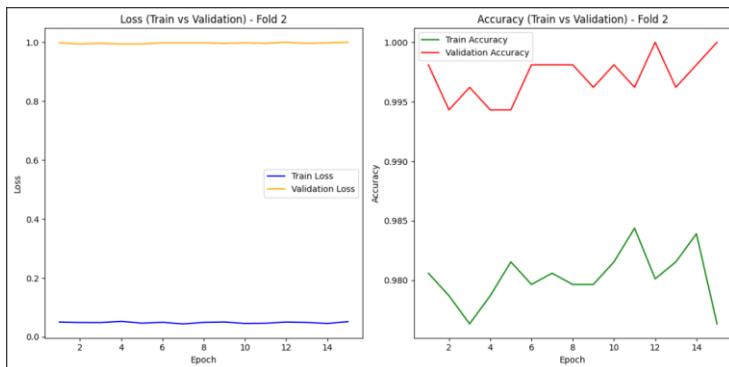
AUC for Fold 1: 0.8217
Evaluation Fold 2



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1700	0.2906	100
meningioma_tumor	0.6939	0.8870	0.7786	115
no_tumor	0.5074	0.9810	0.6688	105
pituitary_tumor	0.9310	0.5143	0.6626	105
accuracy			0.6494	425
macro avg	0.7831	0.6380	0.6002	425
weighted avg	0.7784	0.6494	0.6080	425

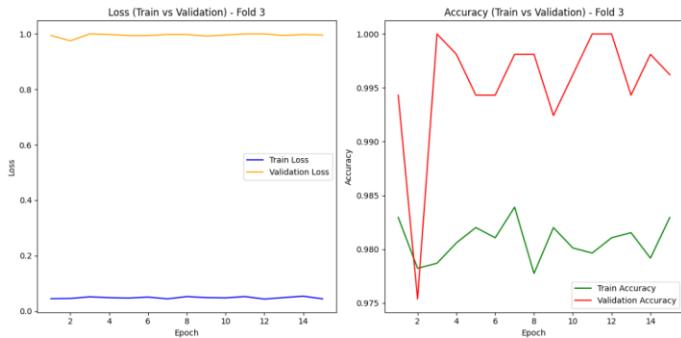
AUC for Fold 2: 0.8189



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7095	0.9130	0.7985	115
no_tumor	0.5074	0.9810	0.6688	105
pituitary_tumor	0.9643	0.5143	0.6708	105
accuracy			0.6588	425
macro avg	0.7953	0.6471	0.6108	425
weighted avg	0.7909	0.6588	0.6188	425

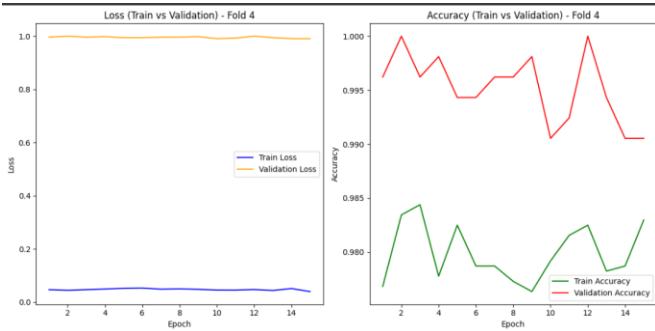
AUC for Fold 3: 0.8206



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.6391	0.9391	0.7606	115
no_tumor	0.5102	0.9524	0.6645	105
pituitary_tumor	0.9000	0.3429	0.4966	105
accuracy			0.6165	425
macro avg	0.7373	0.6036	0.5554	425
weighted avg	0.7331	0.6165	0.5632	425

AUC for Fold 4: 0.8117



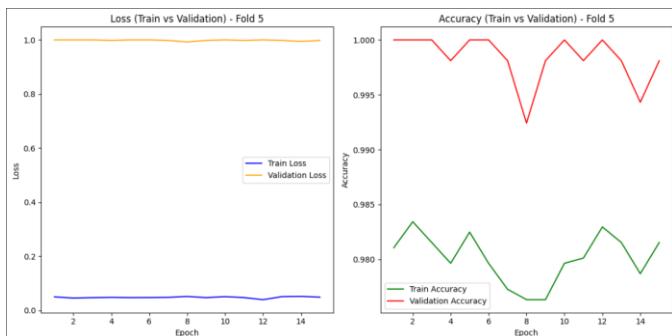
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1800	0.2975	100
meningioma_tumor	0.6543	0.9217	0.7653	115
no_tumor	0.5126	0.9714	0.6711	105
pituitary_tumor	0.9070	0.3714	0.5270	105
accuracy			0.6235	425
macro avg	0.7328	0.6111	0.5652	425
weighted avg	0.7294	0.6235	0.5731	425

AUC for Fold 5: 0.8175

===== Overall AUC on Test Set =====

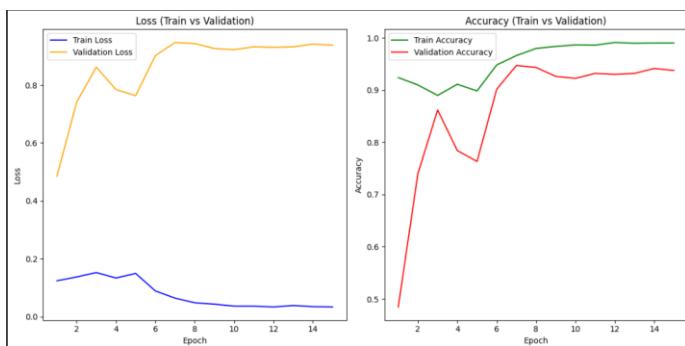
Average AUC: 0.8181



Acurateti mai slabe decat daca aveam learning_rate de 0.001.

Foldul cel mai slab ramane si aici foldul 2.

Scheduler cu weight_decay pentru foldul 2:



```

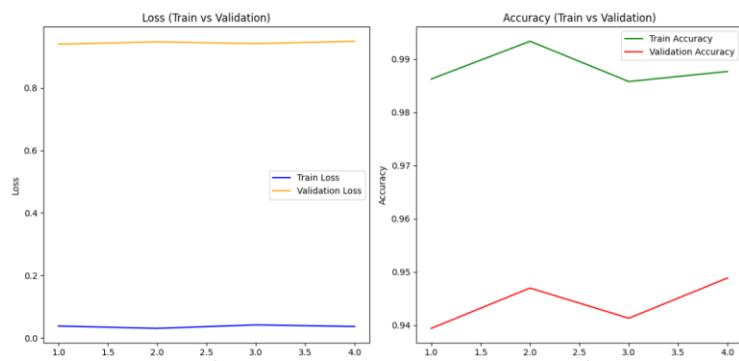
precision    recall   f1-score   support
glioma_tumor      0.7200    0.1800    0.2880     100
meningioma_tumor   0.7132    0.8000    0.7541     115
no_tumor           0.4602    0.9905    0.6284     105
pituitary_tumor    0.9111    0.3905    0.5467     105

accuracy          0.6000
macro avg         0.7011    0.5902    0.5543     425
weighted avg       0.7012    0.6000    0.5621     425

AUC for Fold 2 scheduler: 0.8116
===== Overall AUC on Test Set =====
Average AUC: 0.8116

```

Cu early_stopping:



S-a oprit la epoca 4.

```

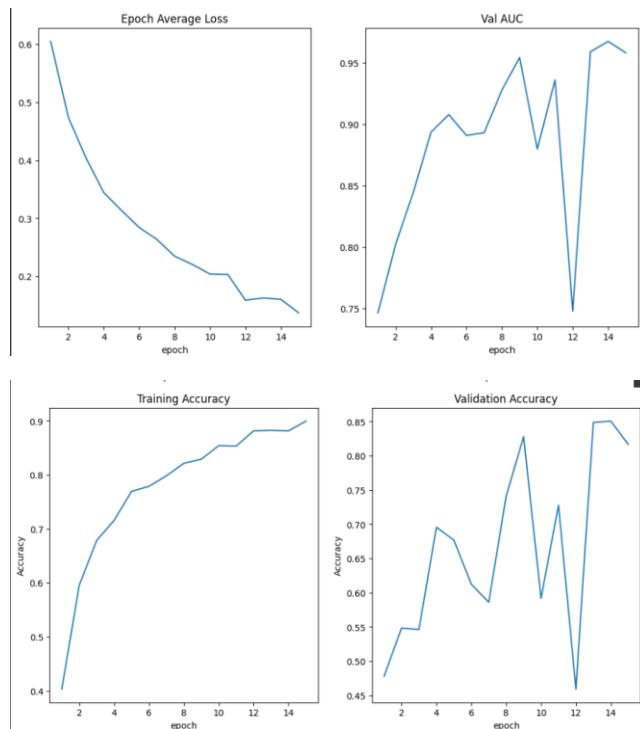
precision    recall   f1-score   support
glioma_tumor      0.7600    0.1900    0.3040      100
meningioma_tumor   0.7209    0.8087    0.7623      115
no_tumor           0.4541    0.9905    0.6228      105
pituitary_tumor    0.9048    0.3619    0.5170      105

accuracy          -         -        0.5976      425
macro avg         0.7100    0.5878    0.5515      425
weighted avg       0.7096    0.5976    0.5594      425

AUC early_stopping: 0.8136
===== Overall AUC on Test Set =====
Average AUC: 0.8136

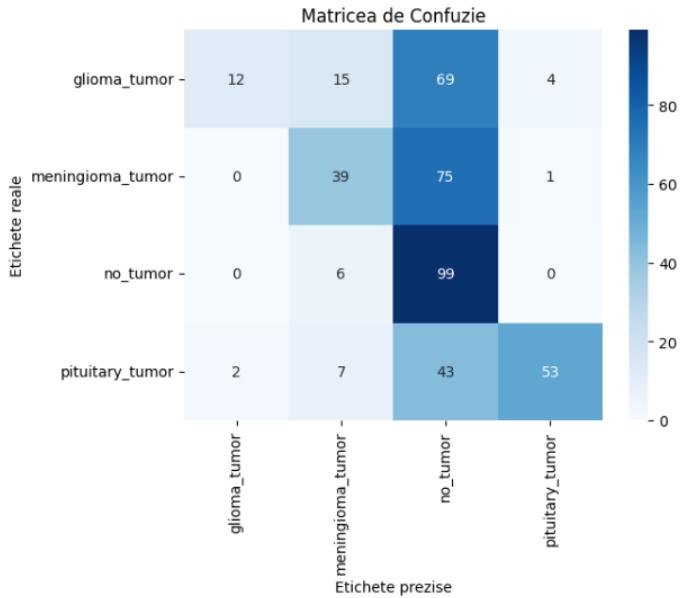
```

Acum introducem dropout-ul si in rest aceleasi specificatii (optimizer= Adam, learning_rate=0.01, batch_size=32)



	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1200	0.2105	100
meningioma_tumor	0.5821	0.3391	0.4286	115
no_tumor	0.3462	0.9429	0.5064	105
pituitary_tumor	0.9138	0.5048	0.6503	105
accuracy	-	-	0.4776	425
macro avg	0.6748	0.4767	0.4489	425
weighted avg	0.6705	0.4776	0.4513	425

Aici a scazut acuratetea dupa ce am adaugat dropout



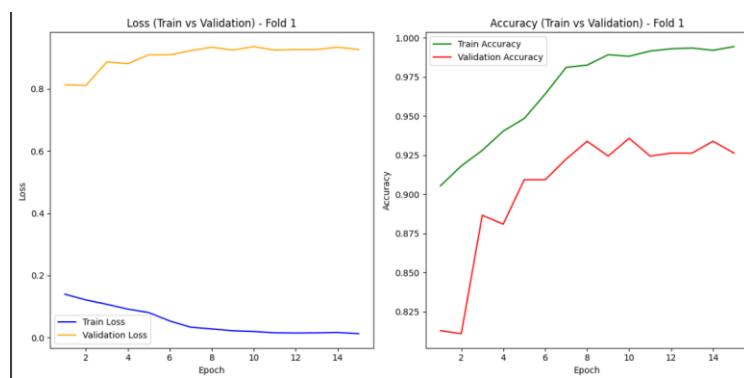
Pentru folduri media metricilor este :

```
Precision: Mean = 0.9833, Std = 0.0311
Recall: Mean = 0.9830, Std = 0.0318
F1-score: Mean = 0.9830, Std = 0.0317
Accuracy: Mean = 0.9830, Std = 0.0318
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.7778	0.1400	0.2373	100
meningioma_tumor	0.6646	0.9130	0.7692	115
no_tumor	0.5316	0.9619	0.6847	105
pituitary_tumor	0.9492	0.5333	0.6829	105
accuracy			0.6494	425
macro avg	0.7308	0.6371	0.5935	425
weighted avg	0.7287	0.6494	0.6019	425

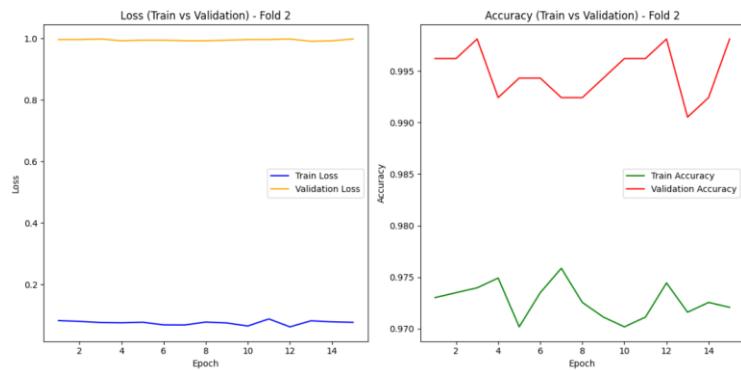
AUC for Fold 1: 0.8541



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9333	0.1400	0.2435	100
meningioma_tumor	0.6347	0.9217	0.7518	115
no_tumor	0.5600	0.9333	0.7000	105
pituitary_tumor	0.9265	0.6000	0.7283	105
accuracy			0.6612	425
macro avg	0.7636	0.6488	0.6059	425
weighted avg	0.7586	0.6612	0.6136	425

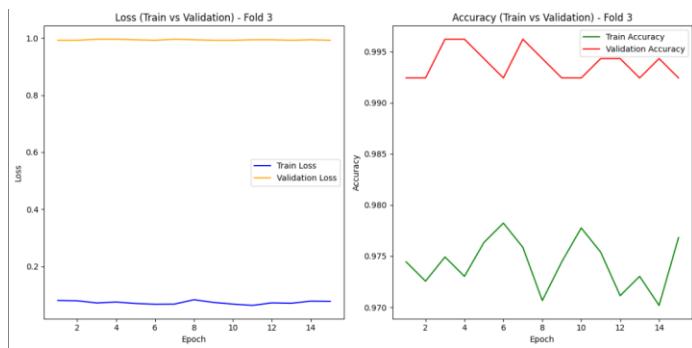
AUC for Fold 2: 0.8542



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1500	0.2609	100
meningioma_tumor	0.7103	0.8957	0.7923	115
no_tumor	0.5024	0.9810	0.6645	105
pituitary_tumor	0.9167	0.5238	0.6667	105
accuracy			0.6494	425
macro avg	0.7824	0.6376	0.5961	425
weighted avg	0.7781	0.6494	0.6047	425

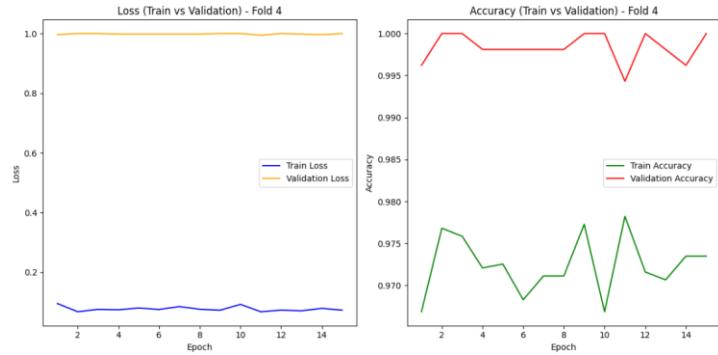
AUC for Fold 3: 0.8434



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.8333	0.1500	0.2542	100
meningioma_tumor	0.6386	0.9217	0.7544	115
no_tumor	0.5780	0.9524	0.7194	105
pituitary_tumor	0.9412	0.6095	0.7399	105
accuracy			0.6706	425
macro avg	0.7478	0.6584	0.6170	425
weighted avg	0.7442	0.6706	0.6245	425

AUC for Fold 4: 0.8585



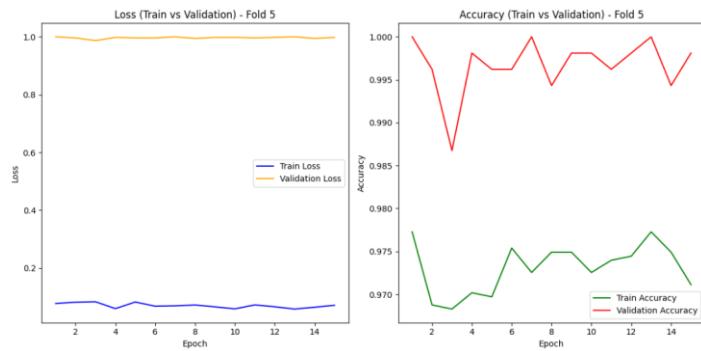
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8500	0.1700	0.2833	100
meningioma_tumor	0.6846	0.8870	0.7727	115
no_tumor	0.5075	0.9619	0.6645	105
pituitary_tumor	0.9298	0.5048	0.6543	105
accuracy			0.6424	425
macro avg	0.7430	0.6309	0.5937	425
weighted avg	0.7403	0.6424	0.6016	425

AUC for Fold 5: 0.8400

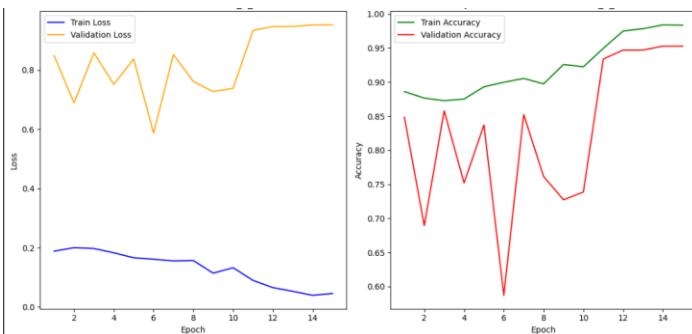
===== Overall AUC on Test Set =====

Average AUC: 0.8500



De data aceasta, cel mai slab fold a fost fold-ul 5

Scheduler cu weight_decay:



	precision	recall	f1-score	support
glioma_tumor	0.8947	0.1700	0.2857	100
meningioma_tumor	0.7164	0.8348	0.7711	115
no_tumor	0.4905	0.9810	0.6540	105
pituitary_tumor	0.9516	0.5619	0.7066	105
accuracy			0.6471	425
macro avg	0.7633	0.6369	0.6043	425
weighted avg	0.7607	0.6471	0.6120	425

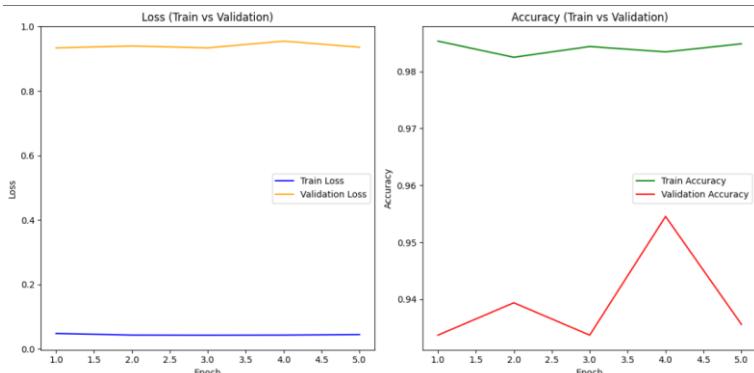
AUC for Fold 5 scheduler: 0.8441

===== Overall AUC on Test Set =====

Average AUC: 0.8441

A crescut acuratetea putin

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.6558	0.8783	0.7509	115
no_tumor	0.5178	0.9714	0.6755	105
pituitary_tumor	0.9444	0.4857	0.6415	105
accuracy			0.6400	425
macro avg	0.7545	0.6289	0.5920	425
weighted avg	0.7505	0.6400	0.5992	425

AUC early_stopping: 0.8399

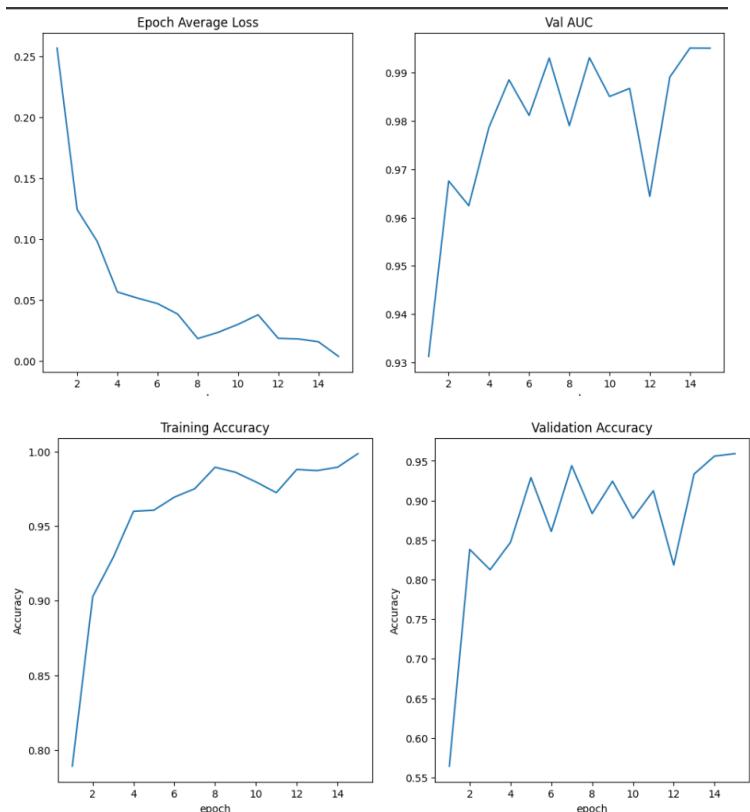
===== Overall AUC on Test Set =====

Average AUC: 0.8399

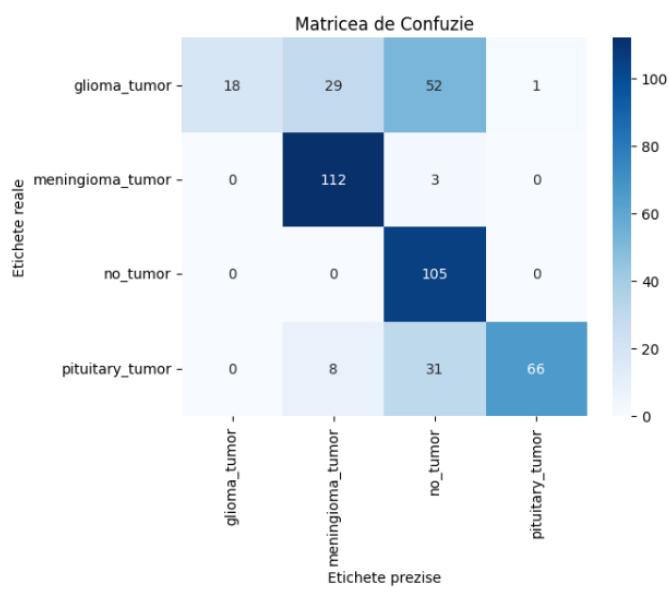
Am avansat pana la epoca 5.

Cazul cu Adam cu learning_rate de 0.001, batch_size=64, fara dropout

Antrenarea fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7517	0.9739	0.8485	115
no_tumor	0.5497	1.0000	0.7095	105
pituitary_tumor	0.9851	0.6286	0.7674	105
accuracy			0.7082	425
macro avg	0.8216	0.6956	0.6576	425
weighted avg	0.8179	0.7082	0.6663	425



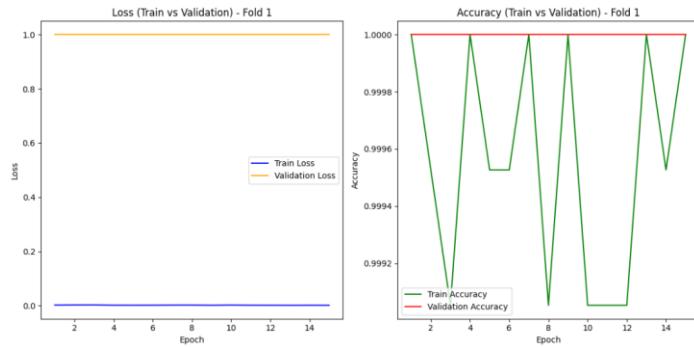
Pentru folduri, , media metricilor la antrenare este:

```
Precision: Mean = 1.0000, Std = 0.0000
Recall: Mean = 1.0000, Std = 0.0000
F1-score: Mean = 1.0000, Std = 0.0000
Accuracy: Mean = 1.0000, Std = 0.0000
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.7115	0.9652	0.8192	115
no_tumor	0.5532	0.9905	0.7099	105
pituitary_tumor	0.9839	0.5810	0.7305	105
accuracy			0.6941	425
macro avg	0.8122	0.6817	0.6447	425
weighted avg	0.8076	0.6941	0.6527	425

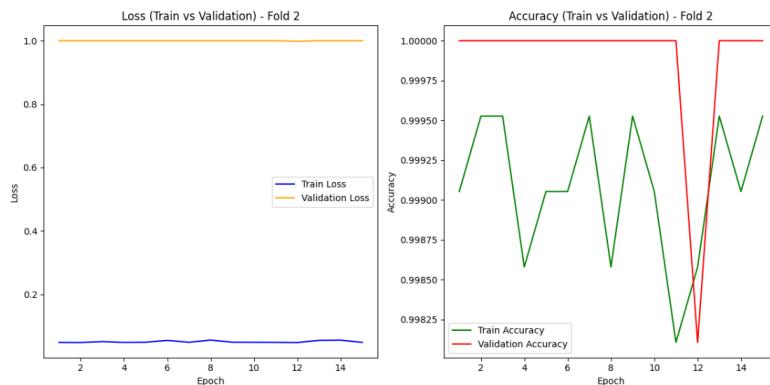
AUC for Fold 1: 0.8858



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1800	0.3051	100
meningioma_tumor	0.7208	0.9652	0.8253	115
no_tumor	0.5532	0.9905	0.7099	105
pituitary_tumor	1.0000	0.6190	0.7647	105
accuracy			0.7012	425
macro avg	0.8185	0.6887	0.6512	425
weighted avg	0.8141	0.7012	0.6594	425

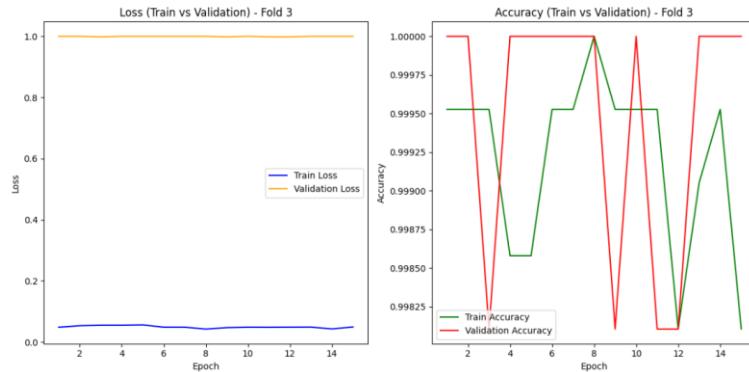
AUC for Fold 2: 0.8902



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.7534	0.9565	0.8429	115
no_tumor	0.5440	1.0000	0.7047	105
pituitary_tumor	0.9851	0.6286	0.7674	105
accuracy			0.7059	425
macro avg	0.8206	0.6938	0.6586	425
weighted avg	0.8169	0.7059	0.6669	425

AUC for Fold 3: 0.8921

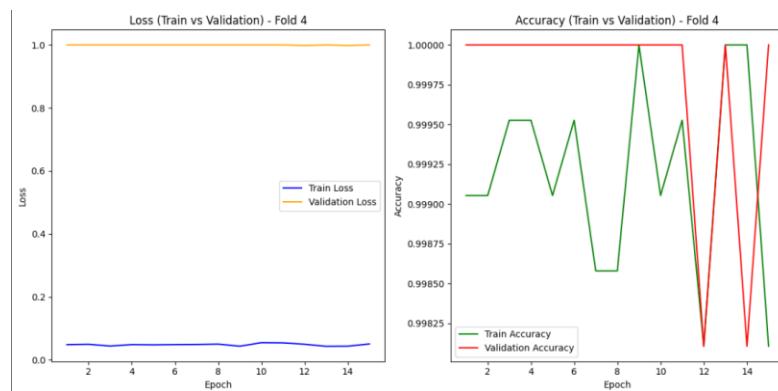


Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7606	0.9391	0.8405	115
no_tumor	0.5306	0.9905	0.6910	105
pituitary_tumor	0.9851	0.6286	0.7674	105
accuracy			0.6988	425
macro avg	0.8066	0.6870	0.6539	425
weighted avg	0.8038	0.6988	0.6623	425

AUC for Fold 4: 0.8837

Evaluation Fold 5



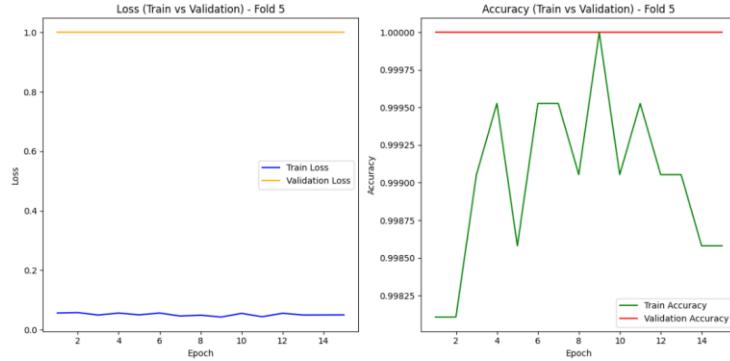
Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.6894	0.9652	0.8043	115
no_tumor	0.5746	0.9905	0.7273	105
pituitary_tumor	1.0000	0.6095	0.7574	105
accuracy			0.7012	425
macro avg	0.8160	0.6888	0.6521	425
weighted avg	0.8109	0.7012	0.6596	425

AUC for Fold 5: 0.9004

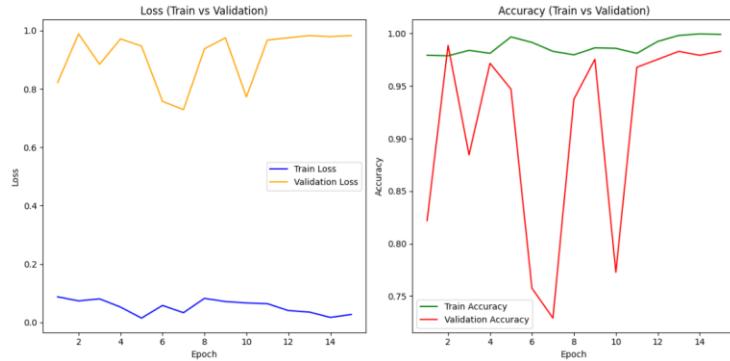
===== Overall AUC on Test Set =====

Average AUC: 0.8904



Cel mai slab fold este foldul 4

Scheduler cu weight_decay pe foldul slab:



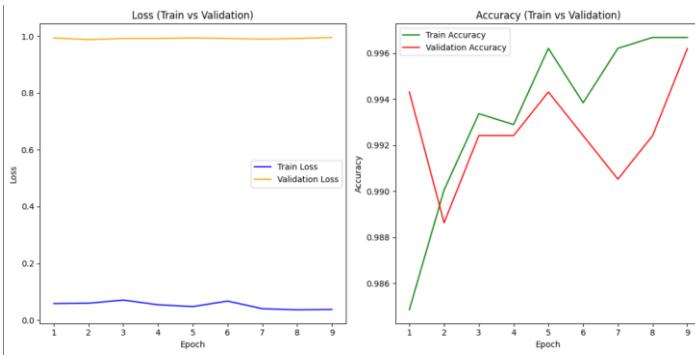
	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1900	0.3193	100
meningioma_tumor	0.7535	0.9304	0.8327	115
no_tumor	0.4860	0.9905	0.6520	105
pituitary_tumor	0.9800	0.4667	0.6323	105
accuracy			0.6565	425
macro avg	0.8049	0.6444	0.6091	425
weighted avg	0.8014	0.6565	0.6177	425

AUC for Fold 2 scheduler: 0.8551

===== Overall AUC on Test Set =====

Average AUC: 0.8551

Cu early_stopping:

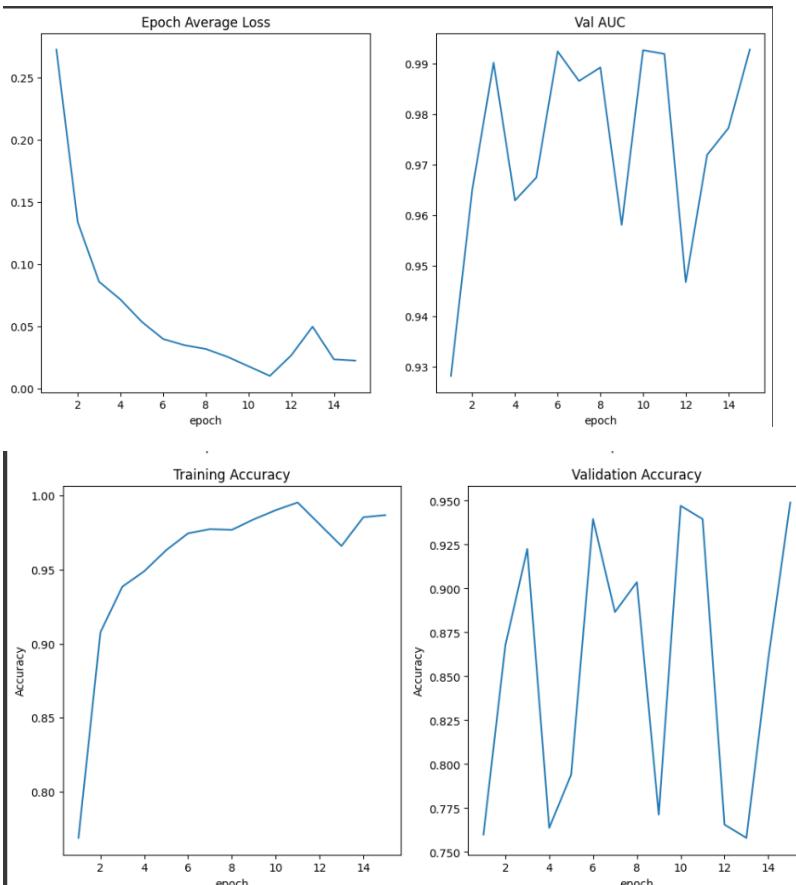


	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.6770	0.9478	0.7899	115
no_tumor	0.5691	0.9810	0.7203	105
pituitary_tumor	0.9355	0.5524	0.6946	105
accuracy			0.6847	425
macro avg	0.7954	0.6728	0.6380	425
weighted avg	0.7902	0.6847	0.6450	425

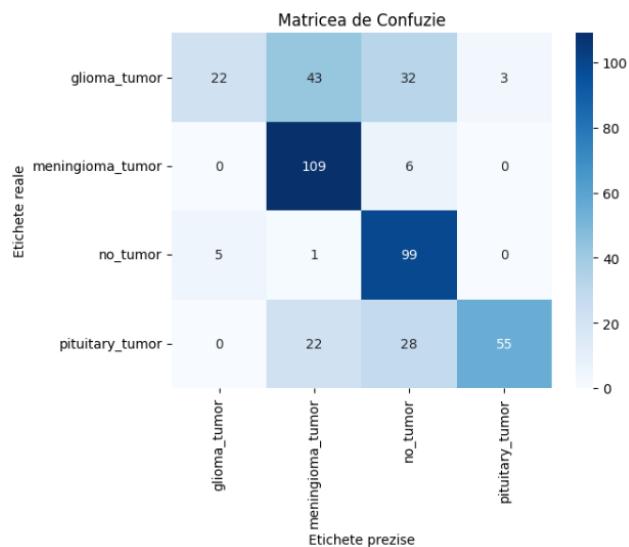
```
AUC early_stopping: 0.8857
===== Overall AUC on Test Set =====
Average AUC: 0.8857
```

Cu dropout batch_size=64, optimizator=Adam, learning_rate=0.001:

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.8148	0.2200	0.3465	100
meningioma_tumor	0.6229	0.9478	0.7517	115
no_tumor	0.6000	0.9429	0.7333	105
pituitary_tumor	0.9483	0.5238	0.6748	105
accuracy			0.6706	425
macro avg	0.7465	0.6586	0.6266	425
weighted avg	0.7428	0.6706	0.6328	425



Antrenarea cu k-folduri:

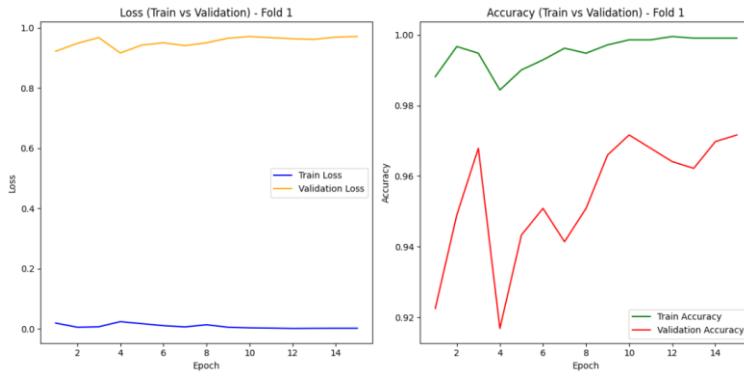
```
Precision: Mean = 0.9936, Std = 0.0121
Recall: Mean = 0.9936, Std = 0.0123
F1-score: Mean = 0.9936, Std = 0.0123
Accuracy: Mean = 0.9936, Std = 0.0123
```

Media metricilor

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.7248	0.9391	0.8182	115
no_tumor	0.5417	0.9905	0.7003	105
pituitary_tumor	0.9688	0.5905	0.7337	105
accuracy			0.6871	425
macro avg	0.7838	0.6750	0.6381	425
weighted avg	0.7811	0.6871	0.6463	425

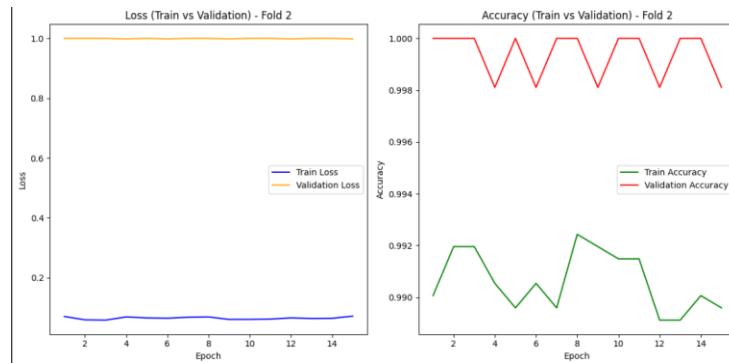
AUC for Fold 1: 0.9177



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.7200	0.9391	0.8151	115
no_tumor	0.5561	0.9905	0.7123	105
pituitary_tumor	0.9565	0.6286	0.7586	105
accuracy			0.6965	425
macro avg	0.7950	0.6845	0.6471	425
weighted avg	0.7915	0.6965	0.6551	425

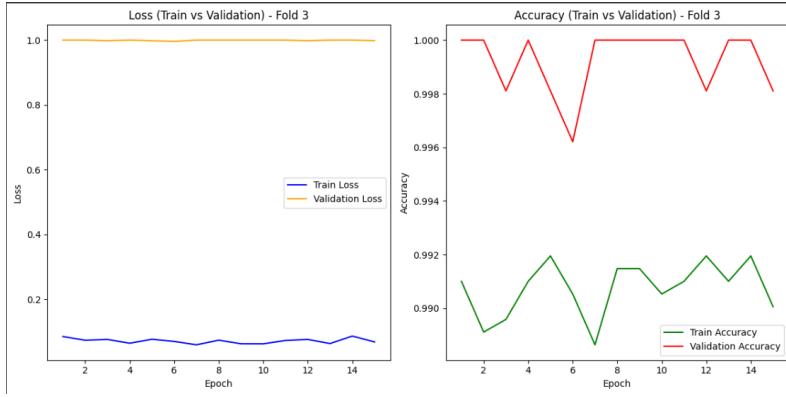
AUC for Fold 2: 0.9199



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9524	0.2000	0.3306	100
meningioma_tumor	0.7097	0.9565	0.8148	115
no_tumor	0.5714	0.9905	0.7247	105
pituitary_tumor	0.9701	0.6190	0.7558	105
accuracy			0.7035	425
macro avg	0.8009	0.6915	0.6565	425
weighted avg	0.7970	0.7035	0.6640	425

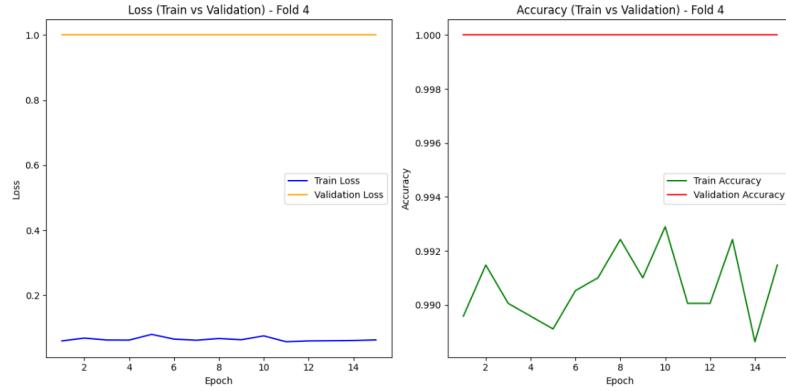
AUC for Fold 3: 0.9250



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.7097	0.9565	0.8148	115
no_tumor	0.5561	0.9905	0.7123	105
pituitary_tumor	0.9688	0.5905	0.7337	105
accuracy			0.6918	425
macro avg	0.7955	0.6794	0.6408	425
weighted avg	0.7917	0.6918	0.6489	425

AUC for Fold 4: 0.9142



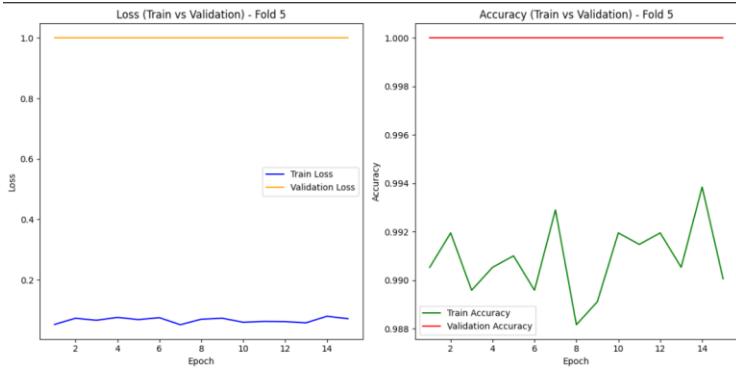
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9444	0.1700	0.2881	100
meningioma_tumor	0.7051	0.9565	0.8118	115
no_tumor	0.5503	0.9905	0.7075	105
pituitary_tumor	0.9839	0.5810	0.7305	105
accuracy			0.6871	425
macro avg	0.7959	0.6745	0.6345	425
weighted avg	0.7920	0.6871	0.6427	425

AUC for Fold 5: 0.9143

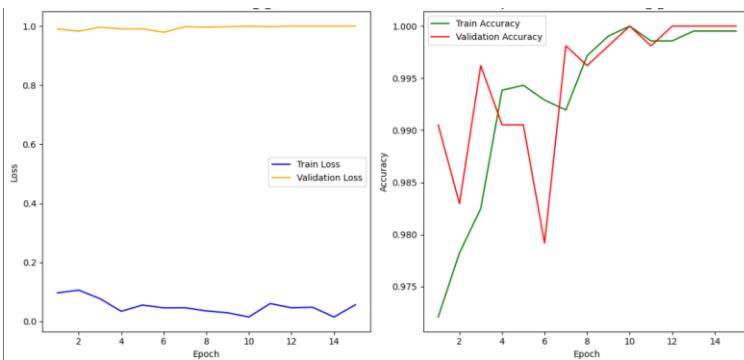
===== Overall AUC on Test Set =====

Average AUC: 0.9182



Cel mai slab fold este foldul 1

Scheduler cu weight_Decay:



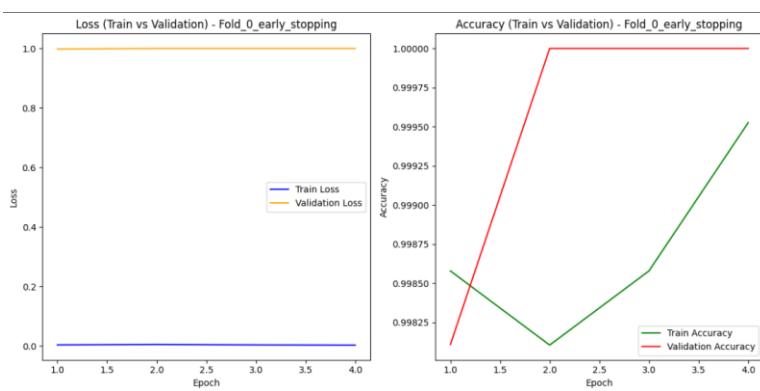
	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.6894	0.9652	0.8043	115
no_tumor	0.5876	0.9905	0.7376	105
pituitary_tumor	0.9851	0.6286	0.7674	105
accuracy			0.7059	425
macro avg	0.8030	0.6936	0.6565	425
weighted avg	0.7986	0.7059	0.6640	425

AUC for Fold 5 scheduler: 0.8912

===== Overall AUC on Test Set ======

Average AUC: 0.8912

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.9444	0.1700	0.2881	100
meningioma_tumor	0.7115	0.9652	0.8192	115
no_tumor	0.5810	0.9905	0.7324	105
pituitary_tumor	0.9722	0.6667	0.7910	105
accuracy			0.7106	425
macro avg	0.8023	0.6981	0.6577	425
weighted avg	0.7985	0.7106	0.6658	425

AUC for Fold 5 early_stopping: 0.8931

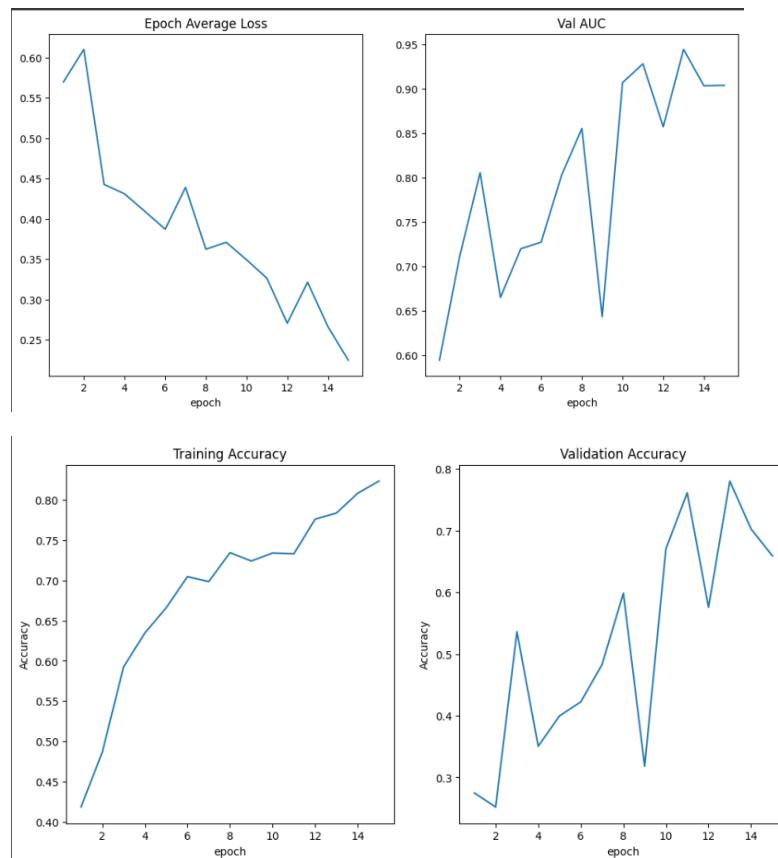
===== Overall AUC on Test Set ======

Average AUC: 0.8931

Am obtinut o acuratete mai buna la early_Stopping decat la scheduler cu weight_decay

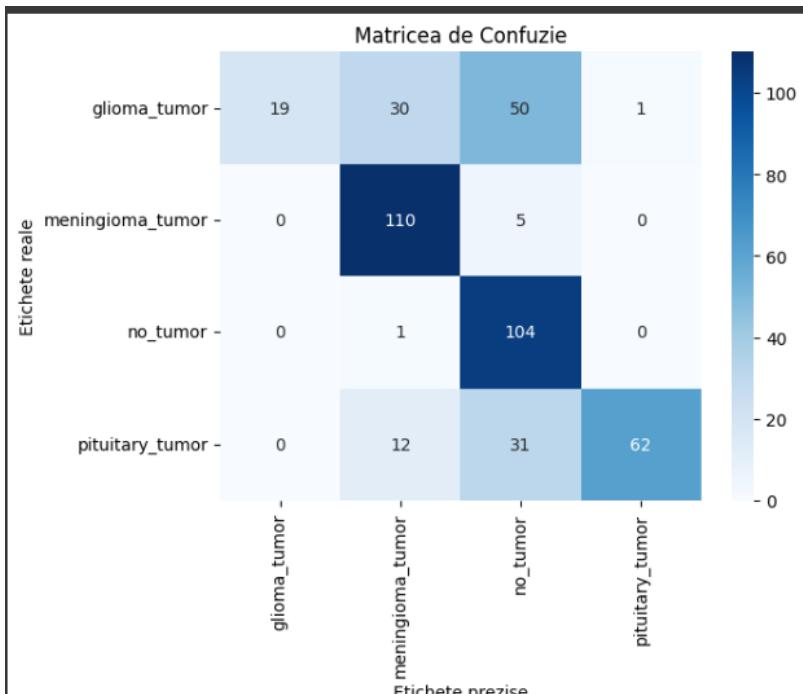
[Acum am testat cu optimizatorul Adam cu learning_rate = 0.01, batch_size = 64, fara dropout](#)

Pentru antrenarea clasica, fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.5833	0.1400	0.2258	100
meningioma_tumor	0.1000	0.0087	0.0160	115
no_tumor	0.2977	0.8762	0.4444	105
pituitary_tumor	0.4634	0.3619	0.4064	105
accuracy			0.3412	425
macro avg	0.3611	0.3467	0.2732	425
weighted avg	0.3524	0.3412	0.2677	425

Dupa cum am vazut prima oara la Adam cu learning_rate 0.01 dar cu batch_size=32, se poate observa ca fata de un learning_rate 0.001 este mult mai slaba acuratetea si la fel si metricile. Acuratetea este foarte slaba

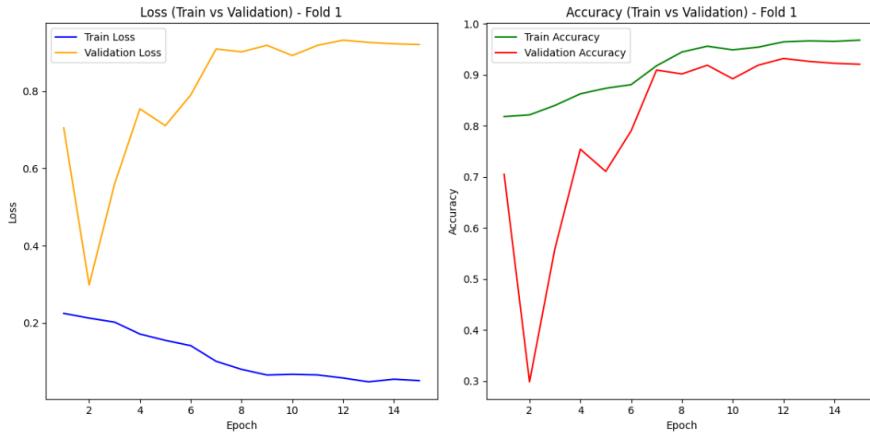


Antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9554, Std = 0.0208
Recall: Mean = 0.9534, Std = 0.0218
F1-score: Mean = 0.9533, Std = 0.0216
Accuracy: Mean = 0.9534, Std = 0.0218
```

Fold1:

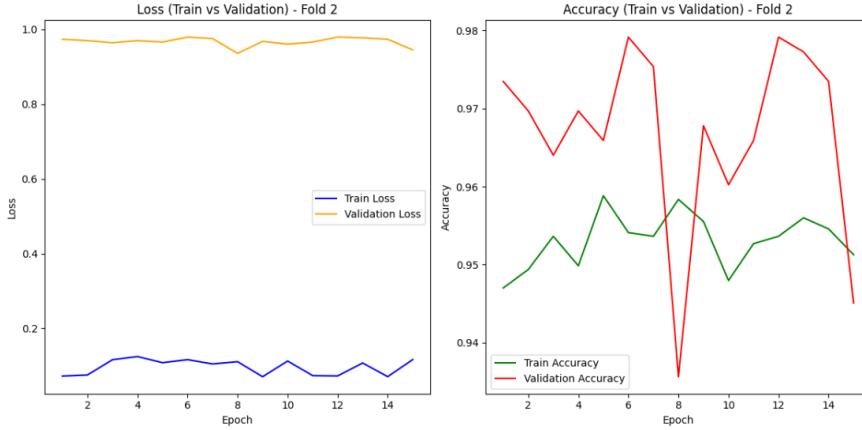
	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1700	0.2906	100
meningioma_tumor	0.6099	0.7478	0.6719	115
no_tumor	0.4762	0.9524	0.6349	105
pituitary_tumor	0.8421	0.4571	0.5926	105
accuracy			0.5906	425
macro avg	0.7321	0.5818	0.5475	425
weighted avg	0.7260	0.5906	0.5534	425
AUC for Fold 1:	0.7974			



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.7826	0.1800	0.2927	100
meningioma_tumor	0.6250	0.6957	0.6584	115
no_tumor	0.4562	0.9429	0.6149	105
pituitary_tumor	0.8421	0.4571	0.5926	105
accuracy			0.5765	425
macro avg	0.6765	0.5689	0.5397	425
weighted avg	0.6740	0.5765	0.5454	425

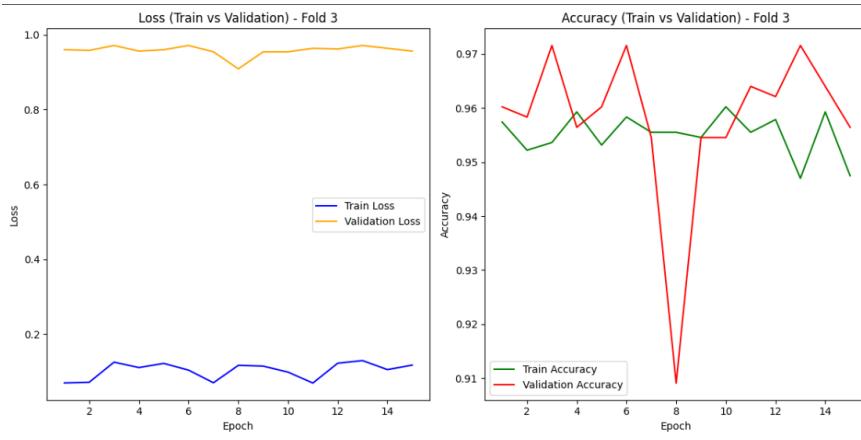
AUC for Fold 2: 0.7864



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1800	0.2975	100
meningioma_tumor	0.6364	0.7304	0.6802	115
no_tumor	0.4720	0.9619	0.6332	105
pituitary_tumor	0.8448	0.4667	0.6012	105
accuracy			0.5929	425
macro avg	0.7026	0.5848	0.5530	425
weighted avg	0.6992	0.5929	0.5590	425

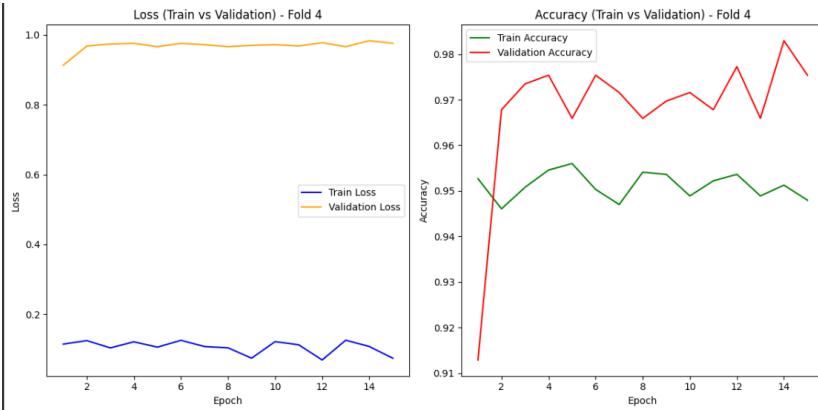
AUC for Fold 3: 0.7989
Evaluating Fold 4



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.7727	0.1700	0.2787	100
meningioma_tumor	0.6364	0.6696	0.6525	115
no_tumor	0.4317	0.9333	0.5904	105
pituitary_tumor	0.8545	0.4476	0.5875	105
accuracy			0.5624	425
macro avg	0.6738	0.5551	0.5273	425
weighted avg	0.6718	0.5624	0.5331	425

AUC for Fold 4: 0.7841



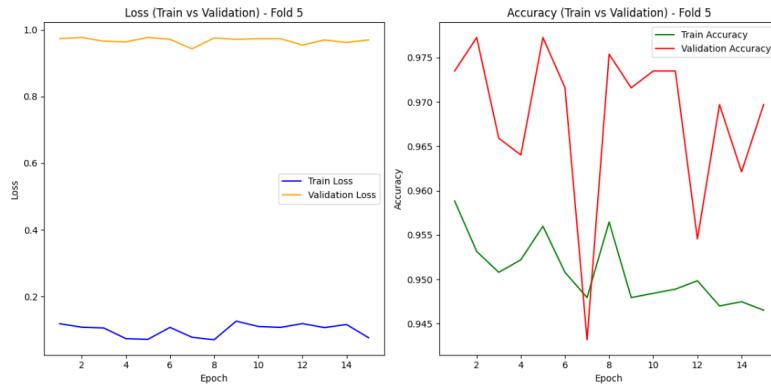
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9412	0.1600	0.2735	100
meningioma_tumor	0.6412	0.7304	0.6829	115
no_tumor	0.4498	0.9810	0.6168	105
pituitary_tumor	0.8958	0.4095	0.5621	105
accuracy			0.5788	425
macro avg	0.7320	0.5702	0.5338	425
weighted avg	0.7274	0.5788	0.5404	425

AUC for Fold 5: 0.7877

===== Overall AUC on Test Set =====

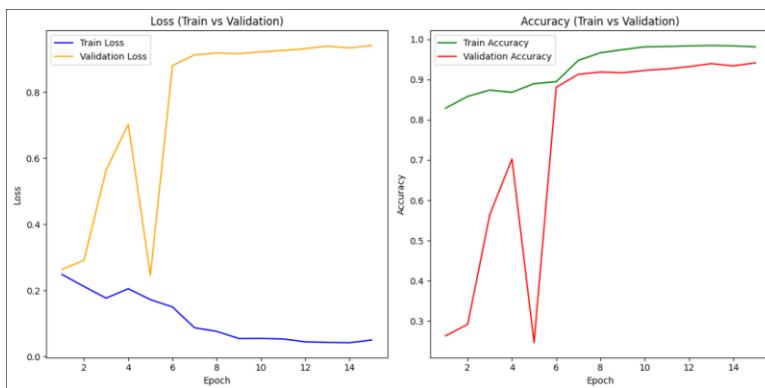
Average AUC: 0.7909



Acurateti mai bune fata de cea obtinuta la antrenarea clasica

Cel mai slab fold este foldul 4.

Antrenarea cu scheduler cu weight_decay

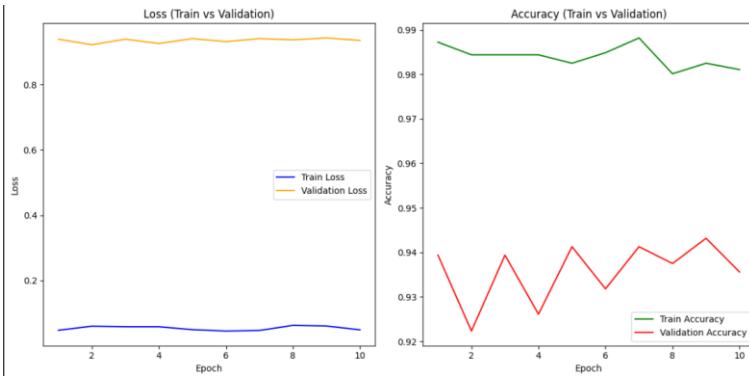


	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1800	0.2975	100
meningioma_tumor	0.6510	0.8435	0.7348	115
no_tumor	0.5024	0.9905	0.6667	105
pituitary_tumor	0.9167	0.4190	0.5752	105
accuracy			0.6188	425
macro avg	0.7318	0.6083	0.5685	425
weighted avg	0.7284	0.6188	0.5757	425

AUC for Fold 2 scheduler: 0.8432

===== Overall AUC on Test Set =====
Average AUC: 0.8432

Cu early_stopping:



Observam ca s-a oprit la epoca 10.

```

precision    recall   f1-score  support
glioma_tumor 1.0000  0.1600  0.2759   100
meningioma_tumor 0.6597  0.8261  0.7336   115
no_tumor       0.4883  0.9905  0.6541   105
pituitary_tumor 0.9038  0.4476  0.5987   105

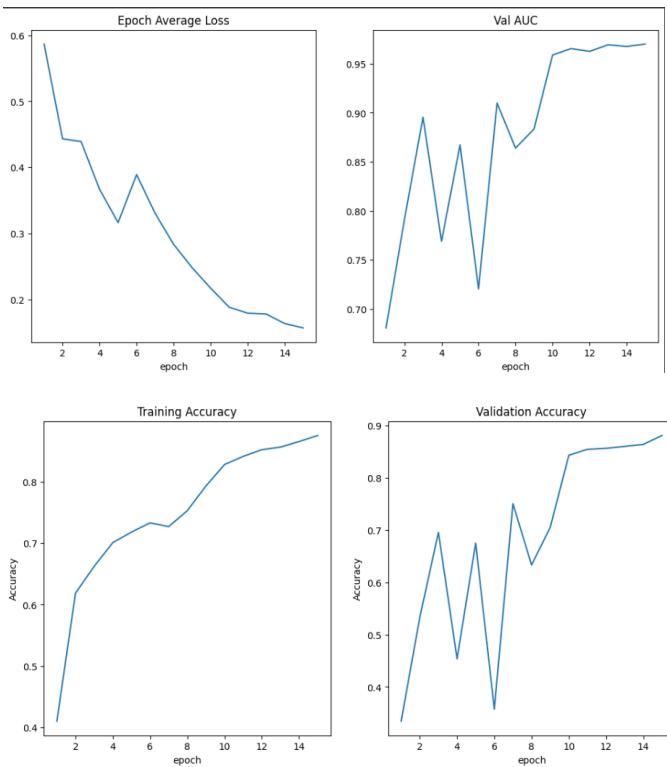
accuracy          0.6165
macro avg        0.7630  0.6060  0.5656   425
weighted avg     0.7577  0.6165  0.5729   425

AUC early_stopping: 0.8428
===== Overall AUC on Test Set =====
Average AUC: 0.8428

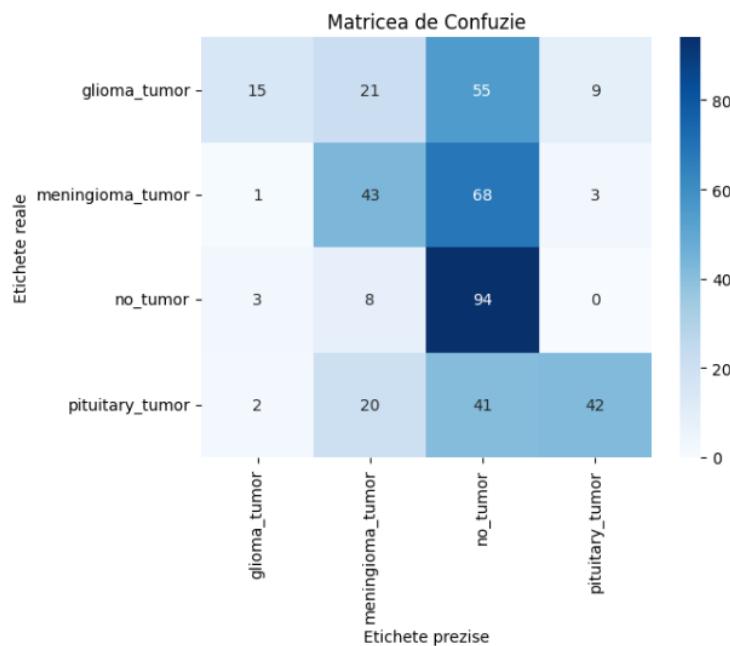
```

Acum am testat cu optimizatorul Adam cu learning_rate = 0.01, batch_size = 64, cu dropout

Pentru antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.7143	0.1500	0.2479	100
meningioma_tumor	0.4674	0.3739	0.4155	115
no_tumor	0.3643	0.8952	0.5179	105
pituitary_tumor	0.7778	0.4000	0.5283	105
accuracy			0.4565	425
macro avg	0.5809	0.4548	0.4274	425
weighted avg	0.5767	0.4565	0.4292	425



Pentru antrenarea cu k-folduri:

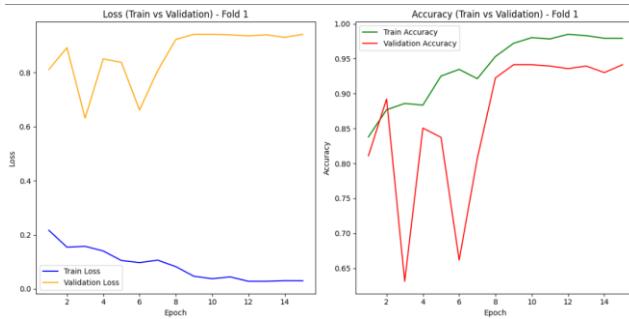
```
Precision: Mean = 0.9535, Std = 0.0209
Recall: Mean = 0.9527, Std = 0.0210
F1-score: Mean = 0.9523, Std = 0.0211
Accuracy: Mean = 0.9527, Std = 0.0210
```

Aceasta este media metricilor

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.7619	0.1600	0.2645	100
meningioma_tumor	0.6296	0.8870	0.7365	115
no_tumor	0.5531	0.9429	0.6972	105
pituitary_tumor	0.9048	0.5429	0.6786	105
accuracy			0.6447	425
macro avg	0.7123	0.6332	0.5942	425
weighted avg	0.7098	0.6447	0.6014	425

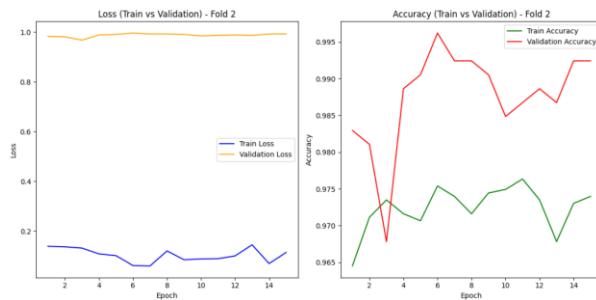
AUC for Fold 1: 0.8488



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.7727	0.1700	0.2787	100
meningioma_tumor	0.7293	0.8435	0.7823	115
no_tumor	0.5126	0.9714	0.6711	105
pituitary_tumor	0.9155	0.6190	0.7386	105
accuracy			0.6612	425
macro avg	0.7325	0.6510	0.6177	425
weighted avg	0.7320	0.6612	0.6255	425

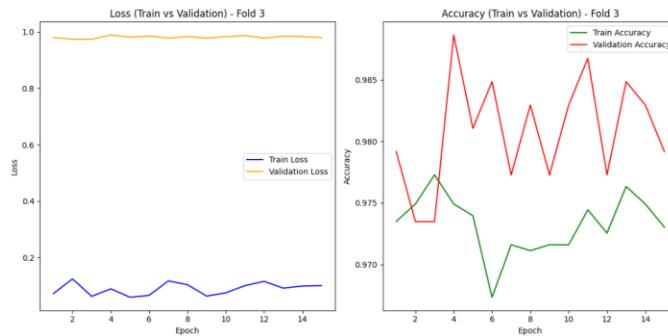
AUC for Fold 2: 0.8488



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.7600	0.1900	0.3040	100
meningioma_tumor	0.6275	0.8348	0.7164	115
no_tumor	0.5176	0.9810	0.6776	105
pituitary_tumor	0.9375	0.4286	0.5882	105
accuracy			0.6188	425
macro avg	0.7106	0.6086	0.5716	425
weighted avg	0.7081	0.6188	0.5781	425

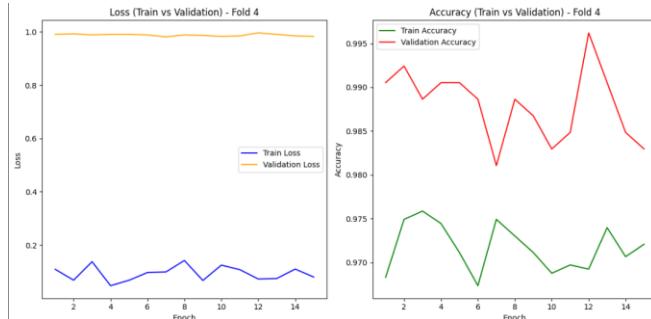
AUC for Fold 3: 0.8511



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.7200	0.1800	0.2880	100
meningioma_tumor	0.6906	0.8348	0.7559	115
no_tumor	0.4951	0.9714	0.6559	105
pituitary_tumor	0.9091	0.4762	0.6250	105
accuracy			0.6259	425
macro avg	0.7037	0.6156	0.5812	425
weighted avg	0.7032	0.6259	0.5888	425

AUC for Fold 4: 0.8354

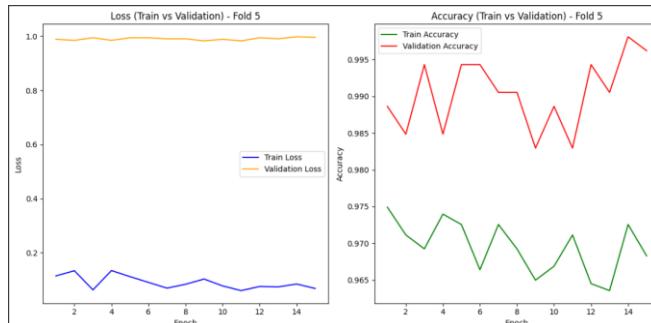


Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8095	0.1700	0.2810	100
meningioma_tumor	0.6831	0.8435	0.7549	115
no_tumor	0.5204	0.9714	0.6777	105
pituitary_tumor	0.9242	0.5810	0.7135	105
accuracy			0.6518	425
macro avg	0.7343	0.6415	0.6068	425
weighted avg	0.7322	0.6518	0.6141	425

AUC for Fold 5: 0.8383

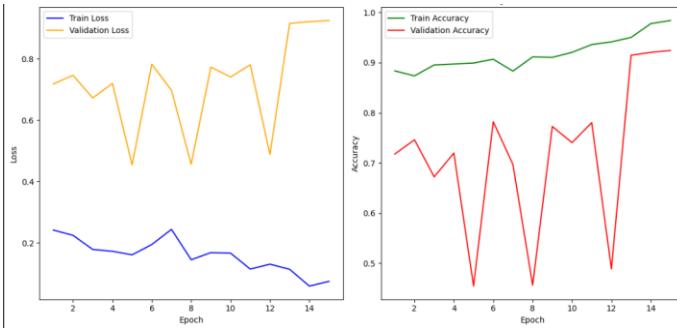
===== Overall AUC on Test Set =====
Average AUC: 0.8445



Observam ca, cu dropout avem acurateti mult mai slabe fata de etapa in care pentru acest learning_rate si batch_size dar fara dropout aveam acurateti mai mari la folduri.

Foldul 4 este cel mai slab din acest set.

Cu scheduler cu weight_decay:

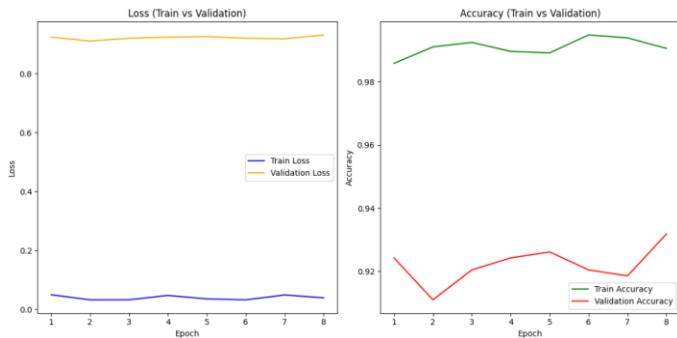


	precision	recall	f1-score	support
glioma_tumor	0.8947	0.1700	0.2857	100
meningioma_tumor	0.7007	0.8348	0.7619	115
no_tumor	0.5050	0.9714	0.6645	105
pituitary_tumor	0.9701	0.6190	0.7558	105
accuracy			0.6588	425
macro avg	0.7676	0.6488	0.6170	425
weighted avg	0.7646	0.6588	0.6243	425

AUC for Fold 2 scheduler: 0.8245
===== Overall AUC on Test Set =====
Average AUC: 0.8245

Observam o crestere a acuratetei, iar la clase, o crestere mica la no_tumor la precision, recall.

Cu early_stopping:



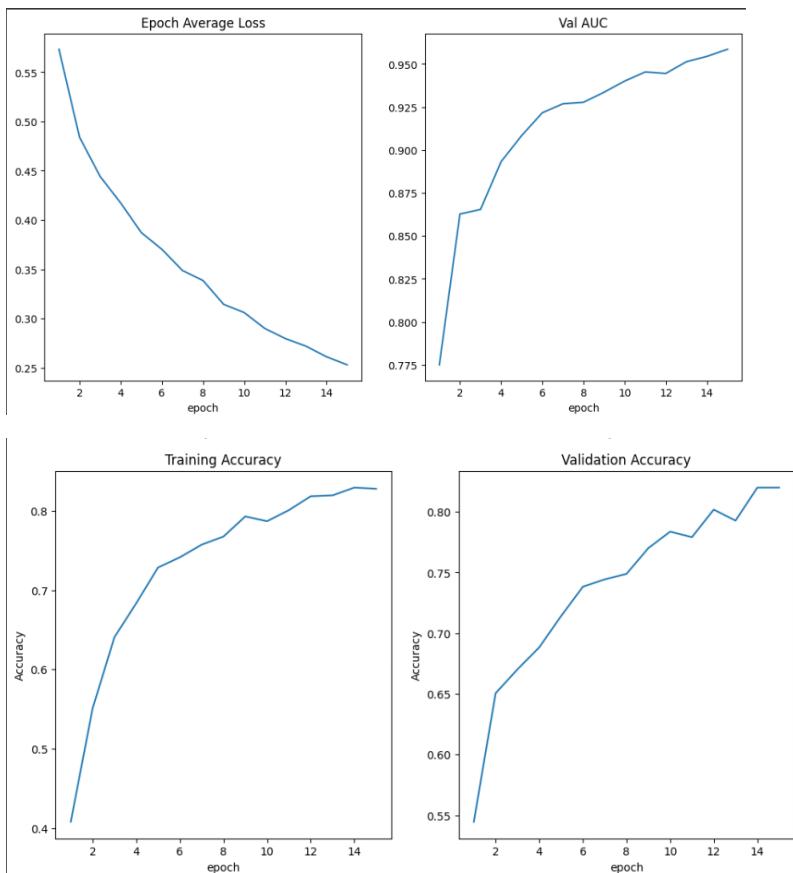
	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma tumor	0.7021	0.8609	0.7734	115
no_tumor	0.5226	0.9905	0.6842	105
pituitary_tumor	0.9846	0.6095	0.7529	105
accuracy			0.6729	425
macro avg	0.7898	0.6627	0.6318	425
weighted avg	0.7859	0.6729	0.6389	425

AUC early_stopping: 0.8452
===== Overall AUC on Test Set =====
Average AUC: 0.8452

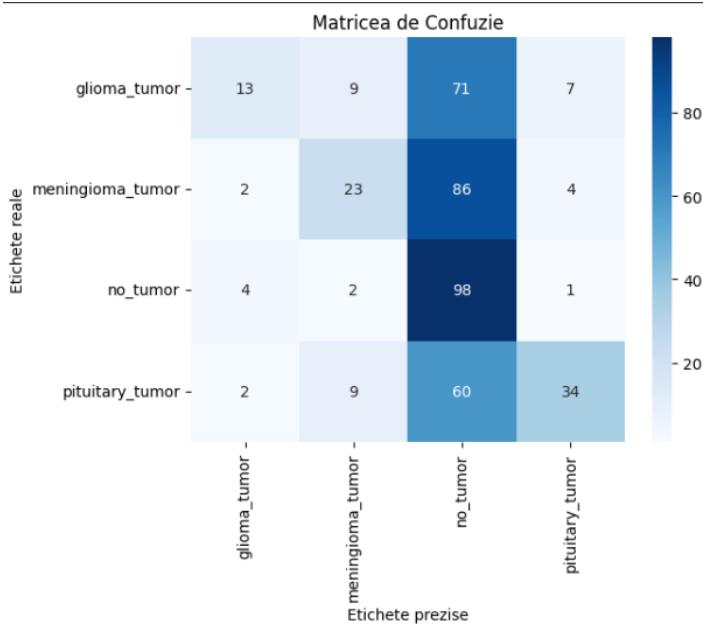
O acuratete mai buna obtinuta aici cu early_stopping, oprirea fiind la epoca 5.

Acum vom testa cu Stochastic Gradient Descent(SGD), batch_size = 32, learning_rate = 0.001 si fara dropout

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.6190	0.1300	0.2149	100
meningioma_tumor	0.5349	0.2000	0.2911	115
no_tumor	0.3111	0.9333	0.4667	105
pituitary_tumor	0.7391	0.3238	0.4503	105
accuracy			0.3953	425
macro avg	0.5510	0.3968	0.3558	425
weighted avg	0.5499	0.3953	0.3559	425



Observam niste metrii destul de slabe fata de cele de la Adam

Antrenarea cu k-folduri:

```
Precision: Mean = 0.8827, Std = 0.0167
Recall: Mean = 0.8819, Std = 0.0181
F1-score: Mean = 0.8783, Std = 0.0195
Accuracy: Mean = 0.8819, Std = 0.0181
```

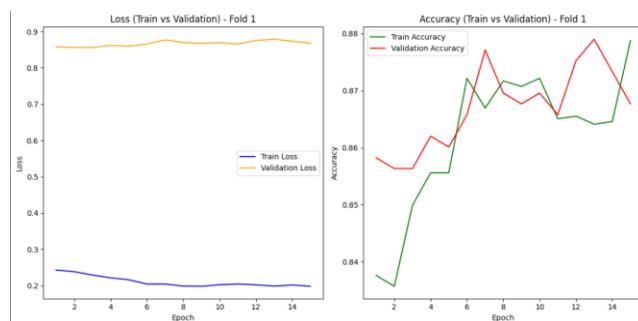
Aceasta este media metricilor

Pentru folduri:

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.6111	0.1100	0.1864	100
meningioma_tumor	0.6230	0.3304	0.4318	115
no_tumor	0.3278	0.9429	0.4865	105
pituitary_tumor	0.7500	0.3143	0.4430	105
accuracy			0.4259	425
macro avg	0.5780	0.4244	0.3869	425
weighted avg	0.5786	0.4259	0.3903	425

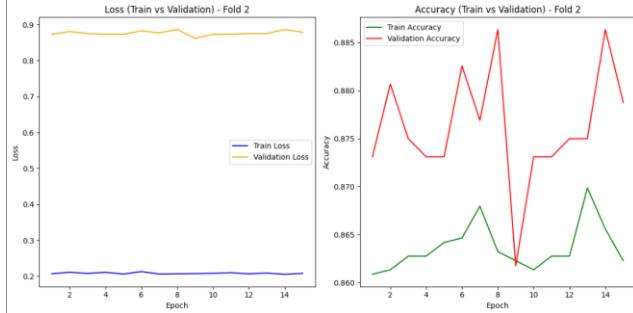
AUC for Fold 1: 0.7350



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.6250	0.1500	0.2419	100
meningioma_tumor	0.6515	0.3739	0.4751	115
no_tumor	0.3368	0.9333	0.4949	105
pituitary_tumor	0.7955	0.3333	0.4698	105
accuracy			0.4494	425
macro avg	0.6022	0.4476	0.4205	425
weighted avg	0.6031	0.4494	0.4238	425

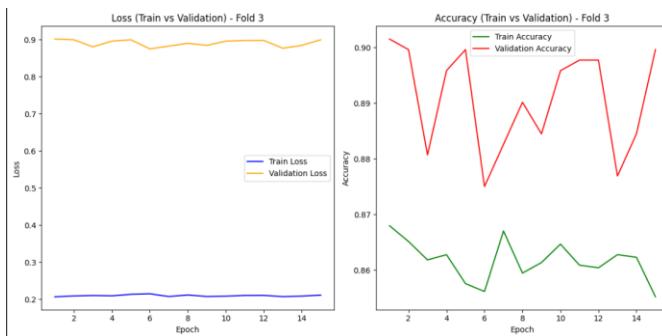
AUC for Fold 2: 0.7319



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.6818	0.1500	0.2459	100
meningioma_tumor	0.6415	0.2957	0.4048	115
no_tumor	0.3268	0.9524	0.4866	105
pituitary_tumor	0.7727	0.3238	0.4564	105
accuracy			0.4306	425
macro avg	0.6057	0.4305	0.3984	425
weighted avg	0.6057	0.4306	0.4004	425

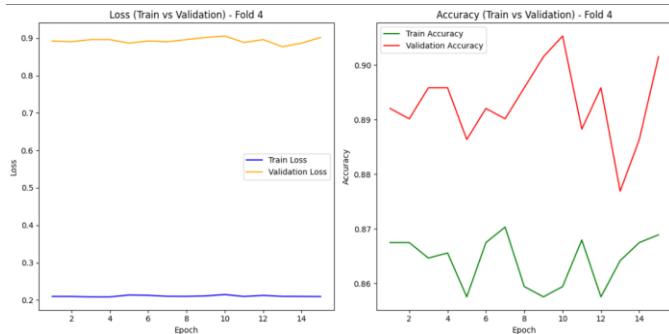
AUC for Fold 3: 0.7392



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.6087	0.1400	0.2276	100
meningioma_tumor	0.6190	0.3391	0.4382	115
no_tumor	0.3357	0.9143	0.4910	105
pituitary_tumor	0.7170	0.3619	0.4810	105
accuracy			0.4400	425
macro avg	0.5701	0.4388	0.4095	425
weighted avg	0.5708	0.4400	0.4123	425

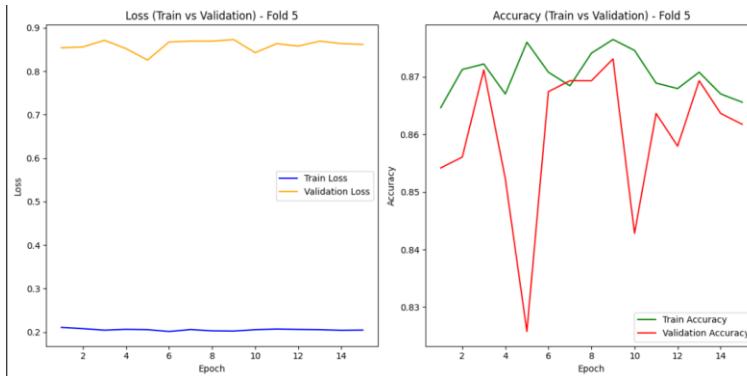
AUC for Fold 4: 0.7238



Fold5:

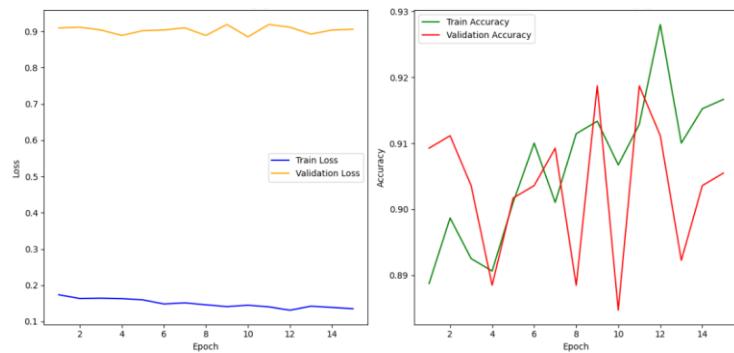
	precision	recall	f1-score	support
glioma_tumor	0.6957	0.1600	0.2602	100
meningioma_tumor	0.6716	0.3913	0.4945	115
no_tumor	0.3451	0.9333	0.5039	105
pituitary_tumor	0.7843	0.3810	0.5128	105
accuracy			0.4682	425
macro avg	0.6242	0.4664	0.4428	425
weighted avg	0.6244	0.4682	0.4462	425

AUC for Fold 5: 0.7355
===== Overall AUC on Test Set =====
Average AUC: 0.7331



In acest caz, cel mai slab fold este foldul 1.

Scheduler cu weight_decay pentru foldul cel mai slab:



	precision	recall	f1-score	support
glioma_tumor	0.6842	0.1300	0.2185	100
meningioma_tumor	0.6796	0.6087	0.6422	115
no_tumor	0.3813	0.9333	0.5414	105
pituitary_tumor	0.7826	0.3429	0.4768	105
accuracy			0.5106	425
macro avg	0.6319	0.5037	0.4697	425
weighted avg	0.6324	0.5106	0.4768	425

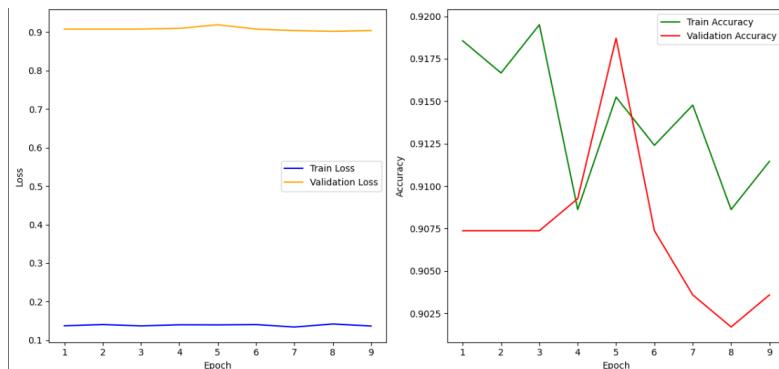
AUC for Fold 1 scheduler: 0.7860

===== Overall AUC on Test Set =====

Average AUC: 0.7860

Observam o crestere generala a metricilor.

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.8421	0.1600	0.2689	100
meningioma_tumor	0.6863	0.6087	0.6452	115
no_tumor	0.3831	0.9524	0.5464	105
pituitary_tumor	0.8140	0.3333	0.4730	105
accuracy			0.5200	425
macro avg	0.6814	0.5136	0.4834	425
weighted avg	0.6796	0.5200	0.4897	425

AUC for Fold 1 early_stopping: 0.7842

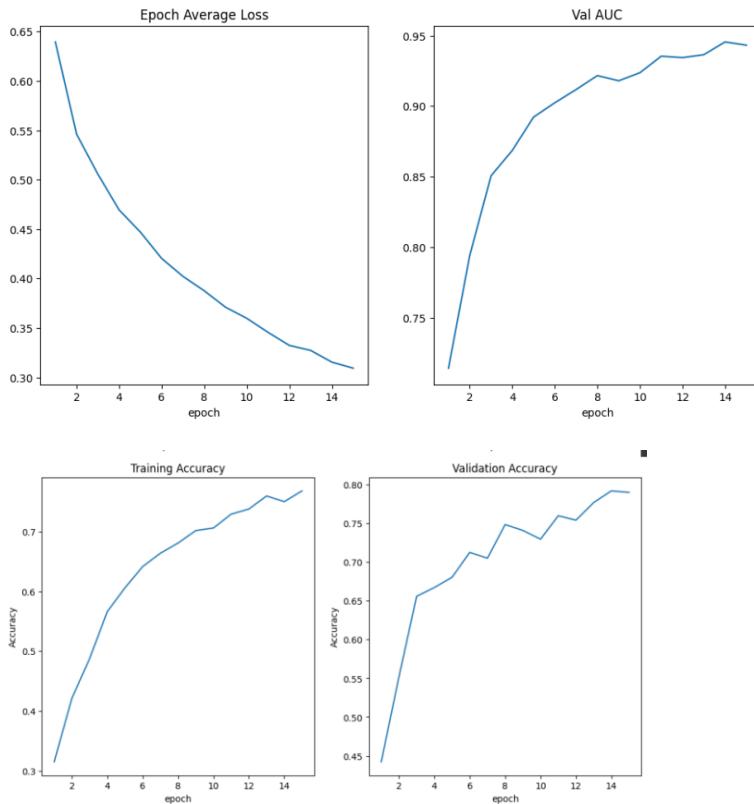
===== Overall AUC on Test Set =====

Average AUC: 0.7842

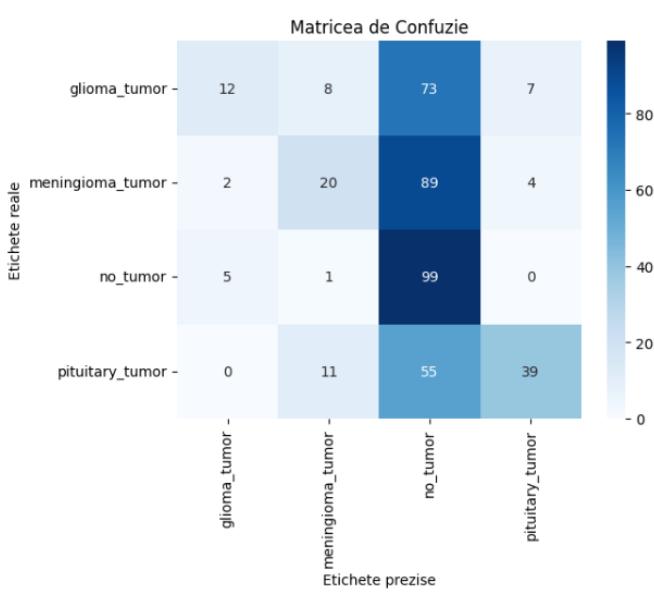
Am avansat pana la epoca 9 si metrii mai bune decat la weight_decay

[Acum vom testa cu Stochastic Gradient Descent, batch_size = 32, lerning_rate = 0.001 si cu dropout](#)

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.6316	0.1200	0.2017	100
meningioma_tumor	0.5000	0.1739	0.2581	115
no_tumor	0.3133	0.9429	0.4703	105
pituitary_tumor	0.7800	0.3714	0.5032	105
accuracy			0.4000	425
macro avg	0.5562	0.4020	0.3583	425
weighted avg	0.5540	0.4000	0.3578	425



Se poate observa din matricea de confuzie ca modelul greseste mai mult fata de etapa precedenta

Antrenarea cu k-folduri:

Media metricilor:

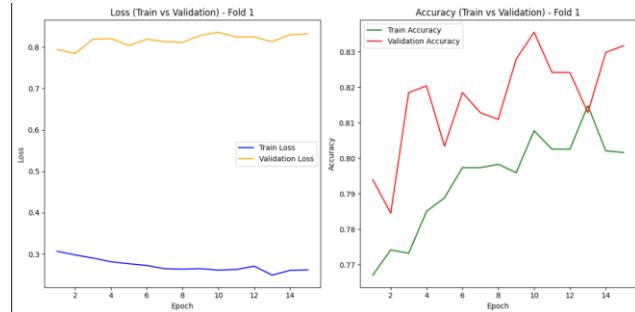
```
Precision: Mean = 0.8338, Std = 0.0178
Recall: Mean = 0.8361, Std = 0.0156
F1-score: Mean = 0.8323, Std = 0.0165
Accuracy: Mean = 0.8361, Std = 0.0156
```

Fold1:

```
model.load_state_dict(torch.load(os.path.join(root_dir, r
precision      recall   f1-score   support
glioma_tumor    0.6316   0.1200   0.2017    100
meningioma_tumor 0.5455   0.2087   0.3019    115
no_tumor         0.3204   0.9429   0.4783    105
pituitary_tumor   0.7736   0.3905   0.5190    105

accuracy          0.5678   0.4155   0.3752    425
macro avg        0.5665   0.4141   0.3755    425
weighted avg     0.5665   0.4141   0.3755    425

AUC for Fold 1: 0.7267
```

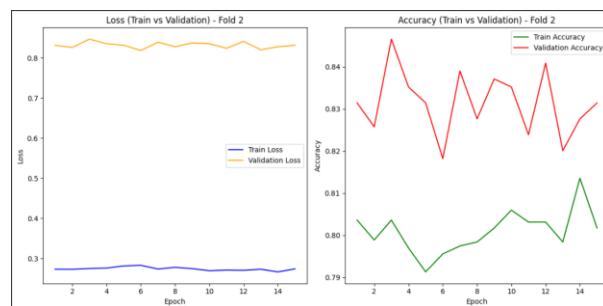


Fold2:

```
precision      recall   f1-score   support
glioma_tumor    0.6250   0.1000   0.1724    100
meningioma_tumor 0.4694   0.2000   0.2805    115
no_tumor         0.3170   0.9238   0.4720    105
pituitary_tumor   0.7407   0.3810   0.5031    105

accuracy          0.5380   0.4012   0.3570    425
macro avg        0.5354   0.4000   0.3574    425
weighted avg     0.5354   0.4000   0.3574    425

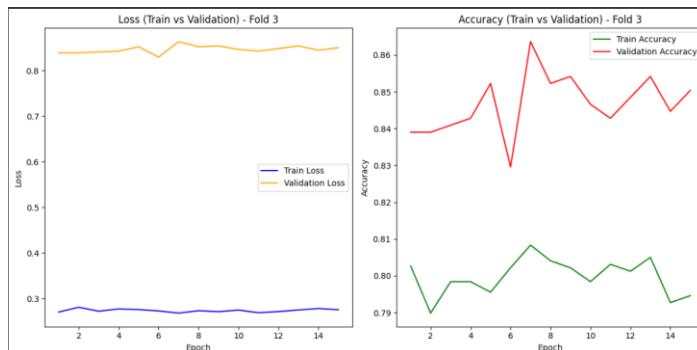
AUC for Fold 2: 0.7291
```



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.5455	0.1200	0.1967	100
meningioma_tumor	0.5122	0.1826	0.2692	115
no_tumor	0.3137	0.9143	0.4672	105
pituitary_tumor	0.6964	0.3714	0.4845	105
accuracy			0.3953	425
macro avg	0.5170	0.3971	0.3544	425
weighted avg	0.5165	0.3953	0.3542	425

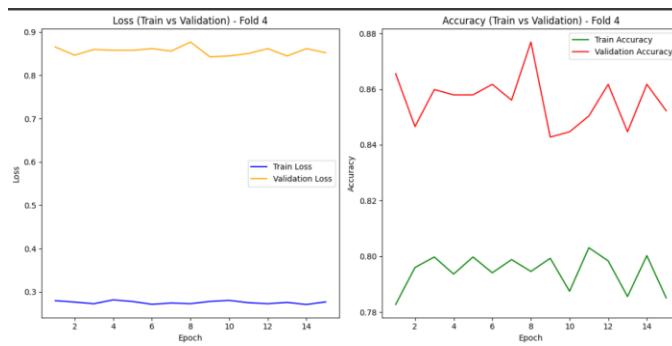
AUC for Fold 3: 0.7322



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.6000	0.1200	0.2000	100
meningioma_tumor	0.5246	0.2783	0.3636	115
no_tumor	0.3405	0.9048	0.4948	105
pituitary_tumor	0.7231	0.4476	0.5529	105
accuracy			0.4376	425
macro avg	0.5470	0.4377	0.4028	425
weighted avg	0.5459	0.4376	0.4043	425

AUC for Fold 4: 0.7359



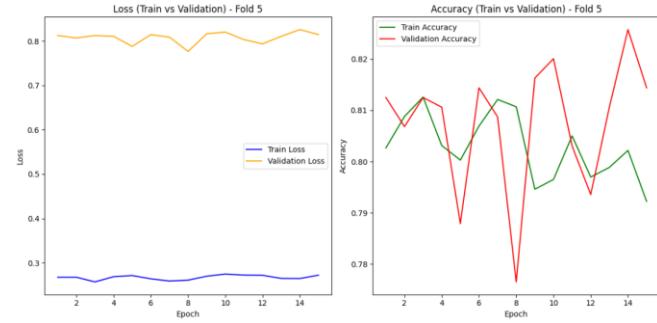
Fold5:

```
precision    recall   f1-score   support
glioma_tumor      0.5455    0.1200    0.1967      100
meningioma_tumor   0.5091    0.2435    0.3294      115
no_tumor           0.3333    0.8952    0.4858      105
pituitary_tumor    0.6818    0.4286    0.5263      105

accuracy          -         -        0.4212      425
macro avg         0.5174    0.4218    0.3846      425
weighted avg       0.5169    0.4212    0.3855      425

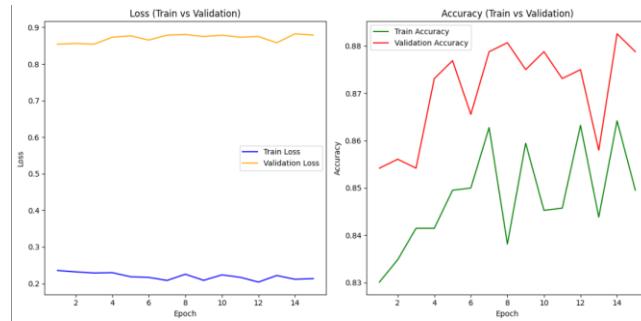
AUC for Fold 5: 0.7419

===== Overall AUC on Test Set =====
Average AUC: 0.7331
```



Cel mai slab este foldul3.

Scheduler cu weight_decay:



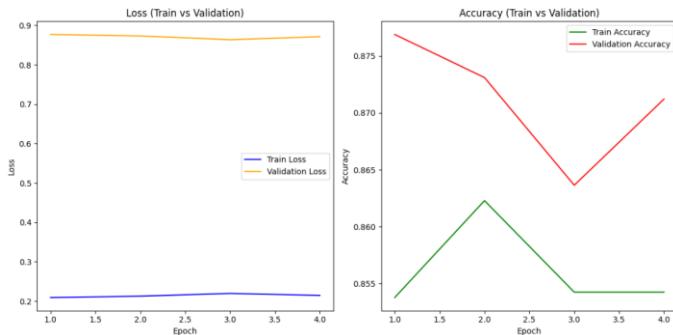
```
precision    recall   f1-score   support
glioma_tumor      0.6800    0.1700    0.2720      100
meningioma_tumor   0.6897    0.3478    0.4624      115
no_tumor           0.3322    0.9238    0.4887      105
pituitary_tumor    0.7600    0.3619    0.4903      105

accuracy          -         -        0.4518      425
macro avg         0.6155    0.4509    0.4284      425
weighted avg       0.6164    0.4518    0.4310      425

AUC for Fold 2 scheduler: 0.7508

===== Overall AUC on Test Set =====
Average AUC: 0.7508
```

Cu early_stopping:



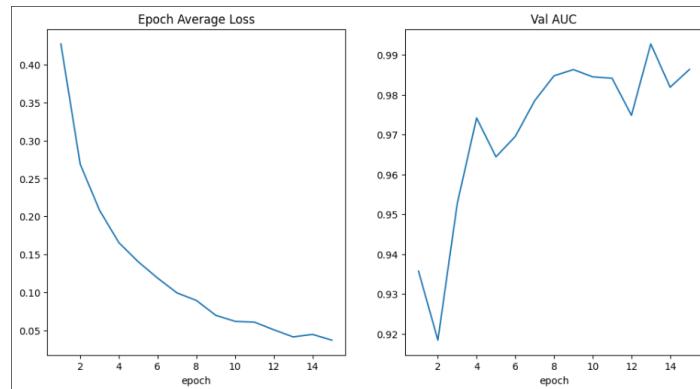
	precision	recall	f1-score	support
glioma_tumor	0.8125	0.1300	0.2241	100
meningioma_tumor	0.6087	0.2435	0.3478	115
no_tumor	0.3119	0.9714	0.4722	105
pituitary_tumor	0.8611	0.2952	0.4397	105
accuracy			0.4094	425
macro avg	0.6486	0.4100	0.3710	425
weighted avg	0.6457	0.4094	0.3722	425

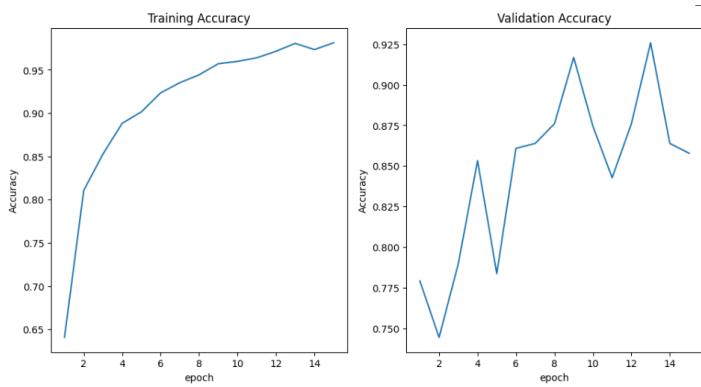
AUC early_stopping: 0.7537
===== Overall AUC on Test Set =====
Average AUC: 0.7537

S-a oprit la epoca 4.

Acum testam cu SGD cu learning_rate de 0.01, batch_size=32 si fara dropout

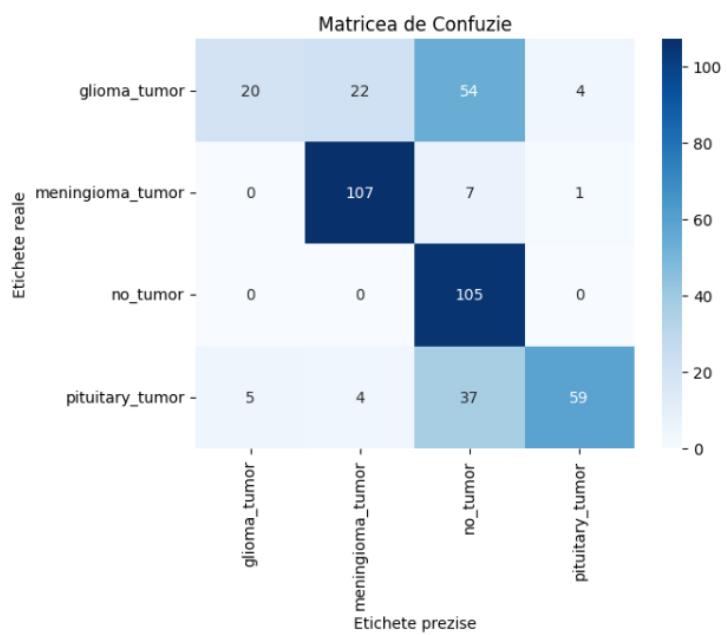
Antrenarea clasica fara k-folduri:





	precision	recall	f1-score	support
glioma_tumor	0.8000	0.2000	0.3200	100
meningioma_tumor	0.8045	0.9304	0.8629	115
no_tumor	0.5172	1.0000	0.6818	105
pituitary_tumor	0.9219	0.5619	0.6982	105
accuracy			0.6847	425
macro avg	0.7609	0.6731	0.6407	425
weighted avg	0.7615	0.6847	0.6497	425

Observam metrii mult mai bune pentru SGD cu un learning_rate mai mic



Antrenarea cu k-folduri:

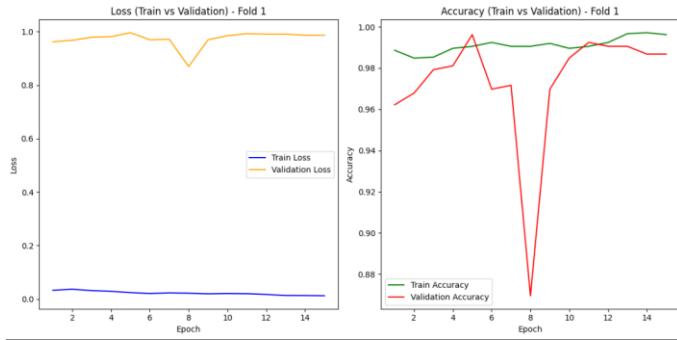
Media metricilor:

```
Precision: Mean = 0.9970, Std = 0.0057
Recall: Mean = 0.9970, Std = 0.0057
F1-score: Mean = 0.9970, Std = 0.0057
Accuracy: Mean = 0.9970, Std = 0.0057
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.8696	0.2000	0.3252	100
meningioma_tumor	0.7051	0.9565	0.8118	115
no_tumor	0.5591	0.9905	0.7148	105
pituitary_tumor	0.9167	0.5238	0.6667	105
accuracy			0.6800	425
macro avg	0.7626	0.6677	0.6296	425
weighted avg	0.7600	0.6800	0.6375	425

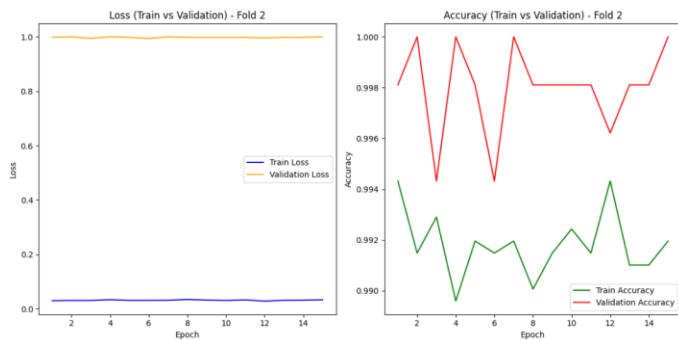
AUC for Fold 1: 0.8687



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7237	0.9565	0.8240	115
no_tumor	0.5532	0.9905	0.7099	105
pituitary_tumor	0.9692	0.6000	0.7412	105
accuracy			0.6965	425
macro avg	0.7990	0.6842	0.6479	425
weighted avg	0.7955	0.6965	0.6560	425

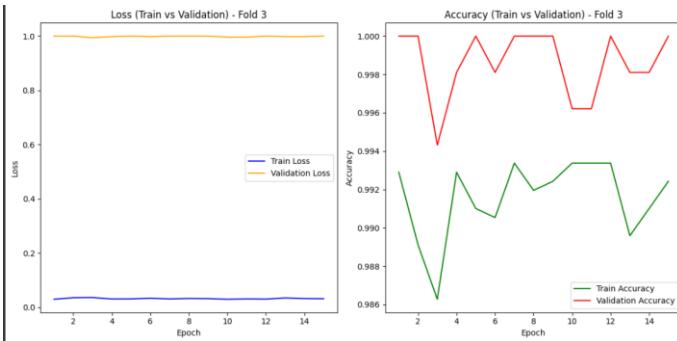
AUC for Fold 2: 0.8682



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.7794	0.9217	0.8446	115
no_tumor	0.5073	0.9905	0.6710	105
pituitary_tumor	0.9219	0.5619	0.6982	105
accuracy			0.6753	425
macro avg	0.7772	0.6635	0.6285	425
weighted avg	0.7758	0.6753	0.6374	425

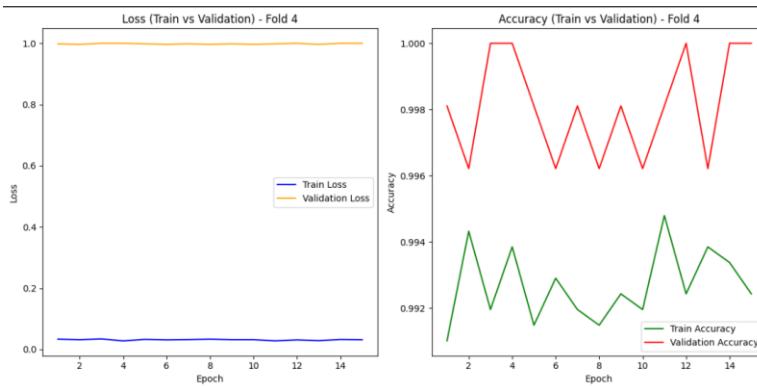
AUC for Fold 3: 0.8617



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.1700	0.2906	100
meningioma_tumor	0.7032	0.9478	0.8074	115
no_tumor	0.5445	0.9905	0.7027	105
pituitary_tumor	0.9355	0.5524	0.6946	105
accuracy			0.6776	425
macro avg	0.7958	0.6652	0.6238	425
weighted avg	0.7912	0.6776	0.6321	425

AUC for Fold 4: 0.8737



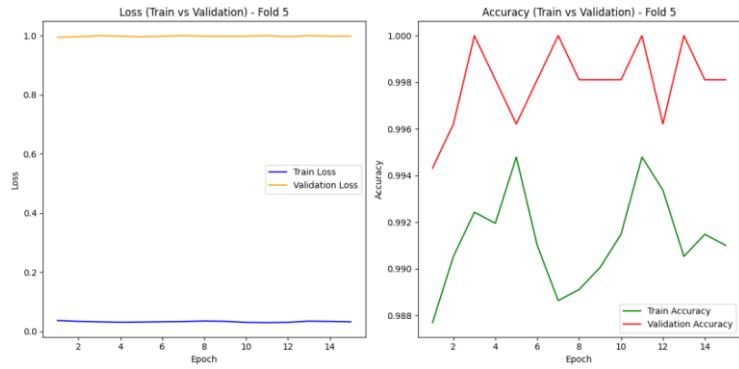
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.8092	0.9217	0.8618	115
no_tumor	0.5098	0.9905	0.6731	105
pituitary_tumor	0.9429	0.6286	0.7543	105
accuracy			0.6941	425
macro avg	0.8030	0.6827	0.6515	425
weighted avg	0.8014	0.6941	0.6604	425

AUC for Fold 5: 0.8712

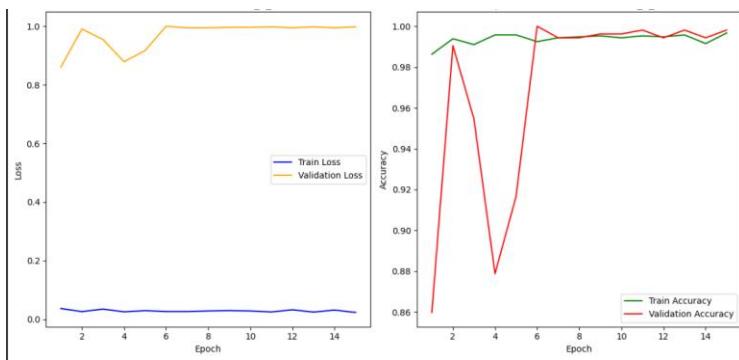
===== Overall AUC on Test Set =====

Average AUC: 0.8687



Cel mai slab fold este 3

Cu scheduler si weight_decay:



```

precision    recall   f1-score   support
glioma_tumor      1.0000    0.1800    0.3051      100
meningioma_tumor   0.7929    0.9652    0.8706      115
no_tumor           0.5147    1.0000    0.6796      105
pituitary_tumor    0.9524    0.5714    0.7143      105

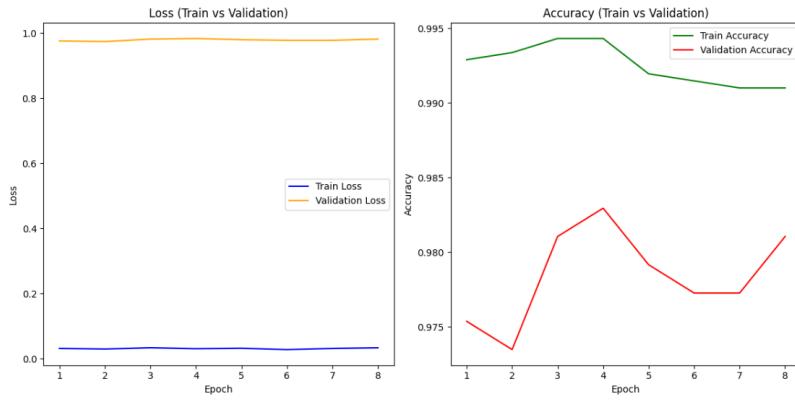
accuracy          -         -        0.6918      425
macro avg         0.8150    0.6792    0.6424      425
weighted avg       0.8123    0.6918    0.6517      425

AUC for Fold 3 scheduler: 0.8748
===== Overall AUC on Test Set =====
Average AUC: 0.8748

```

O imbunatatire generala fata de antrenarea din k-folduri pentru foldul 3

Cu early_stopping:



```

precision    recall   f1-score   support
glioma_tumor      0.7308     0.1900     0.3016     100
meningioma_tumor   0.7241     0.9130     0.8077     115
no_tumor           0.5126     0.9714     0.6711     105
pituitary_tumor    0.8909     0.4667     0.6125     105

accuracy          -          -         0.6471     425
macro avg         0.7146     0.6353     0.5982     425
weighted avg      0.7146     0.6471     0.6066     425

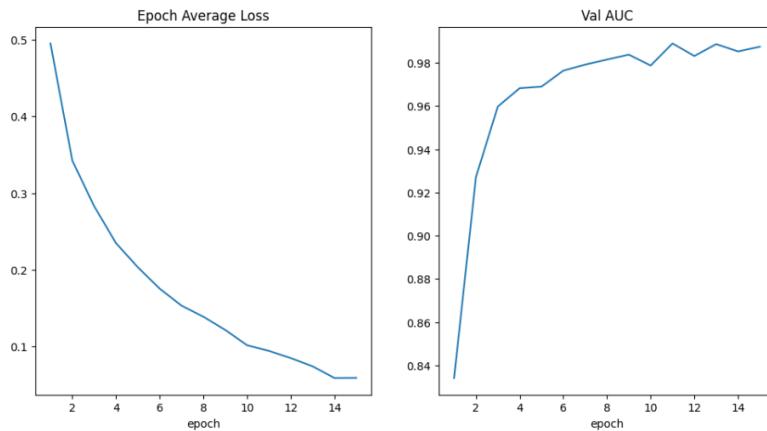
AUC early_stopping: 0.8736
===== Overall AUC on Test Set =====
Average AUC: 0.8736

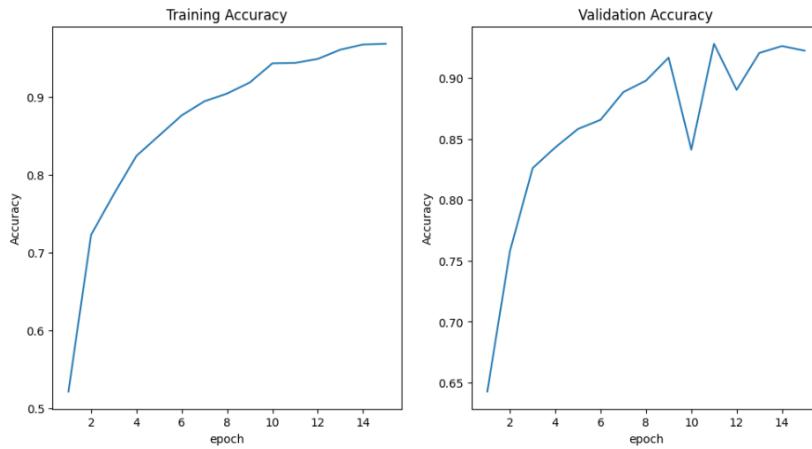
```

Ne-am oprit la epoca 8 si in general sunt metrii mai slabe.

Acum testam cu SGD cu learning_rate de 0.01, batch_size=32 si cu dropout

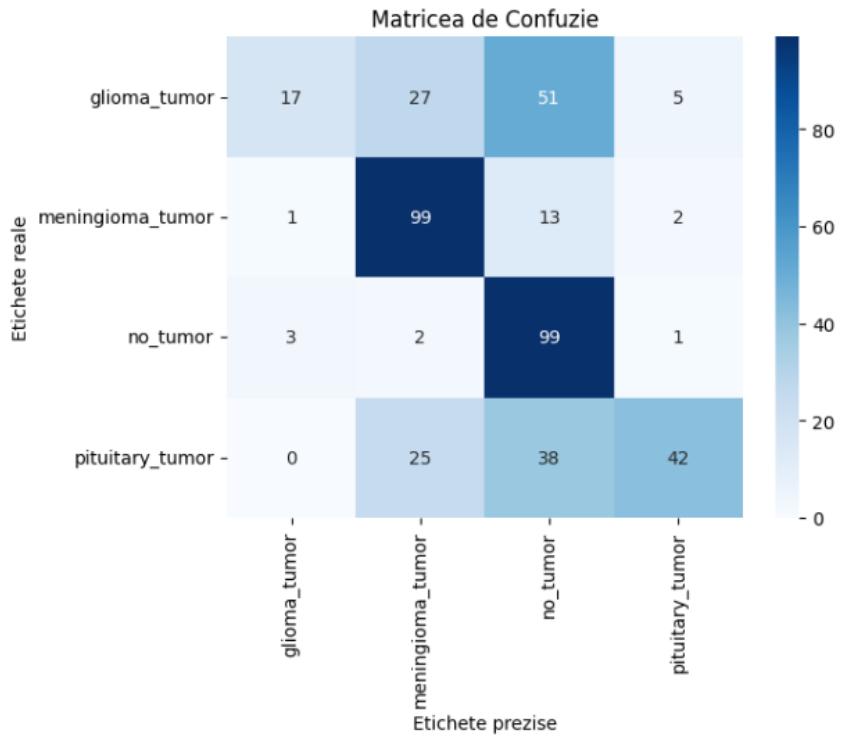
Antrenarea clasica fara k-folduri:





	precision	recall	f1-score	support
glioma_tumor	0.8095	0.1700	0.2810	100
meningioma_tumor	0.6471	0.8609	0.7388	115
no_tumor	0.4925	0.9429	0.6471	105
pituitary_tumor	0.8400	0.4000	0.5419	105
accuracy			0.6047	425
macro avg	0.6973	0.5934	0.5522	425
weighted avg	0.6948	0.6047	0.5598	425

Dropout a afectat performanta modelului negative, lucru vizibil in scaderea acuratetii.



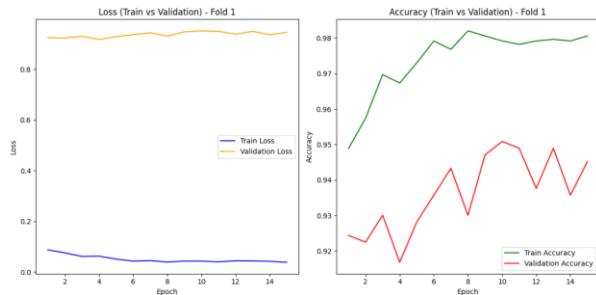
Pentru antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9805, Std = 0.0203
Recall: Mean = 0.9803, Std = 0.0204
F1-score: Mean = 0.9803, Std = 0.0205
Accuracy: Mean = 0.9803, Std = 0.0204
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9375	0.1500	0.2586	100
meningioma_tumor	0.6731	0.9130	0.7749	115
no_tumor	0.5450	0.9810	0.7007	105
pituitary_tumor	0.8906	0.5429	0.6746	105
accuracy			0.6588	425
macro avg	0.7615	0.6467	0.6022	425
weighted avg	0.7574	0.6588	0.6103	425

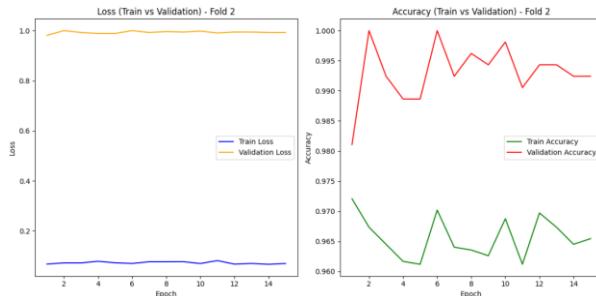
AUC for Fold 1: 0.8428



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.8947	0.1700	0.2857	100
meningioma_tumor	0.6500	0.9043	0.7564	115
no_tumor	0.5074	0.9810	0.6688	105
pituitary_tumor	0.9070	0.3714	0.5270	105
accuracy			0.6188	425
macro avg	0.7398	0.6067	0.5595	425
weighted avg	0.7358	0.6188	0.5673	425

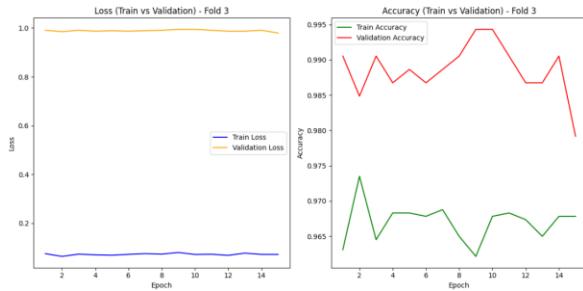
AUC for Fold 2: 0.8346



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.8500	0.1700	0.2833	100
meningioma_tumor	0.7333	0.8609	0.7920	115
no_tumor	0.4769	0.9810	0.6417	105
pituitary_tumor	0.8519	0.4381	0.5786	105
accuracy			0.6235	425
macro avg	0.7280	0.6125	0.5739	425
weighted avg	0.7267	0.6235	0.5825	425

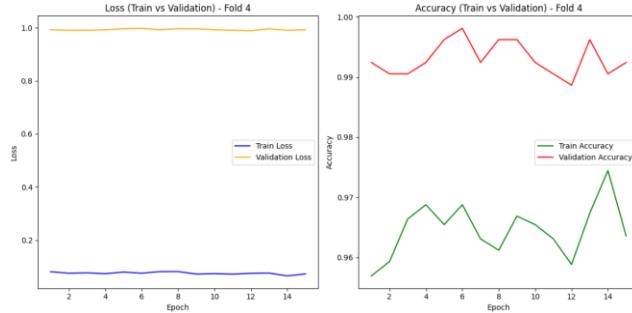
AUC for Fold 3: 0.8435



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.8889	0.1600	0.2712	100
meningioma_tumor	0.6939	0.8870	0.7786	115
no_tumor	0.5202	0.9810	0.6799	105
pituitary_tumor	0.8710	0.5143	0.6467	105
accuracy			0.6471	425
macro avg	0.7435	0.6355	0.5941	425
weighted avg	0.7406	0.6471	0.6022	425

AUC for Fold 4: 0.8464



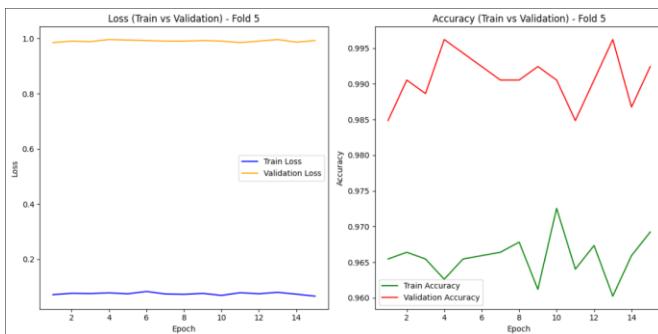
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1800	0.2975	100
meningioma_tumor	0.7103	0.8957	0.7923	115
no_tumor	0.5152	0.9714	0.6733	105
pituitary_tumor	0.9016	0.5238	0.6627	105
accuracy			0.6541	425
macro avg	0.7461	0.6427	0.6064	425
weighted avg	0.7439	0.6541	0.6144	425

AUC for Fold 5: 0.8473

===== Overall AUC on Test Set =====

Average AUC: 0.8429



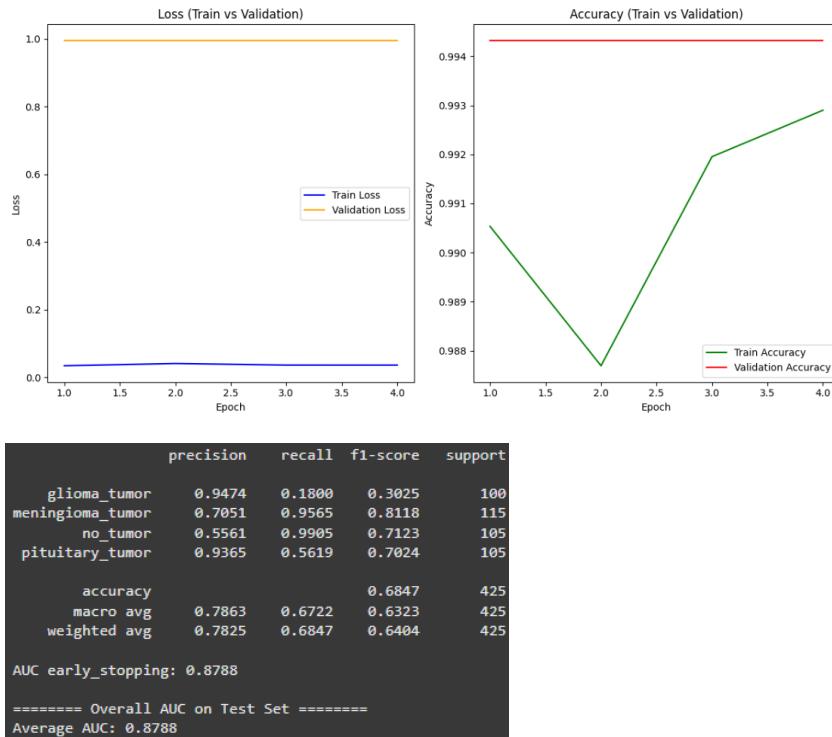
Cel mai slab fold este 2

Cu scheduler cu weight_decay:



Observam o imbunatatire semnificativa a modelului, in mare parte a metricilor fiind imbunatatite

Cu early_stopping:

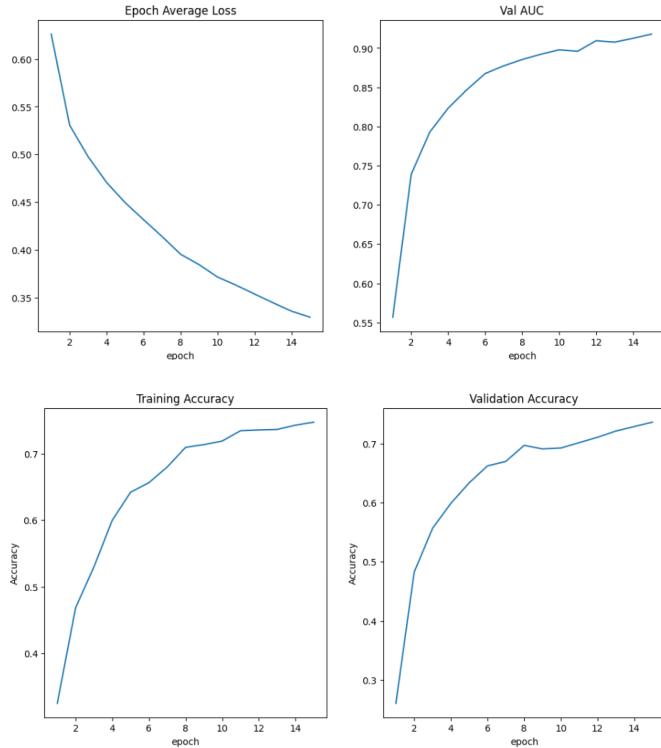


Observam ca sunt destul de apropiate acuratetile, dar la recall pare ca sunt mai bune metricile de la scheduler.

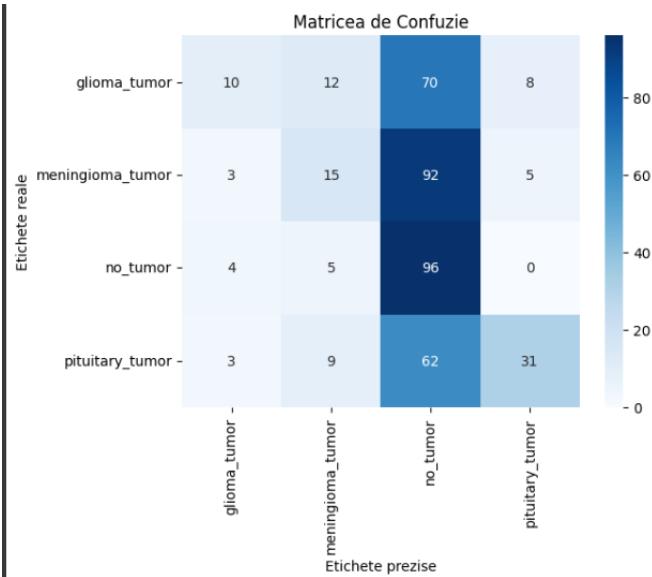
Modelul s-a oprit la epoca 4.

[Acum am testat pentru optimizatorul SGD cu learning_rate = 0.001, batch_size = 64 si fara dropout](#)

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.5000	0.1000	0.1667	100
meningioma_tumor	0.3659	0.1304	0.1923	115
no_tumor	0.3000	0.9143	0.4518	105
pituitary_tumor	0.7045	0.2952	0.4161	105
accuracy			0.3576	425
macro avg	0.4676	0.3600	0.3067	425
weighted avg	0.4648	0.3576	0.3057	425



Din nou, observam ca un learning_rate mai mic decat 0.01, in acest caz 0.001 afecteaza performanta invatarii modelului, precizia fiind slaba afectand mai departe acuratetea, desi evolutia pe parcusul epochilor este ascendent afara spike-uri cum aveam la Adam.

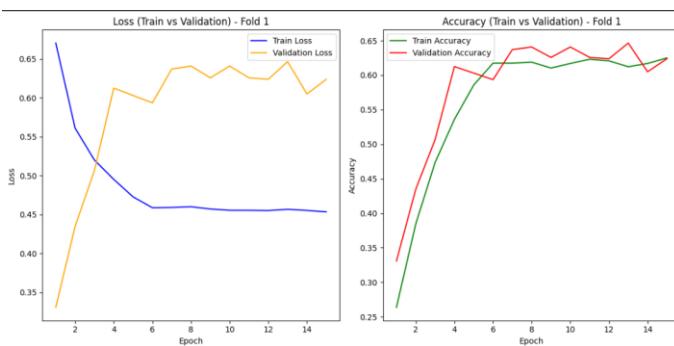
Antrenarea cu k-folduri, media metricilor:

```
Precision: Mean = 0.6062, Std = 0.0216
Recall: Mean = 0.6115, Std = 0.0236
F1-score: Mean = 0.6023, Std = 0.0219
Accuracy: Mean = 0.6115, Std = 0.0236
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.4048	0.1700	0.2394	100
meningioma_tumor	0.3636	0.1043	0.1622	115
no_tumor	0.2559	0.7238	0.3781	105
pituitary_tumor	0.3774	0.1905	0.2532	105
accuracy			0.2941	425
macro avg	0.3504	0.2972	0.2582	425
weighted avg	0.3501	0.2941	0.2562	425

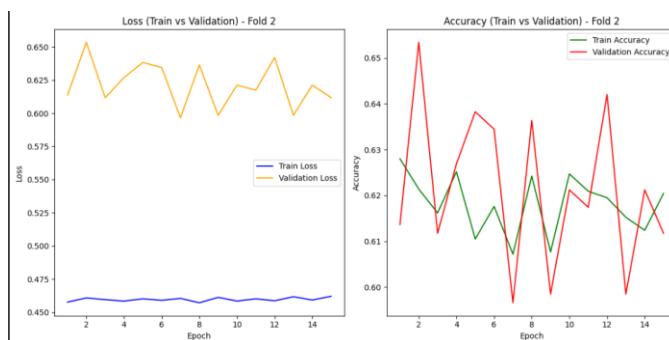
AUC for Fold 1: 0.5778



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.5333	0.1600	0.2462	100
meningioma_tumor	0.3235	0.0957	0.1477	115
no_tumor	0.2750	0.8381	0.4141	105
pituitary_tumor	0.3415	0.1333	0.1918	105
accuracy			0.3035	425
macro avg	0.3683	0.3068	0.2499	425
weighted avg	0.3653	0.3035	0.2476	425

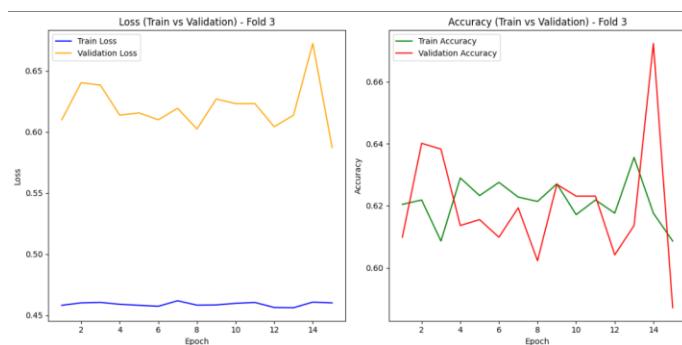
AUC for Fold 2: 0.5645



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.3714	0.1300	0.1926	100
meningioma_tumor	0.3750	0.1043	0.1633	115
no_tumor	0.2533	0.7238	0.3753	105
pituitary_tumor	0.3621	0.2000	0.2577	105
accuracy			0.2871	425
macro avg	0.3405	0.2895	0.2472	425
weighted avg	0.3409	0.2871	0.2459	425

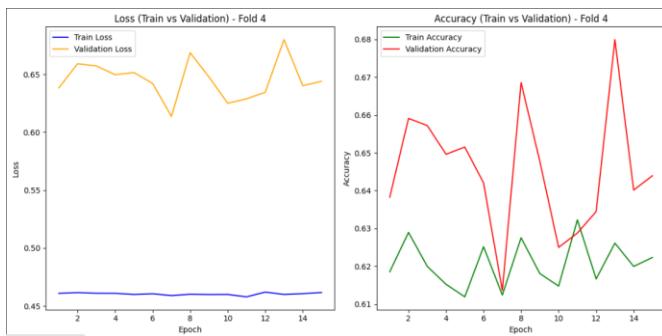
AUC for Fold 3: 0.5846



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.5135	0.1900	0.2774	100
meningioma_tumor	0.3404	0.1391	0.1975	115
no_tumor	0.2656	0.7714	0.3951	105
pituitary_tumor	0.3889	0.1333	0.1986	105
accuracy			0.3059	425
macro avg	0.3771	0.3085	0.2672	425
weighted avg	0.3746	0.3059	0.2654	425

AUC for Fold 4: 0.5895



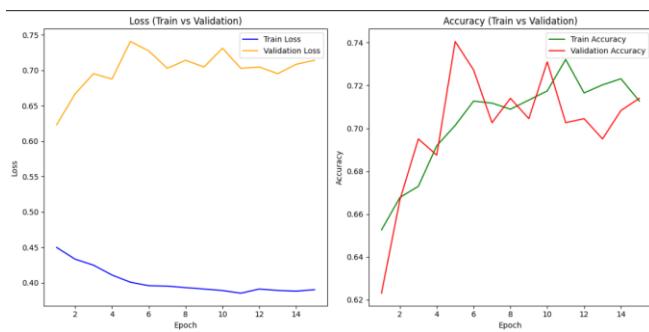
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.5278	0.1900	0.2794	100
meningioma_tumor	0.3590	0.1217	0.1818	115
no_tumor	0.2685	0.7619	0.3970	105
pituitary_tumor	0.3846	0.1905	0.2548	105
			accuracy	0.3129
			macro avg	0.2783
			weighted avg	0.2760
AUC for Fold 5:	0.5661			
===== Overall AUC on Test Set =====				
Average AUC:	0.5765			



Cel mai slab fold este 3

Cu scheduler cu weight decay:



```

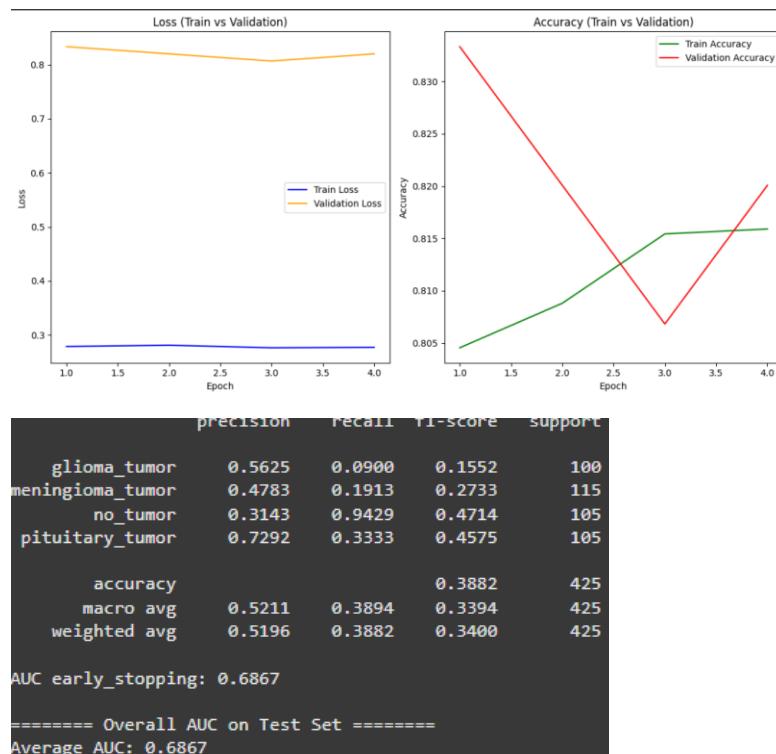
precision    recall   f1-score   support
glioma_tumor      0.5385    0.1400    0.2222      100
meningioma_tumor   0.3226    0.0870    0.1370      115
no_tumor           0.2764    0.8476    0.4169      105
pituitary_tumor    0.6087    0.2667    0.3709      105

accuracy          -         -         -         425
macro avg        0.4365    0.3353    0.2867      425
weighted avg     0.4327    0.3318    0.2840      425

AUC for Fold 2 scheduler: 0.6198
===== Overall AUC on Test Set =====
Average AUC: 0.6198

```

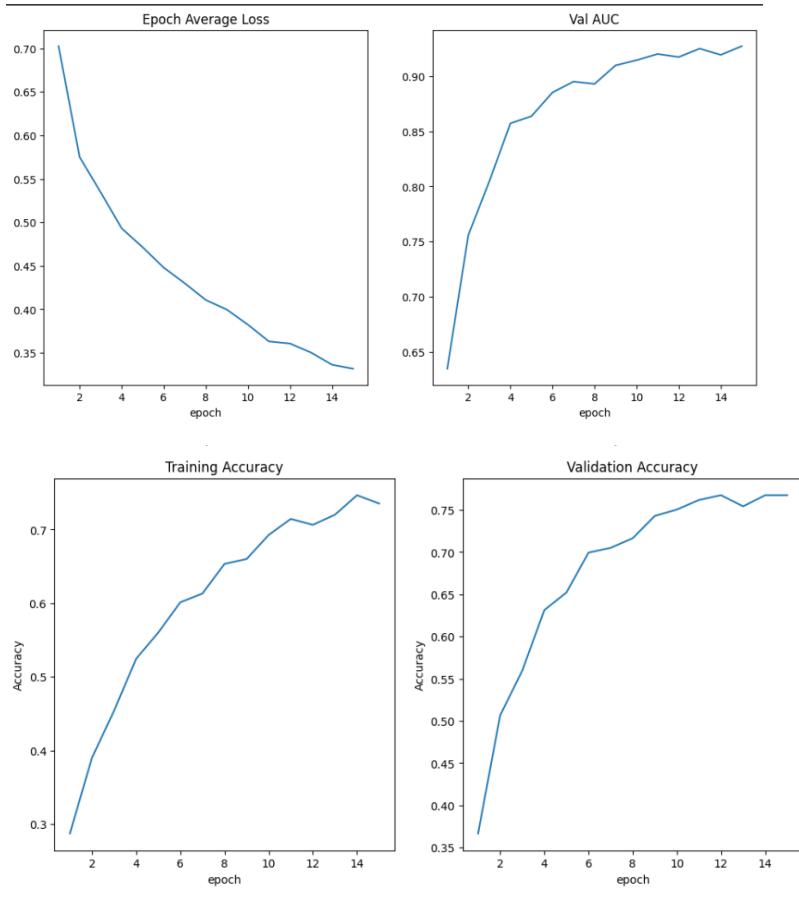
Cu early_stopping:



Dupa weight_decay am avut o crestere in performanta modelului, la fel si dupa early_stopping. Oprirea a fost la epoca 4

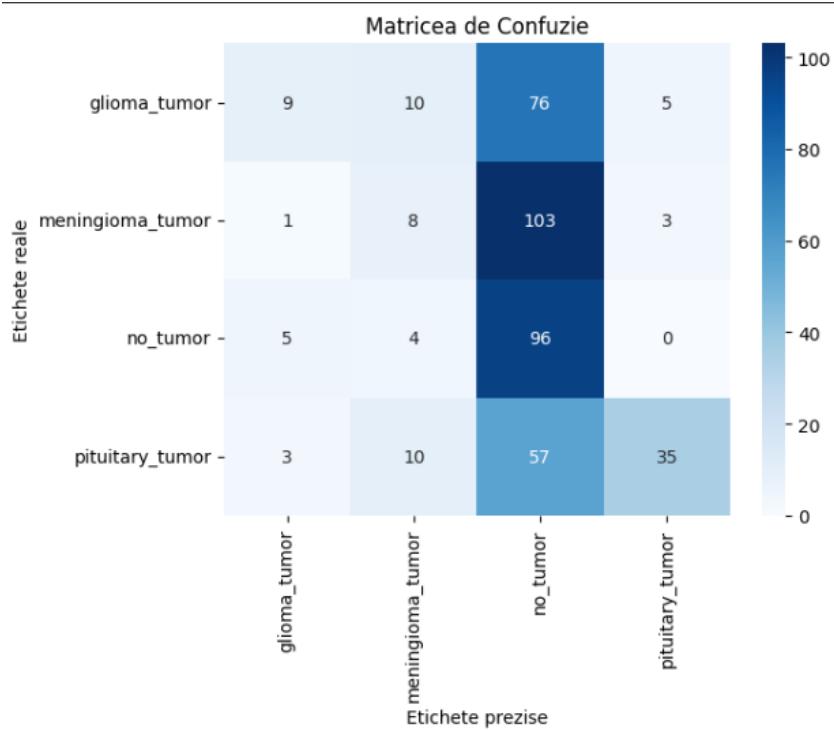
[Acum voi testa cu SGD avand learning_rate de 0.001, batch_size = 64 si cu dropout.](#)

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.5000	0.0900	0.1525	100
meningioma_tumor	0.2500	0.0696	0.1088	115
no_tumor	0.2892	0.9143	0.4394	105
pituitary_tumor	0.8140	0.3333	0.4730	105
accuracy			0.3482	425
macro avg	0.4633	0.3518	0.2934	425
weighted avg	0.4578	0.3482	0.2907	425

Metrici mai slabe fata de etapa trecuta cand nu aveam dropout.



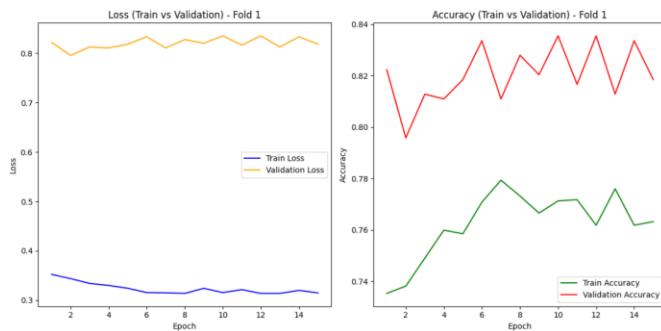
Antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.8217, Std = 0.0217
Recall: Mean = 0.8220, Std = 0.0232
F1-score: Mean = 0.8148, Std = 0.0246
Accuracy: Mean = 0.8220, Std = 0.0232
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.6250	0.1000	0.1724	100
meningioma_tumor	0.2308	0.0522	0.0851	115
no_tumor	0.3043	0.9333	0.4590	105
pituitary_tumor	0.7213	0.4190	0.5301	105
accuracy			0.3718	425
macro avg	0.4704	0.3761	0.3117	425
weighted avg	0.4629	0.3718	0.3080	425

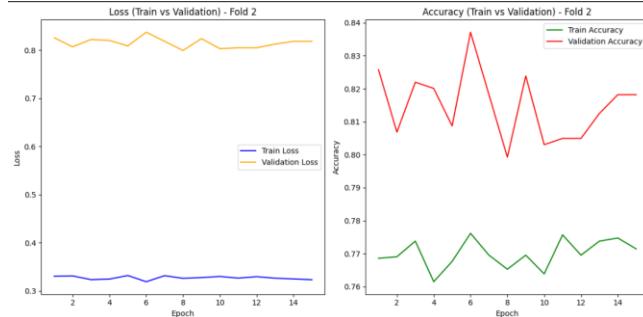
UC for Fold 1: 0.6591



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.7000	0.1400	0.2333	100
meningioma_tumor	0.1111	0.0174	0.0301	115
no_tumor	0.2934	0.9333	0.4465	105
pituitary_tumor	0.7736	0.3905	0.5190	105
accuracy			0.3647	425
macro avg	0.4695	0.3703	0.3072	425
weighted avg	0.4584	0.3647	0.3016	425

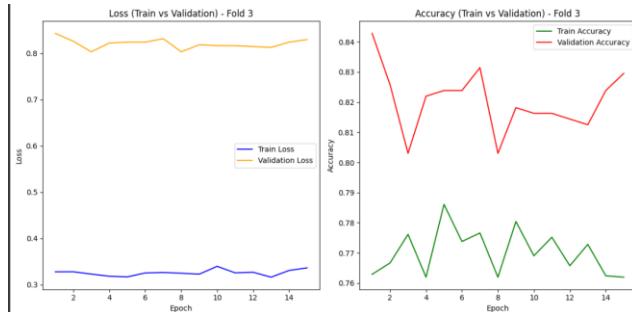
AUC for Fold 2: 0.6438



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.5789	0.1100	0.1849	100
meningioma_tumor	0.2727	0.0522	0.0876	115
no_tumor	0.3056	0.9429	0.4615	105
pituitary_tumor	0.8000	0.4571	0.5818	105
accuracy			0.3859	425
macro avg	0.4893	0.3905	0.3290	425
weighted avg	0.4832	0.3859	0.3250	425

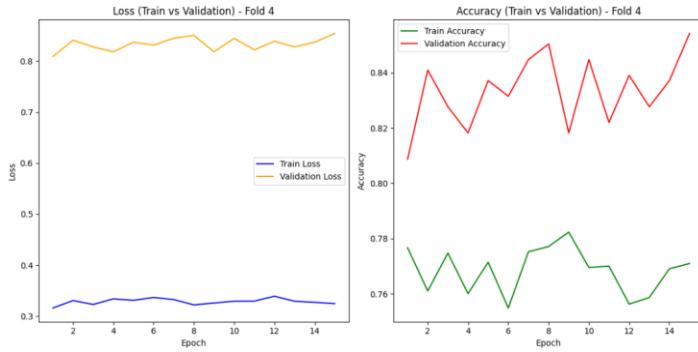
AUC for Fold 3: 0.6426



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.5652	0.1300	0.2114	100
meningioma_tumor	0.3448	0.0870	0.1389	115
no_tumor	0.3074	0.8667	0.4539	105
pituitary_tumor	0.7662	0.5619	0.6484	105
accuracy			0.4071	425
macro avg	0.4959	0.4114	0.3631	425
weighted avg	0.4916	0.4071	0.3596	425

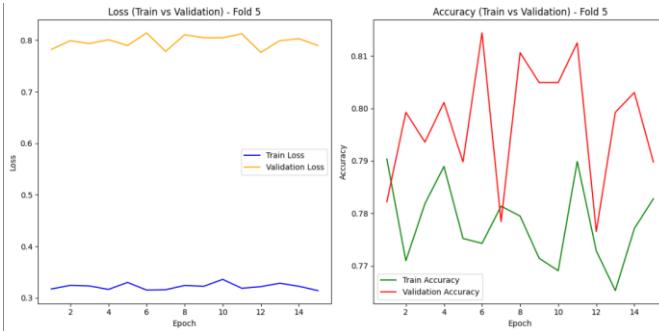
AUC for Fold 4: 0.6640



Fold5:

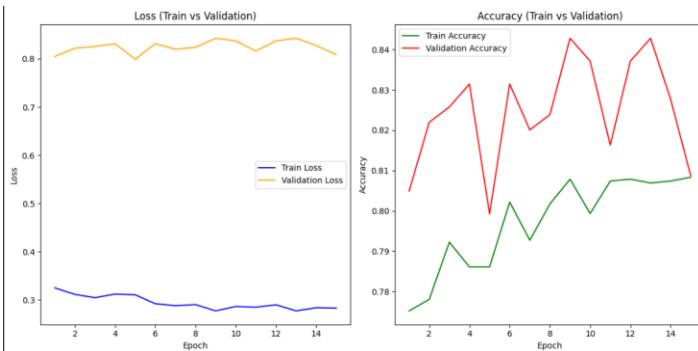
	precision	recall	f1-score	support
glioma_tumor	0.5833	0.1400	0.2258	100
meningioma_tumor	0.3077	0.0696	0.1135	115
no_tumor	0.3125	0.9048	0.4645	105
pituitary_tumor	0.7606	0.5143	0.6136	105
accuracy			0.4024	425
macro avg	0.4910	0.4072	0.3544	425
weighted avg	0.4856	0.4024	0.3502	425

AUC for Fold 5: 0.6578
===== Overall AUC on Test Set ====== Average AUC: 0.6534



Cel mai slab fold este 2

Cu scheduler cu weight_decay:



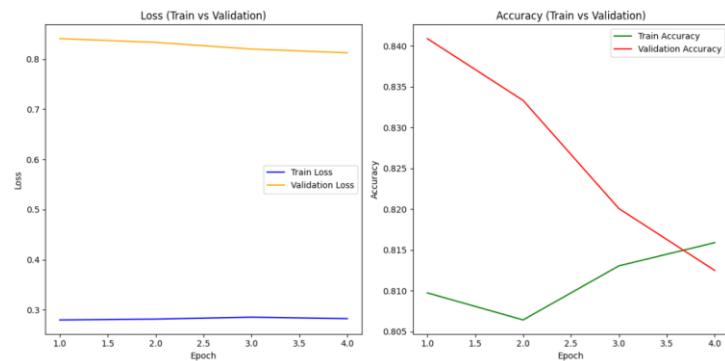
	precision	recall	f1-score	support
glioma_tumor	0.6154	0.1600	0.2540	100
meningioma_tumor	0.4167	0.0870	0.1439	115
no_tumor	0.3142	0.8857	0.4638	105
pituitary_tumor	0.7089	0.5333	0.6087	105
accuracy			0.4118	425
macro avg	0.5138	0.4165	0.3676	425
weighted avg	0.5103	0.4118	0.3637	425

AUC for Fold 2 scheduler: 0.6792

===== Overall AUC on Test Set =====

Average AUC: 0.6792

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.6842	0.1300	0.2185	100
meningioma_tumor	0.3000	0.0522	0.0889	115
no_tumor	0.3061	0.9619	0.4644	105
pituitary_tumor	0.8571	0.4571	0.5963	105
accuracy			0.3953	425
macro avg	0.5369	0.4003	0.3420	425
weighted avg	0.5295	0.3953	0.3375	425

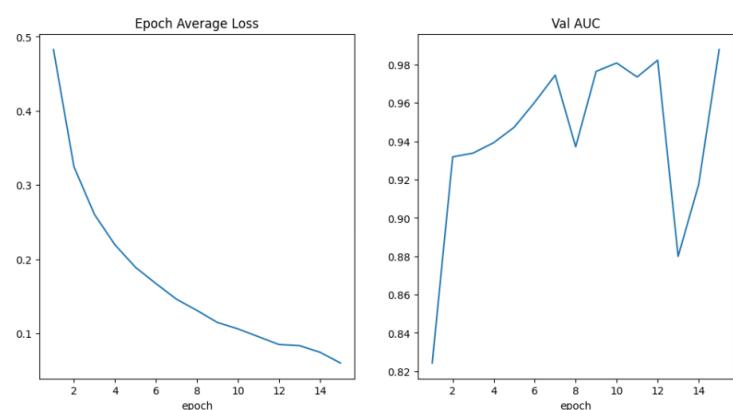
AUC early_stopping: 0.6835

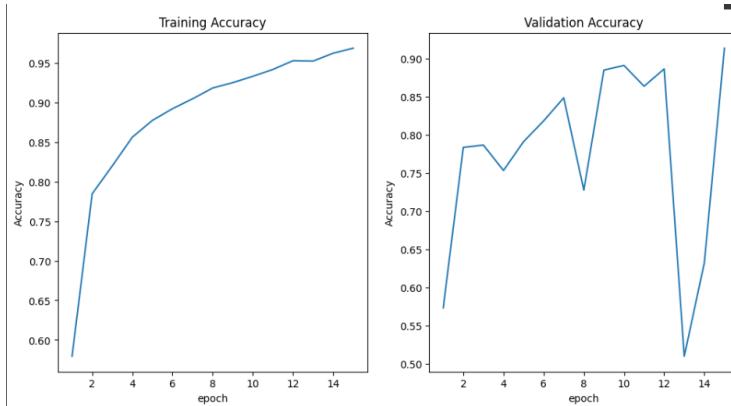
===== Overall AUC on Test Set =====

Average AUC: 0.6835

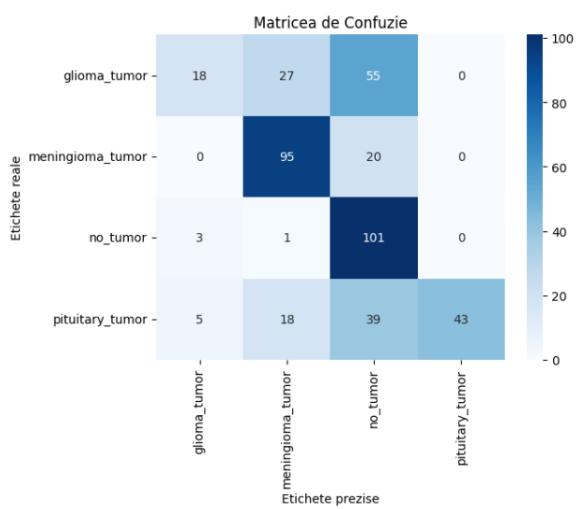
De data aceasta la early_stopping, oprirea a fost la epoca 4, iar acuratetea nu a fost imbunatatita fata de weight_decay.

Acum voi testa cu SGD, learning_rate=0.01, batch_size = 64, fara dropout





	precision	recall	f1-score	support
glioma_tumor	0.6923	0.1800	0.2857	100
meningioma_tumor	0.6738	0.8261	0.7422	115
no_tumor	0.4698	0.9619	0.6312	105
pituitary_tumor	1.0000	0.4095	0.5811	105
accuracy			0.6047	425
macro avg	0.7090	0.5944	0.5661	425
weighted avg	0.7083	0.6047	0.5676	425



Observam ca un learning_rate mai scazut la SGD adduce rezultate mult mai bune la antrenare. Acest lucru se poate intampla datorita faptului ca o rata mai mare de invatare accelereaza convergenta, iar SGD determina modelul sa invete mai repede fata de Adam, unde il imbunatatestea mai lent pe parcurs in functie de valorile gradientilor. Iar in cazul lui SGD o rata de invatare mai mare ajuta la reducerea overfittingului, ceea ce duce la o acuratete mai buna si overall metrii mai bune.

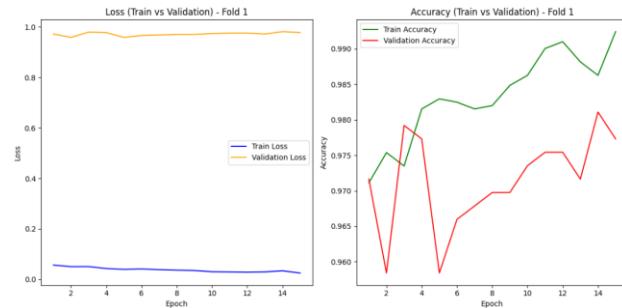
Antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9891, Std = 0.0074
Recall: Mean = 0.9890, Std = 0.0074
F1-score: Mean = 0.9890, Std = 0.0074
Accuracy: Mean = 0.9890, Std = 0.0074
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9000	0.1800	0.3000	100
meningioma_tumor	0.6536	0.8696	0.7463	115
no_tumor	0.5176	0.9810	0.6776	105
pituitary_tumor	0.9811	0.4952	0.6582	105
accuracy			0.6424	425
macro avg	0.7631	0.6314	0.5955	425
weighted avg	0.7589	0.6424	0.6026	425

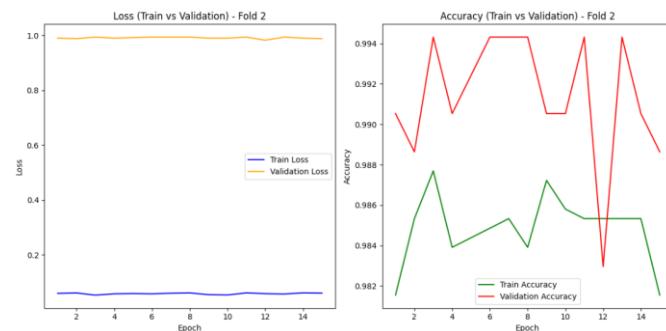
AUC for Fold 1: 0.8330



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9130	0.2100	0.3415	100
meningioma_tumor	0.6689	0.8609	0.7529	115
no_tumor	0.5074	0.9810	0.6688	105
pituitary_tumor	1.0000	0.4857	0.6538	105
accuracy			0.6447	425
macro avg	0.7723	0.6344	0.6042	425
weighted avg	0.7682	0.6447	0.6108	425

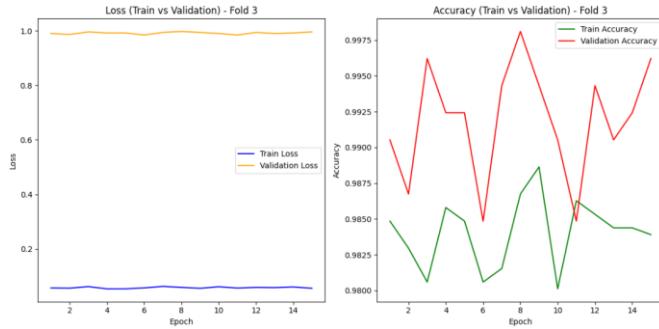
AUC for Fold 2: 0.8409



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9091	0.2000	0.3279	100
meningioma_tumor	0.6688	0.8957	0.7658	115
no_tumor	0.5228	0.9810	0.6821	105
pituitary_tumor	1.0000	0.4952	0.6624	105
accuracy			0.6541	425
macro avg	0.7752	0.6430	0.6096	425
weighted avg	0.7711	0.6541	0.6165	425

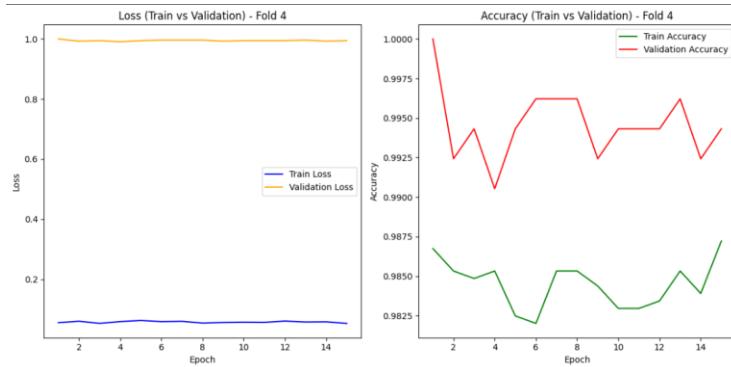
AUC for Fold 3: 0.8438



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.8571	0.1800	0.2975	100
meningioma_tumor	0.7113	0.8783	0.7860	115
no_tumor	0.5149	0.9905	0.6775	105
pituitary_tumor	0.9500	0.5429	0.6909	105
accuracy			0.6588	425
macro avg	0.7583	0.6479	0.6130	425
weighted avg	0.7560	0.6588	0.6208	425

AUC for Fold 4: 0.8532



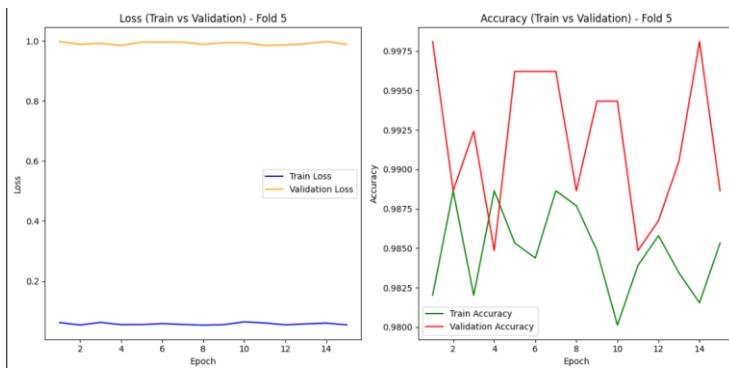
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9048	0.1900	0.3140	100
meningioma_tumor	0.6561	0.8957	0.7574	115
no_tumor	0.5200	0.9905	0.6820	105
pituitary_tumor	1.0000	0.4476	0.6184	105
accuracy			0.6424	425
macro avg	0.7702	0.6309	0.5929	425
weighted avg	0.7659	0.6424	0.6001	425

AUC for Fold 5: 0.8420

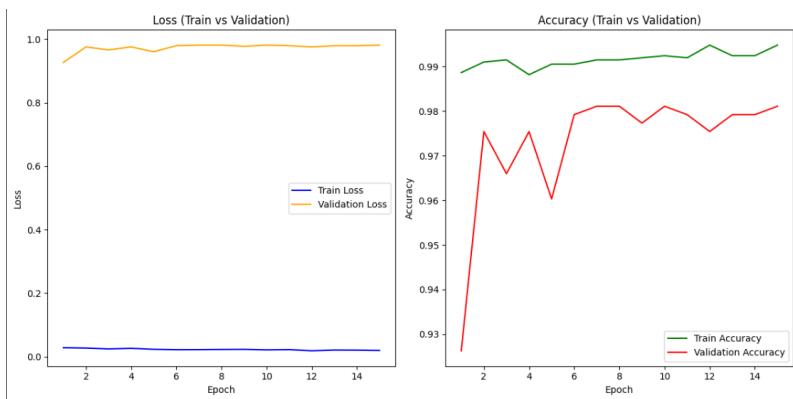
===== Overall AUC on Test Set =====

Average AUC: 0.8426



Observam ca cel mai slab fold este 1

Cu scheduler cu weight_decay:



```

precision    recall   f1-score   support
glioma_tumor      0.9474     0.1800     0.3025      100
meningioma_tumor   0.6646     0.9384     0.7754      115
no_tumor           0.5591     0.9985     0.7148      105
pituitary_tumor    1.0000     0.5619     0.7195      105

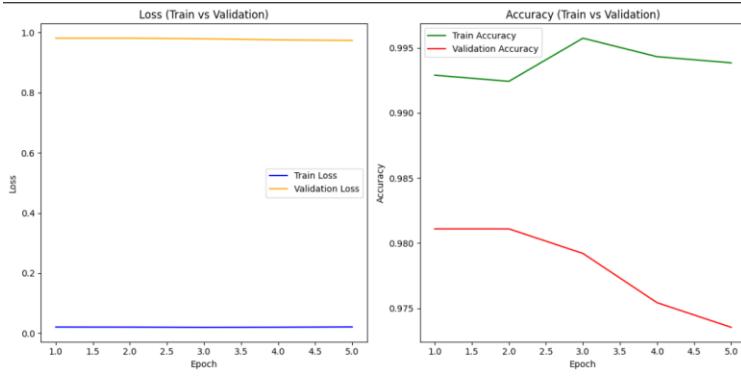
accuracy          -         -         -       425
macro avg         0.7928     0.6657     0.6280      425
weighted avg       0.7879     0.6776     0.6353      425

AUC for Fold 2 scheduler: 0.8510
===== Overall AUC on Test Set =====
Average AUC: 0.8510

```

Observam o imbunatatire in mare parte a metricilor in special la acuratete.

Cu early_stopping:



```

precision    recall    f1-score   support
gloma_tumor      0.8261    0.1900    0.3089     100
meningioma_tumor  0.6774    0.9130    0.7778     115
no_tumor          0.5426    0.9714    0.6962     105
pituitary_tumor   0.9831    0.5524    0.7073     105

accuracy          0.6682
macro avg        0.7573    0.6567    0.6226     425
weighted avg     0.7546    0.6682    0.6299     425

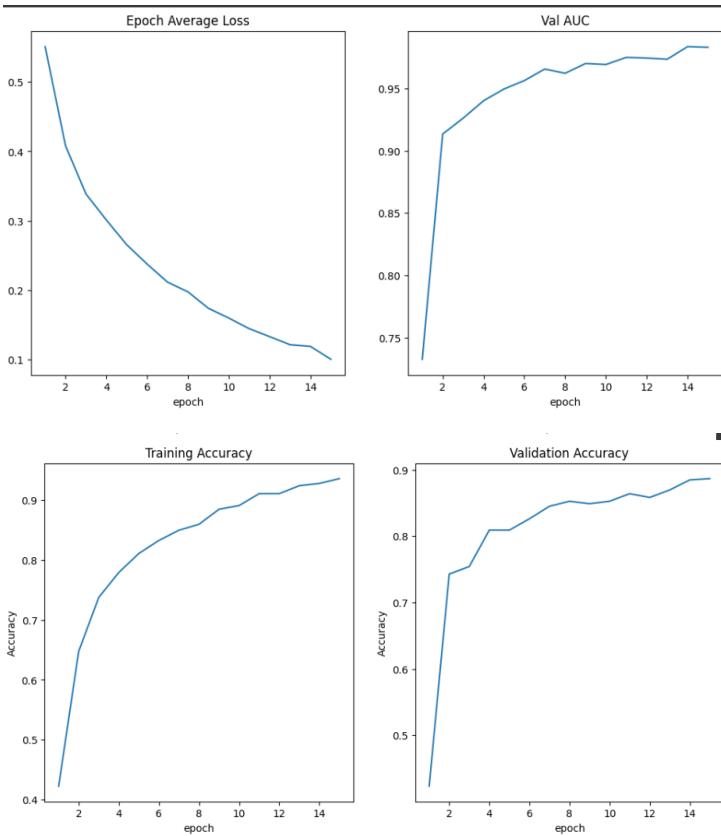
AUC early_stopping: 0.8581
===== Overall AUC on Test Set =====
Average AUC: 0.8581

```

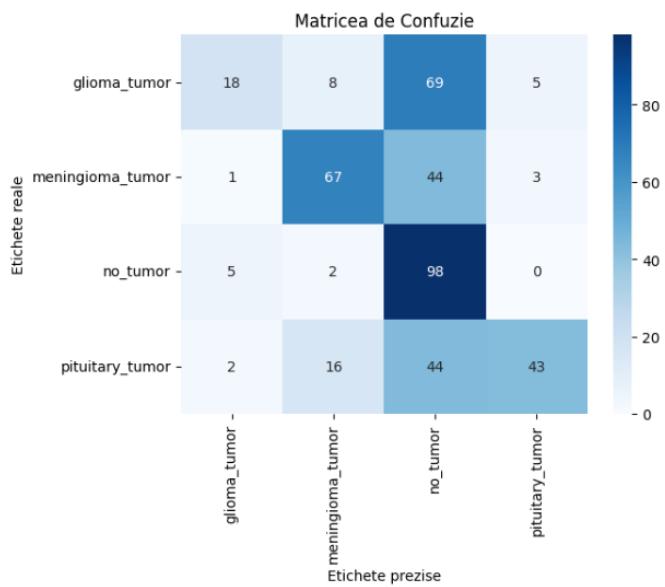
Dupa early_stopping, nu am obtinut metrii mai bune decat de la optimizator.

Acum voi testa cu SGD, learning_rate de 0.01 cu dropout, batch_size = 64, cu dropout.

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.6923	0.1800	0.2857	100
meningioma_tumor	0.7204	0.5826	0.6442	115
no_tumor	0.3843	0.9333	0.5444	105
pituitary_tumor	0.8431	0.4095	0.5513	105
accuracy			0.5318	425
macro avg	0.6600	0.5264	0.5064	425
weighted avg	0.6611	0.5318	0.5123	425



Observam faptul ca dropout afecteaza negativ metricile. Dezactivarea acestor neuroni aleator alesi este esentiala pe parcursul invatarii modelului.

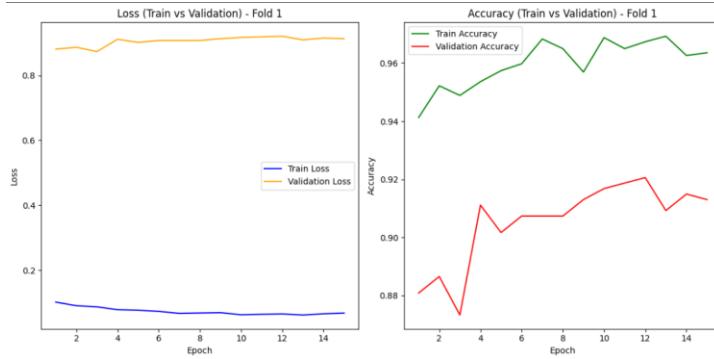
Pentru antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9575, Std = 0.0266
Recall: Mean = 0.9576, Std = 0.0261
F1-score: Mean = 0.9571, Std = 0.0265
Accuracy: Mean = 0.9576, Std = 0.0261
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.6667	0.1800	0.2835	100
meningioma_tumor	0.7203	0.7391	0.7296	115
no_tumor	0.4323	0.9429	0.5928	105
pituitary_tumor	0.9020	0.4381	0.5897	105
accuracy			0.5835	425
macro avg	0.6803	0.5750	0.5489	425
weighted avg	0.6814	0.5835	0.5563	425

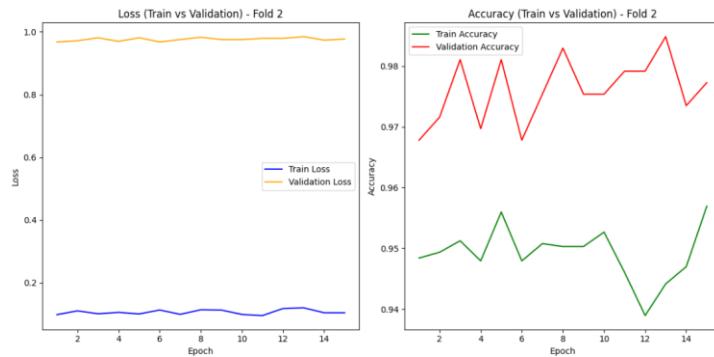
AUC for Fold 1: 0.8362



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.6923	0.1800	0.2857	100
meningioma_tumor	0.7000	0.6696	0.6844	115
no_tumor	0.4167	0.9524	0.5797	105
pituitary_tumor	0.9388	0.4381	0.5974	105
accuracy			0.5671	425
macro avg	0.6869	0.5600	0.5368	425
weighted avg	0.6872	0.5671	0.5432	425

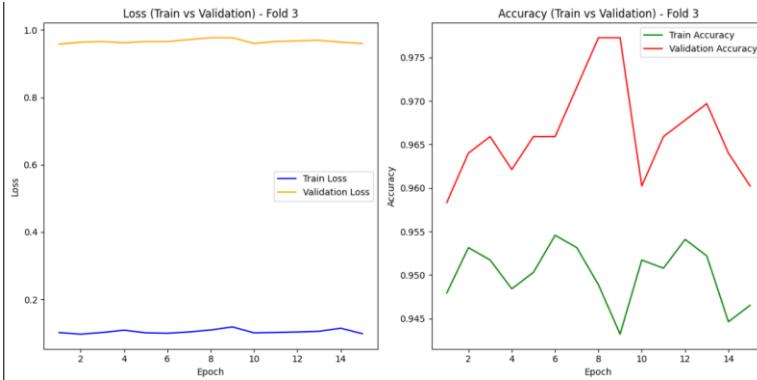
AUC for Fold 2: 0.8445



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.6923	0.1800	0.2857	100
meningioma_tumor	0.6643	0.8087	0.7294	115
no_tumor	0.4605	0.9429	0.6188	105
pituitary_tumor	0.9091	0.3810	0.5369	105
accuracy			0.5882	425
macro avg	0.6815	0.5781	0.5427	425
weighted avg	0.6810	0.5882	0.5501	425

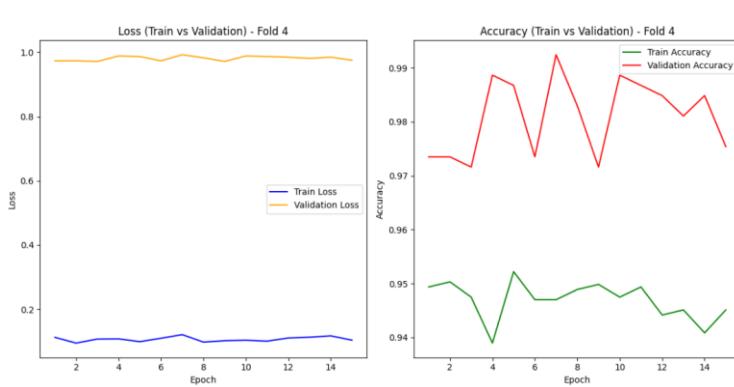
AUC for Fold 3: 0.8400



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.6429	0.1800	0.2812	100
meningioma_tumor	0.7167	0.7478	0.7319	115
no_tumor	0.4558	0.9333	0.6125	105
pituitary_tumor	0.8548	0.5048	0.6347	105
accuracy			0.6000	425
macro avg	0.6675	0.5915	0.5651	425
weighted avg	0.6690	0.6000	0.5724	425

AUC for Fold 4: 0.8475



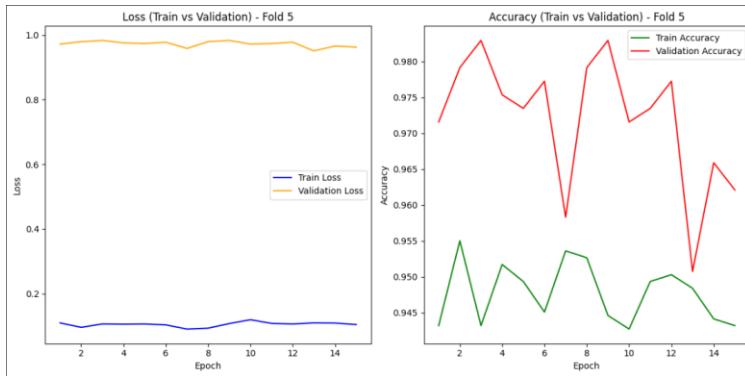
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.7037	0.1900	0.2992	100
meningioma_tumor	0.7453	0.6870	0.7149	115
no_tumor	0.4125	0.9429	0.5739	105
pituitary_tumor	0.9038	0.4476	0.5987	105
accuracy			0.5741	425
macro avg	0.6913	0.5669	0.5467	425
weighted avg	0.6925	0.5741	0.5536	425

AUC for Fold 5: 0.8407

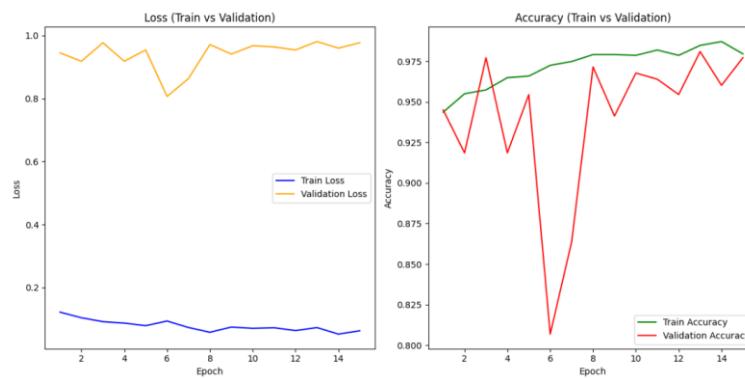
===== Overall AUC on Test Set =====

Average AUC: 0.8418



Cel mai slab fold este 2

Cu scheduler cu weight_decay:



```

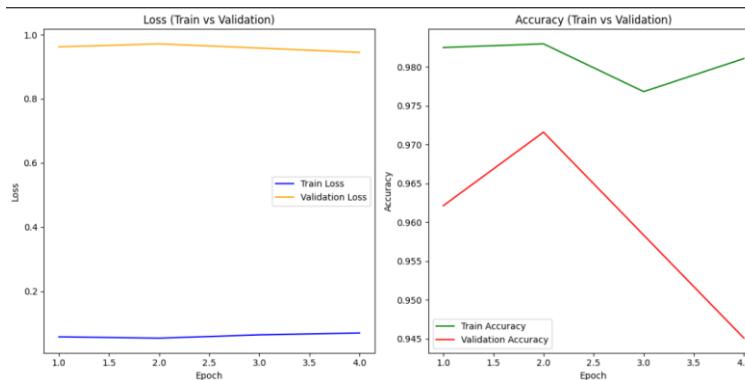
precision    recall   f1-score   support
glioma_tumor      0.7826    0.1800    0.2927      100
meningioma_tumor   0.8017    0.8087    0.8052      115
no_tumor           0.4688    1.0000    0.6383      105
pituitary_tumor    0.9032    0.5333    0.6707      105

accuracy          0.7391    0.6305    0.6017      425
macro avg         0.7400    0.6400    0.6101      425
weighted avg       0.7400    0.6400    0.6101      425

AUC for Fold 2 scheduler: 0.8641
===== Overall AUC on Test Set =====
Average AUC: 0.8641

```

Cu early_stopping:



```

precision    recall    f1-score   support
glioma_tumor      0.9000    0.1800    0.3000      100
meningioma_tumor   0.7742    0.8348    0.8033      115
no_tumor          0.4537    0.9810    0.6205      105
pituitary_tumor    0.9074    0.4667    0.6164      105

accuracy           -         -        0.6259      425
macro avg          0.7588    0.6156    0.5850      425
weighted avg       0.7575    0.6259    0.5935      425

AUC early_stopping: 0.8277
===== Overall AUC on Test Set =====
Average AUC: 0.8277

```

Oprirea a fost la epoca 4, iar acuratetea la early_stopping nu este mai buna decat cea de la weight_decay.

Foldurile slabie le-am ales in functie de acuratete, f1-score, recall si precision.

PS: Imi cer scuze ca mi-a luat foarte multe pagini pana acum la cerinta 2.5

Focal Loss:

Pentru a implementa aceasta cerinta, am importat functia de pierdere din biblioteca kornia.

In urmatoarele experimente am pastrat learning_rate-urile pentru care am obtinut cele mai bune metriki atat pentru Adam cat si pentru SGD. La Adam a fost 0.001, iar la SGD a fost 0.01.

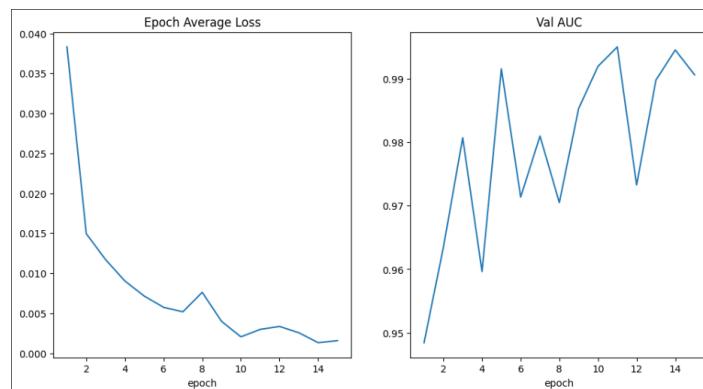
Din ce am citit, am vazut ca Focal Loss se aplica cel mai bine pe clase neechilibrate:

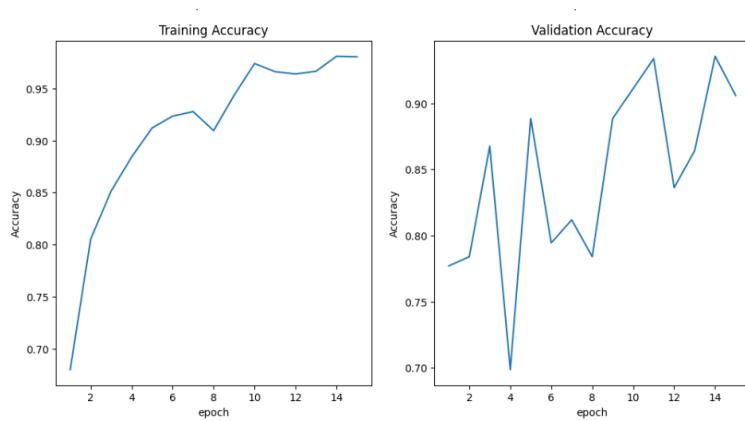
[Use Focal Loss To Train Model Using Imbalanced Dataset - Lei Mao's Log Book](#)

Informatii asemanatoare legate de FocalLoss am gasit si in cursul 8.

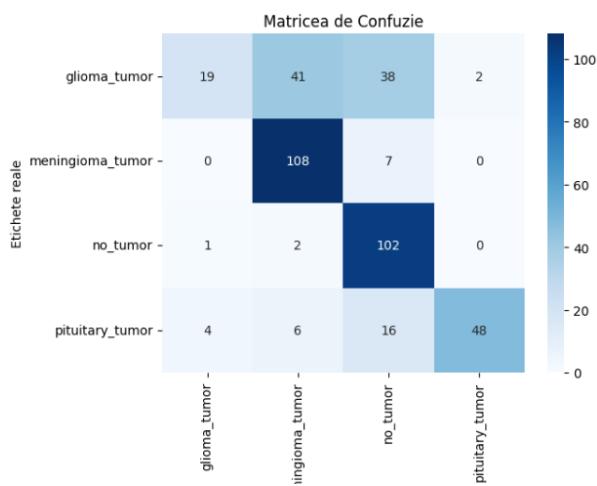
Am aplicat fara sa fi echilibrat clasele mai intai cu dropout, batch_size=32, optimizator Adam cu learning_rate de 0.001.

Pentru antrenarea clasica fara k-folduri:





	precision	recall	f1-score	support
glioma_tumor	0.7917	0.1900	0.3065	100
meningioma_tumor	0.6879	0.9391	0.7941	115
no_tumor	0.6258	0.9714	0.7612	105
pituitary_tumor	0.9600	0.6486	0.7742	74
accuracy			0.7030	394
macro avg	0.7663	0.6873	0.6590	394
weighted avg	0.7488	0.7030	0.6578	394



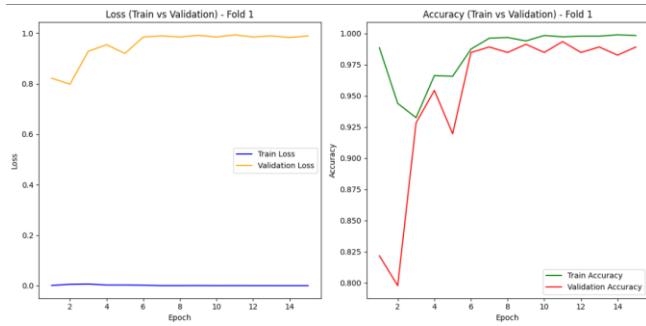
Pentru k-folduri, media rularilor este:

```
Precision: Mean = 0.9974, Std = 0.0047
Recall: Mean = 0.9974, Std = 0.0047
F1-score: Mean = 0.9974, Std = 0.0047
Accuracy: Mean = 0.9974, Std = 0.0047
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.7070	0.9652	0.8162	115
no_tumor	0.6250	1.0000	0.7692	105
pituitary_tumor	0.9583	0.6216	0.7541	74
accuracy			0.7183	394
macro avg	0.8226	0.6992	0.6717	394
weighted avg	0.8067	0.7183	0.6730	394

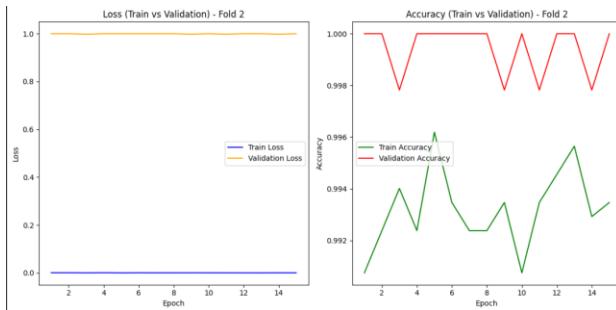
AUC for Fold 1: 0.8687



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9565	0.2200	0.3577	100
meningioma_tumor	0.7333	0.9565	0.8302	115
no_tumor	0.6176	1.0000	0.7636	105
pituitary_tumor	0.9412	0.6486	0.7680	74
accuracy	0.8122	0.7063	0.7234	394
macro avg	0.8122	0.7063	0.6799	394
weighted avg	0.7982	0.7234	0.6809	394

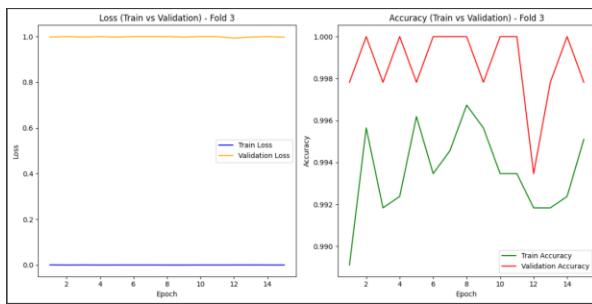
AUC for Fold 2: 0.8657



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.7320	0.9739	0.8358	115
no_tumor	0.6140	1.0000	0.7609	105
pituitary_tumor	0.9592	0.6351	0.7642	74
accuracy	0.8263	0.7048	0.7234	394
macro avg	0.8263	0.7048	0.6770	394
weighted avg	0.8113	0.7234	0.6784	394

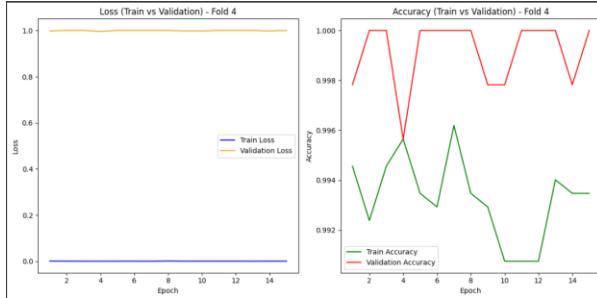
AUC for Fold 3: 0.8667



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2200	0.3607	100
meningioma_tumor	0.7303	0.9652	0.8315	115
no_tumor	0.6176	1.0000	0.7636	105
pituitary_tumor	0.9400	0.6351	0.7581	74
accuracy			0.7234	394
macro avg	0.8220	0.7051	0.6785	394
weighted avg	0.8081	0.7234	0.6801	394

AUC for Fold 4: 0.8691



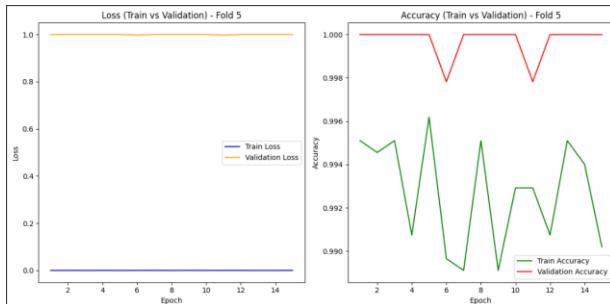
Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.7383	0.9565	0.8333	115
no_tumor	0.6000	1.0000	0.7500	105
pituitary_tumor	0.9592	0.6351	0.7642	74
accuracy			0.7183	394
macro avg	0.8244	0.7004	0.6737	394
weighted avg	0.8093	0.7183	0.6747	394

AUC for Fold 5: 0.8657

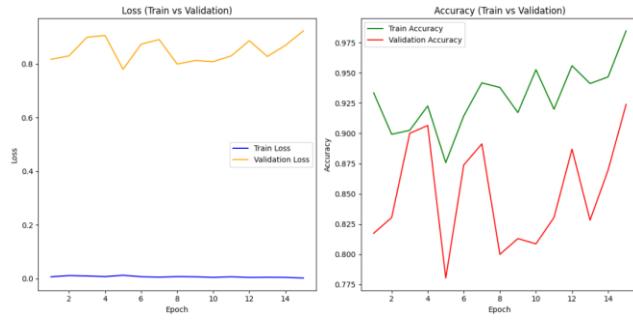
===== Overall AUC on Test Set =====

Average AUC: 0.8672



Foldul 1 este cel mai slab

Scheduler cu weight_decay:



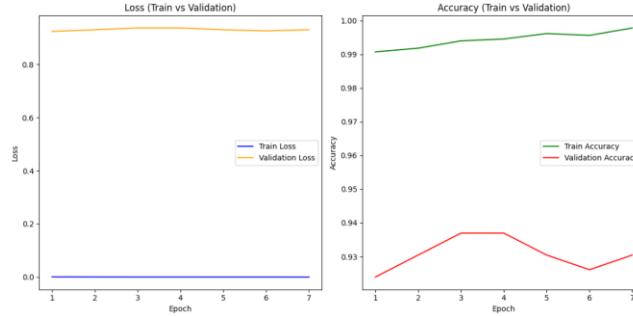
```

precision    recall   f1-score   support
glioma_tumor      0.9130    0.2100    0.3415      100
meningioma_tumor   0.6867    0.8957    0.7774     115
no_tumor           0.6036    0.9714    0.7445     105
pituitary_tumor    0.9808    0.6892    0.8095      74
accuracy          -         -        0.7030      394
macro avg         0.7960    0.6916    0.6682      394
weighted avg       0.7772    0.7030    0.6640      394

AUC for Fold 2 scheduler: 0.8962
===== Overall AUC on Test Set =====
Average AUC: 0.8962

```

Cu early_Stopping:



```

precision    recall   f1-score   support
glioma_tumor      0.9286    0.2600    0.4062      100
meningioma_tumor   0.7431    0.9304    0.8263     115
no_tumor           0.6108    0.9714    0.7500     105
pituitary_tumor    0.9818    0.7297    0.8372      74
accuracy          -         -        0.7335      394
macro avg         0.8161    0.7229    0.7049      394
weighted avg       0.7997    0.7335    0.7014      394

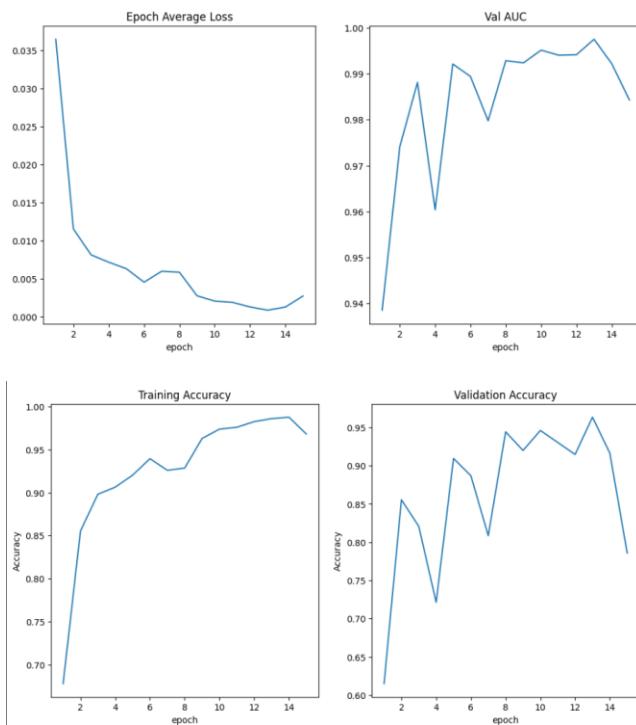
AUC early_stopping: 0.8946
===== Overall AUC on Test Set =====
Average AUC: 0.8946

```

Cu early_stopping ne-am oprit la epoca 7 si am obtinut metrici mai bune in mare parte decat la weight_decay.

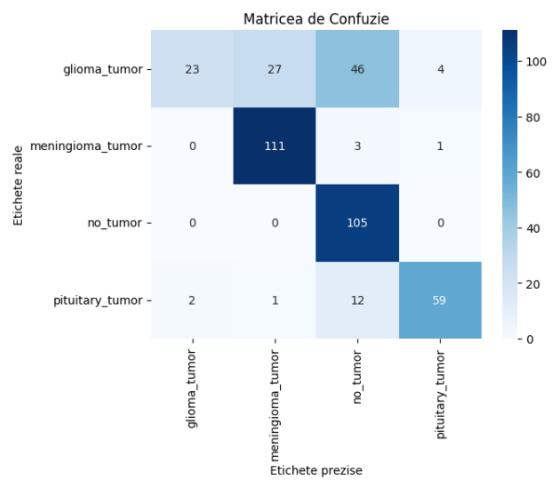
Acum am testat cu Adam, learning_rate = 0.001, batch=32, cu dropout.

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.9200	0.2300	0.3680	100
meningioma_tumor	0.7986	0.9652	0.8740	115
no_tumor	0.6325	1.0000	0.7749	105
pituitary_tumor	0.9219	0.7973	0.8551	74
accuracy			0.7563	394
macro avg	0.8182	0.7481	0.7180	394
weighted avg	0.8083	0.7563	0.7156	394

Cea mai buna acuratete de pana acum obtinuta din toate experimentele.



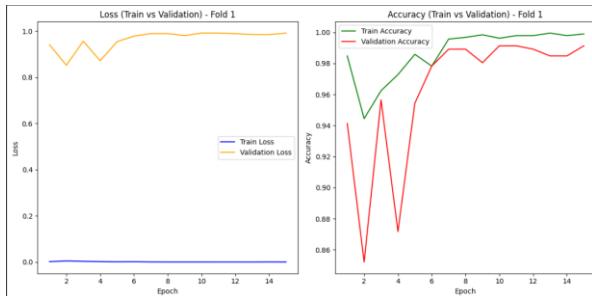
Antrenarea cu k-folduri media metricilor este:

```
Precision: Mean = 0.9974, Std = 0.0035
Recall: Mean = 0.9974, Std = 0.0036
F1-score: Mean = 0.9974, Std = 0.0036
Accuracy: Mean = 0.9974, Std = 0.0036
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2300	0.3740	100
meningioma_tumor	0.6894	0.9652	0.8043	115
no_tumor	0.6500	0.9905	0.7849	105
pituitary_tumor	1.0000	0.6757	0.8065	74
accuracy			0.7310	394
macro avg	0.8349	0.7153	0.6924	394
weighted avg	0.8161	0.7310	0.6903	394

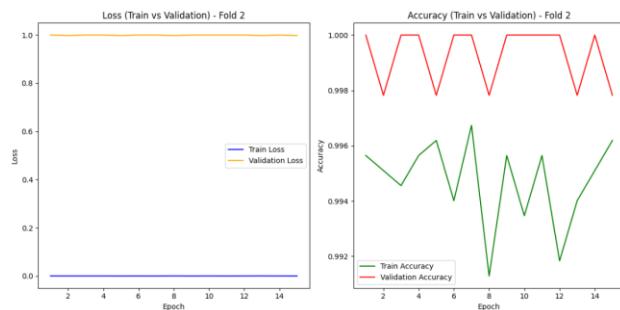
AUC for Fold 1: 0.8820



Fold2:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2300	0.3740	100
meningioma_tumor	0.6975	0.9826	0.8159	115
no_tumor	0.6646	1.0000	0.7985	105
pituitary_tumor	0.9804	0.6757	0.8000	74
accuracy			0.7386	394
macro avg	0.8356	0.7221	0.6971	394
weighted avg	0.8186	0.7386	0.6961	394

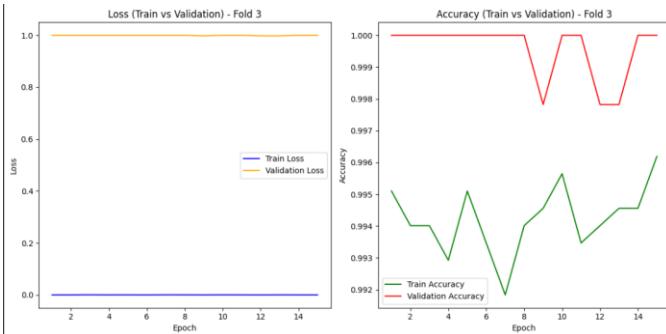
AUC for Fold 2: 0.8829



Fold3:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2100	0.3471	100
meningioma_tumor	0.6957	0.9739	0.8116	115
no_tumor	0.6522	1.0000	0.7895	105
pituitary_tumor	0.9608	0.6622	0.7840	74
accuracy			0.7284	394
macro avg	0.8272	0.7115	0.6830	394
weighted avg	0.8111	0.7284	0.6826	394

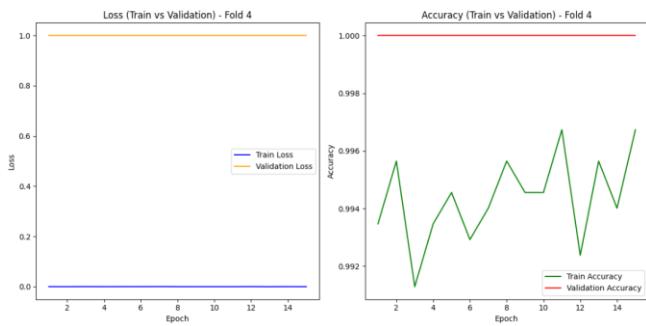
AUC for Fold 3: 0.8858



Fold4:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2300	0.3740	100
meningioma_tumor	0.7025	0.9652	0.8132	115
no_tumor	0.6541	0.9905	0.7879	105
pituitary_tumor	0.9630	0.7027	0.8125	74
accuracy			0.7360	394
macro avg	0.8299	0.7221	0.6969	394
weighted avg	0.8140	0.7360	0.6948	394

AUC for Fold 4: 0.8856



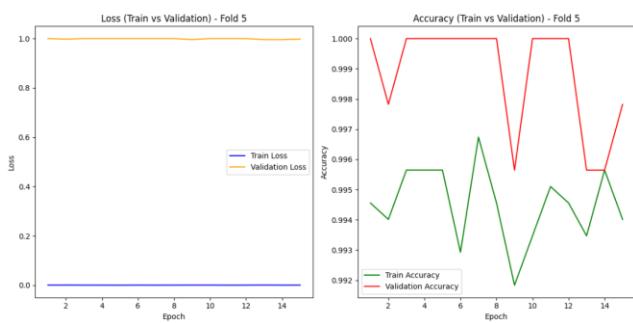
Fold5:

	precision	recall	f1-score	support
glioma_tumor	1.0000	0.2300	0.3740	100
meningioma_tumor	0.7044	0.9739	0.8175	115
no_tumor	0.6582	0.9905	0.7909	105
pituitary_tumor	0.9815	0.7162	0.8281	74
accuracy			0.7411	394
macro avg	0.8360	0.7277	0.7026	394
weighted avg	0.8192	0.7411	0.6998	394

AUC for Fold 5: 0.8810

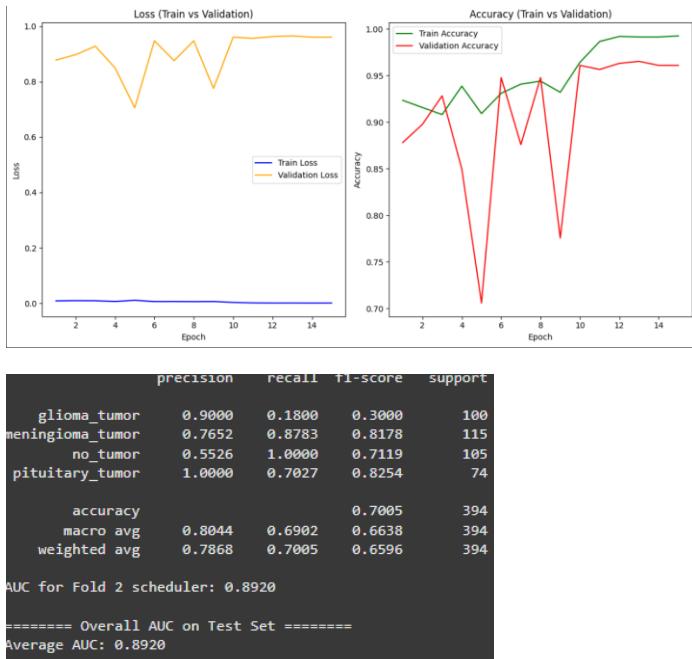
===== Overall AUC on Test Set =====

Average AUC: 0.8835



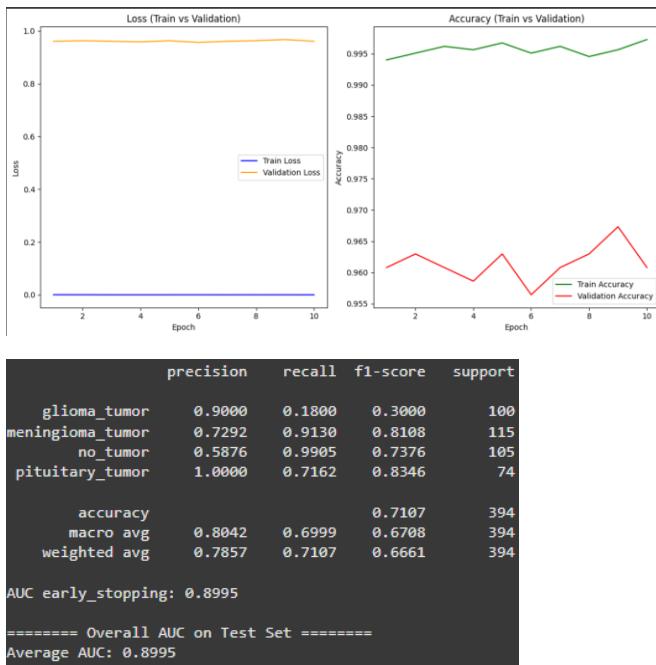
Cel mai slab fold este 2.

Cu scheduler cu weight_decay:



Observam o scadere in acuratete si in restul metricilor de la f1-score

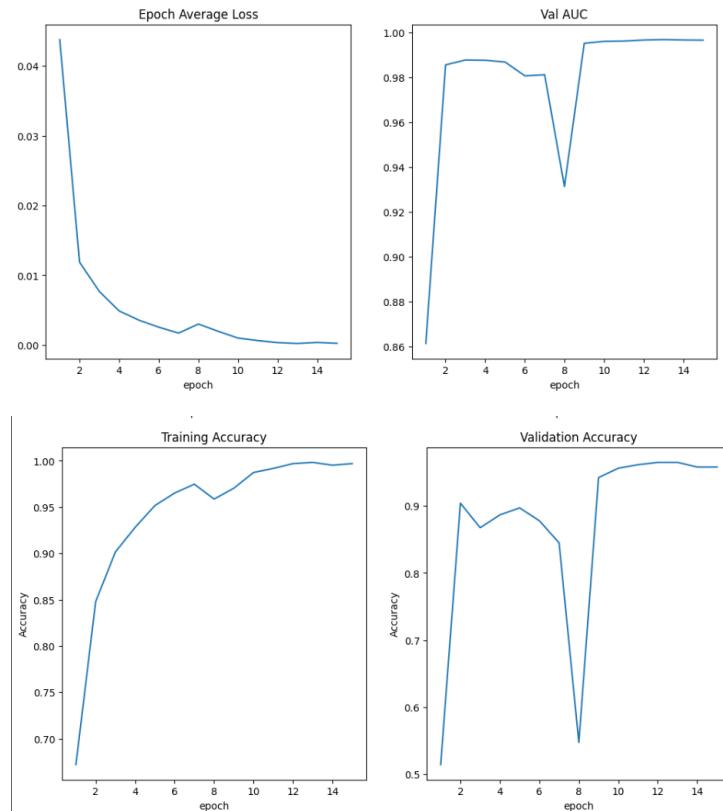
Cu early_stopping:



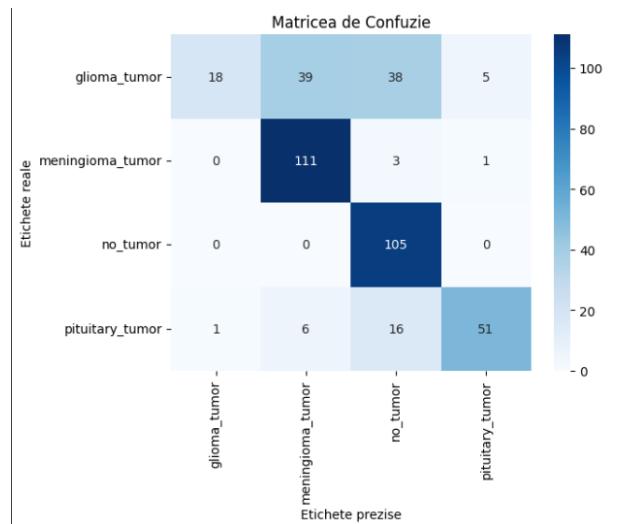
S-a oprit la epoca 10. Im bunatati la f1-score pentru no_tumor si pituitary_tumor, la acuratete.

Acum voi testa cu Adam, learning_rate=0.001, fara dropout dar cu batch_size=64.

Pentru antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.7115	0.9652	0.8192	115
no_tumor	0.6481	1.0000	0.7865	105
pituitary_tumor	0.8947	0.6892	0.7786	74
accuracy			0.7234	394
macro avg	0.8004	0.7086	0.6717	394
weighted avg	0.7889	0.7234	0.6717	394



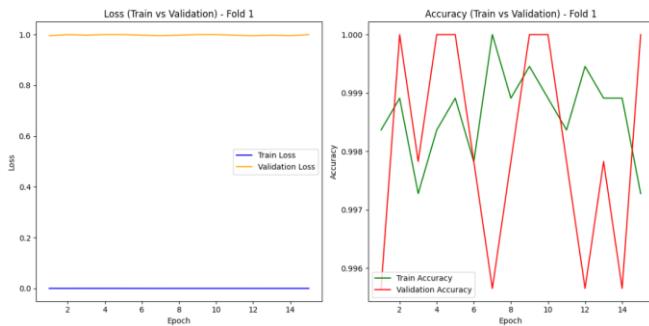
Pentru antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9991, Std = 0.0019
Recall: Mean = 0.9991, Std = 0.0020
F1-score: Mean = 0.9991, Std = 0.0020
Accuracy: Mean = 0.9991, Std = 0.0020
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.9474	0.1800	0.3025	100
meningioma_tumor	0.7273	0.9739	0.8327	115
no_tumor	0.6325	1.0000	0.7749	105
pituitary_tumor	0.9091	0.6757	0.7752	74
accuracy			0.7234	394
macro avg	0.8041	0.7074	0.6713	394
weighted avg	0.7920	0.7234	0.6719	394

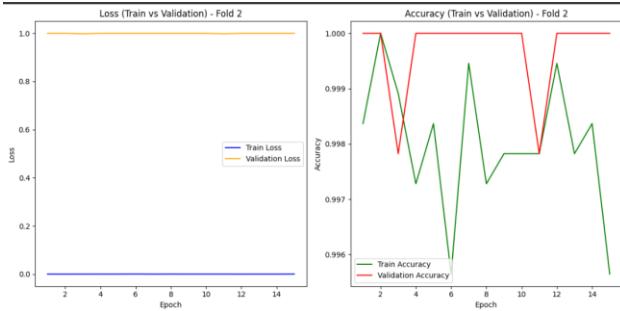
AUC for Fold 1: 0.8680



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7226	0.9739	0.8296	115
no_tumor	0.6420	0.9985	0.7790	105
pituitary_tumor	0.8947	0.6892	0.7786	74
accuracy			0.7259	394
macro avg	0.8023	0.7109	0.6760	394
weighted avg	0.7912	0.7259	0.6764	394

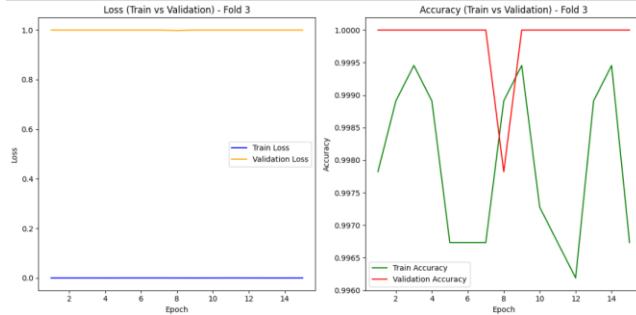
AUC for Fold 2: 0.8735



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7044	0.9739	0.8175	115
no_tumor	0.6460	0.9905	0.7820	105
pituitary_tumor	0.9074	0.6622	0.7656	74
accuracy			0.7208	394
macro avg	0.8019	0.7041	0.6704	394
weighted avg	0.7893	0.7208	0.6712	394

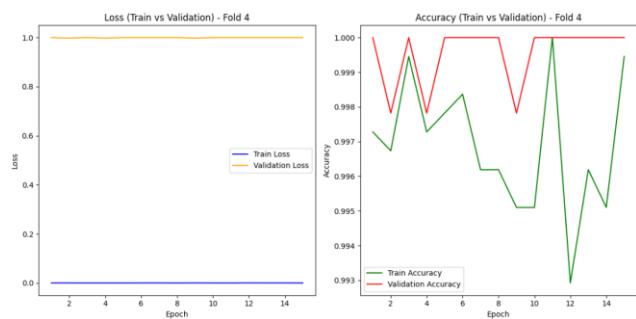
AUC for Fold 3: 0.8731



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9048	0.1900	0.3140	100
meningioma_tumor	0.7134	0.9739	0.8235	115
no_tumor	0.6358	0.9810	0.7715	105
pituitary_tumor	0.9074	0.6622	0.7656	74
accuracy			0.7183	394
macro avg	0.7903	0.7018	0.6687	394
weighted avg	0.7777	0.7183	0.6695	394

AUC for Fold 4: 0.8762

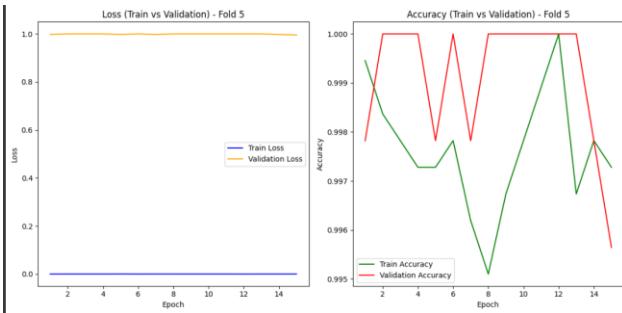


Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.9500	0.1900	0.3167	100
meningioma_tumor	0.7226	0.9739	0.8296	115
no_tumor	0.6420	0.9905	0.7790	105
pituitary_tumor	0.8947	0.6892	0.7786	74
accuracy			0.7259	394
macro avg	0.8023	0.7109	0.6760	394
weighted avg	0.7912	0.7259	0.6764	394

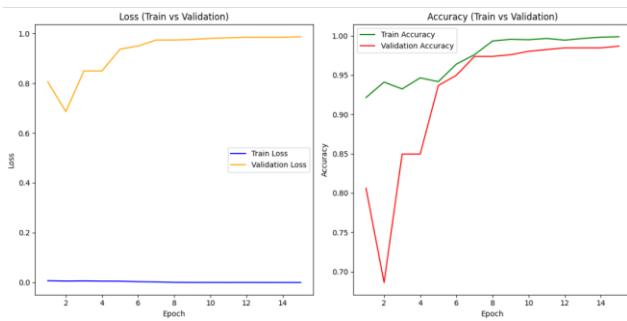
AUC for Fold 5: 0.8753

===== Overall AUC on Test Set =====
Average AUC: 0.8732



Cel mai slab fold este 4.

Cu scheduler cu weight_decay:



```

precision    recall    f1-score   support
glioma_tumor  0.8800   0.2200   0.3520    100
meningioma_tumor 0.6981   0.9652   0.8102    115
no_tumor       0.6519   0.9810   0.7833    105
pituitary_tumor 0.9808   0.6892   0.8095     74

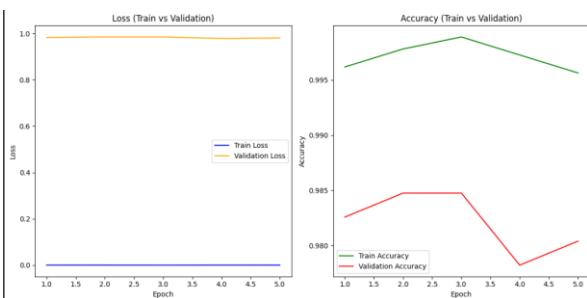
accuracy          0.8802   0.7138   0.6888    394
macro avg        0.8802   0.7138   0.6888    394
weighted avg     0.8802   0.7138   0.6888    394

AUC for Fold 2 scheduler: 0.8638
===== Overall AUC on Test Set =====
Average AUC: 0.8638

```

Observam o imbunatatire la f1-score.

Cu early_stopping:



```

precision    recall   f1-score   support
gloma_tumor      0.9545    0.2100    0.3443     100
meningioma_tumor  0.7208    0.9652    0.8253     115
no_tumor          0.6205    0.9810    0.7601     105
pituitary_tumor   1.0000    0.7027    0.8254      74

accuracy          -         -        0.7284     394
macro avg       0.8240    0.7147    0.6888     394
weighted avg    0.8058    0.7284    0.6859     394

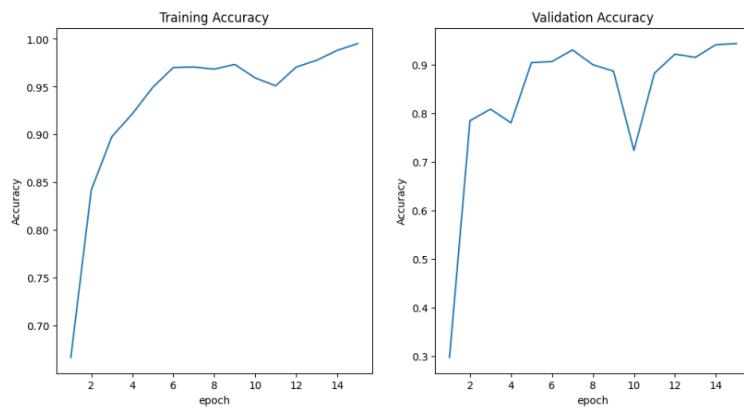
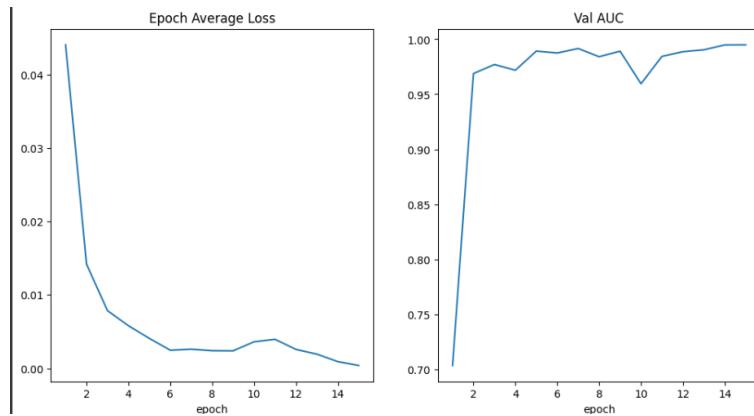
AUC early_stopping: 0.8669
===== Overall AUC on Test Set =====
Average AUC: 0.8669

```

Acuratetea la fel ca la weight_decay.

Acum voi testa cu Adam, learning_rate = 0.001, batch_size=64 si cu dropout.

Antrenarea clasica fara k-folduri:

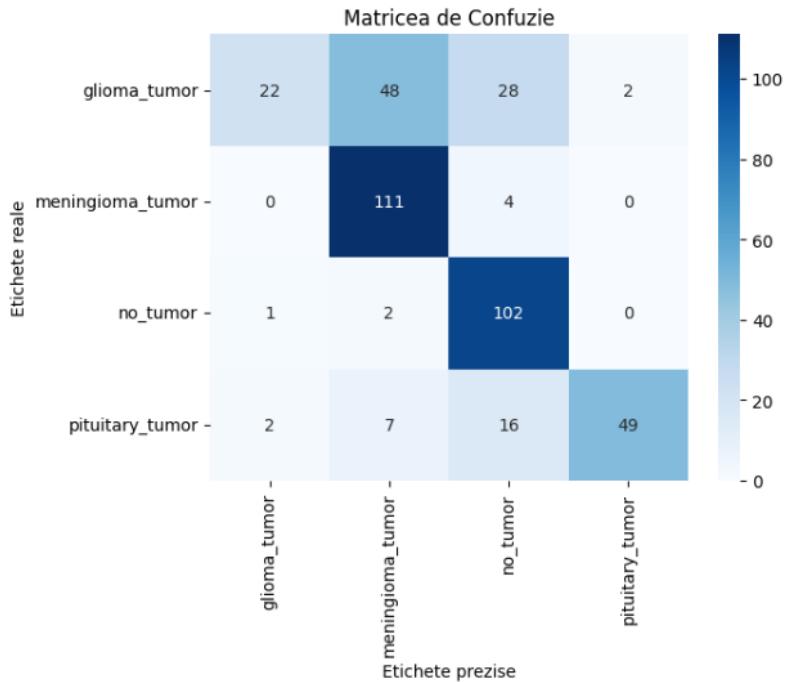


```

precision    recall   f1-score   support
gloma_tumor      0.8800    0.2200    0.3520     100
meningioma_tumor  0.6607    0.9652    0.7845     115
no_tumor          0.6800    0.9714    0.8000     105
pituitary_tumor   0.9608    0.6622    0.7840      74

accuracy          -         -        0.7208     394
macro avg       0.7954    0.7047    0.6801     394
weighted avg    0.7779    0.7208    0.6788     394

```

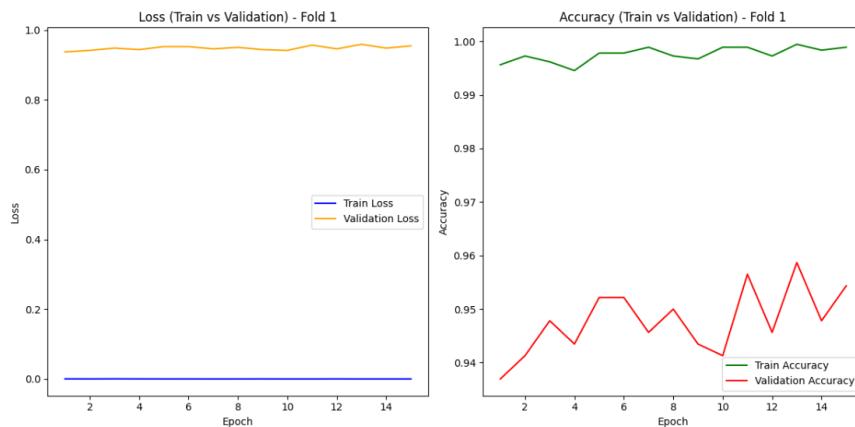


Antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9904, Std = 0.0202
Recall: Mean = 0.9904, Std = 0.0202
F1-score: Mean = 0.9904, Std = 0.0203
Accuracy: Mean = 0.9904, Std = 0.0202
```

Fold1:

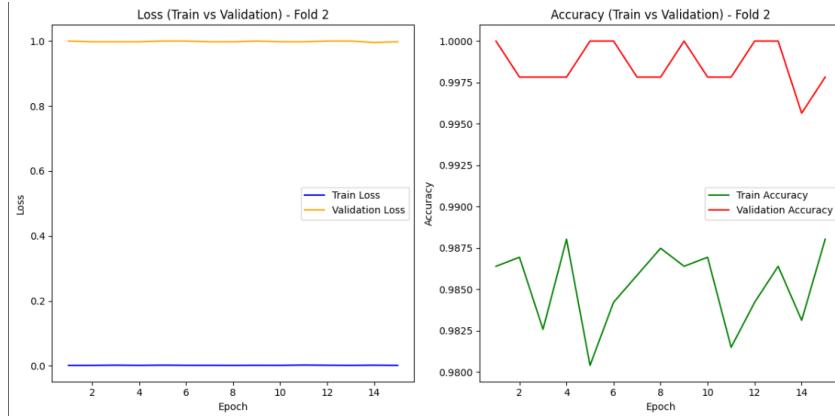
	precision	recall	f1-score	support
glioma_tumor	0.8889	0.2400	0.3780	100
meningioma_tumor	0.6813	0.9478	0.7927	115
no_tumor	0.6581	0.9714	0.7846	105
pituitary_tumor	0.9808	0.6892	0.8095	74
accuracy			0.7259	394
macro avg	0.8022	0.7121	0.6912	394
weighted avg	0.7840	0.7259	0.6884	394
AUC for Fold 1:	0.8480			



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.9167	0.2200	0.3548	100
meningioma_tumor	0.6770	0.9478	0.7899	115
no_tumor	0.6433	0.9619	0.7710	105
pituitary_tumor	0.9615	0.6757	0.7937	74
accuracy			0.7157	394
macro avg	0.7996	0.7014	0.6773	394
weighted avg	0.7823	0.7157	0.6751	394

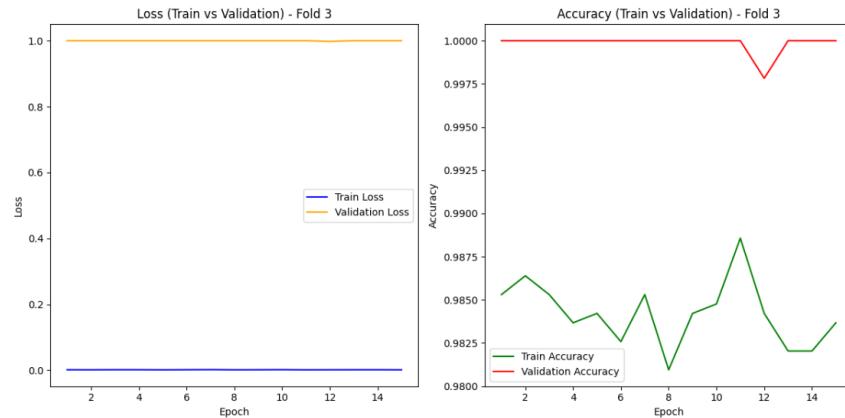
AUC for Fold 2: 0.8496



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.8800	0.2200	0.3520	100
meningioma_tumor	0.6627	0.9565	0.7829	115
no_tumor	0.6601	0.9619	0.7829	105
pituitary_tumor	0.9800	0.6622	0.7903	74
accuracy			0.7157	394
macro avg	0.7957	0.7001	0.6770	394
weighted avg	0.7767	0.7157	0.6749	394

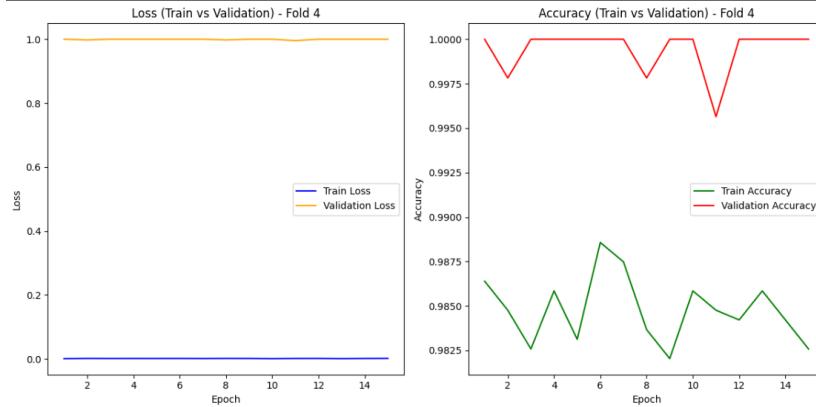
AUC for Fold 3: 0.8488



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.9231	0.2400	0.3810	100
meningioma_tumor	0.6748	0.9565	0.7914	115
no_tumor	0.6601	0.9619	0.7829	105
pituitary_tumor	0.9615	0.6757	0.7937	74
accuracy			0.7234	394
macro avg	0.8049	0.7085	0.6872	394
weighted avg	0.7878	0.7234	0.6854	394

AUC for Fold 4: 0.8473



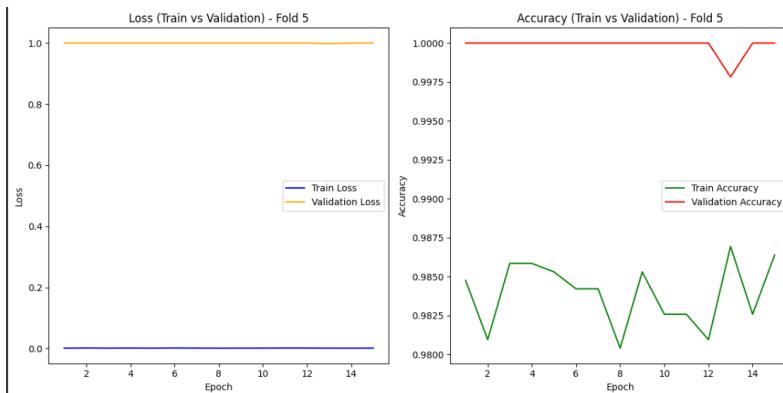
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8846	0.2300	0.3651	100
meningioma_tumor	0.6568	0.9652	0.7817	115
no_tumor	0.6918	0.9619	0.8048	105
pituitary_tumor	0.9623	0.6892	0.8031	74
accuracy			0.7259	394
macro avg	0.7989	0.7116	0.6887	394
weighted avg	0.7813	0.7259	0.6861	394

AUC for Fold 5: 0.8498

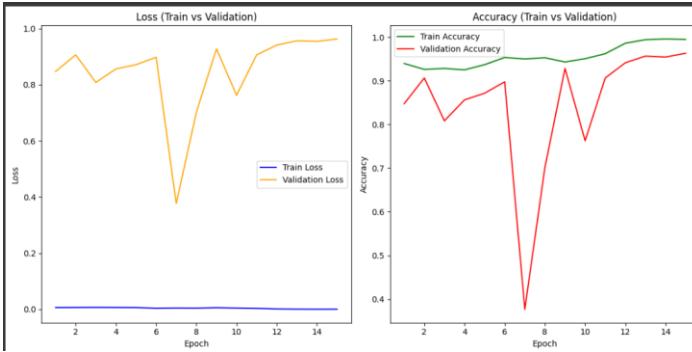
===== Overall AUC on Test Set =====

Average AUC: 0.8487



Cel mai slab fold este 3

Cu scheduler cu weight_decay:

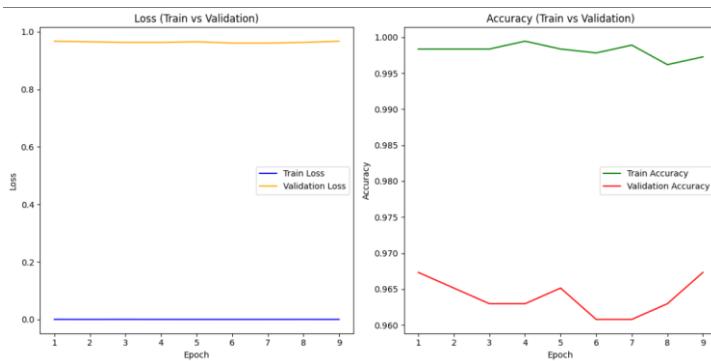


```

precision    recall   f1-score   support
glioma_tumor      1.0000    0.2200    0.3607     100
meningioma_tumor   0.6987    0.9478    0.8044     115
no_tumor          0.6012    0.9905    0.7536     105
pituitary_tumor    0.9778    0.5946    0.7395      74
accuracy           -         -         0.7081     394
macro avg        0.8212    0.6882    0.6646     394
weighted avg      0.8035    0.7081    0.6661     394
AUC for Fold 2 scheduler: 0.8773
===== Overall AUC on Test Set =====
Average AUC: 0.8773

```

Cu early_stopping:



```

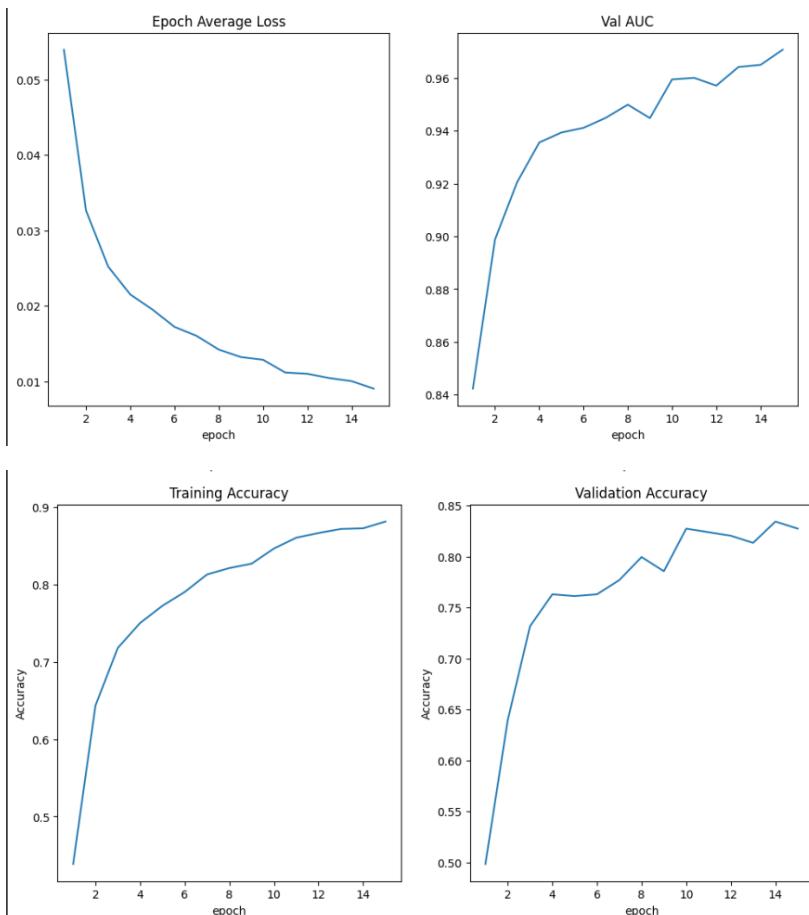
precision    recall   f1-score   support
glioma_tumor      1.0000    0.2000    0.3333     100
meningioma_tumor   0.7315    0.9478    0.8258     115
no_tumor          0.6012    0.9905    0.7482     105
pituitary_tumor    0.9808    0.6892    0.8095      74
accuracy           -         -         0.7208     394
macro avg        0.8284    0.7069    0.6792     394
weighted avg      0.8117    0.7208    0.6771     394
AUC early_stopping: 0.8778
===== Overall AUC on Test Set =====
Average AUC: 0.8778

```

Metrici mai bune decat la weight_decay si s-a oprit la epoca 9.

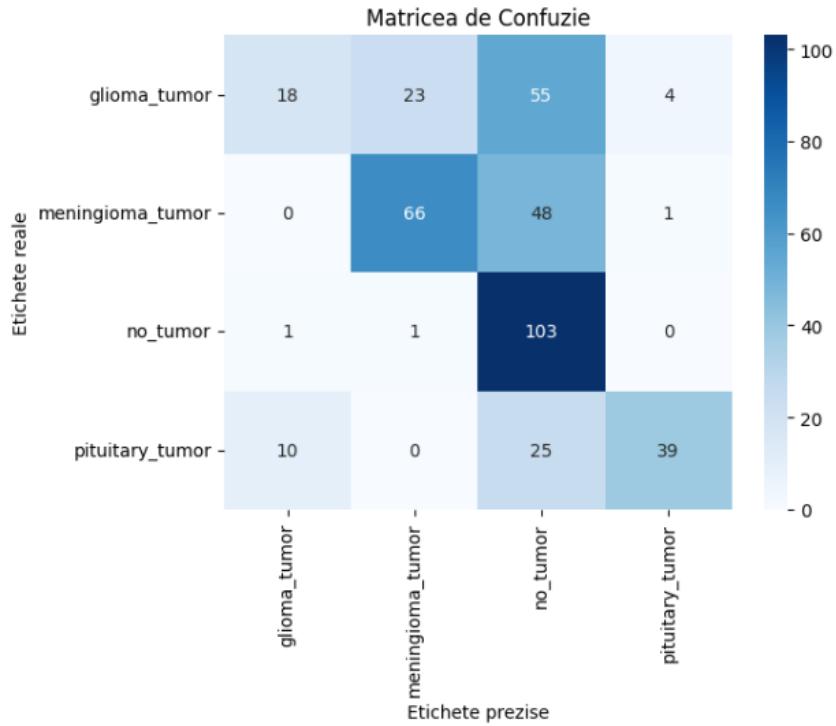
Acum voi testa cu SGD, learning_rate=0.01 batch_size = 32 fara dropout.

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.6207	0.1800	0.2791	100
meningioma_tumor	0.7333	0.5739	0.6439	115
no_tumor	0.4459	0.9810	0.6131	105
pituitary_tumor	0.8864	0.5270	0.6610	74
accuracy			0.5736	394
macro avg	0.6716	0.5655	0.5493	394
weighted avg	0.6569	0.5736	0.5463	394

Metrici mult mai slabe cu SGD cu learning_rate=0.01 decat la Adam cu learning_rate=0.001

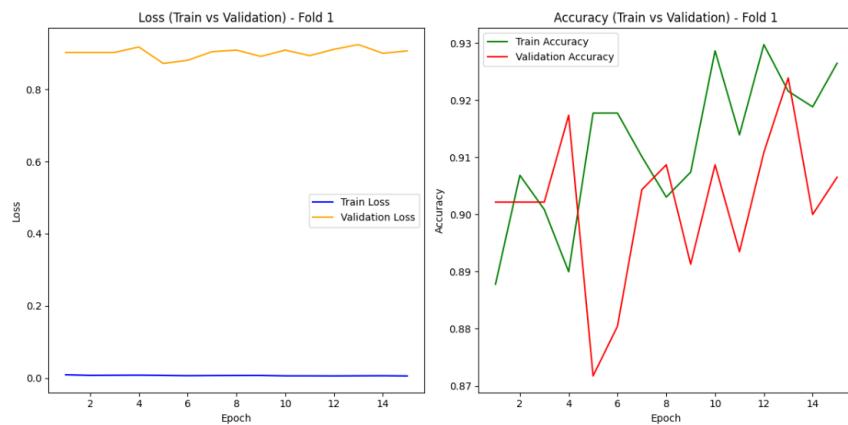


Cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9407, Std = 0.0178
Recall: Mean = 0.9395, Std = 0.0186
F1-score: Mean = 0.9387, Std = 0.0193
Accuracy: Mean = 0.9395, Std = 0.0186
```

Fold1:

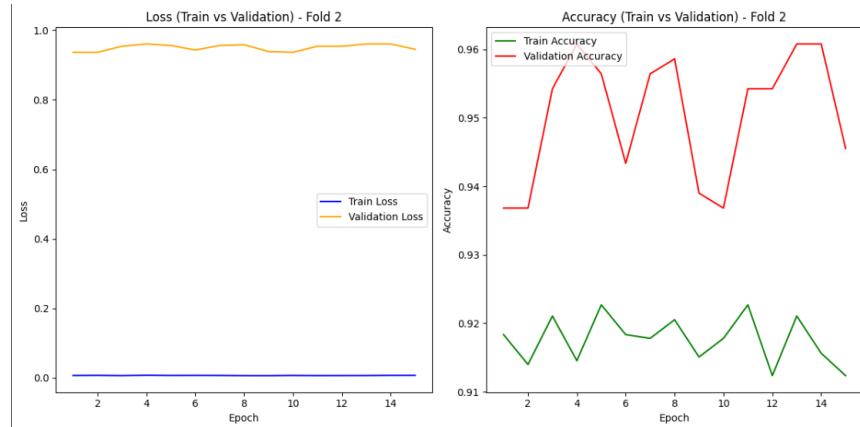
	precision	recall	f1-score	support
glioma_tumor	0.9444	0.1700	0.2881	100
meningioma_tumor	0.6304	0.7565	0.6877	115
no_tumor	0.5176	0.9810	0.6776	105
pituitary_tumor	0.8974	0.4730	0.6195	74
accuracy			0.6142	394
macro avg	0.7475	0.5951	0.5682	394
weighted avg	0.7302	0.6142	0.5708	394
AUC for Fold 1:	0.7566			



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.8500	0.1700	0.2833	100
meningioma_tumor	0.6767	0.7826	0.7258	115
no_tumor	0.5361	0.9905	0.6957	105
pituitary_tumor	0.9149	0.5811	0.7107	74
accuracy			0.6447	394
macro avg	0.7444	0.6310	0.6039	394
weighted avg	0.7279	0.6447	0.6026	394

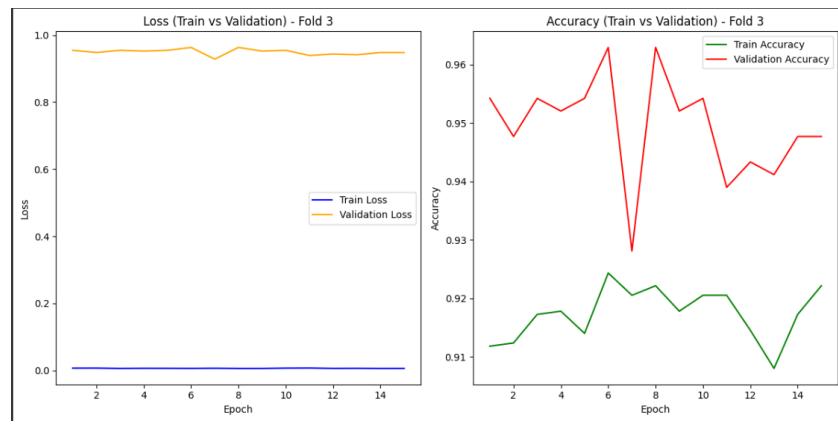
AUC for Fold 2: 0.7790



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.8182	0.1800	0.2951	100
meningioma_tumor	0.6541	0.7565	0.7016	115
no_tumor	0.5233	0.9619	0.6779	105
pituitary_tumor	0.9348	0.5811	0.7167	74
accuracy			0.6320	394
macro avg	0.7326	0.6199	0.5978	394
weighted avg	0.7136	0.6320	0.5949	394

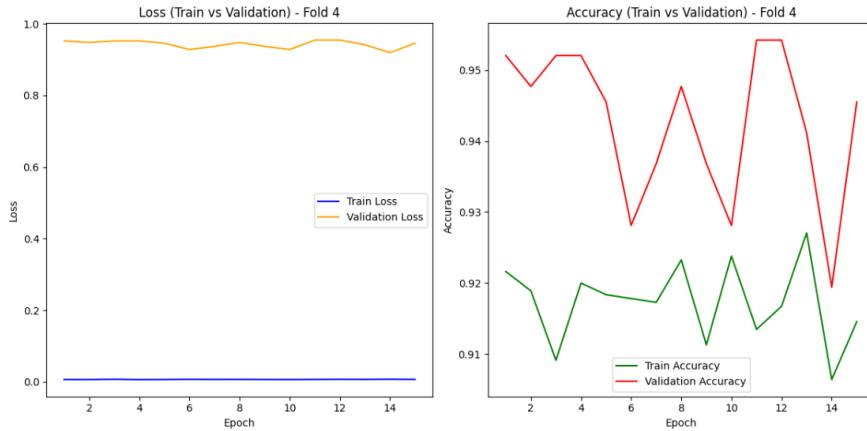
AUC for Fold 3: 0.7712



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.8636	0.1900	0.3115	100
meningioma_tumor	0.6449	0.7739	0.7036	115
no_tumor	0.5410	0.9429	0.6875	105
pituitary_tumor	0.9412	0.6486	0.7680	74
accuracy			0.6472	394
macro avg	0.7477	0.6389	0.6176	394
weighted avg	0.7284	0.6472	0.6119	394

AUC for Fold 4: 0.7737



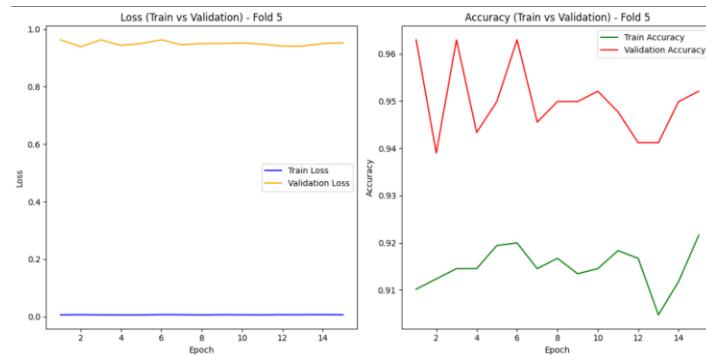
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.8333	0.2000	0.3226	100
meningioma_tumor	0.6389	0.8000	0.7104	115
no_tumor	0.5537	0.9333	0.6950	105
pituitary_tumor	0.8776	0.5811	0.6992	74
accuracy			0.6421	394
macro avg	0.7259	0.6286	0.6068	394
weighted avg	0.7104	0.6421	0.6058	394

AUC for Fold 5: 0.7797

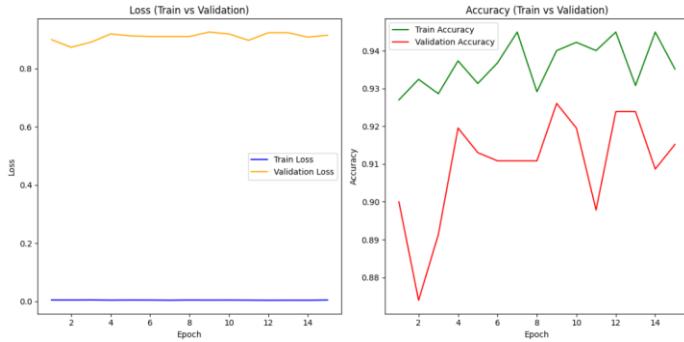
===== Overall AUC on Test Set ======

Average AUC: 0.7720



Cel mai slab fold este 1

Cu scheduler cu weight_decay:



	precision	recall	f1-score	support
glioma_tumor	0.7917	0.1900	0.3065	100
meningioma_tumor	0.6591	0.7565	0.7045	115
no_tumor	0.5255	0.9810	0.6844	105
pituitary_tumor	0.9286	0.5270	0.6724	74
accuracy			0.6294	394
macro avg	0.7262	0.6136	0.5919	394
weighted avg	0.7078	0.6294	0.5921	394

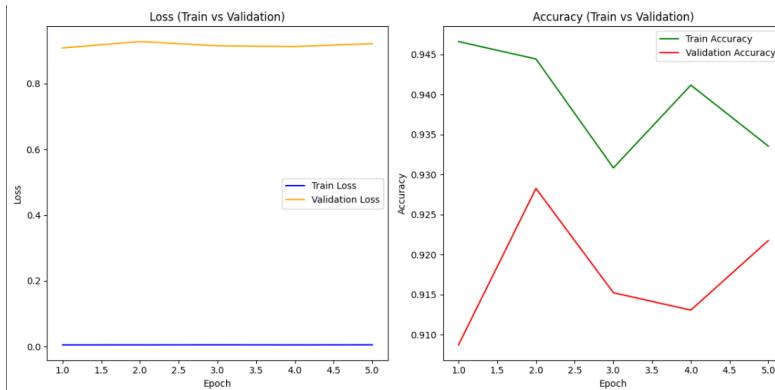
AUC for Fold 2 scheduler: 0.7801

===== Overall AUC on Test Set =====

Average AUC: 0.7801

Am obtinut metrii mai bune decat in antrenarea pe k-folduri

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.8947	0.1700	0.2857	100
meningioma_tumor	0.6547	0.7913	0.7165	115
no_tumor	0.5426	0.9714	0.6962	105
pituitary_tumor	0.8542	0.5541	0.6721	74
accuracy			0.6371	394
macro avg	0.7365	0.6217	0.5927	394
weighted avg	0.7232	0.6371	0.5934	394

AUC early_stopping: 0.7893

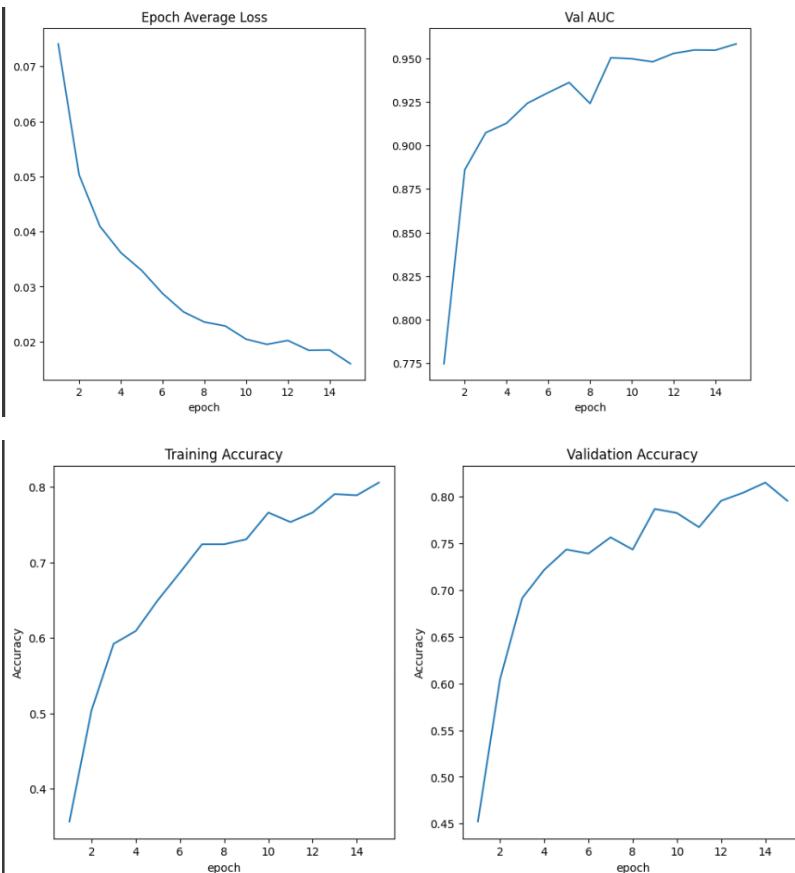
===== Overall AUC on Test Set =====

Average AUC: 0.7893

Ne-am oprit la epoca 5, cu metrii mai bune decat la scheduler.

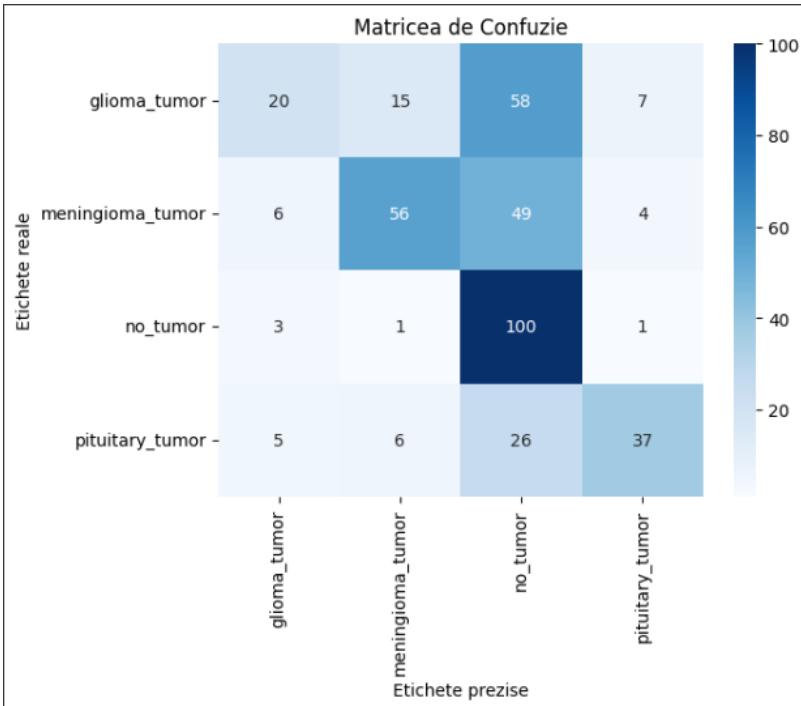
Acum voi testa cu batch_size = 32, learning_rate = 0.01, cu dropout.

Antrenarea clasica fara k-folduri:



	precision	recall	f1-score	support
glioma_tumor	0.5882	0.2000	0.2985	100
meningioma_tumor	0.7179	0.4870	0.5803	115
no_tumor	0.4292	0.9524	0.5917	105
pituitary_tumor	0.7551	0.5000	0.6016	74
accuracy			0.5406	394
macro avg	0.6226	0.5348	0.5180	394
weighted avg	0.6150	0.5406	0.5158	394

Metrici mai slabe fata de experimental anterior la antrenarea clasica.



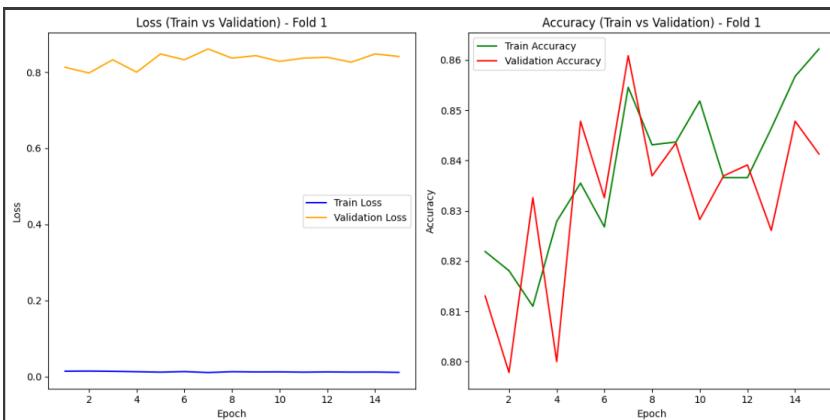
Antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.9000, Std = 0.0329
Recall: Mean = 0.8968, Std = 0.0340
F1-score: Mean = 0.8950, Std = 0.0351
Accuracy: Mean = 0.8968, Std = 0.0340
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.6071	0.1700	0.2656	100
meningioma_tumor	0.6560	0.7130	0.6833	115
no_tumor	0.4776	0.9143	0.6275	105
pituitary_tumor	0.8500	0.4595	0.5965	74
accuracy			0.5812	394
macro avg	0.6477	0.5642	0.5432	394
weighted avg	0.6325	0.5812	0.5461	394

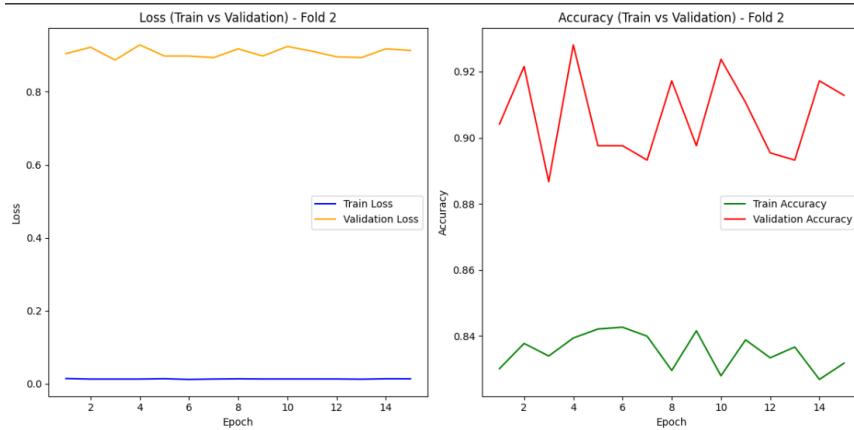
AUC for Fold 1: 0.7707



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.7037	0.1900	0.2992	100
meningioma_tumor	0.6748	0.7217	0.6975	115
no_tumor	0.4663	0.9238	0.6198	105
pituitary_tumor	0.8333	0.4054	0.5455	74
accuracy			0.5812	394
macro avg	0.6695	0.5602	0.5405	394
weighted avg	0.6564	0.5812	0.5471	394

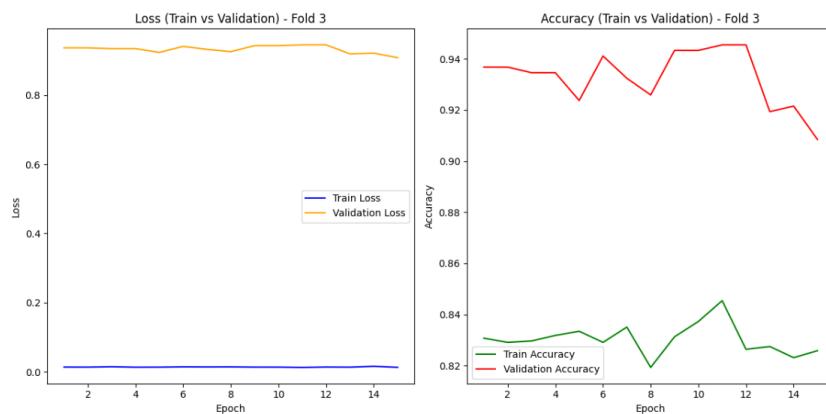
AUC for Fold 2: 0.7633



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.7917	0.1900	0.3065	100
meningioma_tumor	0.6991	0.6870	0.6930	115
no_tumor	0.4645	0.9333	0.6203	105
pituitary_tumor	0.7826	0.4865	0.6000	74
accuracy			0.5888	394
macro avg	0.6845	0.5742	0.5549	394
weighted avg	0.6758	0.5888	0.5580	394

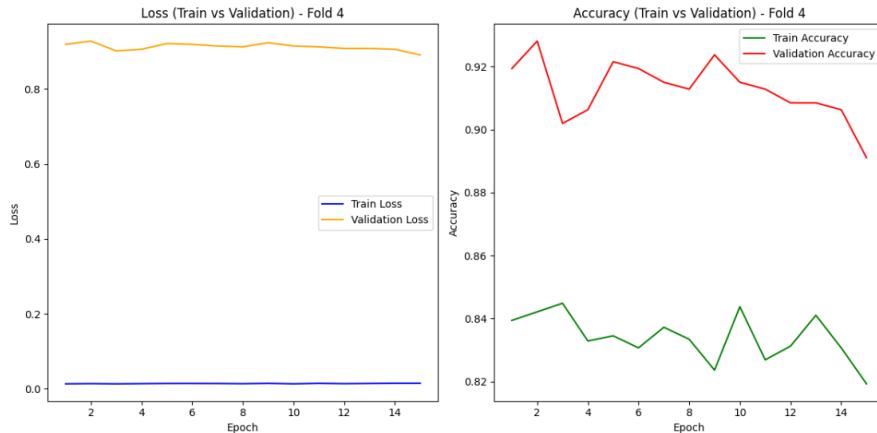
AUC for Fold 3: 0.7762



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.6129	0.1900	0.2901	100
meningioma_tumor	0.5912	0.7043	0.6429	115
no_tumor	0.4947	0.8857	0.6348	105
pituitary_tumor	0.8684	0.4459	0.5893	74
accuracy			0.5736	394
macro avg	0.6418	0.5565	0.5393	394
weighted avg	0.6231	0.5736	0.5411	394

AUC for Fold 4: 0.7811



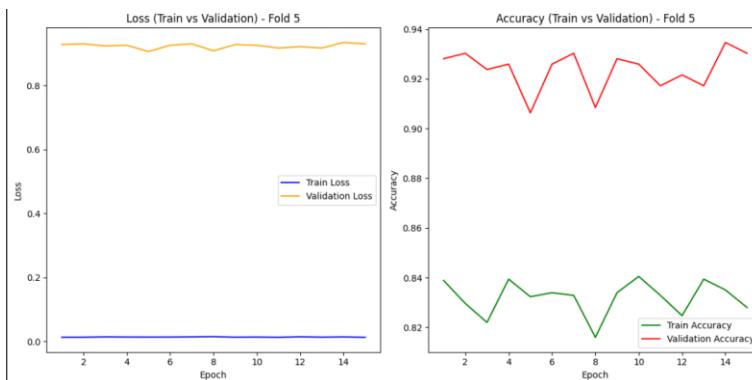
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.6800	0.1700	0.2720	100
meningioma_tumor	0.6557	0.6957	0.6751	115
no_tumor	0.4605	0.9429	0.6188	105
pituitary_tumor	0.8750	0.3784	0.5283	74
accuracy			0.5685	394
macro avg	0.6678	0.5467	0.5235	394
weighted avg	0.6510	0.5685	0.5302	394

AUC for Fold 5: 0.7769

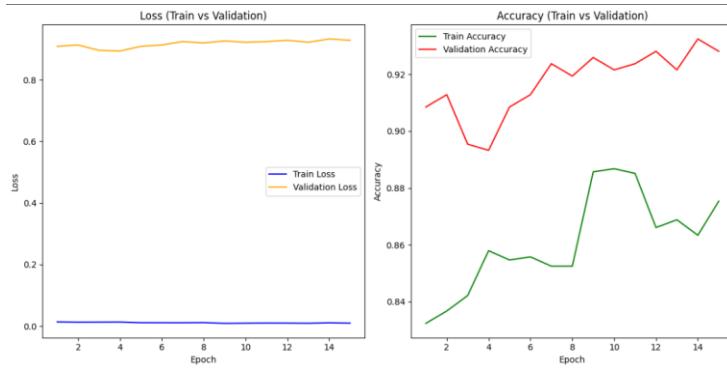
===== Overall AUC on Test Set =====

Average AUC: 0.7736



Cel mai slab fold este 5

Cu scheduler cu weight_decay:



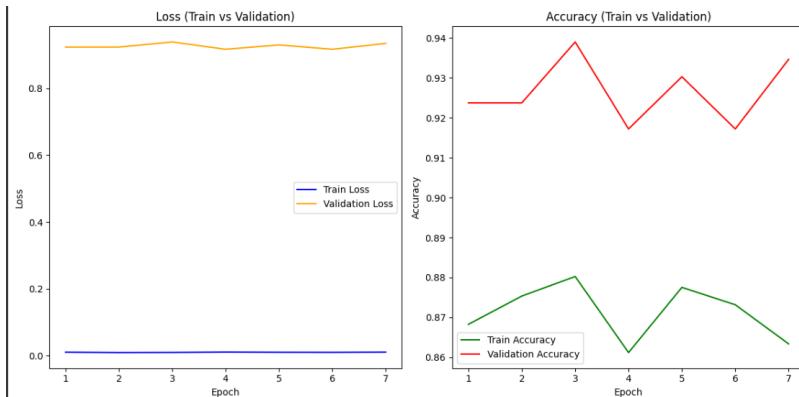
	precision	recall	f1-score	support
glioma_tumor	0.6800	0.1700	0.2720	100
meningioma_tumor	0.6772	0.7478	0.7107	115
no_tumor	0.4879	0.9619	0.6474	105
pituitary_tumor	0.8857	0.4189	0.5688	74
accuracy			0.5964	394
macro avg	0.6827	0.5747	0.5497	394
weighted avg	0.6666	0.5964	0.5559	394

AUC for Fold 2 scheduler: 0.7874

===== Overall AUC on Test Set =====

Average AUC: 0.7874

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.6923	0.1800	0.2857	100
meningioma_tumor	0.6541	0.7565	0.7016	115
no_tumor	0.4950	0.9429	0.6492	105
pituitary_tumor	0.8000	0.3784	0.5138	74
accuracy			0.5888	394
macro avg	0.6604	0.5644	0.5376	394
weighted avg	0.6488	0.5888	0.5468	394

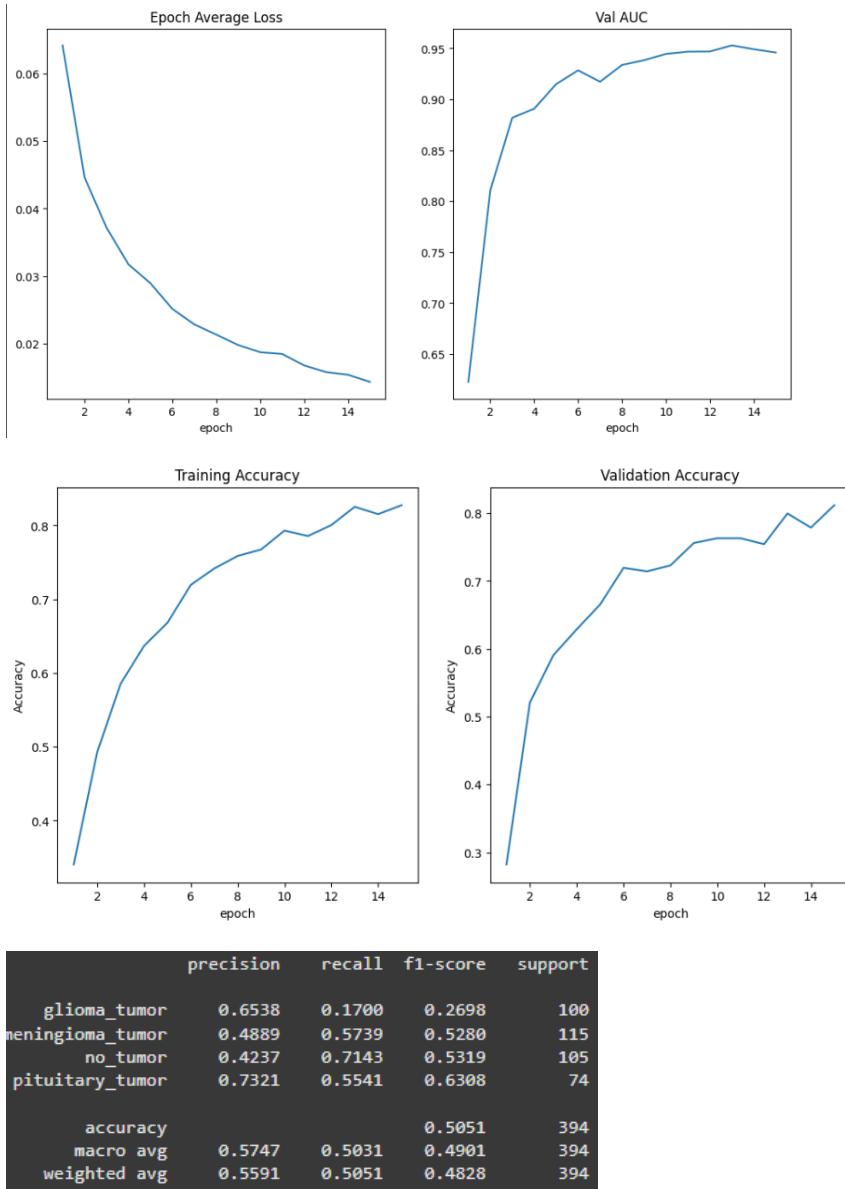
AUC early_stopping: 0.7855

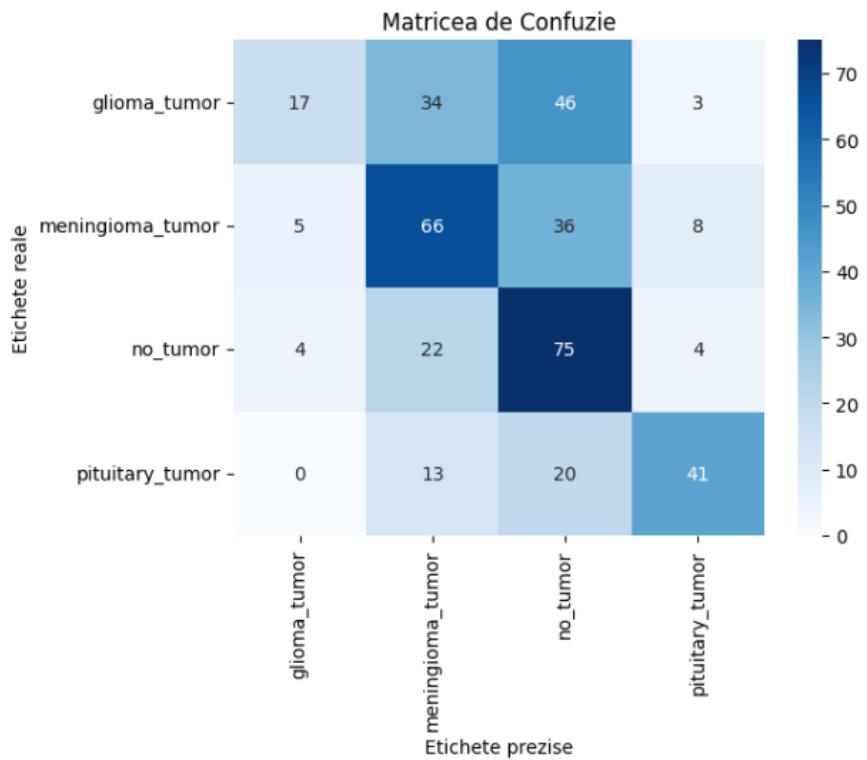
===== Overall AUC on Test Set =====

Average AUC: 0.7855

O acuratete mai slaba decat la weight_decay dar in mare parte metrii mai mari la early_stopping.

Acum voi testa cu SGD, batch_size=64, learning_rate=0.01 fara dropout.



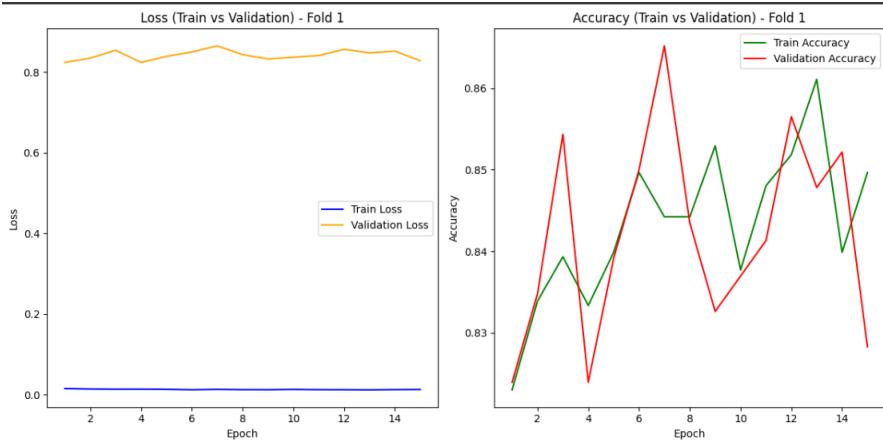


Antrenarea fara k-folduri, media metricilor este:

```
Precision: Mean = 0.8615, Std = 0.0190
Recall: Mean = 0.8576, Std = 0.0199
F1-score: Mean = 0.8549, Std = 0.0202
Accuracy: Mean = 0.8576, Std = 0.0199
```

Fold1:

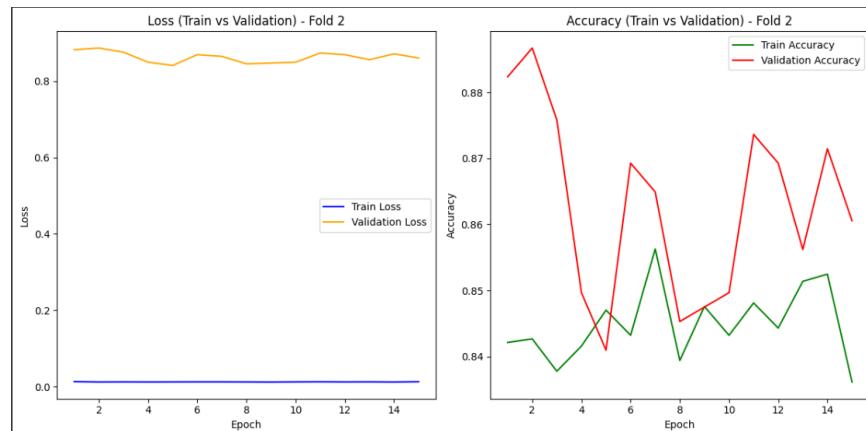
	precision	recall	f1-score	support
glioma_tumor	0.6667	0.2000	0.3077	100
meningioma_tumor	0.6017	0.6174	0.6094	115
no_tumor	0.4410	0.8190	0.5733	105
pituitary_tumor	0.6667	0.4595	0.5440	74
accuracy			0.5355	394
macro avg	0.5940	0.5240	0.5086	394
weighted avg	0.5876	0.5355	0.5109	394
AUC for Fold 1:	0.7398			



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.6538	0.1700	0.2698	100
meningioma_tumor	0.5750	0.6000	0.5872	115
no_tumor	0.4670	0.8095	0.5923	105
pituitary_tumor	0.6515	0.5811	0.6143	74
accuracy			0.5431	394
macro avg	0.5868	0.5402	0.5159	394
weighted avg	0.5806	0.5431	0.5131	394

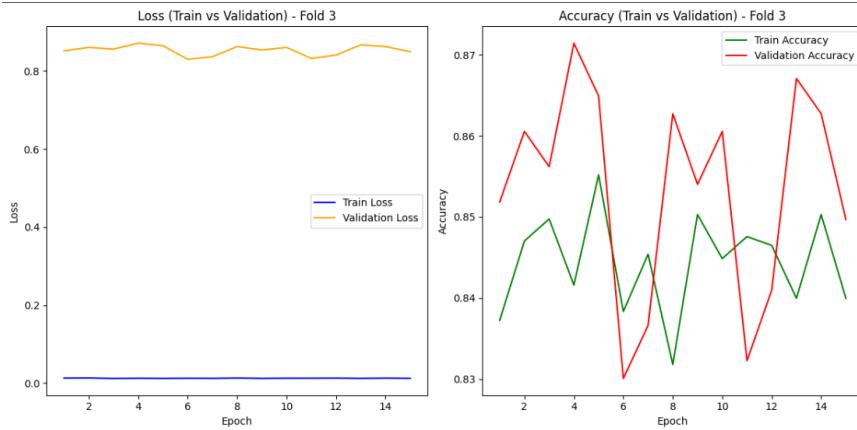
AUC for Fold 2: 0.7274



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.7143	0.2000	0.3125	100
meningioma_tumor	0.5738	0.6087	0.5907	115
no_tumor	0.4603	0.8286	0.5918	105
pituitary_tumor	0.6727	0.5000	0.5736	74
accuracy			0.5431	394
macro avg	0.6053	0.5343	0.5172	394
weighted avg	0.5978	0.5431	0.5172	394

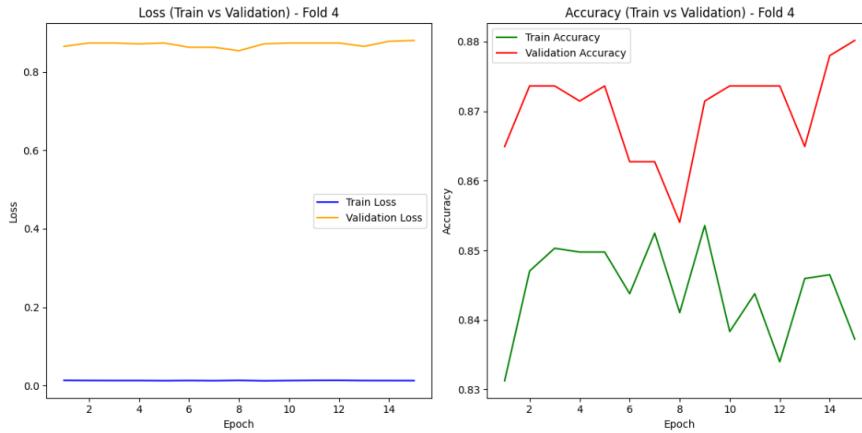
AUC for Fold 3: 0.7227



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.7500	0.1800	0.2903	100
meningioma_tumor	0.5862	0.5913	0.5887	115
no_tumor	0.4356	0.8381	0.5733	105
pituitary_tumor	0.6731	0.4730	0.5556	74
accuracy			0.5305	394
macro avg	0.6112	0.5206	0.5020	394
weighted avg	0.6040	0.5305	0.5027	394

AUC for Fold 4: 0.7347



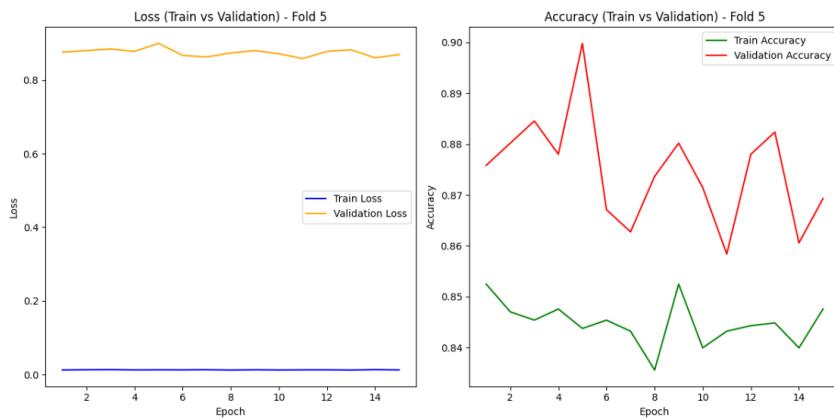
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.6786	0.1900	0.2969	100
meningioma_tumor	0.6018	0.5913	0.5965	115
no_tumor	0.4573	0.8667	0.5987	105
pituitary_tumor	0.6296	0.4595	0.5312	74
accuracy			0.5381	394
macro avg	0.5918	0.5269	0.5058	394
weighted avg	0.5880	0.5381	0.5088	394

AUC for Fold 5: 0.7423

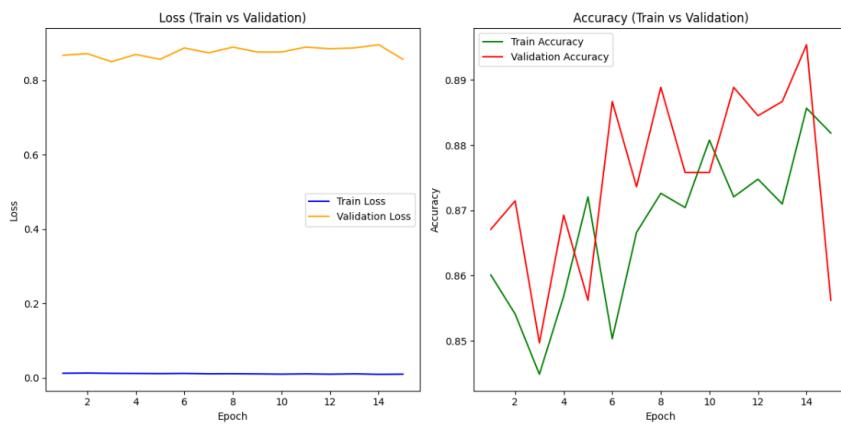
===== Overall AUC on Test Set =====

Average AUC: 0.7334



Cel mai slab fold este 4.

Cu scheduler cu weight_decay:

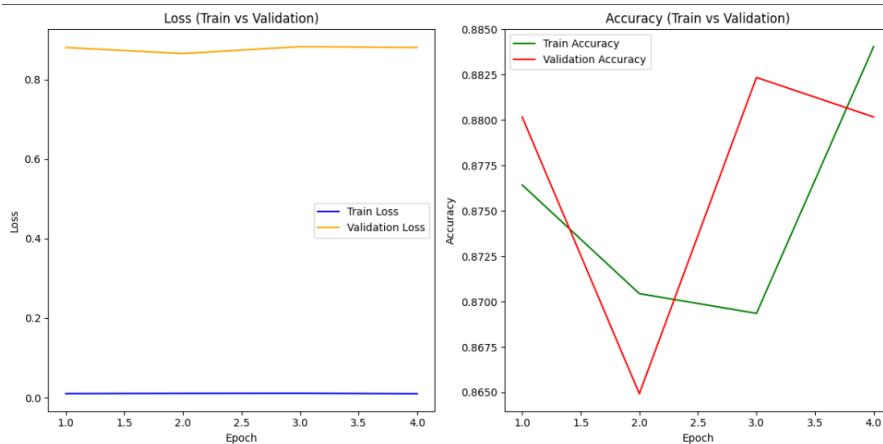


	precision	recall	f1-score	support
glioma_tumor	0.7600	0.1900	0.3040	100
meningioma_tumor	0.6119	0.7130	0.6586	115
no_tumor	0.4921	0.8857	0.6327	105
pituitary_tumor	0.7609	0.4730	0.5833	74
accuracy			0.5812	394
macro avg	0.6562	0.5654	0.5447	394
weighted avg	0.6455	0.5812	0.5476	394

```
AUC for Fold 2 scheduler: 0.7619
===== Overall AUC on Test Set =====
Average AUC: 0.7619
```

Observam o imbunatatire in cadrul metrichilor fata de antrenarea la nivelul k-foldurilor

Cu early_stopping:



```

precision    recall   f1-score   support
glioma_tumor      0.6897    0.2000    0.3101     100
meningioma_tumor   0.6016    0.6696    0.6337     115
no_tumor          0.4762    0.8571    0.6122     105
pituitary_tumor    0.7708    0.5000    0.6066      74

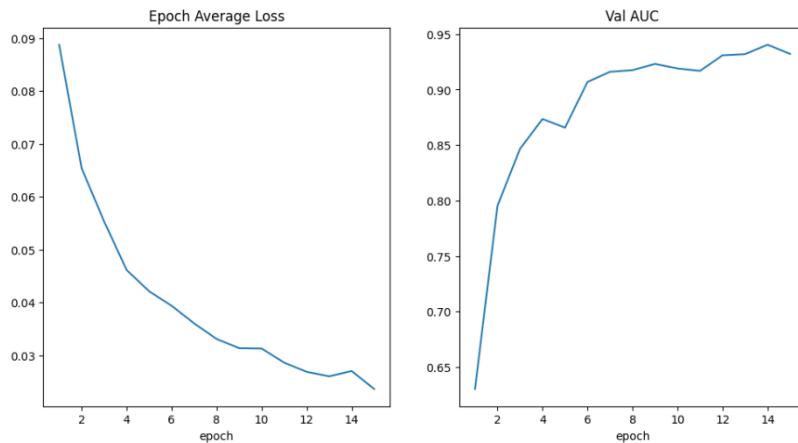
accuracy           0.6346    0.5567    0.5407     394
macro avg         0.6346    0.5567    0.5407     394
weighted avg       0.6223    0.5685    0.5408     394

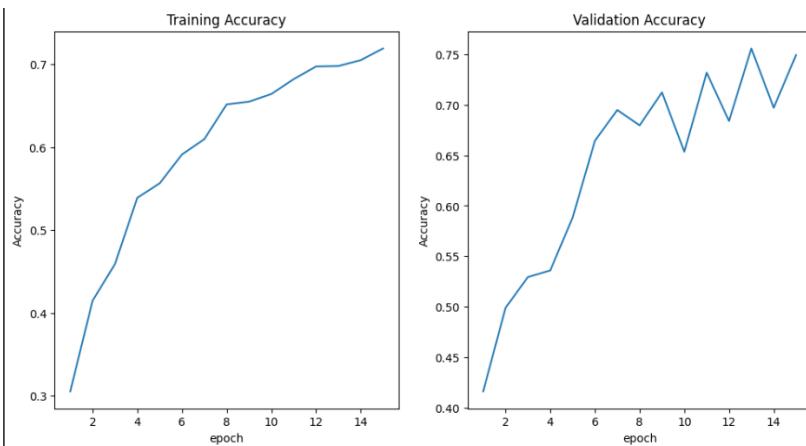
AUC early_stopping: 0.7424
===== Overall AUC on Test Set =====
Average AUC: 0.7424

```

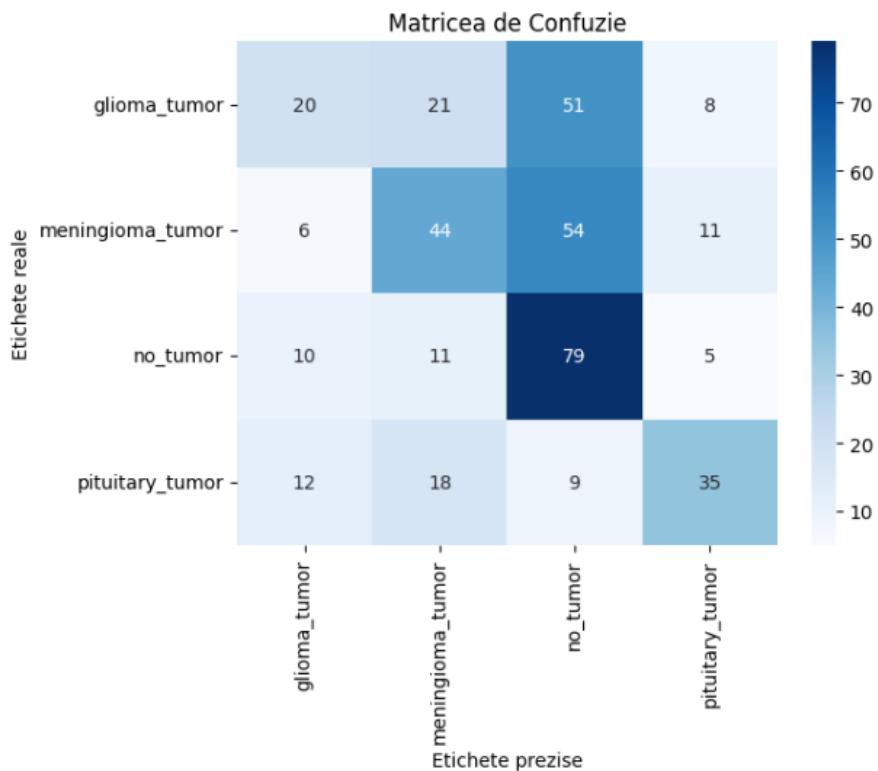
Acum voi testa cu SGD, learning_rate=0.01, batch_size=64, cu dropout

Antrenarea clasica fara k-folduri:





	precision	recall	f1-score	support
glioma_tumor	0.4167	0.2000	0.2703	100
meningioma_tumor	0.4681	0.3826	0.4211	115
no_tumor	0.4093	0.7524	0.5302	105
pituitary_tumor	0.5932	0.4730	0.5263	74
accuracy			0.4518	394
macro avg	0.4718	0.4520	0.4370	394
weighted avg	0.4629	0.4518	0.4316	394



Metrici si mai slabe ca pana acum la FocalLoss pentru SGD.

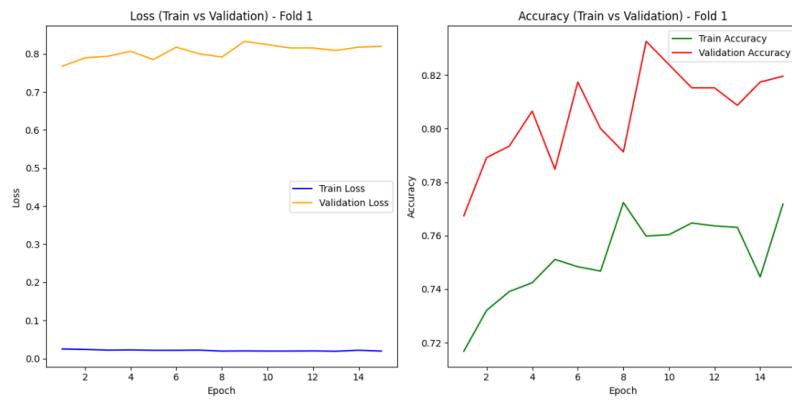
Pentru antrenarea cu k-folduri, media metricilor este:

```
Precision: Mean = 0.8371, Std = 0.0247
Recall: Mean = 0.8319, Std = 0.0242
F1-score: Mean = 0.8270, Std = 0.0244
Accuracy: Mean = 0.8319, Std = 0.0242
```

Fold1:

	precision	recall	f1-score	support
glioma_tumor	0.6296	0.1700	0.2677	100
meningioma_tumor	0.5283	0.4870	0.5068	115
no_tumor	0.4155	0.8190	0.5513	105
pituitary_tumor	0.6481	0.4730	0.5469	74
accuracy			0.4924	394
macro avg	0.5554	0.4872	0.4682	394
weighted avg	0.5465	0.4924	0.4655	394

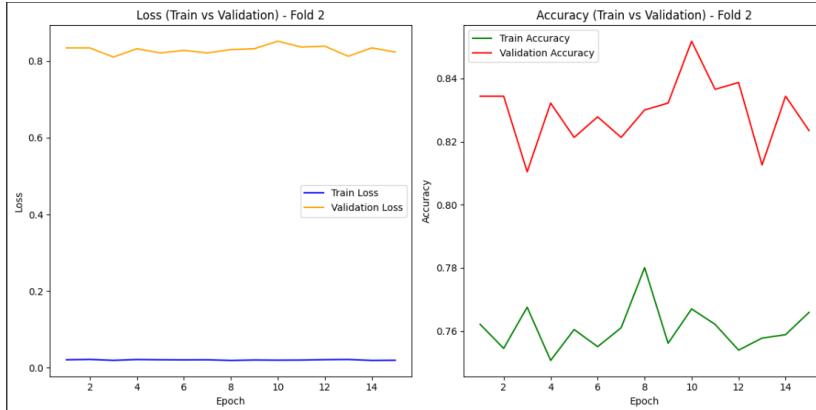
AUC for Fold 1: 0.6998



Fold2:

	precision	recall	f1-score	support
glioma_tumor	0.5714	0.1600	0.2500	100
meningioma_tumor	0.5200	0.4522	0.4837	115
no_tumor	0.4099	0.8667	0.5566	105
pituitary_tumor	0.7273	0.4324	0.5424	74
accuracy			0.4848	394
macro avg	0.5572	0.4778	0.4582	394
weighted avg	0.5426	0.4848	0.4548	394

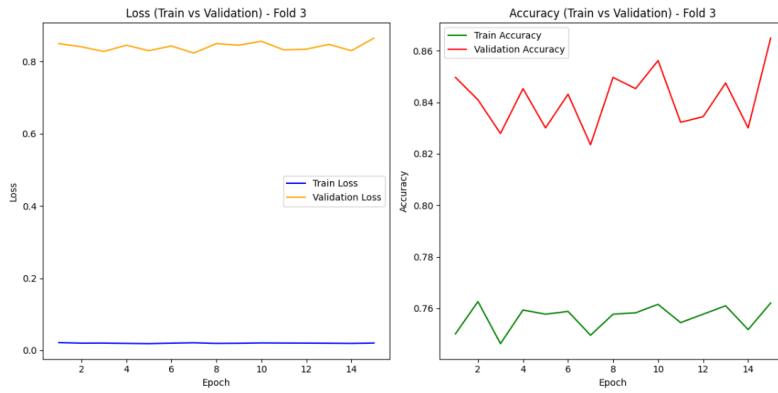
AUC for Fold 2: 0.6919



Fold3:

	precision	recall	f1-score	support
glioma_tumor	0.6071	0.1700	0.2656	100
meningioma_tumor	0.5408	0.4609	0.4977	115
no_tumor	0.4247	0.8857	0.5741	105
pituitary_tumor	0.7143	0.4730	0.5691	74
accuracy			0.5025	394
macro avg	0.5717	0.4974	0.4766	394
weighted avg	0.5593	0.5025	0.4725	394

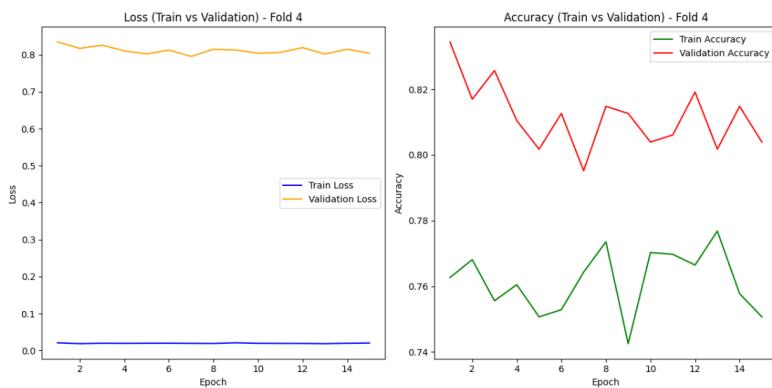
AUC for Fold 3: 0.7059



Fold4:

	precision	recall	f1-score	support
glioma_tumor	0.5185	0.1400	0.2205	100
meningioma_tumor	0.5283	0.4870	0.5068	115
no_tumor	0.4259	0.8762	0.5732	105
pituitary_tumor	0.7333	0.4459	0.5546	74
accuracy			0.4949	394
macro avg	0.5515	0.4873	0.4638	394
weighted avg	0.5370	0.4949	0.4608	394

AUC for Fold 4: 0.6940



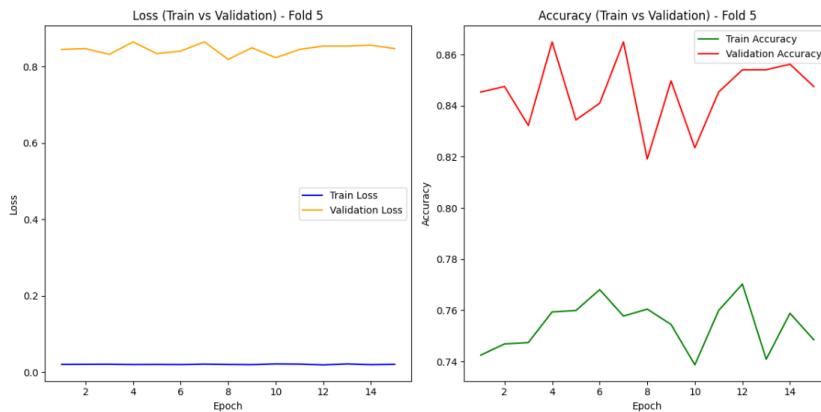
Fold5:

	precision	recall	f1-score	support
glioma_tumor	0.5161	0.1600	0.2443	100
meningioma_tumor	0.5600	0.4870	0.5209	115
no_tumor	0.4174	0.8667	0.5635	105
pituitary_tumor	0.7333	0.4459	0.5546	74
accuracy			0.4975	394
macro avg	0.5567	0.4899	0.4708	394
weighted avg	0.5434	0.4975	0.4684	394

AUC for Fold 5: 0.7109

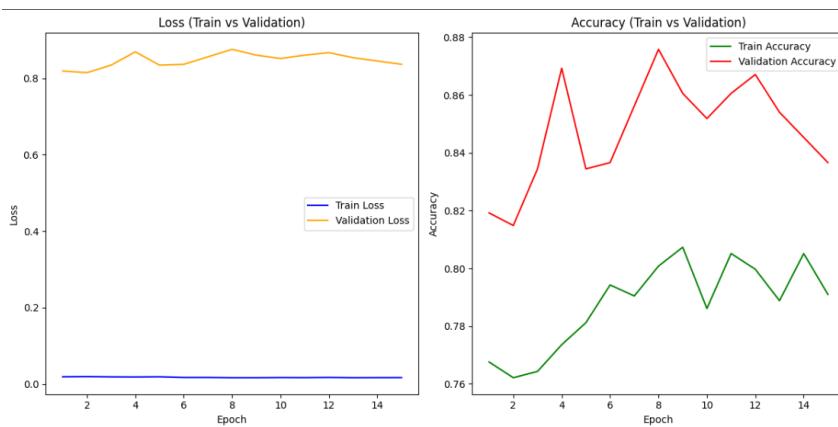
===== Overall AUC on Test Set =====

Average AUC: 0.7005



Cel mai slab fold este 2

Cu scheduler cu weight_decay:



	precision	recall	f1-score	support
glioma_tumor	0.6207	0.1800	0.2791	100
meningioma_tumor	0.5851	0.4783	0.5263	115
no_tumor	0.4017	0.8762	0.5509	105
pituitary_tumor	0.7619	0.4324	0.5517	74
accuracy			0.5000	394
macro avg	0.5924	0.4917	0.4770	394
weighted avg	0.5785	0.5000	0.4749	394

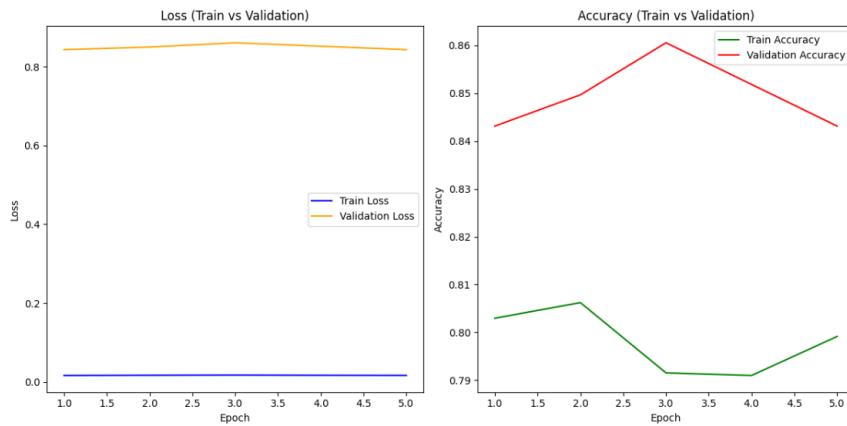
AUC for Fold 2 scheduler: 0.7169

===== Overall AUC on Test Set =====

Average AUC: 0.7169

O imbunatatire drastica in cadrul weight_decay-ului, oferind o imbunatatire generala.

Cu early_stopping:



	precision	recall	f1-score	support
glioma_tumor	0.5714	0.1600	0.2500	100
meningioma_tumor	0.5455	0.5217	0.5333	115
no_tumor	0.4318	0.9048	0.5846	105
pituitary_tumor	0.7500	0.3649	0.4909	74
accuracy			0.5025	394
macro avg	0.5747	0.4878	0.4647	394
weighted avg	0.5602	0.5025	0.4671	394
AUC early_stopping:	0.7213			
===== Overall AUC on Test Set =====				
Average AUC: 0.7213				

S-a oprit la epoca 5 si acuratetea este mai buna decat la weight_decay, iar de la early_stopping la weight_decay sunt scaderi in performanta in general atat la precision, cat si la recall dar si la f1-score.

Din toate aceste experimente de la cerinta 2.5 am obtinut cele mai bune metriki cu functia de pierdere FocalLoss cu optimizatorul Adam cu learning_rate=0.001 batch_size=32 cu antrenarea clasica fara k-folduri ajungand la 75%.

Bibliografie:

- Laboratorul 4
- Laboratorul 2
- Cursul 8
- [Use Focal Loss To Train Model Using Imbalanced Dataset - Lei Mao's Log Book](#)
- [Passing the weights to CrossEntropyLoss correctly - PyTorch Forums](#)
- [Cross Entropy Loss Implementation - PyTorch Forums](#)
- [How to handle overfitting in PyTorch models using Early Stopping - GeeksforGeeks](#)
- [Bjarten/early-stopping-pytorch: Early stopping for PyTorch](#)
- [A Step-by-Step Guide to Early Stopping in TensorFlow and PyTorch | by Vrunda Bhattbhatt | Medium](#)
- [StratifiedKFold — scikit-learn 1.6.1 documentation](#)