

Bone Marrow Pathology Detection

Michael Freeman, Ariana Schindler, Emmanuel Peters, Ziwen Zhou

TA Advisor: Jun Suk Ha

For my capstone project, my group and I investigated a variety of deep learning frameworks and architectures toward classifying bone marrow biopsies. We explored models that were entirely designed and trained by us, as well as models that were reliant on pretrained weights and infrastructure. At best, we were able to achieve categorical accuracies of 70%+ with expected accuracies of 85%+ with additional training time and resources.

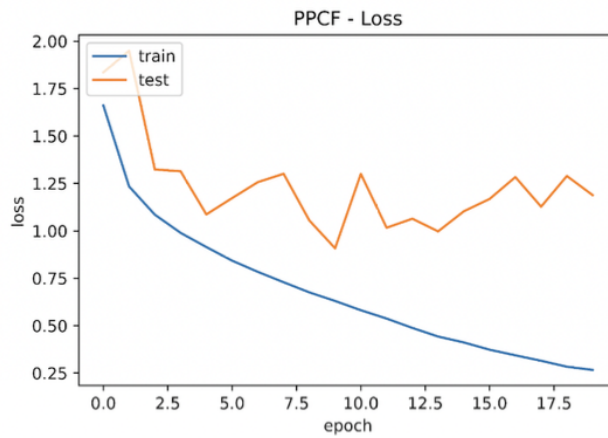


FIG. 1. PPCF Loss

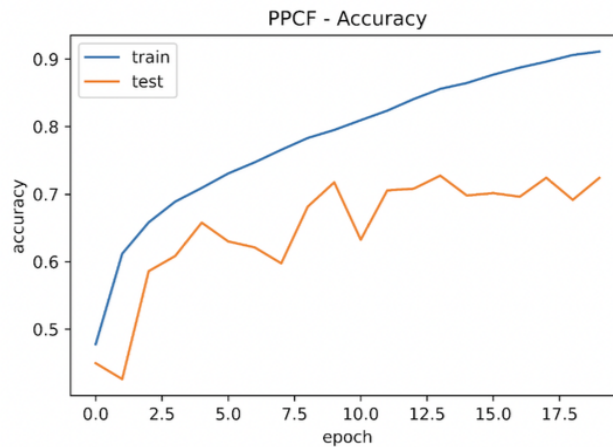


FIG. 2. PPCF Accuracy

	precision	recall	f1-score	support
ABE	0.0	0.0	0.0	2.0
ART	0.72	0.78	0.75	3941.0
BAS	0.26	0.21	0.23	89.0
BLA	0.64	0.61	0.62	2432.0
EBO	0.88	0.87	0.88	5500.0
EOS	0.91	0.81	0.86	1162.0
FGC	0.0	0.0	0.0	11.0
HAC	0.29	0.03	0.05	79.0
KSC	0.0	0.0	0.0	9.0
LYI	0.0	0.0	0.0	13.0
LYT	0.78	0.84	0.81	5277.0
MMZ	0.3	0.28	0.29	631.0
MON	0.41	0.48	0.44	834.0
MYB	0.52	0.44	0.48	1321.0
NGB	0.57	0.46	0.5	2034.0
NGS	0.84	0.84	0.84	5767.0
NIF	0.41	0.34	0.37	720.0
OTH	0.14	0.05	0.07	63.0
PEB	0.58	0.63	0.6	552.0
PLM	0.54	0.82	0.65	1456.0
PMO	0.75	0.64	0.69	2381.0
accuracy	0.73	0.73	0.73	0.73
macro avg	0.45	0.43	0.43	34274.0
weighted avg	0.73	0.73	0.72	34274.0

FIG. 3. Precision Recall

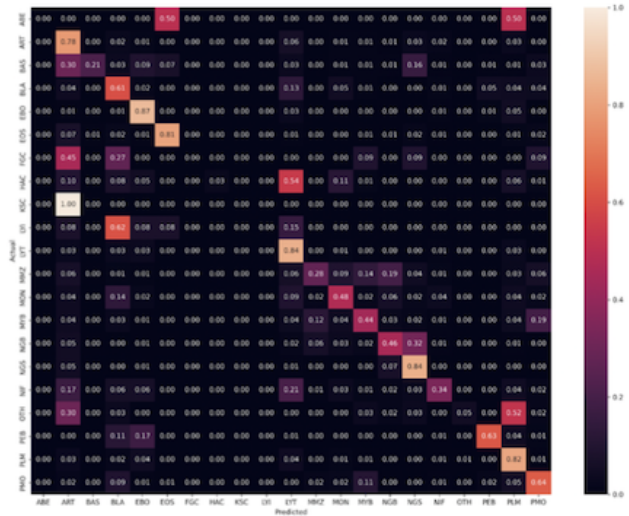


FIG. 4. Confusion Matrix