14th International Conference „Data Analysis Methods for Software Systems“
November 30th – December 2nd, 2023, Druskininkai, Lithuania

VILNIUS TECH
Vilnius Gediminas Technical University

Automatic Tumor Identification Using Deep Neural Network

Edita Mažonienė, Mantas Kundrotas, Dmitrij Šešok
Vilnius Gediminas Technical University, Vilnius, Lithuania

Summary: In this research, we aimed to integrate machine learning (ML) deep neural network (DNN), especially convolutional neural network (CNN) for image analysis in histopathology and cancer research. For this work, the ResNet, DenseNet, MobileNet, EfficientNet, Inception architectures were used from the Tensorflow library, also, mentioned models were already trained on the ImageNet dataset. Using our adapted U-net model (M-model) we managed to reduce model size and increase the accuracy from 0.95491 to 0.95515 AUC. Moreover, the result increased to 0.96870 with the TTA method, and 0.96977 with the addition of the multi-model ensemble. After corrections of image processing parametres AUC increased by 3%, which become 0.96664 AUC and final model result was 0.97673 AUC.

INTRODUCTION

Careful identification of tumors, especially at an early stage, requires extensive expert knowledge, so that cancerous tissue is often identified only after it has been affected. Expanding the ability to identify more precise ML methods and techniques for detecting tumor damaged tissues in histopathology surveys has been a key objective of our study.

DATASETS

One public image classification dataset was used:

- **PatchCamelyon 2020.**

Table 1. Dataset features

Features	
Amount of Images	327680
Pixels Size	96x96
Labels	Yes (positive/negative)
Training Images	6.1 GB
Valid Images	0.8 GB
Test Images	0.8 GB
Balance between positive and negative	50/50

RESEARCH PLAN AND ALGORITHMS

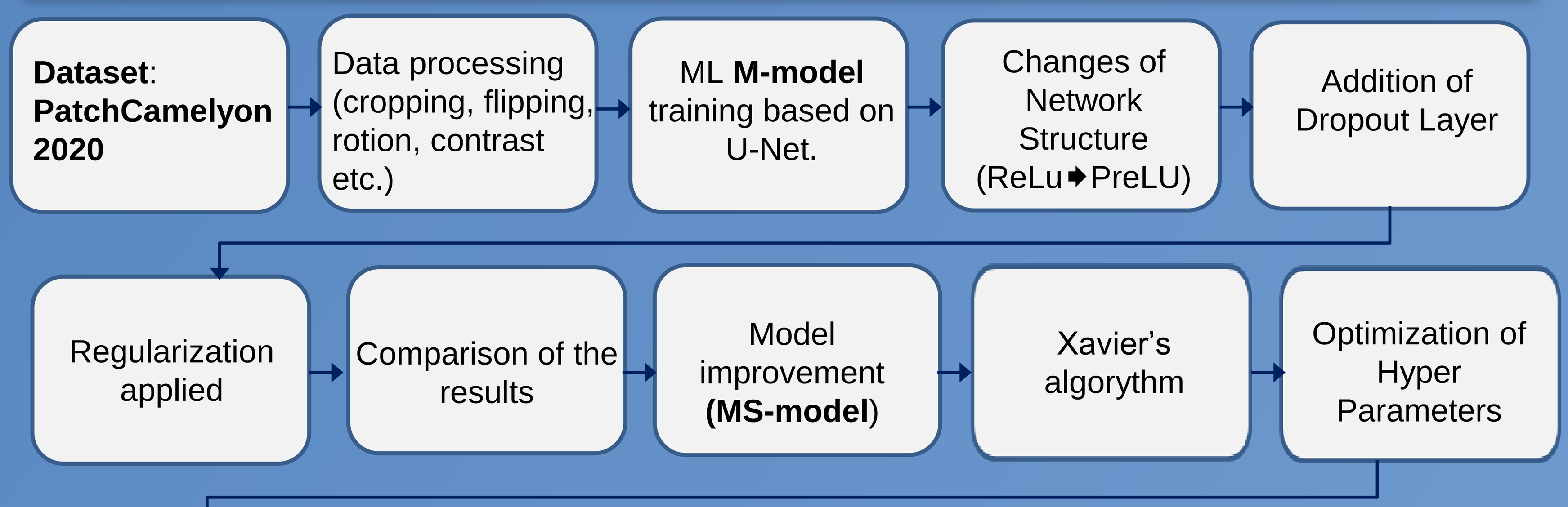

Fig. 1. Research flowchart

Table 2. Architectures and optimization methods

Model Architectures	Optimization Methods
DenseNet121	SGD
ResnNet50	Adam
ResNet50 V2	AdamW
MobileNetV1, MobileNetV2	Ranger
Inception	
EfficientNetB0, EfficientNetB1	
EfficientNetB0 V2, EfficientNetB1 V2	

RESULTS

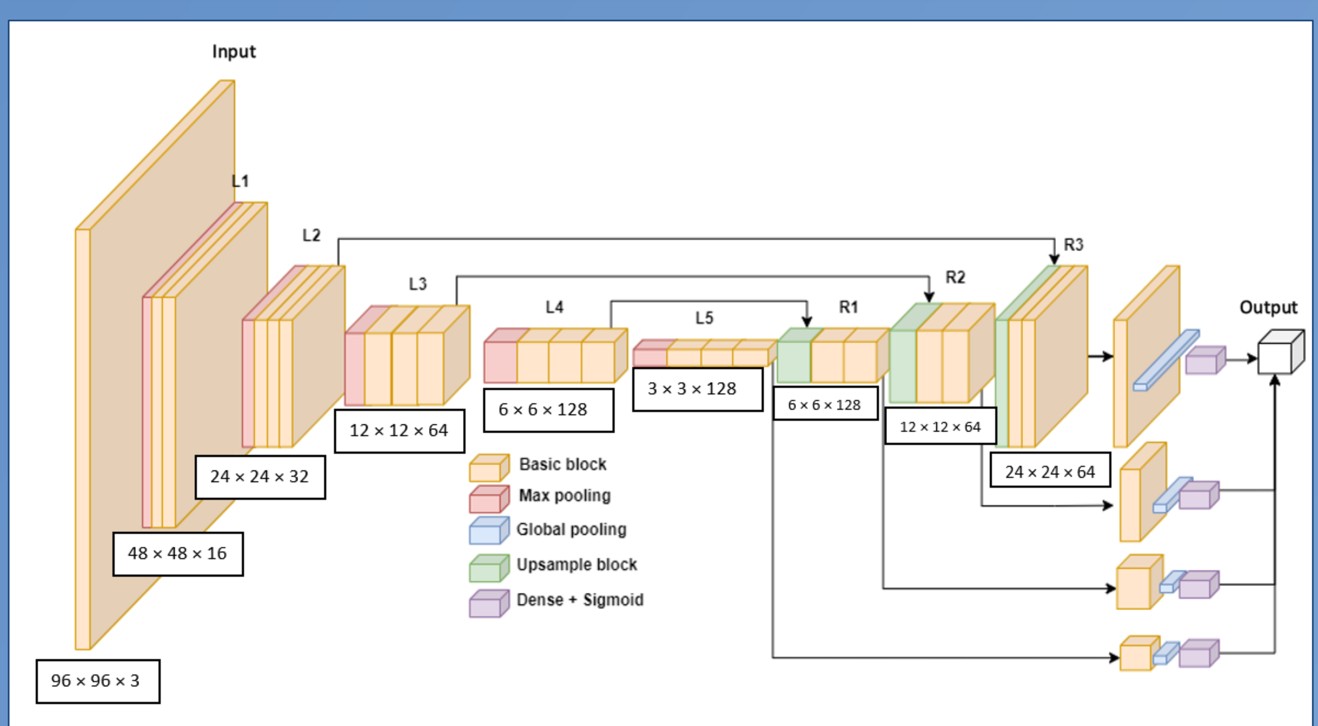

Fig. 2. The M-model based on the U-Net network architecture.

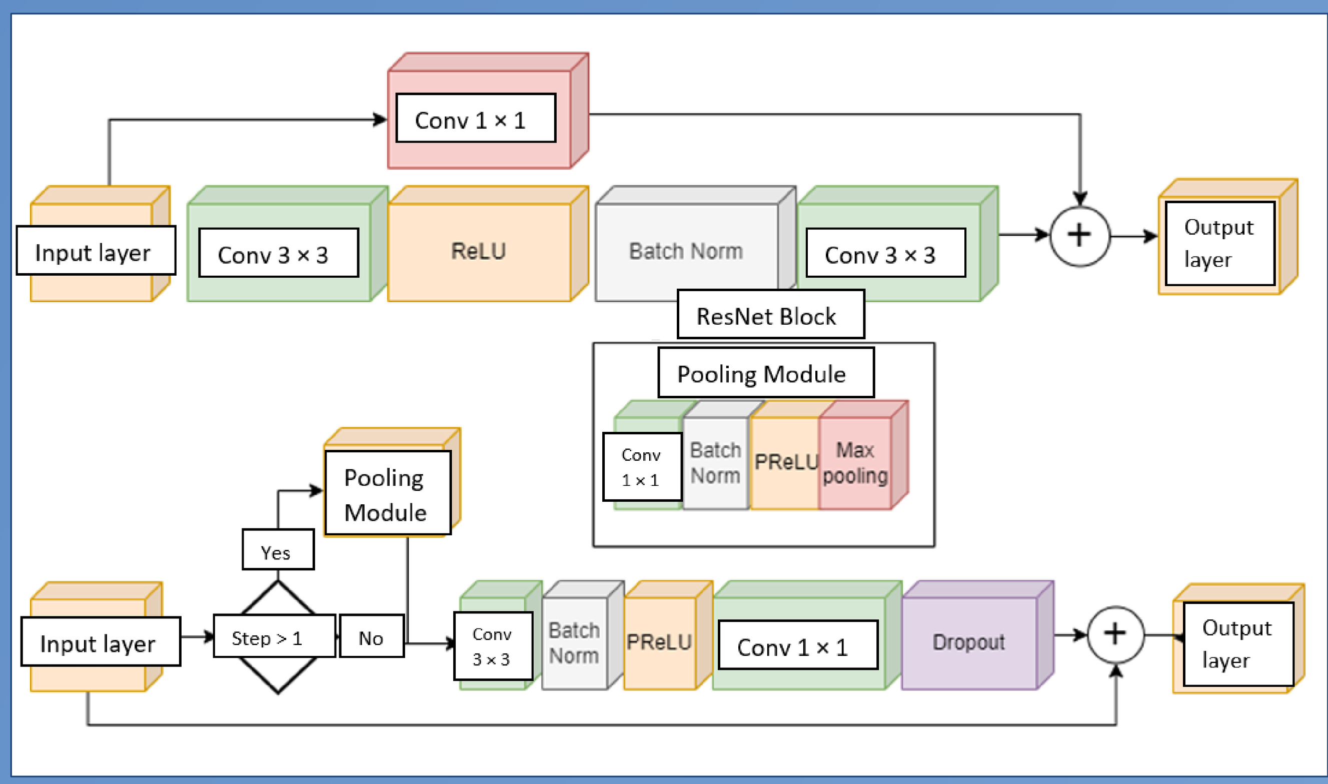

Fig. 3. E-module based on ResNet block design.

Table 3. Model architectures analysis results.

AUC (Area under the Curve)		
Model	ImageNet Weights	Xavier Initialization Weights
DenseNet121	0.95672	0.94560
ResNet50	0.95078	0.94380
ResNet50 V2	0.95078	0.94380
MobileNetV1	0.94954	0.93855
MobileNetV2	0.95065	0.95395
Inception	0.94697	0.94608
EfficientNetB0	0.95121	0.94608
EfficientNetB1	0.93876	0.94608
EfficientNetB0 V2	0.94570	0.75981
EfficientNetB1 V2	0.94287	0.79871

Table 4. MS-model results.

Learning Iteration	AUC
Reusing weights	0.95501
New initialization 1	0.95498
New initialization 2	0.95508
New initialization 3	0.95505

Table 5. Comparison of optimization methods.

Learning Iteration	AUC
SGD	0.95510
Adam	0.95475
AdamW	0.95515
Ranger	0.95500

Table 6. Summary results

AUC (Area under the Curve)		
Ensemble Type	AUC	Difference
DenseNet121	0.95672	-
M-model training 5 outputs together	0.95405	−0.267%
M-model training 5 outputs separately	0.95491	−0.1891%
MS-model	0.95508	−0.164%
MS-model with AdamW	0.95515	−0.157%
MS-model with repeated training	0.95911	0.239%
MS-model TTA	0.96870	1.198%
MS-model ensemble	0.96592	0.920%
MS-model connecting weights	0.96240	0.568%
TTA + weights and models ensemble	0.96922	1.250%
MS-model after corrections	0.96147	0.475%
MS-model after corrections with repeated training	0.96675	1.003%
Group of ensembles from all experiments	0.96977	1.305%
Optimized ensemble based on the best model	**0.97673**	2.001%

CONCLUSIONS

In this work, we proposed to use Ml and different neural network techniques to find a solution to WSIs histopathological data analysis. Our extensive experiments showed that the application of artificial deep neural networks (TTA+ResNet Assembly) for the classification of medical images, compared to other classical methods, are superior in almost all criteria.