Classification of cell types in human kidney tissue using Convolutional Neural Network(CNN)

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Artificial Intelligence (COM2028) Coursework

Introduction

The biological functions and interactions of different cell types of an organ, in our case, the human kidney, requires thorough and accurate evaluation [1]. The complexity of the human kidney organ, makes the image base classification highly challenging. Modern approaches use larger-scale fluorescence 3D imaging[2], which provides higher advantages in cell classification. However, in this approach, 28x28 pixels grey-scale images will be used, which has its own advantages and robustness.
From the many deep learning methods that use data to train neural networks for image classification, convolutional neural network (CNN) is one of the most powerful techniques.
Such a method was used for this coursework. The system learns how to extract many features from the image data set and automatically identify cell types in the human renal cortex.

Data Set

The dataset is provided by Broad Bioimage Benchmark Collection[Ljosa et al., *Nature Methods*, 2012], human kidney cortex cells Accession number BBBC051 and it has been revised into 28X28 grey-scale. A selection of 150000 images belonging to eight classes has been used to train and validate the model, with an extra 50000 images for testing.

- Training: 120000
- Validation: 30000
- Testing: 50000

Cell types

Cell value counts:

- Type 0 – 48074
- Type 1 – 7072
- Type 2 – 5334
- Type 3 – 13965
- Type 4 – 10697
- Type 5 – 7050
- Type 6 – 35608
- Type 7 – 22199

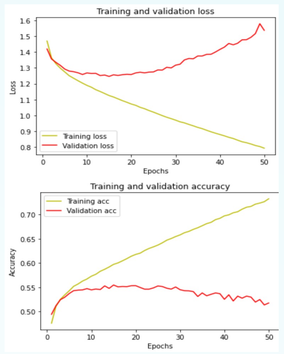
From the above results in the value counts, we conclude that we are dealing with an imbalanced data set.

Analysis

Four Convolutional Neural Network (CNN) models were created to determine the class of each cell type in the human kidney cortex. This models automatically detect the essential features and classify each image based on the raw pixel data. All models are implemented using TensorFlow, NumPy, pandas, and executed on Google Colab Pro. Training and validation loss/accuracy curves are plotted on graphs using the model's performance history data to indicate the performance of the proposed models.

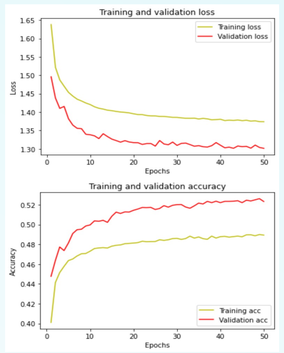
Model I

We start with a simple 32 filters Convolution layer with an L2 regularizer to try and reduce the weights, followed by a Flatten and two Dense layers. Adam optimizer is used for compiling with de default 0.001 learning rate, having accuracy as a metric. The model is clearly overfitting as the training is doing well compared to the validation error, which starts diverging from around 5 epochs.



Model II

To improve our previous model, we try a deeper CNN with added Convolution layer and a Dropout of 0.5 to reduce overfitting. We can see that the training and validation loss starts to converge; however, we are now getting higher validation accuracy compared to training, which may be due to the high drop out rate used and unbalanced bias /variance.

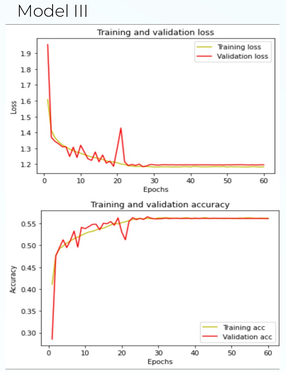


Because we are dealing with a multi-class classification problem, Softmax is used as the activation function in the output layer for all the models to increase the probability of higher classification accuracy. Categorical crossentropy is used for compiling and training all models due to the nature of the problem.

$$\sigma(\vec{z})_i = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}}$$ Softmax

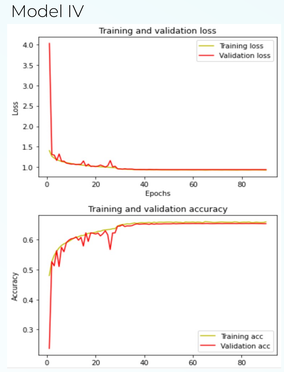
Model III

We now try to reduce the bias from Model II by adding more layers and reducing the drop out to 0.25. We increase the number of instances by applying random horizontal and vertical flips to the model. As our network gets deeper, BatchNormalization is used to stabilize the learning process. Finally, to tackle our variance problem and reduce computation complexity, average polling is introduced after each BatchNormalisation layer. SGD optimizer is used with a 0.001 learning rate and 0.9 momentum. The model performs well now; however, it still lacks accuracy, currently at 56% with some 60 epochs.



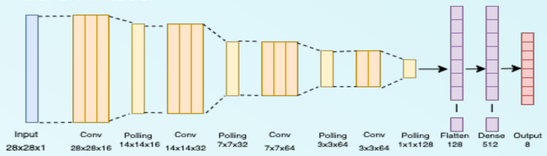
Model IV

We now revert to the Adam optimizer with a lower minim learning rate of 0.000001 to try and improve our accuracy. Non-relevant elements are now removed by adopting max polling over average polling. This also adds improved robustness to the inputs following the random flip changes. The final proposed model now has a 10% increase in accuracy compared to the previous ConvNet. The accuracy on the validation data set stands now at over 65% with some 90 epochs.



Evaluation

Final CNN Model



As our data has an uneven class distribution, we can use the weighted average of precision and recall to calculate the overall F1 score and evaluate our models which in this case can be more useful than accuracy[3].

Model	Params	Overall Precision	Overall Recall	Overall F1 score	Overall Accuracy	Epochs
I	693.704	0.58	0.44	0.49	51.25%	50
II	31.592	0.55	0.27	0.37	52.33%	50
III	264.776	0.72	0.39	0.51	56.11%	60
IV	264.776	0.75	0.54	0.63	65.76%	90

Conclusion

The results above show that our best model achieves a decent 65% accuracy and 0.63 overall F1 scores. Machine learning approaches for kidney cell classification using 3D nuclear stained images have been made using a custom 3D convolutional neural network where a realistic score of 80.26% has been achieved.[4]

Three approaches to solving the uneven class distribution issue would be to under-sample the majority class or oversample the minority classes using duplication or SMOTE(Synthetic Minority Oversampling Technique)

Reference

[1] Tarek M. El-Achkar, Seth Winfree, Niloy Talukder, Daria Barwinska, Michael J. Ferkowicz and Mohammad Al Hasan, Tissue Cytometry With Machine Learning in Kidney: From Small Specimens to Big Data
[2] Andre Woloshuk, Seth Winfree, Tarek M. El-Achkar , Classification of Cell types in the Human Kidney Using 3D Nuclear Morphology
[3] StackOverflow
[4] Andre Woloshuk,Suraj Khochare,Aljohara F. Almulhim,Andrew T. McNutt,Dawson Dean,Daria Barwinska,Michael J. Ferkowicz,Michael T. Eadon,Katherine J. Kelly,Kenneth W. Dunn,Mohammad A. Hasan,Tarek M. El-Achkar,Seth Winfree, In Situ Classification of Cell Types in Human Kidney Tissue Using 3D Nuclear Staining

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