

## Automatic Classifier of Non-Available Chromosome Images Using Convolution Neural Network

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### 1. Introduction

Dicentric Chromosome Assay (DCA) has been used for estimating the absorbed radiation dose following occupational or incidental radiation exposure. The estimating procedure of DCA is labor intensive and time consuming, and therefore, it cannot be widely utilized for radiation mass casualty incidents. Automatic estimation systems of DCA has been studied to improve the efficiency of the estimation procedure in previous studies [1-3]. These methods, however, cause significant problems on the accuracy of the chromosome detection. For improving the accuracy and efficiency of the DCA, an automatic estimation system of DCA using deep learning technique is under development in our research group. As a first step, in this study, a classifier of the chromosome using Convolutional Neural Networks (CNN) is developed to automatically remove the non-available images in using DCA.

### 2. Method

#### 2.1. Scope of image classifier

The automatic system, which is under development in our research group, conducts DCA using the deep learning technique. Before the automatic estimation, the chromosome images, which cannot be clearly identified for DCA, are thrown out with following criteria:

- Two or more chromosome groups mixed in a picture.
- Chromosomes overlapped by background particles.
- The number of chromosomes < 40.

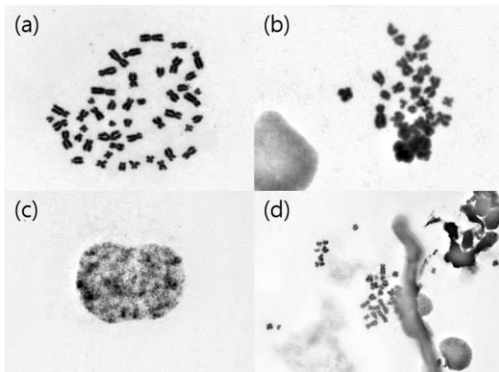


Figure 1. (a) will be kept for DCA and (b)-(d) are thrown out by the criteria.

In this study, a classifier for automatically selecting the available chromosome images in DCA is developed.

#### 2.2. CNN based image classifier

Chromosome images were resized to 299x299 and augmented by flipping and rotating images as shown in Figure 2. The images were fed into the CNN classifier [4, 5].

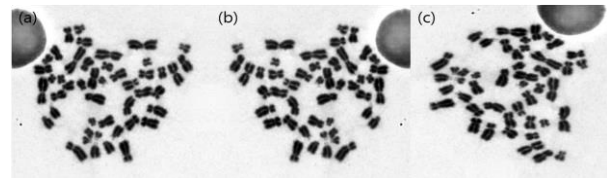


Figure 2.(a) original, (b) flipped, and (c) rotated images.

Inception v3, a widely-used model for image recognition and classification (GoogLeNet) [7 - 10], was used as the networks of the classifier and all layers were initialized by pre-trained data [6] except for logit layer.

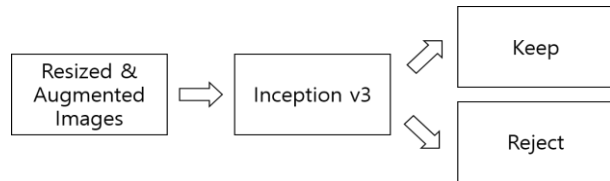


Figure 3. Architecture of classification.

16,400 images were used to train the network and 1,641 images to tune model's hyperparameters. The model was trained using Adam optimizer [11] with a batch size of 32 for 20 epochs. The default parameter settings of TensorFlow [12] were used, such that  $\beta_1 = 0.9$  and  $\beta_2 = 0.999$ . The learning rate is exponentially decayed with initial value of 0.001. The hyperparameters used for the training are summarized in Table 1.

Table 1. Neural network and hyperparameter information.

The number of training images	16,400
The number of validation images	1,641
Batch size	32
Epochs	20
Initial learning rate	0.001
Learning rate decay	0.9
Input image size	299 x 299
Dropout rate	0.2
Optimizer	Adam

### 3. Test and results

As shown in Figure 4, the training and validation losses were converged in 20 epochs. The network yields a training and validation accuracy of above 0.99, respectively. The model parameters were saved and used at the epoch having a lowest validation loss.

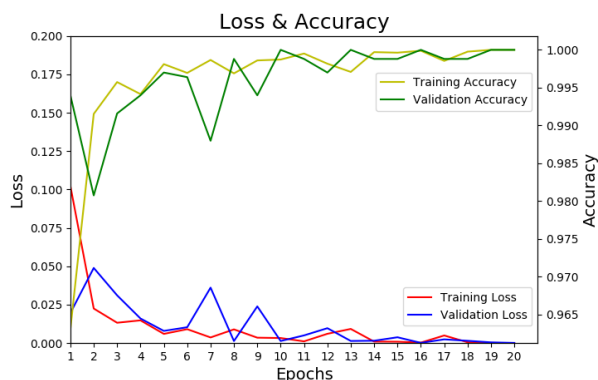


Figure 4. Loss & accuracy vs number of epochs for training and validation data.

2,040 chromosome images were classified by the network as shown in figure 5. The test loss was  $6.623e-5$  and accuracy for test data was 0.995. The results are summarized in Table 2.

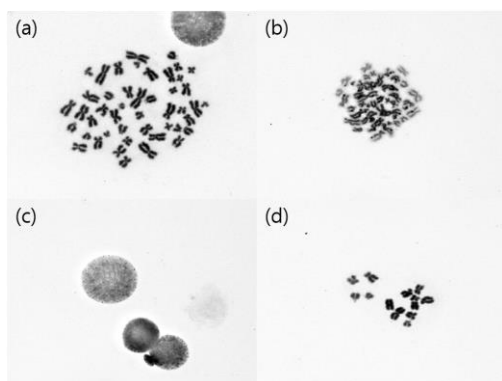


Figure 5. (a) was kept data and (b)-(d) were rejected data.

Table 2. Results of classification of chromosome images.

Number of images to classify	2,040
loss for test data	$6.623e-5$
Accuracy	0.995

### 4. Conclusion

A classifier using Inception v3 network was developed for automatically removing non-available chromosome data in DCA. The 2,040 data were tested with the classifier, and the accuracy was evaluated over 99%. Analysis showed that the classifier has an outstanding performance to distinguish the available data for DCA. This automatic classifier can be directly utilized for reducing the estimation time and resources in DCA.

### Acknowledgment

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