Performance Improvement of Automated Melanoma Diagnosis System by Data Augmentation

Kana KATO,* Mitsutaka NEMOTO,** Yuichi KIMURA,* Yoshio KIYOHARA,*** Hiroshi KOGA,†
Naoya YAMAZAKI,‡ Güstav CHRISTENSEN,‡‡ Christian INGVAR,‡‡ Kari NIELSEN,‡‡ Atsushi NAKAMURA,‡
Takayuki SOTA,** Takashi NAGAOKA*,††

Abstract Color information is an important tool for diagnosing melanoma. In this study, we used a hyperspectral imager (HSI), which can measure color information in detail, to develop an automated melanoma diagnosis system. We therefore integrated the deep convolutional neural network with transfer learning into our system. We tried data augmentation to demonstrate how our system improves diagnostic performance. 283 melanoma lesions and 336 non-melanoma lesions were used for the analysis. The data measured by HSI, called the hyperspectral data (HSD), were converted to a single-wavelength image averaged over plus or minus 3 nm. We used GoogLeNet which was pre-trained by ImageNet and then was transferred to analyze the HSD. In the transfer learning, we used not only the original HSD but also artificial augmentation dataset to improve the melanoma classification performance of GoogLeNet. Since GoogLeNet requires three-channel images as input, three wavelengths were selected from those single-wavelength images and assigned to three channels in wavelength order from short to long. The sensitivity and specificity of our system were estimated by 5-fold cross-validation. The results of a combination of 530, 560, and 590 nm (combination A) and 500, 620, and 740 nm (combination B) were compared. We also compared the diagnostic performance with and without the data augmentation. All images were augmented by inverting the image vertically and/or horizontally. Without data augmentation, the respective sensitivity and specificity of our system were 77.4% and 75.6% for combination A and 73.1% and 80.6% for combination B. With data augmentation, these numbers improved to 79.9% and 82.4% for combination A and 76.7% and 82.2% for combination B. From these results, we conclude that the diagnostic performance of our system has been improved by data augmentation. Furthermore, our system succeeds to differentiate melanoma with a sensitivity of almost 80%.

Keywords: melanoma, hyperspectral imager, deep learning, transfer learning, data augmentation.

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1. Introduction

Melanoma, generally known as ‘mole cancer’, is a superficial malignant tumour. Its incidence in Japan is low, at around 1–2 per 100,000, but is increasing [1]. According to statistics from the American Joint Committee on Cancer, 5-year survival rates for melanoma are approximately 97% in Stage I, but less than 40% in Stage IIIC, and below 15% in Stage IV [2]. Because the prognosis for advanced melanoma is poor, early detection and treatment are important. Today, dermatologists rely heavily on visual inspection to diagnose melanoma. If a lesion cannot be evaluated by visual assessment, it is diagnosed using a dermoscope, a special type of magnifier for observing pigmented skin diseases. However, diagnosis by dermoscopy is also subjective and requires training as well as abundant experience. The accuracy of melanoma diagnosis by dermoscopy, even for skilled dermatologists, is between 75% and 88% [3]. A quantitative diagnostic method for melanoma is therefore urgently needed.

One of the diagnostic guidelines for melanoma is the ABCDE rule [4, 5]. ABCDE is an acronym (Asymmetry,
Border, Color, Diameter, Evolving) that encompasses the form and characteristics of melanoma lesions. Although the guideline is relatively easy to understand, sensitivity and specificity are as low as 66% and 80%, respectively [5, 6], so that a diagnosis of melanoma requires a comprehensive examination of clinical symptoms by a dermatologist. When diagnosis by visual observation is difficult, the dermoscope can be used to enlarge and brighten the image of the lesion by 10 to 30 times, allowing the details to be observed without surface reflected light. Observation with dermoscopy is easy and non-invasive, but quantitative diagnosis by dermoscopy is difficult. Since melanoma is a superficial lesion, many attempts have been made to develop an automatic diagnosis system, but none yet exists that can withstand clinical use [7].

Melanoma is a cancer of melanocytes that produce melanin [8]. Observation of the distribution of pigment molecules in detail is therefore important for its diagnosis. In this study, we used a hyperspectral imager (HSI) [9], a type of spectroscopic. We believe that it is useful for the diagnosis of melanoma because it allows detailed observation of the color information of the lesion.

In recent years, artificial intelligence (AI) technology has progressed remarkably [10]. In the fields of image and speech recognition, the effectiveness of deep learning, a type of AI technology, is widely recognized [11]. Deep learning is composed of multi-layered neural networks [10], with mathematical models that mimic the network structure of neurons in the brain. Several attempts to diagnose melanoma by this approach have been reported. Esteva et al. [12] were the first to introduce deep learning to the diagnosis of melanoma, and they applied deep learning to 129,450 clinical images, 3,374 of which were dermoscopic images. They reported an accuracy of 72.1% in the classification of three groups (melanoma, inflammatory lesions and non-melanoma). Fujisawa et al. [13] applied deep learning to 6,000 dermoscopic images, dividing them into two groups: malignant and benign. They reported accuracy of 92.4% for their system compared to 85.3% for dermatologists. However, these numbers dropped to 59.7% and 74.5% when limited to cases that were difficult to diagnose.

We are developing two automated melanoma diagnosis systems that use deep learning. The first system, which was documented in Proceedings of Japanese Biomedical Engineering Symposium (JBMES) 2019 [14], trains the deep learning network by inputting hyperspectral data (HSD) directly, as we believe that features appropriate for melanoma diagnosis can be extracted by directly training HSD data with a huge amount of colour information. The present paper, part of which was presented at the JBMES 2019 [15], reports on the second system that trains the network by inputting 3-channel images converted from HSD, and has the advantage that many existing networks that receive 3-channel images can be used easily.

In this study, we observed the distribution of melanin in more detail using HSI. Adopting a technique not used in previous studies, we used datasets taken with HSI for deep learning, creating two-group (melanoma or non-melanoma) discriminators.

We are in the process of developing an automated melanoma diagnosis system [16–18]. In previous studies, the entropy of the spectral angle [19] was calculated from HSD and used as a melanoma diagnostic index. Although these indices achieved sensitivity of 96% and specificity of 87%, problems remained. The technique could not cope with lesions, many of which were early, on the fair skin of northern Europeans.

In this study, we integrated transfer learning, a type of deep learning, into our system. Changes in diagnostic performance resulting from data augmentation are reported below.

2. Methods

2.1 Hyperspectral imager

An HSI (MSI-3.1, Mitaka Kohki Co., Ltd, Tokyo, Japan) for pigmented skin lesions (PSLs) was designed and developed de novo. In this study, all lesions were measured hyperspectrally, using a spectrometer to separate light for each wavelength in order to measure color information in greater detail than the three primary colors (blue, red, and green) recorded by a typical digital camera. In our analysis, we used several HSI devices to collect hyperspectral data (HSD). Because the optical system of each device had a slightly different structure from that of all the other HSIs, the measured wavelength range and wavelength resolution also differed. The wavelength in the HSD closest to the desired wavelength was used. The measurement range also differed slightly among the HSIs, but the position coordinates were not corrected because the discrepancies were too small to affect the analysis. Table 1 lists the specifications of the HSI used in the study shown in Fig. 1.

2.2 Materials

The HSD used in this study were collected at four facilities: Shizuoka Cancer Center; Shinshu University; National Cancer Center Japan; and Lund University, Sweden. Table 2 shows the HSD collected at each facility.

A total of 619 lesions, including 283 melanoma lesions and 336 non-melanoma lesions, were used in the analysis. The melanoma group included 72 in situ lesions. All melanoma lesions were diagnosed histopatho-
logically, while obviously benign cases were diagnosed clinically.

We used a protocol approved by our university’s Institutional Review Board and sanctioned for our experiments by all other facilities involved. Only data obtained from subjects who gave informed written consent were used in this analysis.

### 2.3 Deep learning

Deep learning was used to train multi-layered deep neural networks, such as the deep convolutional neural network (DCNN). We adopted the well-known GoogLeNet [20], one of many types of DCNN structure, because it was used in two previous studies [12, 13]. GoogLeNet won the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) in 2014. Inception v3, one of several versions of GoogLeNet, was used in this study. It inputs a $224 \times 224$ pixel, three-channel image and outputs 1,000 image classifications.

Deep learning training requires huge amounts of data. Having only 619 HSD samples, we therefore adopted a method that allows training with a small amount of data.

Transfer learning is a method that reuses knowledge of the source domain to solve a new task of the target domain [21]. Even if the training data are very small or untrained, the classifier can be trained by using the knowledge of the original domain. In this study, we employed a fine-tuning method, re-training the pre-trained model by replacing the output layer of the pre-trained model with two classes, melanoma and non-melanoma.

Our study used GoogLeNet pre-trained by ILSVRC 2012 [22], which consists of 140,000 images and 1,000 classes. These pre-trained networks were also used in previous studies, making comparison possible. Learning by full scratch was not adopted due to low diagnostic ability.

### 2.4 Data augmentation method

Artificially-augmented images as well as the original single-wavelength images were used to fine-tune GoogLeNet. In general, DCNNs, including GoogLeNet, are known to improve classification ability as the number of training datasets increases [23]. Therefore, we attempted to fine-tune more efficiently by augmenting small training datasets.

DCNNs, including GoogLeNet, need a large-scale dataset to train or fine-tune those networks, but our collected HSD dataset was too small to train. The data-augmentation technique enlarges training datasets and often contributes to stable training of deep neural networks with small datasets. In this study, we executed vertical or horizontal inversion (or both) to the original single-wave-
length images, thus increasing the training dataset four-fold. In this study, only the inversion operation was experimentally adopted as an initial trial of the data augmentation method.

2.5 Analysis method

Figure 2 shows our analysis method. The skin reflection spectrum in the visible range is mostly composed of melanin and hemoglobin. Therefore, we think that it is possible to reduce the spectrum, which is multidimensional information, to about three dimensions. In this paper, as an initial study, we adopted a method of selecting three single-wavelength images from HSD and inputting them as three-channel images to deep learning networks.

First, the HSD was converted to multiple single-wavelength images, averaged over plus or minus 3 nm. Every single-wavelength image had reflectance as the luminance value of each pixel. Although the width and height of the single-wavelength image differed slightly from device to device, the difference was processed by resizing, as described below.

Next, three wavelengths were selected from those single-wavelength images. The combination of 530, 560 and 590 nm (hereafter referred to as combination A) and the combination of 500, 620 and 740 nm (hereafter referred to as combination B) were the two sets of three wavelengths used for image input, which were considered to be diagnostically useful in our preliminary study [24]. In the study, the wavelength with the highest diagnostic performance was searched among all combinations of wavelengths in the HSD.

Because GoogLeNet inputs three-channel images, three wavelengths were selected from those single-wavelength images and assigned to three channels, in wavelength order from short to long. The image was then resized to a width of 164 pixels and a height of 224 pixels. The width was 60 pixels too short for input to GoogLeNet. A random noise of 30 pixels was therefore added to the left and right of the image. In general, the aspect ratio was changed to obtain square images. It was experimentally confirmed that the change in aspect ratio resulted in a decrease in accuracy due to the change in lesion shape; therefore, the addition of random noise was adopted in this study. Other resize transformation methods such as squashing and cropping were also tried, but our approach was selected empirically.

DIGITS ver 6.0, manufactured by NVIDIA Corporation, was used as a deep learning environment. The operating system was Ubuntu 16.04 LTS, and the graphics processing unit (GPU) was NVIDIA Quadro P5000. NVIDIA Caffe ver 0.15.14, CUDA ver 9.2 and cuDNN ver 7.1 were used as deep learning programming platforms.

We adopted 5-fold cross-validation for this study. The melanoma and non-melanoma cases were randomly divided into five groups. Of these, four were used for training and the last for validation. The same process was repeated five times because each group was used once for validation. The average values of sensitivity and specificity for the five groups were used as an evaluation index. Our dataset was randomly divided into training data (80%) and validation data (20%). Without data augmentation, the dataset consisted of 495 training and 124 validation data samples. With data augmentation, the dataset increased in size to 1,980 training data samples and 124 validation data samples. With Adaptive Moment Estimation (Adam) as the solver type and the random seed set at 8, the experimental training parameters were batch size 32 and 100 epochs.

A dataset of each wavelength combination was created and the network trained. A classifier was created to discriminate between melanoma and non-melanoma. This system was verified and evaluated by the sensitivity and specificity of the validation data as well as by the area under the receiver operating characteristics (ROC) curve (AUC) analysis of the validation data.

The Student’s t-test was used to test the significance of difference between two groups, with the significance level set at 5%.  

1. Get HSD
2. Create single wavelength image
3. Select 3 wavelengths
4. Create 3 channel image
5. Transfer Learning
6. Diagnosis

Fig. 2 The analysis method of this study. First, HSD was acquired by HSI. Second, the HSD was converted to multiple single-wavelength images. Third, three wavelengths were selected. Fourth, a three-channel image was created by assigning three selected single-wavelength images to each channel in wavelength order from short to long. Fifth, GoogLeNet was trained by the transfer learning method. Sixth, a classifier was created to distinguish between melanoma and non-melanoma.

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3. Results

3.1 Single-wavelength image
Figure 3 shows a single-wavelength image of a melanoma case. Because melanin has high absorbance at short wavelengths, the image is dark overall at 500 nm. The reflectance of the 740 nm image is generally bright and faint because the light absorption of melanin is lower at longer wavelengths.

3.2 Three-channel image
Figure 4 shows an example of a three-channel image used for GoogLeNet input. This image was obtained from the same lesion as the one in Fig. 3. It looks blue because the reflectance of the 740 nm wavelength in the B channel among the three RGB channels is high.

3.3 Analysis results
Figures 5 and 6 show an example of a training process without and with data augmentation, respectively. The vertical axis shows accuracy (right) and loss (left), and the horizontal axis shows the number of epochs. Figures 7 and 8 show the sensitivity and specificity without and with data augmentation, respectively. Without data augmentation, the diagnostic performance of combination A was 77.4% sensitivity and 75.6% specificity. The performance of combination B was 73.1% sensitivity and 80.6% specificity. With data augmentation, the diagnostic performance of combination A was 79.9% sensitivity and 82.4% specificity. The performance of combination B was 76.7% sensitivity and 82.2% specificity. There were no significant differences in sensitivity and specificity between combinations A and B, both without and with data augmentation. Figure 9 shows the sensitivity of melanoma in situ without and with data augmentation. Without data augmentation, the diagnostic performance in sensitivity was 60.1% for combination A, 61.3% for combination B. With data augmentation, the diagnostic performance in sensitivity was 66.9% for combination A, 67.0% for combination B. Here, too, there were also no significant differences in sensitivity between combinations A and B, both without and with data augmentation.

Fig. 3 Single-wavelength images of a melanoma case at 500 nm, 620 nm, and 740 nm. The 500-nm image is dark because the absorbance of melanin is high. The 740-nm image is bright and faint because light absorption of melanin decreases.

Fig. 4 An example of three-channel image used for GoogLeNet input, created from combination B. This lesion is a melanoma. The image looks blue because the reflectance of the 740 nm wavelength in the B channel among the three RGB channels is high.

Fig. 5 An example of the training process without data augmentation. The vertical axis is accuracy (right) and loss (left), and the horizontal axis is number of epochs.

Fig. 6 An example of the training process with data augmentation. The vertical axis is accuracy (right) and loss (left), and the horizontal axis is number of epochs.
**Data augmentation.**

The results of ROC analysis without data augmentation and with data augmentation are shown in Figure 10(a) and Figure 10(b). Without data augmentation, the AUCs of combination A and combination B were 0.837 and 0.841, respectively. With data augmentation, the AUCs of combination A and combination B were 0.863 and 0.864, respectively.

### 4. Discussion

From Figures 5 and 6, it can be seen that the convergence is at around epoch 70, and that the loss changes at about 1. The presence or absence of data augmentation has no effect on the training curve. The network is well converged, and no overlearning is seen. These findings indicated that our parameters were appropriate.

As shown in Figure 7, the sensitivity without data augmentation was 77.4% for combination A and 73.1% for combination B. Compared with the sensitivity of 96.3%
in the previous study reported by Fujisawa et al. [13], our results were about 20% lower. With data augmentation, the sensitivity was 79.9% for combination A and 76.7% for combination B. Our results were also lower, this time by about 16%, than those obtained by Fujisawa et al. However, while Fujisawa et al. trained deep learning using 6,000 dermoscopic images, the HSD of our study consisted of only 619 images. Therefore, the need for data augmentation was recognized.

In this study, data augmentation improved the sensitivity by 2.5% for combination A and 3.6% for combination B. As a result of data augmentation, a high-performance classifier with a sensitivity of close to 80% was achieved. Although the data augmentation tried was relatively simple, its effective improvement of diagnostic performance was confirmed. In deep learning, increasing the amount of data leads to improvement of image classification performance. It is currently believed that larger datasets are necessary for more accurate diagnosis by deep learning. In recent years, deep learning with a small set of data has been studied [25]. In the future, it will be necessary to consider more effective methods for data augmentation.

The results for the in situ lesions without data augmentation (see Fig. 9) show that the sensitivity was 60.1% for combination A, 61.3% for combination B. However, compared with the 74.5% accuracy of Fujisawa et al., our result was about 14% lower. However, even for early lesions that were difficult to diagnose in our previous studies, we found that a certain degree of diagnosis was possible using this system.

For in situ lesions with data augmentation, Fig. 9 shows that the sensitivity was 66.9% for combination A and 67.0% for combination B. Our results were 7% lower than those of Fujisawa et al [13]. On the other hand, Fujisawa et al. reported dermatologist accuracy of only 59.7%. Our system, both without and with data augmentation, out-performed experienced dermatologists. Furthermore, the data of in situ lesions in this study included a large number of northern European patients with fair skin. Melanomas in these patients are often found earlier than in Japanese patients, and darker skin is considered one of the factors that increase the difficulty level of diagnosis. In this study, data augmentation improved classification performance for in situ lesions, with increase in sensitivity of 6.8% for combination A and 5.7% for combination B. Because of the small number of data samples of in situ lesions in the present study, the variation in classification performance is large, but we believe that additional data may reduce this variation.

In this study, there were no significant differences in sensitivity and specificity between combinations A and B, both without and with data augmentation. Combination A is one of the characteristic absorption peaks of oxyhemoglobin. We therefore speculate that there is a correlation with blood accumulation associated with melanoma angiogenesis. Combination B is less affected by oxyhemoglobin and covers a wavelength range where the state of melanin can be more easily confirmed. Melanoma is a cancer of melanocytes, and it is important to observe the state of melanin. It is possible that no significant difference was found because both combinations are suitable wavelengths for observing the state of melanoma.

The results of the ROC analysis showed no significant difference between combination A and combination B. On the other hand, data augmentation increased AUC values by 0.026 for combination A and by 0.023 for combination B. The ROC analysis also confirmed that diagnostic performance was improved by data augmentation.

5. Conclusion

We developed an automated melanoma diagnosis system combined with deep learning. The analysis used 283 melanoma lesions and 336 non-melanoma lesions measured in Japan and northern Europe. We sought to improve diagnostic performance through data augmentation. By performing two-group discrimination between a melanoma group and a non-melanoma group, it was possible to construct a high-performance classifier with 79.9% sensitivity and 82.4% specificity for combination A. In this paper, only the primary augmentation method was adopted. Nevertheless, an improvement in accuracy was confirmed. More effective augmentation methods have been reported [26]. By adopting these methods, further improvement in performance of our system can be expected.

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Kana Kato

Kana Kato received B.E. degree from Kindai University in 2019. She is currently a student at Department of Biomedical System Engineering, Graduate School of Biology-Oriented Science and Technology, Kindai University. Her research interests include automated melanoma diagnosis using deep learning.

Mitsutaka Nemoto

Mitsutaka Nemoto received Ph.D. in Bio-Applications and Systems Engineering from Tokyo University of Agriculture and Technology in 2007. He is currently a lecturer at Department of Biomedical Engineering, Faculty of Biology-Oriented Science and Technology, Kindai University. His research interests include Medical image analysis, Pattern recognition, and Computational anatomy. He is a member of Institute of Electronics, Information and Communication Engineers (IEICE), Japanese Society for Medical and Biological Engineering (JSMBE), Japanese Society of Medical Imaging Technology (JAMIT), Japan Radiological Society (JRS), and Japanese Society of Nuclear Medicine (JSNM).

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Pan SJ, Yang Q: A survey on transfer learning. IEEE Trans Knowledge Data Eng. 22(10), 1345–1359, 2010.
Atsushi Nakamura received Ph.D. in Integrative Bioscience and Biomedical Engineering from Waseda University in 2004. He is currently a junior researcher at Research Institution for Science and Engineering, Waseda University. His research interests include spectroscopic imaging system. He is a member of the Japan Society of Applied Physics, Japanese Association of Forensic Science and technology, and Japanese Skin Cancer Society.

Hiroshi Koga received Ph.D. degree from Shinshu University in 2017. He is currently a Senior Lecturer at Department of Dermatology, Shinshu University Hospital. His research interests include melanoma diagnosis with imaging modality and clinical trial. He is a member of Japanese Society of Dermatology, Japanese Society of Investigative Dermatology, Japanese Society of Medical Oncology, Japanese society of Clinical Oncology, and Japanese Skin Cancer Society.

Naoya Yamazaki
He is a Chief at Department of Dermatologic Oncology, National Cancer Center Hospital, Tokyo, Japan.

Gustav Christensen
He is in Department of Dermatology, Lund University, Skane University Hospital, Department of Clinical Sciences Lund, Dermatology, Lund, Sweden.

Yuichi Kiyohara, M.D. is a Chief at Dermatology Division, Shizuoka Cancer Center, Shizuoka, Japan.

Christian Ingvar
He is in Department of Pathology, Lund University, Skane University Hospital, Department of Clinical Sciences Lund, Pathology, Lund, Sweden.

Kari Nielsen
She is in Department of Surgery, Lund University, Skane University Hospital, Department of Clinical Sciences Lund, Surgery, Lund, Sweden.

Atsushi Nakamura
Atsushi Nakamura received Ph.D. in Integrative Bioscience and Biomedical Engineering from Waseda University in 2004. He is currently a junior researcher at Research Institution for Science and Engineering, Waseda University. His research interests include spectroscopic imaging system. He is a member of the Japan Society of Applied Physics, Japanese Association of Forensic Science and technology, and Japanese Skin Cancer Society.

Takayuki Sota
Takayuki Sota received Ph.D. in Electrical Engineering from Waseda University in 1985. He is currently a professor at Department of Electrical Engineering and Bioscience, Waseda University. His research interests include optical properties of matters. He is a member of the Physical Society of Japan, the Japan Society of Applied Physics, Japanese Association of Forensic Science and technology, and Japanese Skin Cancer Society.

Takashi Nagaoka
Takashi Nagaoka received the Ph.D. degree in engineering from Waseda University, Japan, in 2005. He is lecturer at Faculty of Biology-Oriented Science and Technology, Kindai University, Japan, from 2015. His research fields are medical optics. He is member of Japanese Society for Medical and Biological Engineering, the Society of Instrument and Control Engineers, and Japanese Skin Cancer Society.