# **Classification and Analysis of Liverwort Sperm by Integration-Net**

Haruki Fujii<sup>1</sup>, Naoki Minamino<sup>2</sup>, Takashi Ueda<sup>2,3</sup>, Yohei Kondo<sup>2,3,4</sup> and Kazuhiro Hotta<sup>1</sup>

<sup>1</sup>Meijo University, 1-501 Shiogamaguchi, Tempaku-ku, Nagoya 468-8502, Japan

<sup>2</sup>National Institute for Basic Biology, 38 Nishigounaka, Myoudaiji-cho, Okazaki 444-0867, Japan

<sup>3</sup>The Graduate University for Advanced Studies, 1560-35 Syonankokusai-mura, Hayama-machi, Miura-gun, Japan

<sup>4</sup>Exploratory Research Center on Life and Living Systems (ExCELLS),

5-1 Higashiyama, Myodaiji-cho, Okazaki, 444-8787, Japan

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Abstract: In this paper, we propose a method to classify the videos of wild-type and mutant sperm of liverwort using deep learning and discover the differences between them. In traditional video classification, 3D-Convolution was often used. However, when 3D CNN is used, the information of multiple frames is mixed. Therefore, it is difficult to detect important frames and locations in a video. To solve this problem, we proposed a network that retains video frame information using Depthwise Convolution and Skip Connection, and used gradient-based visualization to analyze the difference between wild type and mutant sperm. In experiments, we compared the proposed method with conventional 3DCNN and show the effectiveness of the proposed method.

# **1 INTRODUCTION**

In recent years, there has been a lot of researches of video recognition based on Convolutional Neural Network (CNN). These techniques have been applied not only to human behavior recognition (Dalal, N., Triggs, B., & Schmid, C., 2006), but also to animal behavior (Anderson, D. J., & Perona, P., 2014). The purpose of this paper is to classify two types of sperm using CNN and to discover the differences between two types of sperm (mutant and wild type) by visualizing the important frames and locations in a video.

We would like to visualize important frames and locations in a video for classification. However, the 3DCNN used for video recognition collapses the frame information as it goes through the layers. Therefore, important frame information cannot be analyzed by gradient-based approaches such as Grad-CAM (Selvaraju, R. R., Cogswell, M., Das, A., Vedantam, R., Parikh, D., & Batra, D., 2017) and Grad-CAM++ (Chattopadhay, A., Sarkar, A., Howlader, P., & Balasubramanian, V. N., 2018). It is necessary to maintain the time-series information of frames in the network to discover important frames and locations in a video.

In this paper, we propose Integration-Net which is the integrated network of two different networks devised to maintain frame information. One network in the integrated network has the structure in which



Figure 1: Example of visualization. Left shows an input image and right shows the result of visualization.

the input frame information is transmitted to the deeper layer by skip connection in order to maintain the frame information. The other network uses the Depthwise convolution. Since the Depthwise convolution applies a single filter to each channel, there is no risk for losing frame information. By integrating the outputs of these two different networks, we can use the advantages of ensemble effect which is expected to improve the accuracy in comparison with a single network.

When a video is classified, our method visualizes which parts in the video are important for Integration-Net to determine whether it is wild type or mutant. We obtain feature maps whose channel is the same number of frames as the input video, and calculate the gradients from the outputs to visualize the important locations and frames in a video.

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Figure 2: Network architecture of Integration-Net. The numbers in the figure represents the shape of feature maps. For example,  $3 \times 32 \times 256 \times 256$  at input represents 3 channels, 32 frames and a size of  $256 \times 256$ . BN represents batch normalization.

In our experiments, we used the videos of liverwort sperm to discriminate between wild type and mutants, and achieved an average classification accuracy 91.79%. In addition, from visualization results, we confirmed that our method discovered important frames and locations in a video for classification. Figure 1 shows the visualization result in which red indicates important locations and blue indicates unimportant locations.

The organization of this paper is as follows. First, section 2 describes related works. Section 3 explains the proposed method. Section 4 describes the experimental methods and shows the experimental results. Finally, in section 5, we describe the conclusion and future works.

# 2 RELATED WORKS

### 2.1 Video Recognition

In recent years, video recognition has been dominated by CNN-based approaches as well as image recognition. Since video has an additional dimension in the time direction to images, and there is a difference in the characteristics of mainly temporal and spatial information. Therefore, simple time dilation, which is an effective method for image recognition, is not always effective for video recognition.

3D CNN (Ji, S., Xu, W., Yang, M., & Yu, K., 2012) is a method that considers the information in temporal direction by 3D-convolutional processing, which is the extension of 2D convolutional processing to the temporal direction.

C3D (Tran, D., Bourdev, L., Fergus, R., Torresani, L., & Paluri, M., 2015) was proposed as a pioneering method for 3DCNN. It can learn taskappropriate spatio-temporal features in an end-to-end manner.

In this paper, we propose the Integration-Net which integrates two different networks. It can use ensemble of two networks, and we can improve the accuracy in comparison with a single network. In this paper, we would like to classify sperm videos and visualize the important frames and locations in a video. However, conventional video classification methods cannot visualize the important frames



Figure 3: Overview of proposed method. We visualized the important frames and locations by weighting the gradients against the network predictions. This allows us to show the differences between wild type and mutant sperm. We compute the gradient of convolutional layer from the prediction result and create weight maps. Weights are calculated by averaging them in channel direction at each frame of the weight maps. For each pixel, we calculate the product between the feature maps and the weights.



Figure 4: How to detect the differences by our method. The "f" and "ch" represent the number of frames and channels in the feature maps. The dimension of the feature maps in the Integration-Net is channel x frame x height x width. We transposed the channels and frames of the feature maps as a preprocessing step for visualization. This allows us to generate a heat map for each frame.

because the number of output channels is different from the number of input frames. Our proposed Integration-Net solved this problem by skip connection of input information and the Depthwise convolution.

### 2.2 Visualization Method

There are researches that visualize where the network pays attention to classification. If the classification accuracy of the model is high, the visualization results can help the people discover problems and new phenomena. Some visualization methods have been proposed; Guided backpropagation (Springenberg, J. T., Dosovitskiy, A., Brox, T., & Riedmiller, M., 2014) and deconvolution (Zeiler, M. D., & Fergus, R., 2014) visualized CNN predictions by highlighting important pixels. These methods emphasized the details of the image at high resolution, but are unable to identify classes. Grad-CAM (Selvaraju, R. R., Cogswell, M., Das, A., Vedantam, R., Parikh, D., & Batra, D., 2017) is a visualization method that improved the problem. It is a technique for visualizing important pixels for classification by weighting their gradients with respect to the predicted value. The weights are calculated by partially differentiating the probability scores and all feature maps are integrated by weighted average into a saliency map. This means that positions that have a large impact on the class decision have a large probability score.

As shown in Figure 2, in the proposed method, the feature maps from two different networks are summed. To use gradient-based method such as Grad-CAM for our method, we extract the summed feature maps and classification results to visualize the important parts. Grad-CAM gives the importance of a pixel by summing in the channel (frames in a video) direction. However, we would like to know the important frames and locations. Thus, we must modify Grad-CAM slightly.

# **3 PROPOSED METHOD**

#### 3.1 Overview of the Proposed Method

Figure 3 shows the overview of the proposed method. Videos of  $256 \times 256$  pixels and 32 frames are fed into Integration-Net. As mentioned above, the number of frames in the feature map used for visualization must be the same as the number of frames in an input video. To classify the videos, we used  $1 \times 1 \times 1$  convolution to set the number of channels to the number of classes, and then Adaptive Average Pooling was used. The output with the highest probability is returned to Integration-Net, where the important features that affect the final probability score are calculated. In this paper, a feature map that summed the outputs of two networks was used for visualization, as shown in Figure 2.



Figure 5: Accuracy and loss function for validation set.

#### 3.2 Details of Network Architecture

Integration-Net is the integration of two different networks. One of two networks has four convolutional layers with 3D-Convolution, and the input video is transmitted to the deeper layer by skip connections. There is a difference in the resolution and number of channels of the skip connection, and we change the resolution of the input by average pooling. The number of channels in the feature map is also changed to the same number of channels in the input video with 1 x 1 x 1 convolution. In general, when we use 3D-Convolution, the information of each frame is mixed up. If the frame information is lost, the important frames cannot be identified when we analyse important frames using gradient information. Therefore, we compensate for the frame information of input video by using skip connections to convey the frame information of the input.

The other network uses the Depthwise convolution. The reason for using the Depthwise convolution is that it applies one filter to each channel. Thus, frame information is not lost. It also reduces the computational cost in comparison with standard convolution. Integration with a network using skip connections uses the sum of feature maps. Therefore, the number of channels is also changed to the same number of channels in the input video by  $1 \times 1 \times 1$  convolution before integration. This allows us to align the shape of the output feature maps from the two networks for integration.

In two networks, the kernel size and stride in the frame direction for all convolutions were set to 1. This allows us to keep the number of frames in the network. After the convolution, batch normalization, FReLU (Ma, N., Zhang, X., & Sun, J., 2020), and dropout were used. FReLU is an activation function specialized for image recognition. Unlike the commonly used ReLU, the function can be changed for each location as shown in equation (1).

$$y=\max(x, T(x)) \tag{1}$$

where  $T(\cdot)$  is Depthwise convolution. Therefore, FReLU is able to learn spatial elements for each pixel, and can decide whether to use the learned pixel or not by max( $\cdot$ ).

#### **3.3** Discover the Difference

Figure 4 shows how our method discover the difference in sperm. The dimension of output feature map in the Integration-Net is channel  $\times$  frame  $\times$  height  $\times$  width. Since Grad-Cam used in image



Figure 6: Results of difference discovery by our proposed method. The upper row is the wild type and the lower row is the mutant. Left column shows the examples of input frames and right column shows the results of difference discovery.

classification is calculated by the weighted sum of each channel, we cannot know the important frames. Thus, as shown in Figure 4, the channels and frames of the feature map are transposed as a preprocessing step. This allows the channels corresponding to each frame to be grouped together. For example, the first frame of the feature map in Figure 4 is shown in red. Thus, by computing the gradients of the feature map and generating a heat map for each frame, we can detect the differences between wild-type and mutant sperm automatically. The difference shows important frames and locations in a video for classification.

# 4 EXPERIMENTS

#### 4.1 Datasets

In experiments, we used video datasets of liverwort sperm. We cropped the areas including a single sperm from videos and created 256 video clips. There is no overlap for cropping areas. The size of video clips is  $256 \times 256$  pixels, and the number of frames is 32. There are two classes; wild type and mutant. We used 128 video clips for training, 64 for validation and 64 for test. We evaluate our method with 4-fold cross validation.

#### 4.2 Implementation Details

In this paper, we used the Pytorch library and trained 500 epochs using Adam optimizer. The initial learning rate was set to 0.001, CosineAnnealingLR was used as scheduler,  $T_0=250$ ,  $T_mult=1.0$ , eta min=0.0, and the batch size was set to 32.

We used Focal Loss (Lin, T. Y., Goyal, P., Girshick, R., He, K., & Dollár, P., 2017) defined in equation 2.

Focal Loss= 
$$-(1-p_t)^{\gamma} \log(p_t)$$
 (2)

where  $\gamma$  is a hyper-parameter and we set  $\gamma$  to 2 according to the original paper.

We chose the model with the lowest loss or the highest accuracy for validation set. The model is used for evaluation.

In experiments, six methods were evaluated as comparison. Six methods are as follows. 3D-ResNet50 (Hara, K., Kataoka, H., & Satoh, Y., 2017) which is commonly used in video classification; Skip-Net which introduces skip connections from the input frame; Depthwise-Net which uses the Depthwise convolution; SS-Integration-Net which integrates two Skip-Nets. DD-Integration-Net which integrates two Depthwise-Nets. Integration-Net which integrates Skip-Net and Depthwise-Net.

### 4.3 **Results of Experiments**

Table 1 shows the evaluation results of each method when we use the model with the lowest loss for validation set. We see that our proposed Integration-Net, which integrates Skip-Net and Depthwise-Net gave the best accuracy. The proposed method improved the accuracy by more than 38% from the conventional 3D-ResNet50. This is because 3D-ResNet50 has a large model and overfitting might occur. Integration of two different networks also gave better classification accuracy than the integration of two same networks. This is because the integration of the two different networks allowed us to use the ensemble effect.



Figure 7: Results of difference discovery by our method when skip connection was removed. The upper row is the wild type and the lower row is the mutant. Left column shows some frames in a video and right column shows the results of difference discovery.

Table 1: Comparison results when the model with the lowest loss for the validation set was chosen.

	wild	mutant	Average
3D-ResNet50	60.94	46.10	53.52
Skip-Net	92.16	70.31	81.25
Depthwise-Net	88.28	89.84	89.06
SS-integration	67.97	93.75	80.86
DD-integration	89.06	91.41	90.24
SD-integration	89.84	93.75	91.79

Table 2: Comparison results when the model with the highest accuracy for the validation set was chosen.

2 U U	wild	mutant	average
3D-ResNet50	61.72	49.22	55.47
Skip-Net	87.50	69.53	78.52
Depthwise-Net	82.81	88.28	85.55
SS-integration	68.75	92.97	80.86
DD-integration	86.72	90.63	88.67
SD-integration	86.72	92.97	89.81

Table 2 shows the results when we choose the model with the highest accuracy for validation set. In comparison with the results in Table 1, the overall accuracy became low. Figure 5 shows the graph of the transition of accuracy and loss for the validation set. The highest accuracy is achieved at around 350 epochs, but the loss function continues to be low until the end of the training. Therefore, it is more accurate to choose the model with the lowest loss for the validation set.

Figure 6 shows the visualization results of important frames and locations for classification by our proposed method. Important parts are shown in red and unimportant parts are shown in blue. In both the wild type and the mutant classes, the flagella that are used for swimming in water were discovered as an important part for classification. This indicates that the wild type and the mutant have the differences in their flagella. The visualization results show that the flagella of wild type is a distinctive feature compared with the mutant's flagella.

#### 4.4 Ablation Study

In this section, we investigate the effectiveness of FReLU and skip connections used in the proposed method. In the experiment, three models were compared. Three models are our proposed method, the proposed method without the skip connection, and the proposed method that the FReLU is replaced by ReLU.

Table 3 shows the results of ablation study. We can confirm that the accuracy was improved by more than 8% by using FReLU as the activation function. FReLU is also effective in video classification using 3D-convolution.

Table 3: Results of the proposed method when skip connection is not used and when the activation function FReLU is replaced by ReLU.

skip connection	activation function	wild	mutant	average
	FReLU	67.97	93.75	80.86
1	ReLU	85.94	81.25	83.60
1	FReLU	89.84	93.75	91.79

Evaluation results showed that the accuracy was improved by more than 10% when the skip connection was used. This is because the information of each frame has been mixed up in the network.

Figure 7 shows the results of difference discovery by our method without skip connection. In comparison with Figure 5, the difference is ambiguous. These results show that providing input information to the feature map by skip connection is effective for visualizing important frames.

# 5 CONCLUSION

This paper proposed the Integration-Net which integrates different networks for classifying wildtype and mutant sperm of liverwort. This allows more accurate classification than conventional video classification methods. We discover the difference between the two types of sperm by using the gradients of network. Our method discovered the difference of the flagella automatically.

However, the heat map may be ambiguous or blurry. Therefore, we would like to use visualization methods that do not depend on gradient calculation such as Score-CAM (Wang, H., Wang, Z., Du, M., Yang, F., Zhang, Z., Ding, S., Mardziel, P. & Hu, X., 2020), or consider more detailed visualization methods that refer to it.

In addition, we would like to use ConvLSTM (Xingjian, S. H. I., Chen, Z., Wang, H., Yeung, D. Y., Wong, W. K., & Woo, W. C., 2015) to use motion information effectively.

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