**Building the convolutional neural network model**

To find the characteristics of the nEMG signal, we used a 1-dimensional convolutional neural network (CNN) named nEMGNet. The structure of nEMGNet includes spatial block-1, which reduces the resolution by half, spatial block-2 which reduces the resolution by quarter, and residual block which solves the problem of poor backward propagation as the layer gets deeper by making a residual connection. (S1 Table)

|  |  |  |
| --- | --- | --- |
| **Spatial reduction block-1**  **(n,k)** | **Spatial reduction block-2**  **(n,k)** | **Residual block**  **(n)** |
| Conv(k)-n,  Stride(1) | Conv(k)-n,  Stride(2) | Conv(5)-n,  Stride(1) |
| BatchNorm | BatchNorm | BatchNorm |
| ReLU | ReLU | ReLU |
| Max-pool(2),  Stride(2) | Max-pool(2),  Stride(2) | Conv(5)-n,  Stride(1) |
|  |  | BatchNorm |

S1 Table. convolutional blocks of nEMGNet. n, the number of channel; k, the number of filter; conv, convolutional layer; BatchNorm, batch normalization; Max-pool, max pooling.

The nEMGNet was tested with 4 versions of nEMGNet-A, nEMGNet-B, nEMGNet-C, and nEMGNet-D with different versions according to the number of residual blocks. (S2 Table)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **nEMGNet-A** | **nEMGNet-B** | **nEMGNet-C** | **nEMGNet-D** |
| Block 1 | SR block-2  (64, 11) | SR block-2  (64, 11) | SR block-2  (64, 11) | SR block-2  (64, 11) |
| Block 2 | SR block-2  (64, 7) | SR block-2  (64, 7) | SR block-2  (64, 7) | SR block-2  (64, 7) |
| Block 3 | SR block-2  (64, 5) | SR block-2  (64, 5) | SR block-2  (64, 5) | SR block-2  (64, 5) |
| Block 4 |  | Residual block  (64) 2 | Residual block  (64) 4 | Residual block  (64) 6 |
| Block 5 | SR block-1  (128, 5) | SR block-1  (128, 5) | SR block-1  (128, 5) | SR block-1  (128, 5) |
| Block 6 |  | Residual block  (128) 2 | Residual block  (128) 4 | Residual block  (128) 6 |
| Block 7 | SR block-1  (256, 5) | SR block-1  (256, 5) | SR block-1  (256, 5) | SR block-1  (256, 5) |
| Block 8 |  | Residual block  (256) 2 | Residual block  (256) 4 | Residual block  (256) 6 |
| Block 9 | SR block-1  (512, 5) | SR block-1  (512, 5) | SR block-1  (512, 5) | SR block-1  (512, 5) |
| Block 10 |  | Residual block  (512) 2 | Residual block  (512) 4 | Residual block  (512) 6 |
| Block 11 | SR block-1  (1024, 5) | SR block-1  (1024, 5) | SR block-1  (1024, 5) | SR block-1  (1024, 5) |
| Block 12 |  | Residual block  (1024) 2 | Residual block  (1024) 4 | Residual block  (1024) 6 |
|  | FC-512 | FC-512 | FC-512 | FC-512 |
|  | FC-256 | FC-256 | FC-256 | FC-256 |
|  | FC-64 | FC-64 | FC-64 | FC-64 |
|  | FC-16 | FC-16 | FC-16 | FC-16 |
|  | FC-10 | FC-10 | FC-10 | FC-10 |
|  | Softmax | Softmax | Softmax | Softmax |

S2 Table. configuration of 4 different versions of nEMGNet. SR block, spatial resolution block; FC, fully connected layer.

A rectified linear unit (ReLU) is applied to the fully connected layer after the convolutional layer. (Figure 1)



Figure 1. nEMGNet structure. Processing composed of convolutional neural network, batch normalization, rectified linear unit (ReLU), max pooling. Light gray box; spatial block-1 and spatial block-2, Dark gray box and bold curved arrow; residual block. 유재성연구원 그림 바꿔서 주면 변경

The initial values of nEMGNet hyperparameter were empirically determined based on values that have been widely used. The learning rate, batch size, and epoch were set to 10-3, 32, and 100. Adam optimizer was used for optimizer, and inversely proportional values were used for the class weight to the number of signal segments for preventing erroneous prediction.

The number of muscles tested with nEMG is different for each subject, and among the tested muscles, abnormal and normal nEMG can coexist. To overcome these limitations, we applied a method called the DiVote (Divide and Vote) algorithm. DiVote divided each nEMG signal into segments of homogeneous length and converted it into 3 signal segment prediction scores through a feature extractor. The muscle signal prediction score was calculated by aggregating the signal segment prediction score and aggregated to derive the subject prediction score through soft voting. When deriving the subject prediction score, two different method were tried. The first method is to calculate and aggregate prediction scores by classifying them by neuropathy, myopathy, and normal without information on the location of the muscle. The second method is to classify whether it is proximal or distal according to the location of the muscle, and calculate and aggregate prediction scores of each neuropathy, myopathy, and normal. After 1500 training, in the process for extracting features of neuropathy, myopathy, and normal the learning rate was adjusted to 10-2 and gradient descent was applied.

There two major methods of aggregated probabilities corresponding to neuropathy, myopathy, and normal of the segment from nEMG signal data for each muscle, hard voting and soft voting. The former is to select one item with the highest probability for each segment, count the number of selected items and finally select the one that occupies the largest number among them. On the other hand, the latter is to select items with highest probabilities after averaging each probability from each segments. In the case of hard voting, where only values with high probability are selected for each segment, data loss might occur, so soft voting was used to reduce data loss. The most probable diagnosis obtained through soft voting in the segment is the muscle prediction score, and the subject prediction score is the soft voting of all muscles by subject after soft voting in the segment.

The classifier to distinguish neuropathy, myopathy, and normal was obtained in two ways and the classified results were compared. First, it was determined through logistic regression analysis with the subject features of each group as the independent variables and the diagnosis as the dependent variable; Second, it was determined by additionally considering muscle locations as an independent variables.