Input sequence window: 1 X 31

Input feature vector 39 X 31

Convolution

MaxPool

Flatten

Fully Connected with Dropout

Output: residue i's numeric propensity for protein binding

Save the weights of the Convolution layer after fine-tuning

Input sequence window: 1 X 31

Input feature vector 39 X 31

Bidirectional GRU

Flatten

Fully Connected with Dropout

Output: residue i's numeric propensity for protein binding
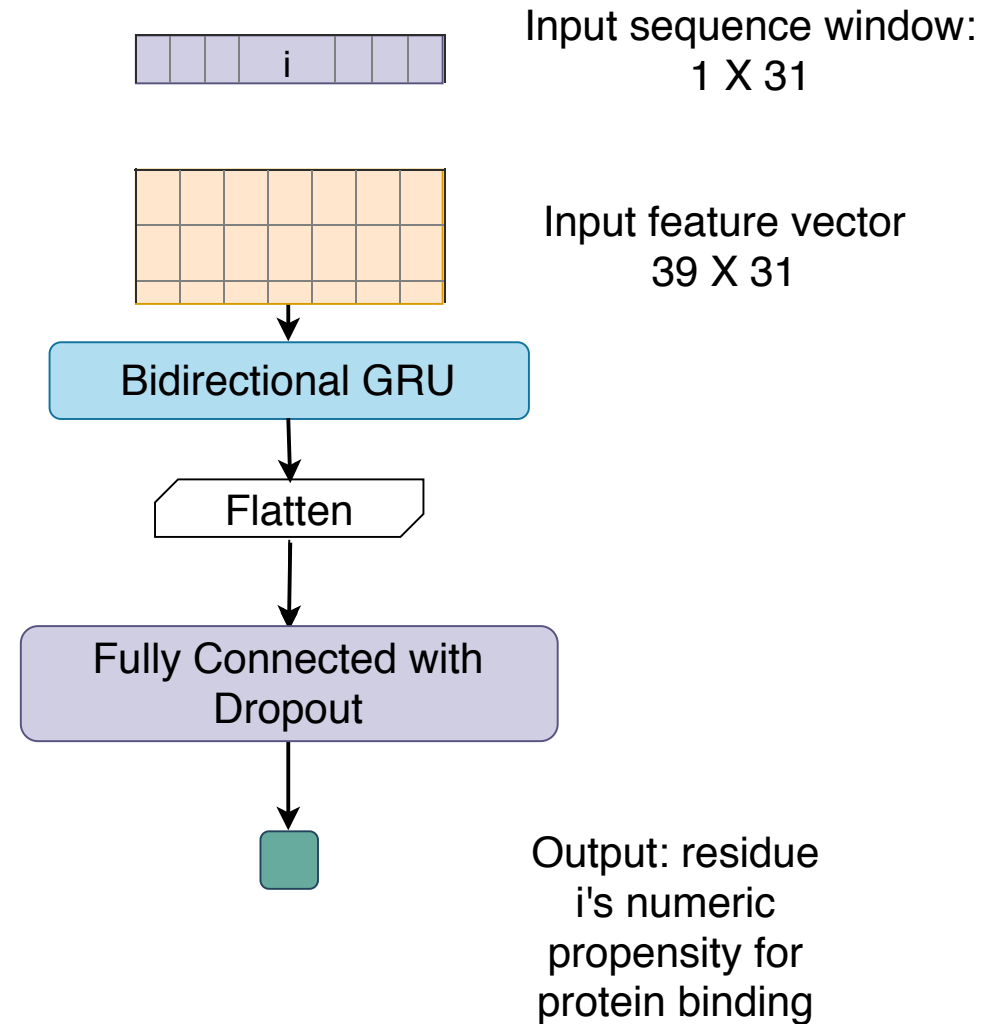
Save the weights of the GRU layer after fine-tuning

Input sequence window: 1 X 31

Input feature vector 39 X 31

Convolution

Bidirectional GRU

MaxPool

Flatten

Flatten

Concatenate

Fully Connect with Dropout

Output: residue i's numeric propensity for protein binding
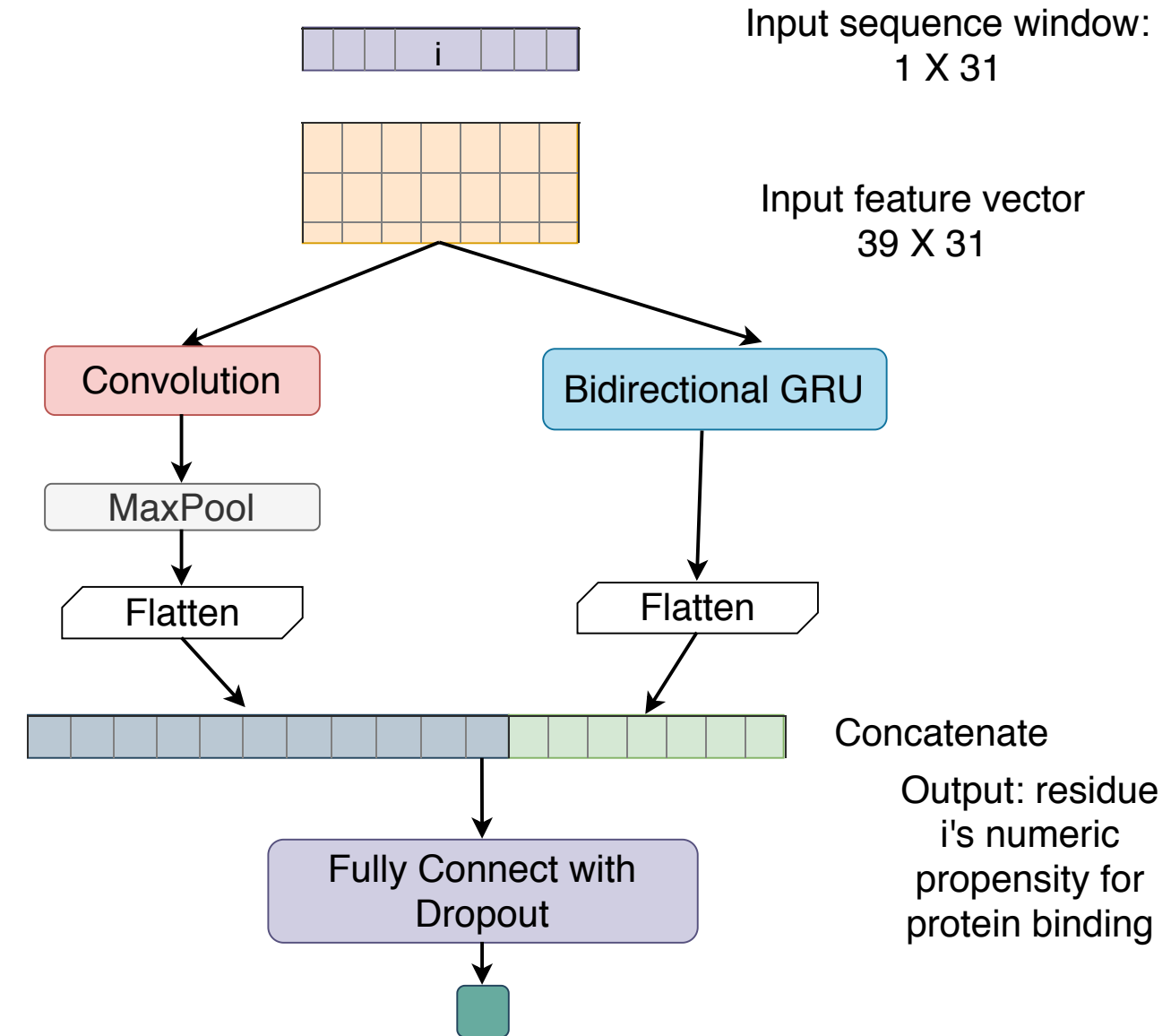
Load the weights of the Convolution and GRU layers