Classifying Muscle Parameters with Long-Short Term Memory Networks and Simulated Lateral Pinch Data

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Introduction: Current musculoskeletal models of the thumb rely on the estimation of over 109 parameters that define joint motion, muscle and bone geometry, and muscle architecture [1]. Many of these parameters are challenging to experimentally measure, which impedes development of subject-specific models and simulations. Machine learning, however, may provide an effective tool for predicting these difficult to measure parameters. In this study, we evaluate whether recurrent neural networks can accurately predict isolated changes in muscle architectural parameters using only lateral pinch strength. We choose to specifically examine recurrent neural networks because this approach can identify dependencies across time, which are important when studying dynamic, human movements.

Materials and Methods: A biomechanical dataset was created by running 120 lateral pinch simulations in OpenSim v 3.3 [2]. For each simulation, the input musculoskeletal model of the wrist and thumb [1] was varied by changing the maximum isometric force of the *abductor pollicis longus* (APL). The output of each simulation was a three-component vector representing dynamic changes in pinch force versus time. Note, that maximum isometric force cannot be directly measured using current experimental methods, while pinch force can be easily measured using a force sensor. The time-series force data was then input into a recurrent neural network designed to classify differences in the APL muscle architecture. Specifically, a long-short term memory (LSTM) algorithm [3] was implemented with 4 input nodes (time and three-component force vectors), 2 output nodes (small vs. large APL maximum isometric force), 4 hidden nodes, and a learning rate of 0.0001. Cross validation was completed using both 5-fold and 10-fold methods. Accuracies and losses for each k-fold method were analyzed.

Results and Discussion: The peak average accuracy for the 5-fold and 10-fold cross validation methods were 87.5% and 93.4%, respectively. The confidence interval of the accuracy decreased with the implementation of the 10-fold validation process, indicating a more consistently accurate model. However, the training losses increased, possibly indicative of a too high learning rate. These results suggest that the present LSTM framework may be used to accurately predict muscle architectural parameters, such as maximum isometric force, but learning rates should be adjusted as needed to fit k-fold validation architectures.

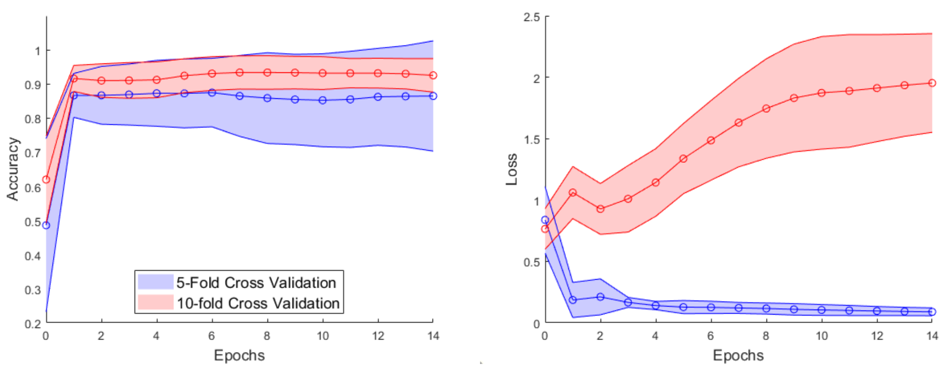

Figure 1. Average test accuracy (left) and average training loss (right) across epochs. Shaded regions represent 95% confidence intervals.

Conclusions: This work informs the future development of machine learning frameworks for analyzing biomechanical time-series datasets. Future work may incorporate more input nodes to represent variations in additional muscle parameters as well as examine more complex biomechanical systems and movements.

References: [1] Nichols et al. *J Biomech.* 2017. 58:97-104. [2] Delp et al., *IEEE Trans Biomed Eng.* 2007. 54(11):1940-50. [3] Gamboa. *Seminar on Collaborative Intelligence* 2016.