INFERENCE OF COMPACT ANALYTICAL FUNCTIONS DESCRIBING TENDON ROUTING IN THE FINGERS

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INTRODUCTION

Computational modeling of biomechanical systems often requires explicit analytical functions representing changes in tendon excursions with joint angles. This is particularly important for the simulation of musculoskeletal dynamics to test theories of motor control where moment arms (obtained by taking partial derivatives of these expressions with joint angles [2]) need to be evaluated iteratively several thousand times. Conventionally, these expressions for tendon excursions are assumed to be of polynomial form and the coefficients are regressed from experimental data obtained from cadaveric specimens (Eg. [2]). Here we present a novel method based on symbolic regression that infers both the form of the analytical functions as well as the parameter values directly from experimental data. We apply it to the inference of analytical functions representing tendon routings in the index finger.

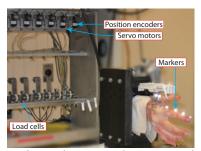


Figure 1: Experimental setup used to generate joint angletendon excursion dataset.

METHODS

We applied a constant tension of 5N on the seven tendons of the index finger (flexor digitorum profundus (FDP), flexor digitorum superficialis (FDS), extensor indicis (EI), extensor digitorum communis (EDC), first lumbrical (LUM), first dorsal interosseous (FDI), and first palmar interosseous (FPI)) of a fresh-frozen cadaveric hand using servo dc motors (Fig. 1). We then moved the finger manually to span the full fourdimensional joint configuration space (ad-abduction at the metacarpophalangeal joint (MCP) and flexion extension at the MCP, the proximal interphalangeal joint (PIP) and the distal interphalangeal joint (DIP). We recorded tendon excursions using optimal encoders and calculated joint angles from marker positions obtained using a Vicon motion capture system. The joint angles and tendon excursion dataset was then divided into a training data set, a cross-validation dataset (interpolated datapoints) and an extrapolation (datapoints outside the range of training). We then used a software package called Eureqa [3] that implements symbolic regression using genetic programming to infer both the form and the parameter values of analytical functions mapping joint angles to each tendon's excursions using the training dataset. We used root mean squared error between measured and

predicted tendon excursions as a measure of the fitness error. We compared errors of these analytical functions against those obtained using polynomial regression, the state-of-the-art technique used in musculoskeletal modeling.

RESULTS

Eureqa gives a family of solutions lying on the Pareto front of the fitness error-complexity plane (complexity defined by number of parameters) and we chose the expressions with smallest extrapolation errors as the optimal solutions. Figure 2 shows the comparison against polynomial regression and sample results for one of the tendons (FDS).

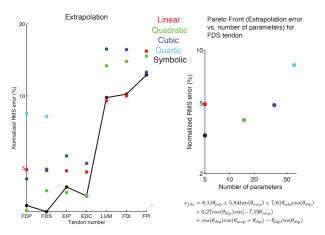


Fig 2: Comparison of symbolic vs. polynomial regressions.

DISCUSSION & CONCLUSIONS

Analytical functions obtained using Eureqa are more accurate than (or in some cases, comparable to) polynomial regressions when tested with cross-validation as well as extrapolated data. They are more compact, require fewer parameters and they do not tend to overfit to the training dataset. Hence, they are more suitable than state of the art, polynomial regressions, to model musculoskeletal systems.

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