Human Musculoskeletal Dynamics Modeling: Current Research and Objectives

Laura Hallock
Ruzena Bajcsy
Semiautonomous Seminar
2017.08.25
Human-Assistive Robotic Technologies (HART) Lab

OVERVIEW
HART Lab Ecosystem

Levels of human modeling abstraction
People (Musculoskeletal Modeling)

UC Berkeley

- R. Bajcsy
- R. Matthew
- L. Hallock
- S. Seko
- J. Zhang
- A. Sy
- S. Sharma
- I. McDonald
- D. Ho
- Y. Tuo
- L. Howard
- S. Nair
- P. Kiran

Stanford

- O. Khatib
- S. Menon
- T. Migimatsu
Why model musculoskeletal dynamics?

Human dynamics modeling is essential for many applications.

- understanding forces imperative in physical HRI
- non-physiological models cannot sufficiently predict dynamics
Why model musculoskeletal dynamics?

Human dynamics modeling is essential for many applications.

- understanding forces imperative in physical HRI
- non-physiological models cannot sufficiently predict dynamics

It’s also difficult.

- complex dynamical system
- morphological variation
- limited sensing (esp. non-invasive)
Objectives & Approach

We seek to:

• develop a dynamical modeling framework of the human arm
• understand the assumptions made when simplifying these models
Objectives & Approach

We seek to:

• **develop a dynamical modeling framework** of the human arm
• **understand the assumptions made** when simplifying these models

For clarity, we define:

• **Project 1**: building a predictive dynamics model of the human arm using multiple sensors (sEMG, AMG, ultrasound, etc.) (**UCB**)
• **Project 2**: characterizing model quality via multi-subject MRI (**Stanford-UCB collaboration**)

Building a Predictive Dynamics Model: Multi-Sensor “Minimal Modeling” of the Human Arm
Goal: Predictive Upper-Limb Model

- predicts contact forces / joint torques of interest
- accommodates musculoskeletal pathology
  - injury
  - disease (e.g., MD)
- individualized
- computationally tractable
Existing Human Dynamics Models

- **(Static) Morphological Data**
  - (MRI, ultrasound)
- **Real-Time Data**
  - (sEMG, AMG, motion capture, ultrasound)
- **Morphological Assumptions**
  - (biomechanics tables, literature values)
- **Contextual Assumptions**
  - (gait cycle, motion primitives)

**DYNAMICS MODEL**

- **Dynamics**
  - (contact forces, joint torques)

**PI: Building a Predictive Dynamics Model**
Our Objective

(Static) Morphological Data
(MRI, ultrasound)

Real-Time Data
(sEMG, AMG, motion capture, ultrasound)

DYNAMICS MODEL

Dynamics
(contact forces, joint torques)

Morphological Assumptions
(biomechanics tables, literature values)

Contextual Assumptions
(gait cycle, motion primitives)
Starting Point: Simplified Model

- single individual
- elbow joint (hinge)
- single aggregate “muscle”
- static

// Diagram and equations

MUSCLE MODEL

\[ F_m = \bar{a} F_0 (\beta_1 \bar{l}^2 + \beta_2 \bar{l} + \beta_3) \]

\[ \bar{l} = \frac{l}{l_{opt}} \]

\[ l = h(r_u, r_l, \theta) \]

assumed morphological parameters

\[ m, F_0, r_u, r_l, l_{opt} \]

normalized muscle activation

\[ \bar{a} = \frac{a}{a_{max}} \]

elbow angle

\[ \theta \]

elbow torque

\[ \tau = g_1(F_m) = g_2(m, F_{in}, \tau_{in}) \]
Starting Point: Simplified Model

- single individual
- elbow joint (hinge)
- single aggregate “muscle”
- static

If we measure \((\bar{a}, \tau, \theta)\), can we infer \(B = [\beta_1 \quad \beta_2 \quad \beta_3]^T\)?
Starting Point: Simplified Model

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Starting Point: Simplified Model

If we measure \((\bar{a}, \tau, \theta)\), can we infer \(B = [\beta_1 \quad \beta_2 \quad \beta_3]^T\)?

By examining many discrete coordinate pairs \((\bar{a}, \tau, \theta)\), we can write the system dynamics as

\[
\begin{bmatrix}
\tau_{in,1} + rF_{in,1} - \frac{1}{2}mg \sin \theta_1 r \\
\vdots \\
\tau_{in,n} + rF_{in,n} - \frac{1}{2}mg \sin \theta_n r 
\end{bmatrix}
= 
\begin{bmatrix}
\tau_1 \\
\vdots \\
\tau_n 
\end{bmatrix}
= F_0 r_1 r_u 
\begin{bmatrix}
\frac{1}{l_{opt}} \sin \theta_1 \bar{a}_1 \\
\vdots \\
\frac{1}{l_{opt}} \sin \theta_n \bar{a}_n 
\end{bmatrix}
\begin{bmatrix}
\frac{1}{l_1} \sin \theta_1 \bar{a}_1 \\
\vdots \\
\frac{1}{l_n} \sin \theta_n \bar{a}_n 
\end{bmatrix}
\begin{bmatrix}
\beta_1 \\
\beta_2 \\
\beta_3 
\end{bmatrix}
\]

which admits linear least-squares optimization

\[
\min_B \|T - WB\|_2^2
\]

to allow the fitting of \(B\) from experimental data.
Activation ($\bar{\alpha}$) Measures: sEMG and AMG

**sEMG** (surface electromyography)
- sensitive, noisy
- aggregate
- based on neurological signals
  
  *neurological disorder $\rightarrow$ poor signal*
- well-explored
- industry standard

**AMG** (acoustic myography)
- improved SNR
- aggregate
- based on physiological signals
- novel
Sample Activation Data

sEMG

AMG
Activation ($\bar{a}$) Measures: Ultrasound

3D View

Muscle Cross-Section

Inactive

Active

Force

Force

Ultrasound Measures

PI: Building a Predictive Dynamics Model
Experimental Setup

~230 \((\ddot{a}, \tau, \theta)\) data points

- \(\ddot{a}\) via single-channel (biceps)
  - sEMG
  - AMG
  - ultrasound
- \(\tau\) via F/T sensor (mounted to UR5 robot)
- \(\theta\) calculated from images (13 waypoints)

50% training, 50% testing (randomly assigned)
Preliminary Results: sEMG vs. AMG

Using both sEMG and AMG:

- **predicted force** using fitted $B$ is reasonable (~5-10% mean error over test set)
Preliminary Results: sEMG vs. AMG

Using both sEMG and AMG:

- **predicted force** using fitted $B$ is reasonable (~5-10% mean error over test set)

- **predicted force-length relation** is biologically reasonable but differs across sensors
  - max force at reasonable location $\Rightarrow l_{opt}$ accurate
  - normalization unreasonable $\Rightarrow F_0$ inaccurate
  - more investigation into other parameters needed
Preliminary Results: Ultrasound

WP 1
(25°)
(extended)

WP 5
(69°)

WP 13
(117°)
(flexed)
## Preliminary Results: Ultrasound

<table>
<thead>
<tr>
<th>WP</th>
<th>Degree</th>
<th>No Force</th>
<th>Max Force</th>
</tr>
</thead>
<tbody>
<tr>
<td>WP 1</td>
<td>25°</td>
<td><img src="image1.png" alt="Image" /></td>
<td><img src="image2.png" alt="Image" /></td>
</tr>
<tr>
<td>WP 5</td>
<td>69°</td>
<td><img src="image3.png" alt="Image" /></td>
<td><img src="image4.png" alt="Image" /></td>
</tr>
<tr>
<td>WP 13</td>
<td>117°</td>
<td><img src="image5.png" alt="Image" /></td>
<td><img src="image6.png" alt="Image" /></td>
</tr>
</tbody>
</table>
**Open question**: could particle tracking yield insight into **dynamics**, or only kinematics?
Current Work: US Muscle Deformation Model

Key questions:

• Can we differentiate muscle deformation associated with kinematic configuration from deformation associated with force output?

• If we account for pure configuration-associated deformation, can we infer a clean relationship between force and deformation that can be used as a control signal?

Possible deformation models:

• cross-sectional area (CSA) changes
• volume changes
• superquadric models
• FEM
**Current Work: US Muscle Deformation Model**

**Model target:** elbow flexors (*biceps brachii, brachialis, brachioradialis*)

**Data set:**
- 3 subjects (1 F, 2 M)
- full arm ultrasound volumetric scan
- 4 elbow flexion angles, 0–90°
- 5 loading conditions
  - fully supported
  - gravity compensation only
  - light wrist weight (~225g)
  - medium wrist weight (~725g)
  - heavy wrist weight (~950g)
Current Work: US Muscle Deformation Model

Next step: segment elbow flexors and characterize deformation

full extension
(0°)

full flexion
(90°)
Future Work: Model Improvements

• Extract and incorporate morphological parameters from
  – MRI (bone volumes, muscle volumes, muscle attachment points)
  – ultrasound (PCSA, tendon length)

• Incorporate knowledge of AMG physics (cross-bridge cycling vs. vibrating string vs. unfused motor unit theory)

• Maintain “minimal modeling” framework while increasing complexity
  – multiple muscles
  – dynamic conditions (Hill model)
Future Work: “Sensor-Driven” Modeling

**Key ideas** moving forward:

- use **an abstraction** for each sensing modality that **generates reliable results**, even at the expense of detail (e.g., sEMG as binary signal)

- determine **which parameters/signals are most critical** to measure correctly, and focus on those

- use **optimization/control techniques** to use signals effectively (e.g., hybrid systems)
Characterizing Model Quality: Multi-Subject MRI Data Analysis and Dynamical Simulation
Motivation

There exist frameworks for human modeling . . .

• OpenSim / AnyBody
• task-specific models
• our own models
Motivation

There exist frameworks for human modeling . . .

• OpenSim / AnyBody
• task-specific models
• our own models

. . . but there do not exist frameworks that tell us how good these models are.
Goal: Quantify Model Accuracy

We seek to examine

- the morphological variation across subjects,
- existing frameworks’ ability to account for this variation, and
- the impact of this variation on dynamical model prediction accuracy

(specifically, for the human arm).
**Dataset: Upper-Limb MRI Scans**

- **~10 subjects**, full arm (hand through torso)

- vary in
  - age
  - health
  - height/weight
  - gender

- **4 separate scans** taken to improve contrast where possible, then stitched together in post-processing
  - hand, forearm, elbow (“bird cage” coil)
  - shoulder (no additional coil)
Approach

- **extract** parameters of interest
  - bone/muscle volumes
  - bone/muscle length
  - muscle-bone attachment points

*Segmented muscle data, Stanford 2016*
Approach

- **extract** parameters of interest
  - bone/muscle volumes
  - bone/muscle length
  - muscle-bone attachment points

- **compare** parameters
  - across subjects
  - across perturbed subjects
  - with best canonical model approximation (e.g., OpenSim)
Approach

- **extract** parameters of interest
  - bone/muscle volumes
  - bone/muscle length
  - muscle-bone attachment points
- **compare** parameters
  - across subjects
  - across perturbed subjects
  - with best canonical model approximation (e.g., OpenSim)
- **evaluate** each parameter’s impact on predicted dynamics (contact forces, joint torques) using Stanford’s SCL
Approach: Bone Segmentation

Arm bones of 4 subjects segmented using

- **MSER** (implemented in MATLAB) (*small* — e.g., *hand* — *bones*)
- **active contours** (built into itk-SNAP) (*larger bones*)
- **manual coloring** in itk-SNAP (*poor contrast* — e.g., *shoulder* — *bones*)
- **manual cleanup** (*required on ALL bones*)
Approach: Bone Segmentation

Arm bones of 4 subjects segmented using

- **MSER** (implemented in MATLAB) *(small — e.g., hand — bones)*
- **active contours** *(built into itk-SNAP) *(larger bones)*
- **manual coloring** *(poor contrast — e.g., shoulder — bones)*
- **manual cleanup** *(required on ALL bones)*

**extensive manual cleanup required!**
Preliminary Results: Hand/MSER
Preliminary Results: Hand/Manual
Preliminary Results: Forearm/AC
Preliminary Results: Forearm/Manual
**Approach: Muscle Segmentation**

Muscle segmentation presents further challenges:

- manual segmentation *prohibitively time-intensive* (*multiple months for single subject by Stanford collaborators*)
Approach: Muscle Segmentation

Muscle segmentation presents further challenges:

• manual segmentation **prohibitively time-intensive**

• **poorly suited** to generic blob/edge detection
  – large inter- and intra-subject contrast variation
  – muscle fascia hard to observe, even for humans
  – artifacts (stitching, motion, etc.)
Approach: Muscle Segmentation

Muscle segmentation presents further challenges:

- **manual segmentation** _prohibitively_ time-intensive
- **poorly suited** to generic blob/edge detection
- **significant non-affine variation** predicted across subjects
  - joint angles (likely need to match segments and stick them back together)
  - overall morphology
Approach: Muscle Segmentation

Muscle segmentation presents further challenges:

• manual segmentation **prohibitively time-intensive**
• **poorly suited** to generic blob/edge detection
• **significant non-affine variation**

→ **Instead of segmenting from scratch, map segmented muscles from one subject to another!**
**Approach:** Muscle Segmentation

**Goal:** Find best transformation $F : R \rightarrow T$

- (segmented) reference subject $R$
- target subject $T$
**Approach:** Muscle Segmentation

**Goal:** Find best transformation $F : R \rightarrow T$

(segmented) reference subject $R \in \mathbb{R}$

atlas

target subject $T$

$P2$: Characterizing Model Quality
**Goal**: Find best transformation $F : R \rightarrow T$

→ This is a canonical MRI registration problem (use same $F$ on raw scans and muscles), so we can explore existing libraries!

**Approach**: Muscle Segmentation

(segmented) reference subject $R \in \mathbb{R}$

$F$

target subject $T$

$P2: \text{Characterizing Model Quality}$
Approach: Muscle Segmentation as Registration

Our problem of finding $F : R \rightarrow T$ can be formulated as registration optimization problem

$$F^* = \arg \min_F -S(F; R, T)$$

**References**

- Similarity function (e.g., MI)
- Target image
- Reference image
- Optimal transformation
Approach: Muscle Segmentation as Registration

Our problem of finding $F : R \rightarrow T$ can be formulated as registration optimization problem

$$\mu^* = \arg \min_{\mu} -S(F_\mu; R, T)$$

optimal transformation parameters
**Approach: Muscle Segmentation as Registration**

Our problem of finding $F : R \rightarrow T$ can be formulated as registration optimization problem

$$\mu^* = \arg \min_{\mu} -S(F_{\mu}; R, T)$$

**Potential DoF**

- # similarity function classes
- # parameters $\mu$
**Approach: Muscle Segmentation as Registration**

Our problem of finding $F: R \rightarrow T$ can be formulated as registration optimization problem

$$
\mu^* = \arg \min_{\mu} -S(F_\mu; R, T) + \lambda P(F_\mu)
$$

**Potential DoF**

- # similarity function classes
- # parameters $\mu$
- # penalty function classes
- # $\lambda$ values
**Approach: Muscle Segmentation as Registration**

Our problem of finding $F : R \rightarrow T$ can be formulated as registration optimization problem

$$
\mu^* = \arg \min_{\mu} -S_{\theta_1}(F_{\mu}; R, T) + \lambda P_{\theta_2}(F_{\mu})
$$

**Potential DoF**

# similarity function classes
* # parameters $\mu$
* # penalty function classes
* # $\lambda$ values
* # similarity function parameters
* # penalty function parameters
Approach: Muscle Segmentation as Registration

Our problem of finding $F : R \rightarrow T$ can be formulated as registration optimization problem

$$\mu^* = \arg \min_\mu -S_{\theta_1}(F_\mu; R, T) + \lambda P_{\theta_2}(F_\mu)$$

Additionally, we have no convexity guarantees.
**Approach: Muscle Segmentation as Registration**

Our problem of finding $F : R \rightarrow T$ can be formulated as registration optimization problem

$$\mu^* = \arg \min_{\mu} -S_{\theta_1}(F_{\mu} ; R, T) + \lambda P_{\theta_2}(F_{\mu})$$

Additionally, we have **no convexity guarantees**.

→ must build **application-specific intuition** for parameter importance and begin optimization **close to good local optimum**

- **Potential DoF**
  - # similarity function classes
  - # parameters $\mu$
  - # penalty function classes
  - # $\lambda$ values
  - # similarity function parameters
  - # penalty function parameters
Most promising results thus far obtained via:

- **intensity-based** registration
- **multi-resolution image pyramids**: registered lower-resolution image initializes that of next highest resolution
- **weighted combination of transform types**: lower-DOF transform results initialize higher-DOF transform
**Approach:** Elastix Parameters

P2: Characterizing Model Quality
Particularly impactful parameters include:

- choice of similarity function
  - **mutual information** appears superior to mean squared difference
- penalty functions
  - **bending penalty** to avoid overfitting
  - **rigidity penalty** associated with areas known to be rigid (i.e., bones)
- error computation at each iteration
  - **uniformly random** voxels vs. random voxels **within a local neighborhood**
- number of iterations
Preliminary Results: Muscle Mapping (sim. only)
Preliminary Results: Muscle Mapping (bending pen.)
Preliminary Results: Muscle Mapping (ground truth)

... we’re working on it.
Preliminary bone segmentation results show significant morphological variation across subjects that cannot be modeled in existing frameworks.
Fig. 5. **Model Scaling Errors.** A. A canonical model’s radius bone side-by-side with an MRI-based subject-specific model’s radius bone. The subject-specific model is accurate to < 1nm, and considered to be ground truth. B. We scaled the canonical model to the subject’s radius with an affine transformation that optimized the distance between five hundred corresponding points between the two bones. C. The scaled canonical model was unable to match the geometry of the subject-specific model. Moreover, affine fits can be expected to be substantially worse when ground truth is unavailable.

*MRI vs. canonical, Stanford 2016*
Preliminary Results: Simulation

Fig. 3. Model Generation. A. MRI-based musculoskeletal models were obtained by segmenting high-resolution anatomical scans. Exemplar sagittal cross-sections for the shoulder are shown, matching the volumetric reconstruction below. B. The model generation pipeline consists of six stages. Stages 1 and 2 involved extracting three dimensional volumes for bones and muscles, Stage 3 involved slicing muscles normal to their direction of force. Stage 4 involved packing fiber-group actuator cross-sections into the muscle slices. Stage 5 involved associating actuator intersection circles across slices. And, finally, stage 6 involved connecting actuators to create piece-wise muscle approximations. Stages 3 and 4 may be parameterized to create families of models.
Preliminary Results: Simulation

Fig. 2. **Comparing Model Accuracy and Analysis Error.** A. Volumetric rendering of bones and muscles extracted from a subject’s anatomical MRI data. B. A family of models generated from the volumetric data. Skeletons are identical. The muscle model on the left very accurately captures muscle volumes (2.5mm radius and 2cm length fiber-group segments). The other two models are parametrically decimated by reducing the number of fiber groups per unit area, without dropping muscles. The musculature in the lower arm is better preserved since the muscles are more numerous and thinner, and thus lose less detail. C. Analyzing a family of MRI-based models with varying accuracy provides insights into the level of detail required for a given biomechanical analysis. A family of models with varying detail can help identify and avoid the model simplifications (or improvements) that increase errors. Ideal models have predictable errors.

*Model resolution comparison, Stanford 2016*
Next Steps

• morphology extraction
  – develop sufficiently fast segmentation pipeline (automated or manual or both)
  – complete segmentation (first bone, then muscle) of initial ~10-subject cohort

• (quantitative) morphology comparison

• dynamics model evaluation
  – validate existing optimization-based control scheme using additional sensing data (ultrasound, sEMG, AMG, etc.)
  – determine morphological parameters to which dynamics is most sensitive
  – characterize model changes across resolution
PROJECT I & II

CONCLUSIONS
Conclusions

By investigating both multi-sensor modeling of a single subject and large-scale morphological modeling of many subjects, we seek to generate a modeling framework that surpasses existing models in predictive accuracy while remaining useful in a wide range of applications.

{lhallock, bajcsy} @ eecs.berkeley.edu
hart.berkeley.edu
Papers

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Technical Reports
PROJECT I & II

FIN