Human Musculoskeletal Dynamics Modeling: Current Research and Objectives

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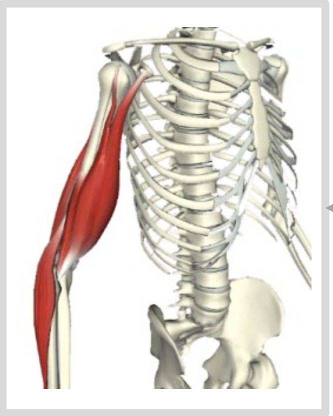
BCCI Seminar
2017.07.26

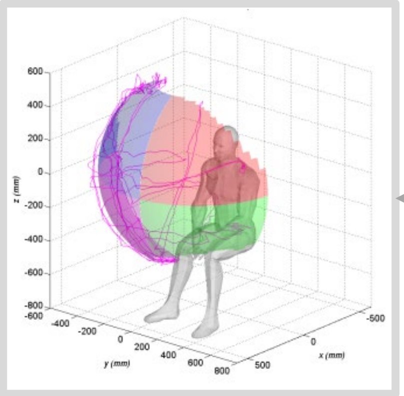
HART Lab
Human-Assistive Robotic Technologies

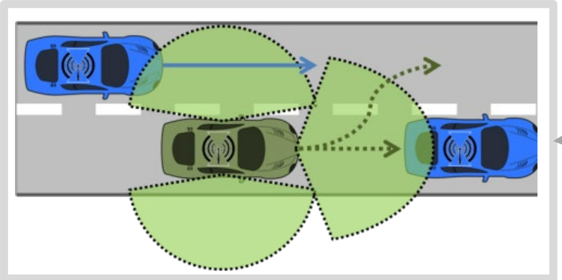
Human-Assistive Robotic Technologies (HART) Lab

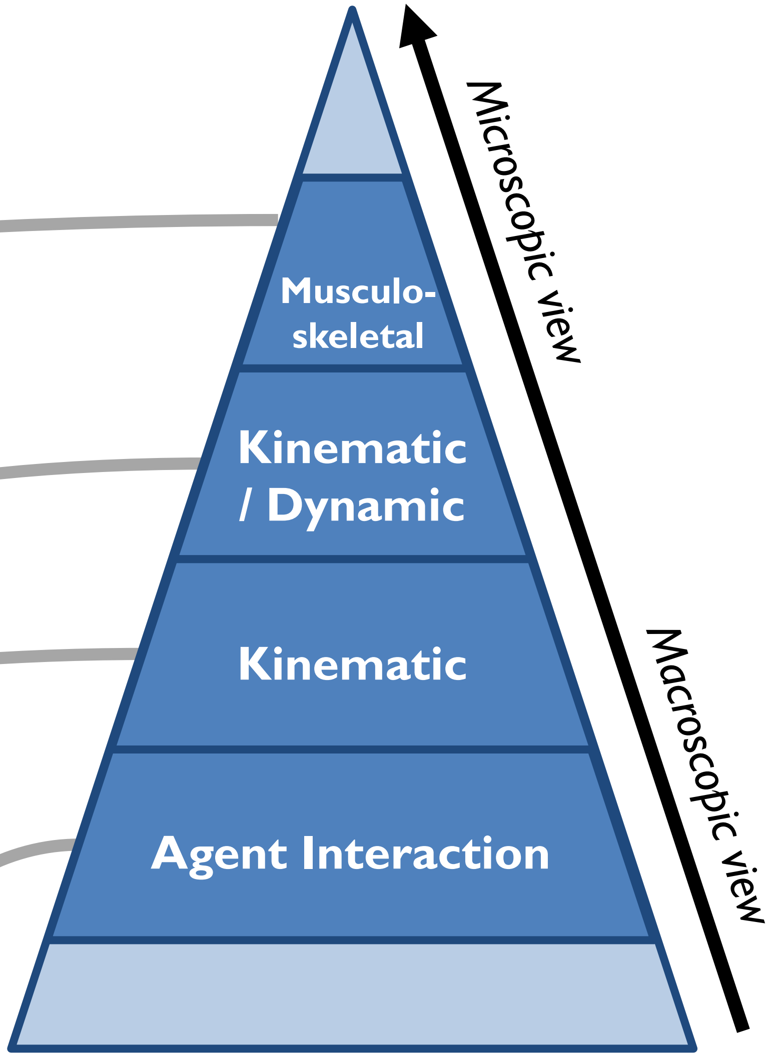
OVERVIEW

HART Lab Ecosystem









Levels of human modeling abstraction

People (Musculoskeletal Modeling)

UC Berkeley


R. Bajcsy


R. Matthew


L. Hallock

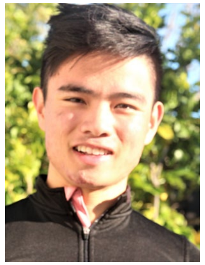

S. Seko


J. Zhang


A. Sy


S. Sharma


I. McDonald


D. Ho


Y. Tuo


L. Howard


S. Nair


P. Kiran

Stanford


O. Khatib

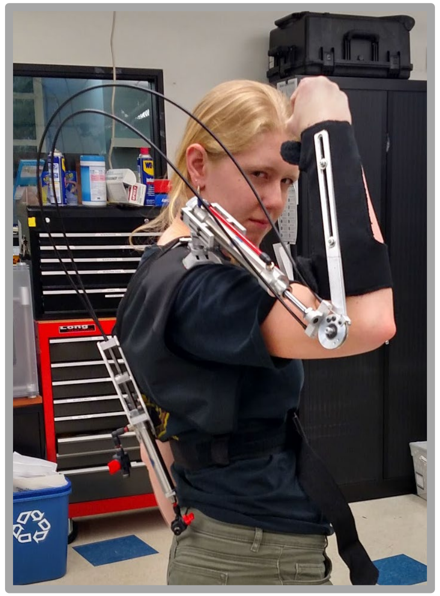

S. Menon


T. Migimatsu

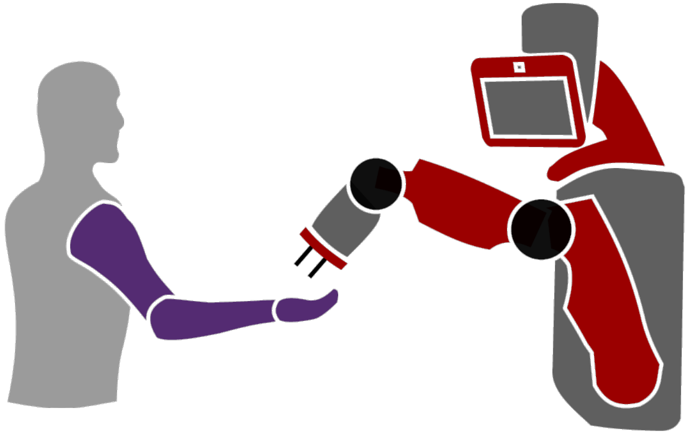
Why model musculoskeletal dynamics?

Human dynamics modeling is essential for many applications.

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



Gamma exoskeleton,
HART Lab 2016



Why model musculoskeletal dynamics?

Human dynamics modeling is essential for many applications.

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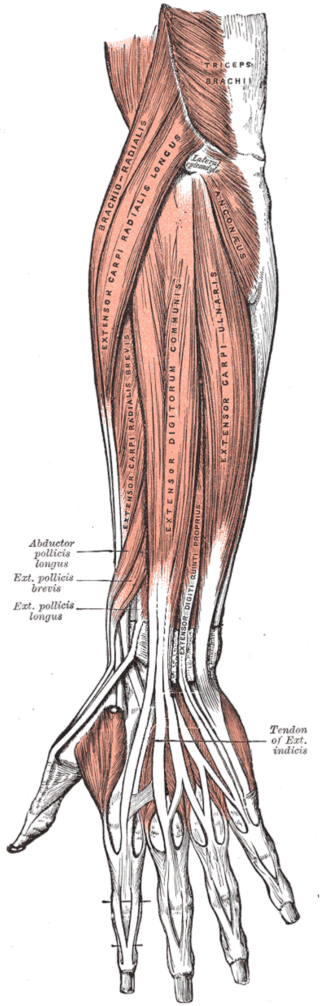
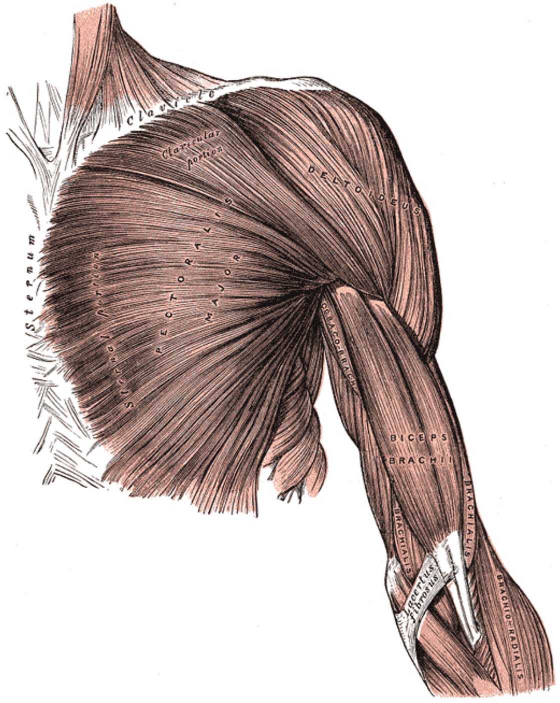
- non-physiological models cannot sufficiently predict dynamics

It's also difficult.

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





Gray's Anatomy, 1858

Objectives & Approach

We seek to:

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

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- **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*)

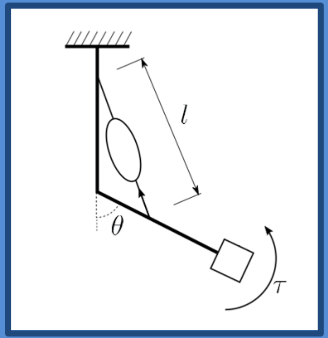
PROJECT 1 (*UCB*)

Building a Predictive Dynamics Model: *Multi-Sensor "Minimal Modeling" of the Human Arm*

Goal: Predictive Upper-Limb Model

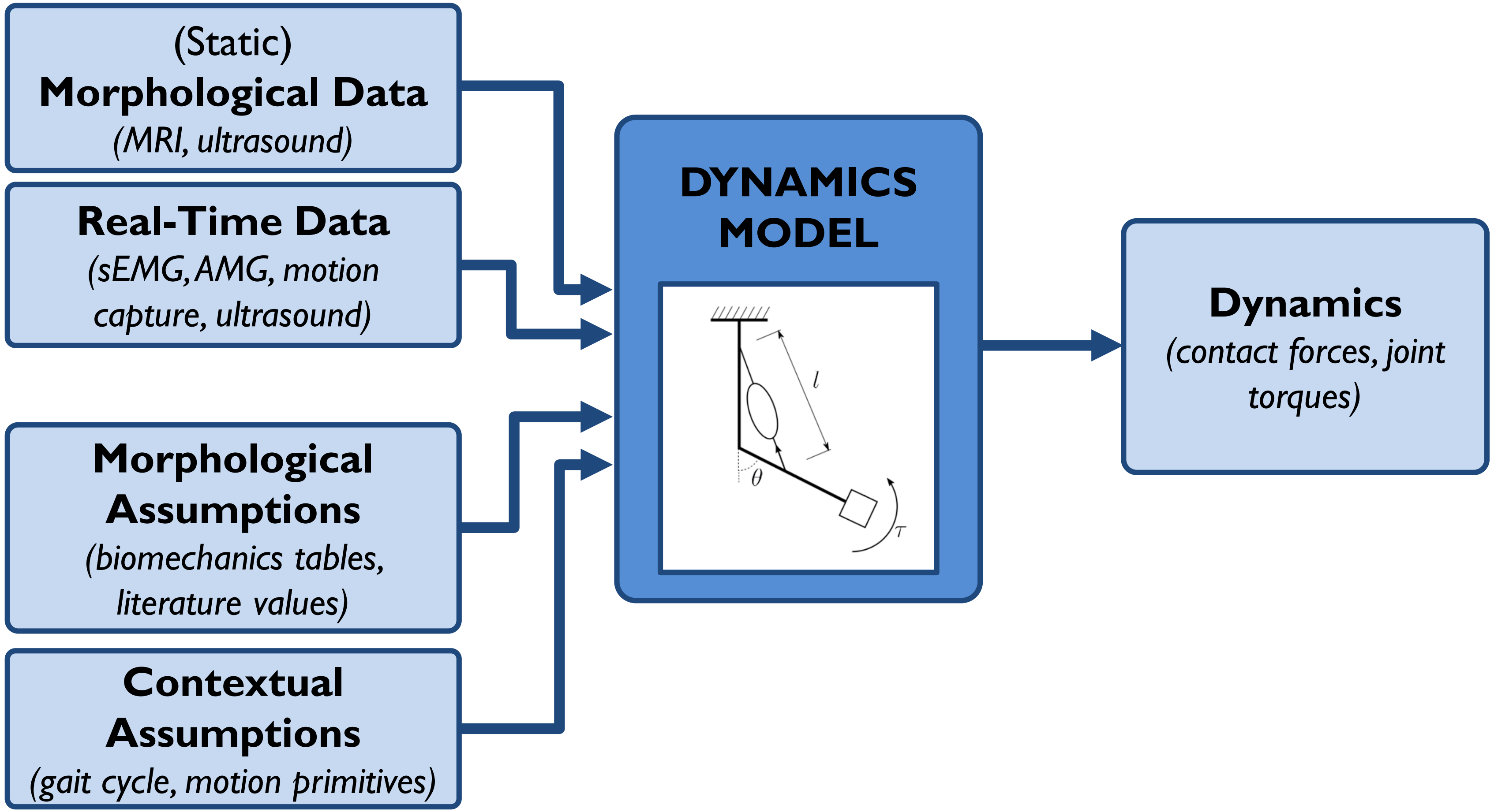
- predicts contact forces / joint torques of interest
- accommodates musculoskeletal pathology
  - injury
  - disease (e.g., MD)
- individualized
- computationally tractable

DYNAMICS MODEL



Dynamics
(contact forces, joint torques)

Existing Human Dynamics Models



Our Objective

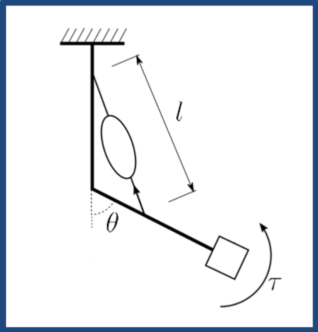
(Static)
Morphological Data
(MRI, ultrasound)

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

Morphological Assumptions
(biomechanics tables, literature values)

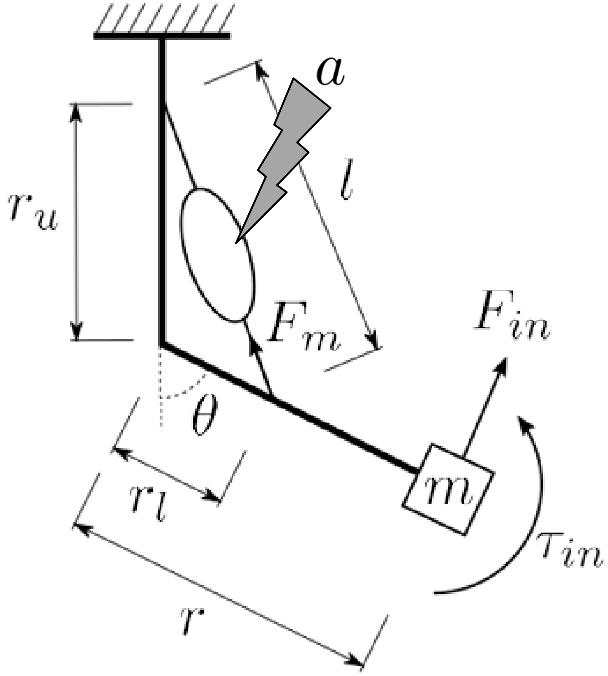
Contextual Assumptions
(gait cycle, motion primitives)

DYNAMICS MODEL



Dynamics
(contact forces, joint torques)

Starting Point: Simplified Model



- single individual
- elbow joint (hinge)
- single aggregate "muscle"
- static

assumed morphological parameters

$m, F_0, r_u, r_l, l_{opt}$

normalized muscle activation

$$\bar{a} = \frac{a}{a_{max}}$$

elbow angle

θ

MUSCLE MODEL

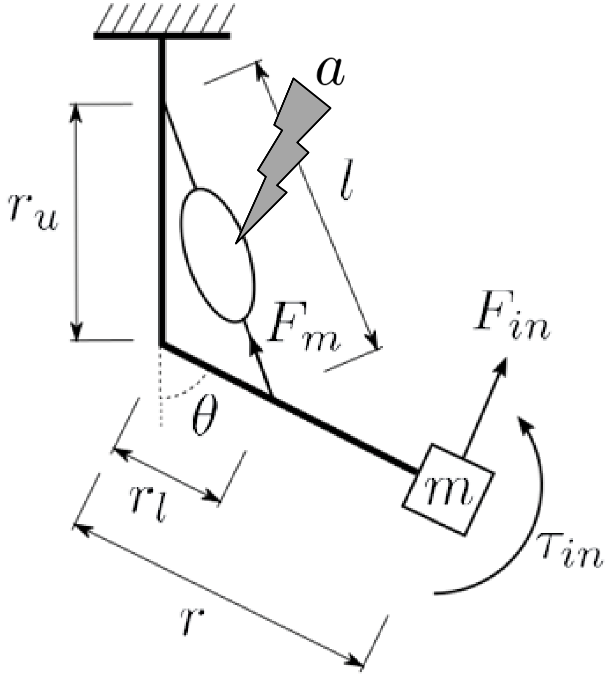
$$F_m = \bar{a}F_0(\beta_1\bar{l}^2 + \beta_2\bar{l} + \beta_3)$$

$$\bar{l} = \frac{l}{l_{opt}}, \; l = h(r_u, r_l, \theta)$$

elbow torque

$$\tau = g_1(F_m) = g_2(m, F_{in}, \tau_{in})$$

Starting Point: Simplified Model



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elbow torque
$$\tau = g_1(F_m) = g_2(m, F_{in}, \tau_{in})$$

If we measure $(\bar{a}, \tau, \theta)$, can we infer $B = \begin{bmatrix} \beta_1 & \beta_2 & \beta_3 \end{bmatrix}^\top$?

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

$$\begin{bmatrix} \tau_{in,1} + rF_{in,1} - \frac{1}{2}mg\sin\theta_1 r \\ \vdots \\ \tau_{in,n} + rF_{in,n} - \frac{1}{2}mg\sin\theta_n r \end{bmatrix} = \underbrace{\begin{bmatrix} \tau_1 \\ \vdots \\ \tau_n \end{bmatrix}}_{T} = \underbrace{F_0 r_l r_u \begin{bmatrix} \frac{l_1}{l_{opt}^2}\sin\theta_1\bar{a}_1 & \frac{1}{l_{opt}}\sin\theta_1\bar{a}_1 & \frac{1}{l_1}\sin\theta_1\bar{a}_1 \\ \vdots & \vdots & \vdots \\ \frac{l_n}{l_{opt}^2}\sin\theta_n\bar{a}_n & \frac{1}{l_{opt}}\sin\theta_n\bar{a}_n & \frac{1}{l_n}\sin\theta\bar{a}_n \end{bmatrix}}_{W} \underbrace{\begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \end{bmatrix}}_{B}$$

which admits linear least-squares optimization

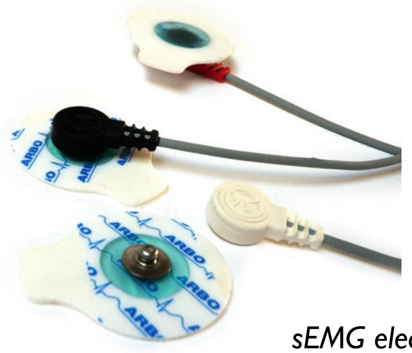
$$\min_B \|T - WB\|_2^2$$

to allow the fitting of B from experimental data.

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

sEMG (surface electromyography)

- sensitive, noisy
- aggregate
- based on neurological signals (*neurological disorder → poor signal*)
- well-explored
- industry standard



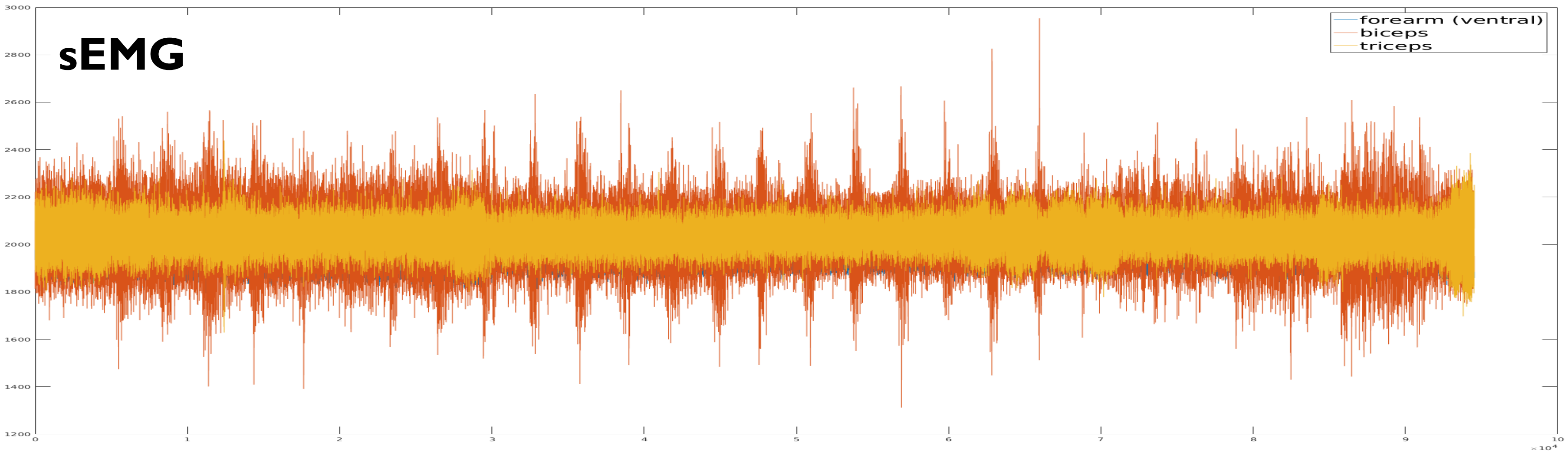
sEMG electrodes

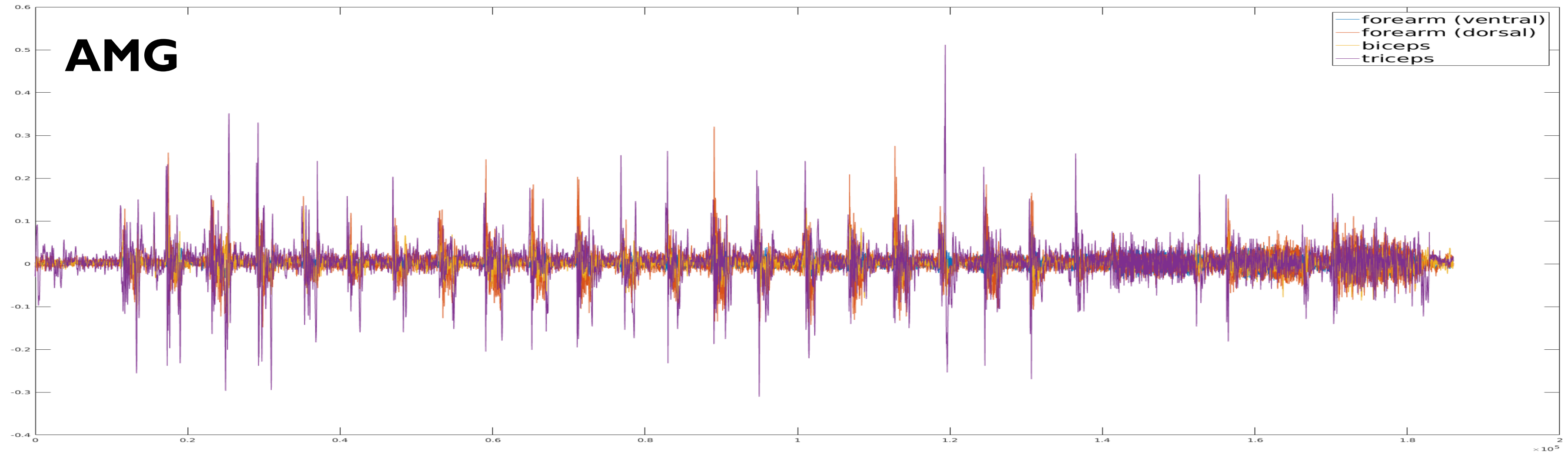
AMG (acoustic myography)

- improved SNR
- aggregate
- based on physiological signals
- novel

CURO

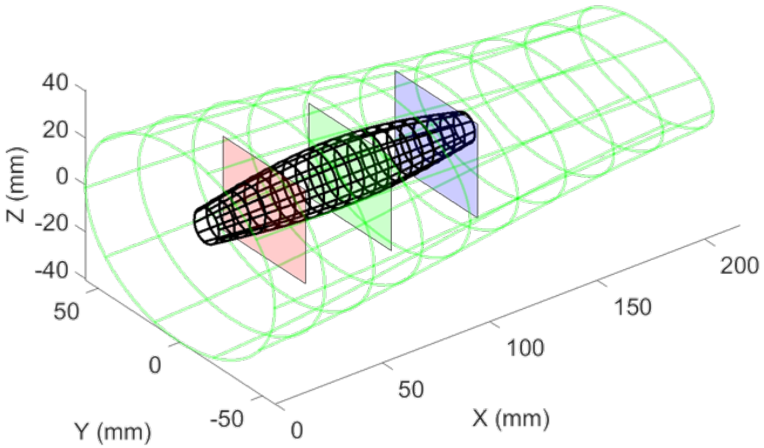
Sample Activation Data





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

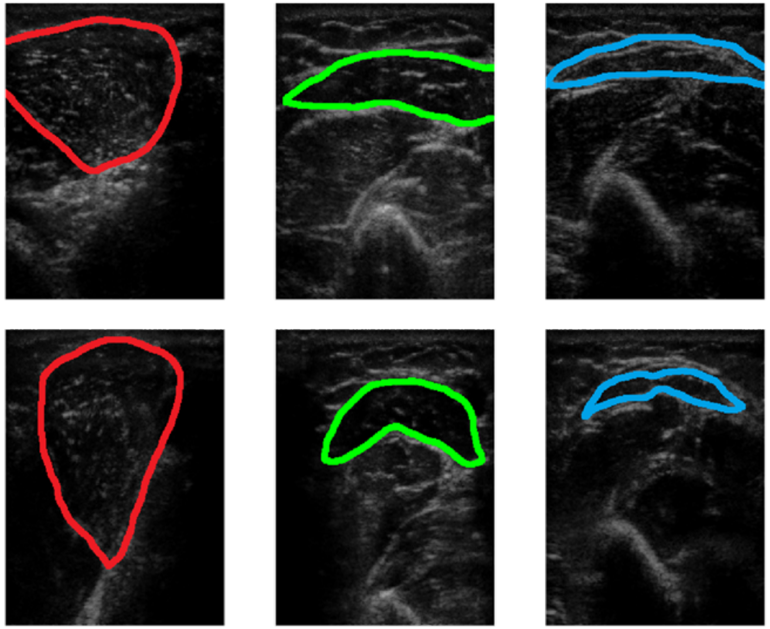
3D View

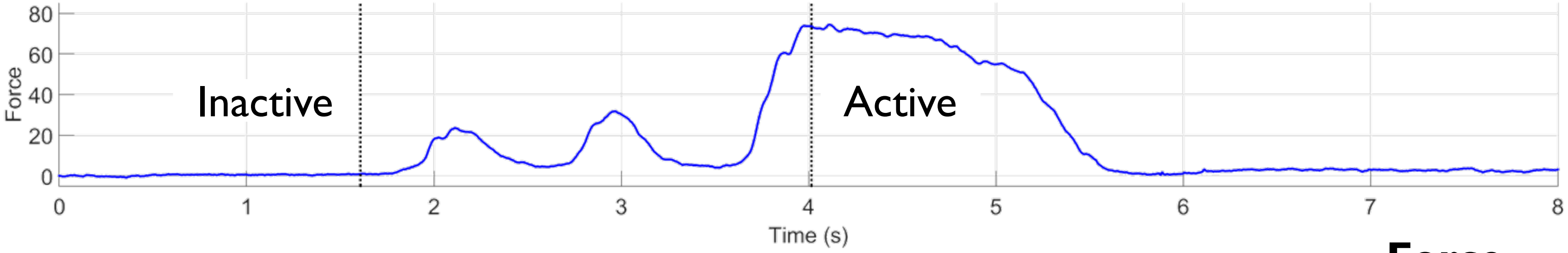


Muscle Cross-Section

Inactive

Active





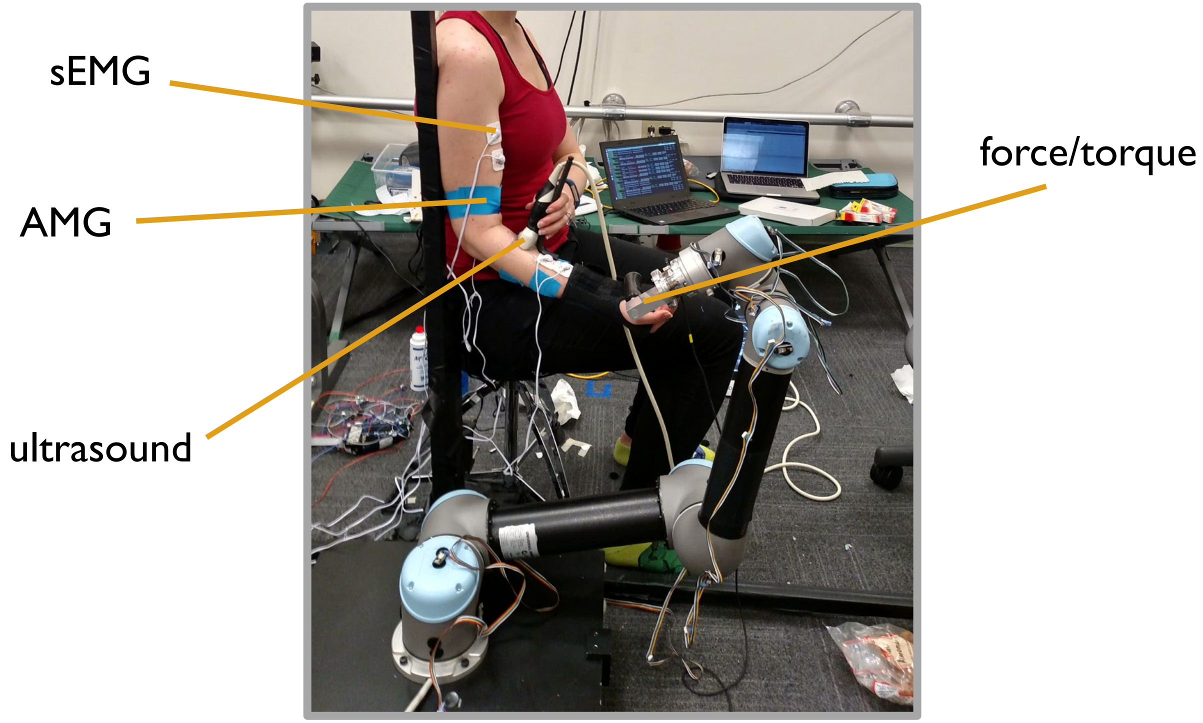
Force

Experimental Setup

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

- $\bar{a}$ via single-channel (biceps)
  - sEMG
  - AMG
  - ultrasound
- τ via F/T sensor (mounted to UR5 robot)
- θ calculated from images (13 waypoints)

50% training, 50% testing (randomly assigned)



Data collection, HART Lab 2017

Preliminary Results: sEMG vs. AMG

Using both sEMG and AMG:

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

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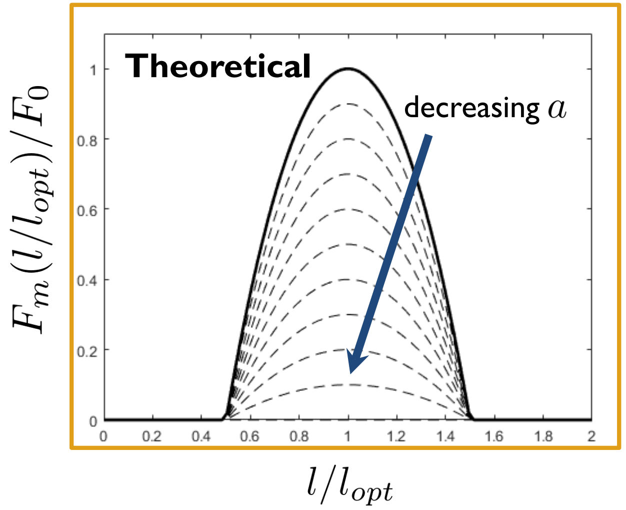
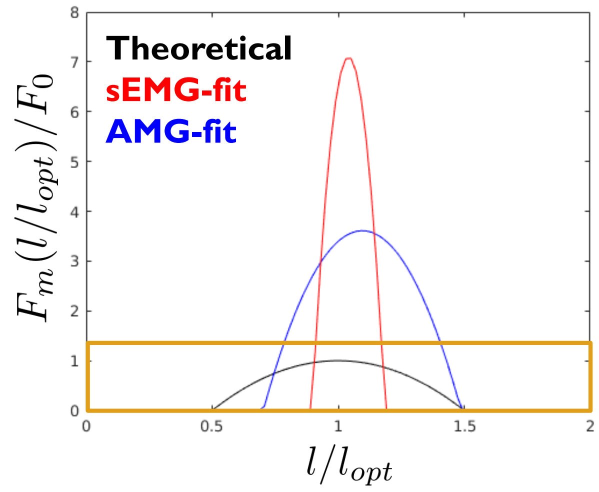
Using both sEMG and AMG:

- **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 → l_{opt} accurate
  - normalization unreasonable → F_0 inaccurate
  - more investigation into other parameters needed

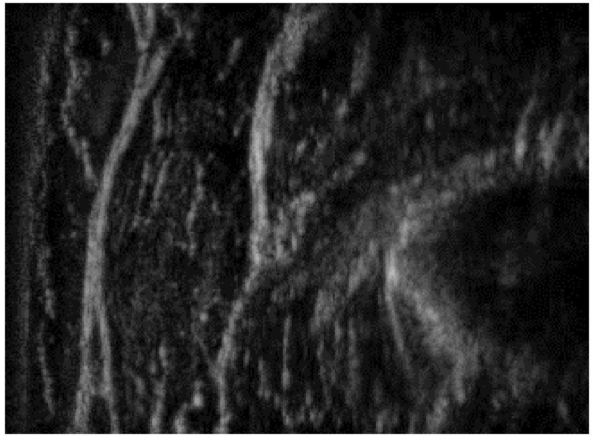




Preliminary Results: Ultrasound

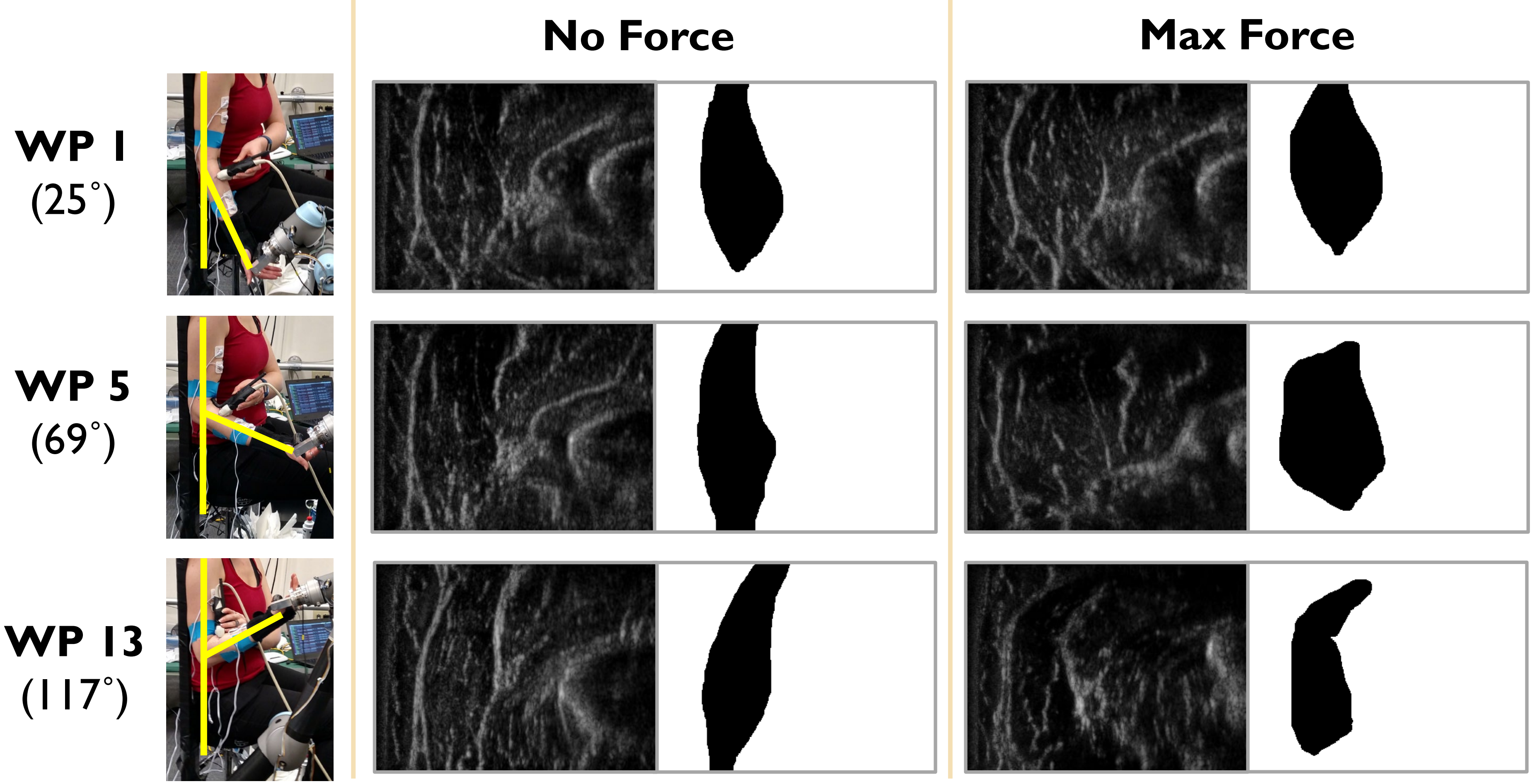
WP 1
(25°)
(extended)

WP 5
(69°)

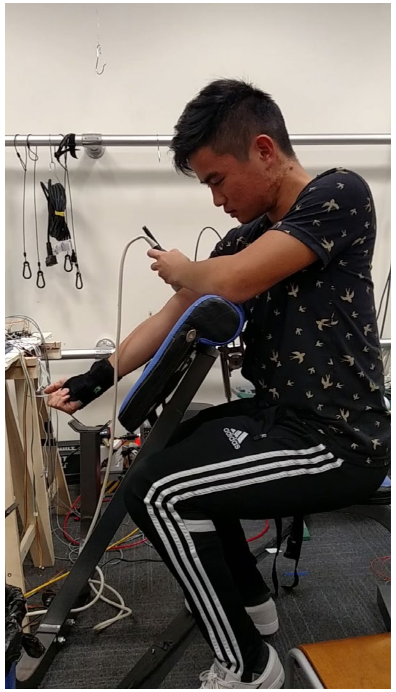


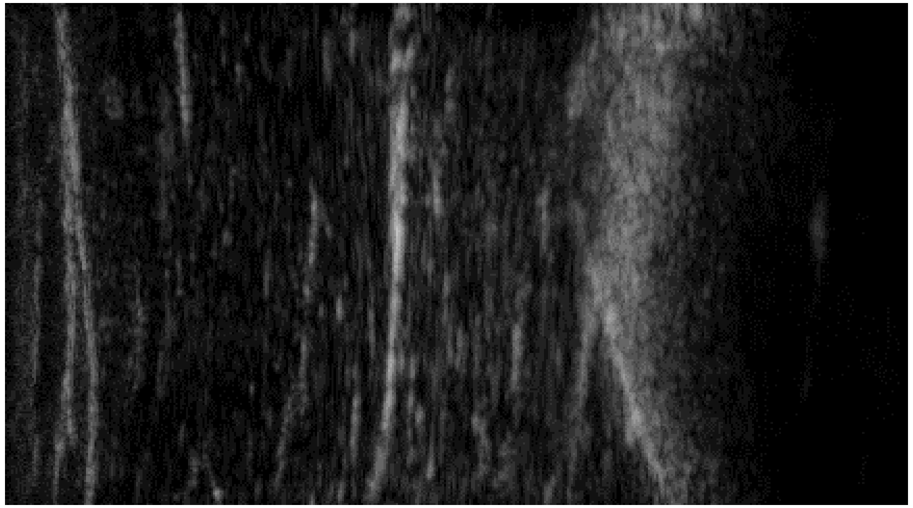
WP 13
(117°)
(flexed)

Preliminary Results: Ultrasound



Preliminary Results: Ultrasound





Open question: could particle tracking yield insight into **dynamics**, or only kinematics?

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)

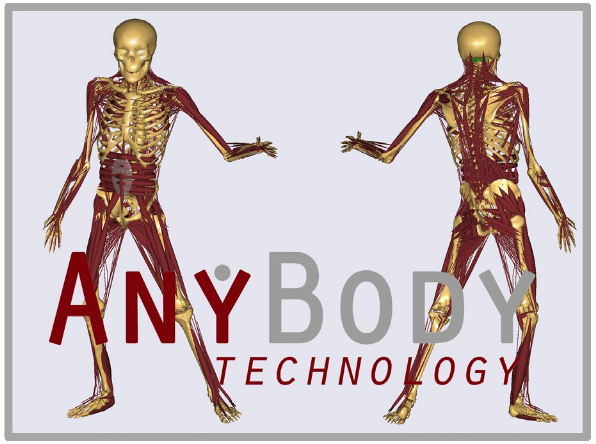
PROJECT II (*Stanford-UCB collaboration*)

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** . . .

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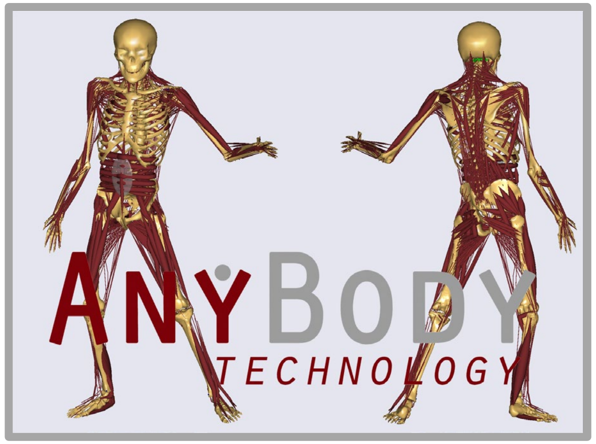
- task-specific models
- our own models

. . . 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

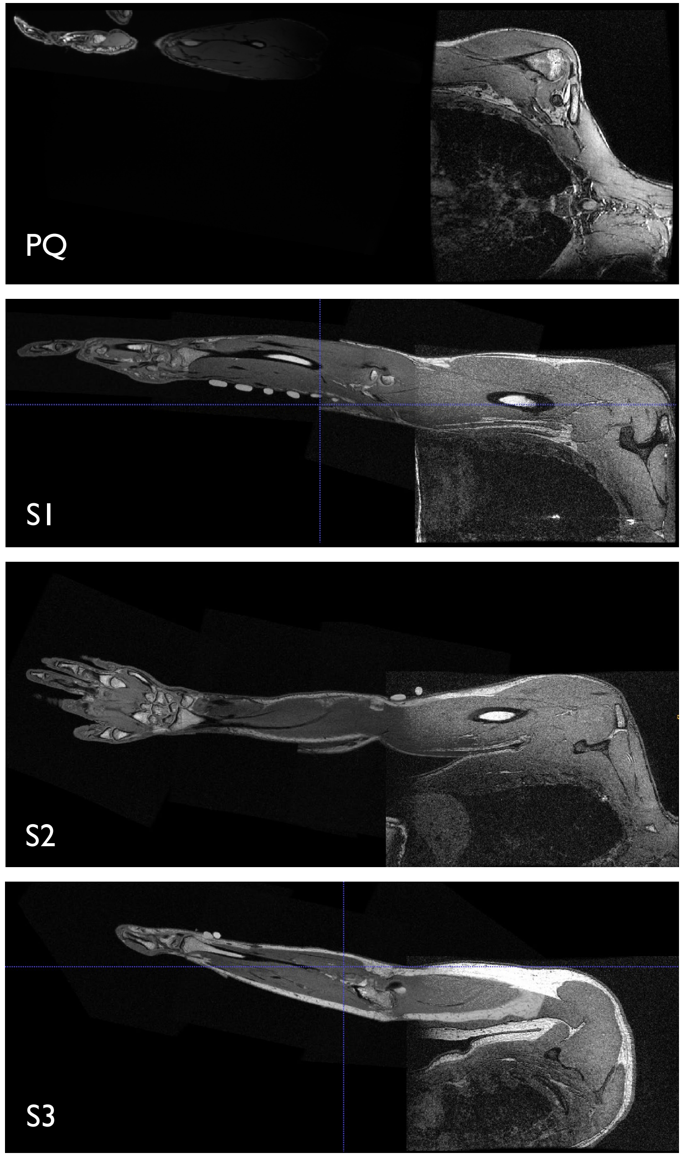
(specifically, for the human arm).

Dataset: Upper-Limb MRI Scans

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

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

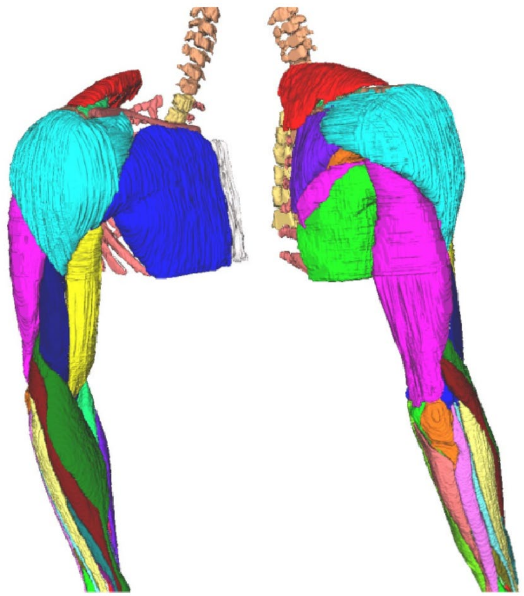
- **4 separate scans** taken to improve contrast where possible, then stitched together in post-processing
  - hand, forearm, elbow (“bird cage” coil)
  - shoulder (no additional coil)



. . .

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
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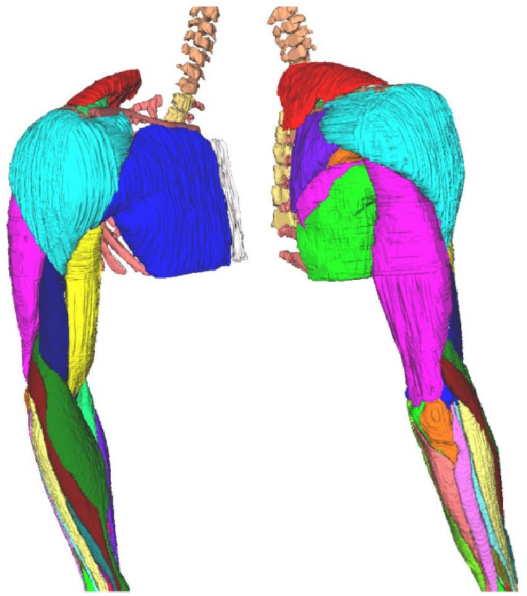
  - muscle-bone attachment points
- **compare** parameters
  - across subjects
  - across perturbed subjects
  - with best canonical model approximation (e.g., OpenSim)



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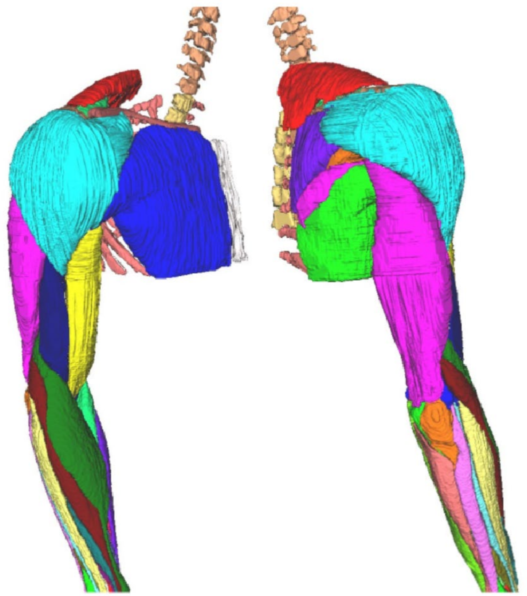
  - bone/muscle length
  - muscle-bone attachment points
- **compare** parameters
  - across subjects
  - across perturbed subjects
  - with best canonical model approximation (e.g., OpenSim)
- **evaluate** each parameter's impact on predicted dynamics (contact forces, joint torques) using Stanford's SCL



Segmented muscle data,
Stanford 2016

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)*

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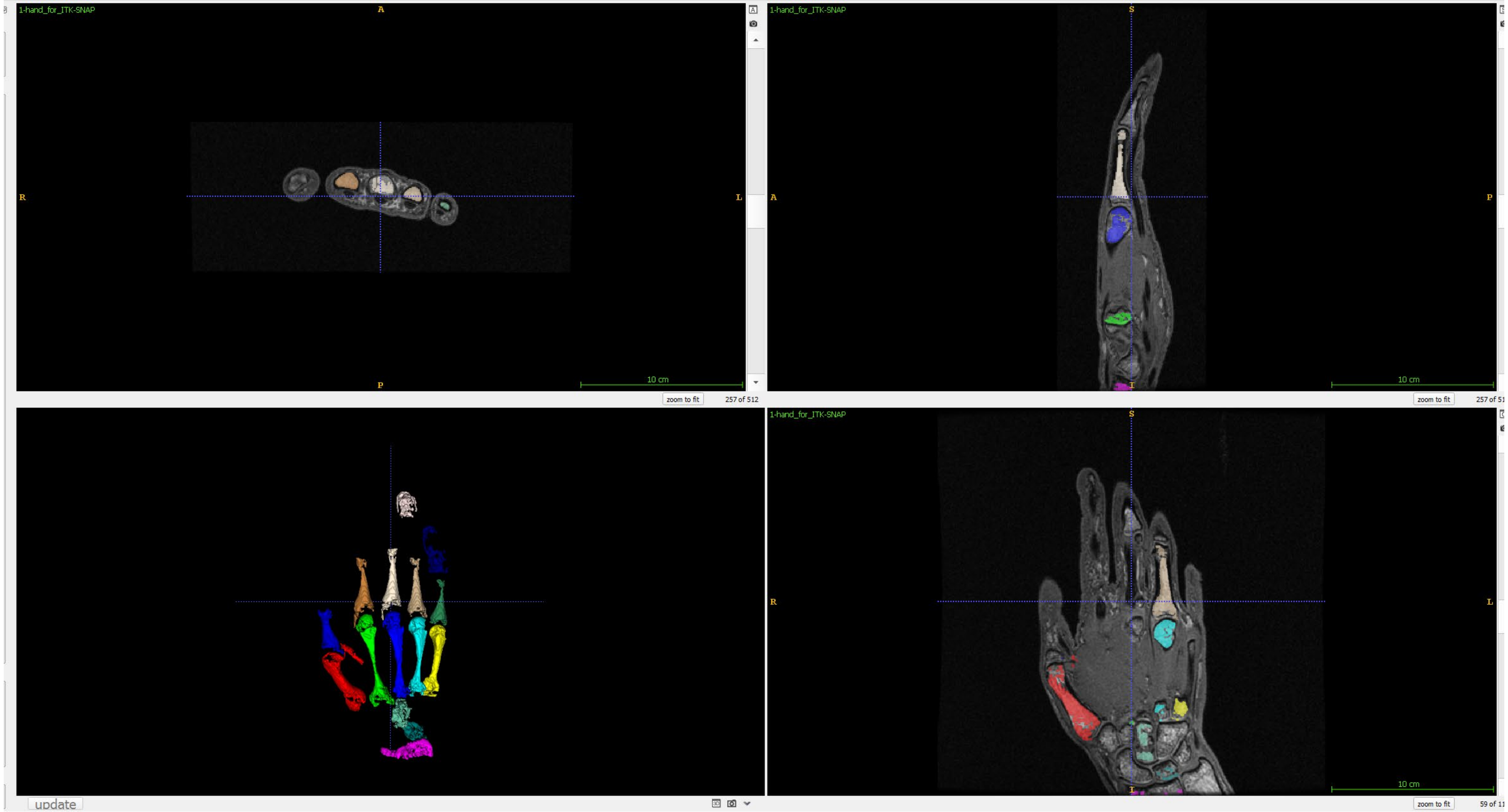
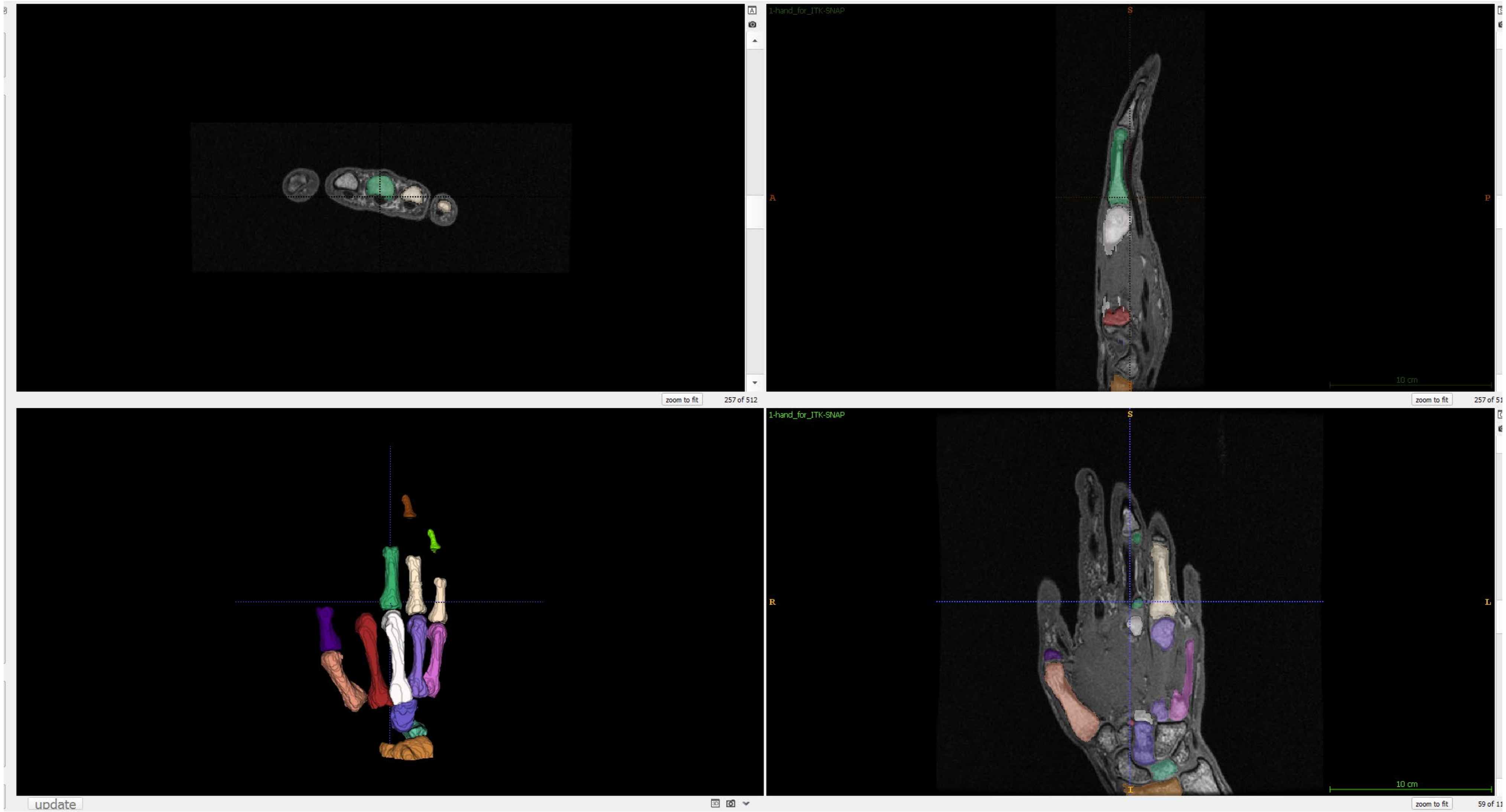
extensive manual cleanup required!

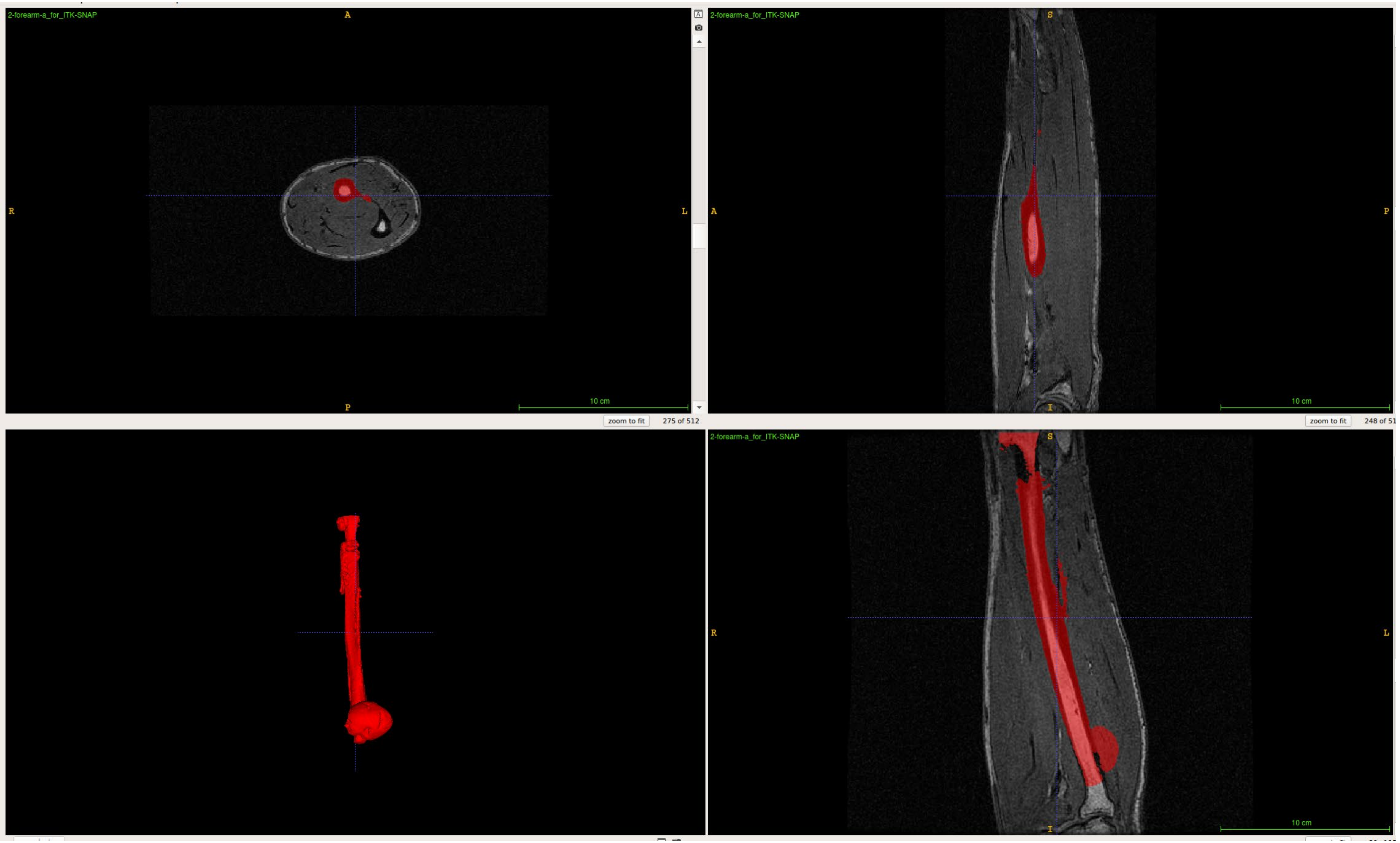
Preliminary Results: Hand/MSER



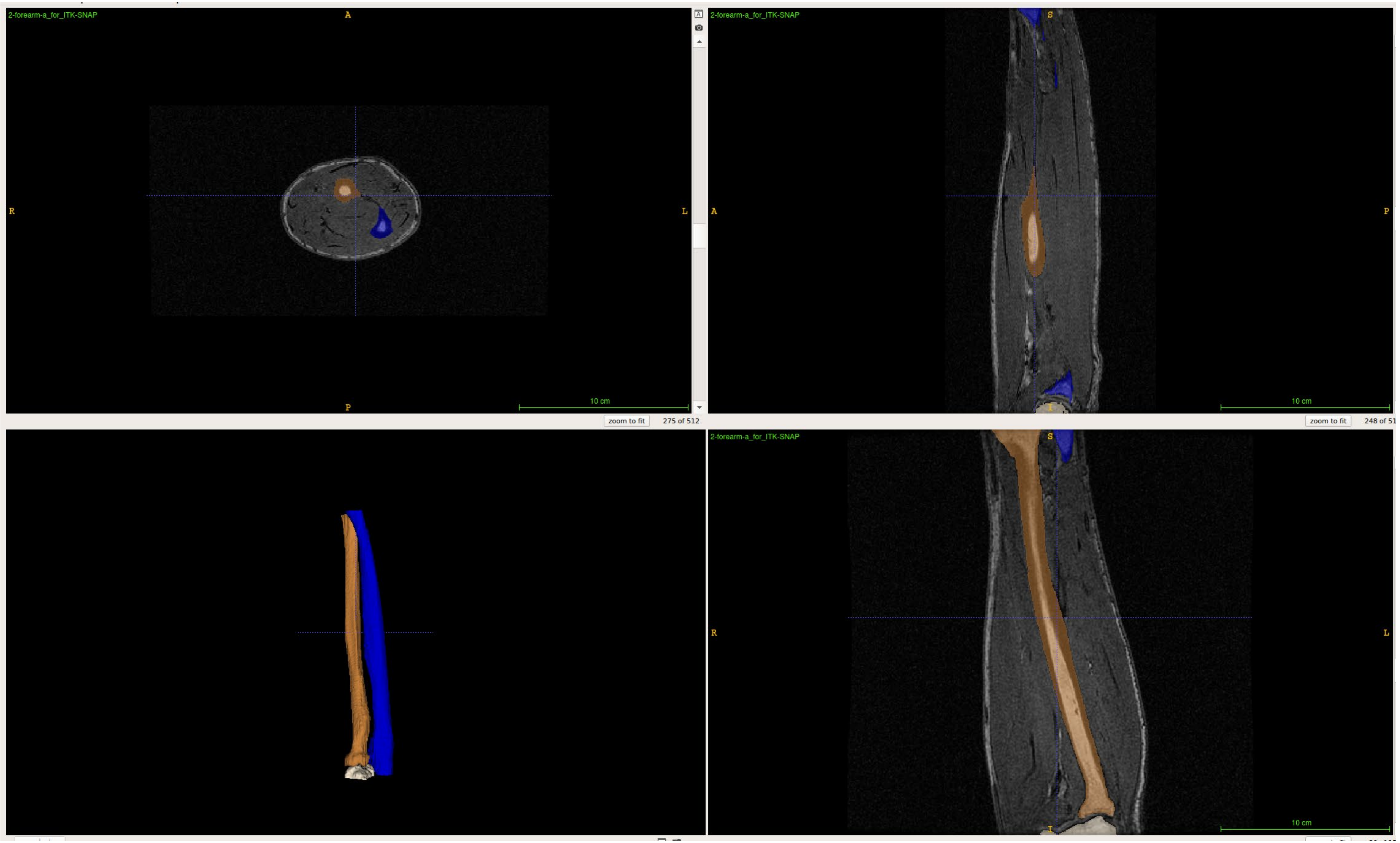
Preliminary Results: Hand/Manual



Preliminary Results: Forearm/AC



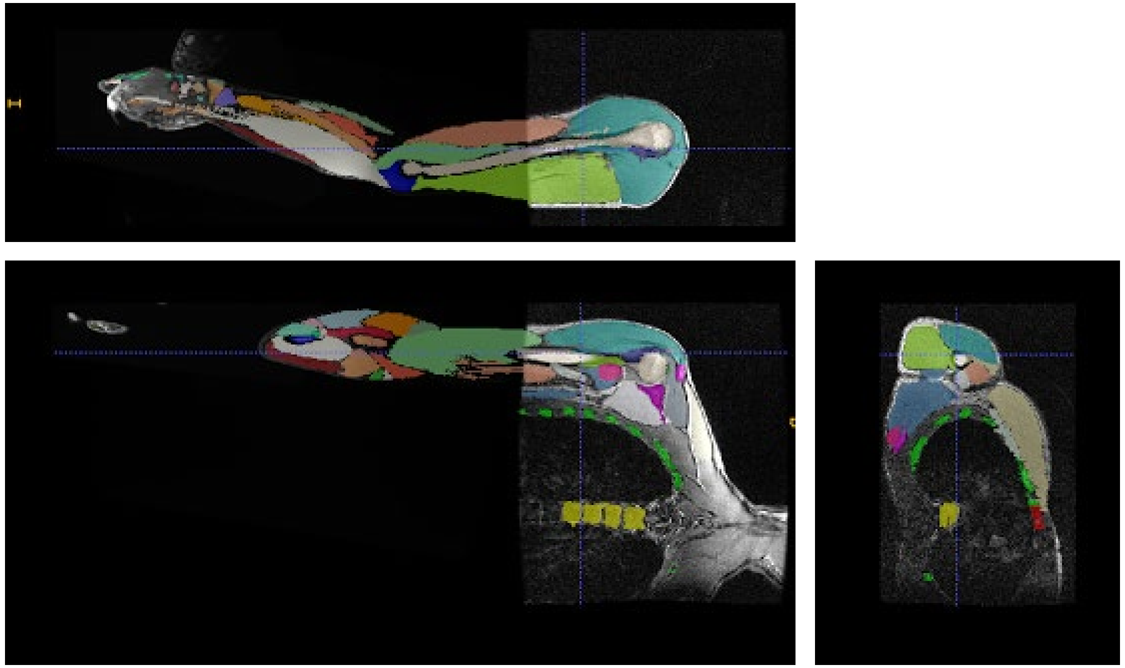
Preliminary Results: Forearm/Manual

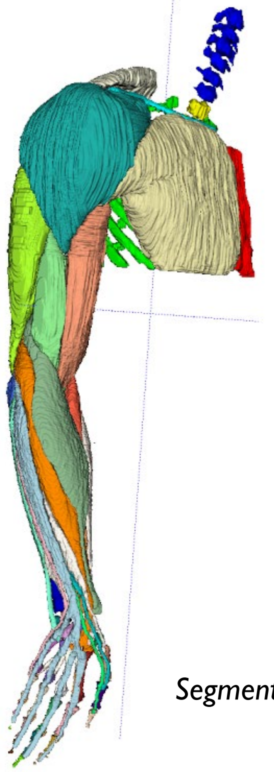


Approach: Muscle Segmentation

Muscle segmentation presents further challenges:

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



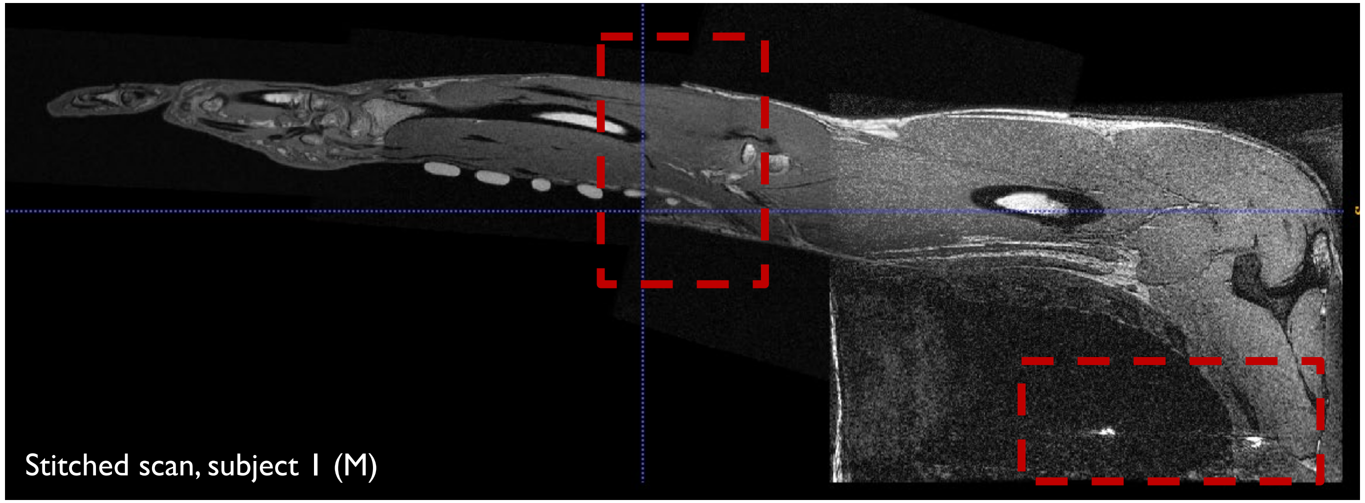


Segmented muscle data,
Stanford 2016

Approach: Muscle Segmentation

Muscle segmentation presents further challenges:

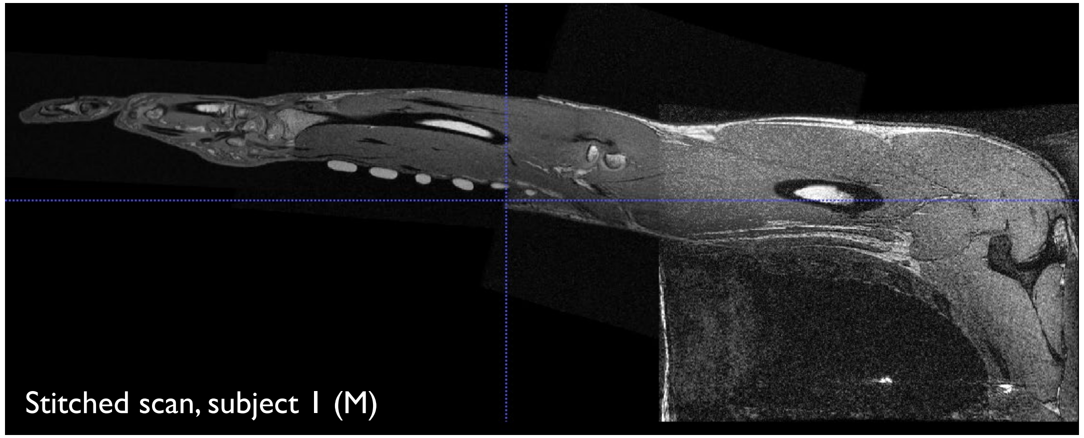
- manual segmentation **prohibitively time-intensive**
- **poorly suited** to generic blob/edge detection
  - large inter- and intra-subject contrast variation
  - muscle fascia hard to observe, even for humans
  - artifacts (stitching, motion, etc.)


Stitched scan, subject 1 (M)

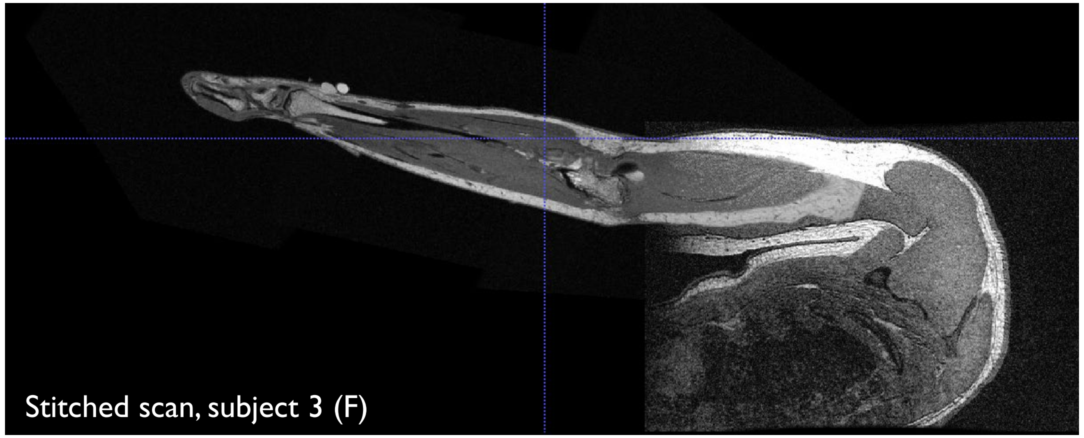
Approach: Muscle Segmentation

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



Stitched scan, subject 1 (M)



Stitched scan, subject 3 (F)

Approach: Muscle Segmentation

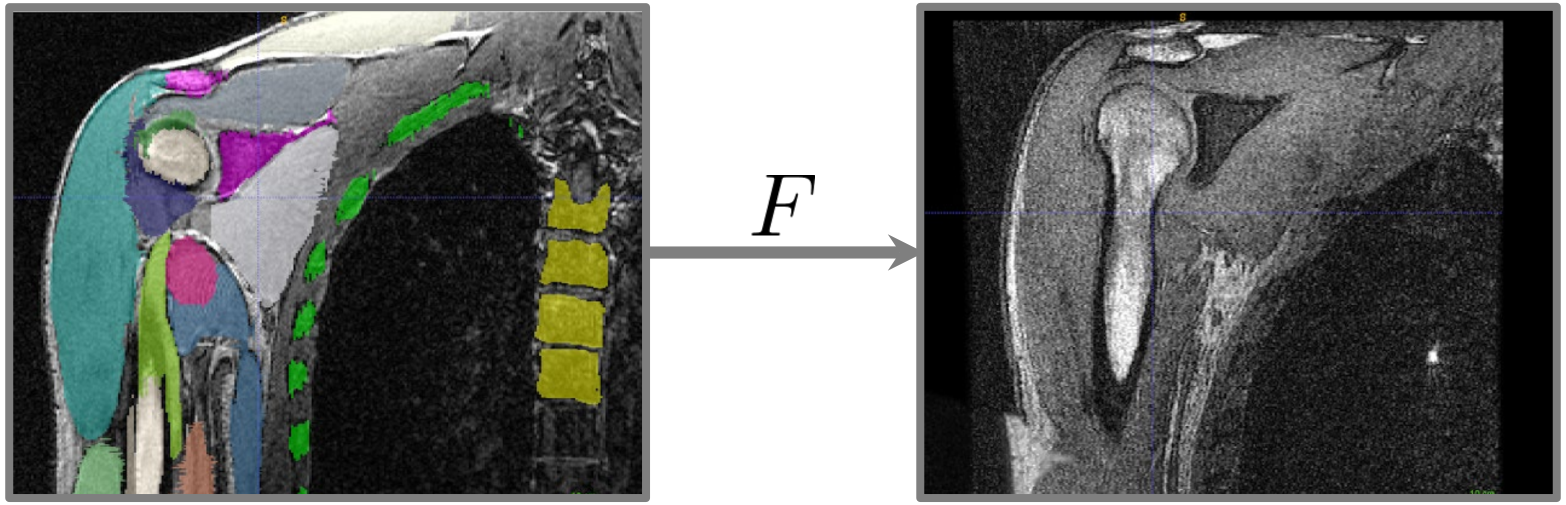
Muscle segmentation presents further challenges:

- 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 $F : R \to T$

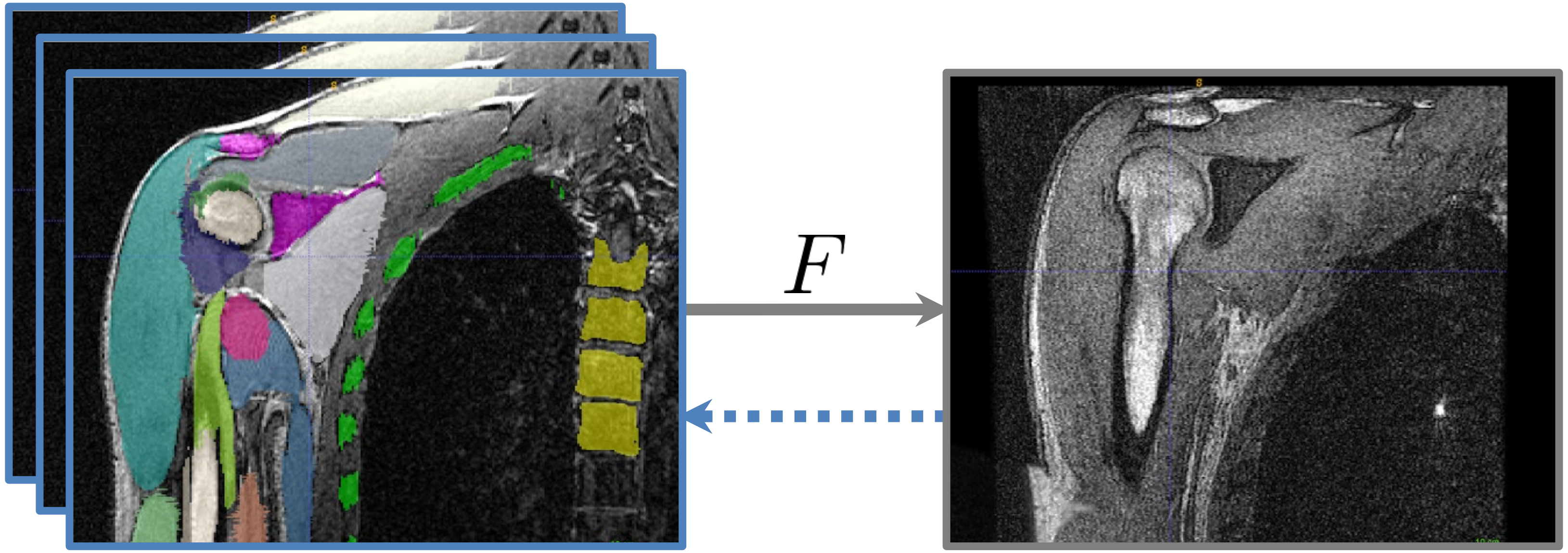


(segmented) reference subject
R

target subject
T

Approach: Muscle Segmentation

Goal: Find best transformation $F : R \to T$



(segmented) reference subject atlas

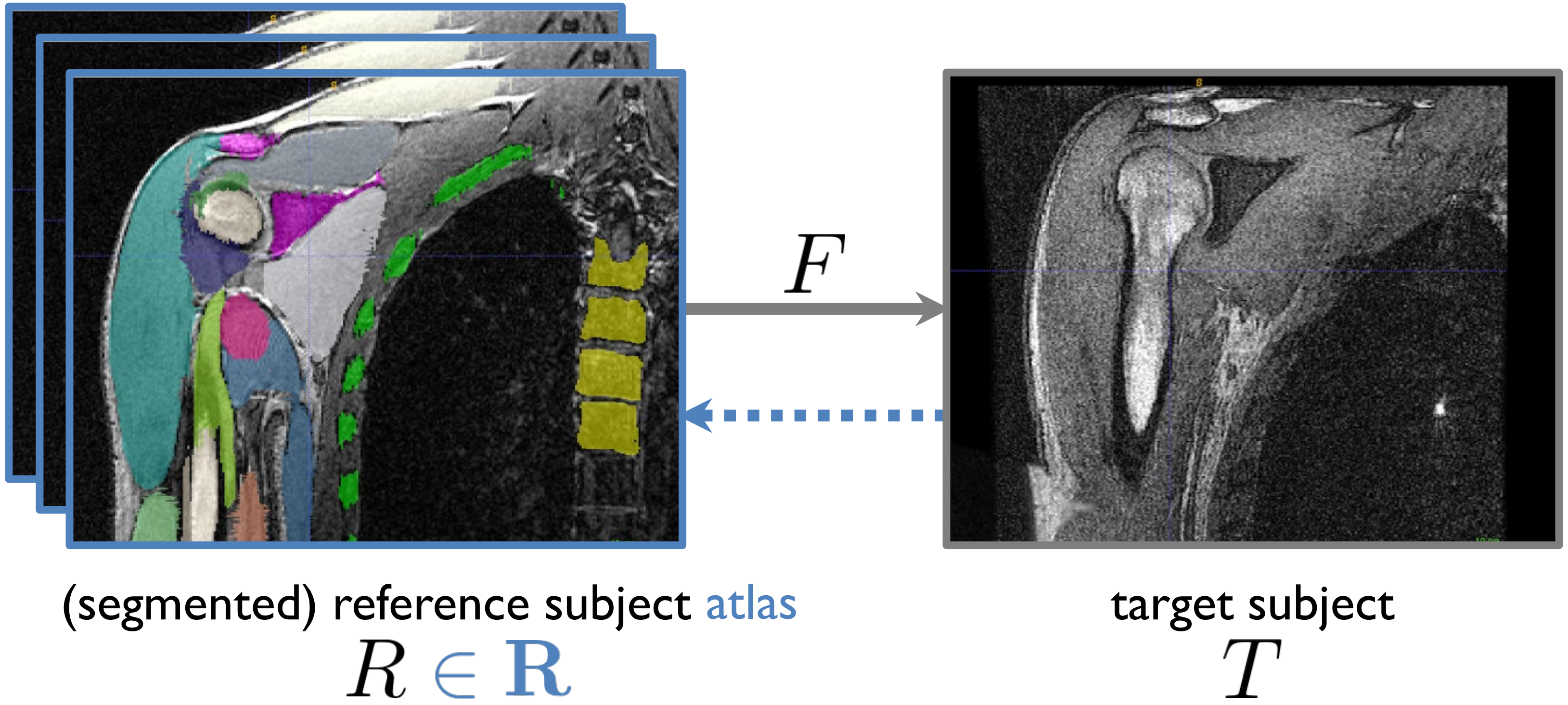
$R \in \mathbf{R}$

target subject

T

Approach: Muscle Segmentation

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 as Registration

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

$$\underbrace{F^*}_{\text{optimal transformation}} = \arg\min_{F} \; -\overbrace{S}^{\substack{\text{similarity function} \\ \textit{(e.g., MI)}}}(F; \underbrace{R}_{\text{reference image}}, \overbrace{T}^{\text{target image}})$$

Approach: Muscle Segmentation as Registration

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$$\underbrace{\mu}_{\substack{\text{optimal}\\\text{transformation}\\\textbf{parameters}}}^* = \arg\min_{\mu} \; -S(F_\mu; R, T)$$

Approach: Muscle Segmentation as Registration

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Potential DoF

 # similarity function classes

*** # parameters μ**

Approach: Muscle Segmentation as Registration

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

penalty function

(e.g., bending penalty)

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

Potential DoF

similarity function classes

* # parameters μ

*** # penalty function classes**

*** # λ values**

Approach: Muscle Segmentation as Registration

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

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

function parameters

Potential DoF

similarity function classes
* # parameters μ
* # penalty function classes
* # λ values
*** # similarity function parameters**
*** # penalty function parameters**

Approach: Muscle Segmentation as Registration

Our problem of finding $F : R \to T$ 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**.

Potential DoF

similarity function classes
* # parameters μ
* # penalty function classes
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Approach: Muscle Segmentation as Registration

Our problem of finding $F : R \to T$ 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**

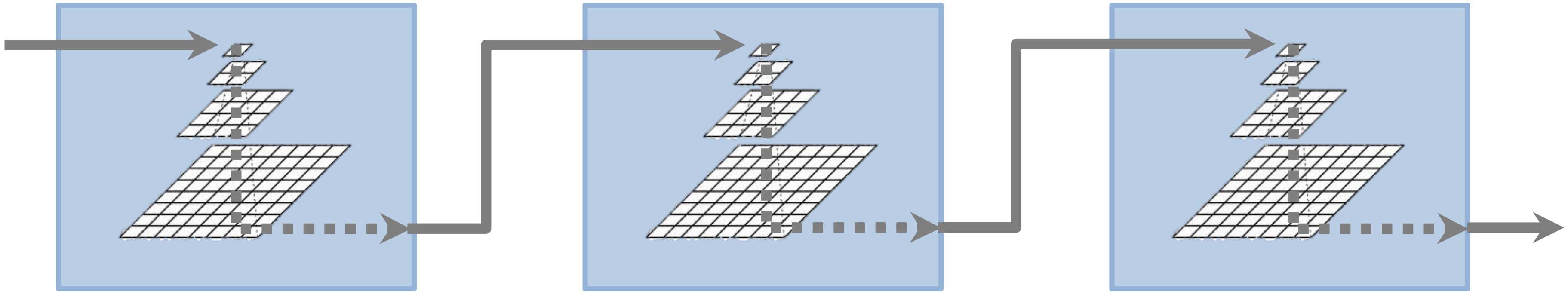
Potential DoF

similarity function classes
* # parameters μ
* # penalty function classes
* # λ values
* # similarity function parameters
* # penalty function parameters

Approach: Registration Pipeline (Elastix)

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



translation + rotation (Euler)

affine transformation

free-form deformation (FFD) *(b-spline parameterized)*

Approach: Elastix Parameters

5. aws server

```
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(CheckNumberOfSamples "true")
(DefaultPixelValue 0)
(FinalBSplineInterpolationOrder 3)
(FinalGridSpacingInPhysicalUnits 8)
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(GridSpacingSchedule 2.80322 1.9881 1.41 1)
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(MaximumNumberOfSamplingAttempts 8)
(Metric "AdvancedMattesMutualInformation" "TransformBendingEnergyPenalty")
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(NumberOfResolutions 4)
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(Registration "MultiMetricMultiResolutionRegistration")
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(Transform "AffineTransform")
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(WriteResultImage "true")

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```

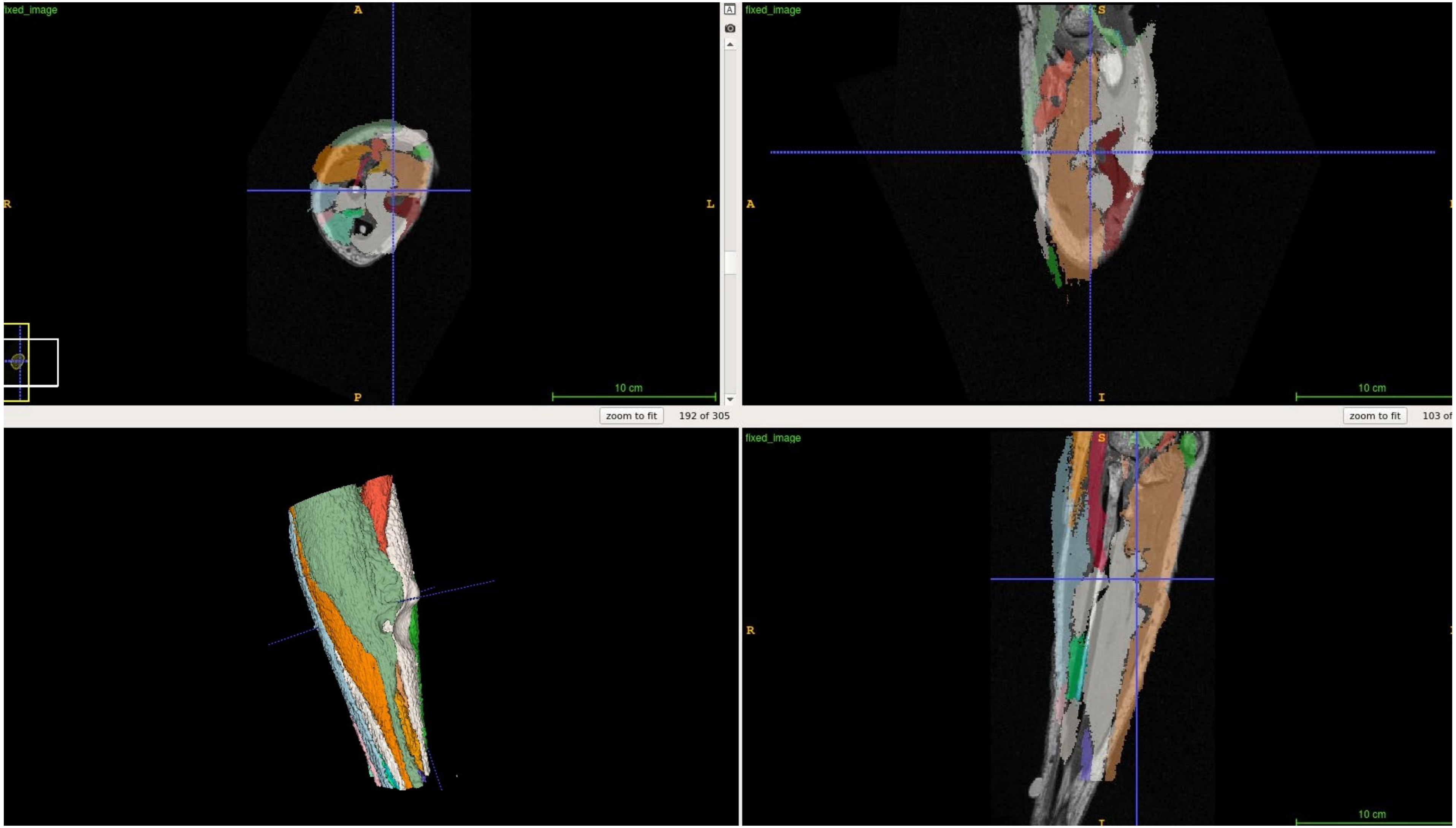
```
[0] 0:bash*                    "ip-172-31-18-22" 00:31 26-Jul-17
```

Approach: Elastix Parameters

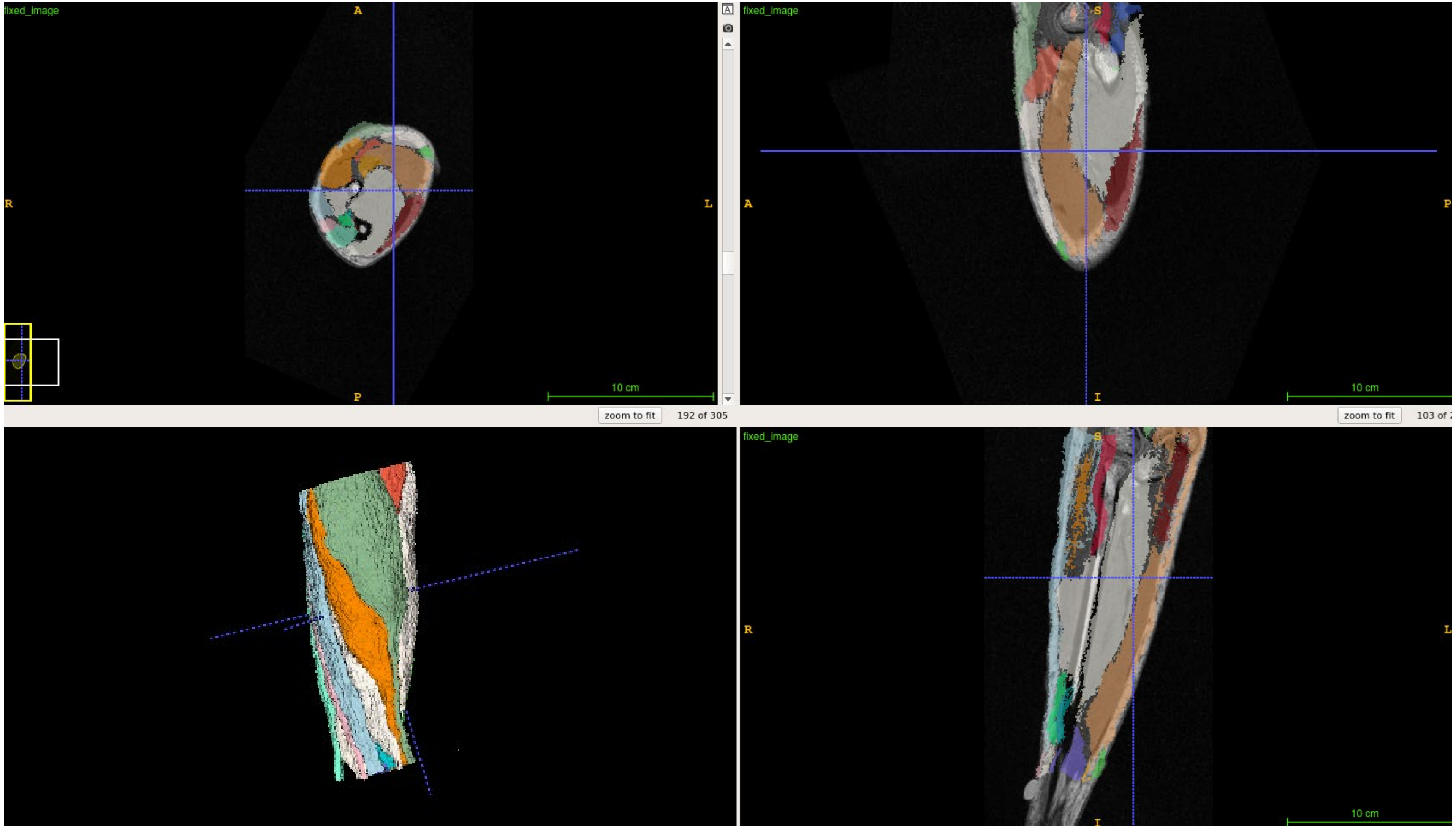
Particularly impactful parameters include:

- 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.)*

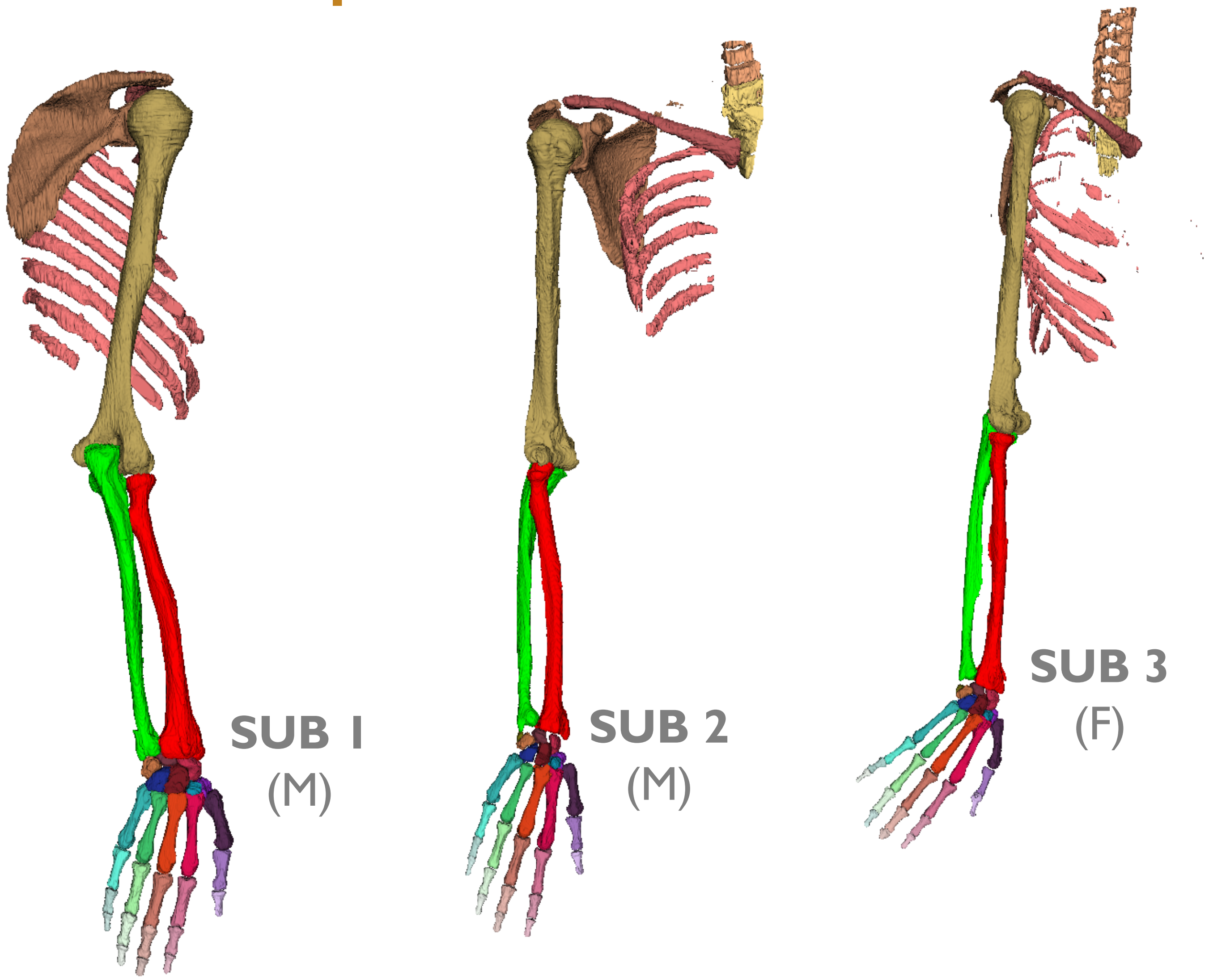


Preliminary Results: Muscle Mapping *(ground truth)*

. . . we're working on it.

Preliminary Results: Comparison

Preliminary bone segmentation results show **significant morphological variation across subjects** that cannot be modeled in existing frameworks.



Preliminary Results: Comparison

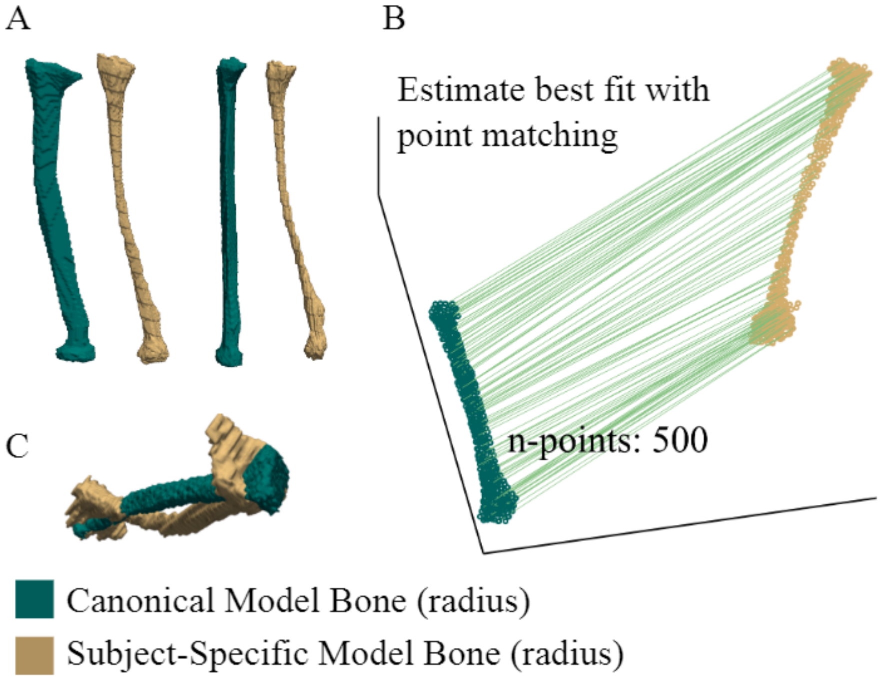


Fig. 5. **Model Scaling Errors. A.** A canonical model's radius bone side-by-side with an MRI-based subject-specific model's radius bone. The subject-specific model is accurate to $<$ 1mm, and considered to be ground truth. **B.** We scaled the canonical model to the subject's radius with an affine transformation 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

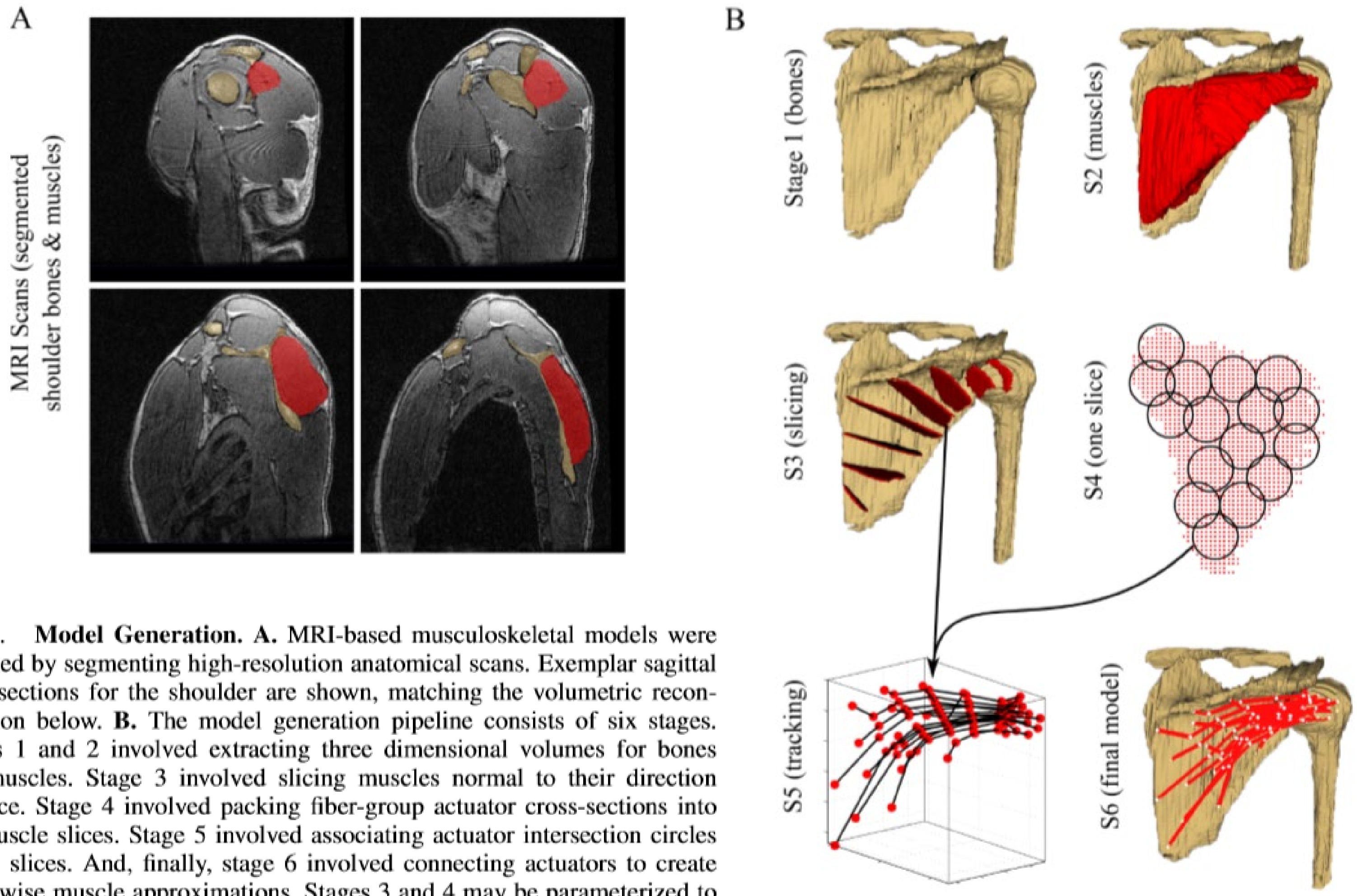


Fig. 3. **Model Generation. A.** MRI-based musculoskeletal models were obtained by segmenting high-resolution anatomical scans. Exemplar sagittal cross-sections for the shoulder are shown, matching the volumetric reconstruction below. **B.** The model generation pipeline consists of six stages. Stages 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.

Dynamics model generation, Stanford 2016

Preliminary Results: Simulation

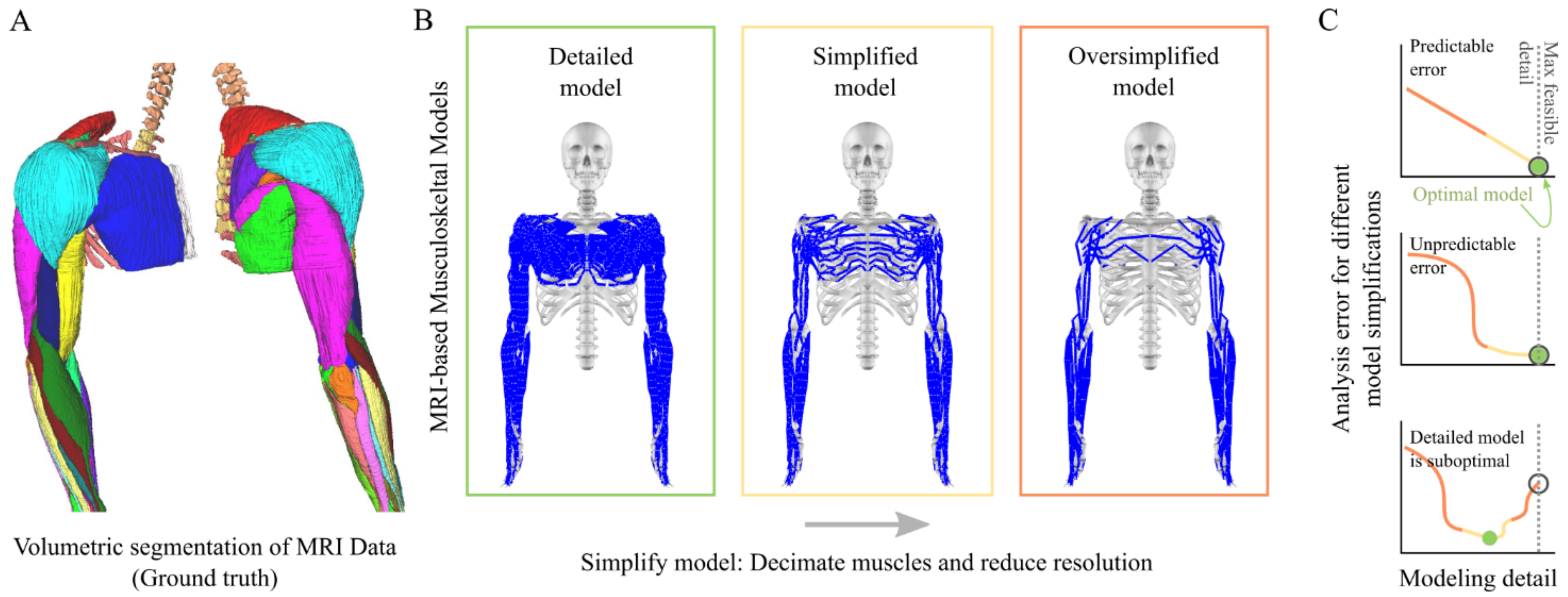


Fig. 2. **Comparing Model Accuracy and Analysis Error. A.** Volumetric rendering of bones and muscles extracted from a subject's anatomical MRI data. **B.** A family of models generated from the volumetric data. Skeletons are identical. The muscle model on the left very accurately captures muscle volumes (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

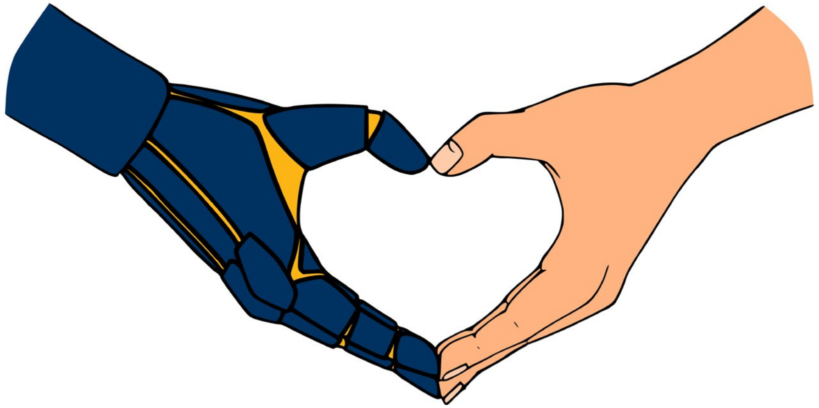
- morphology extraction
  - develop sufficiently fast **segmentation pipeline** (automated or manual or both)
  - **complete segmentation** (first bone, then muscle) of initial ~10-subject cohort
- (quantitative) **morphology comparison**
- dynamics model evaluation
  - **validate existing optimization-based 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**.



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Papers

Conference Papers

L.A. Hallock, R.P. Matthew, S. Seko, and R. Bajcsy. "Sensor-Driven Musculoskeletal Dynamic Modeling." *International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)*, 2016. (late-breaking report)

S. Menon, T. Migimatsu, and O. Khatib. "A Parameterized Family of Anatomically Accurate Human Upper-Body Musculoskeletal Models for Dynamic Simulation & Control." *IEEE RAS International Conference on Humanoid Robots*, 2016.

Technical Reports

L.A. Hallock, R.P. Matthew, S. Seko, and R. Bajcsy. (2016) "Sensor-Driven Musculoskeletal Dynamic Modeling." UC Berkeley EECS, Tech. Rep. UCB/EECS-2016-66.

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