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Computer Graphics Assignment about Kinematics

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master

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Alec Jacobson use libigl v2.4 … on Feb 25 25

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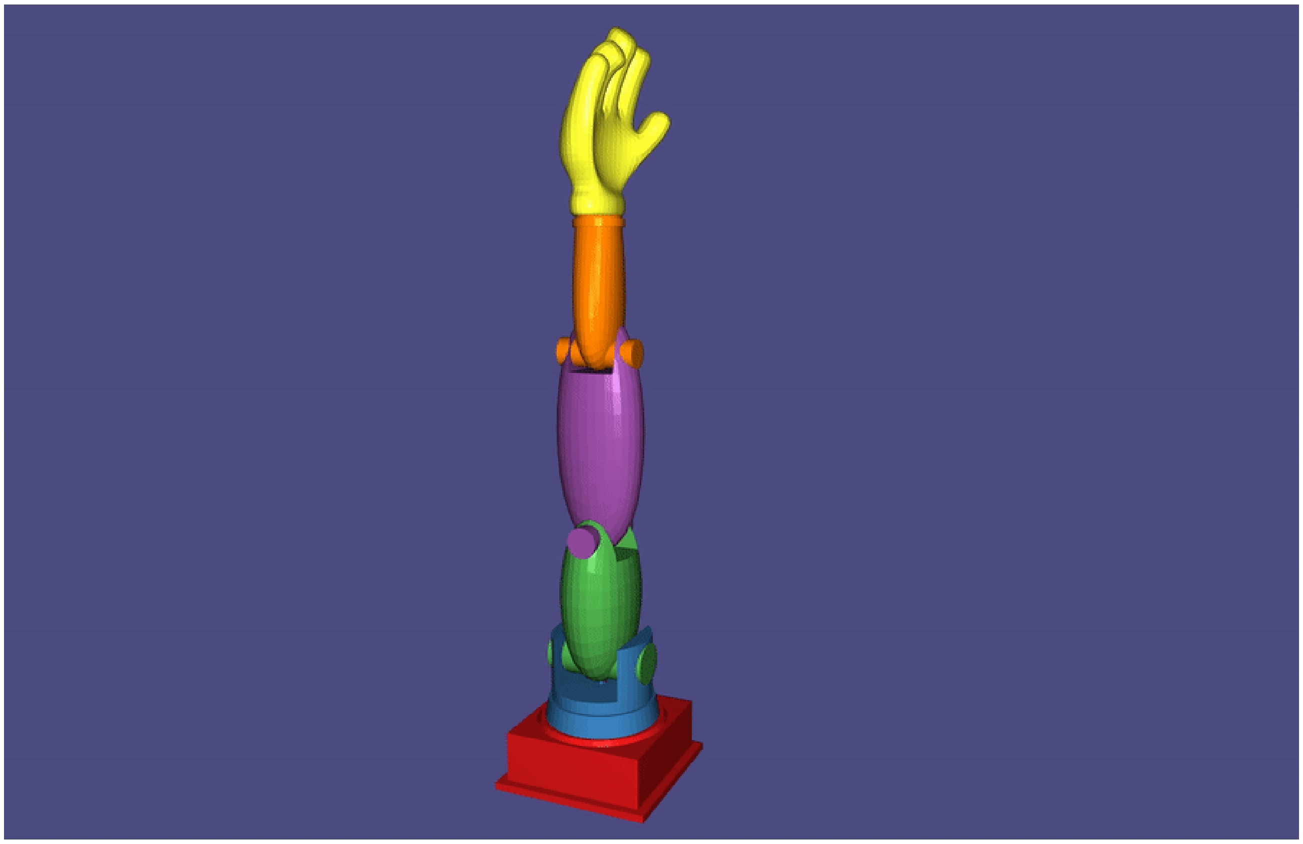
Computer Graphics – Kinematics

> **To get started:** Clone this repository using
>
> ```
> git clone --recursive http://github.com/alecjacobson/computer-graphics-kinematics.git
> ```

Background



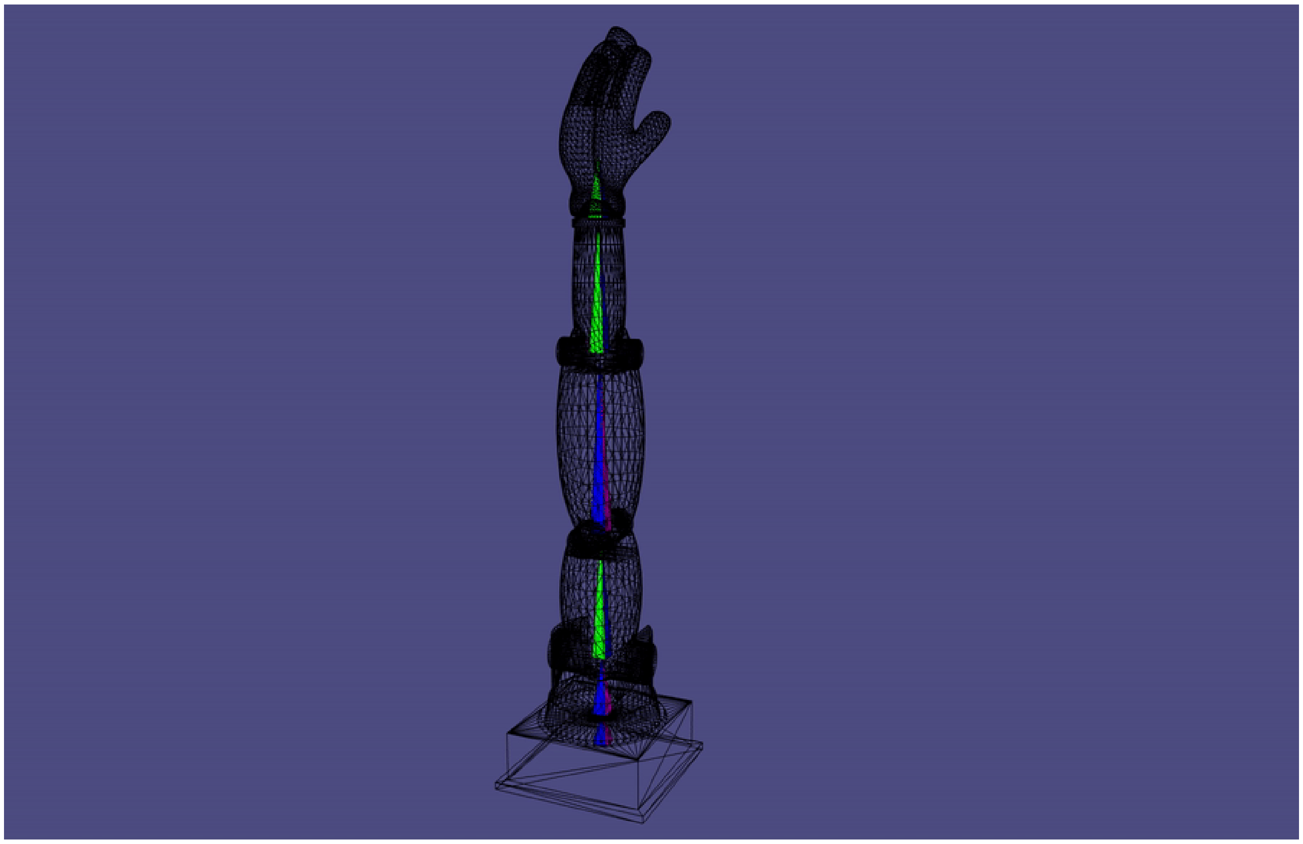
Read Chapter 15.1-15.5 of *Fundamentals of Computer Graphics (4th Edition)*.

Read Chapter 16.1-16.4 of *Fundamentals of Computer Graphics (4th Edition)*.

Skeleton

In this assignment we'll consider animating shapes *rigged* to an internal skeleton. The skeleton is a (graphical) user interface (UI) *metaphor*. A skeleton is a tree of rigid bones, not unlike the anatomical bones in a human or animal.

Each "bone" in the skeleton is really a UI widget for visualizing and controlling a 3D rigid transformation. A common visualization of 3D bone in computer graphics is a long, pointed pyramid shape. This reveals the twisting rotation as well as the tree hierarchy: the bone points toward its children.

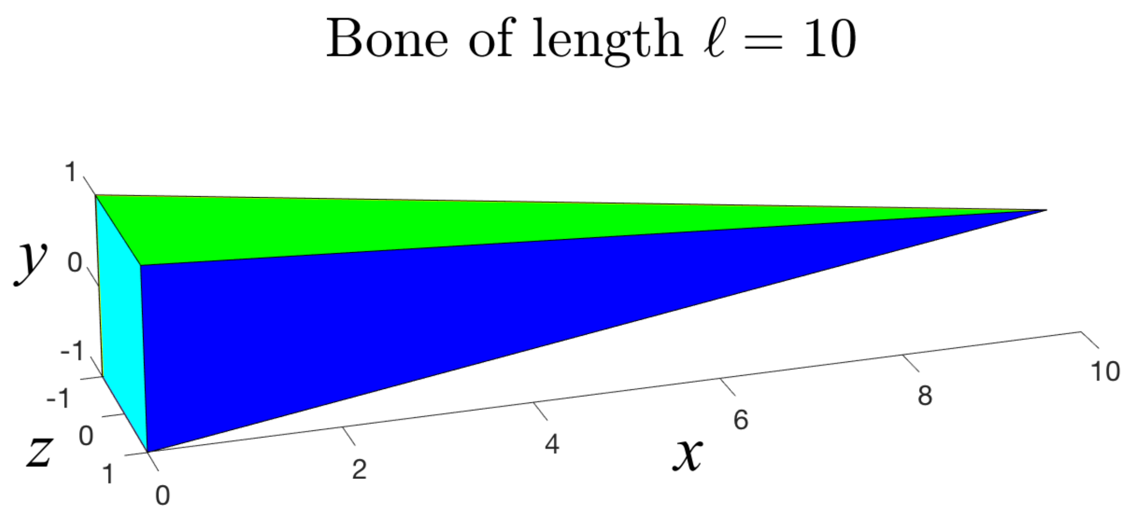


Unlike anatomy where the brain triggers muscles to flex and pull the passive bones around, the bones of a skeleton rig will define the pose of a shape.

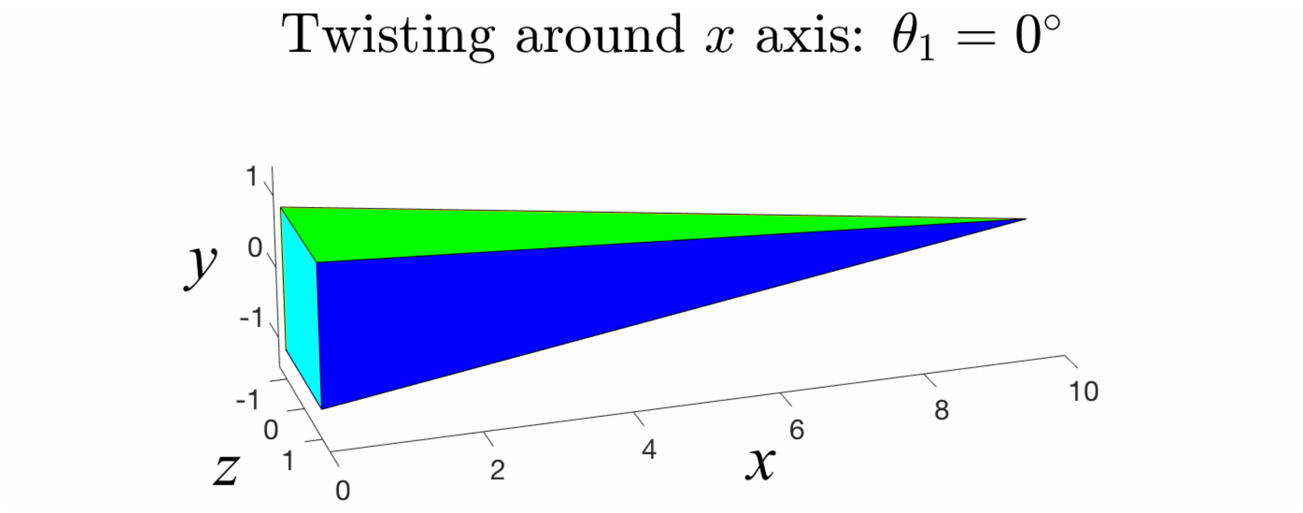
For each bone, we will consider ***three*** "states".

1. Canonical Bone

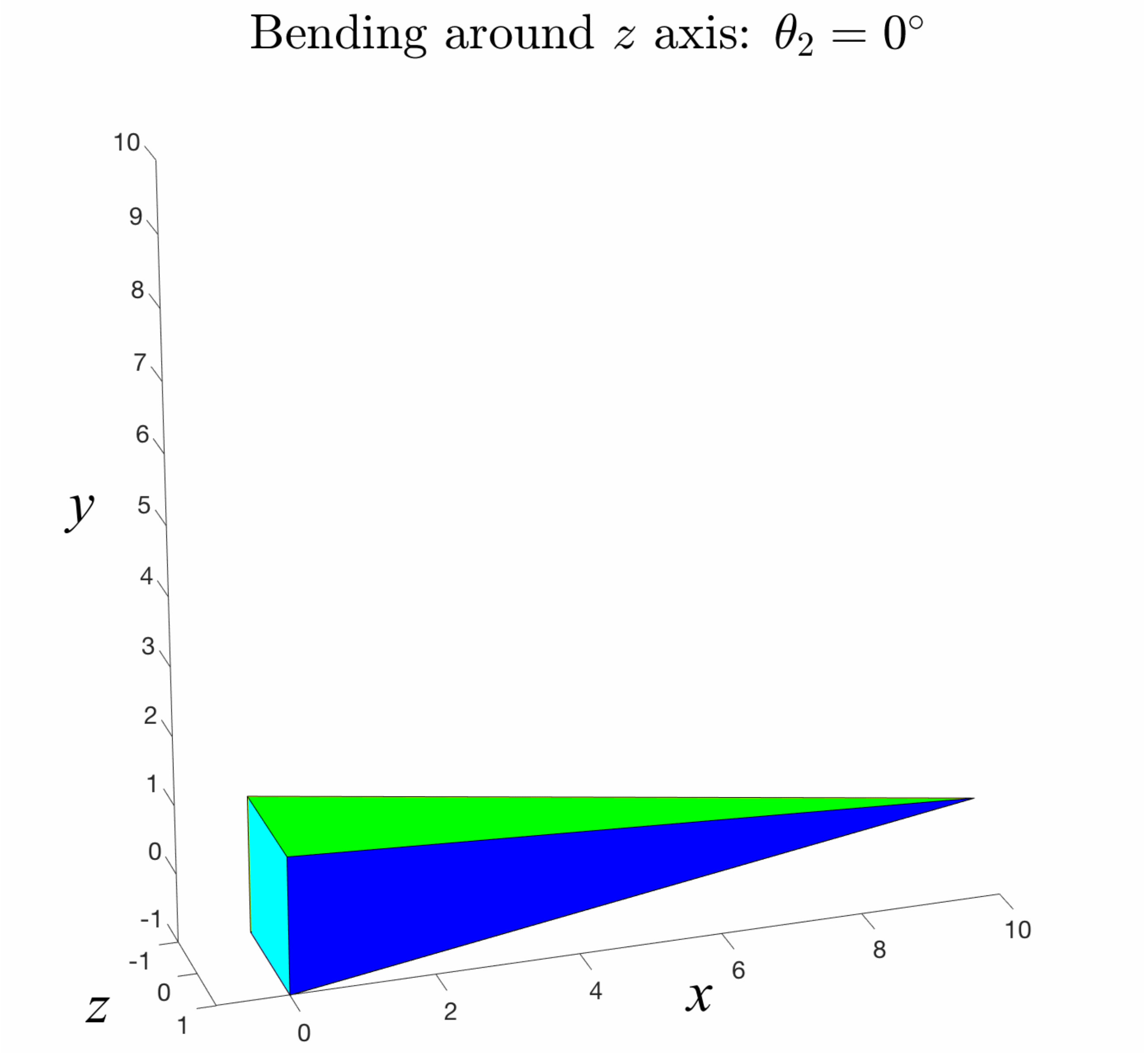
The "Canonical Bone" of length ℓ lies along the x-axis with its "tail" at the origin $(0,0,0)$, its "tip" at $(\ell,0,0)$.



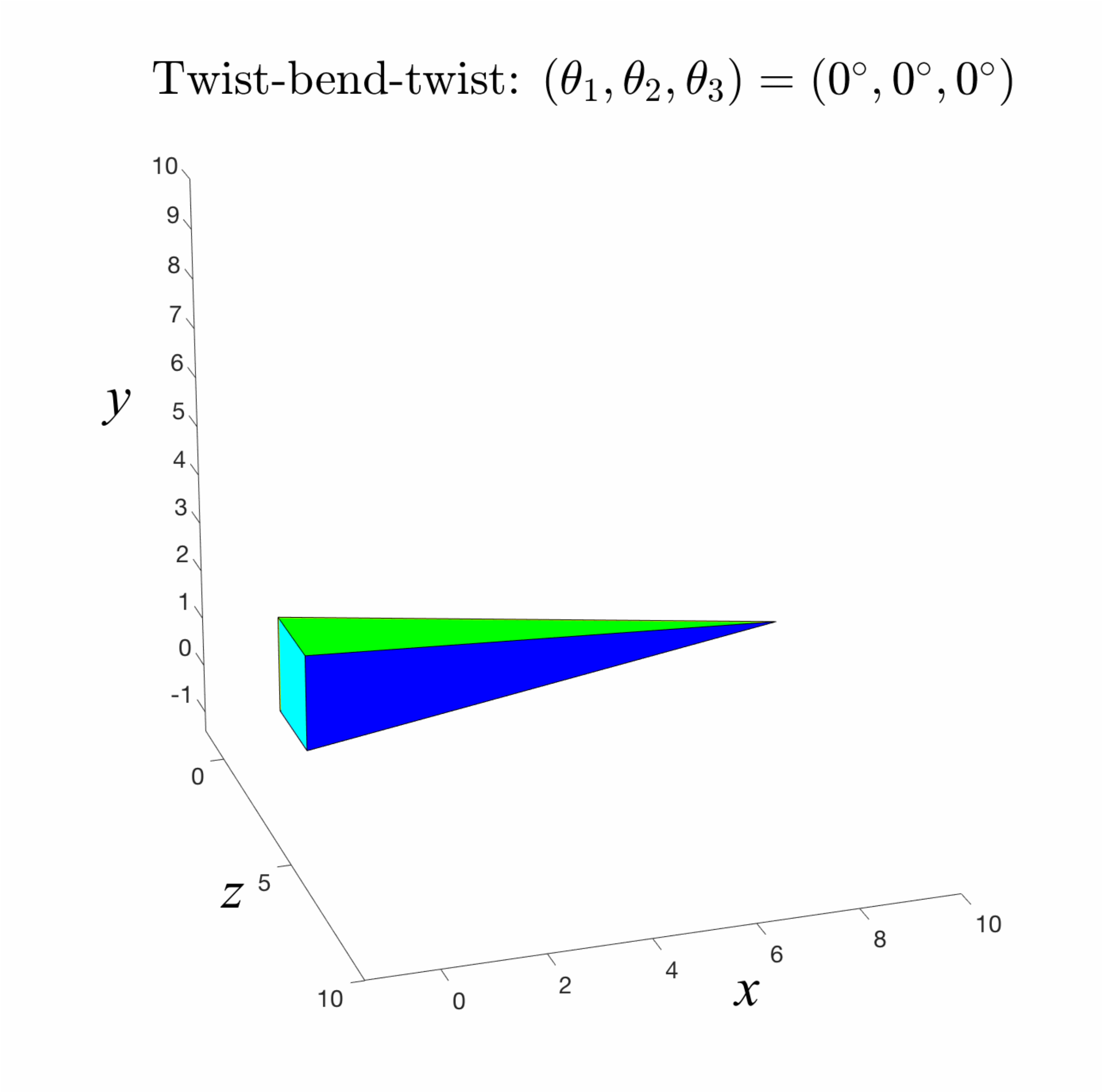
The bone is endowed with an orientation or frame. This helps define a canonical *twisting* direction. We will define twisting as rotating about the x-axis in the canonical frame.



For example, in this assignment, *bending* is accomplished by rotating about the z-axis in the canonical frame.



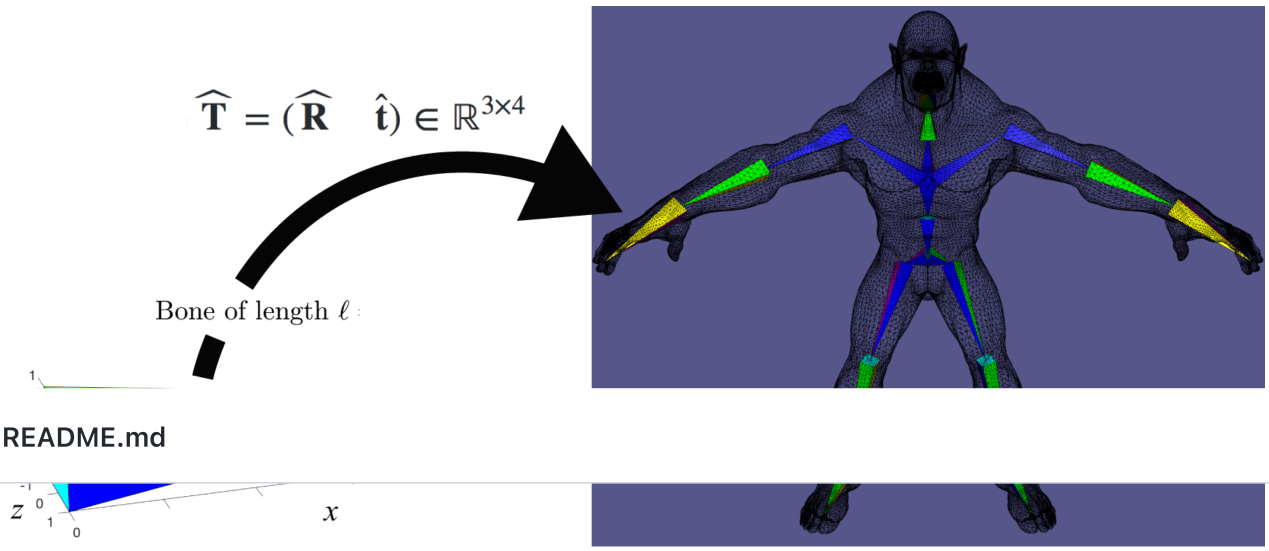
Composing a twist, bend and another twist spans all possible 3D rotations.


Twist-bend-twist: $(\theta_1, \theta_2, \theta_3) = (0^\circ, 0^\circ, 0^\circ)$
y
z
x
10
9
8
7
6
5
4
3
2
1
0
-1
0
5
10
0
2
4
6
8
10

We call the three angles composed into a rotation this way, Euler angles (not to be confused with the homophonous Oiler angles).

2. Rest Bone

To assemble a skeleton inside our shape will we map each bone from its canonical bone to its position *and orientation* in the undeformed model. Maintaining the rigidity of the bone, this means for each bone there's a rigid transformation $\widehat{\mathbf{T}} = (\widehat{\mathbf{R}} \quad \widehat{\mathbf{t}}) \in \mathbf{R}^{3\times 4}$ that places its tail and tip to the desired positions in the model.


$\widehat{\mathbf{T}} = (\widehat{\mathbf{R}} \quad \hat{\mathbf{t}}) \in \mathbb{R}^{3\times4}$
Bone of length ℓ
z
x

We use the convention that the "canonical tail" (the origin $(0,0,0)$) is mapped to the "rest tail" inside the model. This means that the *translation* part of the matrix $\widehat{\mathbf{T}}$ is simply the tail position, $\hat{\mathbf{s}} \in \mathbf{R}^3$:

$$\hat{\mathbf{s}} = \widehat{\mathbf{T}}\begin{pmatrix}0\\0\\0\\1\end{pmatrix} = \widehat{\mathbf{R}}\begin{pmatrix}0\\0\\0\end{pmatrix} + \hat{\mathbf{t}}1 = \hat{\mathbf{t}}.$$

The bone's rotation is chosen so that the "canonical tip" $(\ell, 0, 0)$ maps to the "rest tip" $\widehat{\mathbf{d}} \in \mathbf{R}^3$:

$$\widehat{\mathbf{d}} = \widehat{\mathbf{T}}\begin{pmatrix}\ell\\0\\0\\1\end{pmatrix} = \widehat{\mathbf{R}}\begin{pmatrix}\ell\\0\\0\end{pmatrix} + \hat{\mathbf{t}}.$$

Typically the "rest tail" of is coincident with the "rest tip" of its parent (if it exists):

$$\widehat{\mathbf{d}}_p = \hat{\mathbf{s}}.$$

This still leaves any amount of *twisting* of the bone. In the canonical frame, we can think of this as pre-twisting the bone along the canonical x-axis. Clearly, twisting does not effect the ability to map the tail and tip to the correct position. This twist is *chosen* so that canonical bending aligns with a meaningful direction. For example, we may twist a tibia (shinbone) bone so that canonical bending around the z-axis means bending at the knee.

Each rest transformation $\widehat{\mathbf{T}}$ *places* its corresponding bone inside the undeformed shape.

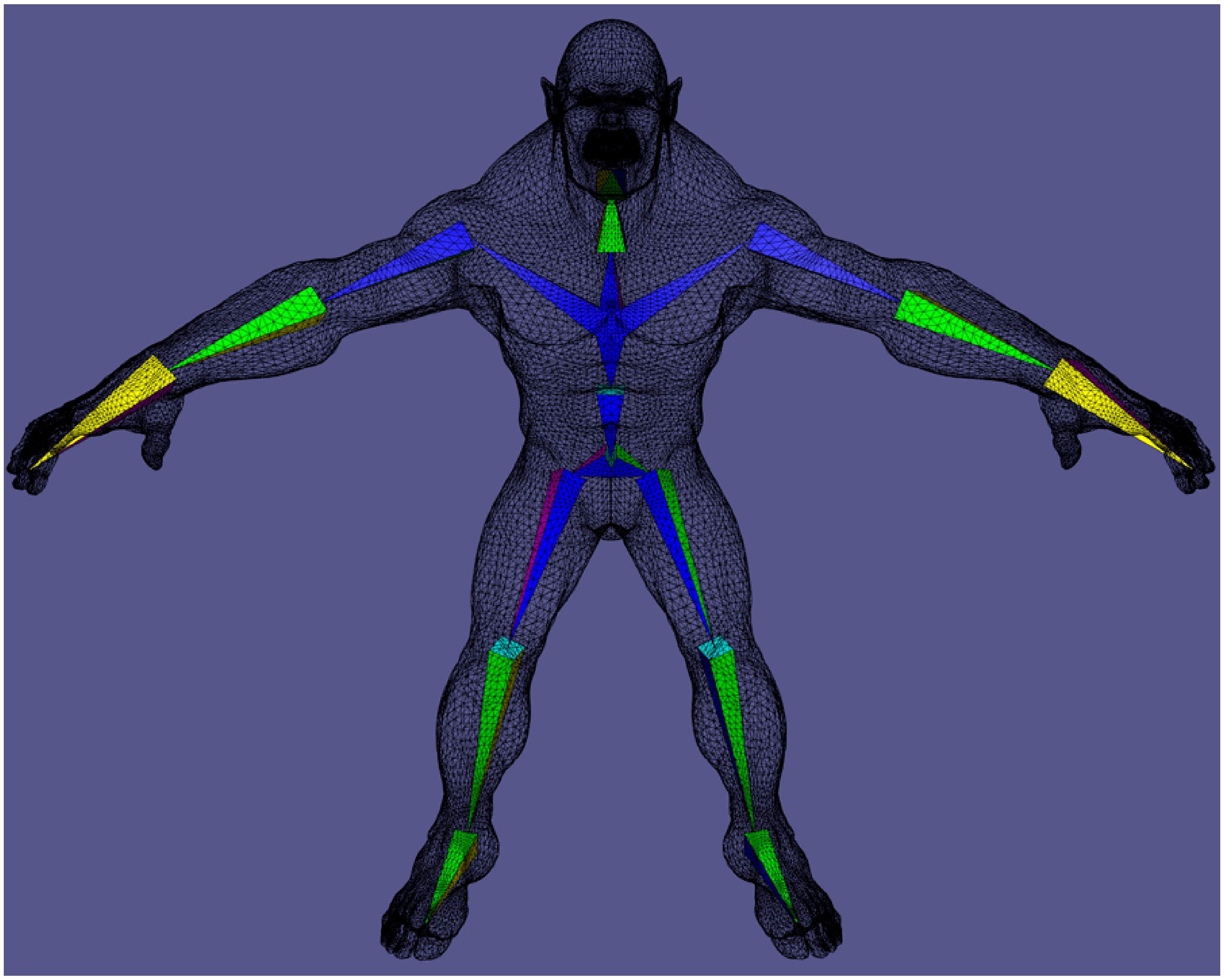
The rest transformations do not measure any deformation of the shape from its original position. Thus, the *pose* of each bone will be measured *relative* to the "rest bone".

3. Pose Bone

The final state to consider is when a bone is *posed*. That is, mapped to a new position and orientation from its rest state.

In general, each rest bone undergoes a rigid transformation $\mathbf{T} \in \mathbf{R}^{3\times 4}$, composed of a rotation $\mathbf{R} \in \mathbf{R}^{3\times 3}$ and a translation $\mathbf{t} \in \mathbf{R}^3$, mapping each of its rest points $\widehat{x} \in \mathbf{R}^3$ to its corresponding posed postion $\mathbf{x} \in \mathbf{R}^3$:

$$\mathbf{x} = \mathbf{T}\widehat{\mathbf{x}}.$$



$\mathbf{T}$ is expressed as a *global* mapping of any point in the rest reference frame to its pose position. This makes it convenient for [blending transformations (see below)][linearblendskinning], but it's not so obvious how to pick coherent values for $\mathbf{T}$. In particular, we would like each bone to rotate about its parent's tip, but this position is determined by the parent's pose transformation $\mathbf{T}_p$, which in turn should rotate about the grandparent's tip and so on.

Forward Kinematics

One way to determine the rigid pose transformations $\mathbf{T}_i \in \mathbf{R}^{3\times 4}$ for each bone i in a skeleton is to aggregate *relative rotations* $\overline{\mathbf{R}}_i \in \mathbf{R}^{3\times 3}$ between a bone i and its parent bone p_i in the skeletal tree. The final transformation at some bone i deep in the skeletal tree is computed via a recursive equation.

For each bone, (reading the effect of transformations *right to left*) we first *undo* the map from canonical to rest (i.e., via inverting $\widehat{\mathbf{T}}_i$), then rotate by our relative rotation $\overline{\mathbf{R}}_i$, then map back to rest (via $\widehat{T}_i$). With our relative transformation accomplished, we continue *up the tree* recursively applying our parent's relative transformation, and our grandparent's and so on:

$$\mathbf{T}_i = \mathbf{T}_{p_i} \begin{pmatrix} \widehat{\mathbf{T}}_i \\ 0\ 0\ 0\ 1 \end{pmatrix} \begin{pmatrix} \overline{\mathbf{R}}_i & \begin{matrix} 0 \\ 0 \\ 0 \end{matrix} \\ 0\ 0\ 0 & 1 \end{pmatrix} \begin{pmatrix} \widehat{\mathbf{T}}_i \\ 0\ 0\ 0\ 1 \end{pmatrix}^{-1}$$

> **Question:** Does using relative rotations ensure that bone tails stay coincident with parent tips?
>
> **Hint:** What do you get if you multiply $\mathbf{T}_i$ and $\widehat{\mathbf{s}}_i$?

As a base case, the *root* transformation can be defined to be the identity (no transformation) or the rigid transformation placing the object/character generally into a larger scene.

This has the great advantage that if the entire model is rotated or translated at the root, the relative transformations still apply correctly. This property holds locally, too. If bone i controls the tibia (shinbone) and $\mathbf{R}_i$ applies a bend at the knee, then twisting and bending at the parent hip bone will naturally *compose* with the knee bend.

It is convenient to express the relative rotations of each bone in the canonical frame. We can utilize canonical twist-bend-twist rotations (three Euler angles, $\theta_1, \theta_2, \theta_3$). Each bone's rotation is conducted in its canonical frame and then *brought* through the rest frame through a change of coordinates:

$$\mathbf{T}_i = \mathbf{T}_{p_i} \widehat{\mathbf{T}}_i \begin{pmatrix} \mathbf{R}_x(\theta_{i3}) & \begin{matrix} 0 \\ 0 \\ 0 \end{matrix} \\ 0\ 0\ 0 & 1 \end{pmatrix} \begin{pmatrix} \mathbf{R}_z(\theta_{i2}) & \begin{matrix} 0 \\ 0 \\ 0 \end{matrix} \\ 0\ 0\ 0 & 1 \end{pmatrix} \begin{pmatrix} \mathbf{R}_x(\theta_{i1}) & \begin{matrix} 0 \\ 0 \\ 0 \end{matrix} \\ 0\ 0\ 0 & 1 \end{pmatrix} \widehat{\mathbf{T}}_i^{-1}$$

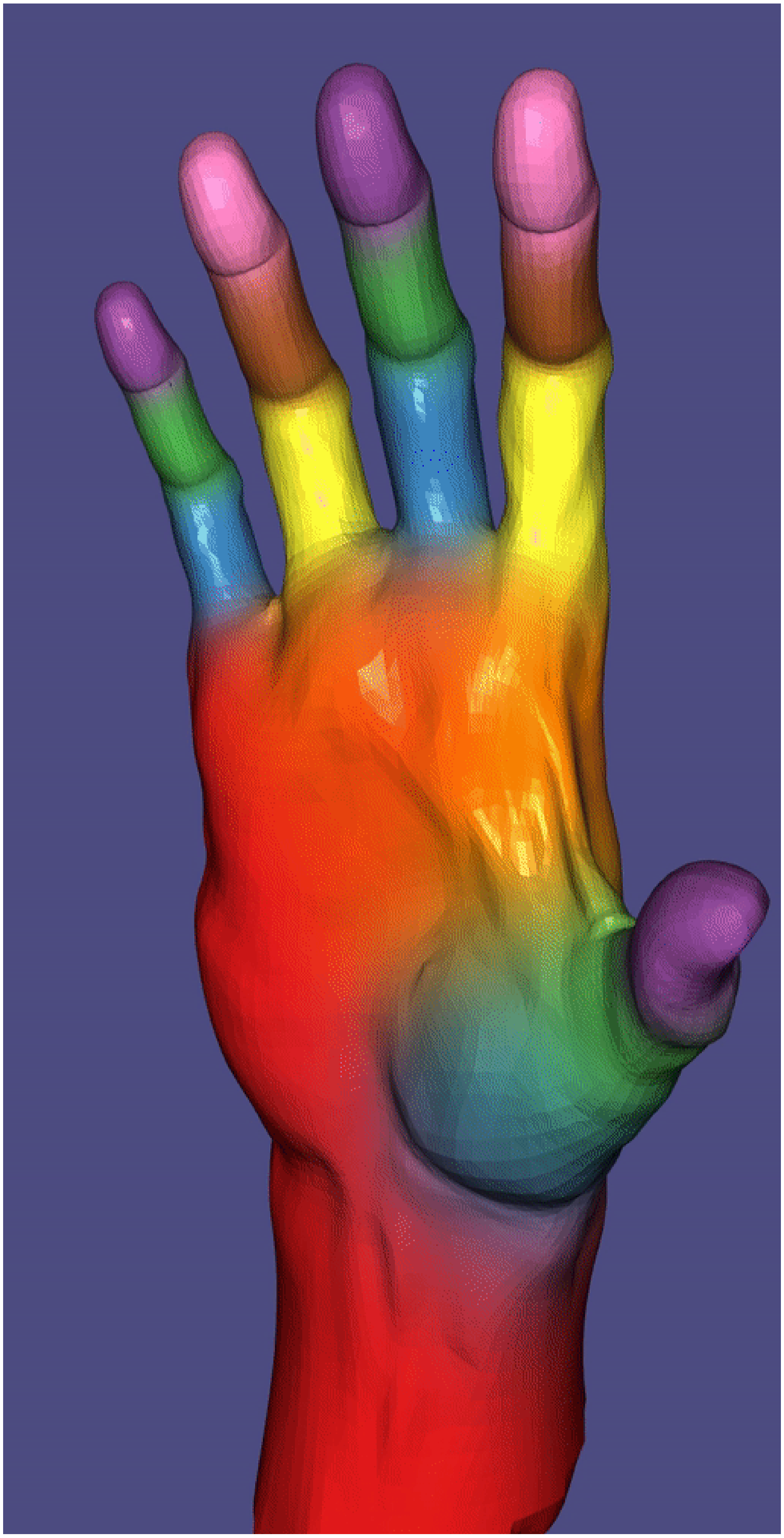
where the matrix $\mathbf{R}_w(\varphi) \in \mathbf{R}^{3\times3}$ is the rotation by φ degrees around the w-axis.

When implementing a skeleton, it is tempting to use a traditional tree data structure where each node (bone) contains a list of pointers to its children (other bones). However, by the *right-to-left* reading of the forward kinematics formulae above, it is more convenient to use a data structure where each node (bone) has a pointer to its (unique) parent (other bone). This is ridiculously named a Spaghetti Stack.

> **Question:** What abstract data-structure is good for ensuring a parent's transformation $\mathbf{T}_{p_i}$ are computed before its child's $\mathbf{T}_i$?
>
> **Hint:** 🥞

Keyframe animation

To create a long animation, specifying three Euler angles for every bone for every frame manually would be too difficult. The standard way to determine the relative bone transformations for each frame is to interpolate values specified at a small number of "key" times during the animation. Linear interpolation will lead to a choppy, robotic animation (try this first!). Instead Catmull-Rom interpolation will produce a smooth animation. Fancier interpolation such as the Kochanek-Bartels method (called TCB in the book) allow better control of easing between key poses.



In this assignment, we will interpolate Euler angles directly. This works well when only a single angle is changing at a time. However, Euler angles do not provide easy movement in every rotational direction. Euler angles model rotations as *twist-bend-twist*. For our canonical bones, bending around the z-axis is easy, but bending around the y-axis requires first twisting by $90°$ and then "un"-twisting by $-90°$ after bending.

So, for more complex interpolation of rotations, a different representation such as unit quaternions would be needed. This is outside the scope of this assignment.

Inverse Kinematics

In the [forward kinematics][forwardkinematics] model, the final position of the tip of a finger is determined by setting (manually or via interpolation) the relative transformations of each joint in the finger, the hand, the elbow, the shoulder, ... This indirect control makes it difficult to achieve basic poses. Instead, we can treat the problem of setting relative rotations of internal bones (shoulder, elbow, hand, ...) as an optimization problem where we try to minimize the distance between the tip of the finger and where we want it to be.

Stated mathematically, for a skeleton with m bones, if we create a vector $\mathbf{a} \in \mathbf{R}^{3m}$ stacking all the Euler angles of each bone vertically:

$$\mathbf{a} = \begin{pmatrix} \theta_{11} \\ \theta_{12} \\ \theta_{13} \\ \theta_{21} \\ \theta_{22} \\ \theta_{23} \\ \vdots \\ \theta_{m1} \\ \theta_{m2} \\ \theta_{m3} \end{pmatrix}$$

then we can ask for the best vector of angles θ. Best-ness must be quantified by an cost/energy/obective-function E. This energy is typically first written with respect to the (global, non-relative) pose positions of certains bones $\mathbf{x}_b \in \mathbf{R}^3$ (often the "tip" of a leaf bone of the skeletal tree, called an end effector). For example, we then we could design our energy to measure the squared distance between the pose tip $\mathbf{x}_b$ of some bone b and a desired goal location $\mathbf{q} \in \mathbf{R}^3$:

$$E(\mathbf{x}_b) = \|\mathbf{x}_b - \mathbf{q}\|^2.$$

Using forward kinematics, we can express $\mathbf{x}_b$ and in turn E with respect to relative rotations:

$$\mathbf{x}_b(\mathbf{a}) = \mathbf{T}_b \widehat{\mathbf{d}}_b$$

where $\mathbf{T}_b$ depends on $\theta_{b1}, \theta_{b2}, \theta_{b2}$ and $\mathbf{T}_{p_b}$ which depends on $\theta_{p_b 1}, \theta_{p_b 2}, \theta_{p_b 2}$. In this way our energy can be written as a function of $\mathbf{a}$:

$$E(\mathbf{x}_b(\mathbf{a})) = \|\mathbf{x}_b(\mathbf{a}) - \mathbf{q}\|^2.$$

We can design arbitrarily complex energies to satisfy our interaction needs. In this assignment, we consider that there is a list of constrained end effectors $b = \{b_1, b_2, \ldots, b_k\}$ and our objective is that all selected end effectors b_i go to their prescribed locations (provided by the mouse-drag UI). using the simple squared distance measure above.

So, over all choices of $\mathbf{a}$ we'd like to optimize:

$$\min_{\mathbf{a}} \quad \underbrace{\Sigma_{i=1}^{k} \|\mathbf{x}_{b_i}(\mathbf{a}) - \widehat{\mathbf{x}}_{b_i}\|^2}_{E(\mathbf{x}_b(\mathbf{a}))}$$

We will further constrain our problem by imposing upper and lower bounds on our angles $\mathbf{a}$. These correspond to joint limits. For example, the joint limits of a hinge or elbow type joint may look like:

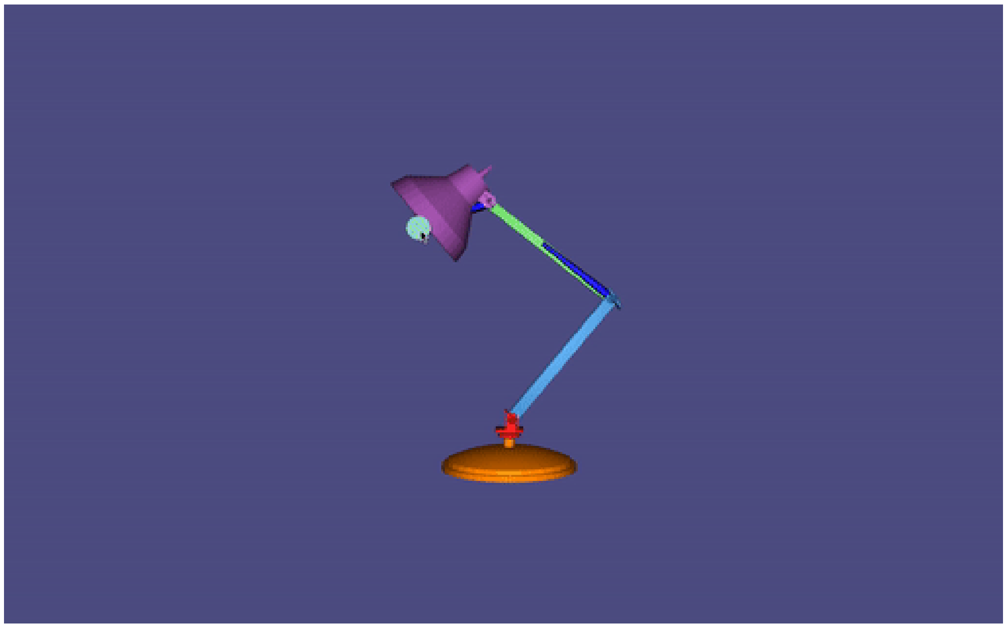
$$0^\circ \leq \theta_1 \leq 0^\circ, \quad 0^\circ \leq \theta_2 \leq 170^\circ, \quad 0^\circ \leq \theta_3 \leq 0^\circ.$$

These would ensure that our joint cannot twist, and can only bend in one direction.

So our full optimization problem becomes

$$\min_{\mathbf{a}^{\min} \leq \mathbf{a} \leq \mathbf{a}^{\max}} \quad E(\mathbf{x}_b(\mathbf{a}))$$

where $\mathbf{a}^{\min}/\mathbf{a}^{\max}$ stack lower/upper bounds correspondingly to $\mathbf{a}$.



This type of minimization is non-trivial. Our energy is a quadratic sum of squares in $\mathbf{x}_b$, but $\mathbf{x}_b$ is a non-linear function of $\mathbf{a}$. In turn, this means to minimize E as a function of $\mathbf{a}$ we must solve a non-linear least squares problem.

Projected Gradient Descent

We're faced with a bound constrained non-linear optimization problem. To solve it, we will construct an initial guess and then iteratively improve the guess by moving in a direction that decreases E, after each step *snap* or project the guess to stay within the bounds if necessary. This algorithm is called *projected gradient descent*.

The idea behind *gradient descent* is intuitive: if you want to get to the bottom of a canyon, look at the ground and walk in the direction that goes downhill.

So, we iteratively take a step in the *negative* gradient direction of our objective function $E(\mathbf{x}(\mathbf{a}))$:

$$\mathbf{a} \leftarrow \mathbf{a} - \sigma \left(\frac{dE(\mathbf{x}(\mathbf{a}))}{d\mathbf{a}}\right)^T$$

Applying the chain rule, this iteration becomes

$$\mathbf{a} \leftarrow \mathbf{a} - \sigma \left(\frac{d\mathbf{x}(\mathbf{a})}{d\mathbf{a}}\right)^T \left(\frac{dE(\mathbf{x})}{d\mathbf{x}}\right)$$

where $\frac{dE}{d\mathbf{a}} \in \mathbf{R}^{|\mathbf{a}|}$, $\frac{dE}{d\mathbf{x}} \in \mathbf{R}^{|\mathbf{x}|}$, and $\frac{d\mathbf{x}}{d\mathbf{a}} \in \mathbf{R}^{|\mathbf{x}| \times |\mathbf{a}|}$

The change in tip positions $\mathbf{x}$ with respect to joint angles $\mathbf{a}$ does not depend on the choice of energy E. We call this matrix of changes the kinematic Jacobian, $\mathbf{J} \in \mathbf{R}^{|\mathbf{x}| \times |\mathbf{a}|}$:

$$\mathbf{J} = \frac{d\mathbf{x}}{d\mathbf{a}}.$$

Written in terms of $\mathbf{J}$ our step becomes,

$$\mathbf{a} \leftarrow \mathbf{a} - \sigma \mathbf{J}^{\mathsf{T}} \left(\frac{dE(\mathbf{x})}{d\mathbf{x}} \right)$$

> **Question:** Can we take an arbitrarily large step $\sigma >> 0$?
>
> **Hint:** What if we just need to change $\mathbf{a}$ by a small, non-zero amount? What would chooing $\sigma = 1,000,000$ do to $\mathbf{a}$? What would that in turn do to $E(\mathbf{x}(\mathbf{a}))$?

For sufficiently small σ, each step will decrease the objective energy E.

If the gradient of E becomes zero, then we're at a stationary point and likely at a minimum.

To ensure that our bounds are obeyed, after each step we need to *project* onto our constraints by snapping each value to its respective bound if necessary:

$$\mathbf{a}_i \leftarrow \max[\mathbf{a}_i^{\min}, \min[\mathbf{a}_i^{\max}, \mathbf{a}_i]].$$

We'll refer to this as a projection filter acting on the entire vector $\mathbf{a}$:

$$\mathbf{a} \leftarrow \mathrm{proj}(\mathbf{a}).$$

> **Newton's method**
>
> The local gradient of a function can be very different from the "best" descent direction. The choice of σ reflects how much we "trust" this direction. Unfortunately, if σ is too large our iterations may diverge. If σ is too small, we will have to do many iterations.
>
> In order to find a *better* descent direction, let's assume we knew *more* about E. That is, suppose we also knew its second derivatives: $\frac{d^2E}{d\mathbf{x}^2}$.
>
> Given an initial guess $\mathbf{x}^0$ we're looking to find a change $\Delta\mathbf{x}$ so that $E(\mathbf{x}^0 + \Delta\mathbf{x})$ is a stationary point.
>
> Starting with our equilibrium equation,
>
> $$\frac{dE(\mathbf{x})}{d\mathbf{x}} = \mathbf{0}$$
>
> we substitute in $x = \mathbf{x}^0 + \Delta\mathbf{x}$

$$\frac{dE(\mathbf{x}^0+\Delta\mathbf{x})}{d\Delta\mathbf{x}}=\mathbf{0}$$

Plugging in a Taylor series expansion

$$E(\mathbf{x}^0+\Delta\mathbf{x})\approx E(\mathbf{x}^0)+\frac{dE(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}}\Delta\mathbf{x}+>\frac{d^2E(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}^2}\frac{(\Delta\mathbf{x})^2}{2}+\dots$$

and dropping higher order terms $(\dots)$, we get:

$$\frac{d}{d\Delta\mathbf{x}}(E(\mathbf{x}^0)+\frac{dE(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}}\Delta\mathbf{x}+\underbrace{\frac{d^2E(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}^2}}_{\mathbf{H}}\frac{(\Delta\mathbf{x})^2}{2})=\mathbf{0},$$

where we call $\mathbf{H}\in\mathbf{R}^{|x|\times|x|}$ the Hessian matrix.

Applying the differentiation by $\Delta\mathbf{x}$ we get a system of equations:

$$\frac{dE(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}}+\frac{d^2E(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}^2}\Delta\mathbf{x}=\mathbf{0}.$$

Solving for the change Δx we get:

$$\Delta x=-\mathbf{H}^{-1}\frac{dE(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}}.$$

So a *raw* Newton's method update would be:

$$\mathbf{x}\leftarrow\mathbf{x}-\mathbf{H}^{-1}\frac{dE(\mathbf{x}^0+\Delta\mathbf{x})}{d\mathbf{x}}.$$

If our Taylor series approximation was perfect (no high order terms in $\dots$; in otherwords E was quadratic), then Newton's method would be perfect: a single update immediately takes us to the minimum.

Newton's method is problematic for a number of reasons.

1. We built our step purely based on the equations for a stationary point. Nothing says we won't get sent toward a maximum or saddle-point.
2. $\mathbf{H}$ is often difficult or expensive to compute.
3. $\mathbf{H}$ may be singular.
4. Inverting $\mathbf{H}$ (even if possible) is often slow.
5. Our system is built off a local approximation of E so the descent direction may *still* point in the wrong direction.

Since we're approximating E at every iteration anyway, we'll skirt many of these issues by considering various approximations of the Hessian matrix $\mathbf{H}$. We'll never actually compute $\mathbf{H}$.

Gradient Descent *Revisited*

The simplest approximation of $\mathbf{H}$ is the identity matrix $\mathbf{I}$. Plugging this into our truncated Taylor series expansion above, our approximation would read:

$$E(\mathbf{x}^0) + \frac{dE(\mathbf{x}^0 + \Delta\mathbf{x})}{d\mathbf{x}} \Delta\mathbf{x} + \mathbf{I}\frac{(\Delta\mathbf{x})^2}{2}.$$

and our step reduces to good ol' gradient descent:

$$\mathbf{x} \leftarrow \mathbf{x} - \frac{dE(\mathbf{x}^0 + \Delta\mathbf{x})}{d\mathbf{x}}.$$

Gauss-Newton

Given that we have already computed first derivatives in the Jacobian $\mathbf{J} >= \frac{d\mathbf{x}(\mathbf{a})}{d\mathbf{a}}$, an even better approximation for Hessian $\mathbf{H}$ than the identity $\mathbf{I}$ would be to use $\mathbf{J}^{\mathsf{T}}J$. The resulting update becomes:

$$\mathbf{a} \leftarrow \mathbf{a} + (\mathbf{J}^{\mathsf{T}}\mathbf{J})^{-1}\,\mathbf{J}^{\mathsf{T}}\frac{dE(\mathbf{x})}{d\mathbf{x}}$$

Unlike $\mathbf{H}$, $\mathbf{J}^{\mathsf{T}}\mathbf{J}$ is easy to compute if we're already computing $\mathbf{J}$. It is guaranteed to be positive semi-definite and it is possible to invert or reliably pseudo-invert ($\mathbf{J}^{+}$ acting in place of $(\mathbf{J}^{\mathsf{T}}\mathbf{J})^{-1} > \mathbf{J}^{\mathsf{T}}$).

The descent directions are often significantly better than gradient descent. As a result this method, called Gauss-Newton, requires many fewer iterations to converge.

It still may try to descend in bad directions. In particular, for inverse kinematics, this Gauss-Newton method performs poorly if the desired positions are not reachable: over extending an arm. First the solution locks in place and then diverges. This happens when our Hessian approximation $\mathbf{J}^{\mathsf{T}}\mathbf{J}$ starts misbehaving.

A good fix is to blend between the gradient descent and Gauss-Newton search directions. That is blend between $\mathbf{I}$ and $\mathbf{J}^{\mathsf{T}}\mathbf{J}$. This is called the Levenberg-Marquadt algorithm.

Finite Differencing

But how do we compute the kinematic Jacobian $\mathbf{J}$? Since each entry in $\mathbf{x}$ is the result of forward kinematics and not just a math expression, it's not immediately obvious how to determine its derivatives. However, a derivative is nothing more than the limit of a small change output divided by a small change in the input:

$$\mathbf{J}_{i,j} = \lim_{h \to 0} \frac{\mathbf{x}_i(\mathbf{a} + h\delta_j) - \mathbf{x}_i(\mathbf{a})}{h},$$

where $\delta_j \in \mathbf{R}^{|a|}$ is a vector of zeros except a 1 at location j.

We can numerically approximate this limit by fixing h to a small value (e.g., $h = 10^{-7}$). This is called the finite difference approximation:

$$\mathbf{J}_{i,j} \approx \frac{\mathbf{x}_i(\mathbf{a} + h\delta_j) - \mathbf{x}_i(\mathbf{a})}{h}.$$

For inverse kinematics, we will need to compute $\mathbf{x}_i(\mathbf{a} + h\delta_j)$ once for each Euler angle of each bone j. This requires $3m$ calls to our forward kinematics function (each with a slightly different input), which is in turn $O(m)$. This makes the total cost $O(m^2)$ to fill in our $\mathbf{J}$ matrix.

> **Automatic Differentiation**
>
> Forward differencing requires $O(m)$ evaluations but doesn't require us to change our code for function evaluation *at all*: we just evaluate it. If we're willing to sprinkle some special types on top of our code (but otherwise leave in all the sub-routine calls, if statements, for loops, etc.), we could use automatic differentiation to compute $\mathbf{J}$.
>
> The are two extremes when it comes to autodiff: forward mode and backward mode.
>
> **Forward mode** works like finite differencing, except the perturbation to the differentiation variable is symbolic and derivatives are tracked through each basic operation (`+` , `-` , `sin` ,etc.): the total computational cost to construct $\mathbf{J}$ is again $O(m^2)$
> .
>
> **Backward mode** works by pushing each function call and basic operation onto a list. Derivatives for all variables are then computed as we pop backward through the evaluation: identical to how we read right-to-left on our recursive kinematics formula. This means we compute derivatives with respect to all variables $\mathbf{a}$ in a single *backwards* evaluation. The total cost is only $O(m)$ to fill $\mathbf{J}$.

Line Search

Whether we're using gradient descent, Newton's method or Gauss-Newton, we a generally *attempting* improving our guess by iteratively moving in a descent direction $\Delta \mathbf{a}$, followed by projecting onto constraints:

$$\mathbf{a} \leftarrow \mathrm{proj}(\mathbf{a} + \Delta \mathbf{a}).$$

Despite our best efforts, this step is not guaranteed to actually decrease our energy E. We can think of the descent *direction* $\Delta \mathbf{a}$ as defining a line (or really a *ray*) and we'd like to find a positive amount σ to move along this line that actually does decrease the energy:

$$E(\mathrm{proj}(\mathbf{a} + \sigma \Delta \mathbf{a})) < E(\mathbf{a}).$$

While there exists an optimal step σ, we don't want to spend too long finding it as we would be better off spending our computational efforts improving the descent *direction* for the next step. So, starting with a large value σ (e.g., 10,000), we decrease σ by a constant factor (e.g., $\frac{1}{2}$) until our inequality passes.

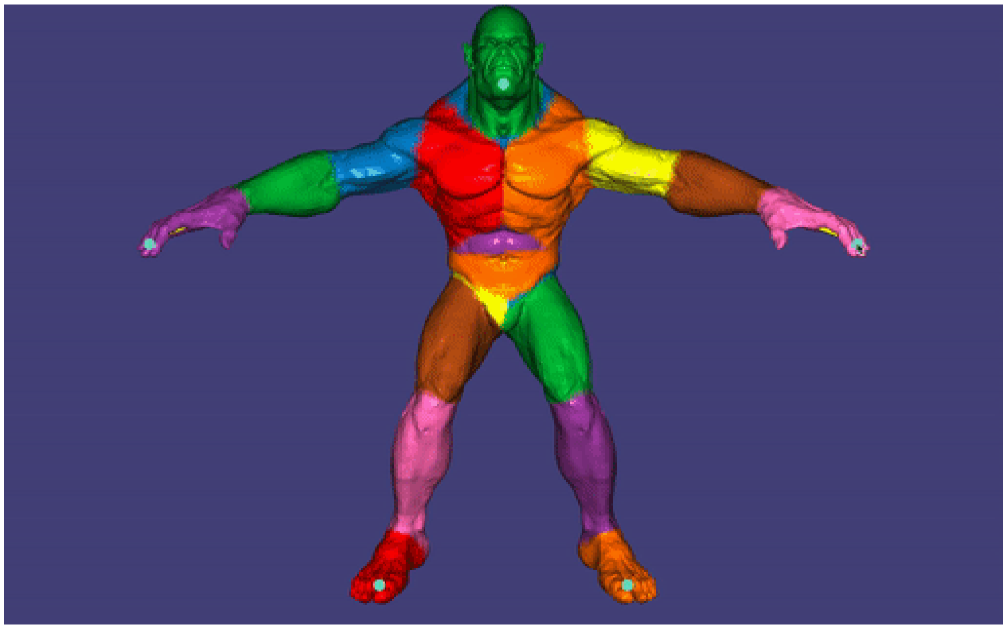
Depending on the configuration, it may or may not be possible to exactly satisfy the constraints (i.e., $E = 0$). But after many iterations, the solution should converge to a local minimum (i.e., $E > 0$, but $dE/d\mathbf{a} = 0$). In our assignment, a thin line will appear if the user-given constraint is not coincident with the end-effector tip position.

Linear Blend Skinning

So far we have only discussed bones floating and moving around in space. Ultimately, we would like to deform interesting models: for example, animals and characters. Unlike robots or mechanical objects, the animals tend to deform smoothly, even near joints: an elbow does not tear into two rigid parts when bent. Instead, the skin around the elbow stretches and smoothly warps. Skin closer to the forearm deforms more like the rigid rotation and translation of the forearm, and likewise the skin near the upper arm deforms like the rigid upper arm bone. In between, we see a smooth transition or blend.

To approximate this smooth blending quickly on the computer, we begin with a 3D triangle mesh in its "rest" position. The "rest bones" are embedded inside of this model. Each vertex i of the mesh is assigned a weight $w_{i,j}$ for each bone j corresonding to how much it is "attached" to that bone on a scale of 0% to 100%. Generally, if the rest position of the vertex $\widehat{\mathbf{v}}_i$ is nearer to a bone j then its weight $w_{i,j}$ will be larger. A vertex in the middle of the elbow may have a weight of 50% for the upper arm and 50% the forearm and 0% for all other bones (toes, fingers, legs, spine, etc.).

Smoothly varying weights produce a smooth deformation. In constrast, piecewise-constant weights lead to a piece-wise rigid deformation.



The "pose" position $\mathbf{v}_i$ of this vertex i will be computed as a weighted average or linear combination of each bone's pose transformation $\mathbf{T}_j$ applied to the vertex's rest position $\widehat{\mathbf{v}}_i$:

$$\mathbf{v}_i = \sum_{j=1}^{m} w_{i,j} \mathbf{T}_j \begin{pmatrix} \widehat{\mathbf{v}}_i \\ 1 \end{pmatrix}.$$

> **Question:** What happens to per-vertex normals after applying a skinning deformation?

> **Hint:** 🤯

Linear blend skinning has many defects. Good "rigging artists" can mitigate these by carefully painting (yes, painting) weight functions and position the rest bones. However, some of the linear blend skinning defects are theoretical: most notably problems that occur by averaging rotations as matrices.

> **Question:** What transformation matrix do you get if you compute: $\frac{1}{2}\mathbf{R}_x(90^\circ) + \frac{1}{2}\mathbf{R}_x(-90^\circ)$?
>
> **Hint:** It's not $\mathbf{R}_x(0^\circ)$.

Tasks

White List

- `Eigen::Affine3d`
- `Eigen::AngleAxis`
- `#include <Eigen/Geometry>`
- c++ lambda functions and capturing `#include <functional>`

Black List

- `igl::lbs`
- `igl::forward_kinematics`

`src/euler_angles_to_transform.cpp`

`src/forward_kinematics.cpp`

`src/transformed_tips.cpp`

`src/catmull_rom_interpolation.cpp`

`src/linear_blend_skinning.cpp`

`src/copy_skeleton_at.cpp`

`src/end_effectors_objective_and_gradient.cpp`

`src/kinematics_jacobian.cpp`

`src/projected_gradient_descent.cpp`

`src/line_search.cpp`

> ## Notes for TAs editing the README
>
> This README file is too complex for texify to render. Use readme2tex locally to render the TeX to SVGs.
>
> `python -m readme2tex --output README.md README.tex.md --nocdn`
>
> `sed -i 's/invert_in_darkmode\"/invert_in_darkmode\&sanitize=true\"/g' README.md`

Releases

No releases published

Packages

No packages published

Languages

● **C++** 93.4% ● **MATLAB** 3.5% ● **CSS** 1.9% ● **Other** 1.2%