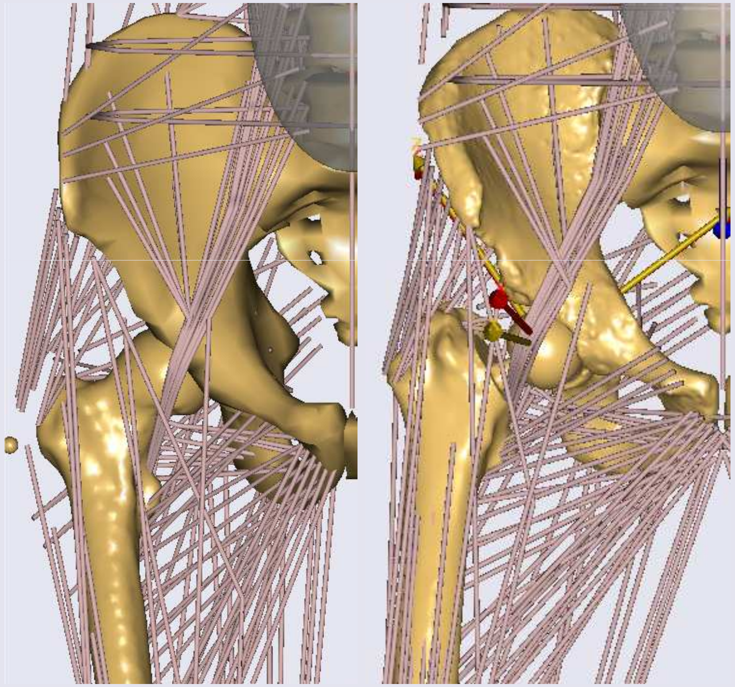
Patient-specific morphing of musculoskeletal models



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People

John Rasmussen
(Presenter)

Søren Tørholm
(Host)

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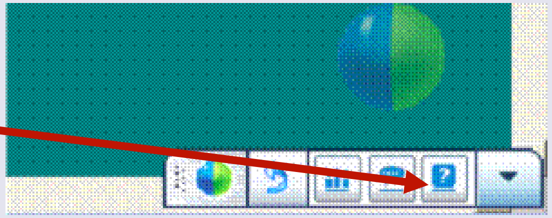
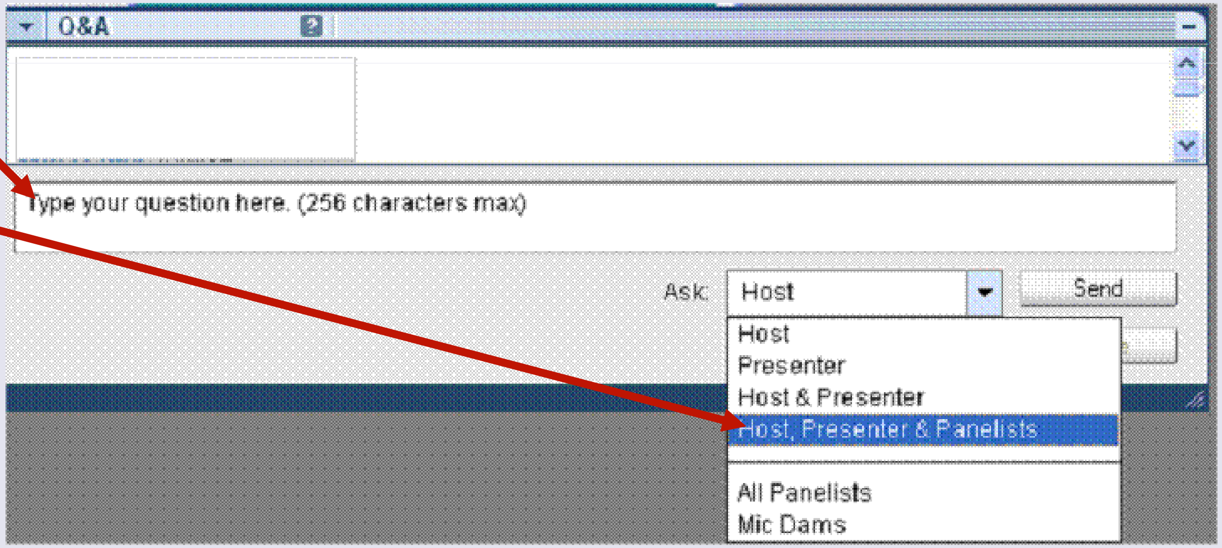
Q&A Panel

- Søren Tørholm
- Launch the Q&A panel here.
- Type your questions in the Q&A panel.
- Send the question to ”Host, Presenter & Panelists”
- Notice the answer displays next to the question in the Q&A box. You may have to scroll up to see it.





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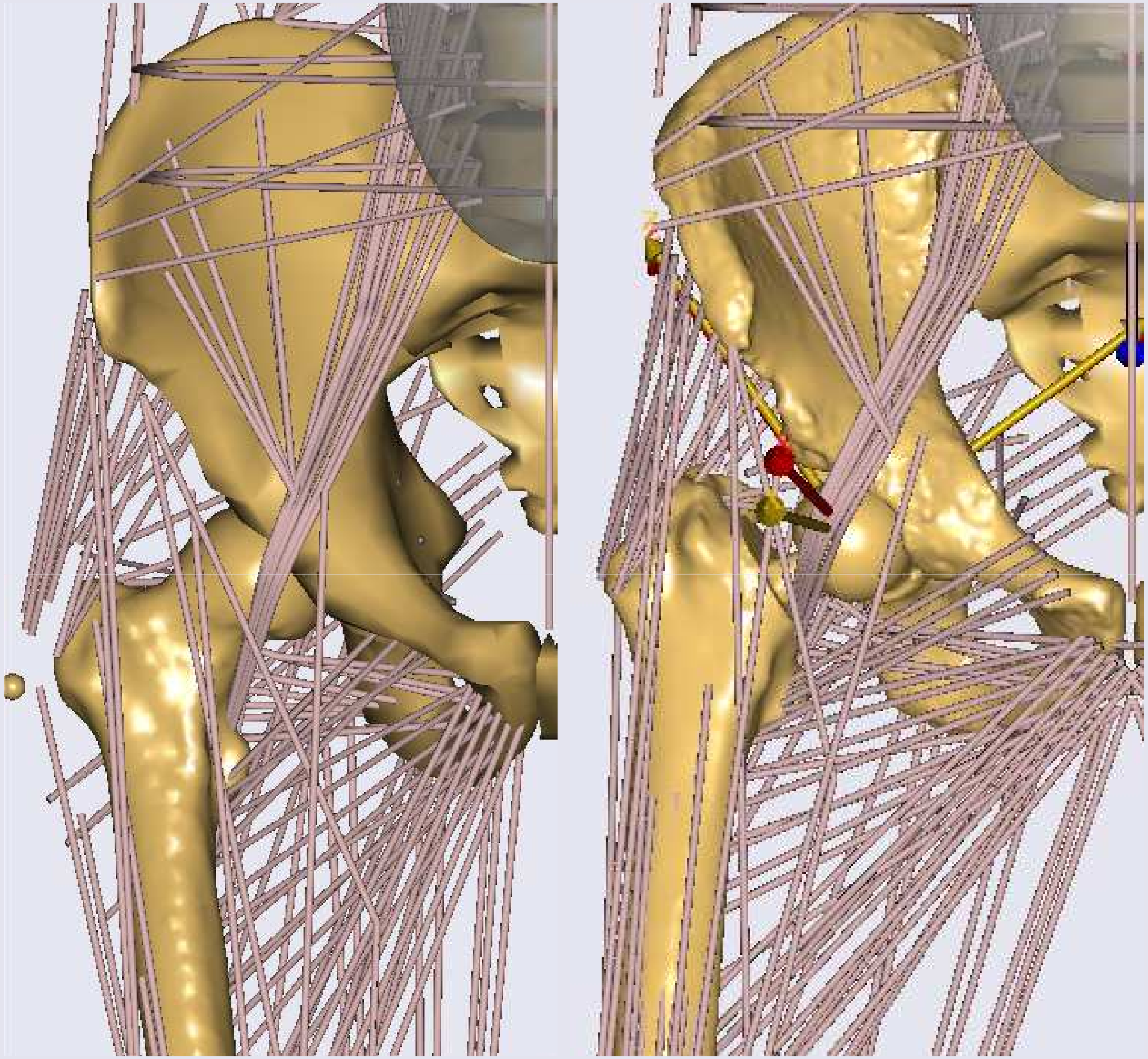
Scaling Scenarios

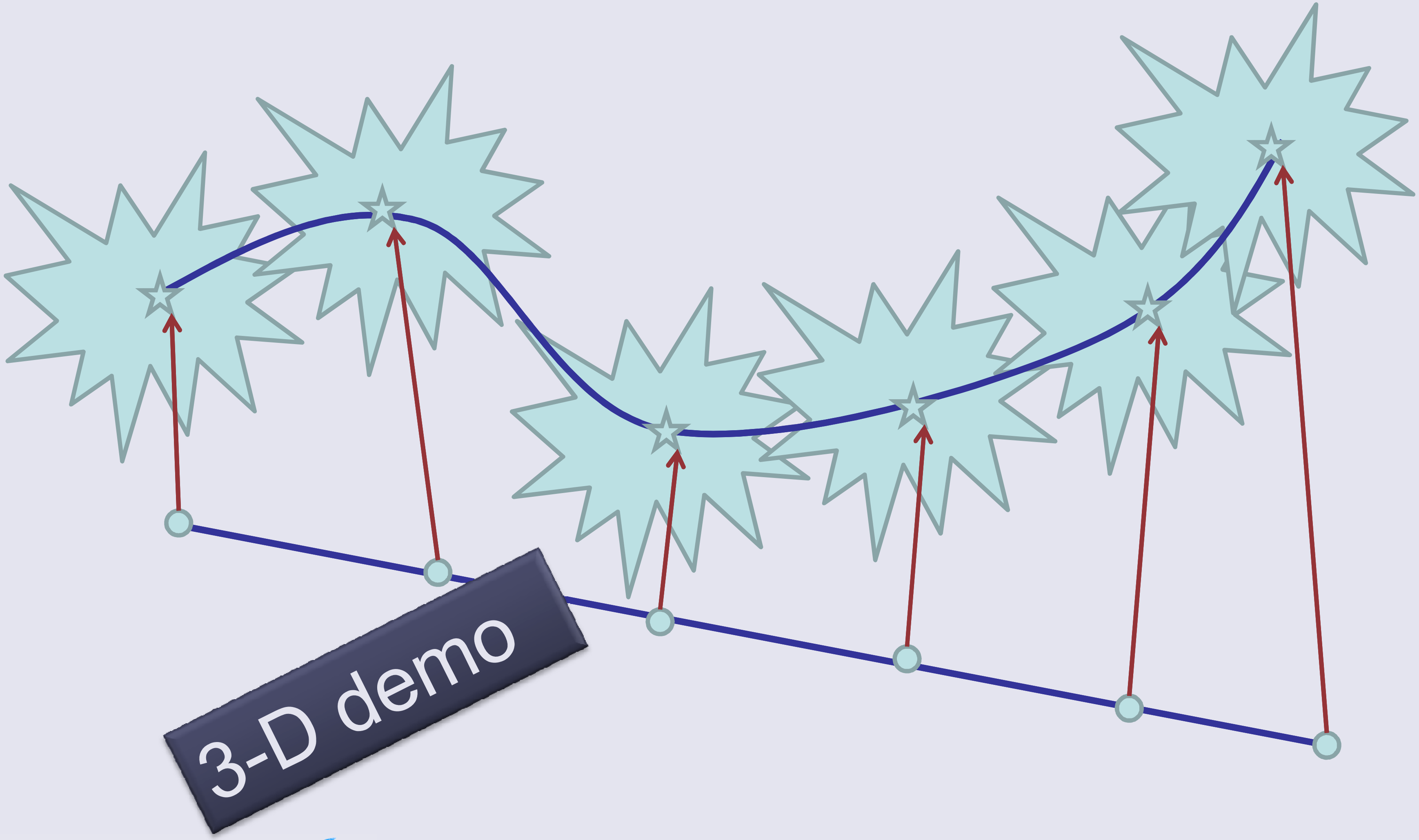
- Detailed level
  - Purpose-specific modeling based on scans, ultrasound data, and similar.
  - Detailed data for each model element.
- Individual level
  - Sports biomechanics for a particular athlete
  - Gait analysis of a particular individual
- Overall population level
  - Investigate ergonomic compatibility for a broad range of the population
  - Based on anthropometric databases



Ingredients

- Scanned patient-specific data from MRI, CT or similar.
- Software to process the raw data like Mimics™ or Simpleware™.
- The AnyBody Modeling System
- The AnyScript Managed Model Repository

Radial Basis Functions (RBF)



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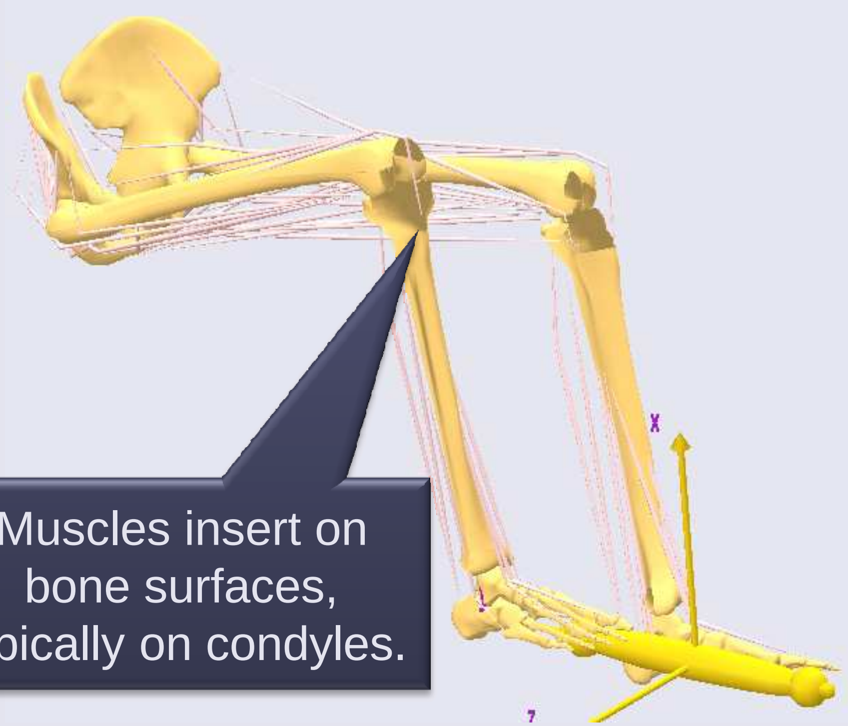
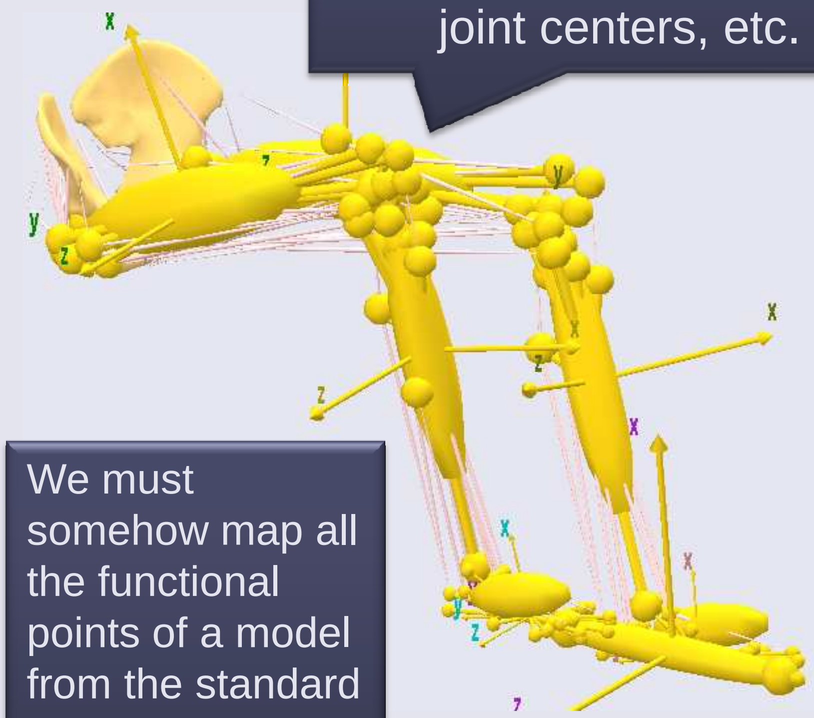
Observations

- Morphing maps one set of points on another set of points.
- Origin and target points are finite sets, i.e. not infinitely many.
- The mapping between the finite sets is then used on the entire geometry, i.e. infinitely many points.

How a segment is defined in AnyBody



Muscles insert on bone surfaces, typically on condyles.



Geometry – point cloud of muscle insertion points, joint centers, etc.

We must somehow map all the functional points of a model from the standard locations to the patient-specific locations

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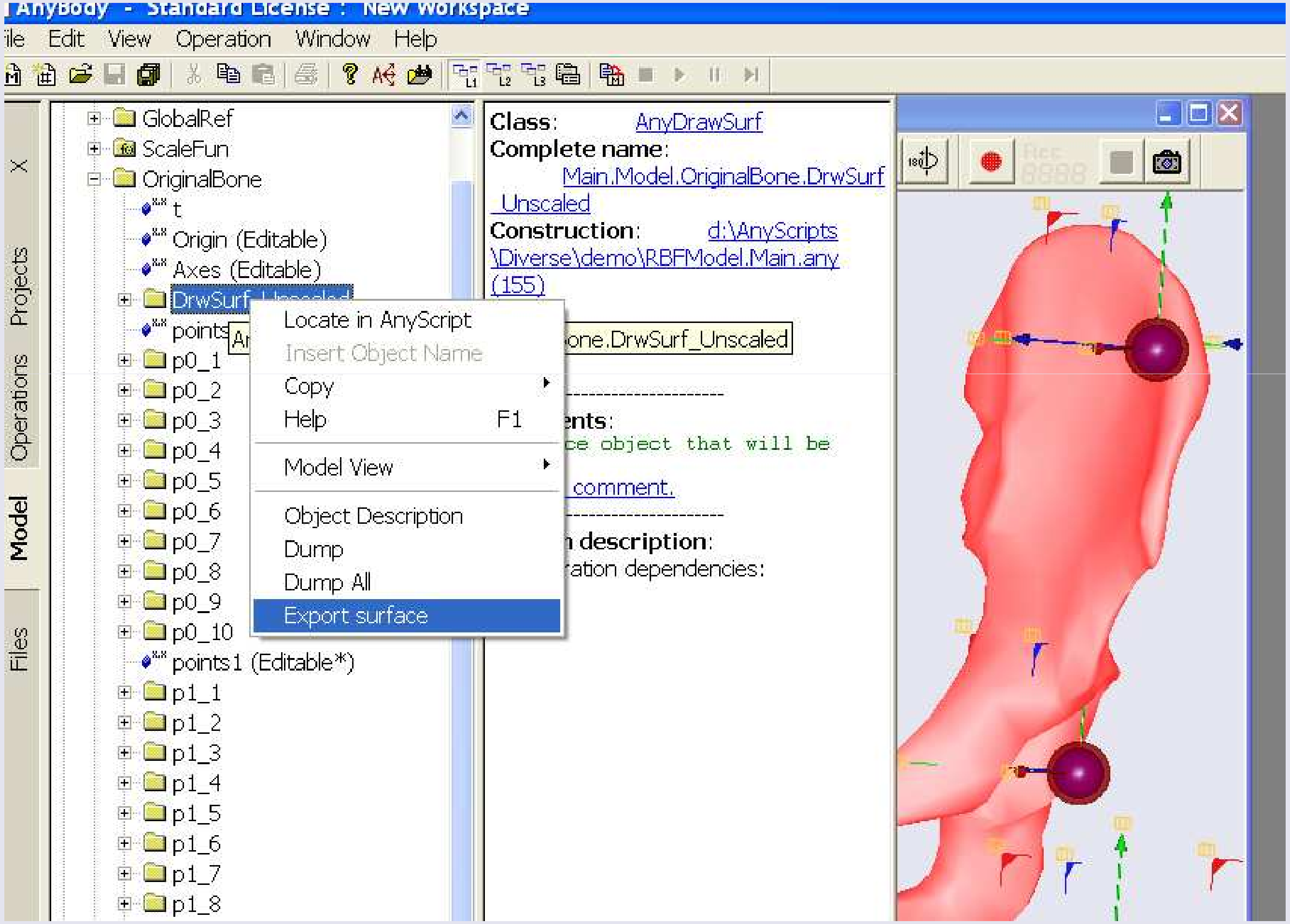
Export original surface from AnyBody



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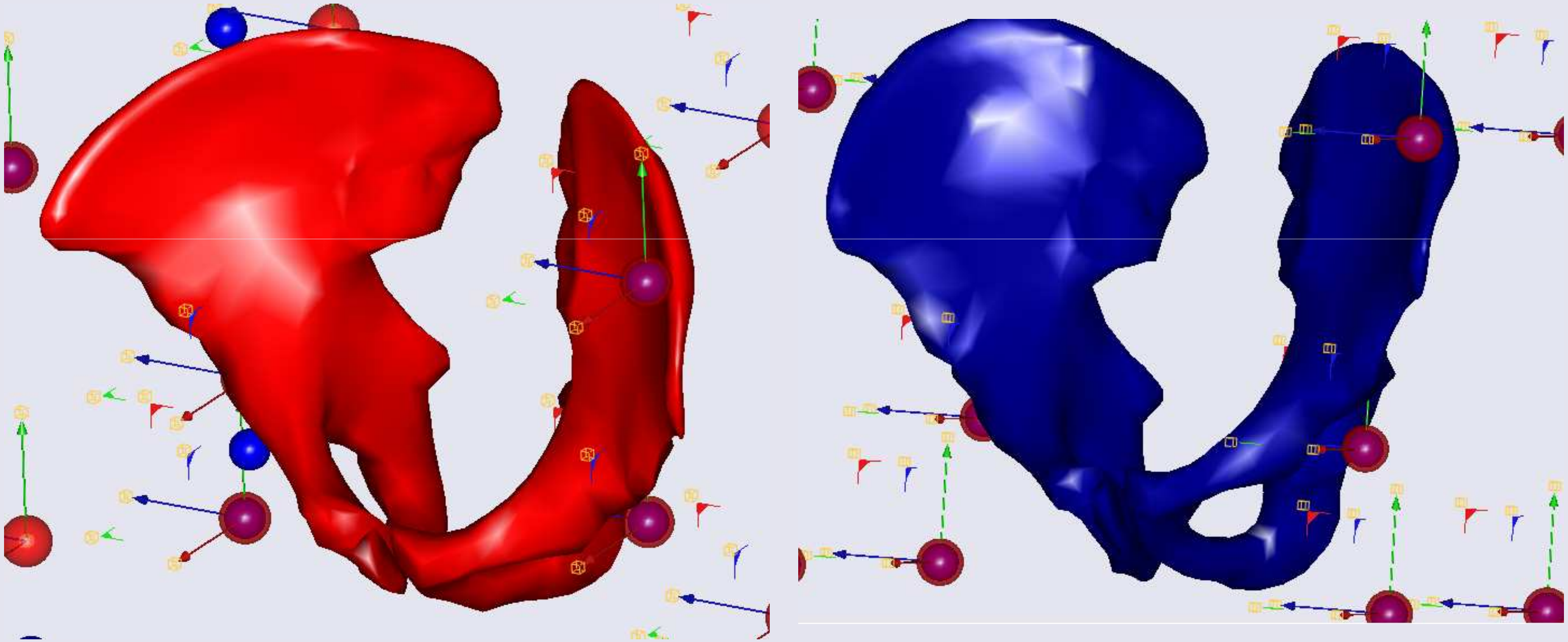
Import AnyBody bone and patient-specific bone into the image processing software



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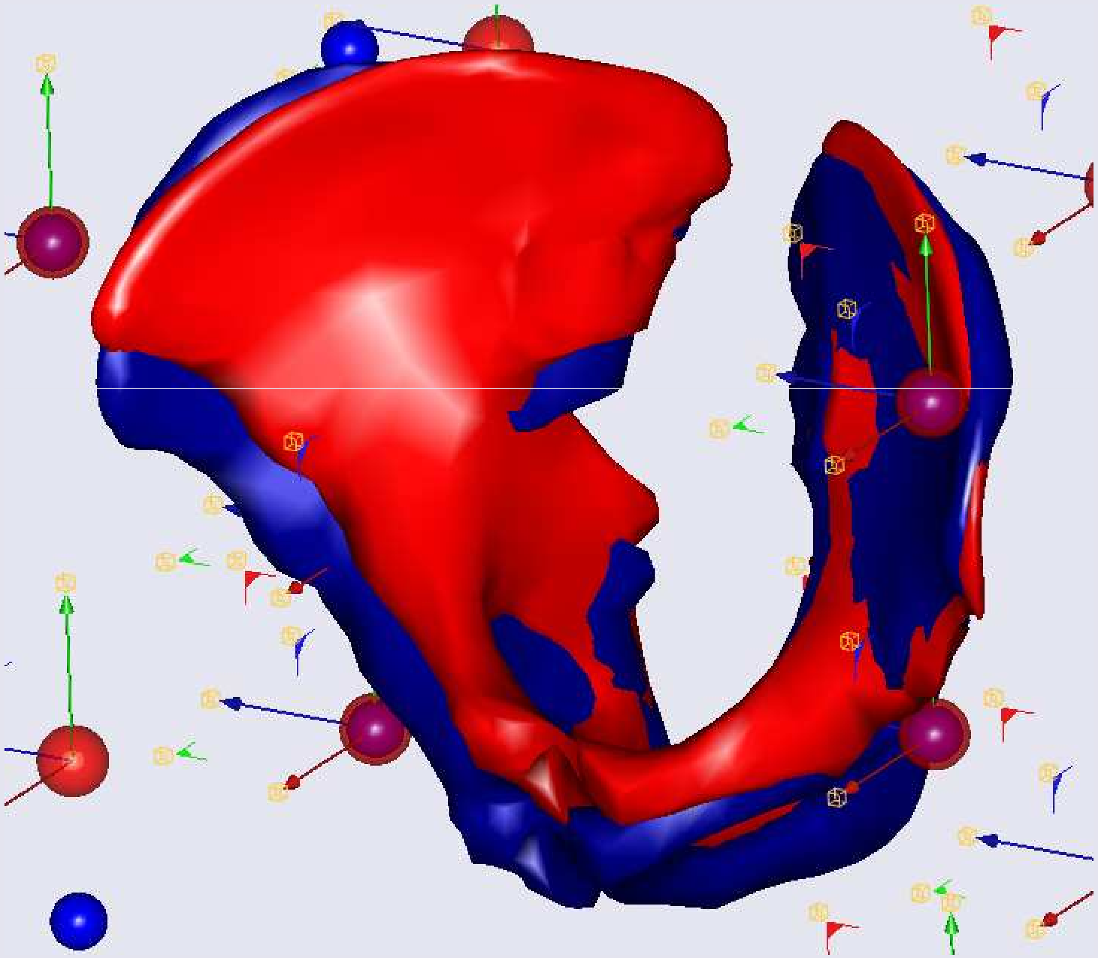
Register the patient-specific bone on the original



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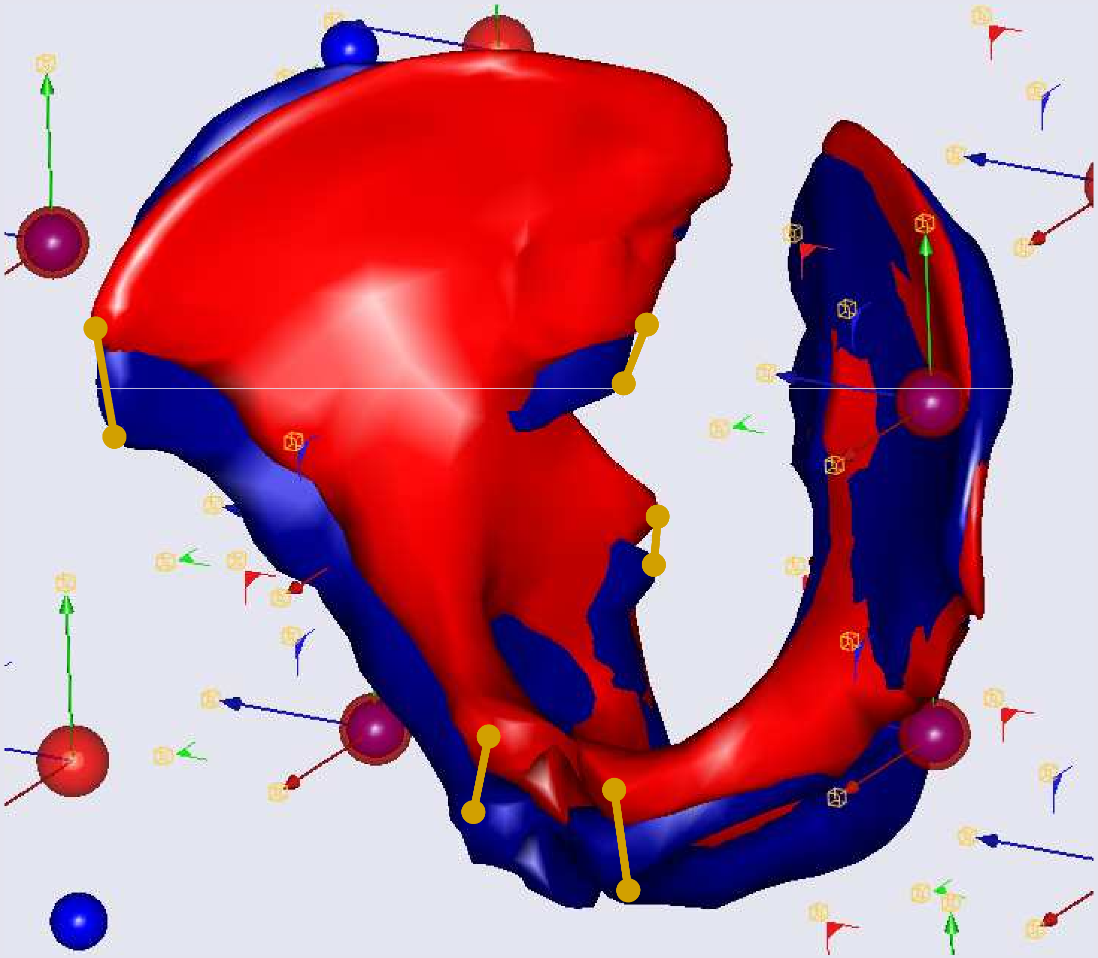
Identify pairs of bony landmarks and save their coordinates



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Import the coordinate pairs into AnyBody

```
AnyFolder Model = {
  AnyFunTransform3DRBF ScaleFunctionL5 = {
    RBFDef.Type = RBF_Gaussian;
    RBFDef.Param = 1;
    PolynomDegree = 1;

    AnyMatrix randomshift = {
      {-0.003895,    -0.001451,     0.001701},
      {-0.008618,     0.001028,    -0.002344},
      {-0.001458,     0.002645,    -0.002440},
      {-0.002999,    -0.002629,    -0.001487},
      { 0.002042,    -0.001206,    -0.002876},
      {-0.002533,     0.002108,     0.002388},
      { 0.002364,    -0.001066,     0.001906},
      { 0.001912,     0.001885,    -0.000878},
      { 0.002069,    -0.001692,     0.001183},
      {-0.002830,    -0.001915,    -0.002315},
      {-0.002085,    -0.001003,    -0.002280},
      {-0.001388,     0.002440,    -0.002179},
      { 0.009382,     0.001788,    -0.001514},
      { 0.002813,     0.002817,     0.001695},
      {-0.002273,     0.002215,    -0.002401}
    };
    Points0 = {
      { 0.072462,     1.180805,    -0.036767},
      { 0.072462,     1.180805,     0.036767},
      { 0.044390,     1.173952,     0.000001},
      { 0.063322,     1.190380,    -0.022513},
      { 0.063322,     1.190380,     0.022513},
      { 0.065274,     1.155646,    -0.013893},
      { 0.065274,     1.155646,     0.013893},
      { 0.117145,     1.179924,     0.000001},
      { 0.107595,     1.150322,     0.000001},
      { 0.085754,     1.186174,     0.000001},
      { 0.081586,     1.161476,     0.000001},
      { 0.099929,     1.182663,    -0.023310},
      { 0.099929,     1.182663,     0.023310},
      { 0.093791,     1.158033,    -0.023417},
      { 0.093791,     1.158033,     0.023417}
    };
    Points1 = Points0 + randomshift;
```

- Define a scaling function of type AnyFunTransform3DRBF
- Define two sets of points
  - Points0
  - Points1

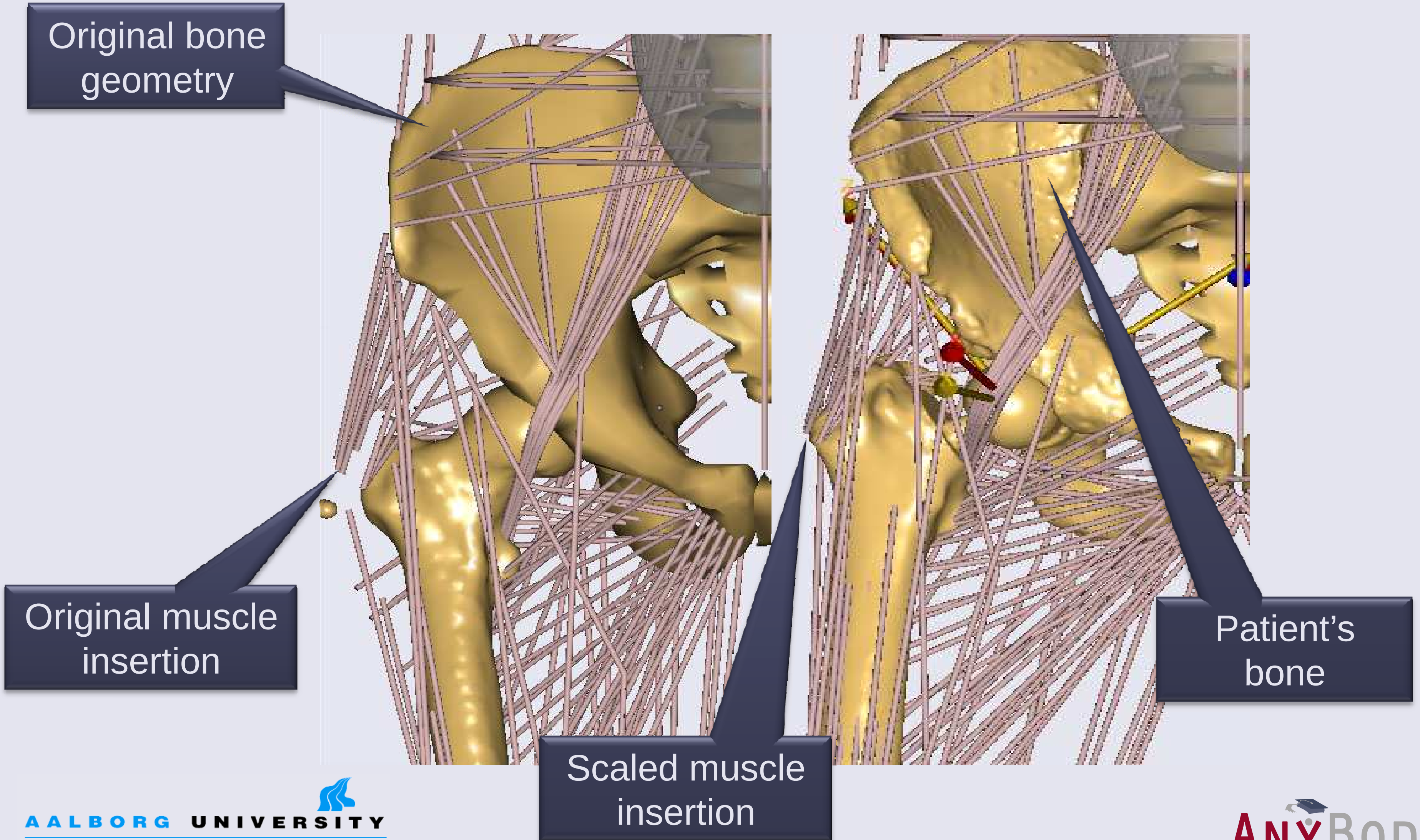
Use the scaling function for the definition of any other node

```
AnyRefNode s1 = {
    sRel= ..ScaleFunctionL5({0.075, 1.19, -0.0322});
};
```

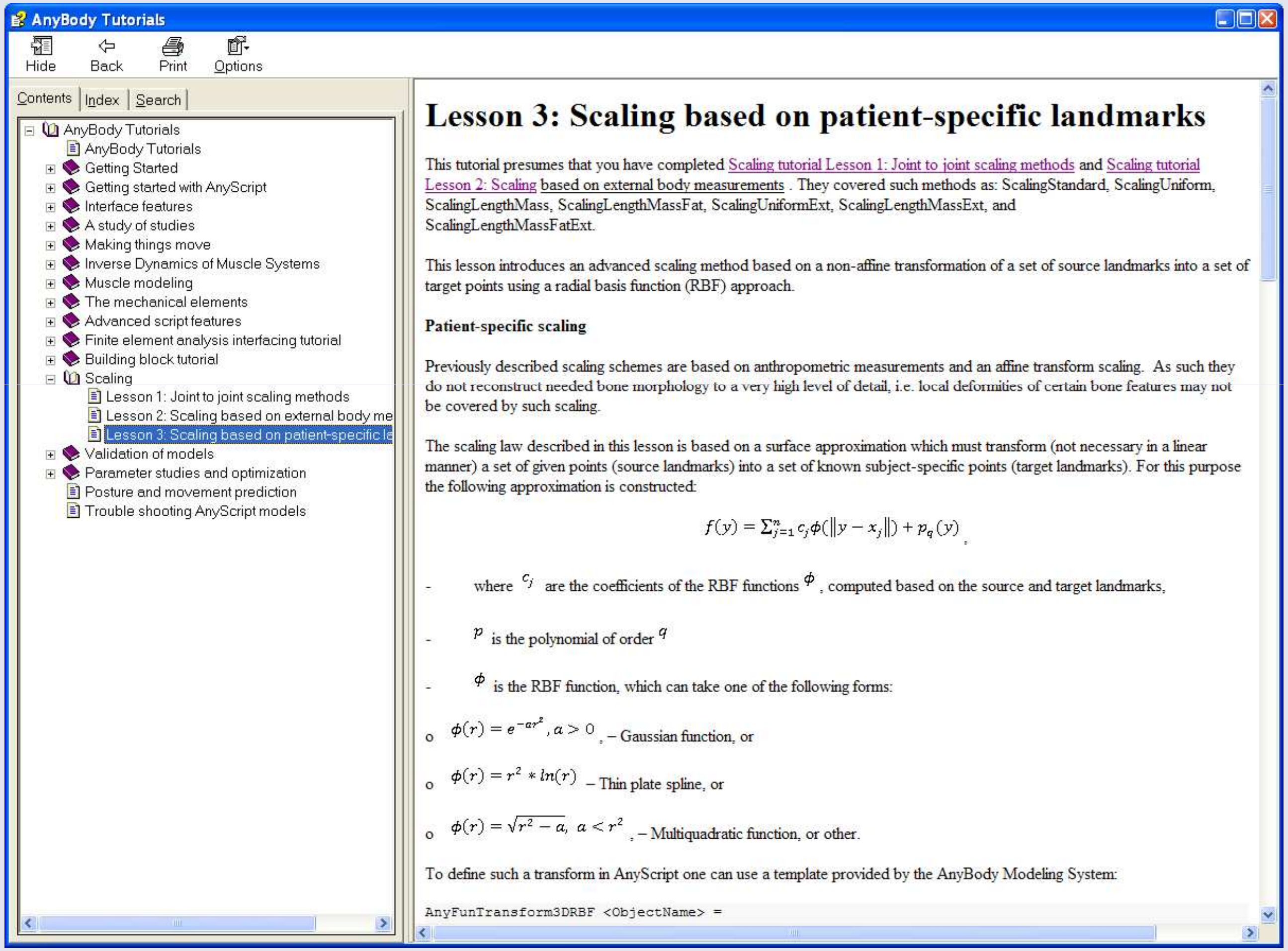
Scaling function defined by point pairs

Any other point, for instance a muscle attachment point sent through the function.

A closer look at our example



Tutorial



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Lesson 3: Scaling based on patient-specific landmarks
This tutorial presumes that you have completed Scaling tutorial Lesson 1: Joint to joint scaling methods and Scaling tutorial Lesson 2: Scaling based on external body measurements . They covered such methods as: ScalingStandard, ScalingUniform, ScalingLengthMass, ScalingLengthMassFat, ScalingUniformExt, ScalingLengthMassExt, and ScalingLengthMassFatExt.
This lesson introduces an advanced scaling method based on a non-affine transformation of a set of source landmarks into a set of target points using a radial basis function (RBF) approach.
Patient-specific scaling
Previously described scaling schemes are based on anthropometric measurements and an affine transform scaling. As such they do not reconstruct needed bone morphology to a very high level of detail, i.e. local deformities of certain bone features may not be covered by such scaling.
The scaling law described in this lesson is based on a surface approximation which must transform (not necessary in a linear manner) a set of given points (source landmarks) into a set of known subject-specific points (target landmarks). For this purpose the following approximation is constructed:
$f(y) = \sum_{j=1}^{n} c_j \phi(\|y - x_j\|) + p_q(y)$
- where c_j are the coefficients of the RBF functions ϕ , computed based on the source and target landmarks,
- p is the polynomial of order q
- ϕ is the RBF function, which can take one of the following forms:
o $\phi(r) = e^{-ar^2}, a > 0$ – Gaussian function, or
o $\phi(r) = r^2 * ln(r)$ – Thin plate spline, or
o $\phi(r) = \sqrt{r^2 - a},\ a < r^2$ – Multiquadratic function, or other.
To define such a transform in AnyScript one can use a template provided by the AnyBody Modeling System:
AnyFunTransform3DRBF <ObjectName> =

Final remarks

- RBF scaling is <u>not primarily</u> a method to morph a standard bone to a patient's bone – we already have the patient's bone from the scan.
- RBF scaling uses the difference between the two bones to map existing musculoskeletal data that we do not have from scans from the standard model to the patient.

Online resources

- www.anybodytech.com
  - Free demo license for the AnyBody Modeling System
- www.AnyScript.org
  - Discussion forum
  - Wiki
  - Model repository
- www.anybody.aau.dk
  - Homepage of the research group

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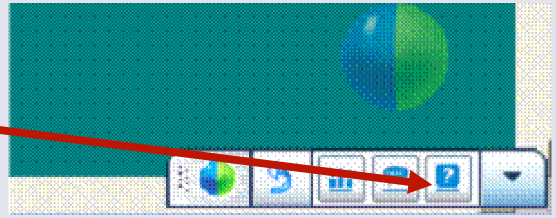

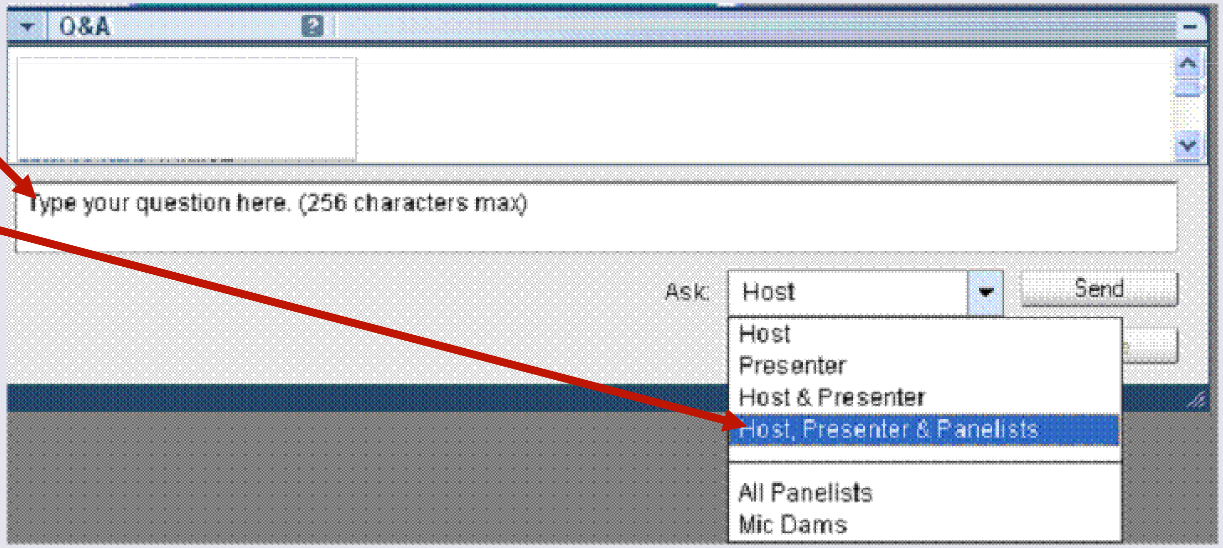

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