A Human Pose Prior based on Pose-Conditioned Joint-Angle Limits

In this code, we provide our pose-dependent joint-angle limits that
can be used to decide whether a 3D pose is valid or not. We can also
formulate a human pose prior based on these joint-angle limits. The
proposed prior can be used for problems where estimating
3D human pose is ambiguous.

Defining the 3D Pose
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The 3D pose is defined by a 3-by-17 matrix consisting of 3D
coordinates of joints. The joints in the matrix should have the
following order.

1: belly, 2: R-shldr, 3: R-elbow, 4: R-wrist, 5: L-shldr, 6: L-elbow,
7: L-wrist, 8: Neck, 9: face, 10: R-hip, 11: R-knee, 12: R-ankle,
13: R-foot, 14: L-hip, 15: L-knee, 16: L-ankle, 17: L-foot

If you don't have feet in your model then you can use NaN as their 3D
coordinates in the pose matrix.

Using the code
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There is an isvalid function in this directory which takes a 3D pose
as input and returns a binary vector telling whether the corresponding
bone is valid or not. Run demo to see how to use this function.

We can also use the isvalid function to define a prior on human pose.
This prior can be used to constrain your optimization problem, if you
don't have enough constraints to ensure the validity of 3D pose. The
proposed prior will make sure that the 3D pose remains valid in every
iteration of the optimization. This can be done by adding a penalty-
term C_{prior} to the cost you want to minimize. C_{prior} will be zero if all the
bones in the 3D pose are valid and ∞ otherwise.

$$C_{prior} = 0 \ \text{if} \ \text{all}(isvalid(\mathbf{X}))$$
$$\infty \ \text{else}$$

C_{prior} does not require you to change the jacobian or do any other change
in the optimization. The only thing you need to make sure is that the
initialization of the optimization should be a valid 3D pose.

Note: If you are using our prior in an optimization, then for time-
efficiency, you may want to avoid the loading of training parameters
in isvalid function in each iteration of the optimization. You may
consider pre-allocation of all the parameters in jointAngleModel.mat
in the parent function. You can declare them as global there.

What is there in JointAngleModel.mat?
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angleSprd: a cell array of binary matrices. This is used to evaluate
the limits for left and right elbow and knee.

boundaries: a cell array consisting of bounadry

sepPlane: a cell array of 3D matrices to define the separating planes
for local coordinates of joints. The values ranges between [-1,1].

bounds: a cell array to define bounding boxes for 2D projections of
local 3D coordinates. The values ranges between [-1,1].

E2: a cell array of 3D matrices consisting of normal vectors for 2D
projection. The values ranges between [-1,1].

The rest: arrays di and a are used to define local coordinate axes for
each joint. jmp (equal to 3) is the discretization we used for binning
the polar and azimuthal angles. edges consists of the connectivity of
points in the 3D pose. chlds and prnts define the child and parent
relationship in the skeleton.

Visualization of Joint-Angle-Limits
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In order to have a sense of what are the joint angle limits, we also
provide a visualization. For this purpose, go to the visualization
directory and run runJointLimitsVisualization. This will create the
following figure.
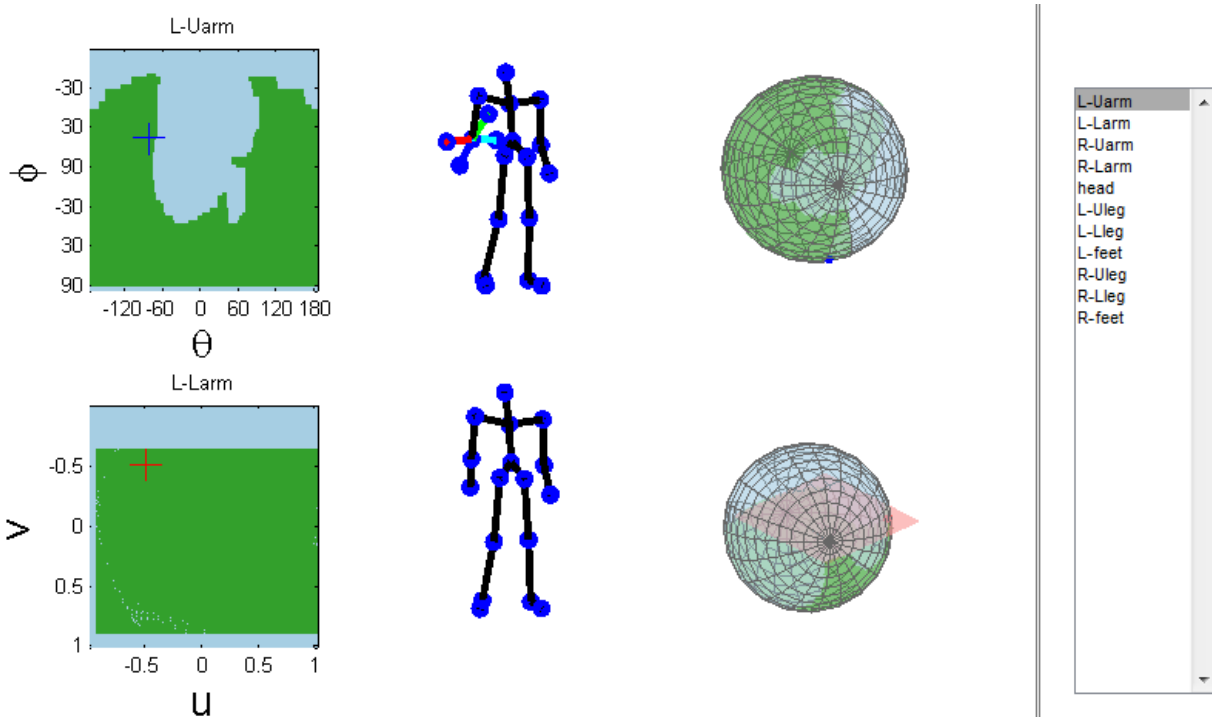
On the right panel you can select different bones in the human skeleton. For the selected bone you will see corresponding six subplots. In the figure we selected right lower-arm. The top-right are the plots of 3D local coordinates of right-elbow in all the instances of training data. The top left shows the corresponding polar and azimuthal angles. White area shows the valid region for the elbow whereas black is invalid. Moving around the pink plus sign shows the corresponding elbow location in the bottom middle. The corresponding conditional instances of wrist are shown in the bottom right. The planar patch define the separating plane for the wrist. The 2D projection of the wrist locations are plotted in the bottom left. You can move the green plus sign to see the corresponding wrist location in bottom middle.

You can press R to rotate the right and middle plots. Pressing R again will stop the rotation.

License
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Ijaz Akhter and Michael Black, "Pose-conditioned joint angle limits for 3D human pose reconstruction", CVPR 2015