H3WB: Human3.6M 3D WholeBody Dataset and Benchmark (Supplementary Material)

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1. Supplementary material – Overview

In this supplementary material:

- We share the link to download the H3WB dataset annotation files (Section 2);
- We provide the H3WB 3D whole-body dataset keypoint layout with 133 keypoints. H3WB dataset follows exactly the same layout as COCO WholeBody dataset [4] (Section 3);
- We provide the statics regarding the diversity of H3WB dataset (Section 4);
- We present web interface of the quality assessment (Section 5);
- We provide more qualitative results for all tasks, as well as qualitative results in the wild evaluated on the COCO dataset (Section 6);
- We study failure cases from SMPL-X extracted from the literature (Section 7);
- We report the results of our 5-fold cross-validation experiments (Section 8);
- We clarify long-term support planning and the license issue (Section 9).

2. H3WB annotations

To download the H3WB dataset annotations click here. The zip file contains following:

- 2Dto3D_train.json has the training annotations for 2D→3D and I2D→3D tasks. Since this file is too big, we split it into 4-parts to ease the training and data loading pipeline. We provide the splitted files as well.
- RGBto3D_train.json has the training annotations for RGB \rightarrow 3D task.

- 2Dto3D_test_2d.json and I2Dto3D_test_2d.json include test instances for 2D→3D and I2D→3D tasks, respectively.
- RGBto3D_test_img.json includes test samples for RGB \rightarrow 3D task.

3. H3WB dataset keypoint layout

We use the COCO WholeBody dataset layout with 133 keypoints illustrated in Figure 1. H3WB dataset has the same keypoints for the whole-body layout.



Figure 1. Whole-body keypoint layout defined in the COCO WholeBody dataset [4]. H3WB dataset follows exactly the same layout. H3WB dataset has total of 133 keypoints annotations for each human: 17 human body keypoints (top-left), 68 face (top-right), 42 hand (21 keypoints for each) (bottom-right) and 6 foot (3 for each) (bottom-left). Image source: https://github.com/jin-s13/COCO-WholeBody

H36M	602.7	540.0	576.3	569.3	578.7	512.8	513.3	527.7	545.3	551.3	552.8	556.5	525.7	518.9	534.8	584.5	624.1	637.4
H3WB	518.8	437.9	433.5	444.3	428.9	453.6	422.3	473.1	427.5	505.0	440.2	519.1	419.9	456.1	430.5	462.6	440.3	473.1
										1.0	1 0 1				•			

Table 1. Standard deviation in mm on average (1st column) and for each of the original 17 body joints.



Figure 2. Distributions of Human3.6 and H3WB datasets per action class

4. Dataset diversity

The distribution of pose per action for H36M and H3WB using the original action labels is shown in Figure 2. Apart from *SittingDown*, they are about the same. Quantitatively, we show the standard deviation in mm on average (bold) and for each of the original 17 body joints in Table 1 which shows H3WB has slightly lower diversity than H36M, but no collapse.

5. Quality assessment study

We assessed the quality of the H3WB dataset by manually annotating 80K keypoints from 600 randomly selected images from the dataset. We presented a web interface to annotators and ask them to zoom-in on the body parts and correct mis-aligned keypoints by drag and drop. Sample screenshots from our web interface are presented in Figure 3.

6. More Qualitative Results

We provide more qualitative outputs obtained by Large SimpleBaseline [6] and Jointformer [5] models in Figure 4. Despite slight mis-alignments, the predicted skeletons are realistic.

We also show some examples in Figure 5 of a model trained on our H3WB benchmark for the task $I2D\rightarrow 3D$ and evaluated on COCO dataset[4]. We can see that even when there are missing points in the 2D input, the model still can predict the 3D wholebody pose accurately. This validates the usefulness of the $I2D\rightarrow 3D$ in real world scenario.

7. SMPL-X failure cases

Parametric body models like SMPL-X have many seminal advantages such as always producing biologically plausible poses or taking into account the shape of the person. This enables powerful applications, for example in augmented reality or animation. However, because very accurate pose is not a requirement in these application, a model like SMPL-X is not yet able to reach satisfactory accuracy, especially on extremities like the hands and the feet. This is what we show in Figure 6, where we extracted images from several articles [8, 9, 2] and zoom on the extremities to visually assess that it is well below the accuracy provided in H3WB. We also ran SMPL-X on Human3.6M to see if it can be used to generate pseudo-labels and show selected zooms on the extremities on Figure 7. Here also, the accuracy is well below what our label generation process managed to get. As such, datasets relying on SMPL-X for their groundtruth are thus by design less accurate and thus not usable for accurate pose estimation, especially on the extremities. Furthermore, assessing quantitatively the accuracy is almost impossible to do with these methods, whereas we provide an estimate for H3WB showing our benchmark is rigorous.

8. Cross validation experiments

We do not provide a validation set for the H3WB dataset. We recommend 5-fold cross-validation for model selection and hyper-parameters tuning. We split the training set into 5 sets. We take the set cvi as a hold out (test set), use remaining sets to train the models, and report the results on cvi. We present the cross-validation results together with the test set results in Tables 2, 3, 4 for all tasks. We observe that cross-validation results are consistent and compatible with the test results which are listed in the main paper.

9. Other issues

We plan to setup a server for test set evaluation. We will also release the test data after 3-5 years once they are well studied to allow long term use without relying on our evaluation server.

Concerning the license, we only release entirely new labels, which fits the license agreement allowing research output.



Figure 3. Sample screenshots from the annotation interface. Annotators are asked to select area of interest, zoom in on that area and correct the mis-aligned keypoints by drag-drop.



Figure 4. Example predictions from Large SimpleBaseline model for $2D \rightarrow 3D$ (1st row) and $I2D \rightarrow 3D$ (2nd row) tasks. 3rd row shows predictions from Jointformer for RGB $\rightarrow 3D$ task. Colored skeletons correspond to predictions and gray skeletons correspond to groundtruths. First two columns show almost-aligned successful front/side predictions, and the last column shows slightly mis-aligned predictions.



Figure 5. Visual examples of lifting on COCO. The labels on the images are the incomplete inputs.



Figure 6. Several examples of failures on hands and feet with SMPL-X model copied from [8, 9, 2]



Figure 7. Our runs with SMPL-X models on the annotation, it is not as visually accurate as we require as annotations.

method	all	body	face		hand		
				†		‡	
SimpleBaseline [6]							
cv1	134.0	128.9	126.8	34.8	148.4	46.2	
cv2	128.9	126.4	120.5	29.0	136.7	42.8	
cv3	136.0	130.6	135.8	23.6	139.1	44.0	
cv4	132.8	131.4	126.9	29.0	143.3	46.6	
cv5	130.0	130.0	120.7	22.7	150.0	46.6	
Cystd	139.9	5 1	6.1	1 1	57	40.0	
Cv sid	4.1	121 4	129.7	20.0	142.5	1.7	
Test	125 4	125.7	115.0	24.6	145.5	43.2	
lest	125.4	123.7	115.9	24.0	140.7	42.5	
Large SimpleBaseline [6]							
cv1	106.8	105.1	105.8	22.7	109.2	33.6	
cv2	103.9	104.3	107.7	16.7	97.6	31.9	
cv3	101.8	102.4	105.5	14.2	95.6	30.6	
cv4	108.7	107.0	111.6	14.3	105.0	32.3	
cv5	111.8	109.0	112.0	15.6	113.1	35.5	
Cv std	3.9	2.5	3.1	3.5	7.5	1.9	
Cv mean	106.6	105.6	108.5	16.7	104.1	32.8	
Test	112.3	112.6	110.6	14.6	114.8	31.7	
CanonPose [10]							
cv1	173.4	177.8	180.0	30.3	160.4	46.4	
cv2	152.9	160.7	162.0	23.2	133.0	44.2	
cv2	163.9	167.4	176.5	21.1	141.5	44.9	
ev5	195.0	197.4	100.2	22.0	160.5	49.1	
cv4	172.6	177.0	199.2	23.0	154.1	46.9	
Cystd	172.0	177.9	102.2	22.1	110	40.0	
Cv sid	12.0	174.2	190.0	22.0	150.1	1.0	
CV mean Test	109.0	1/4.2	100.0	23.9	190.1	40.1	
Test	180.7	193.7	100.4	24.0	160.2	40.9	
CanonPose $[10] + 3D$ sv.							
cv1	121.1	121.9	116.8	27.6	127.5	42.1	
cv2	115.4	118.6	116.4	20.6	111.9	40.6	
cv3	112.4	113.2	113.7	16.5	110.0	38.9	
cv4	116.2	117.9	115.5	17.5	116.2	40.2	
cv5	168.7	170.5	180.3	22.1	149.0	49.2	
Cv std	23.7	23.7	29.0	4.4	16.1	4.1	
Cv mean	126.8	128.4	128.5	20.9	122.9	42.2	
Test	117.7	117.5	112.0	17.9	126.9	38.3	
Jointformer [5]							
cv1	94 3	85.0	76.0	29.8	129.0	48 1	
cv2	87.4	80.0	71.2	21.6	117.8	47.0	
cv3	94 5	86.3	84 5	16.5	115 3	49.2	
cv4	91.0	88.1	74.6	16.5	123.7	48.8	
cv5	104 3	96.3	82.6	19.0	143.0	53.5	
Cv std	62	50.5	56	5 5	11 4	25	
Cymean	04.4	87.1	77.8	20.7	125.0	40.3	
Cy mean Test	24.4 00 2	07.1 94.0	66.5	17.9	125.9	49.5	
1051	00.5	04.7	00.5	17.0	125.5	45.7	

Table 2. Results for $2D \rightarrow 3D$ task on each 5-fold and test sets. Results are shown for MPJPE metric. All results are pelvis aligned, except \dagger and \ddagger show nose and wrist aligned results for face and hands, respectively. Sv. is supervision.

method	all	body	fac	e	hand		
			t			‡	
SimpleBaseline [6]							
cv1	259.9	242.9	220.1	40.9	333.9	84.0	
cv2	271.0	244.9	229.3	34.9	352.7	86.7	
cv3	268.6	251.3	237.9	33.2	327.8	83.7	
cv4	259.1	246.8	225.5	33.8	320.4	81.9	
cv5	269.7	251.0	226.4	33.1	350.0	87.9	
Cv std	5.7	3.7	6.5	3.3	14.0	2.4	
Cv mean	265.7	247.4	227.8	35.2	337.0	84.8	
Test	268.8	252.0	227.9	34.0	344.3	83.4	
Large SimpleBaseline [6]							
cv1	1377	130.8	134.9	33 3	146.2	47 5	
cv2	125.5	124.9	123.6	23.1	129.1	46.0	
cv3	126.3	124.6	125.7	19.6	128.0	44.7	
cv4	136.1	129.9	134.7	19.9	141.7	47.3	
cv5	139.0	135.7	133.4	21.4	149.8	51.2	
Cv std	6.5	4.6	5.4	5.7	9.9	2.4	
Cv mean	132.9	129.2	130.5	23.5	139.0	47.3	
Test	131.4	131.6	120.6	19.8	148.8	44.8	
CanonPose [10]							
cv1	256.7	237.1	278.9	39.1	231.4	55.1	
cv2	255.5	244.2	284.1	35.6	215.4	56.1	
cv3	261.4	245.0	201.1	31.5	210.1	54.8	
cv4	261.3	243.0	285.5	31.6	231.7	56.8	
cv5	270.6	250.2	202.5	35.0	246.2	61.0	
Cy std	59	47	5 5	3.2	11.6	2.5	
Cymean	261.1	244.0	286.4	34.6	229.4	56.8	
Test	285.0	264.4	319.7	31.9	240.0	56.2	
$C_{amon}P_{one}\left[\frac{101}{2}+2D_{am}\right]$							
culture cult	163.6	155 7	160.2	33.7	173 5	40.1	
cv2	158.5	153.0	161.0	25.8	157.4	49.1	
cv3	157.9	150.0	161.5	21.8	156.5	47.3	
cv4	157.3	154.1	155.5	21.0	162.1	49.0	
cv5	175.1	168.9	169.3	25.4	187.9	55.5	
Cy std	75	7 3	5.0	47	13.3	33	
Cy mean	162.5	156 3	161 5	25.9	167.5	49.8	
Test	163.6	155.9	161.3	22.2	171.4	47.4	
Lointformer [5]							
cv1	121.5	114.8	100.9	34 3	158.6	55.9	
cv2	112.5	104.9	93.4	25.2	147.5	56.6	
cv3	110.5	101.2	94 3	20.6	141.9	56.2	
cv4	123.5	115.7	104 5	21.1	158.7	58.2	
cv5	129.4	116.0	107.9	22.5	171.6	61.1	
Cy std	79	7.0	63	5.6	11.5	2.1	
Cy mean	119.5	110.5	100.2	24.7	155.7	57.6	
Test	109.2	103.0	82.4	19.8	155.9	53.5	

method All Body Hand Face t t SHN [7]+SimpleBaseline [6] 191.0 177.9 159.8 41.4 248.7 66.1 cv1 cv2 159.4 151.0 135.8 30.4 202.3 62.6 cv3 170.8 169.9 157.0 25.8 193.9 64.7 192.9 27.7 225.5 cv4 204.8 202.3 68.0 204.8 192.7 173.8 30.2 261.5 71.8 cv5 20.0 21.2 29.0 Cv std 20.4 6.1 3.5 186.2 178.8 163.9 226.4 66.6 Cv mean 31.1 182.5 32.5 189.6 138.7 249.4 64.3 Test CPN [1]+Jointformer[5] 100.8 101.6 75.5 29.9 141.3 53.5 cv1 52.9 cv2 91.9 89.8 70.6 22.8 127.5 cv3 75.7 77.5 62.5 14.9 96.0 51.0 82.0 58.4 107.6 cv4 78.1 16.9 52.7 cv5 100.8 98.3 73.1 19.5 147.2 59.0 Cv std 12.1 10.3 5.9 3.0 7.3 21.8 Cv mean 89.5 68.0 20.8 123.9 53.8 89.8 132.6 142.8 192.7 56.9 91.9 20.7 Test Resnet50 [3] 123.8 117.7 97.6 169.6 34.9 58.3 cv1 cv2 111.8 107.1 88.3 25.3 152.4 57.2 cv3 102.5 103.8 81.9 20.0 135.0 57.8 113.5 89.9 21.2 151.3 58.5 cv4 114.5 cv5 122.8 119 5 91.7 23.1 1751 62.6 5.78 5.9 Cv std 8.8 6.8 16.0 2.1 114.9 112.5 89.9 58.9 24.9 156.7 Cv mean 244.9 63.1 151.6 26.3 Test 166.7 123.6

Table 4. Results for RGB \rightarrow 3D task on each 5-fold and test sets. Results are shown for MPJPE metric. All results are pelvis aligned, except † and ‡ show nose and wrist aligned results for face and hands, respectively.

Table 3. Results for I2D \rightarrow 3D task on each 5-fold and test sets. Results are shown for MPJPE metric. All results are pelvis aligned, except † and ‡ show nose and wrist aligned results for face and hands, respectively. Sv. is supervision. We observe that *CanonPose* fails to generalize to new subject in the test set and performs worse on the test set.

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