**Supplementary methods**

DXA measurement

The densitometer is operated by multiple radiology technicians. In CGMH, all technicians need to be certified to operate the densitometer. The scans were analyzed following recommendations issued by the Taiwan Radiological Society[46] (amended from International Society for Clinical Densitometry, ISCD).[47] The recommendation briefly: 1. All DXA technicians need to complete the ISCD training course (basic and advanced) and operate at least 120 cases of DXA examination before the independent operation of DXA. 2. All technicians need to obtain the SOP provided by the manufacturer and conduct BMD measurements accordingly. 3. All DXA scanners need to have a detailed SOP at the examination site, which needs to be updated regularly and reviewed by relevant professionals. 4. All DXA scanners need to comply with the local radiation safety guideline. 5. Spine phantom BMD measurement is performed regularly to document the stability of DXA performance over time. BMD values must be maintained within an error of ±1.5%. A monitoring plan is needed for a correction approach when the error has been exceeded. 6. All DXA technicians need to establish a personal least significant change (LSC). The current recommendation is that the personal LSC should be within 5.3% for the lumbar spine, 5.0% for the whole hip, and 6.9% for hip neck BMD measurement.

Deep Adaptive Graph (DAG)

In DAG, the anatomical landmarks are formulated as a graph, $\mathrm{G} = (\mathrm{V}, \mathrm{E}, \mathrm{F})$, where the vertices $\mathrm{V}$ represent the landmarks, the edges $\mathrm{E}$ represent the relationships between them, and the features $\mathrm{F}$ encode visual patterns in the neighborhoods of the vertices. For a specific input image, the graph vertices are first initialized in the image using the mean shape of the anatomy, and a neural network is used to

displace the vertices from the initial position to the target anatomy in the image. By formulating the anatomical landmarks as a graph and modeling their displacements by the convolutional neural network–graph convolutional network (GCN), DAG can effectively exploit the structural information and shape prior to the anatomical landmarks. Therefore, DAG provides robust and accurate anatomical landmark detection on both hip and spine radiographs.

The neural network consists of a convolutional neural network to encode the input image to produce graph features $\mathrm{F}$, and a GCN to process the graph to locate its vertices. Specifically, the GCN consists of two parts: a global transformation GCN and multiple local refinement GCNs. The global transformation GCN produces an affine transformation matrix, $\mathrm{M}$, which brings the initial graph vertices closer to the target. The transformed vertices are written as follows:

$$\text{Equation (4): } \mathrm{V}^1 = \{\mathrm{v_i}^1\} = \{\mathrm{M}\mathrm{v_i}^0\},$$

where $\mathrm{V}^0 = \{\mathrm{v_i}^0\}$ and $\mathrm{V}^1 = \{\mathrm{v_i}^1\}$ denote the initial graph vertices before and after the estimated affine transformation, respectively. The local refinement GCNs then iteratively estimate the displacements of the graph vertices $\mathrm{V}^1$. In each iteration, the vertices are displaced as follows:

$$\text{Equation (5): } \mathrm{v_i}^{t+1} = \mathrm{v_i}^t + \Delta\mathrm{v_i}^t,$$

where $\Delta\mathrm{v_i}^t$ is the displacement estimated by the local refinement GCN at the t-th step.

The training loss is calculated for both the global transformation GCN and the local refinement GCNs. Because the goal of global transformation GCN is to locate the anatomy coarsely, the following margin loss is used:

$$\text{Equation (6): } L_{global} = \left[\frac{1}{N}\sum_{i \in N}|v_i^{1} - v_i| - m\right]_+,$$

where $[u]_+ = \max(0, u)$; $v_i^{1}$ and $v_i$ Denote the globally transformed and ground truth vertices, respectively; and $m$ is a hyperparameter representing a margin that aims to achieve high robustness for coarse landmark detection and forgive small errors. To encourage the local refinement GCNs to learn a precise localization, the L1 loss is directly applied to all vertices after the refinements, written as follows:

$$\text{Equation (7): } L_{local} = \frac{1}{N}\sum_{i \in N}|v_i^{T} - v_i|,$$

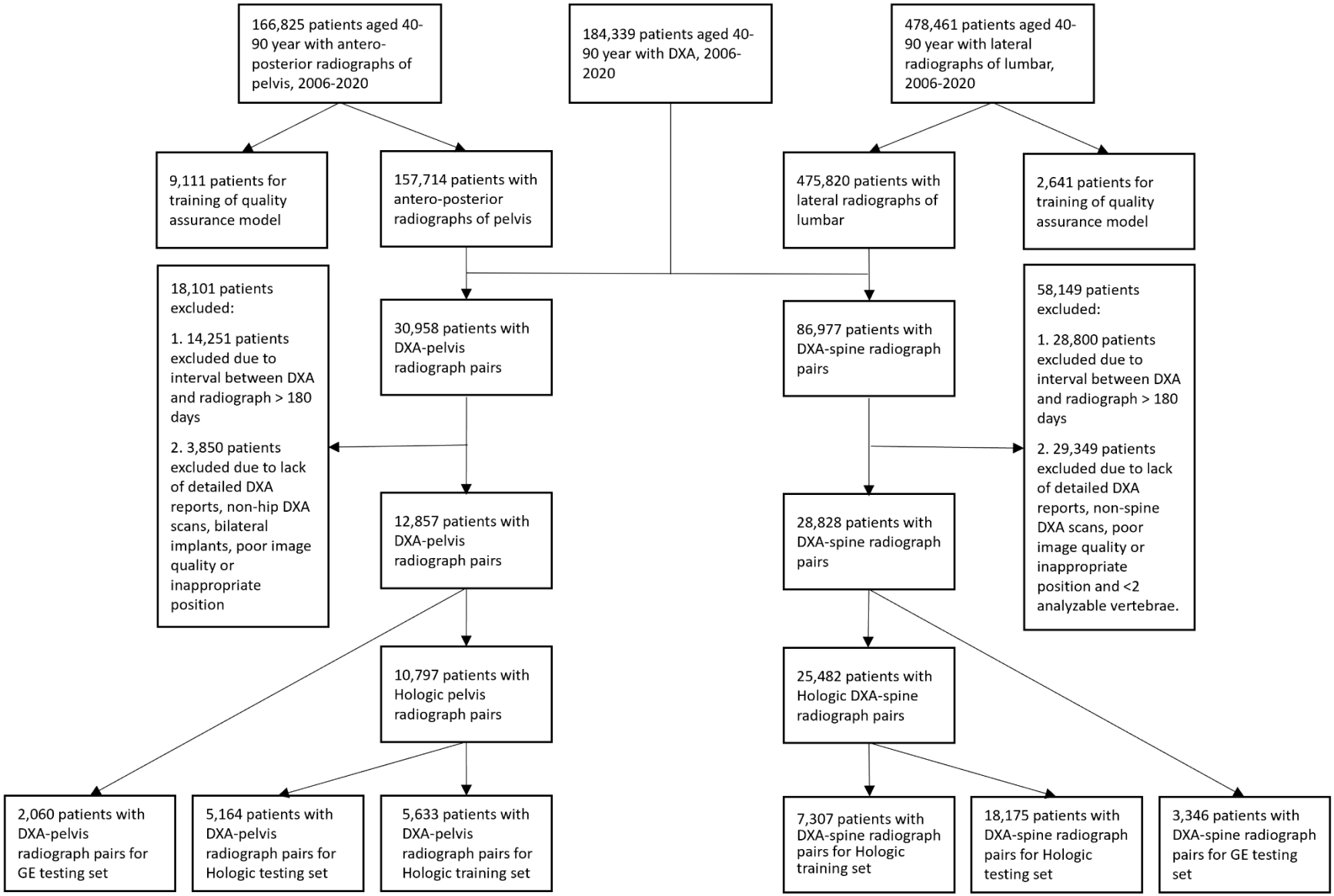
where $v_i^{T}$ denotes the vertices after the last local refinement GCN. The graph edge weights are treated as learnable parameters, which are initialized randomly at the beginning of training and updated via back-propagation during training.

Implementation details

Deep learning models were developed on a workstation with a single Intel Xeon E5-2650 v4 CPU @ 2.2 GHz, 128 GB RAM, and 4 NVIDIA TITAN V GPUs running Ubuntu 18.04 LTS. All code used in this study was developed in Python v3.6, and deep learning models were implemented using PyTorch v1.3. Image preprocessing was performed using the Python Imaging Library. ImageNet pre-trained weights were used to initialize the backbone network VGG-16 block. The Adam optimizer was used to train the model for 200 epochs with a batch size of 8, a starting learning rate of 1e−4, and a weight decay of 1e−4. The learning rate was reduced to 1e−5 after the first 100 training epochs. The following augmentations are performed during training: 1) color jittering on both the brightness (+-0.2) and contrast (+-0.2). 2) random up-down and left-right flipping, 3) random affine transformation (rotation +-30, shear +- 0.2, translation +- 25 pixels, scaling

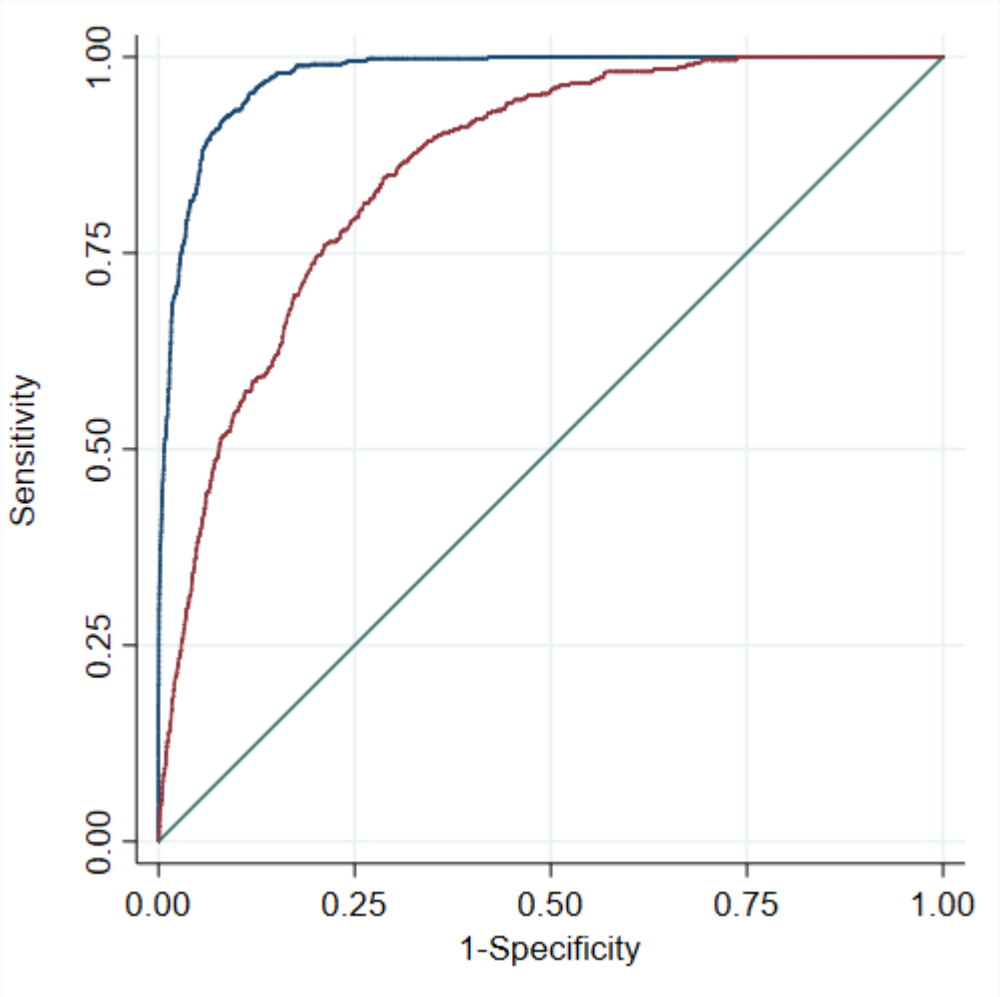
+-10%). The trained model was evaluated on the validation set after each training epoch, and the model with the highest validation correlation coefficient r-value was selected as the best model.

Supplementary Figure 1. Flowchart of the study population.

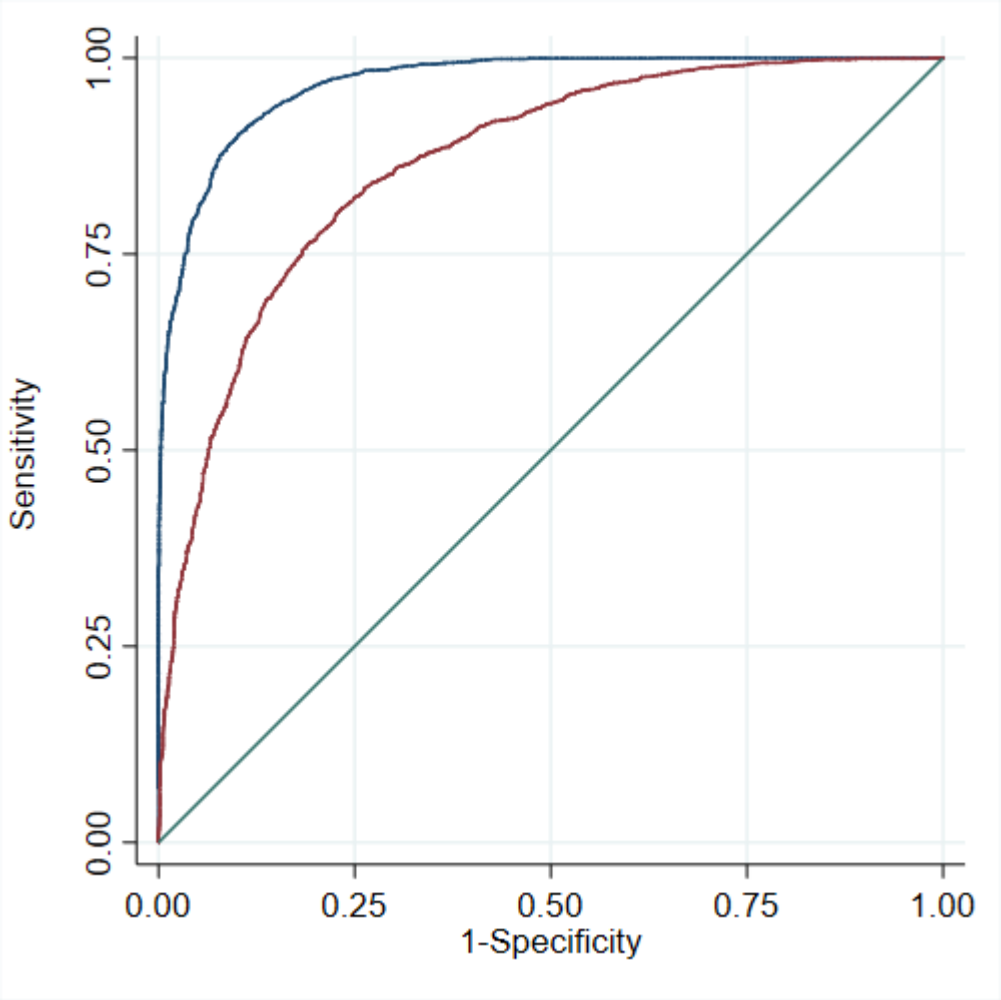


Supplementary Figure 2 Comparison of the receiver-operator curve between FRAX-AI (Navy blue line) and FRAX-NB tools (Maroon line) to classify high 10-year risk groups for (a) major fracture (>=20%) and (b) hip fracture (>=3%)

(a)

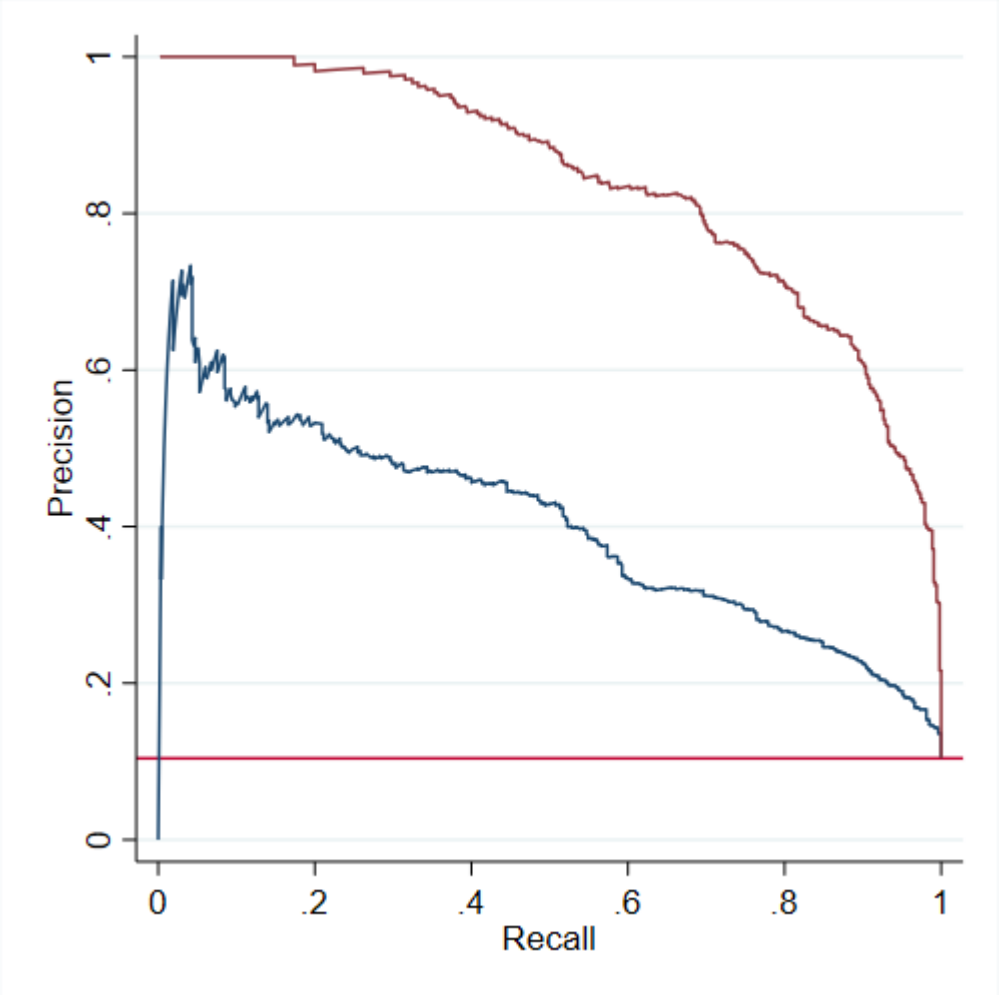


(b)

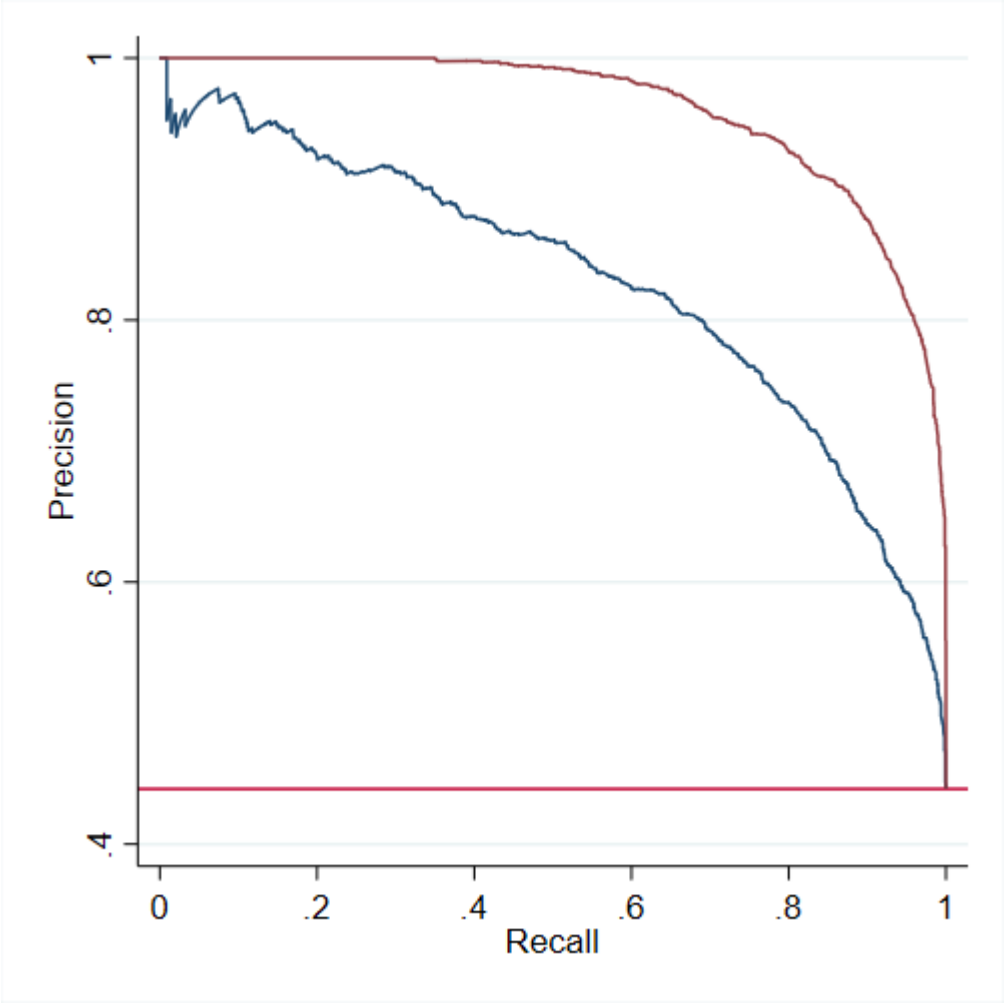

Sensitivity
0.00
0.25
0.50
0.75
1.00
0.00
0.25
0.50
0.75
1.00
1-Specificity

Supplementary Figure 3 Comparison of the precision-recall curve between FRAX-AI (Navy blue line) and FRAX-NB tools (Maroon line) to classify high 10-year risk groups for (a) major fracture (>=20%) and (b) hip fracture (>=3%)

(a)

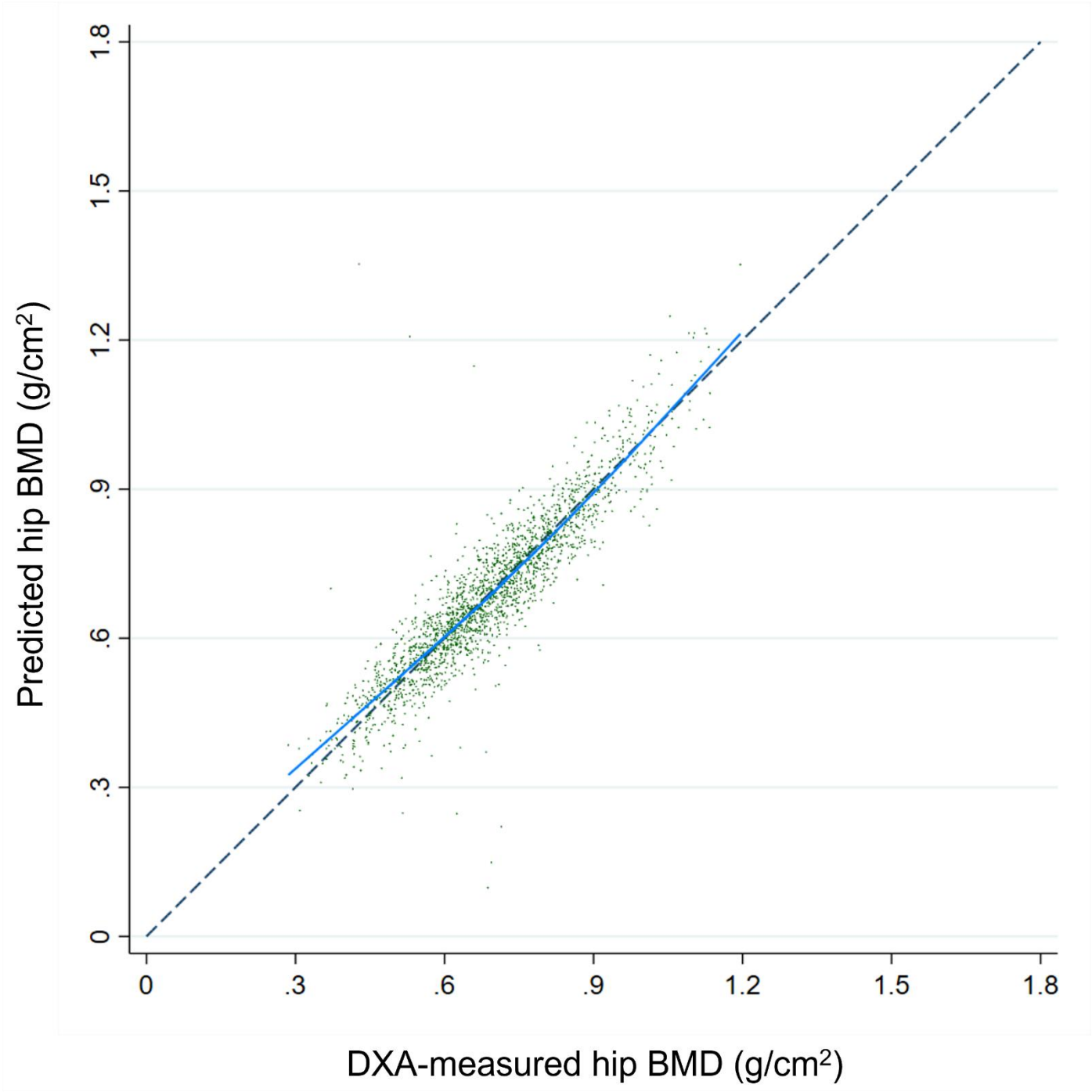



(b)

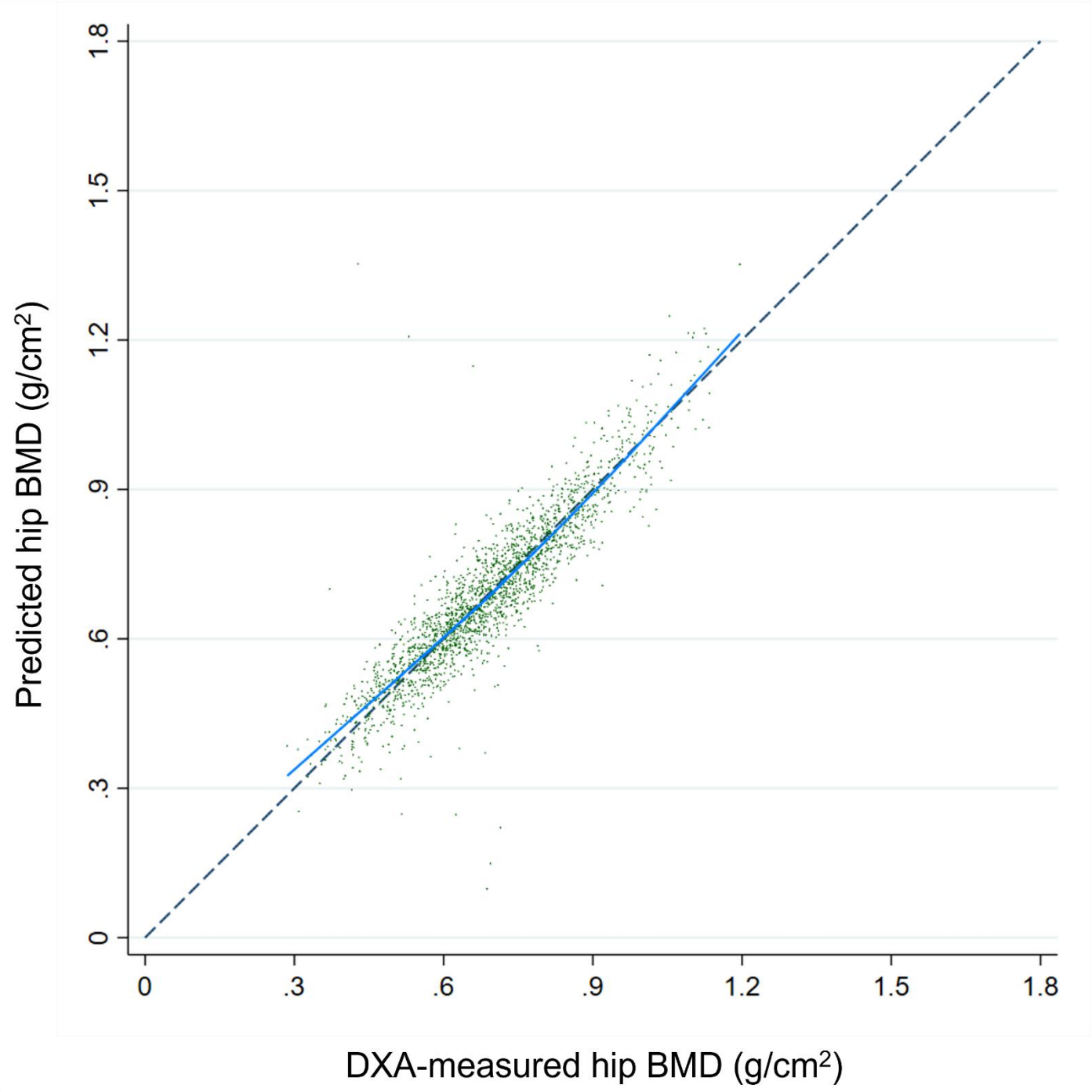

Precision
1
.8
.6
.4
0
.2
.4
.6
.8
1
Recall

Supplementary Figure 4 The calibration plots for predicted-measured BMD. (a) 2060 pairs of predicted-measured hip BMD (2060 patients) and (b) 11027 pairs of predicted-measured lumbar vertebral BMD (3346 patients). The DXA BMD was based on the measurement by the GE Lunar iDXA. Each point represents a data pair of predicted and measure BMD. The points close to the diagonal line suggests good calibration.

(a)

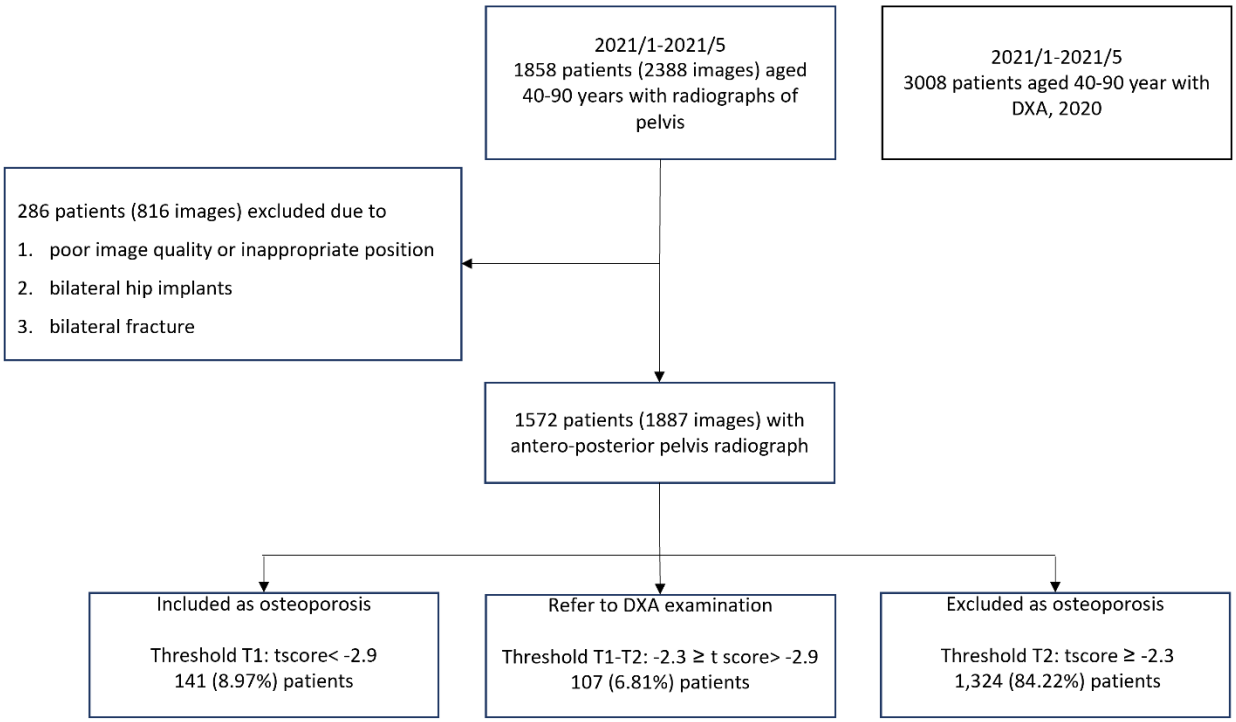



(b)

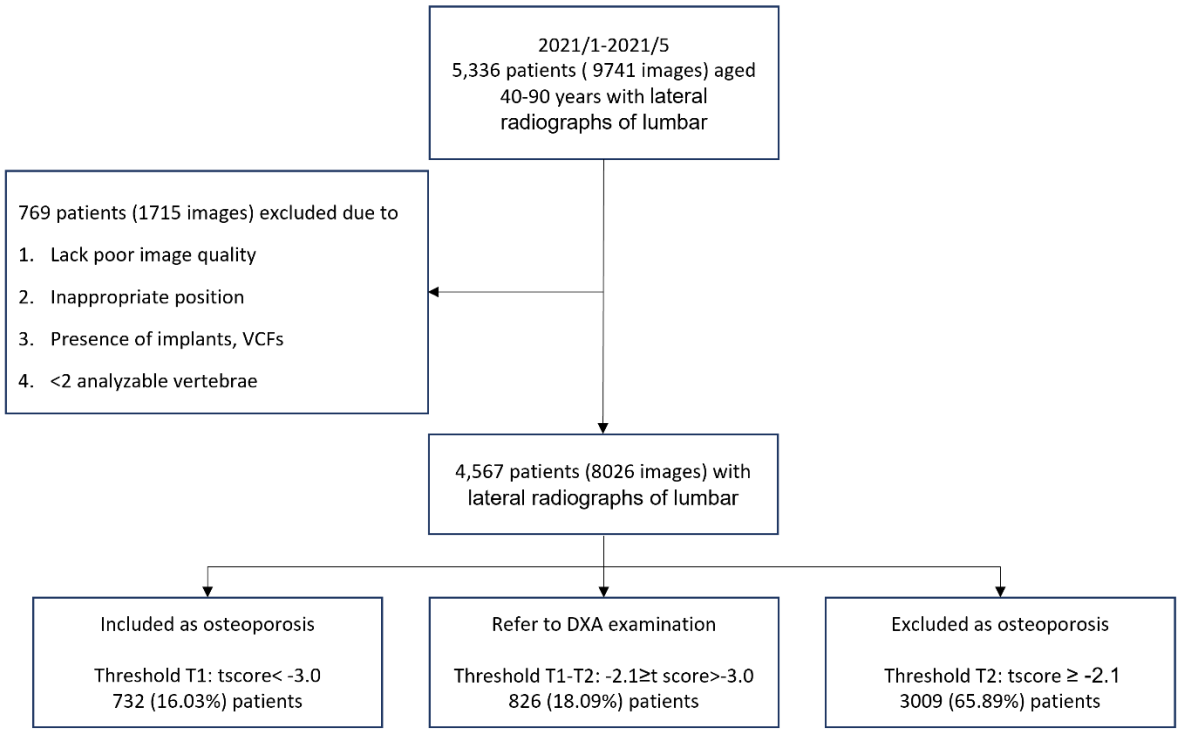

Predicted hip BMD (g/cm²)
0
.3
.6
.9
1.2
1.5
1.8
DXA-measured hip BMD (g/cm²)

Supplementary Figure 5 Data flow chart for the real-world clinical test. (a) hip BMD predictions and (b) spine BMD prediction. In this real-world test, we collected all patients receiving plain film for the hip and lateral plain film of the lumbar spine during January–May 2021. These images were fed into our tool and estimate the number (%) of images that can pass quality check, the distribution of predicted BMD, and the categorization based on the threshold reported in table 4.

(a)



(b)


2021/1-2021/5
5,336 patients ( 9741 images) aged 40-90 years with lateral radiographs of lumbar
769 patients (1715 images) excluded due to
1. Lack poor image quality
2. Inappropriate position
3. Presence of implants, VCFs
4. <2 analyzable vertebrae
4,567 patients (8026 images) with lateral radiographs of lumbar
Included as osteoporosis
Threshold T1: tscore< -3.0
732 (16.03%) patients
Refer to DXA examination
Threshold T1-T2: -2.1≥t score>-3.0
826 (18.09%) patients
Excluded as osteoporosis
Threshold T2: tscore ≥ -2.1
3009 (65.89%) patients

**Supplementary tables**

Supplementary Table 1 Network performance across age and sex subsets

| Discriminatory measures | Hip osteoporosis | | 10-year risk of major osteoporotic fracture >=20% | | 10-year risk of hip fracture >=3% | | Lumbar vertebral osteoporosis | |
|---|---|---|---|---|---|---|---|---|
| Hologic | | | | | | | | |
| | AUROC/AUPRC | OR (95% CI) | AUROC/AUPRC | OR (95% CI) | AUROC/AUPRC | OR (95% CI) | AUROC/AUPRC | OR (95% CI) |
| Female | 0.96/0.90 | 64.84 (52.23–80.48) | 0.97/0.84 | 82.44 (62.49–108.75) | 0.97/0.97 | 82.79 (67.15–102.07) | 0.91/0.91 | 35.23 (32.10–38.64) |
| Male | 0.97/0.78 | 103.23 (55.98–109.35) | NA* | NA* | 0.95/0.86 | 46.01 (31.13–68.00) | 0.92/0.76 | 37.74 (30.55–46.63) |
| Age: <60 years | 0.98/0.78 | 106.99 (46.98–243.69) | NA* | NA* | 0.98/0.80 | 205.33 (74.08–569.14) | 0.92/0.81 | 43.23 (35.17–53.15) |
| Age: 60-74 years | 0.97/0.86 | 95.75 (63.59–144.19) | 0.98/0.82 | 154.61 (87.01–274.73) | 0.95/0.89 | 42.37 (31.43–57.11) | 0.91/0.89 | 36.09 (31.92–40.82) |
| Age: 75-90 years | 0.95/0.91 | 52.66 (41.18–67.34) | 0.96 /0.84 | 69.22 (50.52–94.86) | 0.97/0.97 | 59.93 (46.56–77.12) | 0.91/0.92 | 31.93 (27.54–37.03) |

* The number of patients with a 10-year risk of major osteoporotic fracture >=20% is less than 3.

Supplementary Table 2. Patient characteristics of the GE dataset for testing*

| | Hip testing set | Spine testing set |
|---|---|---|
| Number | 2060 | 3346 |
| Female, n (%) | 1554 (75.4) | 2244 (67.1) |
| Mean age (sd), years | 71.5 (12.1) | 64.8 (11.7) |
| Median time (IQR) between DXA and radiographs | 24 (6, 75) | 28 (4, 95) |
| Mean BMI (sd), $kg/m^{2}$ * | 23.7 (3.8) | 24.5 (3.7) |
| Mean BMD (sd) $g/cm^{2}$ ** | 0.689 (0.160) | 0.831 (0.183)** |
| Median T-score (IQR) | -1.5 (-2.3, -0.6) | -1.5 (-2.6, -0.3)** |
| Osteoporosis, n (%) | 427(20.7) | 975 (29.1)** |

* Converted to the Hologic equivalent

** Calculated based on vertebrae with the lowest BMD.

Supplementary Table 3 BMD value conversion equations for GE Lunar to Hologic DXA scanners.

| Measurement Site | Conversion Equation |
|---|---|
| Lumbar Spine | Hologic BMD= 0.918 x Lunar BMD – 0.038 |
| Total Hip | Hologic BMD= 0.971 x Lunar BMD – 0.037 |

Supplementary Table 4. Summary of performance metrics of the predictive model for BMD* (GE DXA scanner)

| Patient strata | Number of ROIs | Predicted vs. measured mean BMD (sd, $g/cm^2$); p | Correlation coefficient | Linear regression $R^2$, RMSE | Calibration slop, CITL | Bland-Altman bias ($g/cm^2$; sd) |
|---|---|---|---|---|---|---|
| The hip testing set (GE)* | | | | | | |
| Overall | 2060 | 0.690 (0.151) vs. 0.689 (0.160); p=477 | 0.90 | 0.81, 0.071 | 0.955, -0.001 | -0.001 (0.071) |
| Female | 1554 | 0.667 (0.143) vs. 0.670 (0.156); p<0.108 | 0.89 | 0.79, 0.071 | 0.968, 0.003 | 0.003 (0.068) |
| Male | 506 | 0.762 (0.152) vs. 0.749 (0.161); p<0.001 | 0.91 | 0.82, 0.068 | 0.957, -0.013 | -0.013 (0.069) |
| 40-59 years | 358 | 0.811 (0.158) vs 0.803 (0.135); p=0.076 | 0.85 | 0.72, 0.084 | 0.992, 0.008 | 0.008 (0.084) |
| 60-74 years | 685 | 0.726 (0.139) vs. 0.722 (0.147); p<0.03 | 0.91 | 0.82, 0.062 | 0.961, -0.005 | -0.005 (0.062) |
| 75-90 years | 1017 | 0.626 (0.131) vs. 0.625 (0.137); p<0.001 | 0.86 | 0.74, 0.070 | 0.895, -0.002 | -0.002 (0.072) |
| The spine testing set (GE)** | | | | | | |
| Overall | 11027 | 0.899 (0.172) vs. 1.036 (0.196); p<0.001 | 0.89 | 0.79, 0.090 | 1.011, 0.015 | 0.015 (0.090) |
| Female | 7404 | 0.859 (0.1164) vs. 0.867 (0.187); p<0.001 | 0.88 | 0.788, 0.089 | 1.005, 0.008 | 0.008 (0.089) |
| Male | 3623 | 0.978 (0.159) vs. 1.007 (0.179); p<0.001 | 0.86 | 0.73, 0.093 | 0.964, 0.028 | 0.028 (0.093) |
| 40-59 years | 3884 | 0.970 (0.155) vs. 0.991 (0.175); p<0.001 | 0.88 | 0.78, 0.083 | 0.993, 0.022 | 0.022 (0.083) |
| 60-74 years | 4598 | 0.878 (0.165) vs. 0.889 (0.188); p<0.001 | 0.88 | 0.77, 0.091 | 1.001, 0.011 | 0.011 (0.091) |
| 75-90 years | 2545 | 0.827 (0.168) vs. 0.838 (0.198); p<0.001 | 0.86 | 0.74, 0.100 | 1.015, 0.010 | 0.010 (0.100) |
| L1 | 2476 | 0.807 (0.153) vs. 0.821 (0.169); p<0.001 | 0.86 | 0.74, 0.085 | 0.946, 0.014 | 0.014 (0.085) |
| L2 | 3027 | 0.879 (0.164) vs. 0.887 (0.188); p<0.001 | 0.89 | 0.79, 0.087 | 1.020, 0.007 | 0.007 (0.087) |
| L3 | 2967 | 0.934 (0.163) vs. 0.959 (0.193); p<0.001 | 0.88 | 0.78, 0.091 | 1.046, 0.025 | 0.025 (0.091) |
| L4 | 2557 | 0.968 (0.165) vs. 0.980 (0.192); p <0.001 | 0.86 | 0.74, 0.097 | 1.005, 0.012 | 0.012 (0.097) |

* GE BMD were converted to the Hologic equivalent.

** Calculated per eligible vertebrae.

Supplementary Table 5 Discriminatory performance (%) of the predicted BMD to classify hip/lumbar vertebral osteoporosis and high-risk groups for major osteoporotic or hip fractures (GE DXA scanner).

| Discriminatory measures | Hip osteoporosis (T-score <= -2.5 | Lumbar vertebral osteoporosis (vertebrae with the lowest T-score<= 2.5) | 10-year risk of major osteoporotic fracture >=20% | 10-year risk of hip fracture >=3% |
|---|---|---|---|---|
| Number of patients, % | 427 20.7 | 975, 29.1 | 208, 10.4 | 922, 46.2 |
| OR (95% CI) | 66.38 (48.32–91.18) | 39.47 (32.00–48.68) | 101.10 (66.40–153.92) | 102.20 (75.15–138.98) |
| AUROC/AUPRC | 0.96/0.87 | 0.92/0.89 | 0.94/0.79 | 0.96/0.93 |
| Accuracy (%; 95% CI) | 91.4 (90.1–92.6) | 87.6 (86.4–88.7) | 94.8 (93.8–95.8) | 91.0 (89.7–92.2) |
| Sensitivity (%; 95% CI) | 78.9 (74.7–82.7) | 80.6 (78.0–83.1) | 74.0 (67.5–78.0) | 89.9 (87.8–91.8) |
| Specificity (%; 95% CI) | 94.7 (93.5–95.7) | 90.5 (89.2–91.6) | 97.3 (96.4–98.0) | 92.0 (90.2–93.5) |
| PPV (%; 95% CI) | 79.4 (75.8–82.7) | 77.7 (75.4–79.8) | 75.9 (70.2–80.7) | 90.6 (88.7–92.2) |
| NPV (%; 95% CI) | 93.5 (94.1–95.4) | 87.6 (86.4–88.7) | 97.0 (93.8–95.8) | 91.4 (89.7–92.8) |

Supplementary Table 6 Model performance in different x-ray machines and tanges of peak kilovolt (kV) for hip and lumbar radiographs.

| Hip radiographs | | | | Spine radiographs | | | |
|---|---|---|---|---|---|---|---|
| kVp distribution | n | % | Correlation coefficient | kVp distribution | n | % | Correlation coefficient |
| 60-69 kV | 1245 | 24.11 | 0.909 | 70-80 kV | 5157 | 28.37 | 0.896 |
| 70-74 kV | 995 | 19.27 | 0.921 | 90 kV | 4637 | 25.51 | 0.889 |
| 75 kV | 1394 | 26.99 | 0.917 | 95 kV | 4747 | 26.12 | 0.898 |
| Other | 1530 | 29.63 | 0.922 | Other | 3634 | 19.99 | 0.889 |
| Machine type | n | % | Correlation coefficient | Machine type | n | % | Correlation coefficient |
| Canon CDXI 710C | 2576 | 49.88 | 0.919 | Canon CDXI 710C | 12337 | 67.88 | 0.896 |
| Shimadzu MUX-100H | 1161 | 22.48 | 0.914 | Shimadzu MUX-100H | 3501 | 19.26 | 0.885 |
| Other | 1427 | 27,63 | 0.917 | Other | 2337 | 12.86 | 0.887 |

Supplementary Table 7. Summary of performances using different backbone networks for hip BMD prediction (Hologic DXA).

| Models | R-value | RMSE | R squared | Calib. slope | Calib. intercept | Mean diff | Std diff | Mean GT | Mean Pred | p-value |
|---|---|---|---|---|---|---|---|---|---|---|
| VGG-11 | 0.910 | 0.064 | 0.828 | 0.984 | -0.002 | 0.002 | 0.064 | 0.689 | 0.690 | 0.034 |
| VGG-16 | 0.906 | 0.065 | 0.821 | 0.966 | 0.013 | -0.013 | 0.065 | 0.689 | 0.676 | 0.000 |
| ResNet-18 | 0.917 | 0.062 | 0.839 | 0.985 | -0.002 | 0.002 | 0.062 | 0.689 | 0.691 | 0.007 |
| ResNet-34 | 0.917 | 0.062 | 0.841 | 0.984 | -0.004 | 0.004 | 0.062 | 0.689 | 0.693 | 0.000 |
| VGG-11 with age/gender | 0.912 | 0.063 | 0.832 | 0.988 | 0.004 | -0.004 | 0.063 | 0.689 | 0.684 | 0.000 |
| VGG-16 with age/gender | 0.909 | 0.064 | 0.827 | 0.973 | -0.007 | 0.007 | 0.064 | 0.689 | 0.696 | 0.000 |
| ResNet-34-retrain | 0.917 | 0.062 | 0.841 | 0.982 | -0.003 | 0.003 | 0.062 | 0.689 | 0.692 | 0.000 |

* Means were compared using student t test. Two-sided p values were reported.

Supplementary Table 8. Summary of performances using different backbone networks for spine BMD prediction (Hologic DXA).

| Models | R-value | RMSE | Linear Regression R squared | Calibration slope | Calibration intercept (CITL) | Mean of difference | Std of difference | Mean GT BMD | Mean Pred BMD | p-value |
|---|---|---|---|---|---|---|---|---|---|---|
| VGG11 | 0.899 | 0.082 | 0.807 | 1.007 | 0.012 | -0.012 | 0.082 | 0.839 | 0.827 | 0.000 |
| VGG16 | 0.900 | 0.081 | 0.811 | 0.978 | 0.003 | -0.012 | 0.082 | 0.839 | 0.837 | 0.000 |
| ResNet18 | 0.893 | 0.084 | 0.798 | 0.971 | -0.004 | -0.003 | 0.081 | 0.839 | 0.843 | 0.000 |
| ResNet34 | 0.896 | 0.083 | 0.803 | 0.980 | 0.000 | 0.003 | 0.084 | 0.839 | 0.839 | 0.168 |
| VGG11 with age/gender | 0.900 | 0.081 | 0.810 | 0.983 | -0.001 | 0.001 | 0.081 | 0.839 | 0.840 | 0.002 |
| VGG16 with age/gender | 0.902 | 0.080 | 0.814 | 0.977 | -0.007 | 0.006 | 0.081 | 0.839 | 0.846 | 0.000 |

* Means were compared using student t test. Two-sided p values were reported.

Supplementary Table 9. Pseudo code for hip BMD estimation in python style.

```
Input: hip X-ray image, I
```

```
def hip_bmd(I):
    """
    Estimate hip BMD from pelvic X-ray images
    """
    lmks = DagModel(I)             # Apply the DAG model
    score_fx = FranctureModel(I)    # Apply the fracture detection model
    score_implant = ImplantModel(I) # Apply the implant detection model

    box_l, box_r = roi_bounding_box(lmks) # Generate bounding boxes

    fx_l = roi_pooling(score_fx, box_l) > 0.5 # Fracture classification
    fx_r = roi_pooling(score_fx, box_r) > 0.5

    impl_l = roi_pooling(score_impl, box_l) > 0.5 # Implant classification
    impl_r = roi_pooling(score_impl, box_r) > 0.5

    if not fx_l and not impl_l:         # if no fracture and implant
        roi_l = roi_extraction(I, box_l) # extract ROI of the left hip
        bmd_l = BmdModel(roi_l)         # Apply the BMD model
    else:
        bmd_l = None

    in not fx_r and not impl_r:
        roi_r = roi_extraction(I, box_r)
        bmd_r = BmdModel(roi_r)
```

```
    else:
        bmd_r = None


    return bmd_l, bmd_r # return left and right hip BMDs
```

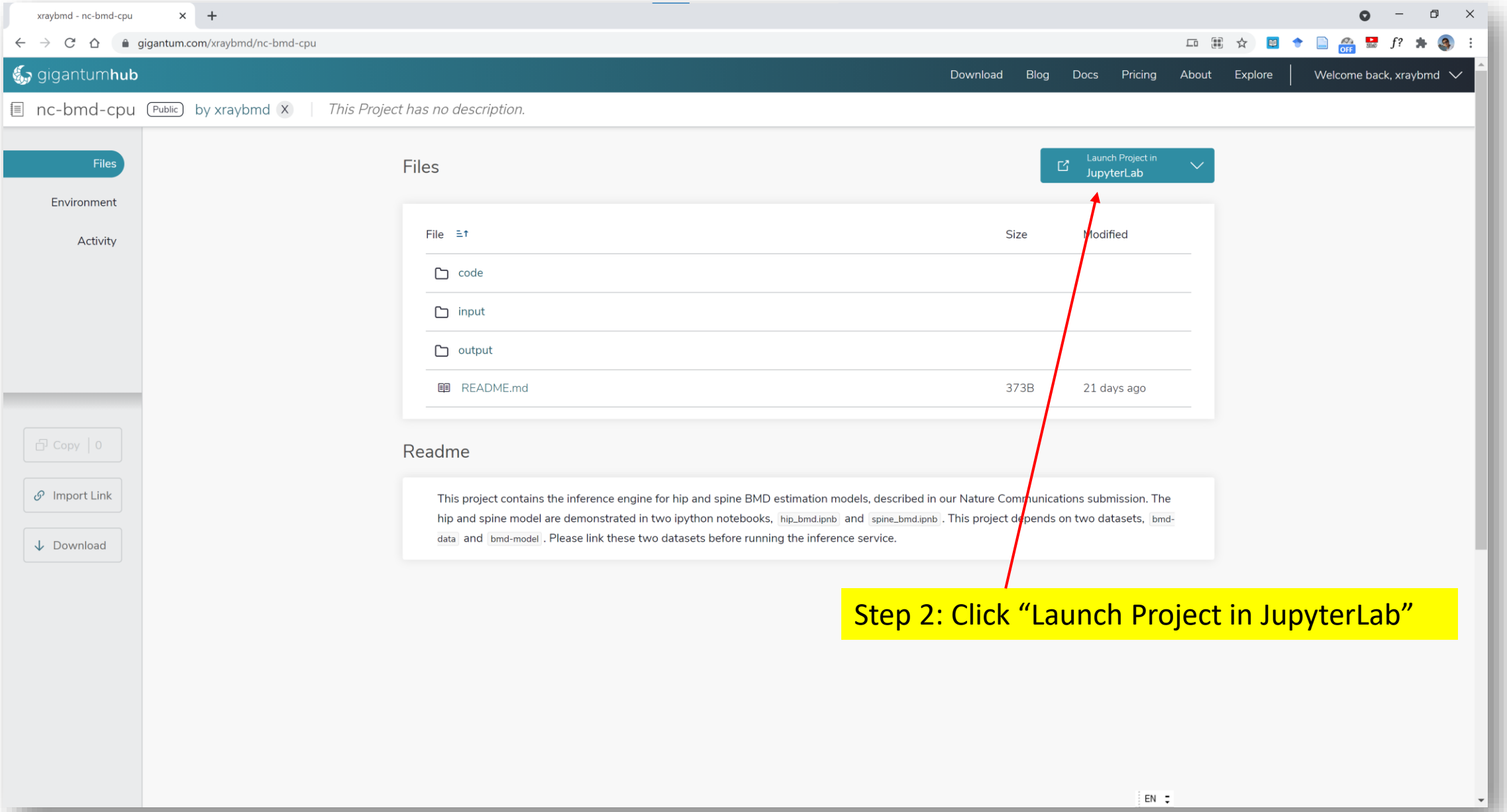
Supplementary Table 10. Pseudo code for spine BMD estimation in python style.

```
Input: Spine X-ray image, I
```

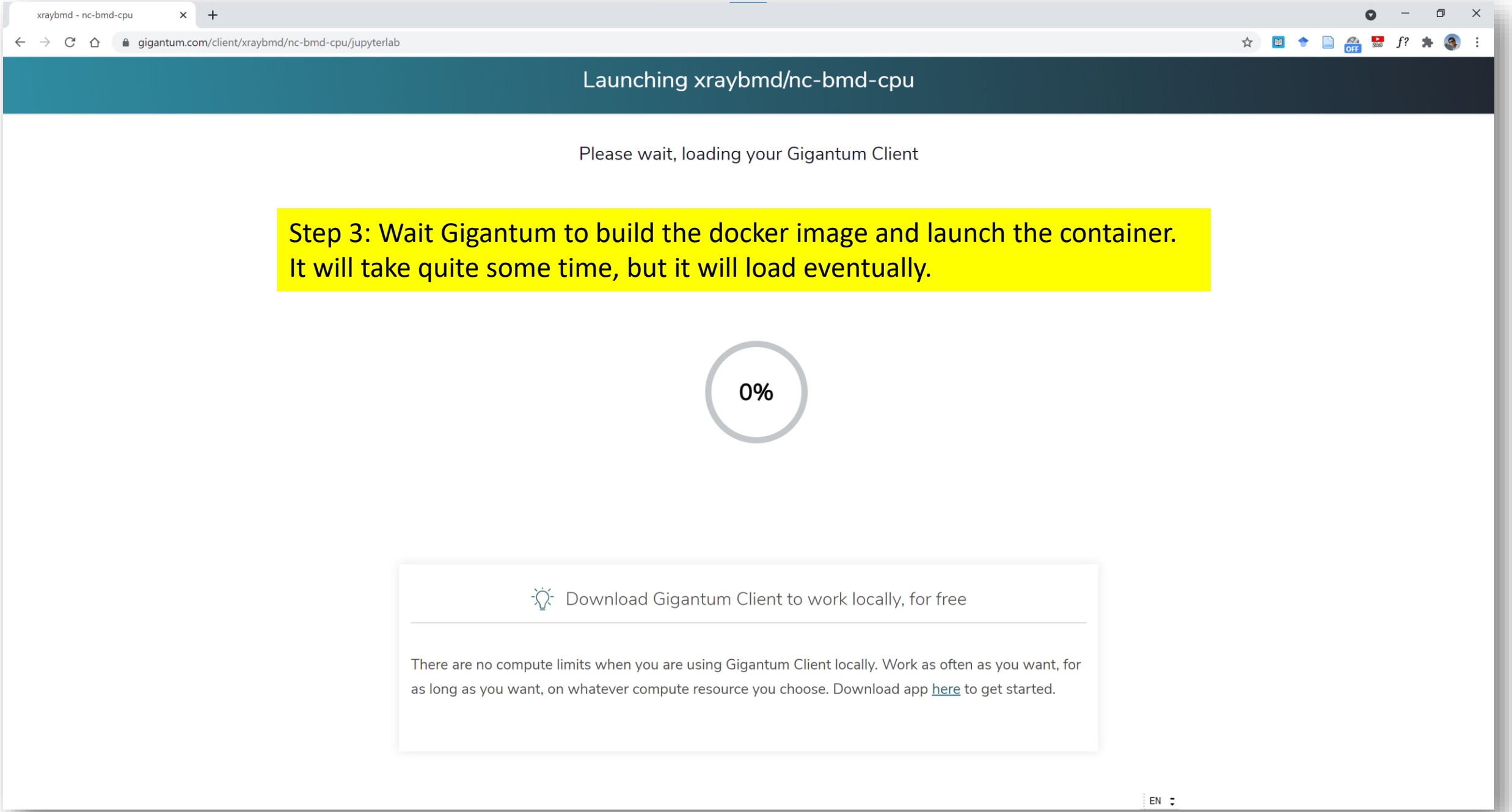
```
def spine_bmd(I):
    """
    Estimate spine BMD from lateral spine X-ray images
    """
    lmks = DagModel(I)             # Apply the DAG model
    score_fx = FractureModel(I)    # Apply the fracture detection model
    score_implant = ImplantModel(I) # Apply the implant detection model

    boxes = roi_bounding_box(lmks) # Generate bounding boxes as a dictionary

    bmd = {}
    for vert in ['L1', 'L2', 'L3', 'L4']:
        fx = roi_pooling(score_fx, boxes[vert]) > 0.5 # Fracture classification
        impl = roi_pooling(score_impl, boxes[vert]) > 0.5 # Implant classification
        ap_ratio, mid_ratio, height_ratio = \
            six_point_morph(boxes[vert]) # Calculate 6-point morphology metrics

        if not fx and not impl and \
            ap_ratio > 0.8 and mid_raio > 0.6 and height_ratio > 0.55: # If there is no fracture or implant and the morphology
is normal
            roi = roi_extraction(I, boxes[vert])
            bmd[vert] = BmdModel(roi)
        else:
            bmd[vert] = None
```

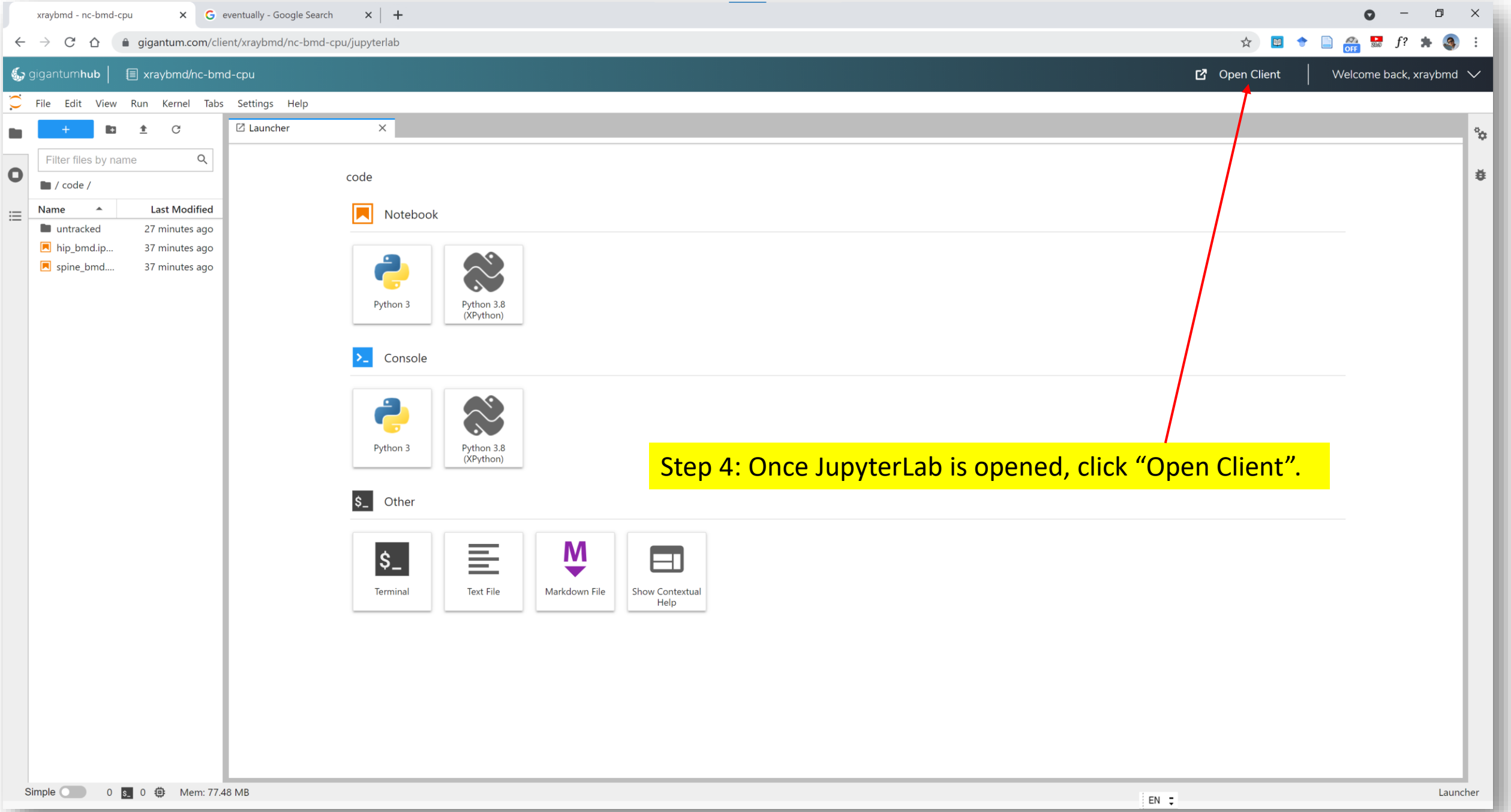
```
    return bmd['L1'], bmd['L2'], bmd['L3'], bmd['L4'] # Return 4 L-spine BMDs
```

Step 1: Open the project page https://gigantum.com/xraybmd/nc-bmd-cpu




Step 2: Click “Launch Project in JupyterLab”


xraybmd - nc-bmd-cpu
gigantum.com/client/xraybmd/nc-bmd-cpu/jupyterlab
Launching xraybmd/nc-bmd-cpu
Please wait, loading your Gigantum Client
Step 3: Wait Gigantum to build the docker image and launch the container.
It will take quite some time, but it will load eventually.
0%
Download Gigantum Client to work locally, for free
There are no compute limits when you are using Gigantum Client locally. Work as often as you want, for as long as you want, on whatever compute resource you choose. Download app here to get started.
EN


xraybmd - nc-bmd-cpu
eventually - Google Search
gigantum.com/client/xraybmd/nc-bmd-cpu/jupyterlab
gigantumhub
xraybmd/nc-bmd-cpu
Open Client
Welcome back, xraybmd
File Edit View Run Kernel Tabs Settings Help
Launcher
Filter files by name
/ code /
Name
Last Modified
untracked 27 minutes ago
hip_bmd.ip... 37 minutes ago
spine_bmd.... 37 minutes ago
code
Notebook
Python 3
Python 3.8 (XPython)
Console
Python 3
Python 3.8 (XPython)
Other
Terminal
Text File
Markdown File
Show Contextual Help
Step 4: Once JupyterLab is opened, click “Open Client”.
Simple
Mem: 77.48 MB
EN
Launcher

xraybmd - nc-bmd-cpu | Gigantum - Build it. Move it. Sha

gigantum.com/client#

gigantumhub

Welcome back, xraybmd

gigantum client

Projects

Datasets

Gigantum Hub

xraybmd

v1.5.3

# xraybmd / nc-bmd-cpu

Add description...

Collaborators
zandis...+1

Branch: master | Sync

Launch: jupyterlab | Running

Overview | Activity | Environment | Code | Input Data | Output Data

## Recent Activity

10:38 am

**xraybmd -** Executed cell in notebook code/hip_bmd.ipynb and generated a result

Step 5: Stop the container by clicking “Running”

## Readme

Step 6: Go to “Input Data” tab

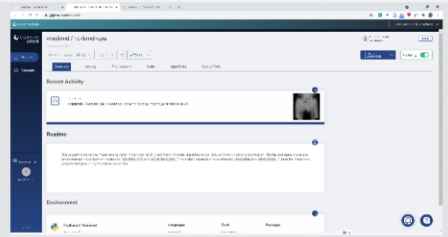
This project contains the inference engine for hip and spine BMD estimation models, described in our Nature Communications submission. The hip and spine model are demonstrated in two ipython notebooks, hip_bmd.ipnb and spine_bmd.ipnb. This project depends on two datasets, bmd-data and bmd-model. Please link these two datasets before running the inference service.

## Environment

**Python3 Minimal**

Revision: 12

| Languages | Tools | Packages |
|---|---|---|
| python3 | jupyterlab | |

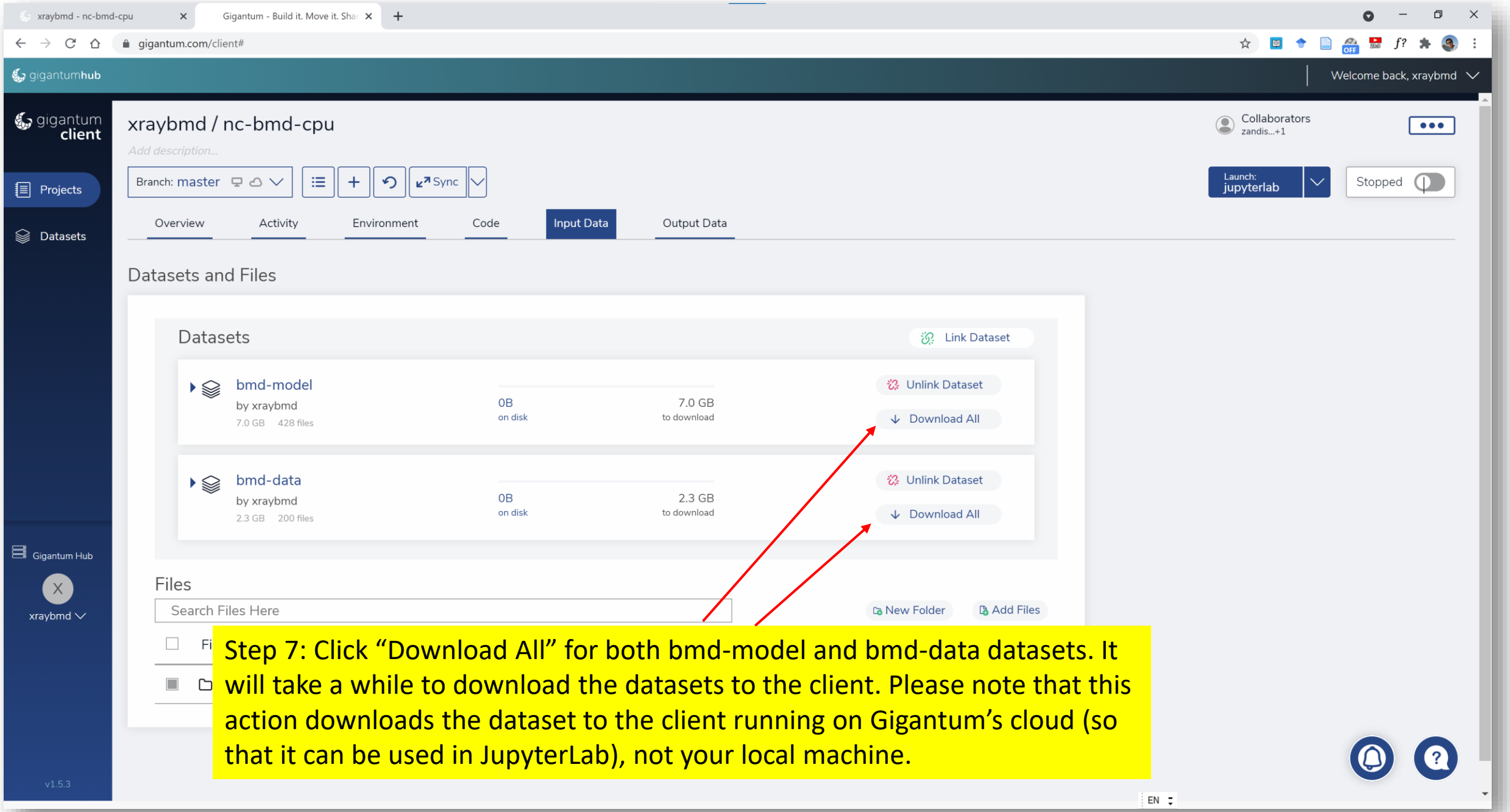


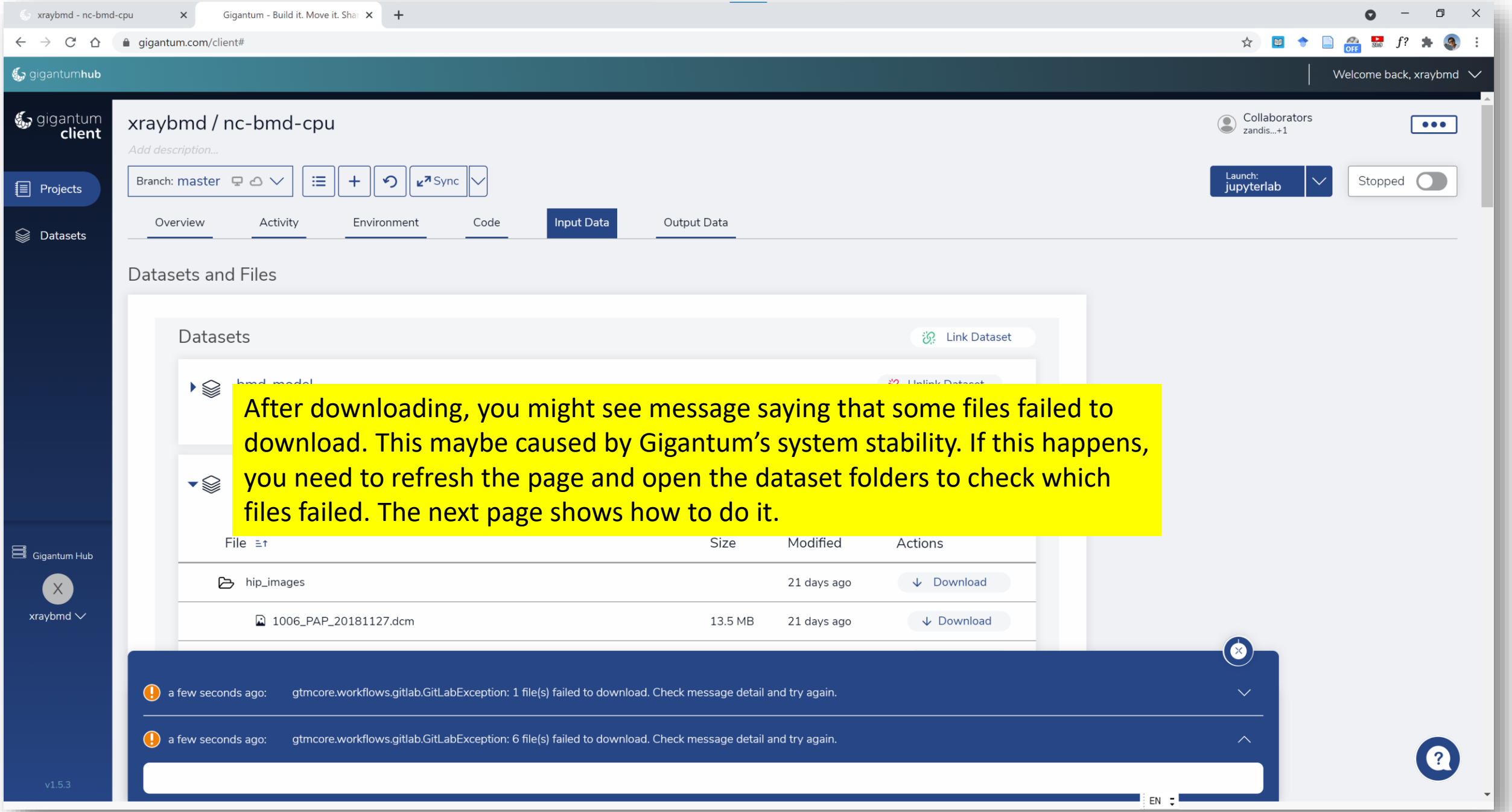
Snip & Sketch

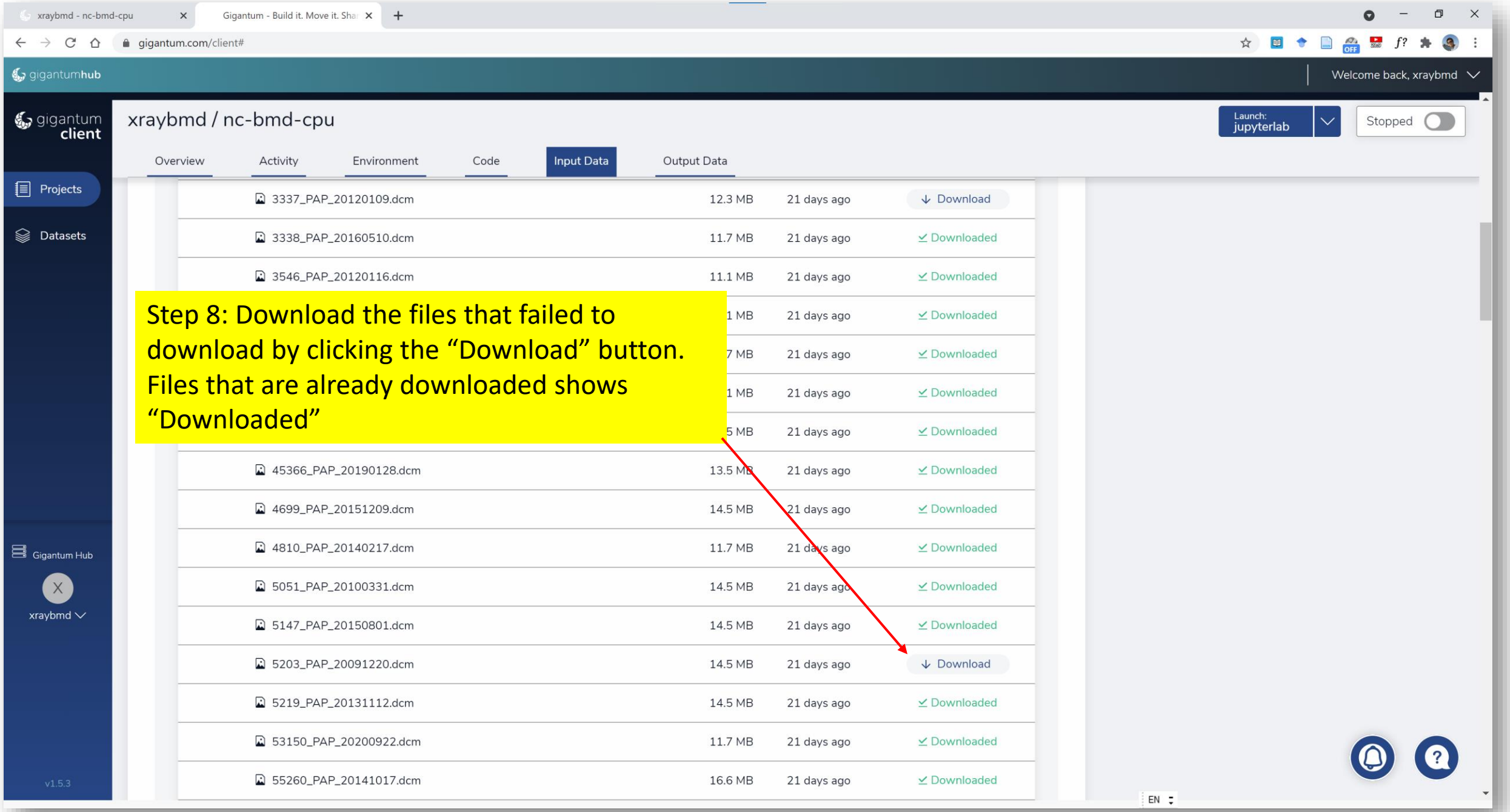
**Snip saved to clipboard**

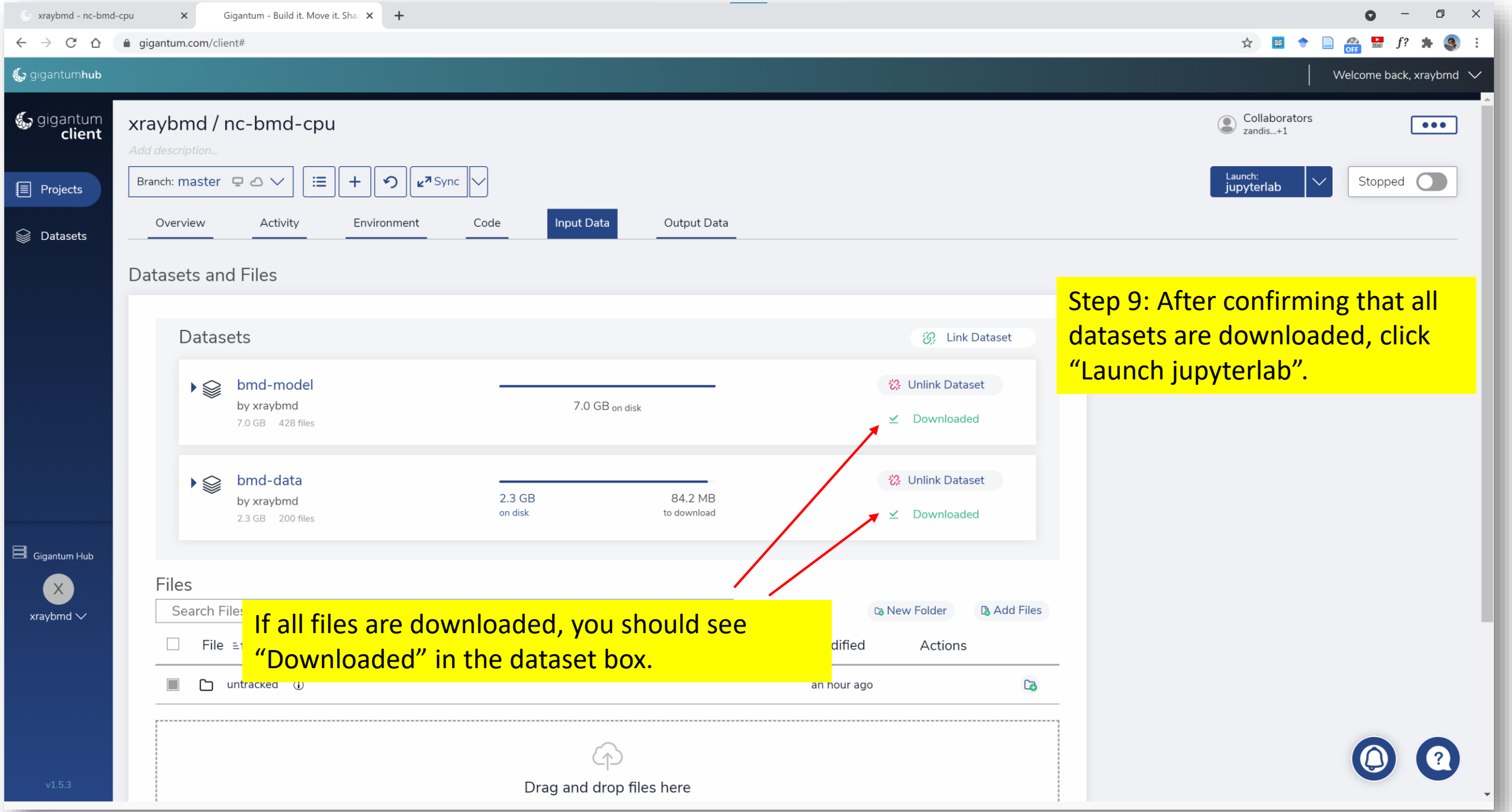
Select here to mark up and share the image

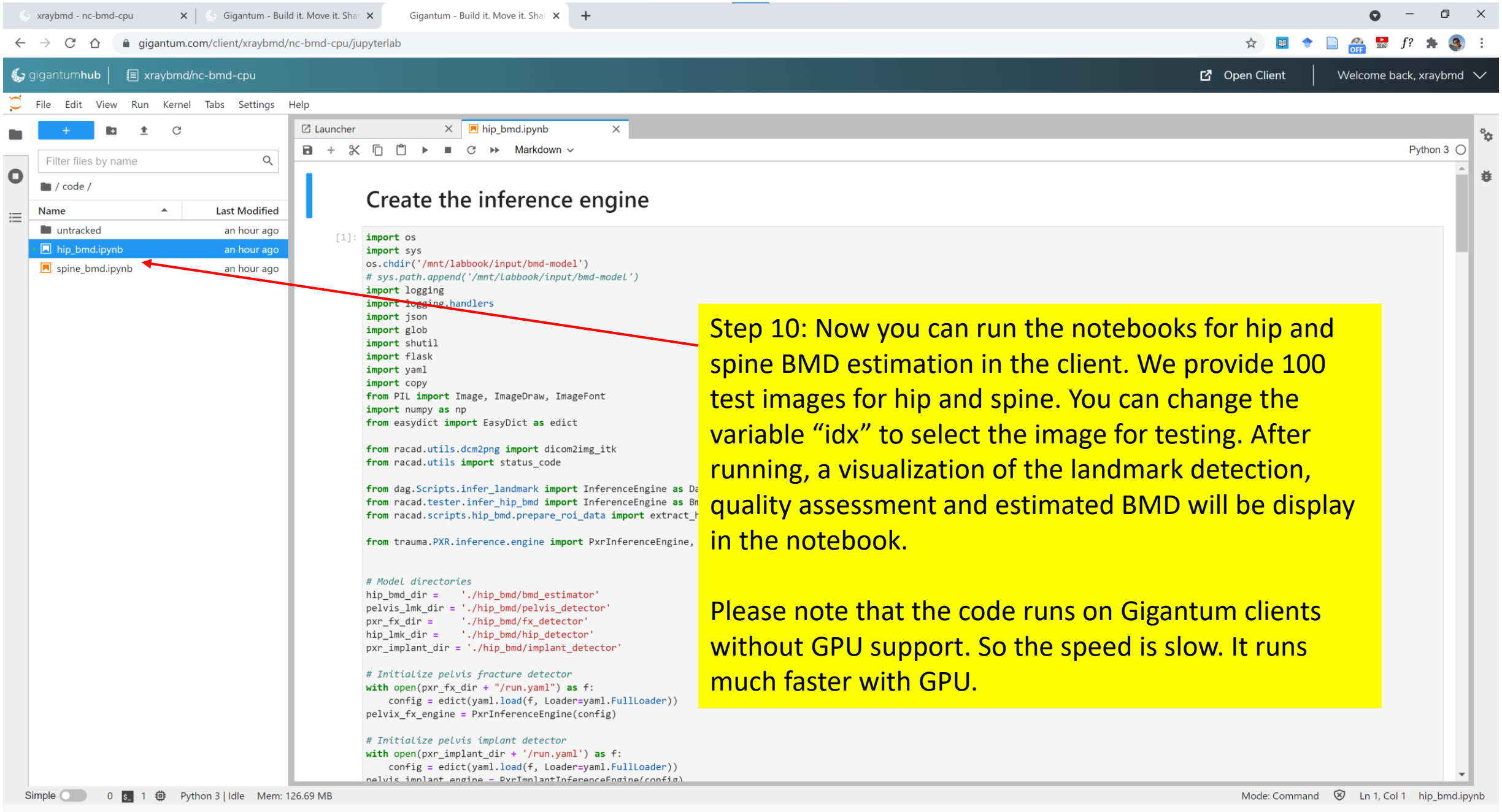
EN


xraybmd - nc-bmd-cpu
Gigantum - Build it. Move it. Sha
gigantum.com/client#
gigantumhub
Welcome back, xraybmd
gigantum client
Projects
Datasets
xraybmd / nc-bmd-cpu
Add description...
Collaborators
zandis...+1
Branch: master
Sync
Launch: jupyterlab
Stopped
Overview
Activity
Environment
Code
Input Data
Output Data
Datasets and Files
Datasets
Link Dataset
bmd-model
by xraybmd
7.0 GB 428 files
0B
on disk
7.0 GB
to download
Unlink Dataset
Download All
bmd-data
by xraybmd
2.3 GB 200 files
0B
on disk
2.3 GB
to download
Unlink Dataset
Download All
Files
Search Files Here
New Folder
Add Files
Gigantum Hub
xraybmd
v1.5.3
EN
Step 7: Click “Download All” for both bmd-model and bmd-data datasets. It will take a while to download the datasets to the client. Please note that this action downloads the dataset to the client running on Gigantum’s cloud (so that it can be used in JupyterLab), not your local machine.


xraybmd - nc-bmd-cpu
Gigantum - Build it. Move it. Sha
gigantum.com/client#
gigantumhub
Welcome back, xraybmd
gigantum client
Projects
Datasets
xraybmd / nc-bmd-cpu
Add description...
Collaborators
zandis...+1
Branch: master
Sync
Launch: jupyterlab
Stopped
Overview
Activity
Environment
Code
Input Data
Output Data
Datasets and Files
Datasets
Link Dataset
bmd_model
Unlink Dataset
After downloading, you might see message saying that some files failed to download. This maybe caused by Gigantum's system stability. If this happens, you need to refresh the page and open the dataset folders to check which files failed. The next page shows how to do it.
File
Size
Modified
Actions
hip_images
21 days ago
Download
1006_PAP_20181127.dcm
13.5 MB
21 days ago
Download
Gigantum Hub
xraybmd
v1.5.3
a few seconds ago: gtmcore.workflows.gitlab.GitLabException: 1 file(s) failed to download. Check message detail and try again.
a few seconds ago: gtmcore.workflows.gitlab.GitLabException: 6 file(s) failed to download. Check message detail and try again.
EN


xraybmd - nc-bmd-cpu
Gigantum - Build it. Move it. Sha
gigantum.com/client#
gigantumhub
Welcome back, xraybmd
gigantum client
xraybmd / nc-bmd-cpu
Launch: jupyterlab
Stopped
Overview
Activity
Environment
Code
Input Data
Output Data
Projects
Datasets
Gigantum Hub
xraybmd
v1.5.3
3337_PAP_20120109.dcm 12.3 MB 21 days ago Download
3338_PAP_20160510.dcm 11.7 MB 21 days ago Downloaded
3546_PAP_20120116.dcm 11.1 MB 21 days ago Downloaded
21 days ago Downloaded
21 days ago Downloaded
21 days ago Downloaded
21 days ago Downloaded
45366_PAP_20190128.dcm 13.5 MB 21 days ago Downloaded
4699_PAP_20151209.dcm 14.5 MB 21 days ago Downloaded
4810_PAP_20140217.dcm 11.7 MB 21 days ago Downloaded
5051_PAP_20100331.dcm 14.5 MB 21 days ago Downloaded
5147_PAP_20150801.dcm 14.5 MB 21 days ago Downloaded
5203_PAP_20091220.dcm 14.5 MB 21 days ago Download
5219_PAP_20131112.dcm 14.5 MB 21 days ago Downloaded
53150_PAP_20200922.dcm 11.7 MB 21 days ago Downloaded
55260_PAP_20141017.dcm 16.6 MB 21 days ago Downloaded
Step 8: Download the files that failed to download by clicking the “Download” button. Files that are already downloaded shows “Downloaded”
EN


xraybmd - nc-bmd-cpu
Gigantum - Build it. Move it. Sha
gigantum.com/client#
gigantumhub
Welcome back, xraybmd
gigantum client
xraybmd / nc-bmd-cpu
Add description...
Collaborators
zandis...+1
Projects
Datasets
Branch: master
Sync
Launch: jupyterlab
Stopped
Overview
Activity
Environment
Code
Input Data
Output Data
Datasets and Files
Datasets
Link Dataset
bmd-model
by xraybmd
7.0 GB 428 files
7.0 GB on disk
Unlink Dataset
Downloaded
bmd-data
by xraybmd
2.3 GB 200 files
2.3 GB on disk
84.2 MB to download
Unlink Dataset
Downloaded
Files
Search Files
New Folder
Add Files
File
Actions
untracked
an hour ago
Drag and drop files here
Gigantum Hub
xraybmd
v1.5.3
Step 9: After confirming that all datasets are downloaded, click “Launch jupyterlab”.
If all files are downloaded, you should see “Downloaded” in the dataset box.


xraybmd - nc-bmd-cpu
Gigantum - Build it. Move it. Sha
Gigantum - Build it. Move it. Sha
gigantum.com/client/xraybmd/nc-bmd-cpu/jupyterlab
gigantumhub
xraybmd/nc-bmd-cpu
Open Client
Welcome back, xraybmd
File Edit View Run Kernel Tabs Settings Help
Launcher
hip_bmd.ipynb
Markdown
Python 3
Filter files by name
/ code /
Name
Last Modified
untracked
an hour ago
hip_bmd.ipynb
an hour ago
spine_bmd.ipynb
an hour ago
Create the inference engine
[1]:
import os
import sys
os.chdir('/mnt/labbook/input/bmd-model')
# sys.path.append('/mnt/labbook/input/bmd-model')
import logging
import logging.handlers
import json
import glob
import shutil
import flask
import yaml
import copy
from PIL import Image, ImageDraw, ImageFont
import numpy as np
from easydict import EasyDict as edict
from racad.utils.dcm2png import dicom2img_itk
from racad.utils import status_code
from dag.Scripts.infer_landmark import InferenceEngine as Da
from racad.tester.infer_hip_bmd import InferenceEngine as Bm
from racad.scripts.hip_bmd.prepare_roi_data import extract_h
from trauma.PXR.inference.engine import PxrInferenceEngine,
# Model directories
hip_bmd_dir = './hip_bmd/bmd_estimator'
pelvis_lmk_dir = './hip_bmd/pelvis_detector'
pxr_fx_dir = './hip_bmd/fx_detector'
hip_lmk_dir = './hip_bmd/hip_detector'
pxr_implant_dir = './hip_bmd/implant_detector'
# Initialize pelvis fracture detector
with open(pxr_fx_dir + "/run.yaml") as f:
config = edict(yaml.load(f, Loader=yaml.FullLoader))
pelvix_fx_engine = PxrInferenceEngine(config)
# Initialize pelvis implant detector
with open(pxr_implant_dir + '/run.yaml') as f:
config = edict(yaml.load(f, Loader=yaml.FullLoader))
Step 10: Now you can run the notebooks for hip and spine BMD estimation in the client. We provide 100 test images for hip and spine. You can change the variable “idx” to select the image for testing. After running, a visualization of the landmark detection, quality assessment and estimated BMD will be display in the notebook.
Please note that the code runs on Gigantum clients without GPU support. So the speed is slow. It runs much faster with GPU.
Simple
Python 3 | Idle
Mem: 126.69 MB
Mode: Command
Ln 1, Col 1
hip_bmd.ipynb