# Pelvic Bone Segmentation on DRR generated pelvic Xrays from CT image.

## Project Report

Sadi Mohammad Siddiquee
Research Assistant, CCDS Lab
Independent University, Bangladesh.

Saadia Binte Alam
Associate Professor
Independent University, Bangladesh.

Annotation Assisted by -

Mahfuzur Rahman
Nabilah Tabassum Oshin
Sadia Khan
Syed Mohaimin Ul Hoque
Mir Sayad Bin Almas

**Brief Description:**
This project's primary work is generating Bone Segments of pelvic X-rays. As there is no such available open-source dataset we are aware of providing annotation for Pelvic Xrays, we needed to annotate our own dataset. CT images from the open-source CTPelvic1k[1] dataset were used for the Digitally reconstructed radiograph (DRR) generation of the X-ray image. A group of 5 students then teamed up for Pelvic Xray bone annotation. Finally, a benchmarking on a subset of dataset was done using the widely used Convolutional Neural Network-based model (UNet).

**Project Stages:**

**Stage 1: Data Annotation.**
Our first work was to ready a dataset of DRR-generated pelvic Xrays and label them for bone segmentation. We used *dataset6 split* of the CTPelvic1k dataset as these CT images do not have metal artifacts in them. A general overview of *dataset6[2] split*:

| Dataset name[split] | # | Mean spacing(mm) | Mean size | # of Tr/Val/Ts | Source and Year |
|---|---|---|---|---|---|
| CLINIC [*dataset6*] | 103 | (0.85, 0.85, 0.80) | (512, 512, 345) | 61/21/21 | Collected 2020 |

We proposed a standalone Data Annotation Pipeline. This pipeline has two phases - CT image ROI selection, Bone labeling from drr generated pelvic X-rays.

  *a. CT image ROI selection*
For drr generation, we need to measure the ROI of the pelvic bones in CT images. For this, we used *MITK workbench[3]* software and navigate through the axial, sagittal and coronal planes for the ROI measurement. This ROI measurement was distributed between 5 students, resulting in this sheet.

Drr generation code was run in MATLAB. This code needs a text file named *ListFile.txt* which holds all the CT file paths, file tikas and ROIs. This was made using above mentioned *ROI sheet* and *pandas module* from python. Hyperparameters of the drr generation code: Degree of Angle = 0, Intensity range = 60:10:120. So for every CT image, there were 7 drr generated Xrays with 7 intensity levels. One file was chosen from them based on visibility.

[1] "MIRACLE-Center/CTPelvic1K: Resources of the paper ... - GitHub."
https://github.com/ICT-MIRACLE-lab/CTPelvic1K. Accessed 8 Aug. 2022.
[2] "Deep learning to segment pelvic bones: large-scale CT datasets ...." 16 Apr. 2021,
https://link.springer.com/article/10.1007/s11548-021-02363-8. Accessed 8 Aug. 2022.
[3] "The Medical Imaging Interaction Toolkit (MITK) - mitk.org." 29 Apr. 2022,
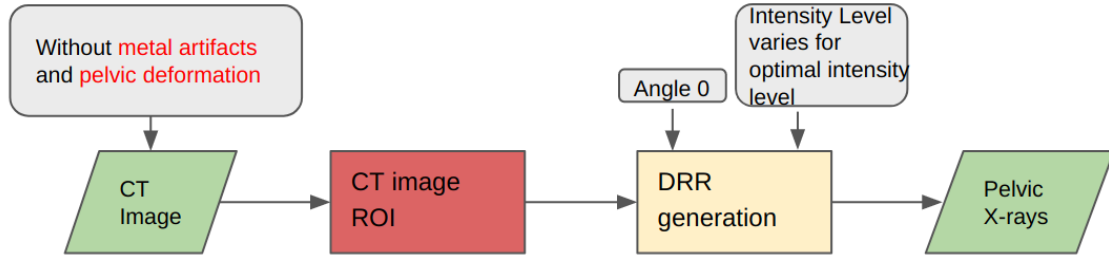https://www.mitk.org/wiki/The_Medical_Imaging_Interaction_Toolkit_(MITK). Accessed 8 Aug. 2022.

Fig 1: Overview of phase 1.

### b. Bone Annotation

We proposed a novel annotation pipeline maintaining SOTA for bone annotation. The proposed Annotation Pipeline:
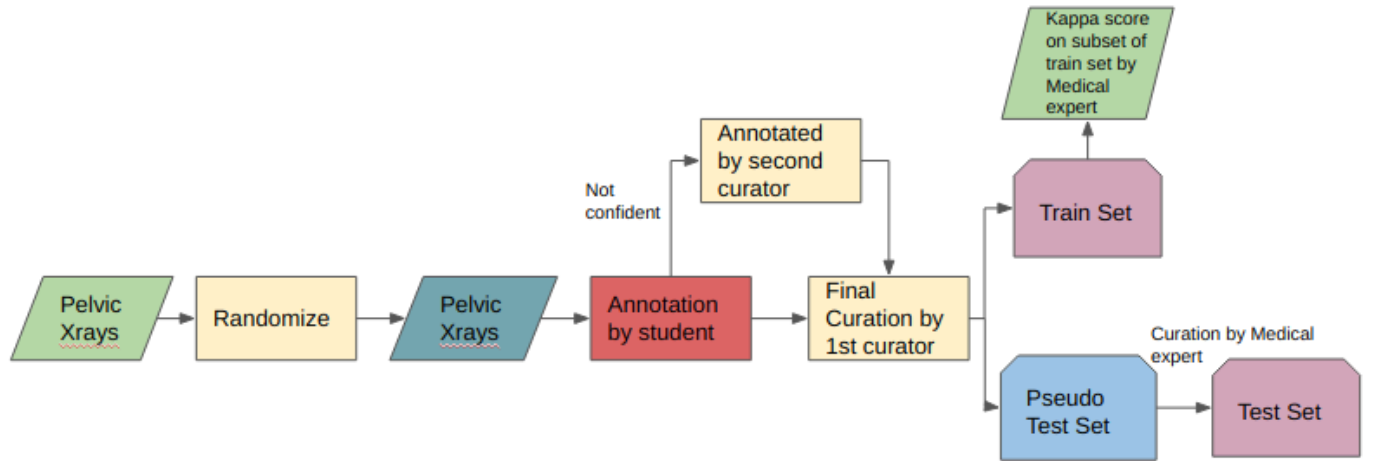


Fig 2: Proposed Data Annotation Pipeline.

Till now, we finished our work on *Annotation by student* step (Randomize step was deserted). As we have a team of 5 members, data was distributed between them in three parts - dist1, dist2, and dist3. Following chart showing data distribution between students (person name anonymized):

| distribution | Student 1 | Student 2 | Student 3 | Student 4 | Student 5 |
|---|---|---|---|---|---|
| dist1 | patch1_8 | patch9_16 | patch17_24 | patch33_40 | patch25_32 |
| dist2 | patch41_53 | | patch67_79 | patch54_66 | patch80_92 |
| dist3 | | | patch98_103 | patch93_97 | |

Here, patch{start}_{end} denotes the filename range from drr generated file. As we told earlier, for every CT image, there were 7 drr generated Xrays, Student first finds the best visible file and uses that for annotation. *MITK workbench* was used for annotation purposes too.
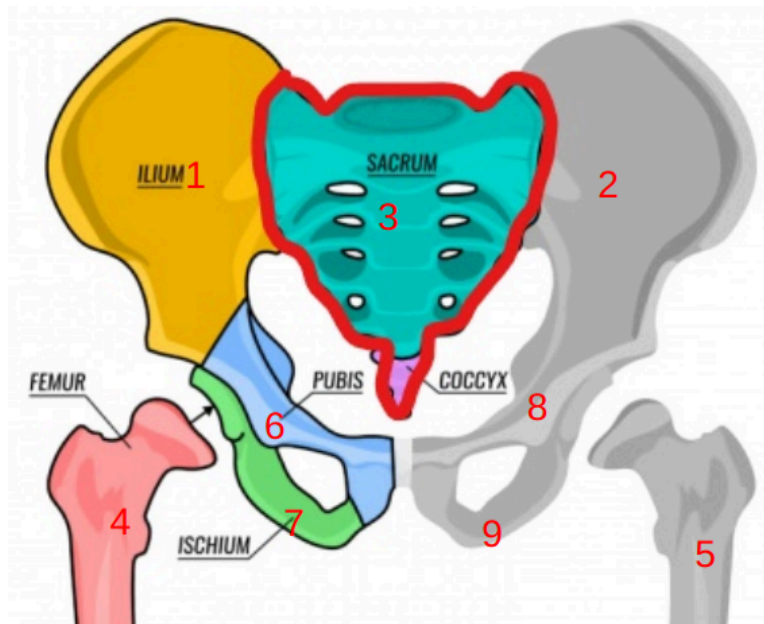


Fig 3: Labeling Protocol of Bones.

As we see in Fig 3, we used a unique labeling protocol for pelvic bones. We gave every bone a unique value and maintain it throughout our annotation process. Also, drr generation errors and annotation confusion were collected from students at the time of annotation ([spreadsheet](#)).
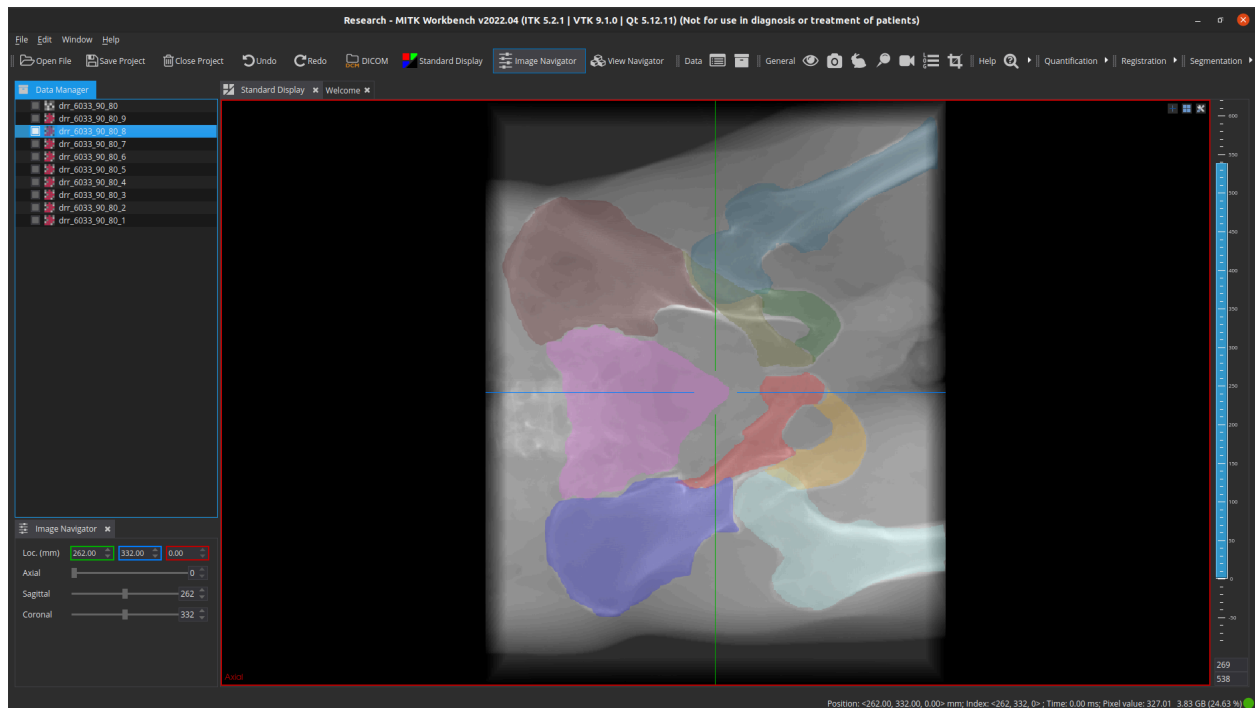


Fig 4: Bone Annotation in MITK workbench.

After the *preliminary stage of data annotation* by the students, the total number of annotated files is 79.

| # of CT files | # of DRR generation error | # of preliminary stage annotated files |
|---|---|---|
| 103 | 24 | 79 |

**Stage 2: Benchmarking Dataset.**

We used Convolutional Neural Network-based model (UNet[4]) for benchmarking. UNet is widely used in medical image segmentation and is acknowledged by many medical experts. We use a subset of the dataset containing 48 data for benchmarking. This subset was randomly split into train and validation sets.

| # of Total File | # of Train files | # of Valid files |
|---|---|---|
| 48 | 38 | 10 |

Training protocol:  input size - (256, 256), batch size - 12, optimizer - Adam, no of epochs - 50, learning rate - 0.0001, gpu - GTX 1070Ti.

Result: In this initial benchmarking, we got a mean *dice coefficient of 0.8724* on the valid set.



a.  Model Prediction.                                       b. Annotation.

Fig 5: Model's prediction on validation sample.

---

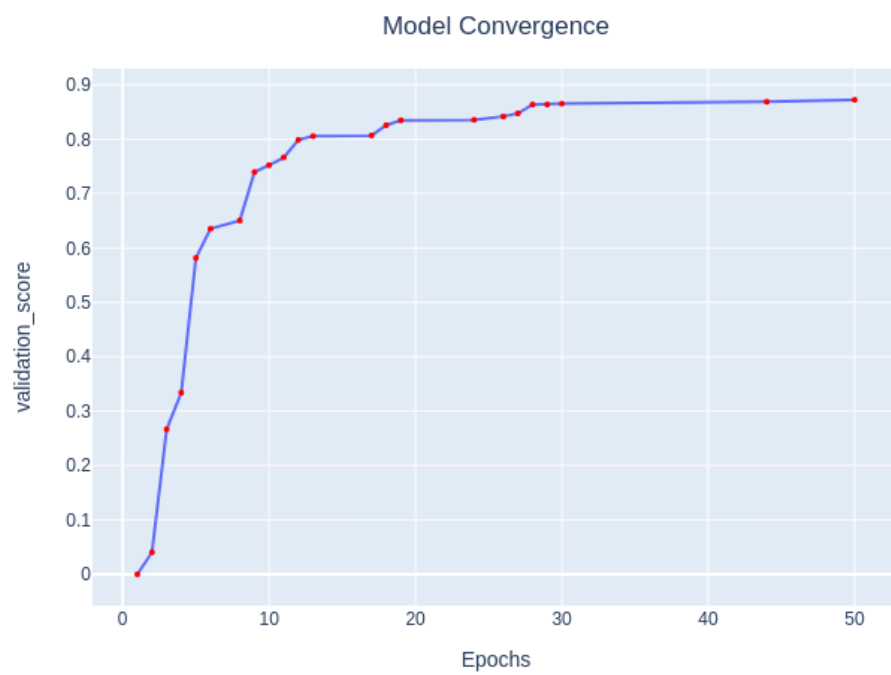[4] "U-Net: Convolutional Networks for Biomedical Image Segmentation." 18 May. 2015, https://arxiv.org/abs/1505.04597. Accessed 8 Aug. 2022.

Fig 6: Model Convergence during training.