

Anatomy-Driven Automated Subsegmentation of Pelvic and Proximal Femoral CT into Clinically Relevant Subregions and Landmark

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Abstract

Background.

The pelvis is among the most demanding regions in musculoskeletal imaging, and CT is its reference standard. Available automated tools, however, largely produce whole-bone or single-task masks, leaving the finer surgical subregions to slow, operator-dependent manual work. We developed a rule-based pipeline that converts pelvic and proximal femoral masks into a structured map of surgically meaningful subregions and landmarks and evaluated the extent to which it reduces this manual burden.

Methods.

Anonymized pelvic CT scans were collected retrospectively; after predefined quality criteria, 757 of 1,316 screened normal adult cases were processed by a one-click pipeline in 3D Slicer. Parent structures from TotalSegmentator were divided by fixed anatomical rules into columns, acetabular regions, sacral zones, and proximal femoral regions. In 100 randomly selected cases, every segment was expert-reviewed and corrected where needed; correction frequency was the primary endpoint, with accuracy computed for corrected segments only.

Results.

Of 8,100 segment observations, 93.8% were accepted without correction, and 51 of 81 segments required no correction in any case. Correction clustered in a few boundary regions, mainly the ischium and femoral neck (median 4.5 segments per case). Computed only on the corrected segments, the median Dice was 0.94, indicating that errors were modest where they occurred. A secondary symmetry analysis showed median surface agreement of 90% within 2 mm and 99.9% within 5 mm.

Conclusions.

Validated in normal adult anatomy, this rule-based pipeline converts pelvic and proximal femoral CT into a structured hierarchy of clinically relevant subregions, needing only limited, predictable correction. It substantially reduces manual workload while preserving the anatomical detail needed for morphometry, surgical planning, and dataset generation. Extension to fracture, deformity, or clinical decision-making requires dedicated validation in abnormal anatomy.

Introduction

Pelvic CT segmentation is central to trauma assessment, deformity analysis, and preoperative surgical planning in orthopedic practice[1]. It further enables patient-specific extraction of pelvic parameters and

optimization of arthroplasty planning and morphological evaluation[2]. However, manual segmentation remains time-consuming and technically dependent on operator expertise[1], [3].

Automated pelvic CT segmentation has been achieved using atlas-based, statistical shape model, and graph-based approaches[1], [4], [5]. These methods primarily produced segmentation of whole pelvic bones or limited hip structures[1], [4], [6], [7]. Deep-learning models have enabled multi-class segmentation of pelvic structures including the sacrum and bilateral hip bones[8], [9].

Recent advances in CT-based pelvic segmentation have produced task-specific outputs such as coarse pelvic bone masks, fracture-fragment masks, and radiotherapy-oriented pelvic bone contours[10], [11], [12], [13], [14]. However, these approaches do not provide a detailed anatomical hierarchy of pelvic and proximal femoral subsegments. Such structured regional mapping could support subregion-specific morphometry, symmetry-based pelvic assessment, bone-quality mapping, fracture localization, fixation-corridor planning, and arthroplasty measurement workflows[15], [16], [17], [18] .

The current study therefore developed a rule-based automated pipeline that transforms parent pelvic and proximal femoral CT masks into a structured hierarchy of clinically relevant anatomical subregions and landmarks. Its primary aim was to evaluate to what extent automated subsegmentation reduces the manual correction burden required to achieve anatomically acceptable outputs across a large normal adult dataset.

Methods – Patient Selection and CT Acquisition

Pelvic CT datasets were retrospectively collected from fully anonymized imaging archives of multiple hospitals affiliated with the Directorate of Health Affairs in Sharqia, Egypt, under formal authorization for research and healthcare innovation. The datasets were collected between July 2025 and March 2026.

Inclusion criteria. Adult CT normal scans were included if they encompassed the entire pelvis and proximal femora, extending from at least the L5 vertebral level superiorly to below the lesser trochanters inferiorly. Native CT quality required near-isotropic acquisition, with in-plane voxel size ≤ 1.0 mm and slice spacing ≤ 1.25 mm, predefined to preserve reliable 3D reconstruction and segmentation. Cases with marked pelvic malposition on CT were excluded[19]. Malposition was defined as $> 5^\circ$ coronal tilt or $> 5^\circ$ axial rotation and was applied as a study-defined quality criterion, as pelvic orientation can affect CT-based measurements[20]. Bone quality was additionally screened at L5, where mean trabecular attenuation ≥ 160 HU was required as an indicator of sufficient bone density for reliable segmentation[21]. Voxel spacing, pelvic positioning, and L5 attenuation were assessed algorithmically using a custom Python-based workflow implemented in 3D Slicer. Morphological abnormalities, fractures, implants, major imaging artifacts, and eligibility decisions were reviewed by an experienced orthopaedic surgeon (Fig. 1).

Exclusion criteria

CT scans were excluded if they were obtained in paediatric patients or showed fracture, major deformity, post-surgical change, metallic implants, severe imaging artifacts, incomplete anatomical extent, or failure to satisfy the predefined technical criteria.

Segmentation workflow

An end-to-end segmentation pipeline for the pelvis and proximal femur was implemented as a custom 3D Slicer module [22], designed for one-click batch processing of large datasets (Fig. 2). The Slicer environment was chosen to leverage its native CT volume handling, segmentation infrastructure, and spatial processing tools within a single reproducible workflow. Manual correction was performed exclusively during reference mask creation for validation and forms no part of the routine processing workflow

TotalSegmentator was integrated to identify the major parent structures required for downstream processing, including L5, the sacrum, both hemipelves, and both femora[9]. The initial sacral mask frequently showed incomplete coverage and was therefore refined using a dedicated rule-based reconstruction step. The confirmed parent masks were then transferred automatically into the rule-based subsegmentation workflow, where deterministic anatomy-based rules were applied across the batch to generate the final subsegmented anatomy (Fig. 3). Detailed segmentation logic for individual regions and the anatomical definitions of framework-defined labels are provided in the Supplementary Material.

Anatomical Design of the Segmentation Tree

The segmentation hierarchy was designed to reflect orthopedic surgical anatomy rather than generic bone parcellation. The acetabulum is the osseous convergence of the ilium, ischium, and pubis—the three fused components of the hemipelvis[23]. Accordingly, these four structures were defined as the principal pelvic components and then organized into anterior and posterior column divisions, reflecting the structural logic of pelvic surgical anatomy[24]. The hierarchy was then extended to finer surgically relevant regions, for instance, the acetabular walls and quadrilateral plate support assessment of acetabular containment and column integrity[25], [26]. The sciatic buttress and femoral calcar provide pelvic and proximal femoral reference regions for hip load transfer and regional bone stock [27], [28], [29]. Denis-based sacral zones convert the sacrum from a single mask into a fracture-oriented map of alar, foraminal, and central involvement[30].

Segmentation Pipeline Architecture

The pipeline operates through sequential parent-to-child geometric derivation. Confirmed parent masks, the sacrum, bilateral hemipelves, and femora, served as the geometric foundation for all downstream subsegmentation. The femoral head was localized using a best-fit circular reference derived from axial and coronal proximal femoral core masks; its detected center and radius then guided acetabular

confinement and extraction. Acetabular subsegmentation was performed within a standardized roof-centered reference frame, partitioning the socket into anterior wall, posterior wall, and quadrilateral plate by positional assignment relative to reproducible anatomical axes. The hemipelvis was divided into anterior and posterior column domains by a deterministic plane connecting the iliac crest apex to the mid-roof point. Each downstream subregion was derived by Boolean operations on confirmed parent masks, geometric thresholding, or proportional mediolateral partitioning, with no region boundary drawn by manual delineation. This architecture ensures that the segmentation output is fully reproducible across cases and operators. Full definitions and segmentation logic for each region are provided in the Supplementary Methods.

Landmark Generation

Anatomical landmarks were generated automatically within the same subsegmentation pipeline and require no manual input. Each landmark was derived directly from the relevant parent mask using extremal geometry, prominence detection, or midline inference. The ASIS and PSIS were identified as the most anterior and most posterior points of the iliac mask, respectively. The iliac crest apex was extracted as the superolateral extremal point of the iliac mask. The AIIS was localized from the anterior iliac prominence below the crest level. The symphysis pubis was defined as the most anterior midline point between the bilateral hemipelvis masks. The lesser trochanter was identified from the posteromedial prominence of the proximal femoral mask. All landmarks were generated as named segment masks or point-sphere regions and are integral outputs of the segmentation tree, not externally placed fiducials.

Validation

A randomly selected subset of 100 eligible cases from the final cohort was used for validation. The automated pipeline generated the complete segmentation tree for each case as the starting point for all reference masks. All generated segments were visually inspected on a per-structure basis by an experienced orthopedic pelvic surgeon. Segments deemed anatomically acceptable were retained without modification; segments with identifiable anatomical errors were manually corrected. All segments were subsequently reviewed and confirmed by a second experienced pelvic surgeon. The resulting outputs served as the expert-corrected reference masks.

This validation design constitutes expert-audited correction-burden validation, in which the primary practical endpoint is correction frequency, the proportion of segments requiring expert correction per case. Accepted segments are reported as counts and percentages. Among segments requiring correction, the Dice similarity coefficient (DSC), absolute percentage volume difference (APVD), center-of-mass distance (CMD), average symmetric surface distance (ASSD), and 95th-percentile Hausdorff distance (HD95) were computed from corrected observations only and quantify the actual magnitude of pipeline error.

Secondary validation assessed anatomical plausibility by left–right symmetry analysis after contralateral mirroring and rigid surface registration, summarized by root-mean-square surface distance (RMSD) and the proportions of corresponding surface points within 1, 2, 3, 4, and 5 mm.

Statistical Analysis

Exported validation outputs were consolidated and analyzed using a custom Python script incorporating predefined integrity checks for case count, segment count, primary observations, and secondary symmetry observations. Accepted segments, those retained without expert correction, were reported as counts and percentages at the segment and case levels; no accuracy metrics were computed for these observations. Correction frequency was defined as Dice < 1.0 at the segment level and as the number of corrected segments per case at the case level. Accuracy metrics, DSC, CMD, ASSD, and HD95, were computed exclusively from corrected observations and are reported as mean $\pm$ standard deviation with median and interquartile range. Right and left observations were pooled within predefined bilateral anatomical categories where appropriate. Secondary symmetry results were summarized by RMSD and threshold-based surface agreement proportions at the regional level.

Results

A total of 1316 pelvic CT cases were screened for eligibility. Of these, 559 cases were excluded: 72 pediatric cases, 218 fracture cases (98 femoral, 69 pelvic-ring, and 51 acetabular fractures), 61 cases with metallic implants or hardware, 32 cases with advanced coxarthrosis or relevant pelvic/hip deformity, and 176 cases with technical or eligibility-related imaging limitations caused by incomplete L5-to-lesser-trochanter coverage of required segmentation components, marked osteoporosis, pelvic malposition/rotation, or inadequate image quality. The final dataset comprised 757 normal adult pelvic CT cases, all processed successfully by the automated segmentation pipeline; 100 cases were randomly selected for detailed primary and secondary validation.

Expert-Audited Validation Overview

Across all 100 validation cases, the automated pipeline generated anatomically acceptable outputs in the substantial majority of segments without requiring expert intervention. Correction was confined to a minority of observations and concentrated within a predictable anatomical subset rather than distributed across the segmentation tree. The overall acceptance and correction profile across all 8,100 case-segment observations is summarized in Table 1.

Table 1
Expert-audited validation overview across the 100-case validation dataset

Item	n	%
Total segment observations	8,100	—
Accepted without expert correction	7,595	93.8
Required expert correction	505	6.2
Segments never requiring correction across all 100 cases	51 of 81	63.0
Segments requiring correction in at least one case	30 of 81	37.0
Cases requiring zero corrections	4 of 100	4.0
Cases requiring correction in ≤ 5 segments	52 of 100	52.0
Cases requiring correction in ≤ 10 segments	96 of 100	96.0

Table 1: Validation overview across 8,100 case-segment observations in the 100-case validation dataset. Median corrected segments per case: 4.5 (range 0–19). Values are reported as counts and percentages.

Among segments requiring correction, error magnitude remained moderate across all geometric metrics. Median Dice exceeded 0.93 and median surface deviation remained within clinically acceptable limits, indicating that corrections addressed anatomically meaningful but bounded errors (Table 2).

Table 2
Accuracy metrics among corrected observations (n = 505 of 8,100)

Metric	Mean $\pm$ SD	Median [Q1, Q3]
Corrected observations, n	505 of 8,100	—
Dice	0.8821 $\pm$ 0.1471	0.9353 [0.8457, 0.9751]
HD95 (mm)	6.8961 $\pm$ 10.0434	5.0000 [2.0254, 8.5701]
ASSD (mm)	1.5769 $\pm$ 4.6458	0.6673 [0.2991, 1.6453]
COM (mm)	3.7943 $\pm$ 6.8007	2.1145 [0.8712, 4.5543]

Table 2: Metrics were calculated exclusively from corrected observations (Dice < 1.0); accepted observations contribute no values to this table. Abbreviations: Dice, Dice similarity coefficient; HD95, 95th-percentile Hausdorff distance; ASSD, average symmetric surface distance; COM, center-of-mass distance. Values are reported as mean $\pm$ SD and median [Q1, Q3].

Segment-Level Expert-Correction Frequency

Stable anatomical reference structures, including the sacrum, bilateral ilium, acetabulum, anterior and posterior columns, sciatic buttress, and all column subcomponents, were accepted without correction in

every case. Correction was concentrated in boundary-dependent regions, with the ischium and femoral neck requiring intervention most frequently and showing the greatest geometric error among corrected observations. Acetabular subsegments, sacral zones, and iliac subregions required only occasional or isolated correction (Table 3).

Table 3
Segment-level expert-correction frequency across the 100-case validation dataset

Segment	Corrected, n	Corrected, %	Mean Dice	Mean HD95 (mm)	Mean ASSD (mm)
Ischium	135	67.5	0.9344	3.5542	0.5188
Femoral neck	82	41.0	0.8235	10.2144	2.5116
Intertrochanteric region	64	32.0	0.9431	6.1140	0.9318
Femoral head	45	22.5	0.9441	5.8172	0.8332
Proximal femur	41	20.5	0.9615	5.1871	0.5651
Subtrochanteric region	37	18.5	0.7665	9.4384	2.5444
Pubis	27	13.5	0.7294	16.6918	4.2516
Greater trochanter	22	11.0	0.9868	1.0942	0.2286
Calcar region	17	8.5	0.6621	11.0916	2.8749
Anterior wall	11	5.5	0.9014	4.2802	0.7032
Posterior wall	10	5.0	0.9151	3.8701	0.7370
Acetabular roof	4	2.0	0.7194	6.1836	1.9282
Lesser trochanter	4	2.0	0.4166	18.9365	13.4503
Quadrilateral plate	4	2.0	0.9776	1.4578	0.2735

Table 3: A segment was classified as corrected when its Dice coefficient was < 1.0; right and left observations were pooled within each bilateral category. Dice, HD95, and ASSD values reflect corrected observations only. Abbreviations: HD95, 95th-percentile Hausdorff distance; ASSD, average symmetric surface distance. Values are reported as counts, percentages, mean Dice, mean HD95, and mean ASSD.

Case-Level Expert-Correction Burden During Validation

The distribution of correction burden across individual cases confirmed that workload remained manageable throughout the validation dataset. The majority of cases required correction in fewer than seven segments, and a small proportion required no correction at all. No case exceeded 19 corrected segments out of 81 analyzed (Table 4).

Table 4
Case-level expert-correction burden during validation

Corrected segments per case, n	Cases, n	Cases, %	Corrected segments per case, n	Cases, n	Cases, %
0	4	4.0	7	6	6.0
1	7	7.0	8	11	11.0
2	16	16.0	9	6	6.0
3	13	13.0	10	3	3.0
4	10	10.0	11	2	2.0
5	2	2.0	14	1	1.0
6	18	18.0	19	1	1.0

Table 4: Case-level correction burden was defined as the number of analyzed segments with Dice < 1.0 within an individual validation case. Values are reported as counts and percentages.

Landmark Structures

Landmark segmentation also remained highly accurate. Complete agreement with the reference standard was observed for the symphysis pubis, ASIS, AIIS, PSIS, and iliac crest apex, whereas the lesser trochanter showed slightly lower but still high agreement.

Overall Secondary Symmetry Validation

Secondary symmetry analysis confirmed excellent bilateral agreement. The median RMS surface mismatch was 1.2494 mm [1.0456, 1.5772]. Threshold-based agreement increased progressively with wider tolerance levels, reaching a median of 99.8537% within 5 mm (Table 5).

Table 5
Overall secondary symmetry validation metrics

Metric	Mean $\pm$ SD	Median [Q1, Q3]
RMS (mm)	1.4840 $\pm$ 1.5039	1.2494 [1.0456, 1.5772]
Within 1 mm (%)	63.4942 $\pm$ 12.0345	63.0662 [56.0684, 72.4334]
Within 2 mm (%)	88.5457 $\pm$ 8.5802	90.4710 [85.2930, 94.2608]
Within 3 mm (%)	95.8609 $\pm$ 5.8051	97.7556 [94.9489, 98.9801]
Within 4 mm (%)	98.0124 $\pm$ 4.3905	99.3767 [97.7988, 99.8698]
Within 5 mm (%)	98.8264 $\pm$ 3.6654	99.8537 [99.0414, 99.9933]

Table 5: Secondary symmetry metrics were calculated across all regional bilateral comparisons in the 100-case validation dataset; threshold values indicate the percentage of surface points within each distance tolerance. Abbreviation: RMS, root-mean-square surface mismatch. Values are reported as mean ± SD and median [Q1, Q3].

Secondary Symmetry Validation by Region

Regional symmetry also remained high. The lowest RMS values were observed in the acetabulum, femoral head, and ilium, whereas relatively higher values were seen in the pubis, ischium, and column-based regions (Table 6).

Table 6
Secondary symmetry validation metrics by region

Region	Group	RMS, mean ± SD (mm)	RMS, median [Q1, Q3] (mm)
Acetabulum	Primary	1.0307 ± 0.2022	1.0014 [0.9043, 1.1029]
Femoral head	Primary	1.0732 ± 0.3138	0.9645 [0.8733, 1.2163]
Ilium	Primary	1.2229 ± 0.2298	1.1783 [1.0598, 1.3199]
Hemipelvis	Primary	1.3847 ± 0.3013	1.3391 [1.2181, 1.4632]
Proximal femur	Primary	1.2992 ± 0.4328	1.1863 [1.0846, 1.3337]
Ischium	Primary	1.4377 ± 0.6894	1.2701 [1.0029, 1.7670]
Pubis	Primary	2.0513 ± 4.1376	1.2833 [0.8760, 1.9214]
Anterior column	Secondary	1.8778 ± 0.6937	1.6734 [1.4014, 2.1497]
Posterior column	Secondary	1.9781 ± 0.8773	1.6985 [1.4349, 2.2086]

Table 6: Regional RMS values summarize bilateral surface agreement for each mirrored anatomical category. Values are reported as mean ± SD and median [Q1, Q3].

Discussion

Pelvic anatomy poses a distinct three-dimensional analytical challenge [31]. CT remains the gold standard for detailed evaluation of the pelvis [32]. Its assessment requires integration of diverse findings, including acetabular measurements, pelvic alignment, bone stock, symmetry, and fracture classification [20], [33], [34]. Therefore, segmentation is particularly valuable in pelvic CT, as it converts complex anatomy into structures that can be consistently visualized, localized, and measured [35].

Manual workflows remain a major barrier in pelvic CT analysis[3], [36]. Previous reports showed that CT-based 3D model segmentation took 90–120 minutes for each hip joint, while manual CT-based THA

planning averaged 185.40 ± 21.76 minutes per case [3], [36]. Additionally, prior data showed that some pelvic landmarks were frequently mislabeled by 10 mm or more [33]. CT-based pelvic analysis is also challenging in several clinically important and research-oriented tasks [2], [23]. These include pelvimetric extraction, fracture classification, fixation planning, deformity correction, and large-scale generation of structured anatomical data for research use [2], [37]. Together, these limitations underscore the value of automated segmentation for structured and reproducible pelvic CT analysis [35].

Earlier pelvic CT studies established the feasibility of atlas-based segmentation, landmark transfer, and targeted hip-joint extraction [1], [5], [6], [4], [38], [7]. Recent CT-based pelvic segmentation work has remained task-specific. Coarse bone-segmentation approaches produced lumbar spine, sacrum, bilateral hemipelvises, femoral, or whole-pelvis labels [8], [9], [11], [12], [39]. Trauma-focused pipelines targeted pelvic fracture masks, fragment segmentation, or fracture-reduction planning [10], [14], [40]. Measurement- and landmark-based frameworks automated selected outputs such as 3D pelvimetry, acetabular lunate-surface analysis, or landmark detection in defective pelvis CTs [2], [41], [42]. Therefore, current literature supports automated pelvic CT analysis for defined tasks, but a unified fully automated sub segmentation framework of normal pelvic and proximal femoral subregions remains insufficiently established.

In the current study, sub segmentation was reframed from coarse bone-mask extraction into an orthopaedic anatomical mapping system. Each output region was selected and defined according to anatomical units with direct clinical applicability in pelvic assessment and surgical planning. This segmentation design is particularly relevant for future fracture mapping, regional morphometry, and planning-oriented CT analysis, where interpretation depends on precise anatomical location rather than whole-bone volume alone.

Pelvic CT segmentation remains boundary-sensitive even before fine sub segmentation. Recent work has described challenges related to small targets, thin boundaries, and separation of adjacent hip bone segments [10]. In the present study, stable reference structures, including the sacrum, ilium, acetabulum, anterior and posterior columns, sciatic buttress, and all column subcomponents, required no expert correction in any of the 100 validation cases. Among femoral and acetabular subsegments, the femoral head, greater trochanter, acetabular walls, and dense sacral compartments were accepted without correction in most cases. Correction was confined to boundary-dependent or bridging regions, principally the femoral neck, ischium, pubis, subtrochanteric region, calcar region, and intertrochanteric region, where anatomical continuity makes discrete voxel-level separation inherently less deterministic. This boundary profile explains why correction frequency was concentrated in a small subset of transition-related segments rather than distributed uniformly across the anatomical tree.

The primary question this study addresses is practical: to what extent does the pipeline reduce manual segmentation workload in pelvic CT analysis. Correction frequency is therefore the central endpoint, reflecting how many segments required expert intervention and how large the remaining errors were. Across 100 validation cases, 93.8% of segments were accepted without correction, and correction where

required was moderate in magnitude and confined to a predictable anatomical subset. Several boundaries in this framework are defined by anatomical rules of inherent geometric precision, applied identically across every case. The acetabular roof, for instance, corresponds to the superior weight-bearing portion of the lunate articular surface [43] identified in the pipeline as the superior acetabular surface at the level where femoral head contact first disappears. Here the anatomical rule is the definition, and its consistent execution across cases represents a standard of reproducibility that freehand delineation does not achieve. These findings indicate that the pipeline generates anatomically acceptable pelvic and proximal femoral subsegmentations in most cases, with a limited and predictable correction burden.

Symmetry analysis served as a secondary plausibility check for segmentation consistency. In the present study, contralateral mirroring and rigid surface registration were applied across 100 CT cases and paired regions including the acetabulum, femoral head, ilium, innominate, ischium, proximal femur, pubis, and anterior and posterior columns; median surface agreement reached 90.4710% within 2 mm and 99.8537% within 5 mm. These findings are consistent with previous 3D studies of intact pelvic symmetry[44], [45], [46]. Ead et al. analyzed 14 pelvic CT scans using Mimics-based 3D reconstruction and Geomagic deviation analysis, reporting an RMS deviation of 1.14 ± 0.26 mm and $91.9 \pm 5.55\%$ of surface points within ± 2 mm[44]. Zheng et al. analyzed 50 pelvic CT scans using Mimics, Geomagic, and closest-point alignment, reporting a mean surface deviation of 1.15 ± 0.16 mm and $90.82 \pm 4.67\%$ of points within the permissible ± 2 mm range[45]. Bakhshayesh et al. analyzed ten healthy adult CT scans using STL reconstruction, hemipelvis mirroring, volume fusion, and CT motion analysis, showing that right–left differences remained within approximately 3 mm translation and 2° rotation[46]. These studies establish bilateral pelvic symmetry as a reliable reference concept; the current study extends this concept from whole-pelvis comparison to region-level segmentation, supporting its use for side-to-side quality control, normal-variation assessment, and detection of abnormal asymmetry.

Beyond validation, the segmentation framework was integrated into a custom one-click 3D Slicer workflow to assess its feasibility for quantitative analysis and clinically relevant secondary applications. These included automated regional bone-quality assessment in predefined load-bearing areas, selected pelvic and proximal femoral morphometric measurements, and planning-oriented workflows for fracture fixation and arthroplasty. The same framework may also support structured annotation of abnormal or excluded cases, where automated segmentation followed by selective manual refinement could accelerate the creation of curated datasets for future deep-learning models. These outputs remain extensions of the core pipeline and represent planned directions for follow-up studies; each requires application-specific validation before clinical use. Technical details for these secondary applications are provided in the Supplementary Material.

Strengths and limitations

To our knowledge, this is the first automated pelvic CT framework to move beyond coarse bone segmentation or single-task measurement and provide a fully automated, anatomy-based orthopedic

subsegmentation map of the pelvis and proximal femur, validated through expert-audited correction-burden analysis across 100 cases. Its main strength is that pelvic CT segmentation is treated as a reproducible anatomical framework, preserving clinically meaningful regions, landmarks, and spatial relationships rather than generating isolated masks. This design provides a transparent and reusable foundation for downstream morphometric, measurement, and planning workflows. The primary limitation of the validation design is that reference masks were initialized from pipeline output and corrected where needed, rather than generated independently from scratch; the results should therefore be interpreted as expert-audited anatomical acceptability and correction burden rather than conventional independent agreement. Independent manual validation of selected key subregions remains a direction for future work. A further limitation is that the pipeline was validated exclusively in normal adult CT scans; performance in fractures, deformity, severe degeneration, implants, or marked morphological alteration remains unproven and requires dedicated evaluation before application to abnormal cohorts or clinical decision-making.

Conclusion

This study presents a rule-based automated pipeline that transforms pelvic and proximal femoral CT into a structured hierarchy of clinically relevant anatomical subregions and landmarks. Across 100 validation cases, 93.8% of segments were accepted without expert correction, with correction confined to a predictable anatomical subset and moderate in magnitude where required. The pipeline substantially reduces manual segmentation workload while preserving the anatomical detail necessary for morphometric analysis, surgical planning, and structured dataset generation. Further validation in abnormal anatomy is required before extension to fracture, deformity, or clinical decision-making workflows.

Abbreviations

AIIS

Anterior inferior iliac spine

APVD

Absolute percentage volume difference

ASSD

Average symmetric surface distance

ASIS

Anterior superior iliac spine

CMD

Center—of—mass distance

DSC

Dice similarity coefficient

HD95

95th—percentile Hausdorff distance

HU

Hounsfield unit

PSIS

Posterior superior iliac spine

RMSD

Root—mean—square surface distance

RMS

Root—mean—square

THA

Total hip arthroplasty

VOLDiff

Absolute volume difference (%)

Declarations

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Competing Interests

None of the authors has any conflicts of interest to declare.

Ethics Approval and Consent to Participate

All methods were carried out in accordance with relevant guidelines and regulations and with the principles of the Declaration of Helsinki. Access to and use of the anonymized CT imaging data were formally authorized by the Directorate of Health Affairs – Sharqia Governorate, Ministry of Health and Population, Arab Republic of Egypt, through an official “Authorization Approval for the Use of Anonymized CT Imaging Data” dated 1 July 2025. The relevant local institutional review board is the Institutional Review Board of the Directorate of Health Affairs – Sharqia Governorate, Egypt.

For this retrospective study using fully anonymized imaging data, separate individual consent to participate was deemed unnecessary/not required according to Egyptian ethical regulations, as stated in the authorization. All imaging data were fully de-identified and contained no names, national identification numbers, or direct personal identifiers, and the data were handled under the conditions of secure storage, ethical use, and no patient re-identification.

Consent to Publish

Not applicable.

Authors' Contributions

Mohammed Rashed: Conceptualization, study design, data collection, eligibility screening, pipeline development, framework design, segmentation workflow implementation, validation analysis, and manuscript writing.

Hatem Al-Abdulrahman: Data evaluation, secondary observer agreement assessment, and review of the reference-standard segmentations.

Simon D. Westfechtel: Methodology review, manuscript review and editing.

Frank Hildebrand: Supervision, manuscript review.

Daniel Truhn: Supervision, methodology guidance, manuscript review and editing.

Availability of Data and Materials

The datasets analyzed and generated during the current study are not publicly available because they consist of retrospectively collected anonymized medical imaging data subject to institutional data-governance requirements. The datasets will be stored securely at the authors' institution for 10 years in accordance with institutional data-retention policy. Data may be made available from the corresponding author upon reasonable request and subject to applicable ethical, institutional, and data-protection approvals.

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Figures



Figure 1

Pelvic CT eligibility and quality-control screening. Representative CT examples show excluded cases and an eligible normal case after assessment of coverage, resolution, bone density, pelvic orientation, and morphology.

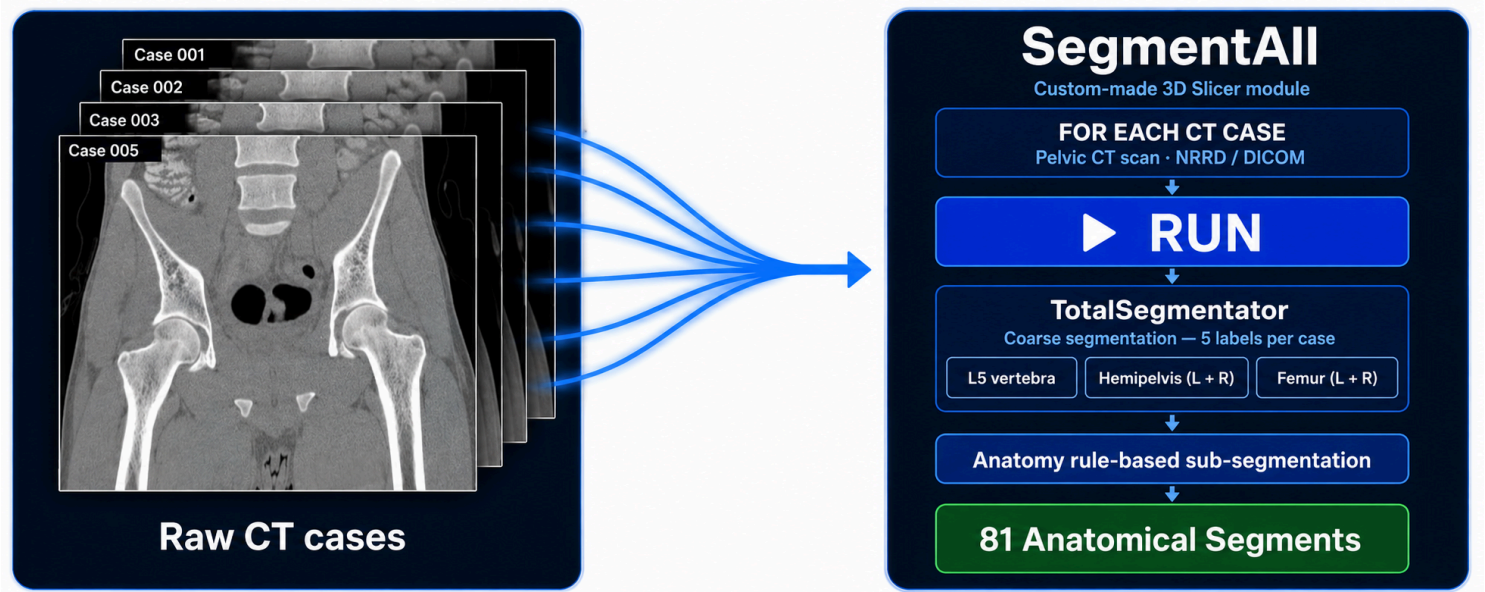


Figure 2

SegmentAll workflow from raw pelvic CTs to the final pelvic and proximal femoral segmentation tree.

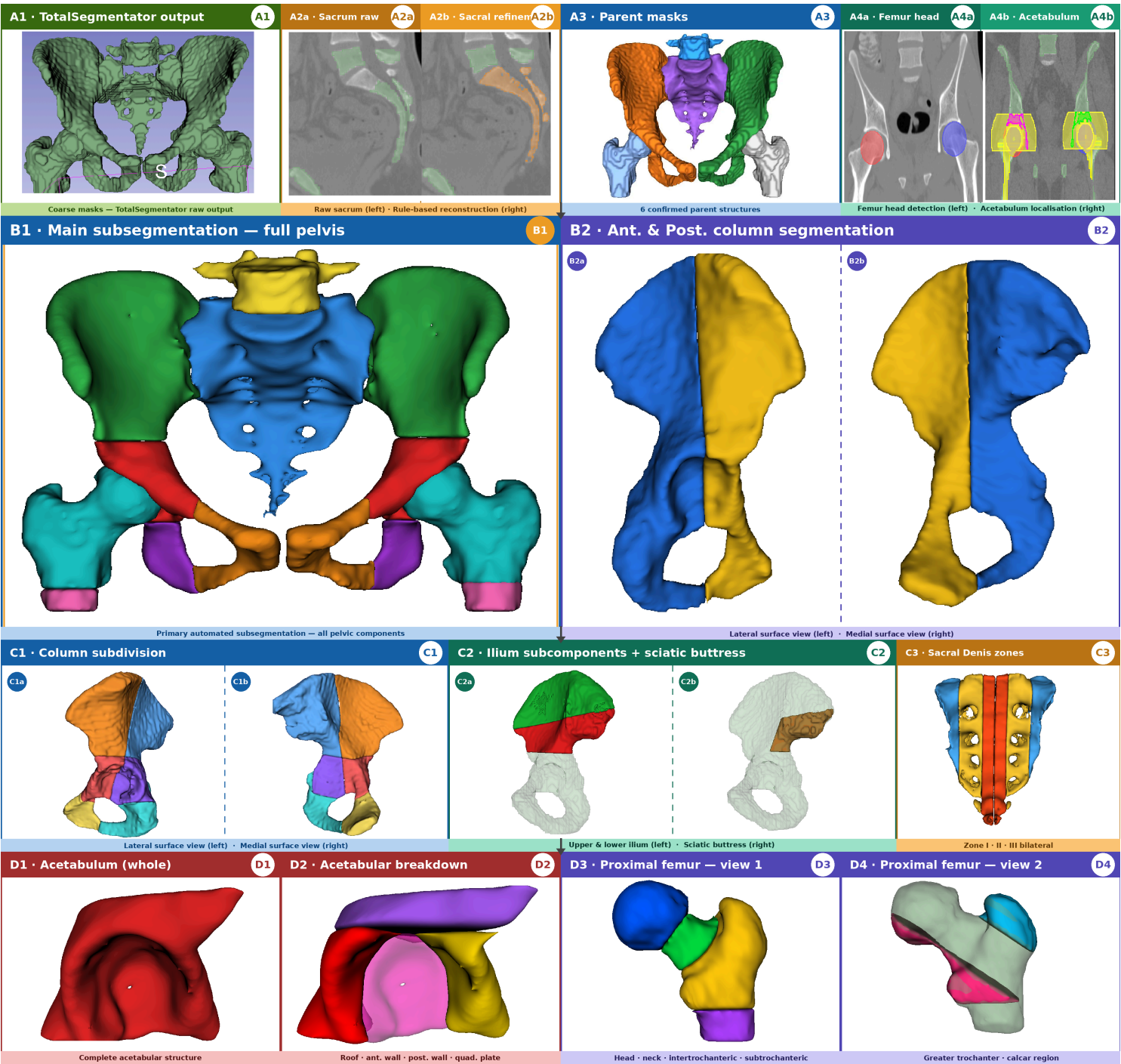


Figure 3

Automated rule-based pelvic CT subsegmentation workflow. (A1) TotalSegmentator coarse masks. (A2) Sacrum raw output (left) and rule-based reconstruction (right). (A3) Six confirmed parent structures. (A4) Bilateral femoral head detection (left) and acetabulum localisation (right) on coronal CT. (B1) Full-pelvis automated subsegmentation result. (B2) Anterior and posterior column segmentation; lateral (left) and

medial (right) surface views. (C1) Column subdivision; lateral (left) and medial (right) views. (C2) Ilium subcomponents — upper and lower ilium (left) and sciatic buttress (right). (C3) Sacral Denis zones I–III, bilateral. (D1) Complete acetabulum. (D2) Acetabular breakdown: roof, anterior wall, posterior wall, and quadrilateral plate. (D3) Proximal femur: head, neck, intertrochanteric, and subtrochanteric regions. (D4) Proximal femur: greater trochanter and calcar region.

Supplementary Files

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