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Technical Note: SegMed, a 3D Slicer module for standardized post mortem CT segmentation of lower-limb long-bone diaphyses

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Abstract

Post mortem computed tomography is increasingly used in forensic medicine and anthropology, but quantitative analysis of skeletal and peri-skeletal structures remains limited by heterogeneous anatomical sampling and manual segmentation procedures. This Technical Note presents SegMed, a Python-based 3D Slicer module developed to standardize segmentation and metric extraction from lower-limb long-bone *post mortem* CT data. In its current version, SegMed is restricted to the lower limb, and the present manuscript focuses on femoral and tibial diaphyseal workflows. The module integrates four steps: semi-automatic extraction of the diaphyseal region from an expert-defined cortical seed point, anatomical alignment of the selected bone segment, Hounsfield unit (HU)-based segmentation of medullary compartments, and optional quantification of peridiaphyseal soft tissues. The module exports quality-control masks, compartment volumes, volumetric fractions, longitudinal profiles, metadata files and analysis-ready CSV/XLSX tables. Optional exploratory indices describing the spatial distribution of segmented compartments are exported for research purposes but are not evaluated in this Technical Note. By combining expert-guided initialization with standardized image processing and structured outputs, SegMed is intended to improve reproducibility in forensic imaging research. The software does not provide diagnostic conclusions, and all outputs require expert visual review and contextual interpretation.

1. Introduction

Post mortem computed tomography (PMCT) has become an important tool in forensic pathology and forensic anthropology [1, 2]. It allows non-destructive documentation of skeletal trauma, anatomical variation, foreign bodies, decomposition-related changes and peri-skeletal structures [1, 3]. However, the quantitative use of PMCT remains limited by the difficulty of defining comparable anatomical regions across cases and by the time required for repeated manual segmentation, particularly in decomposed remains [4, 5].

Lower-limb long-bone diaphyses are particularly suitable for standardized image analysis because they provide elongated anatomical structures that can be aligned, sampled and compared across individuals. Nevertheless, manual selection of the diaphyseal region and manual measurement of internal or surrounding compartments remain operator-dependent [4, 5]. SegMed was developed to address this methodological issue by providing a reproducible protocol for diaphyseal extraction, compartment segmentation and structured export of imaging-derived variables.

The aim of this Technical Note is to describe the design, operational workflow and outputs of SegMed. The module is presented as a technical tool for standardized segmentation and metric extraction. It is not intended to provide automated diagnosis, cause-of-death assessment, *post mortem* interval estimation or medico-legal conclusions. Rather, it provides standardized imaging-derived variables for the study of *post mortem* changes within lower-limb long-bone diaphyseal cavities.

2. Scope of the module

In its current version, SegMed is restricted to lower-limb long bones. The present Technical Note focuses on femoral and tibial diaphyseal analysis, which represents the intended practical use of the module at this stage. Preliminary fibular parameters are implemented in the software, but fibular analysis is not evaluated in this manuscript and should not be considered part of the currently assessed analysis.

This restriction is important because the module relies on lower-limb anatomical assumptions, including proximodistal orientation, diaphyseal sampling, cortical extraction and peridiaphyseal soft-tissue analysis around the selected bone. Extension to other skeletal elements would require dedicated anatomical constraints, orientation rules and validation.

3. Software design

SegMed version 3.2.3 is implemented as a scripted module for 3D Slicer using Python and standard image-processing libraries, including SimpleITK, NumPy and SciPy [6–9]. The graphical interface is organized into four functional tabs: extraction, medullary analysis, peridiaphyseal soft-tissue analysis and export. The overall SegMed processing pipeline is summarized in Fig. 1.

The extraction tab allows the operator to select the CT volume, specify the bone type and laterality, define the case identifier, place a cortical seed point and adjust anatomical limits when necessary. The analysis tab performs Hounsfield unit (HU)-based segmentation of the medullary region using CT values preserved from the original image. The peridiaphyseal tab quantifies a soft-tissue sleeve around the same aligned diaphyseal segment. The export tab centralizes structured outputs, including masks, tables and metadata files.

This organization was designed to preserve expert supervision while reducing repetitive manual operations and improving traceability.

4. Diaphyseal extraction and anatomical alignment

The process begins with an expert-defined seed point placed on the cortical bone. SegMed identifies cortical voxels using HU thresholding and isolates the connected component associated with the selected bone [4, 5]. The long axis of the extracted bone is then estimated using principal component analysis. This axis is used to orient the volume and define a standardized anatomical frame.

The diaphyseal region is delimited using predefined bone-specific anatomical ratios. For the present Technical Note, the relevant workflows are the femur and tibia. These ratios can be adjusted by the operator when necessary, allowing expert control in atypical or altered cases. The module also includes quality-control checks related to bone length and extraction consistency.

The extracted diaphysis can be exported as a binary mask and as an aligned CT volume preserving the original HU values. This allows subsequent analyses to be performed on standardized anatomical

segments while retaining the quantitative information required for HU-based segmentation.

5. Medullary compartment segmentation

The medullary analysis uses HU thresholds to classify internal diaphyseal content into coarse imaging compartments. These compartments are CT attenuation-based classes rather than direct anatomical or histological tissue labels [5]. They are intended to provide reproducible descriptive outputs, not definitive tissue identification.

Gas-related outputs are included because gas detection and distribution are common PMCT findings and may be documented quantitatively, although their interpretation remains case-dependent [3, 10]. The main medullary outputs are defined in Table 1.

Table 1
Operational definitions of SegMed medullary outputs.

SegMed output	Operational definition
Gas total	Voxels of very low attenuation compatible with gas within the medullary cavity.
Gas pure	Subclass of very low-density gas-like voxels.
Gas mixed/aerated content	Subclass of gas-like voxels with higher attenuation, potentially reflecting partial-volume or mixed density effects.
Fat-like content	Voxels with attenuation compatible with fat-like or residual fatty medullary content.
Fluid-like content	Voxels with attenuation compatible with fluid-like content.
Intermediate-density material	Voxels with intermediate attenuation that are not assigned to gas-like, fat-like or fluid-like classes.
Debris-like material	Higher-density voxels within the medullary region, considered an exploratory CT attenuation class rather than a specific biological compartment.
Residual medullary content	Remaining medullary voxels not otherwise assigned by the segmentation sequence.
Endosteal-adjacent shell	A geometric proxy generated along the inner cortical boundary adjacent to the medullary cavity. It should not be interpreted as direct segmentation of the histological endosteum.

Default HU ranges are pre-set for each segmented compartment and can be adjusted by the operator when necessary. To avoid double voxel assignment, medullary HU ranges are required to be correctly ordered and non-overlapping [5]. The software includes internal validation checks to stop the analysis if invalid or overlapping ranges are entered. This constraint improves computational consistency, but it does not imply that the corresponding biological materials are sharply separated on CT.

For each compartment, SegMed computes volumetric measurements, volumetric fractions and spatial descriptors. Longitudinal profiles can also be generated along the aligned diaphyseal axis. These outputs are intended for downstream statistical analysis, comparison between cases or methodological evaluation.

The module also produces quality-control outputs, including segmentation masks, HU summaries and tabular files. These are essential because HU-based segmentation may be affected by scanner parameters, reconstruction kernels, partial-volume effects, metallic artefacts, severe decomposition, incomplete field of view or contact with adjacent anatomical structures.

6. Peridiaphyseal soft-tissue analysis

SegMed includes an optional peridiaphyseal module designed to quantify the soft-tissue envelope surrounding the same aligned diaphyseal segment. This module uses the aligned bone axis and the same proximal-distal limits as the diaphyseal extraction. A radial margin is applied around the target bone to define a reproducible peri-osseous region of interest.

Within this region, HU-based classes can be used to describe broad attenuation-based components, including gas-like, fat-like, fluid-like, muscle-like and dense soft-tissue-compatible areas. These are HU-compatible classes and not definitive anatomical labels. Because *post mortem* changes may alter normal soft-tissue planes, the peridiaphyseal module uses broad HU-compatible attenuation classes rather than discrete anatomical segmentation of the skin, subcutaneous tissue, fascia or individual muscles.

For peridiaphyseal analysis, narrow HU classes are also checked for ordering and exclusivity. However, the broad muscle-compatible window is treated as an independent descriptive metric and may overlap with other attenuation ranges. This distinction should be maintained when interpreting exported variables.

The purpose of the peridiaphyseal module is to provide additional contextual variables related to the preservation or alteration of peri-skeletal tissues. It does not modify the medullary SegMed outputs. Specific safeguards are included to reduce contamination from the scanner table, adjacent structures or the contralateral limb when both lower limbs are visible. As with the medullary analysis, visual inspection remains mandatory [4, 11].

7. Exported outputs

SegMed exports both image-based and tabular outputs. Image outputs include segmentation masks and quality-control files. Tabular outputs include compartment volumes, volumetric fractions, longitudinal summaries, HU statistics, metadata and analysis-ready CSV/XLSX tables [12]. SegMed 3.2.3 also exports variable catalogues in which output fields are classified as primary, derived or quality-control

(QC) variables. This classification is intended to facilitate data interpretation and downstream variable selection; it does not imply biological validity or predictive relevance.

Volumetric fraction variables are exported with different denominators. Variables ending in *_frac* are calculated relative to the total medullary cavity volume. Variables ending in *_frac_nogas* are calculated relative to the non-gas cavity volume, defined as the cavity volume minus total gas volume. Variables ending in *_frac_bio* are calculated relative to the sum of fat-like, fluid-like, intermediate-density and residual medullary content volumes. These suffixes therefore indicate normalization choices and should not be interpreted as additional segmented compartments. Using multiple denominators allows the same segmented compartment to be described from complementary perspectives: relative to the entire medullary cavity, relative to the non-gas portion of the cavity, or relative to selected residual medullary content. This provides flexible normalization for downstream descriptive or statistical analyses, while preserving the distinction between segmented compartments and derived fraction variables.

The export structure also improves auditability by preserving case identifiers, selected parameters, anatomical settings and run metadata.

Optional exploratory indices describing the spatial distribution of segmented compartments are exported for research purposes but are not evaluated in this Technical Note. These variables should therefore be considered descriptive outputs awaiting dedicated methodological assessment.

8. Forensic relevance

SegMed may be useful in forensic anthropology and legal medicine as a standardized research tool for PMCT feature extraction [4, 12]. Its main contribution is methodological: it reduces repeated manual segmentation, applies consistent anatomical sampling, preserves HU-based quantitative information and generates structured outputs suitable for statistical analysis.

Possible research uses include comparative studies of medullary and peri-skeletal imaging features, assessment of segmentation reproducibility, evaluation of CT-visible *post mortem* changes and development of standardized imaging datasets [3–5]. However, SegMed does not replace expert interpretation and should not be used as an autonomous decision-making tool.

9. Limitations

Several limitations must be acknowledged. First, SegMed is currently restricted to lower-limb long bones, and the present Technical Note focuses on femoral and tibial diaphyseal analysis. Although preliminary fibular parameters are implemented in the software, fibular analysis is not evaluated here.

In disarticulated, commingled or bulk-scanned skeletal remains, overlapping or contacting bones may prevent reliable isolation of the target femoral or tibial diaphysis and may require prior manual cropping

or separate scanning. Poor cortical preservation, fragmentation, severe taphonomic alteration or low CT contrast may also compromise seed-based extraction and long-axis estimation.

The segmented compartments are HU-based imaging classes and should not be interpreted as histological tissue types [5]. This is particularly important for intermediate-density, debris-like and residual categories, which may include heterogeneous material, partial-volume effects or artefacts. Similarly, the endosteal output corresponds to a geometric endosteal-adjacent proxy generated from the inner cortical boundary, rather than direct segmentation of the histological endosteum.

The software requires medullary HU ranges to be correctly ordered and non-overlapping, preventing double voxel assignment and improving computational reproducibility [5]. However, this technical constraint does not eliminate the biological and radiological ambiguity inherent to PMCT. Scanner settings, reconstruction kernels, partial-volume effects and decomposition-related heterogeneity may still affect compartment assignment [3, 5].

Finally, SegMed remains a supervised segmentation and metric-extraction tool requiring expert input for seed placement, anatomical review and quality control. The exploratory spatial-distribution indices included in the export files have not yet been validated, and their forensic relevance, repeatability and interpretation remain outside the scope of this Technical Note.

10. Conclusion

SegMed provides an integrated 3D Slicer method for standardized segmentation and metric extraction from lower-limb long-bone PMCT data. In its current version, the module is intended primarily for femoral and tibial diaphyseal workflows. By combining expert-guided initialization, anatomical alignment, HU-based compartment segmentation, peridiaphyseal analysis and structured exports, SegMed offers a reproducible technical framework for forensic imaging research. Its outputs are descriptive and research-oriented, requiring expert review and further validation before any forensic interpretation. A short user guide is provided as supplementary material.

Declarations

Competing interests:

The authors declare that they have no competing interests.

Ethics approval:

No ethics committee approval was sought. All PMCT examinations had been performed for medicolegal purposes, independently of the present study, as part of judicial death investigations under the authority of the competent judicial authorities. The present work involved only the secondary use of fully

anonymised data, and no additional procedure was performed on the deceased. The study did not constitute research involving the human person (*recherche impliquant la personne humaine*, RIPH) under French law and was conducted in accordance with the French CNIL MR-004 reference methodology applicable to research not involving the human person, as well as Article 86 of the French Data Protection Act concerning the use of data relating to deceased individuals.

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Author Contribution

Author contributions: P.N. contributed to the conceptualization of the project, software development, code revision, software testing, and preparation of the manuscript. K.M., F.D., N.T. and F.S. reviewed and critically revised the manuscript. All authors read and approved the final manuscript.

Data availability:

A short user guide describing the software workflow, output structure, and principal variables, are provided as supplementary material. No additional study dataset was generated or analysed for the purposes of this Technical Note.

Code availability:

The SegMed source code will be made publicly available at a later stage. The repository URL and archived release information will be provided when available.

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Figures

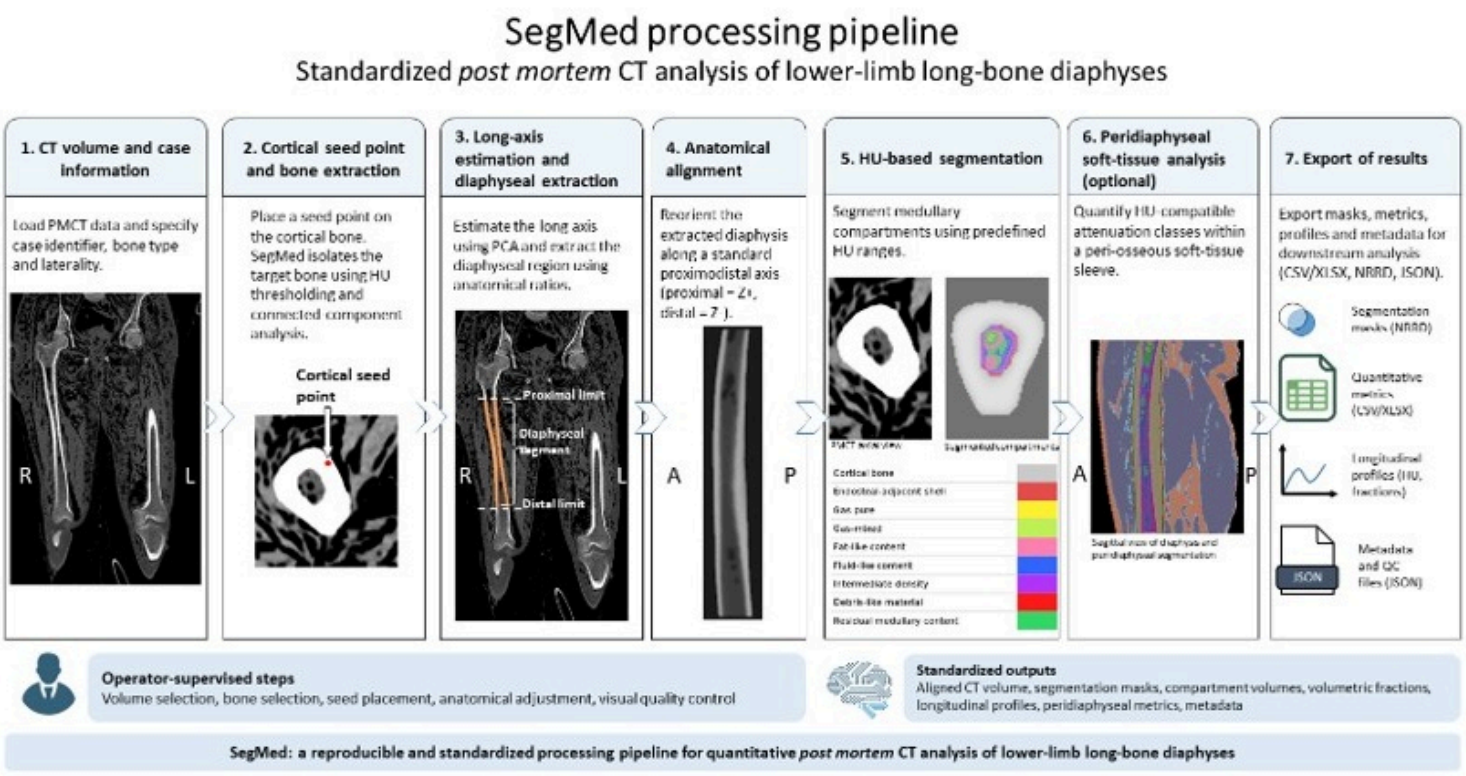


Figure 1

SegMed processing pipeline for standardized *post mortem* CT analysis of lower-limb long-bone diaphyses. The module combines operator-supervised case selection, cortical seed placement, target bone extraction, long-axis estimation, diaphyseal alignment, HU-based medullary segmentation, optional peridiaphyseal soft-tissue analysis, and structured export of segmentation masks, quantitative metrics, longitudinal profiles and metadata. Panel 6 illustrates HU-compatible peridiaphyseal attenuation classes within a peri-osseous soft-tissue sleeve and does not represent discrete anatomical segmentation of individual soft-tissue structures.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SegMed3.2.3UserGuide.docx