

A Modular Computational Pipeline for Quantitative Analysis of Infrared Thermal Images in Digital Health Systems*

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Abstract

Infrared thermal imaging (IRT) is increasingly used in telemedicine and telerehabilitation for non-invasive assessment of physiological processes. However, the absence of unified computational frameworks limits reproducibility and quantitative interpretation of thermal data. This study presents a modular Python-based pipeline for structured analysis of infrared thermal images, integrating segmentation, anatomical normalization, symmetry estimation, and region-based statistical evaluation. The proposed framework supports both isoline-based and equal-interval segmentation strategies, enabling systematic comparison of their influence on spatial and thermal characteristics of extracted regions. The pipeline incorporates run-length encoded mask reconstruction, gradient-based segmentation alternatives, pose-guided anatomical alignment, and symmetry-axis computation using landmark-based principal component analysis. Quantitative evaluation includes region area, temperature statistics, left-right asymmetry metrics, and thermal variability indicators. Experimental results demonstrate that equal-interval segmentation provides more uniform thermal partitioning and higher sensitivity to local temperature variations, while isoline-based methods preserve global thermal structures and exhibit saturation in temperature reduction between regions. The developed framework operates in near real-time and is suitable for integration into distributed digital health systems. The results highlight trade-offs between segmentation granularity and structural stability, providing insights for selecting appropriate thermal analysis strategies in remote medical applications.

Keywords

infrared thermography, thermal mapping, image segmentation, medical image processing, digital health

1. Introduction

Recent advances in telemedicine and telerehabilitation have expanded the use of remote physiological monitoring. Digital health systems increasingly rely on non-invasive imaging integrated into distributed computational environments for real-time analysis. Thermal infrared imaging is particularly promising, as it enables contactless assessment of blood perfusion, inflammation, and metabolic activity.

In telerehabilitation, thermal imaging provides quantitative data for remote monitoring of patient condition and recovery. Modern digital health infrastructures emphasize scalable, data-driven approaches in cloud and edge environments [1,2]. At the same time, telemedicine platforms require automated pipelines that reduce dependence on expert interpretation and ensure standardized processing of imaging data [3,4].

Despite widespread availability of infrared devices, unified frameworks for structured thermal image analysis remain limited. Existing methods often focus on visualization or isolated metrics without a full pipeline integrating segmentation, anatomical alignment, and region-based statistics. This is especially critical in telerehabilitation, where reproducibility and computational efficiency are required for scalable deployment [5,6].

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A further challenge is variability in thermal representations depending on segmentation strategy. Isoline-based methods capture continuous temperature fields but are sensitive to noise and threshold selection. In contrast, equal-interval discretization provides structured partitions but may introduce artificial boundaries unrelated to physiology.

To address these issues, this study proposes a modular Python pipeline for quantitative infrared image analysis, combining segmentation, anatomical normalization, and region-level statistics. It supports both isoline and equal-interval strategies, enabling systematic comparison under varying parameters. The approach follows current trends in computational telerehabilitation, where reproducible processing frameworks are essential for clinical translation [5,7].

The main contribution is a unified framework for structured thermal region analysis, including spatial, statistical, and symmetry features. The study evaluates how segmentation parameters affect region stability and thermal variability, clarifying trade-offs between resolution and structural robustness in infrared imaging for remote healthcare.

2. Related Works

Infrared thermal imaging (IRT) is a non-invasive, radiation-free modality that maps surface temperature reflecting underlying physiological processes [8, 9]. It detects long-wave infrared radiation (8–14 μm) from skin, which has high emissivity (~ 0.98), enabling accurate temperature measurement [10, 11]. Modern systems evolved from cooled single detectors to uncooled focal plane arrays with high resolution and sensitivity below 0.05°C [12, 13].

From the computational perspective, modern infrared thermography increasingly relies on image processing, computer vision, and machine learning methods for automated extraction of diagnostically relevant thermal patterns. Contemporary approaches combine segmentation, contour analysis, feature extraction, symmetry estimation, and deep neural networks to transform raw temperature fields into quantitative descriptors suitable for clinical decision support. In this context, infrared thermography can be considered not only as an imaging modality, but also as a source of spatially distributed physiological data requiring computational modelling and numerical analysis. Therefore, the development of reproducible computational pipelines for thermal image segmentation and quantitative region analysis represents an important task within computer science and digital health systems.

Clinical relevance is based on thermal symmetry: healthy contralateral regions typically differ by $\leq 0.5\text{--}0.7^\circ\text{C}$, while higher deviations may indicate inflammation, perfusion changes, or neoplasms [10,14]. This allows detection of functional abnormalities years before structural imaging [9, 15, 16].

Standardisation is a key issue. Ring and Ammer [12] define strict acquisition conditions (temperature, humidity, acclimatisation, calibration). However, compliance is poor: only 4.2% of studies follow IACT guidelines [17], and most report no protocol at all [14]. This heterogeneity limits reproducibility and clinical translation [15,18]. Although ISO/IEC and CE standards exist [8,10], the gap between guidelines and practice remains a major barrier [17].

Breast cancer is the most studied application [8,11,14]. Thermographic abnormalities may precede diagnosis by 8–10 years and show high sensitivity when combined with other modalities [9]. Large datasets report associations between thermal asymmetry and later cancer diagnosis [13]. However, IRT is not recommended as a standalone screening tool [19], though it may be useful as an adjunct, especially in dense breast tissue [14,17]. For pulmonary infections, Zhang et al. [20] demonstrate strong diagnostic performance (AUC 0.933, sensitivity 90.36%, specificity 92.28%) with defined thermal thresholds and strong correlation with radiographic severity. Deep learning significantly improves performance. Pandey et al. [15] report very high accuracy for multiple pathologies using CapsNet, while She et al. [21] achieve strong dermatological classification using DenseNet and balanced loss strategies. These studies also address dataset limitations through new thermal datasets. AI integration is the dominant trend [18,19,21,22]. Deep learning architectures (CNNs, Transformers) now replace handcrafted features, with applications mainly in oncology, diabetic screening, and fever detection. Reported performance

ranges roughly 78–94% sensitivity and 75–90% specificity [18], though comparisons are limited by dataset heterogeneity [12].

Overall, IRT combined with AI shows strong potential due to non-invasiveness, cost efficiency, and early functional sensitivity [8,9,14,17,18,20]. However, progress is constrained by poor standardisation, limited datasets, and lack of large validation studies [12,14,17,18]. The mismatch between guidelines and real practice remains a critical unresolved issue [17].

3. Materials and Methods

3.1. Overview of the computational pipeline

A modular Python pipeline was developed for quantitative analysis of infrared thermal images for medical diagnostics. It processes three inputs: a 2D temperature matrix from a calibrated infrared camera, a binary segmentation mask (RLE-encoded or gradient-derived), and anatomical keypoints obtained from a visible-light image using a pre-trained pose estimation model (e.g., MediaPipe Pose). Implementation is based on Python 3.10 with NumPy, SciPy, scikit-image, OpenCV, and Matplotlib.

The workflow (Figure 1) includes data loading and validation, mask generation/refinement, spatial normalization (rotation, scaling, cropping), symmetry axis estimation, thermal region extraction (isolines and connected components), region-wise quantification (area, mean/min/max temperature, left–right partitioning), mapping of anatomical keypoints to thermal zones, and result visualization.

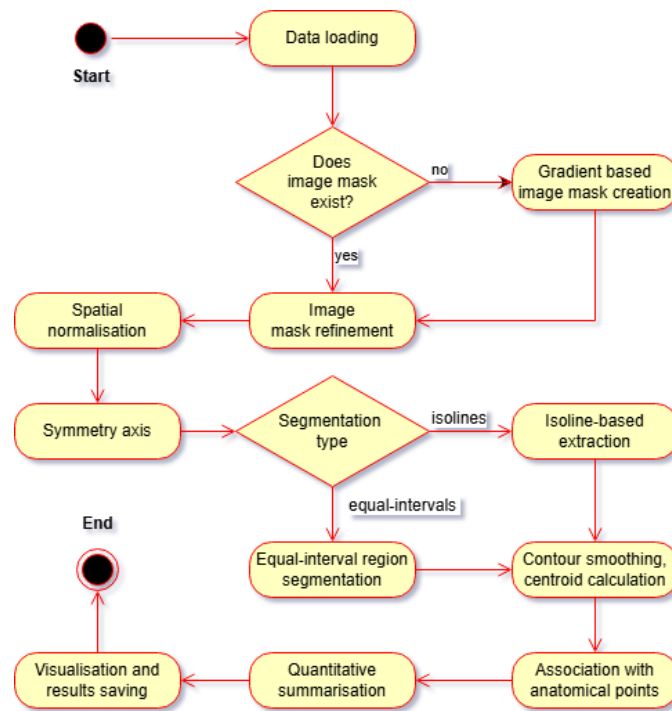


Figure 1: The overall workflow of infra-red image data analysis.

3.2. Data acquisition and input formats

Thermal imaging data were acquired using an uncooled infrared camera with a resolution of 256×192 pixels and $12 \mu\text{m}$ pixel pitch. The detector sensitivity (NETD) is $<50 \text{ mK}$ at 25°C , enabling detection of small temperature variations. The system operates at 25 Hz and covers a wide temperature range (-15°C to $+600^\circ\text{C}$), while medical use is restricted to $10\text{--}45^\circ\text{C}$ (clinically relevant: $28\text{--}42^\circ\text{C}$). Accuracy is $\pm 2^\circ\text{C}$ or $\pm 2\%$, whichever is greater. Measurement modes include point, line, and area analysis, with automatic extrema detection and threshold alarms. The optical system uses a 3.2 mm F1.1 lens with a $56^\circ \times 42^\circ$ field of view and fixed focus.

Thermal images were assigned a predefined colour palette and subsequently processed to generate segmentation masks and joint coordinates using MediaPipe.

For each study, data were stored in a unified JSON structure containing: (i) a temperature matrix (“temp_matrix”) with image dimensions and flattened pixel values (°C), (ii) a run-length encoded segmentation mask (“segmentation_mask”) stored as a compressed base64 string with dimensions, and (iii) pose landmarks (“pose_landmarks”) including key points (e.g., nose, shoulders, hips) with coordinates and confidence scores.

Optional parameters such as “temp_min” and “target_height” were used to suppress cold artefacts and standardise spatial resolution across subjects.

3.3. Mask preparation: RLE decoding and gradient-based alternative

The binary segmentation mask was reconstructed from the RLE payload by decoding the base64 string, decompressing it with zlib, and parsing the resulting byte stream as 5-byte packets. Each packet contained a binary pixel value (0/1) and a 4-byte little-endian run length. The resulting flat array was reshaped to the original image dimensions.

If no precomputed mask was available, a gradient-based method was used. The temperature matrix was first smoothed with a Gaussian filter ($\sigma = 1.0$), then the gradient magnitude was computed using the Sobel operator:

$$G(x, y) = \sqrt{S_x(x, y)^2 + S_y(x, y)^2} \quad (1)$$

where S_x and S_y are horizontal and vertical Sobel gradients of the smoothed temperature field.

Pixels exceeding 30% of the maximum gradient were retained, small connected components (<100 pixels) were removed, and the largest region was selected as the final mask:

$$M(x, y) = \begin{cases} 1, & G(x, y) > \alpha \times \max(G) \\ 0, & \text{otherwise} \end{cases} \quad (2)$$

where $\alpha=0.3$ in the present implementation.

This method is suitable when body boundaries are not explicitly segmented but the skin-air temperature gradient is pronounced [8,20].

3.4. Thermal zone extraction: isolines and connected regions axis computation

To determine the spatial distribution of skin temperature, it was implemented two complementary approaches: isoline-based extraction (following traditional thermography practice [16,19]) and equal-interval region segmentation (more suitable for quantitative comparison across subjects).

3.4.1. Isoline-based extractions

Given the temperature matrix and the binary mask, the appropriate function generates “n levels” equally spaced temperature levels between the minimum and maximum temperature inside the mask:

$$T_i = T_{\min} + \frac{i}{n-1} (T_{\max} - T_{\min}), \quad i = 0, \dots, n-1 \quad (3)$$

where $T_{\min}$ and $T_{\max}$ are the minimum and maximum temperatures inside the segmentation mask.

For each level, contours are extracted using `skimage.measure.find_contours`. Contour points that fall outside the mask are discarded. For the lowest level (minimum temperature), all connected pixels to be considered at or below that level as a set of regions rather than a thin contour, to capture the coldest areas completely.

The function `extract_regions` then convert these isolines into connected regions. For each temperature level, each closed contour defines a region. The following attributes are computed for every region (4):

- area_pixels: number of pixels inside the contour (intersected with the mask).

- mean_intensity, min_intensity, max_intensity: temperature statistics.
- left_pixels, right_pixels: number of pixels lying to the left and right of the symmetry line.
- contour: the smoothed contour points.

$$\bar{T}_r = \frac{1}{|R_r|} \sum_{(x,y) \in R_r} T(x,y) \quad (4)$$

where R_r denotes the set of pixels belonging to region r .

Finally, thermal zones summary data structure incorporates the levels by increasing mean temperature (so that level 0 is the coldest) and aggregates the data per level.

3.4.2. Equal-interval region segmentation

For applications where a fixed number of temperature intervals is desired (e.g., to compare thermal patterns across patients), it was developed an alternative method. This approach first computes “ n intervals” equal-width temperature bins between the global minimum and maximum inside the mask. Each pixel is then assigned a bin index (quantisation):

$$Q(x,y) = \left\lceil \frac{T(x,y) - T_{\min}}{\Delta T} \right\rceil \quad (5)$$

where

$$\Delta T = \frac{T_{\max} - T_{\min}}{n} \quad (6)$$

Connected components within each bin are extracted as separate regions. The same left/right partition and temperature statistics are computed. The resulting regions are independent of the presence of closed isolines and are more robust to noise in the temperature field [18,19].

3.5. Contour smoothing and centroid calculation

Raw contours extracted often contain jagged steps due to pixel discretisation. For visualisation and more stable centroid computation, we implemented smoothing contours using a B-spline (via `scipy.interpolate.splprep` and `splev`). The smoothing factor is user-adjustable (default value is 3). If the contour has fewer than five points or spline fitting fails, the original contour is returned.

The centroid of each region is determined by constructing a binary mask of the region (using `polygon` from `skimage.draw`), then applying a Euclidean distance transform and selecting the pixel with the maximum distance to the boundary:

$$C_r = \arg \max_{(x,y) \in R_r} D(x,y) \quad (7)$$

where $D(x,y)$ is the Euclidean distance transform inside region R_r .

This ensures the label is placed inside the region and away from edges, improving readability of the visualisation.

To link the thermal analysis to clinically relevant landmarks, each region’s “Inner points” and “Nearest points” are computed:

$$d(p, R) = \min_{q \in R_r} \|p - q\|_2 \quad (8)$$

Points that fall inside the region’s polygon are marked as ‘Inner points’. For each point outside the region, the minimum Euclidean distance to any pixel of the region is calculated, and the five closest points are stored as “Nearest points”. This information allows a physician to answer questions such as “Which thermal zone covers the left breast?” or “Is the liver area warmer than the surrounding tissue?”.

4. Results and discussion

Examples of the segmented and marked infra-red images obtained through the system developed are presented in Figure 2.

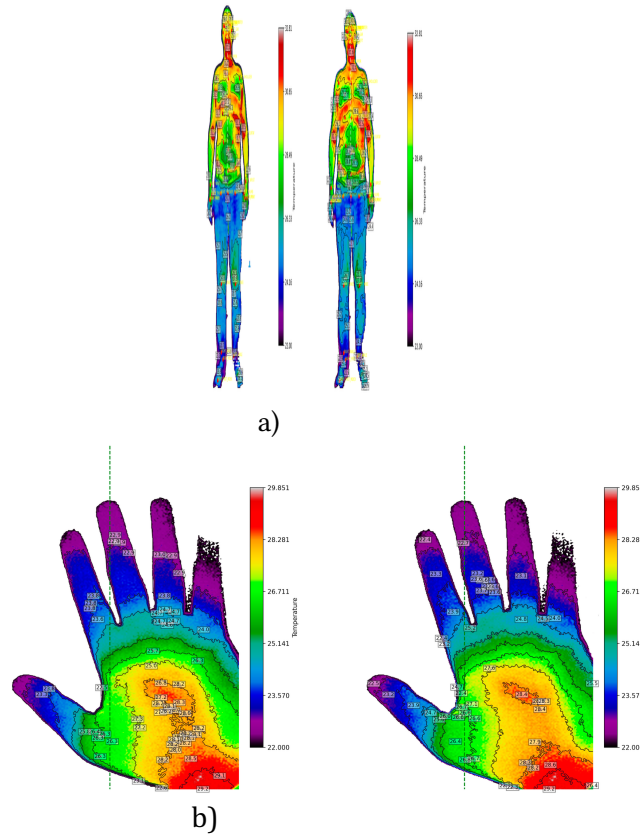


Figure 2: Examples of the infra-red images marked using isoline-based extraction (right images) and equal-interval region segmentation (left images), low temperature cut-off is 22 °C: a) whole body front image, partially undressed person: 7 temperature levels, with temperature labels, anatomic points and mask from MediaPipe; b) hand only image: 10 temperature levels, with temperature labels, no anatomic points, using gradient mask.

Equal-interval and isoline-based segmentation show distinct responses to spatial temperature distributions. Equal-interval segmentation better resolves small, localized thermal zones, producing finer partitioning under subtle but local variations. It remains stable even in sharply localized heating/cooling. In contrast, isoline-based extraction is more sensitive to global temperature structure and tends to form large, merged regions in smooth gradient areas, especially in cooler zones. Increasing the number of temperature levels refines equal-interval segmentation, while in isoline-based methods it may lead to contour fragmentation or region splitting.

Separate analyses were performed for full-body and hand images (Figure 3). The number of regions increases approximately linearly with temperature levels for both methods. For full-body images, equal-interval segmentation yields slightly more regions. For hand images, the trend is less regular, with small fluctuations; at low levels equal-interval dominates, while at higher levels (>7–8) isoline-based segmentation can match or slightly exceed it. Overall differences remain modest.

Mean region area decreases with increasing levels in both methods. At low discretization (3–8 levels), isoline-based regions are larger, but both methods converge at higher levels, where differences become negligible for both full-body and hand images. Standard deviation of region area shows stronger dependence on image scale. For full-body images, equal-interval segmentation produces higher variability, decreasing with more levels, while isoline-based results are more stable; both converge at high levels. For hand images, differences are minimal, and at higher levels both methods become nearly identical.

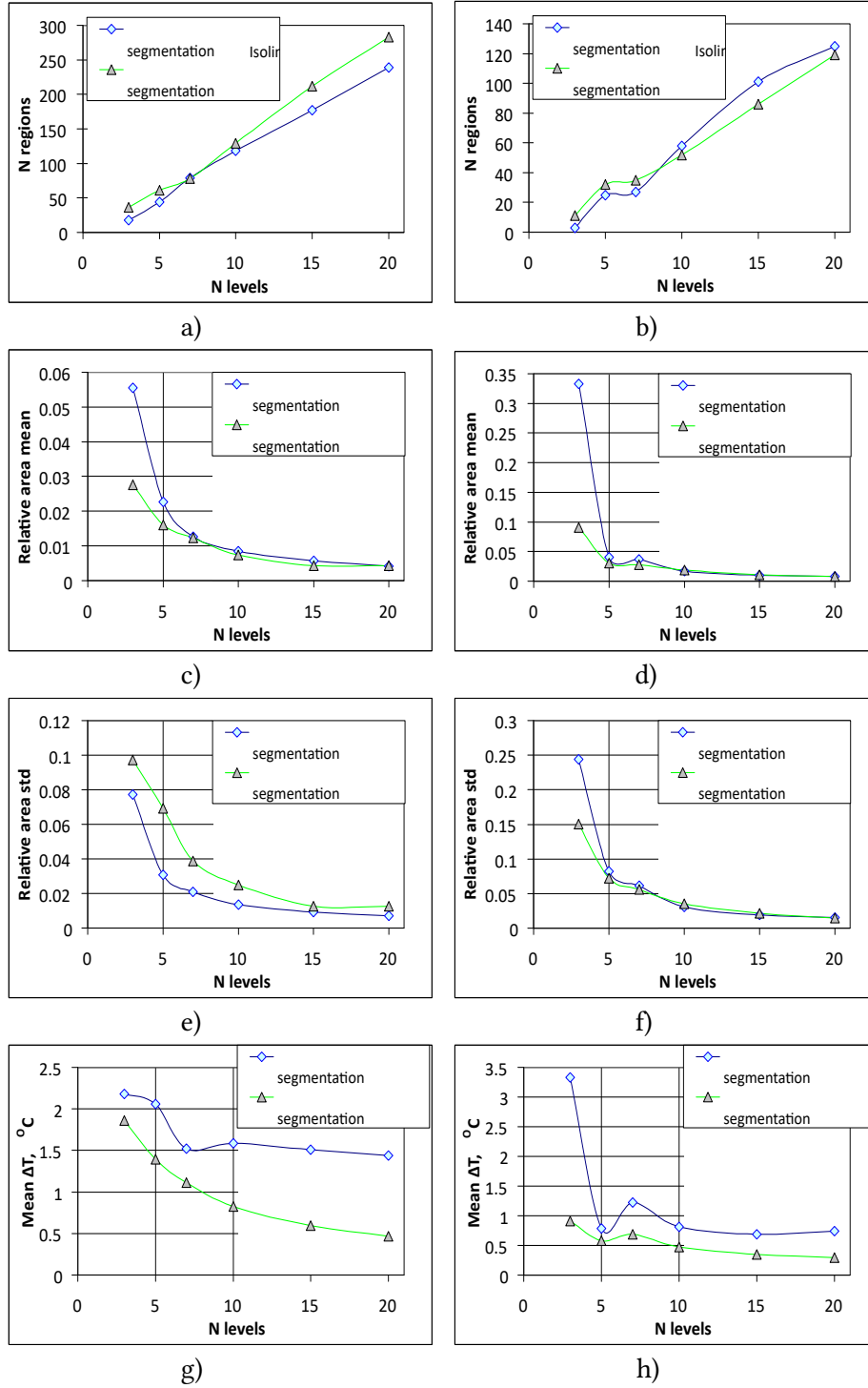


Figure 3: Dependences of regions detected (a, b), mean region area in relation to the image mask whole area (c, d), standard deviation of the relative mean region area (e, f), and mean ΔT per region on the number of predefined temperature levels: a, c, e, g – full-body images; b, d, f, h – localized regions (hands)

The most pronounced effect is observed in mean intra-region temperature difference (ΔT). For full-body images, isoline-based segmentation shows non-monotonic behaviour with initial decrease (3–7 levels) followed by saturation, while equal-interval segmentation decreases more smoothly and consistently yields lower ΔT . For hand images, isoline-based ΔT shows sharp changes at low levels (3–5), a local peak around 7, and stabilization, whereas equal-interval segmentation decreases gradually without abrupt transitions.

Overall, segmentation strategy mainly affects region granularity and thermal homogeneity rather than spatial coverage. With increasing levels, both methods converge in region count and size, but

differences persist in thermal variability, with equal-interval producing more uniform partitioning and isoline-based preserving larger thermal gradients at low levels. At low discretization, isoline-based segmentation preserves larger, more thermally heterogeneous regions, while equal-interval enforces uniform partitioning with smaller, more homogeneous zones. Variability analysis confirms this: equal-interval is more sensitive to local fluctuations in full-body images, while isoline-based better preserves global structure. For localized regions (hands), these differences largely disappear.

ΔT analysis shows the strongest methodological divergence: equal-interval provides a predictable reduction with increasing levels, while isoline-based exhibits saturation, indicating dependence on intrinsic smoothness of the temperature field. Practically, equal-interval is better for fine quantitative partitioning and local variation analysis, while isoline-based is preferable for preserving global thermal structure and avoiding over-segmentation.

Limitations include dependence of symmetry estimation on MediaPipe pose accuracy, where errors propagate to left-right partitioning; potential failure of gradient-based masks under physiological or environmental thermal noise [18]; and absence of anatomical registration, limiting cross-subject comparability. Integration of non-rigid registration using landmarks is planned. The current clinical validation is preliminary and requires larger multi-centre studies following IACT guidelines [12,17].

5. Conclusions

This study proposed a unified Python-based framework for quantitative infrared thermal image analysis, integrating segmentation, anatomical normalization, symmetry estimation, and region-level statistics within a reproducible pipeline for telemedicine and telerehabilitation.

Comparative analysis showed that isoline-based and equal-interval segmentation converge at high discretization levels in terms of region number and size, but differ substantially at low levels. Isoline-based methods preserve larger, more heterogeneous thermal regions, while equal-interval segmentation produces smaller, more uniform partitions.

The strongest methodological difference was observed in intra-region temperature variability (ΔT). Equal-interval segmentation yields a consistent reduction in ΔT with increasing resolution, whereas isoline-based segmentation shows saturation, indicating limited sensitivity to further refinement. Thus, equal-interval is better suited for fine-grained quantitative analysis, while isoline-based methods better preserve global thermal structure.

The framework enables robust estimation of left-right thermal asymmetry using a landmark-based symmetry axis, producing clinically relevant descriptors and operating with computational efficiency (<2 s per subject), supporting near real-time use.

Overall, the proposed approach provides a flexible bridge between raw infrared data and clinically interpretable quantitative metrics, supporting the development of standardized computational thermography in remote healthcare systems.

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Declaration on Generative AI

The author(s) have not employed any Generative AI tools.

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