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Aim

Automatic segmentation of skin lesions (e.g. naevi, melanoma) from surrounding healthy skin tissue is essential for designing effective and efficient computer-based methods for diagnosis and prognosis of melanocytic diseases.

Challenges

Fully automatic tumor segmentation is hard due to variability of several factors:
- tumor morphology (shape, size, structure, occluding hair)
- intrinsic image attributes (skin pigmentation, color, contrast)
- acquisition parameters (imaging devices, image resolution, lens deformation)
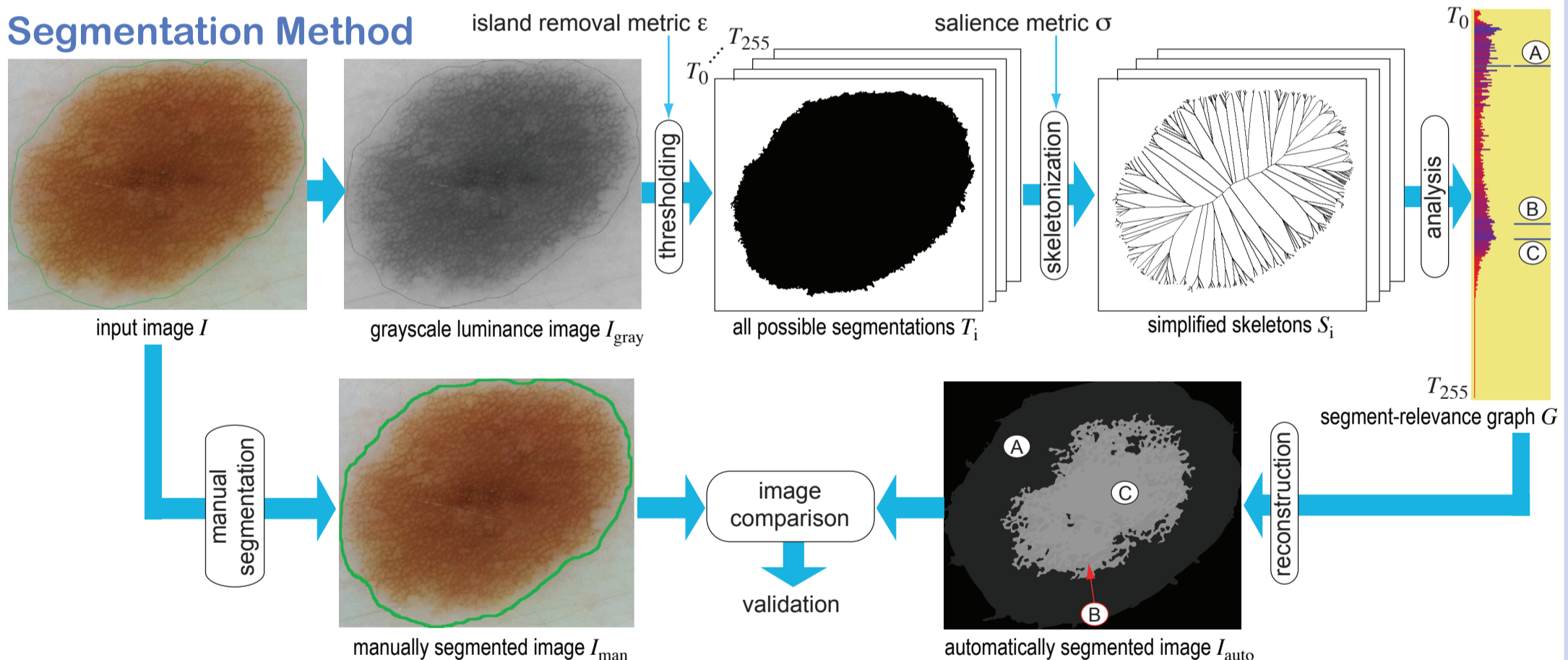
Contribution

We present a fully automatic method for skin lesion segmentation from healthy tissue. The method is based on a novel image representation: multiscale skeletons. We compared our automatic segmentation results with manual segmentations performed by dermatologists. The comparison showed a high similarity in terms of obtained segmentation results for all tested input images.

Materials and Methods

We acquired over 50 images of a wide variety of naevi types using a Handyscope device at 2448 x 3264 pixels. After conversion to grayscale luminance images, we compute all **possible** segmentations T_i ($1<i<255$) of each image by luminance thresholding. Small islands (few pixels size) are next eliminated. Each possible segmentation T_i is next reduced to its so-called **skeleton** S_i [1]. Simplifying skeletons further removes small-scale noise from the segment boundary [2]. Next, we compute how much of the surface of the input image I is encoded in each segment T_i, and encode this data into a segment-relevance graph G. The key to our method is that **maxima** of G correspond to **relevant segmentations** I_{auto} of I. From each such maximum, we reconstruct one segment of I using the skeleton-to-image reconstruction algorithm presented in [1].

To validate our automatic segmentation pipeline, we compare our automatic segmentations I_{auto} with tumor segmentations I_{man} manually performed by dermatologists directly on the input images I. A qualitative comparison of the two shows a high similarity, resistance to image-acquisition noise, insensitivity to the type of tumor structures, occlusion artifacts (hairs), image tints, and image acquisition parameters. The automatically computed segments exhibit the same smooth borders and tumor inclusion features shown by the manual segmentations - compare *e.g.* the segment A (automatically found) with the manually obtained segmentation I_{man} shown in the example below.

Segmentation Method

island removal metric ε — salience metric σ

input image I · grayscale luminance image I_{gray} · all possible segmentations T_i · simplified skeletons S_i · segment-relevance graph G

manually segmented image I_{man} · image comparison · validation · automatically segmented image I_{auto}

Discussion

Ease of use: Our proposed method is entirely automatic, requiring **no user input**.
Robustness: Testing all possible segmentations T_i of the input image eliminates all possible image acquisition biases (contrast, illumination, tint variation) and captures a wide tumor-structure variability.
Smoothness: Inherent small-scale noise (e.g. small fractal-like boundary details [3] is **automatically** eliminated by skeleton simplification but keeps key tumor features e.g. size, outline, and shape [1,2,3].
Efficiency: Our entire pipeline is implemented using parallel graphics hardware, which delivers a performance of roughly **20 image-segmentations / second** on a modern PC (for details, see [4])

Ongoing Work

Quantification: Skeleton descriptors are arguablly effective instruments to quantify all aggregated tumor features (e.g. ABCDE criteria). In particular they directly measure the 'fractal dimension' [3,5,6].
Analysis: The proposed multiscale segmentation and skeletal representation could be used to detect and measure more specific, finer-scale, tumor properties, e.g. the presence of specific structures (*e.g.* globular, cobblestone, (a)typical network and blue/gray pepper-like patterns)
Comparison: Hausdorff distance metrics can be directly used to measure the **segmentation quality** [7]

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More details and software: http://www.cs.rug.nl/svcg/Shapes/SkinImaging