SarcomAI L3 v1.00
User Manual

ver 10.2023

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1. Introduction

Welcome to SarcomAI L3 (short for SarcoMeas AI), optimized software for automatic body composition measurements in CT slices at L3 level. This manual will show you step-by-step how to efficiently perform sarcopenia/body composition measurements with SarcomAI L3.

2. General prerequisites

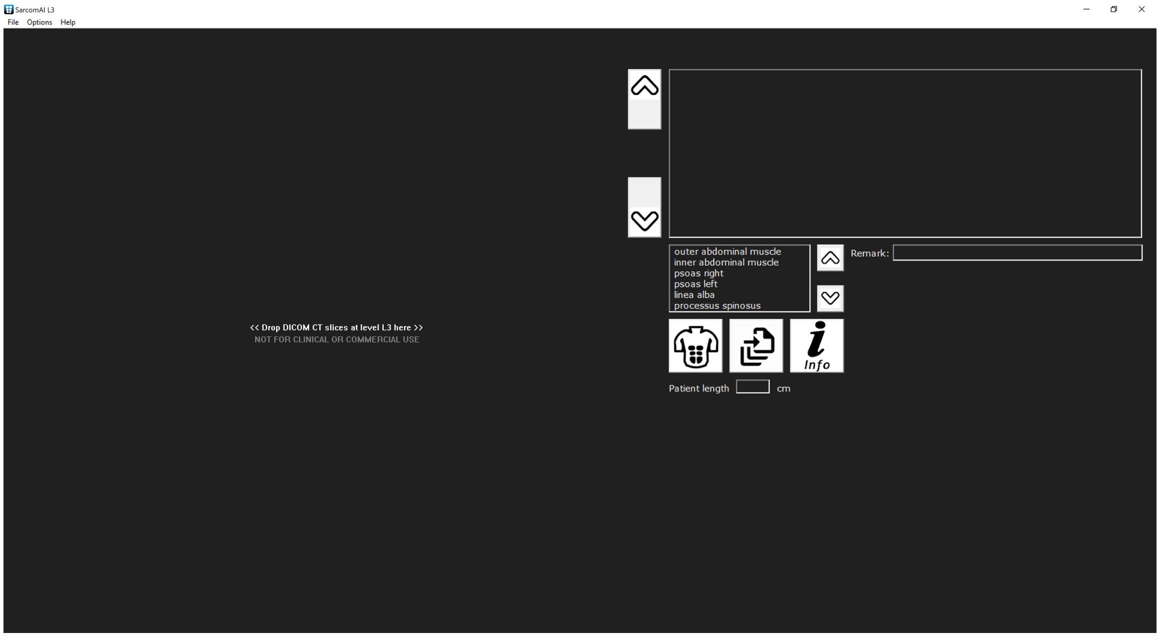
The software expects anonymized axial uncompressed DICOM CT greyscale images at the level of vertebra L3, through the transverse processes, with dimensions of 512x512 pixels, bitdepth 16-bit, and a slice thickness ranging from 1 mm to 5 mm.
The software will run on most modern PCs with 64-bit Windows 7, 8, 10 or 11 installed. A full HD (1920 x 1080 pixels) or larger monitor and a mouse are needed.

3. Starting the software

SarcomAI L3 is portable, standalone analysis software, which means it can run on most PCs without administrator rights and without installation. Simply copy the executable to your Desktop or other folder and double-click the icon to start the program. Make sure the program has write access to the chosen folder, for storing the analysis results.

When the software is run for the first time, a registration dialog is shown, asking for the registration name and license key. Please fill in the required fields, by copying the requested information from the registration email you received, then press the 'Register' button. The program will exit.

The next time SarcomAI L3 is started, it will start in analysis mode (if the provided license information is valid).

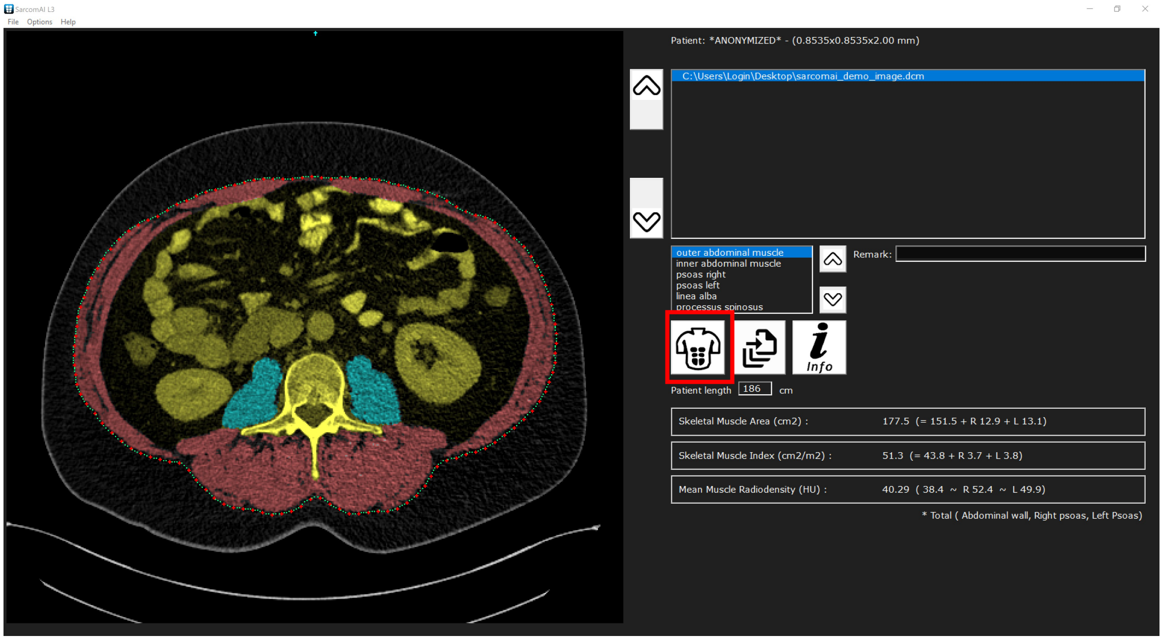


<< Drop DICOM CT slices at level L3 here >>
NOT FOR CLINICAL OR COMMERCIAL USE

4. Loading CT slices

Select the anonymized DICOM L3 CT images in Windows Explorer and drop them on the SarcomAI window, or use the menu option File > Load Dicom Images to select one or more Dicom files. The filenames will now be listed in the upper right box.

The first file will be loaded automatically, and the abdominal muscle wall and psoas muscles automatically are outlined by our builtin state-of-the-art AI algorithm.



Patient: *ANONYMIZED* - (0.8535x0.8535x2.00 mm)

C:\Users\Login\Desktop\sarcomai_demo_image.dcm

Patient length 186 cm

Skeletal Muscle Area (cm2) : 177.5 (= 151.5 + R 12.9 + L 13.1)

Skeletal Muscle Index (cm2/m2) : 51.3 (= 43.8 + R 3.7 + L 3.8)

Mean Muscle Radiodensity (HU) : 40.29 (38.4 ~ R 52.4 ~ L 49.9)

* Total (Abdominal wall, Right psoas, Left Psoas)

5. Contour editing

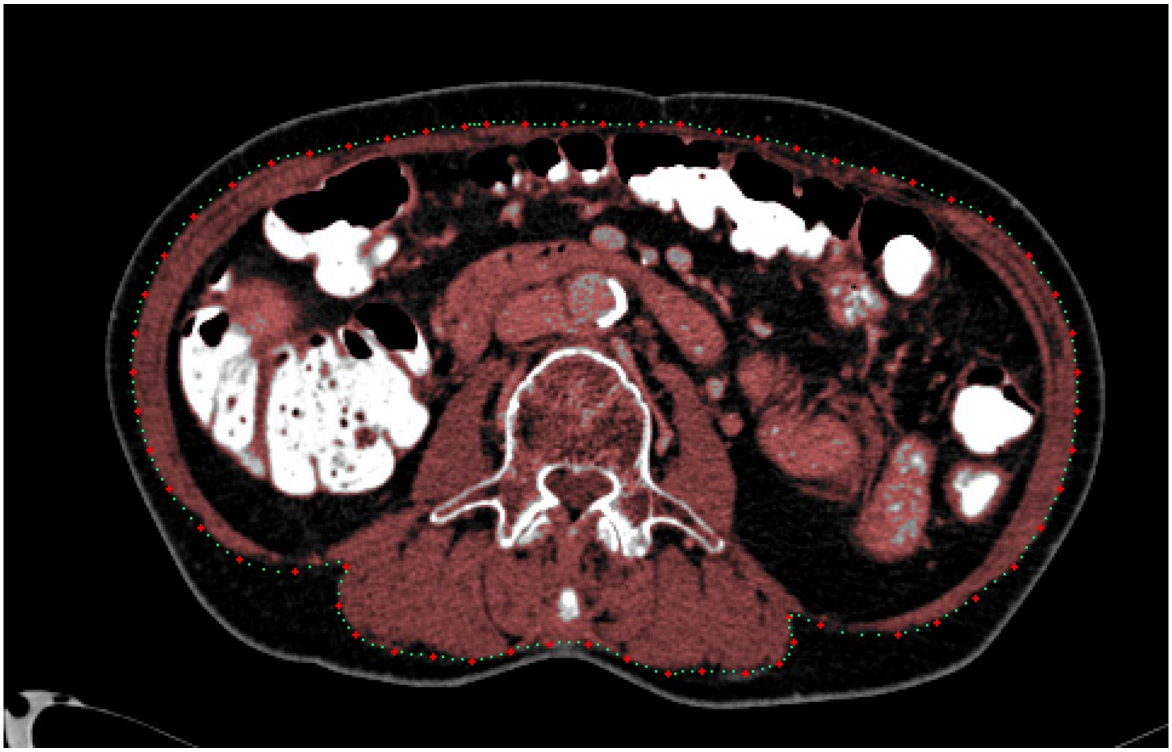
You can adjust contours if needed, by dragging the red contour control points (click and move them by pressing the left mouse button). To revert all contours to the original AI predictions, you can press the auto-detect button.

Contours can be refined by clicking with the right mouse button one of the green intermediate contour points, which will then be converted into a red control point.

Contours have to be positioned just outside the muscle, to make sure all muscle is included, with as little as possible surrounding fat.

To locally simplify a contour, select a red contour control point and drag it over one of its adjacent red control points to fuse them.

The contours will be automatically stored on harddisk during drawing or adjusting.
Contours can be deleted by pressing the Del key.



6. Contour selection

To select another contour, the mouse scroll wheel can be used when hovering over the CT slice. Alternatively, the contour can be selected in the contour list on the right.
A drawn contour can also be selected by clicking the outlined muscle or abdominal cavity in the CT slice.

When the contour is active, it can be edited as described above.

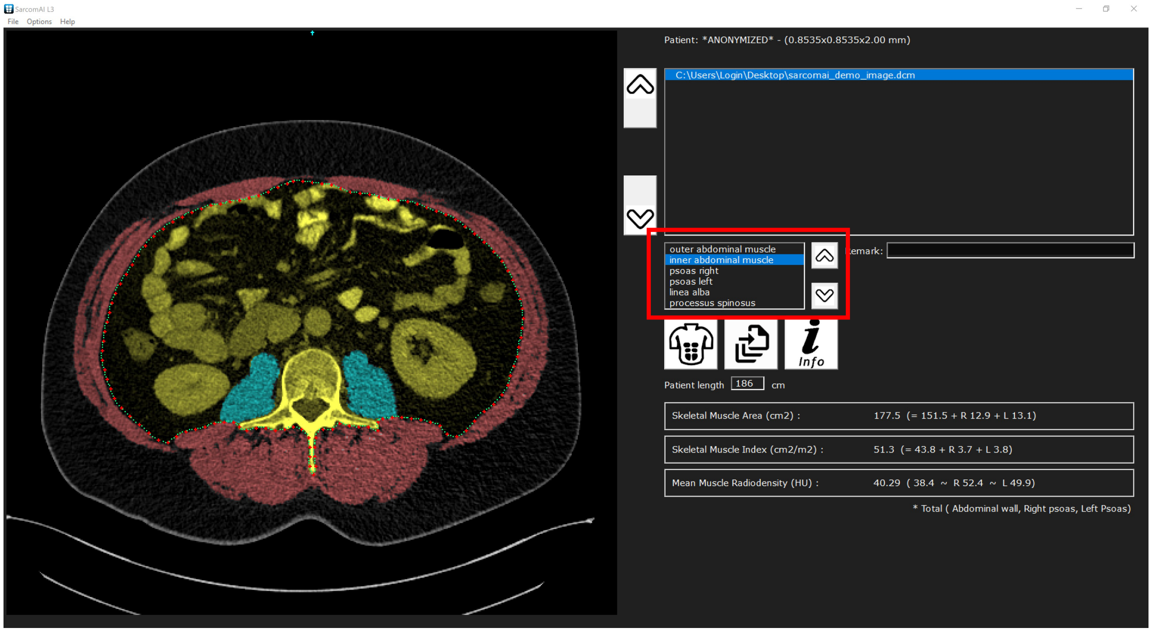
To completely redraw a contour manually, select it in the contour list, delete it with the Del key and draw it in one motion by keeping the left mouse button pressed.

For drawing the inner abdominal wall contour, the transverse and spinous processes have to be included, drawing the contour dorsally from the psoas muscles as depicted below.
After drawing, the contour will be automatically optimized. You can further finetune the contour points by dragging them.

To temporarily hide the contours, to show the original greyscale image, press the Space-bar.

Draw the contours carefully just outside the muscle, and make sure no ligaments or blood vessels are included within the contours.

The last (optional) drawing step is to mark the anterior midline (linea alba) and the posterior midline (processus spinosus). These can be used for comparing the left and right patient sides, but these are not necessary for conventional analysis.



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7. Analysis

After drawing all contours (and optionally placing the midline markers), the image will automatically be analyzed. The measurements will be automatically stored in a file (analysis.txt), in the same folder as the main program. When contours are changed, the data in analysis.txt will be updated automatically for this patient.

The results are stored in analysis.txt in tab-separated format. It can easily be imported into other software, like Microsoft Excel, for further analysis. The data is stored in US format, with decimal points, not commas. Please make sure your other software expects this US formatting convention.

8. Patient length

For computing the Skeletal Muscle Index, the computed muscle area has to be indexed using the patient length. SarcomAI will try to import the patient length from the Dicom image header, but this information is not always available.

If the patient length is missing, the program will show a length of 280 cm, and a warning that the SMI can't be calculated will be displayed.

In this case, the length can be entered manually in the patient length text box. The measurements will be updated accordingly on-screen and in analysis.txt.

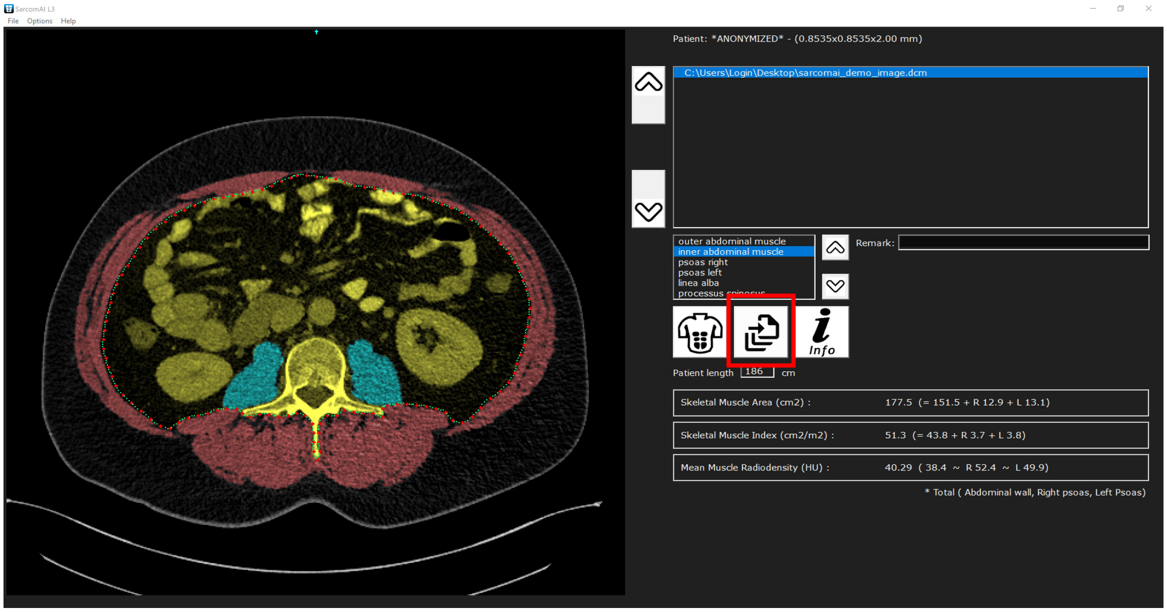
For batch processing, there is an option to import multiple patient lengths at once. For this case, a text file can be imported using the program menu option File > Import Patient Lenghts. This text file should contain two tab-delimited columns. The first column holds the patient ID, the second column holds the patient length in centimeters.
Such a file can easily be created, for instance by selecting two columns in Excel, copy them with Ctrl+C, and pasting them in Windows Notepad.

9. Miscellaneous functions

SarcomAI has some extra functions, which can be useful when analyzing CT slices.

Adding remarks
The first function is the option to add text comments to a slice. For instance, when a slice contains too much noise, movement or other artifacts or when the abdominal wall isn't completely scanned. In the Remark text box this info can be typed, and it will automatically be added to analysis.txt, making it easier to identify deviating cases in the results.

Batch processing
When more than one images are imported, batch processing can be used to quickly delineate them. Of course, always check them carefully to assure high accuracy of your measurements.



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Hide patient information
To ensure double-blinded analysis, patient names can be hidden using the menu option Options > Hide Patient Information.

Display colours
Default, the segmentation is shown in blended mode.
To hide the colours of the segmented muscles in the CT slice, press the Space bar.
To view the complete segmentation colours, press the C key.

10. Best scanning and delineating practices

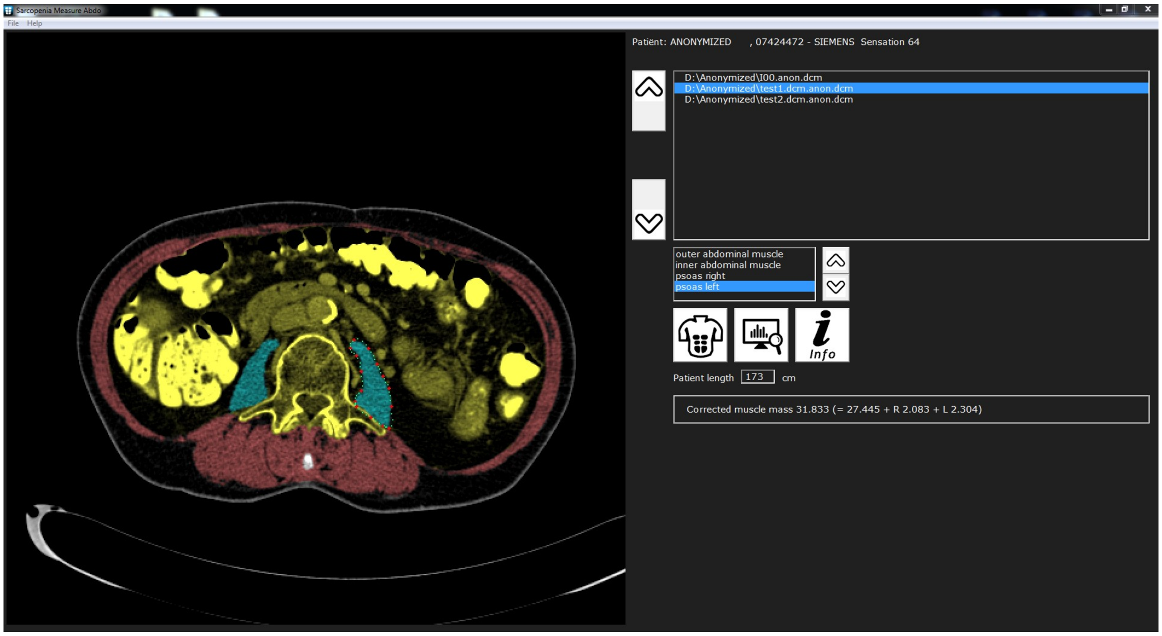
To ensure the best analysis results, it is recommended to use standard CT-scans. Low dose scans contain more noise, which will result in pixels with values that fall outside the defined ranges (-29 to +150 Hounsfield Units). These pixels will therefore not be counted as muscle and will usually lead to underestimation of muscle mass.

The software works on unenhanced and contrast enhanced CT scans. Administration of intravenous contrast will increase density by approximately 10 Hounsfield units. Therefore unenhanced and contrast enhanced CT scans cannot readily be compared.

CT slice thickness between 1 and 5 mm is recommended. Thinner slices may result in more noise, which will affect measurements. Thicker slices will increase the influence of partial volume effects, which also will decrease accuracy of the measurements.

CT scans of the abdomen have to be performed with the patient arms up, to prevent beam hardening artifacts. These artifacts cannot be corrected for and will lead to measurement errors, in both area and density. Scanning the patient in supine position is preferred for our AI algorithm. However, the software automatically detects other patient positioning.

Contours have to be drawn closely around the muscles, including all muscle tissue, but including as less surrounding fat as possible.



Patiënt: ANONYMIZED , 07424472 - SIEMENS Sensation 64

D:\Anonymized\I00.anon.dcm
D:\Anonymized\test1.dcm.anon.dcm
D:\Anonymized\test2.dcm.anon.dcm

Patient length 173 cm

Corrected muscle mass 31.833 (= 27.445 + R 2.083 + L 2.304)