

Automated BCA

Introduction

This is a brief introduction into how to use the Automated **B**ody **C**omposition **A**alysis (Automated BCA) user interface for analyzing 3rd lumbar vertebrae CT scans. This interface does not require installation or knowledge about programming; however, it will only run on the CPU (i.e. analysis will be the same, just much slower – ~30 seconds/scan vs <0.5 second/scan on GPU). The interface will only run on windows machines.

Steps for analysis

1) Preparing CT scan folders

CT scans for analysis should be loaded into a single directory/folder, which may or may not contain sub directories/folders containing the actual scans.

For example:

PC > Desktop > BCA > Automated_Body_Composition_Analysis > Example CT scans >				
Name	Date modified	Type	Size	
dicom_dir	28-01-2022 20:08	File folder		
anon_L3_1.dcm	28-01-2022 19:22	DCM File	515 KB	
anon_L3_2.dcm	28-01-2022 19:22	DCM File	515 KB	
anon_L3_3.dcm	28-01-2022 19:22	DCM File	516 KB	

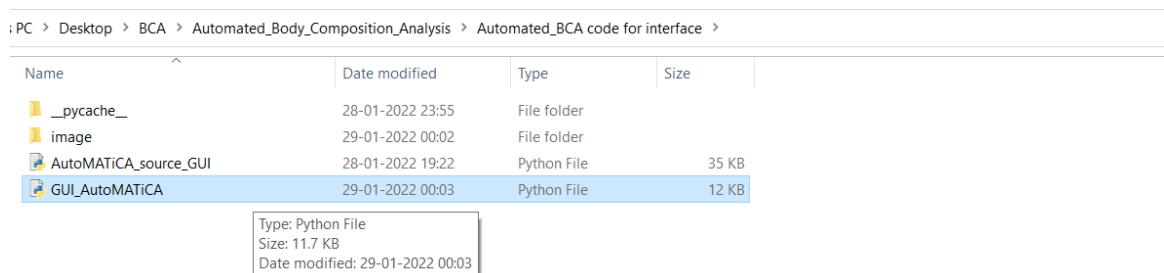
Here is a folder containing 5 CT scans (3rd lumbar vertebrae) from 5 different patients for analysis. In this example, all CT scans are in a single folder. This is an acceptable format.

CT scans should be in the DICOM format (i.e. JPEG and TIFF CT scans are not supported). Some CT scanning software will export the scans without a “.dcm” (DICOM) extension, these are acceptable for input (the software will convert them). **It is best to exclude non-DICOM files from these folders. This is particularly important for files without a file extension, as they will be renamed to contain a “.dcm” tag and cause an error.**

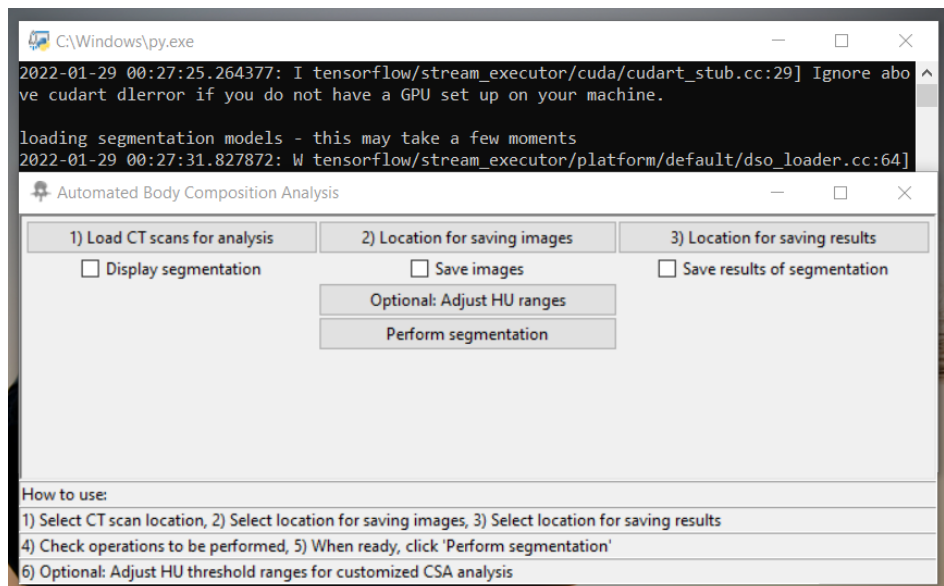
Note: It is important to ensure all subfolders within the selected analysis folder only contain scans you wish to analyze. For example, do not place the landmarked L3 scan in a folder which has subfolders containing the full CT scans - this will lead to the program analyzing every CT scan in the set.

2) Opening user interface

When opening the user interface executable, ensure nothing has been modified from the original download folder. Double click the application file (see below) in the user interface folder.



A terminal command line will open - loading of the user interface will take several moments. The terminal command line will keep you updated on the current status of the analysis (see below).

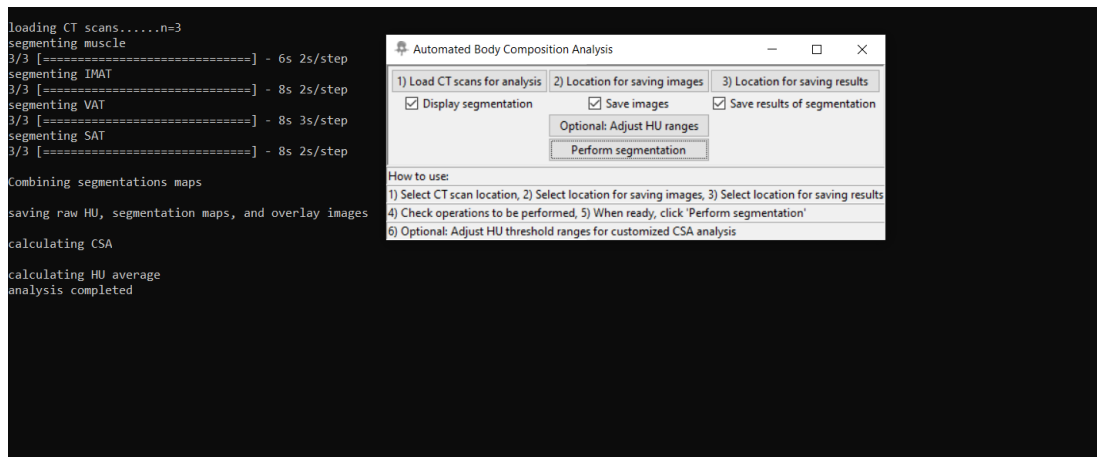


3) Using Automated BCA

The user interface is basic, but easy to use. Brief instructions are placed at the bottom of the interface

Detailed instructions

- I. “Load CT scans for analysis” – this is used to select the folder that contains the CT scans. If the scans are contained within multiple patient folders, select the base folder containing sub folders. When selecting the folder for analysis, the individual CT scans will not appear, simply select the folder for analysis.
- II. “Location for saving images” – this is used to select where the raw CT scans, segmentation maps, and the combined (raw CT + segmentation map) images will be saved
 - a. Images will be labelled using the CT scan’s patient id from the DICOM metadata. If patient id is missing due to an anonymization process or have overlapping id’s from different scans, a number indicating the order in which the scan was analyzed will be used for saving.
- III. “Location for saving results” – this is used to select where the excel file will be created for exporting CT parameters and body composition analysis results.
- IV. Checkboxes are available for displaying segmentation results, saving analyzed scans, and saving body composition analysis results
- V. Once satisfied with the analysis parameters, press “Perform segmentation”
 - a. the command line terminal will output current analysis stage.



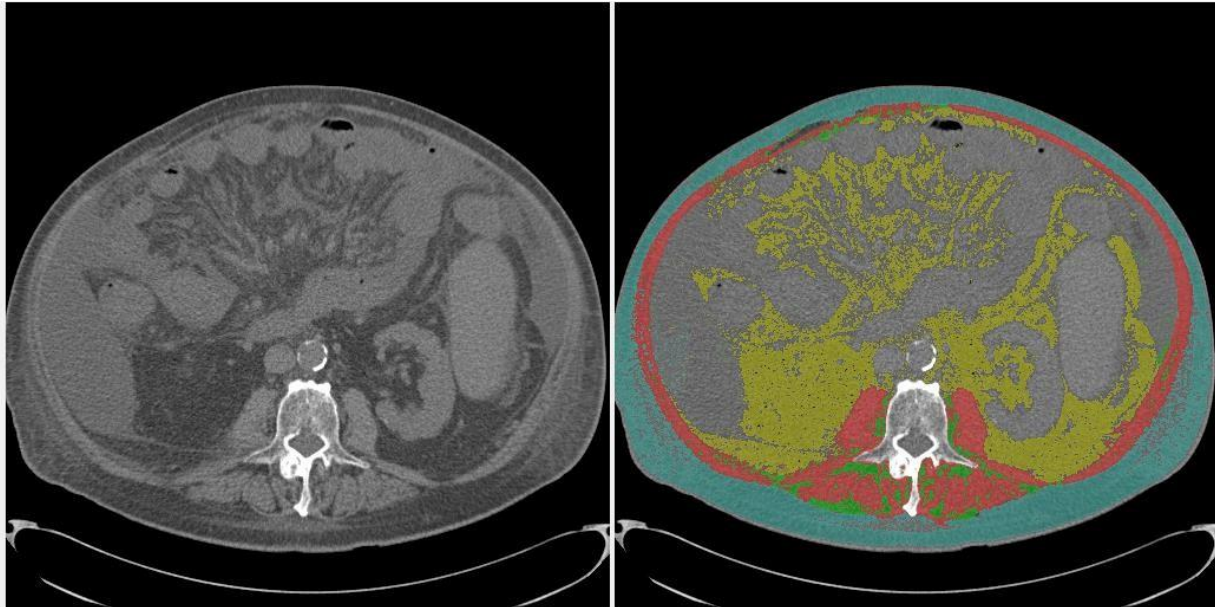
Note: A minimum of 8GB of RAM is suggested for running this software (has not been tested with less).

- VI. Optional: Adjust the HU ranges for Automated BCA muscle, IMAT/SAT, and VAT analysis
- a. These values are initially set at standard ranges
 - i. Muscle: -29 to +150
 - ii. IMAT/SAT: -190 to - 30
 - iii. VAT: -150 to -50
 - b. Only narrower ranges can be applied (e.g. muscle HU range from -29 to 150 TO 30 to 150)
 - c. enables specific HU ranges for CSA analysis (e.g. more dense muscle tissue 30 to 150)
 - d. After setting your preferred values, ensure you press “Okay” to set your ranges

Muscle HU lower boundary	-29	Muscle HU upper boundary	150
IMAT and SAT HU lower boundary	-190	IMAT and SAT HU upper boundary	-30
VAT HU lower boundary	-150	VAT HU upper boundary	-50
<div style="border: 1px solid black; display: inline-block; padding: 5px 20px; background-color: #e6f2ff;">Okay</div>			

4) Displaying analysis output

If display segmentation was selected, once the analysis has completed, a new blank window will appear. By pressing left and right on the keyboard, you can cycle through the raw and analyzed patient scans.



press left and right arrow keys to scroll through scans

5) What is exported

The raw CT scans, segmentation maps, and combined images will be available (labelled based on the extracted Patient ID) if save images was selected. An excel file containing several patient/CT imaging parameters (e.g. age, sex, voltage, etc.) and body composition metrics (cross-sectional area and average Hounsfield units for muscle, intermuscular adipose tissue, visceral adipose tissue, and subcutaneous adipose tissue) will be created based on the date and time of analysis

Note: depending on the anonymization process, the patient characteristics (e.g age, sex, etc.) included within the CT parameters may be incorrect.