User's Guide

CSC_quantification: A MATLAB-based tool for cervical spinal cord atrophy quantification using MRI images

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Brief Description of CSC_quantification

CSC_quantification is a software tool developed on MATLAB, specifically designed to help neurologists measuring Cervical Spinal Cord atrophy and tracking Multiple Sclerosis patients.

System Requirements

CSC_quantification is developed on MATLAB R2023b, thus its system requirements are identical to those of MATLAB. The following are the minimum system requirements for running CSC_quantification.

- Operating Systems
 - For Windows: Windows 11, Windows 10 (version 21H2 or higher), Windows Server 2019, Windows Server 2022.
 - For Linux Ubuntu 22.04 LTS, Ubuntu 20.04 LTS, Debian 11, Red Hat Enterprise Linux 9, Red Hat Enterprise Linux 8 (minimum 8.6), Red Hat Enterprise Linux 7 (minimum 7.9), SUSE Linux Enterprise Desktop 15, SUSE Linux Enterprise Server 12 (minimum SP2), SUSE Linux Enterprise Server 15.
 - For Mac macOS Sonoma (14), macOS Ventura (13), macOS Monterey (12.6),
- Processor

Minimum: Any Intel or AMD x86-64 processor with two or more cores Recommended: Any Intel or AMD x86-64 processor with four or more cores and AVX2 instruction set support.

RAM

Minimum: 8 GB, Recommended: 16 GB

Storage

3.8 GB for just MATLAB; 4-6 GB for a typical installation; 23 GB for an all products installation. An SSD is strongly recommended.

Graphics

No specific graphics card is required, but a hardware accelerated graphics card supporting OpenGL 3.3 with 1GB GPU memory is recommended.

Installation

We propose two solutions to run the CSC_quantification software.

■ First solution: CSC_quantification_MATLAB_GUI

The first solution is a CSC_quantification GUI and shared as repository (CSC_quantification_MATLAB_GUI) including all required matlab files (*.m and *.fig). Matlab software (version R2023b) should be installed with all required toolboxes on your computer. The CSC_quantification GUI does not need any installation. You have only to add the whole repository to your Matlab search path by Home -> Set Path -> Add Folder.

To read MRI image, SPM is needed. In fact, SPM is an academic software toolkit for the analysis of functional imaging data, for users familiar with the underlying statistical, mathematical and image processing concepts. It is made freely available to the imaging community, to promote collaboration and a common analysis scheme across laboratories. The software represents the implementation of the theoretical concepts of Statistical Parametric Mapping in a complete analysis package. The SPM software is a suite of (MATLAB) functions and subroutines with some externally compiled C routines. SPM was written to organise and interpret our functional neuroimaging data. More details about SPM and link to download the adequate version are available here. SPM folder should be added to your Matlab search path by Home -> Set Path -> Add Folder.

Step 1(a): Ensure that Matlab has been installed on your computer. Then, open Matlab and go to the directory where is contained the downloaded CSC_quantification_MATLAB_GUI folder. Therefore, open the main file of our software: Patient_Information.m file. Once you have located the file and opened it, select the "Run" button to execute it.

```
Patient_Information.m X SC_Preprocessing_Segmentation.m X SC_Partition.m
      function varargout = Patient_Information(varargin)
2 🖨
      % PATIENT_INFORMATION MATLAB code for Patient_Information.fig
3
             PATIENT_INFORMATION, by itself, creates a new PATIENT_INFORMATION or raises the existing
4
      %
             singleton*.
5
      %
             H = PATIENT_INFORMATION returns the handle to a new PATIENT_INFORMATION or the handle to the existing !
6
      %
7
             PATIENT_INFORMATION('CALLBACK',hObject,eventData,handles,...) calls the local
8
      %
             function named CALLBACK in PATIENT INFORMATION.M with the given input arguments.
9
      %
10
      %
             PATIENT_INFORMATION('Property','Value',...) creates a new PATIENT_INFORMATION or raises the
      %
11
             existing singleton*. Starting from the left, property value pairs are
12
      %
             applied to the GUI before Patient Information OpeningFcn gets called. An
13
      %
             unrecognized property name or invalid value makes property application
      %
14
             stop. All inputs are passed to Patient_Information_OpeningFcn via varargin.
      %
15
      %
16
             *See GUI Options on GUIDE's Tools menu. Choose "GUI allows only one
17
      %
             instance to run (singleton)".
18
      %
19
      % See also: GUIDE, GUIDATA, GUIHANDLES
20
21
      % Edit the above text to modify the response to help Patient Information
22
23
      % Last Modified by GUIDE v2.5 12-Jan-2024 15:41:14
24
25
      % Begin initialization code - DO NOT EDIT
       gui_Singleton = 1;
26
27
      gui State = struct('gui Name',
                                          mfilename, ...
```

Figure 1. The display of the Patient_Information.m file

Spinal Cord Quantification Software

Patient information block

Date 28-01-2024

Name

Family Name

Date of Study Select Date of Study

National ID

Start Reset Exit

Once "Run" button is pressed, the following main *Patient_Information* block is opened.

Figure 2. The display of the Patient_Information block

Second solution: CSC quantification Compiled App

The second solution is a compiled MATLAB application shared as a repository (*CSC_quantification_Compiled_App*) including an Executable file (CSC_quantification.exe). This solution gives users the ability to run our compiled MATLAB application without installing MATLAB software. However, MATLAB Runtime (R2023b) should be installed. It is possible to download and install the adequate version of the MATLAB Runtime for R2023b (available for Windows, Linux and Mac) from the following link.

Step 1(b): Ensure that MATLAB Runtime for R2023b has been installed on your computer. Then, open the directory where is contained the downloaded CSC_quantification_Compiled_App folder. Therefore, open the executable file of our software: CSC_quantification.exe file. The Patient_Information block, presented by Fig.3., and the same as presented by Fig.2., is displayed.

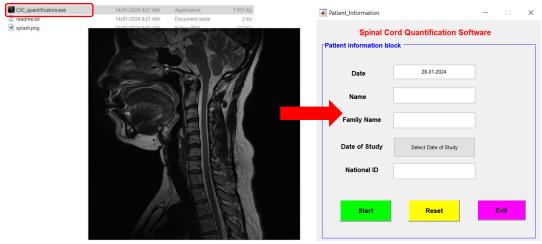


Figure 3. The display of the Patient_Information block

Patient_information block is used to collect and save basic information, especially Study date, Name, Family Name, and National ID, related to a particular patient. In addition, this block included three buttons labeled as Start, Reset and Exit useful to, respectively, open SC_preprocessing_segmentation block, reset all information of the considered patient and exit the block. An example of this block is presented in Fig.2.

All following blocks of the software and their corresponding description are identical for both presented solutions.

Step 2: SC_Preprocessing_Segmentation block include five blocks. The first is image and slice selection block used to load sagittal T2-w MRI and select and display the best slice.

The proposed software was configured by default to operate with *.nii Sagittal T2-w MRI. However, additional image formats such as *.img and .*dcm are also supported. As depicted in Figure 4, it could be selected at line 97 of the source code of the SC_Preprocessing_Segmentation matlab function (SC_Preprocessing_Segmentation.m file).

Figure.4. The display of the SC_Preprocessing_Segmentation.m file

The image to be uploaded should be placed in the <u>main folder</u> of the proposed software (*CSC_quantification_MATLAB_GUI* folder for the first solution and CSC_quantification_Compiled_App folder for the second solution). An example of Sagittal T2-w MRI (T2_medull_sag_X055.nii) is included in both folders and could be considered to test our proposed software.

The user must select the T2-w MRI to be uploaded and the number of corresponding slices will be automatically calculated. The user must therefore select the and display the best slice.

To improve the illumination information of the selected slice and display the generated enhanced image, a contrast enhancement block is considered. Since the principal task of this research work is the quantification of the CSC, ROI selection block is integrated to define the desired region of the SC. Furthermore, a SC segmentation block is considered to extract the CSC using the localized active contour method. We note here that user needs to point the cursor inside the SC to initialize the segmentation process. When the desired segmentation result of SC is achieved, the stop segmentation button is pressed as well as the display button to get extracted SC. Finally, the Start SC partition button opens the SC Partition block. Reset button could be used to restart all the already described steps.

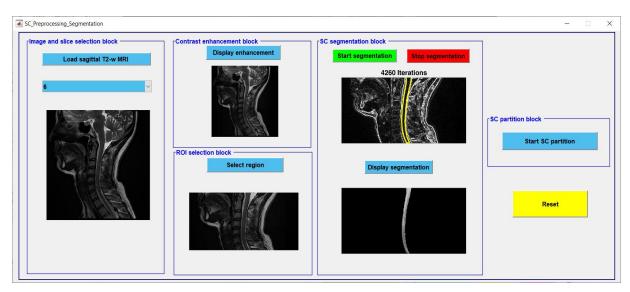


Figure.5. SC_Preprocessing_Segmentation block in CSC quantification software

Step 3: SC_partition block contains three blocks. The first SC partition block is used to shift the squelotonized SC shown in red colour towards vertebrae by changing shifting value. Once red line has been well positioned, the second SC display block is used to display fragmented and labeled SC for all vertebral levels. In fact, a specific color and number is attributed to each SC fragment. The indicated number corresponds to patient vertebrae level. Finally, the SC measures block opens the SC quantification block. While, reset button could be used to restart all the already described steps.

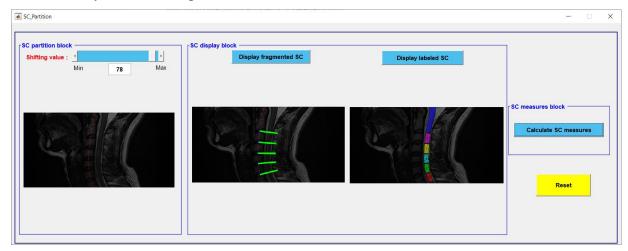


Figure.6. SC_partition block in CSC quantification software

Step 4: SC_quantification block included several buttons used to display considered measurements related to lower-diameter, upper-diameter, length and volume for all segments with numbers indicated in the first column. Also, total CSC length and total CSC volume could be computed and displayed using adequate buttons. A saving button is designed to export SC measurements in Excel file with a name generated as: Name_FamilyName_NationalID specified in the first block of the software.

For a particular patient, imaged several times and so having multiple MRIs, SC measurements of the different follow-up images could be saved in different sheets of the same Excel file. The date of MRI acquisition, specified as the date of study in the *Patient_information* block, is used to rename a particular sheet. This file serves as a reliable source of information. It assists neurologist in making their reports and facilitate their results analysis.

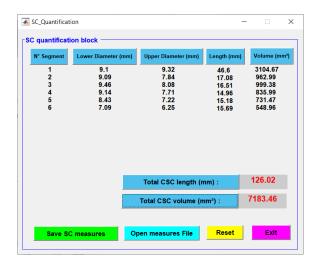


Figure.7. SC_quantification block in CSC quantification software

The following figure illustrates an example of a particular patient imaged 3 times and so having 3-follow-up MRIs. We note here that three different sheets are generated, each one with the date of each Study date.

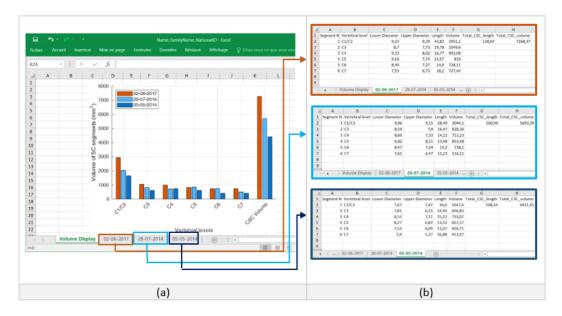


Figure.8. Generated Excel file for 3 follow-up MRIs of RRMS patient; (a) Volume display of SC segments and total CSC volume per vertebral levels, (b) 3 follow-up MRIs measures of a given RRMS patient