SPECKLE QUALITY TEST

V1.0

USER GUIDE

January 2014

Funding

Project developed at Centre for Development of Applied Instrumentation in Agriculture, under supervision of professor DSc. Roberto Alves Braga Jr, from Engineering Department of Federal University of Lavras (UFLA), and was partially by FAPEMIG, CNPq, CAPES and FINEP.

Team

Research team linked to development, Professor DSc. Roberto Alves Braga Jr (robbraga@gmail.com), Michel Melo da Silva (michelms@comp.ufla.br).

Objective

Help researchers in the Dynamic Laser Speckle area evaluate the sequence image captured at their experiments, providing them a feedback before the main assays.

Dates

Project Start: 10/10/2012

Last Actualization: 11/02/2014

Software Register in National Institute of Industrial Property

Registration Protocol:

Registration Number:

Type of Registration: *Software free to use.*

References:

1- Moreira, J., Cardoso, R.R., Braga, R.A. Quality test protocol to dynamic laser speckle analysis, Optics and Lasers in Engineering 2014 *In Press*

2- Godinho, R.P.; et al; Online biospeckle assessment without loss of definition and resolution by motion history image. Optics and Lasers in Engineering, v. 50, p. 366-372, 2012. doi: 10.1016/j.optlaseng.2011.10.023

3- R.A. Braga; et al; Biospeckle numerical values over spectral image maps of activityOptics Communications 285 (2012) 553–561 doi: 10.1016/j.optcom.2011.10.079

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1. Basic considerations

1.1 Programming language utilized

The project was implemented using the programming language C++ with the assistance of Qt 4.7.4 (32-btis) © *Nokia Corporation* Framework for development of graphical user interface and use of additional basic structures. The Qt Creator 2.4.1 was the Integrated Development Environment utilized. It was also used computer vision library Open Source Computer Vision 2.0 (OpenCV) for efficient manipulation of images.

1.2 Generated files

The program saves the images resulted from the speckle quality test processing in Join Photographic Expert Group image format (".jpg").

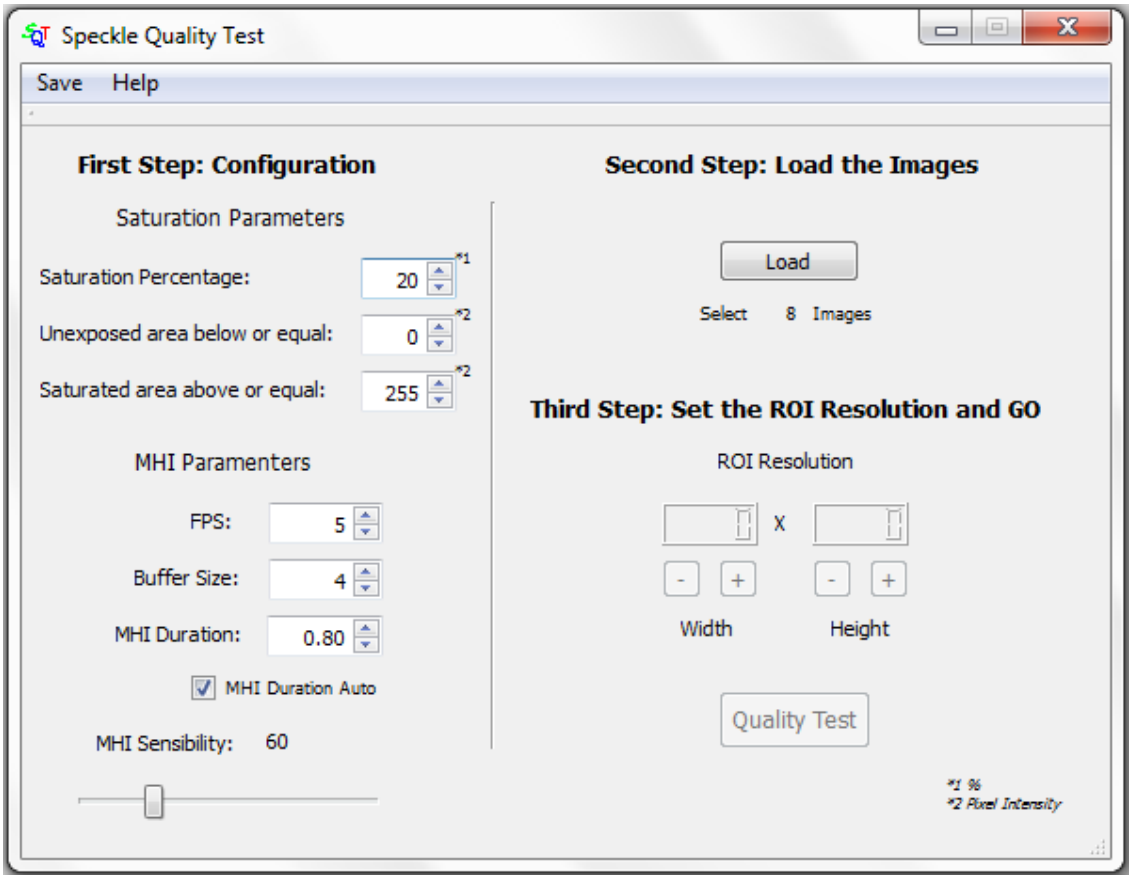
1.3 Installation and execution

This is an executable program (for Windows), so it is not necessary to install it. To run it just copy the folder to your Hard Disk (HD). In this folder there are some files that are essential for the proper functioning of the program,such as: sub-folders named “icons” and “img”, and nine (9) Dynamic Link Library files (".dll") called: libcv200.dll, libcxcore.dll, libcc_s_dw2-1.dll, libhighgui200.dll, mingwm10.dll, QtCore4.dll, QtCored4.dl, QtGui4.dll e QtGuid4.dll.

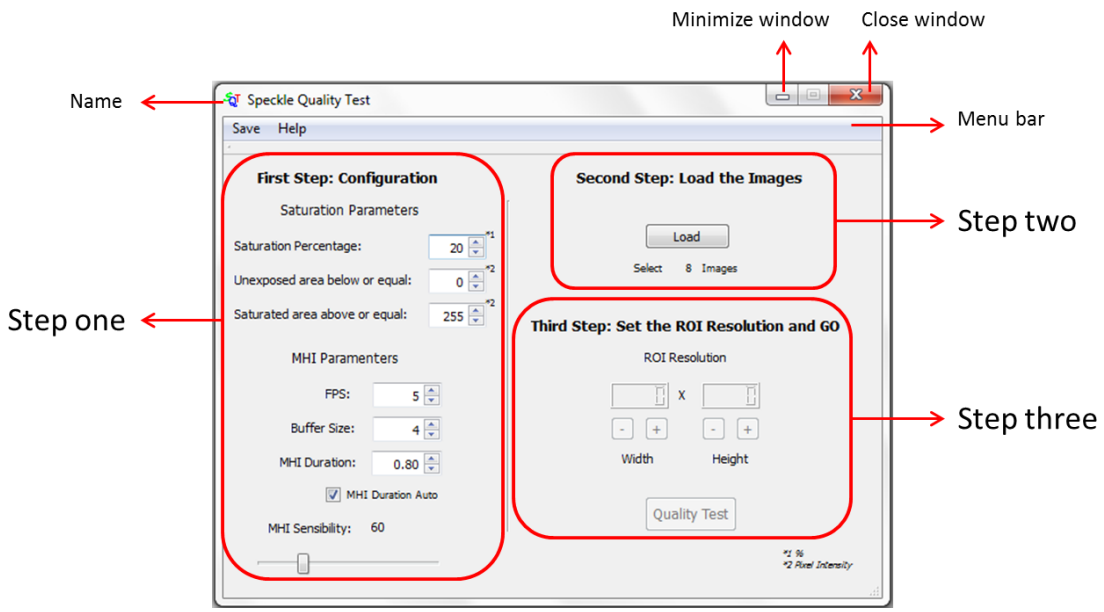
All of these files are already inside the folder. Do **not** remove the program executable file from this folder because it will not work anymore. It is possible to create a shortcut for easy access to the executable file.

2. Overview

This is the Speckle Quality Test v1.0 main window.



This window is divided into steps to facilitate interaction with the user.



- Name:

At the top left there is the name of the program you are using, always check if the manual, documentation and/or information that you have refer to the same program and the same version that you are using.

- Minimize and close the window:

At the top right there are buttons to minimize and to close the window. **There is no** button to maximize the window, it cannot be resized.

- Menu bar:

In the menu bar there are two menus. The "Save" menu only will be enabled when you finish the processing. The "Help" menu is always enabled. In this menu you can find a short program tutorial and the program details, such as the version that you are using.

- First Step

In the First Step there are the configurations for the parameters of the methods Saturation and Motion History Image (Godinho et al. 2012).

- Second Step

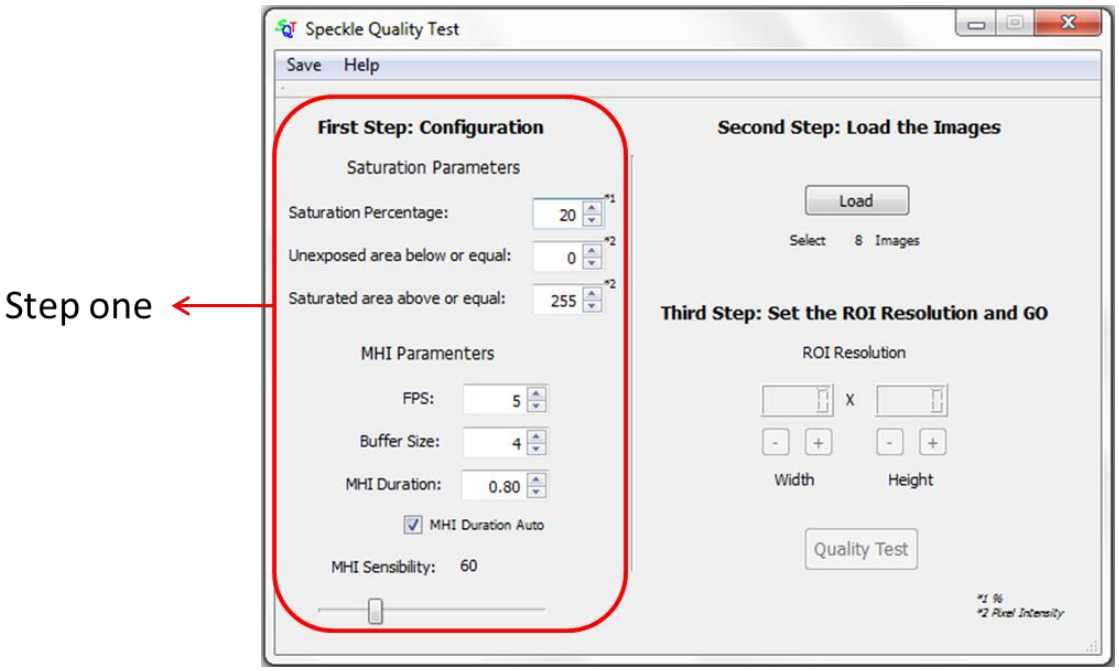
On this step you can load the images to process.

- Third Step

It is responsible for the image division and where you run the analysis. The three parameters are tested within the sub-windows defined as Region of Interest (ROI)

3. First Step

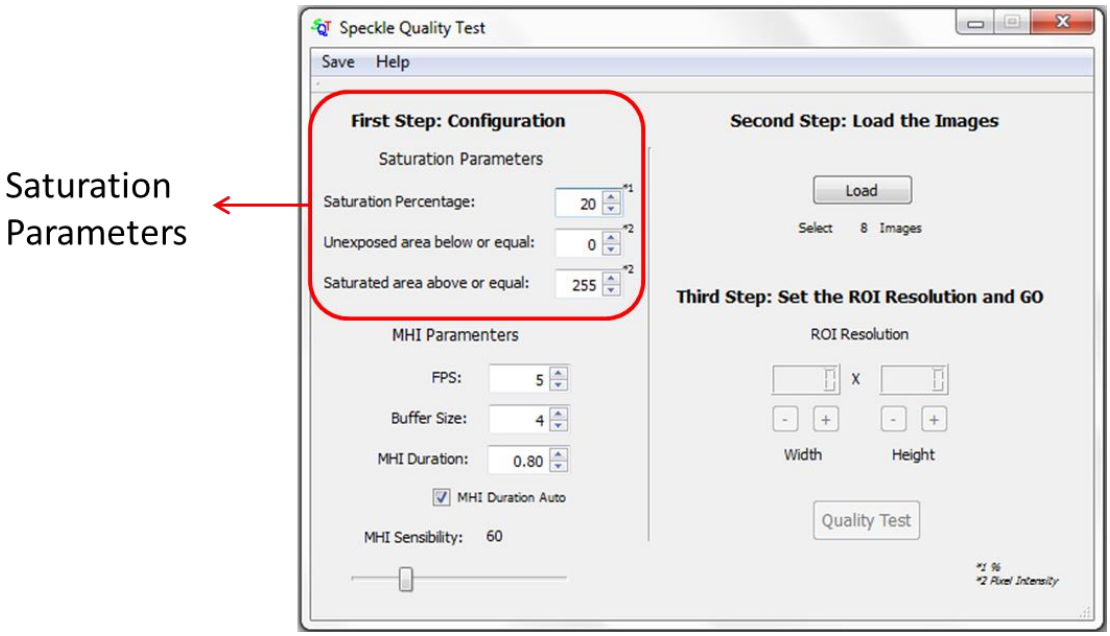
This step is responsible to configure the parameters of the methods applied on the processing.



The methods utilized on the processing to generate the results are the contrast, the saturation and the homogeneity. The contrast doesn't have any adjustable parameters. The Saturation and Homogeneity test have adjustable parameters, and the parameters to Homogeneity test are represented since MHI parameters, because de MHI algorithm is applied to check the activity of the windows (ROIs).

3.1. Saturation Parameters

The saturation method has three configurable parameters: saturation percentage, unexposed area below or equal and saturated area above or equal. All of them will be explained in this section.



3.1.1. Saturation Percentage

The saturation percentage assumes an integer value from 0 to 100. This number represents the threshold to each ROI and for example it will consider a ROI as saturated or underexposed if the percentage of pixels above or below the limit is greater than the saturation percentage chosen.

3.1.2. Unexposed area below or equal

This parameter represents the pixel intensity on gray scale, and it can assume an integer value between 0 and 255. Ever pixel with value equal or below this will be classified as unexposed pixel.

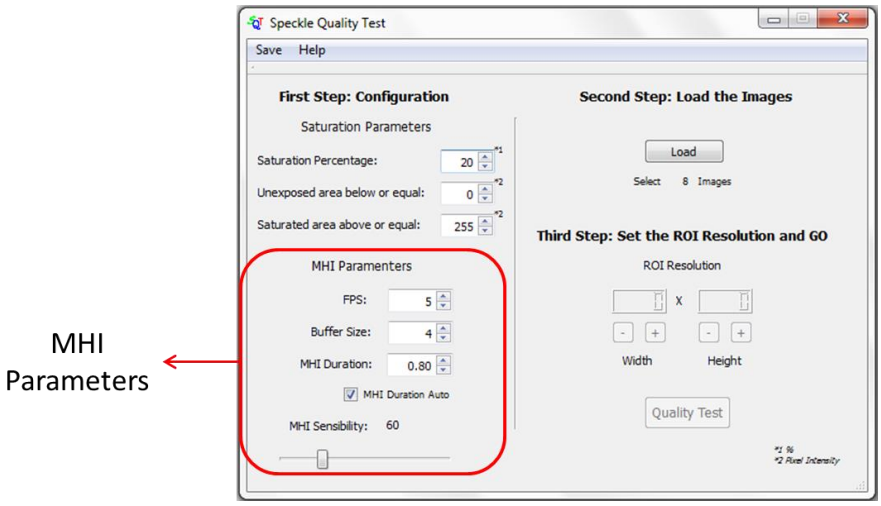
3.1.3. Saturated area above or equal

This parameter represents the pixel intensity on gray scale, can assume an integer value between 0 and 255. Ever pixel with value equal or above this will be classified as saturated pixel.

3.2. MHI parameters

The MHI method has five configurable parameters: FPS, Buffer size, MHI duration and MHI sensibility. All of them will be explained in this section.

To understand more about the utilization of the MHI on speckle experiments read the paper: Online biospeckle assessment without loss of definition and resolution by motion history image (DOI: 10.1016/j.optlaseng.2011.10.023).



3.2.1. FPS

This is an integer parameter, and it can assume values from 0 up to 30. FPS means Frames Per Second. This parameter has to be set with the camera device configuration.

3.2.2. Buffer size

This is an integer parameter, and it can assume values from 2 up to 128. It controls the buffer size of the MHI algorithm, i.e., how many images are used to execute the algorithm processing.

3.2.3. MHI duration

This is a decimal parameter, can assume values between 0.1 and 128. It controls the MHI duration parameter used in the algorithm. The MHI duration represents the lifetime of the image in the processing. At the end of this time, the image is no longer part of the set of the historical images used in the processing.

The check box "MHI Duration Auto", when is checked, automatically calculates MHI Duration value. Given that the lifetime of a frame is the "Buffer Size" value divided by "FPS" value. It is the conventional way to set this processing.

Use **comma** for decimal numbers.

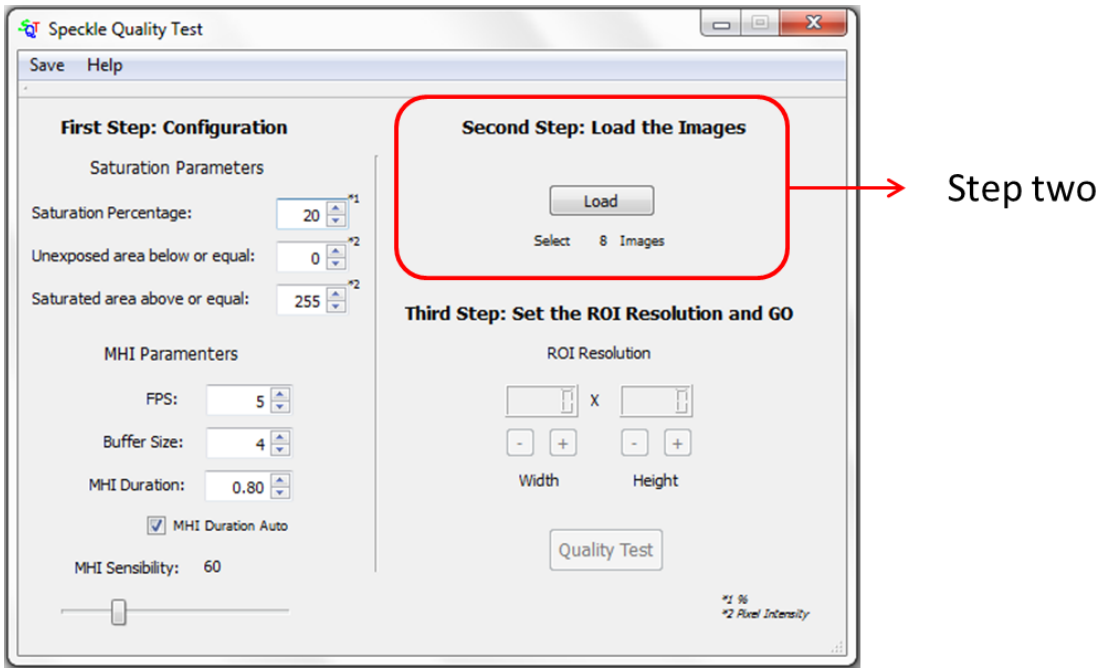
3.2.4. MHI sensibility

This is an integer parameter, and it can assume values from 0 up to 255. It controls the threshold parameter value used to modify the motion sensibility of MHI algorithm.

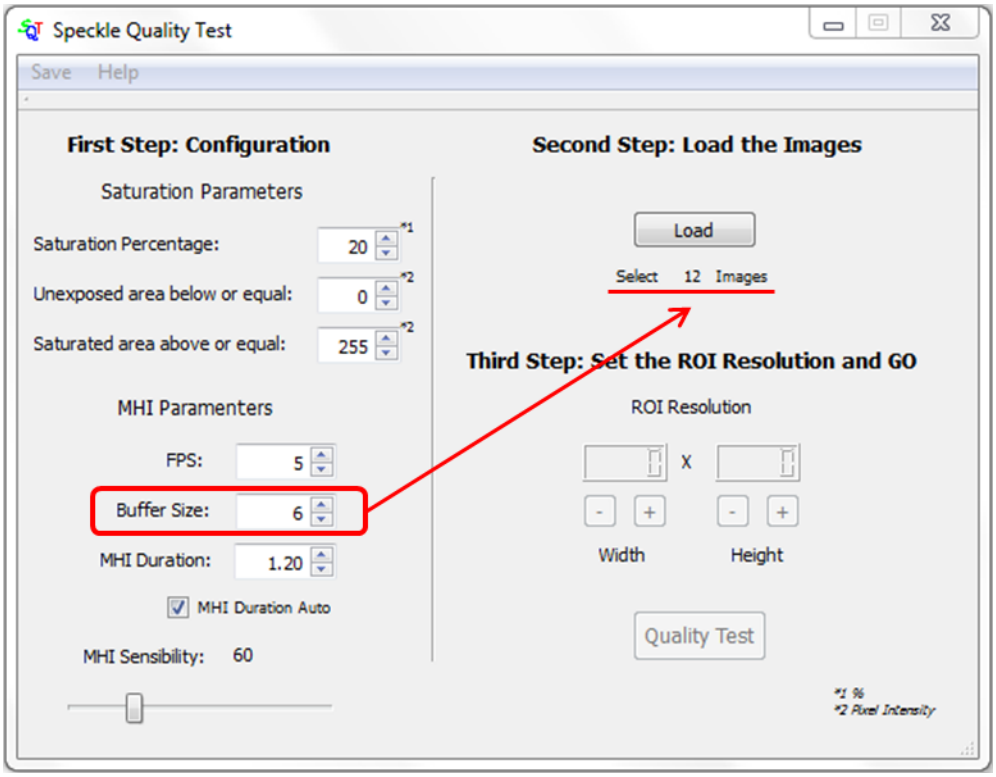
The lower the MHI sensibility value the more sensitive is the algorithm and more discrete changes are analyzed. With a very high MHI sensibility value only abrupt changes will be captured by the algorithm.

4. Second Step

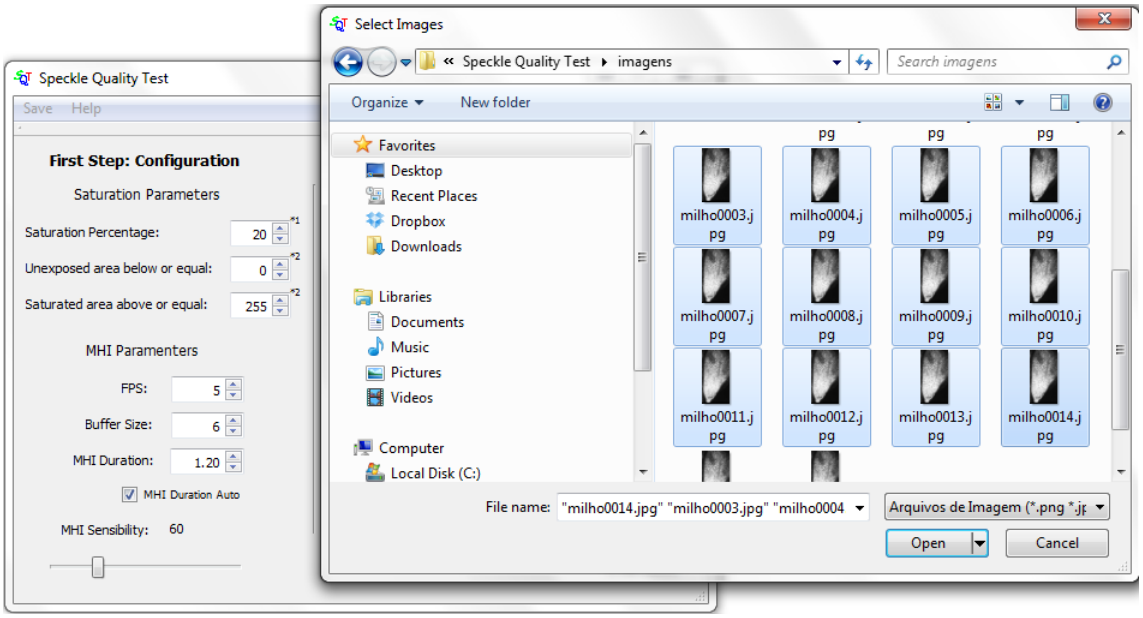
The step two is where images are loaded.



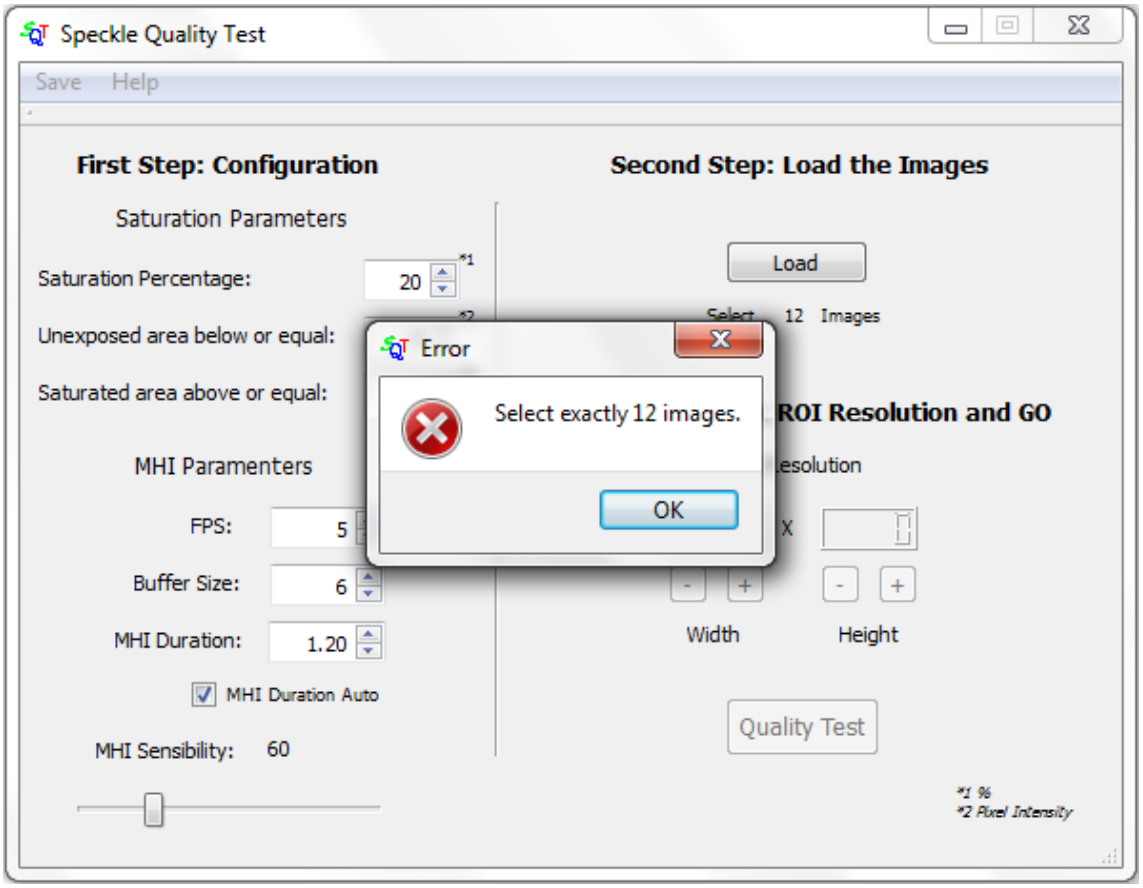
The amount of images that have to be loaded is displayed on the interface. This number is twice the buffer size.



When the button load is selected, a new window opens to let you find the collection of images you need. All images have to be loaded at same time using the <shift> key.

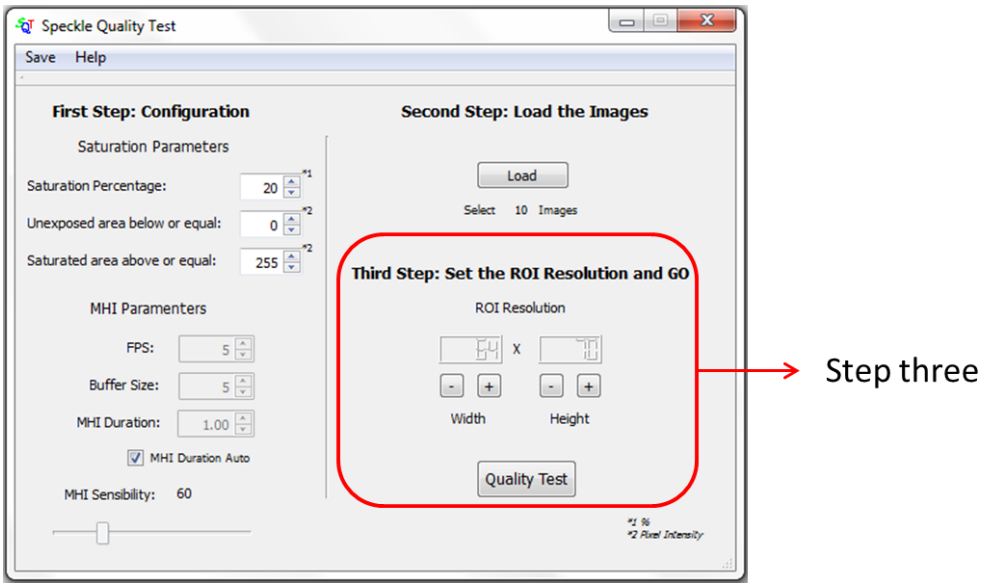


If a wrong number of images are loaded, an error message appears.

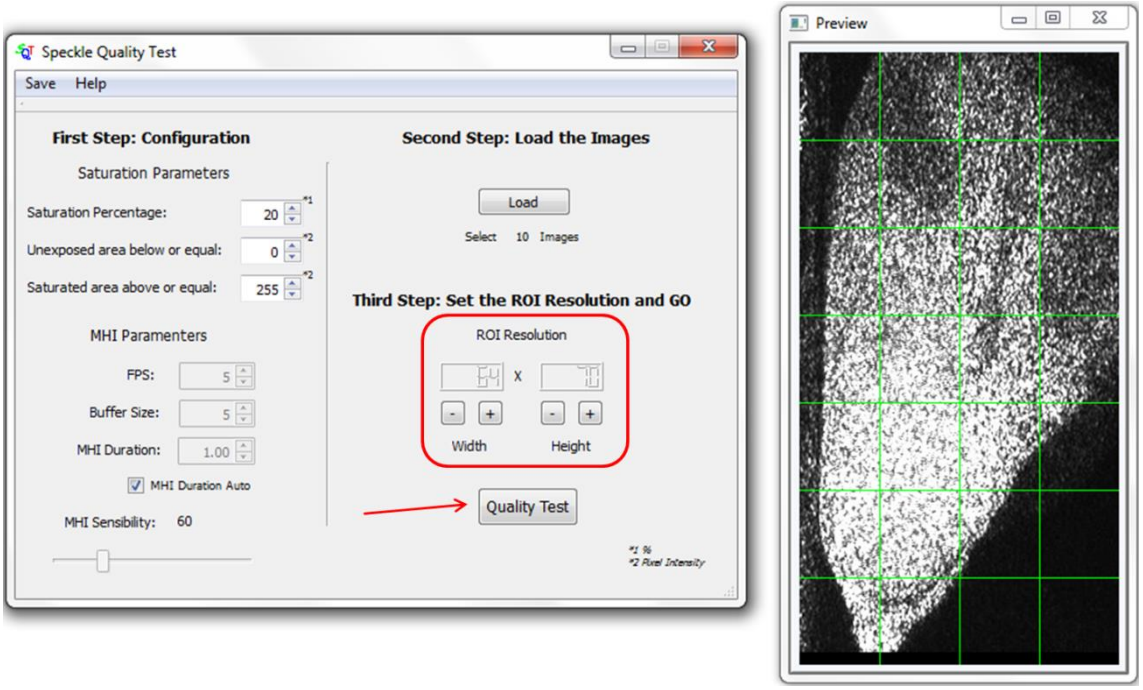


5. Third Step

After set all the parameters and after load the correct number of images, the last step has to be done. The ROI resolution is set and the processing is started. Before the first and the second step are finished, all the buttons of the step three will be disabled.



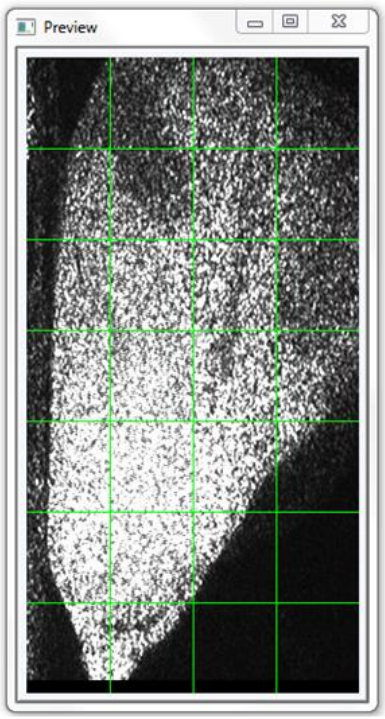
At the end of the step two, a preview window will appear showing the first image of the set of images loaded. This preview has lines that delimit ROIs. Using the + and - buttons, the width and height of the ROIs can be changed. The possible values for width and height are related to an integer numbers of ROIs within the image.

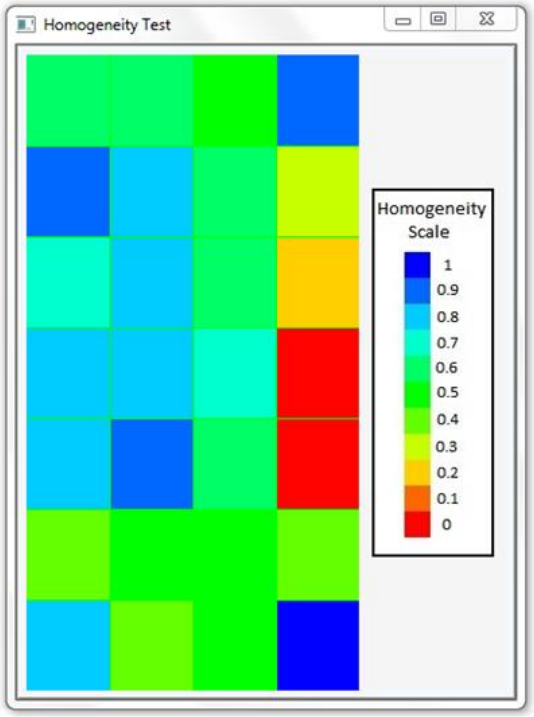


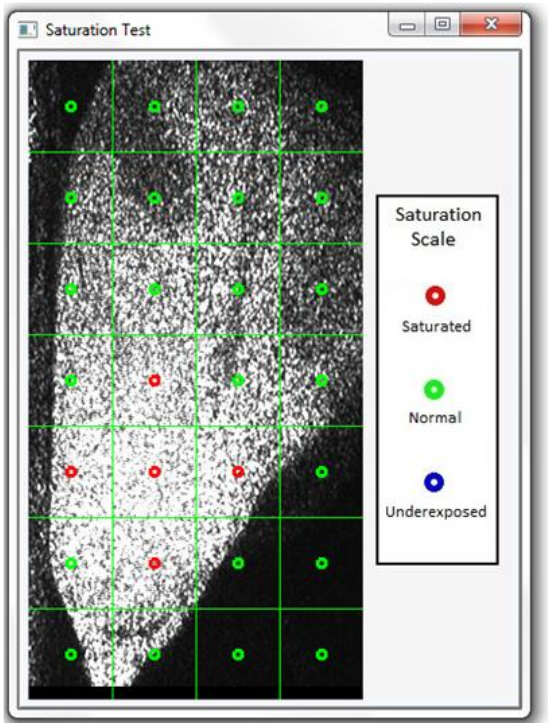
After the selection of the best resolution to your work, press the button “Quality Test”.

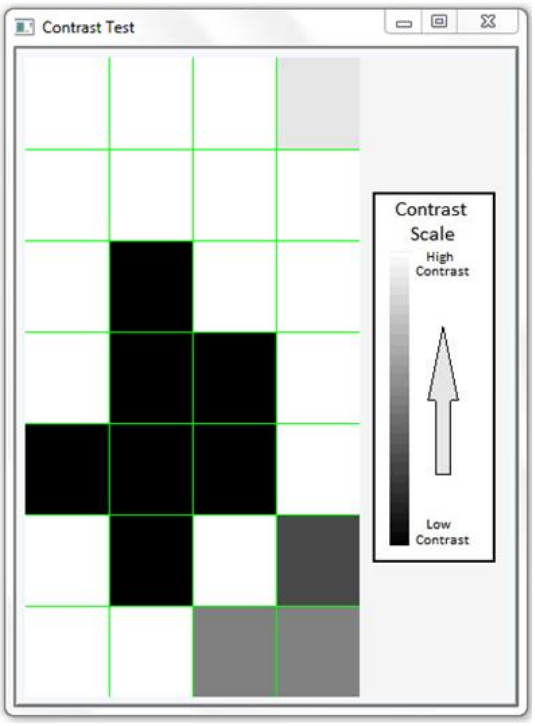
6. Results

When the button “Quality Test” is pressed, the processing starts on background and only the final results are showed. Three windows are presented: contrast test, homogeneity test and saturation test. All windows have a legend with a scale to help you understand them. To understand more about each test applied on speckle experiments read the paper of Moreira et al. (2014).



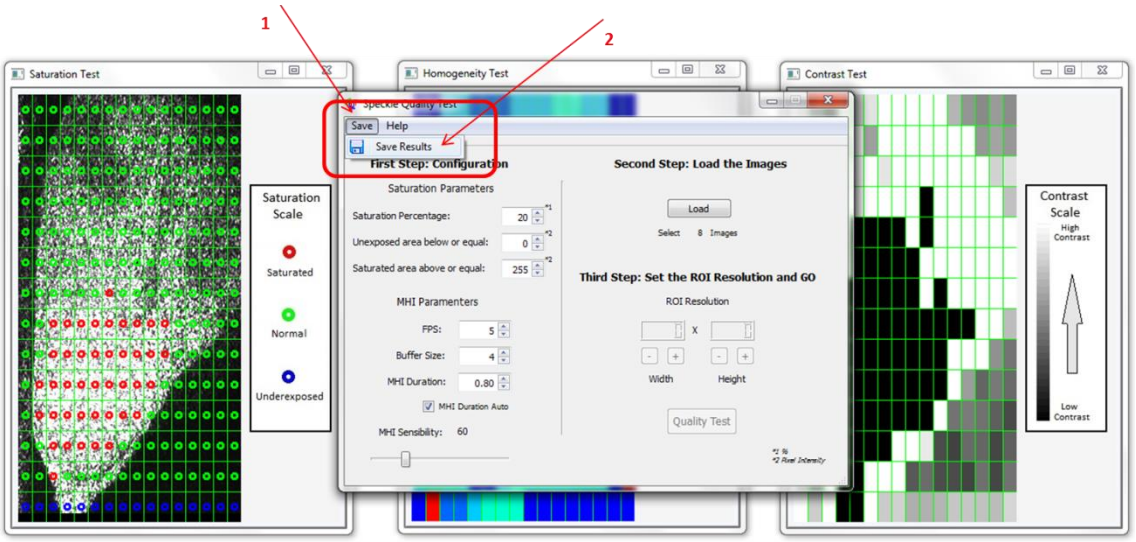




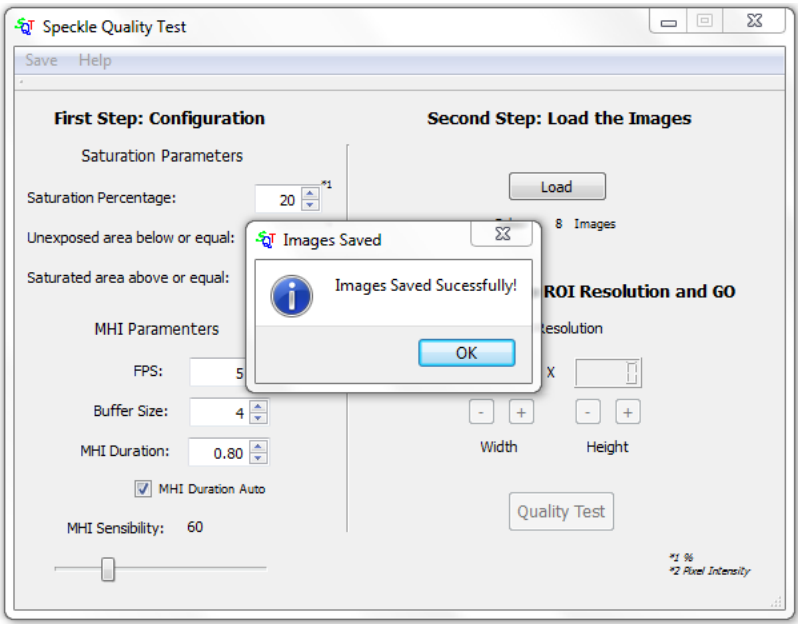


7. Save Results

The outputs can be saved using the option “Save -> Save Results” on menu bar. You will be able to choice a folder where result images will be saved. On the selected, four images will be saved, three of the tests and one of the preview image with the lines delimiting the ROIs. The file names will be: contrast_test.jpg, homogeneity_test.jpg, saturation_test.jpg and preview.jpg.



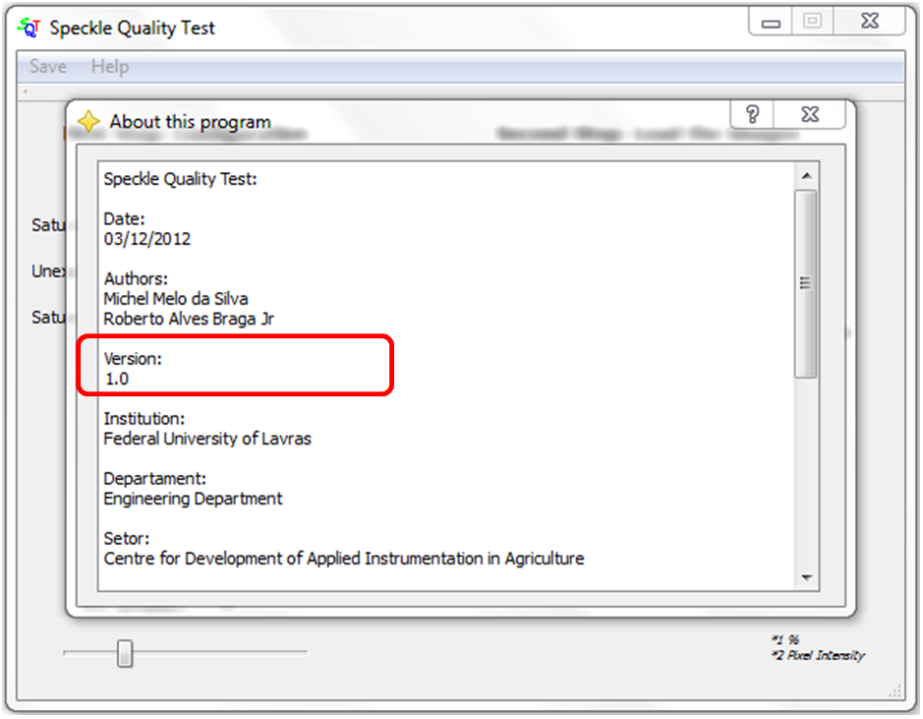
The program shows a feedback window to notify that images were saved.



If you choice a folder that already contains files with the same name the created files, the older ones **will be overwritten without a warning message**, be careful.

8. Program version and details

The program details as version and authors contact can be found on menu “Help -> About” on menu bar.



Thanks for using our program.

This software is totally free for use in research and other activities noncommercial. If you used it in your experiments please cite the follow papers in your paper:

Moreira, J., Cardoso, R.R., Braga, R.A. Quality test protocol to dynamic laser speckle analysis, Optics and Lasers in Engineering 2014 *In Press*

R.A. Braga; et al; Biospeckle numerical values over spectral image maps of activity
Optics Communications 285 (2012) 553–561
doi: 10.1016/j.optcom.2011.10.079

Godinho, R.P.; et al; Online biospeckle assessment without loss of definition and resolution by motion history image. Optics and Lasers in Engineering, v. 50, p. 366-372, 2012.
Doi: 10.1016/j.optlaseng.2011.10.023

Any doubt or suggestion, please get in touch by email or phone.