

Getting started with Tapestry ToolKit

A guide to using the software package

The software is used to generate numerically deformed images of a known deformation field and then compares the DIC results of the deformed images with the known strain field from a finite element analysis

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Installation

The software name is Tapestry_ToolKit and is hereafter referred to as the software except where otherwise stated in this guide.

Requirements:

1. To use the software at its current development stage:
 - You need to have access to Abaqus finite element analysis software installed in the same PC as the Software
 - Or use the in-built finite element analysis function in the software. Only linear elastic material properties and static analysis are available in this case
 - You should either have access to Vic 2D DIC (digital image correlation) analysis software or download and install the free DIC software ncorr (see page 27)
2. The Vic 2D software could be on the same or different PC as the software.

To install the software for the first time, you need to have a stable internet connection

1. Double click on the file named: Tapestry_ToolKit_Installer.exe. Wait for the software to install.
 2. The software is the file named Tapestry_ToolKit .exe
-
- ❖ While the guidelines provided in this manual is focused on the compiled standalone version of the Software. Alternatively, one can run the ToolKit from MATLAB if they have the MATLAB scripts. You do this by changing your working directory to the folder containing the MATLAB scripts and then type Tapestry_ToolKit from the MATLAB command window. Every other steps to using the Software is the same as presented in this manual.

Performing Analysis with the Software following these steps

Step 1. Creating your working directory

Copy and paste the software (Tapestry_ToolKit.exe) in a folder. This folder is known as your working directory and will be referred to as such in this guide. You can create this folder and give it any name you like. All generated files including deformed images folder(s) and results will be saved in this folder.

- Please note that step 1 does not need to be repeated for subsequent analysis with the software unless you want to run analysis from a another working directory.
- This working directory (folder) could be saved any where in your computer. It is preferable to save it in a drive with enough memory that you have rights to.

Step 2. From your working directory, double click on the file named: Tapestry_ToolKit.exe and wait for the software to open. At start up, the software interface will look as shown in the Figure 1.

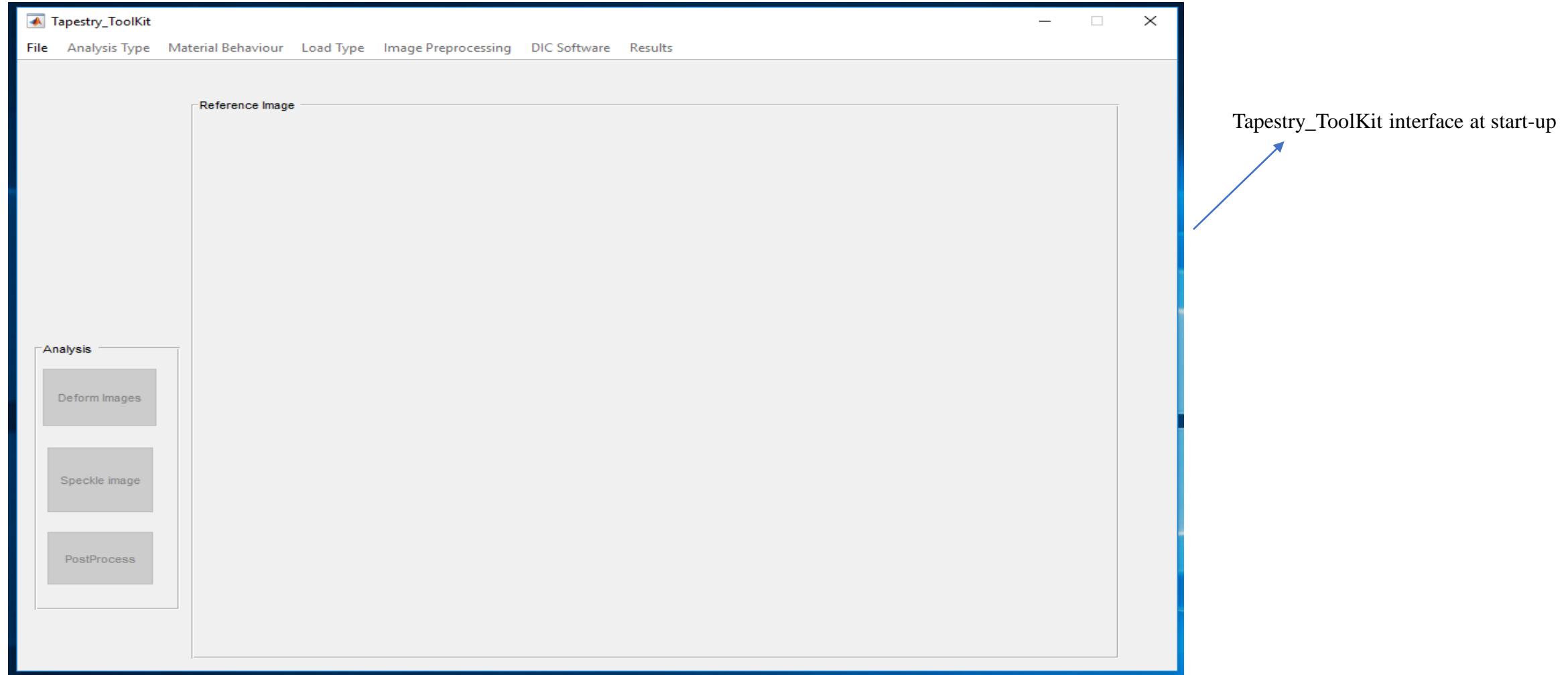


Figure 1

- At start-up (see Figure 2), only the **File** menu is active!

Step 2. Click on **File** menu and select **Open Reference Image**: This will prompt you to select your initial undeformed image.

The initial undeformed image is known as the reference image.

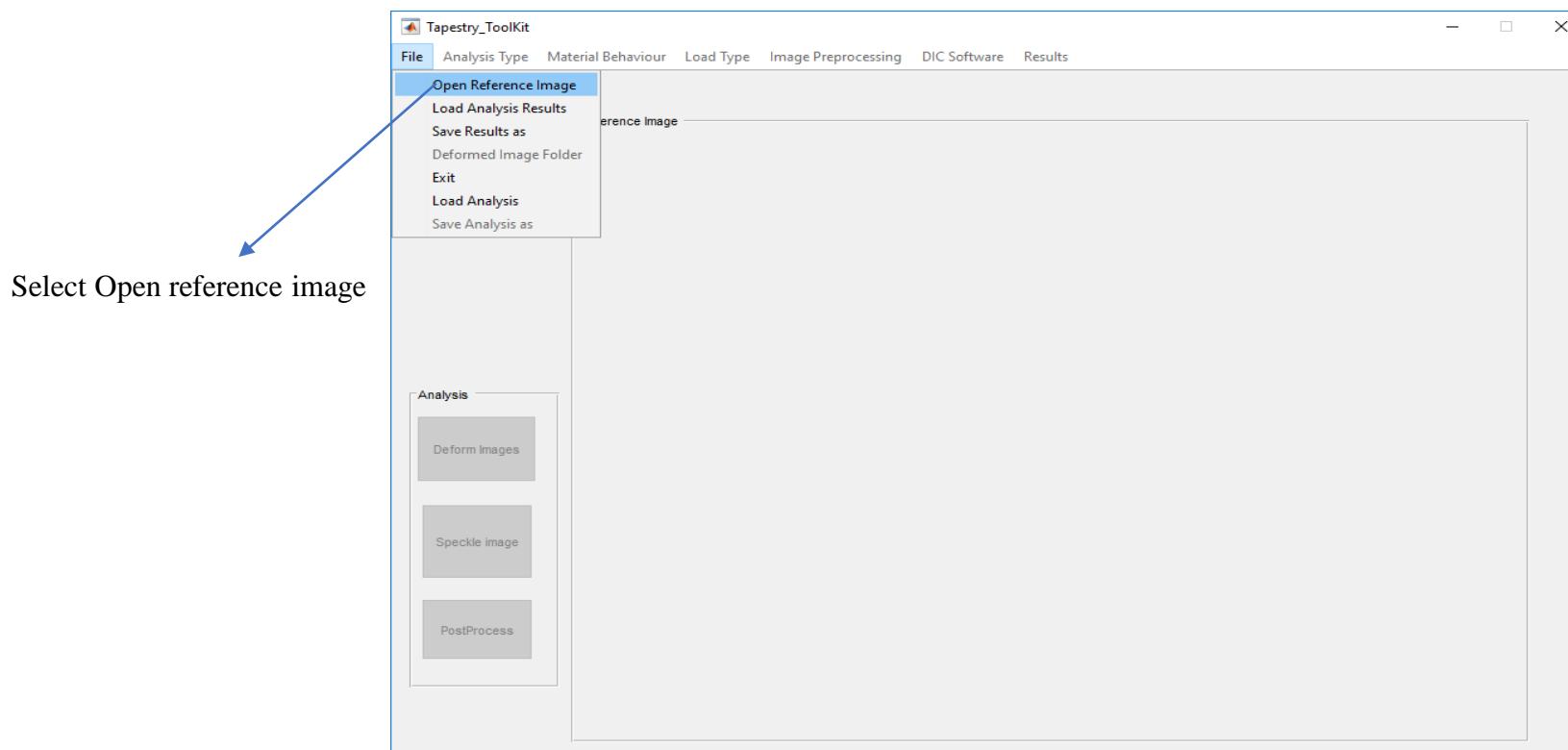


Figure 2

Note:

After selecting the reference image, you will be asked if you know (and want to use) the physical dimensions of the tapestry in the analysis. This is necessary because the finite element model dimensions are determined by the size of the tapestry. If you want to use the actual physical size of the tapestry, select yes in the dialogue box and enter the values (height and width in meters) in the dialogue box, then press enter to continue. In this case, the digital image dimensions will be resized to match the finite element model dimensions and you should enter the actual material properties in MPa (mega Pascal) while the areal density and gravity values should be in mm (millimetres). If you do not want to use the physical dimensions of the tapestry in the analysis, select no in the dialogue box. In this case, the software uses the digital image dimensions (number of pixels) to determine the finite element model dimensions. You should then scale the material properties to match your expected deformation level.

- Once the reference image has been selected, the **Analysis Type** menu becomes active (see Figure 3)!

Step 3. Click on **Analysis Type** menu and select analysis type. Then enter the number of materials in the tapestry.

Currently, **Static** and **Explicit dynamics** analysis are available in the software.

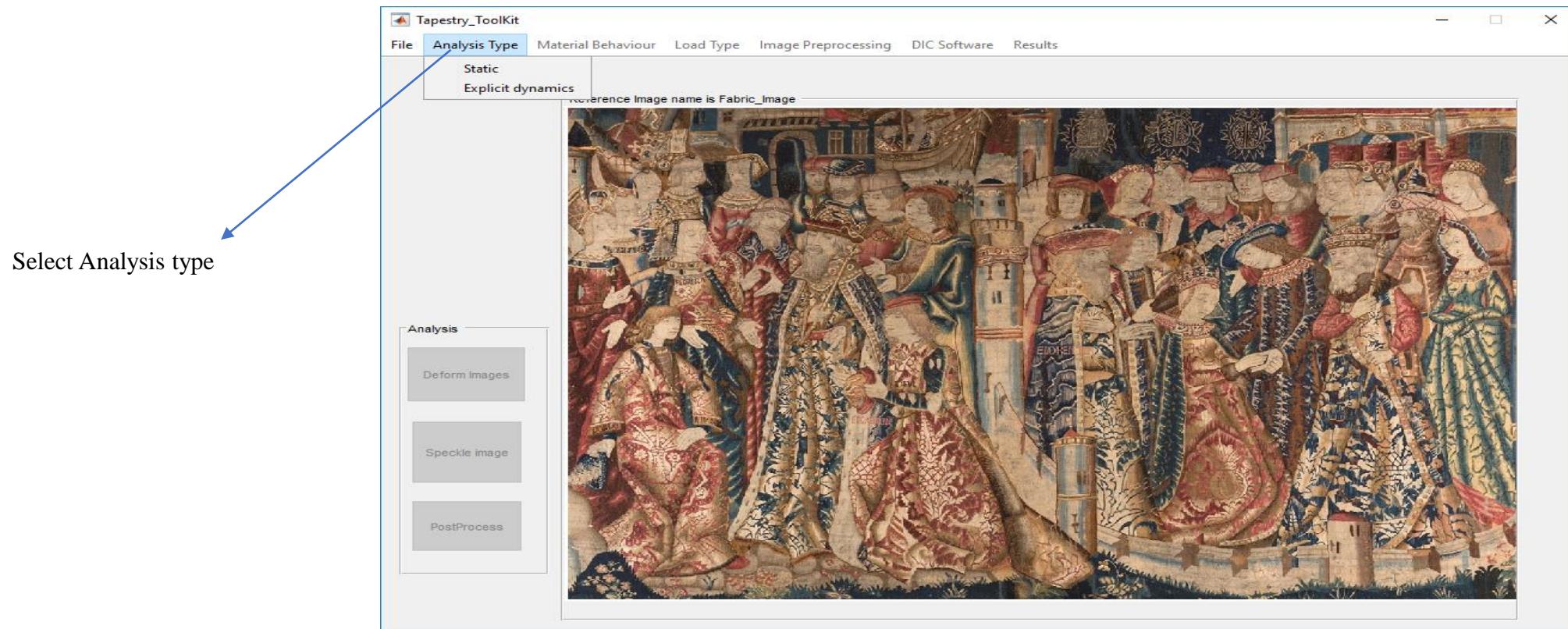


Figure 3

Note:

The analysis type is the kind of analysis you want to perform. Static analysis is appropriate for small deformation and is independent of inertia and dynamics (no free body motion). Explicit dynamics considers inertia, waves, free body motion and very large deformation. It is recommended to use static analysis always except when inertia and dynamic effects are present, or when large deformations are expected.

It has been assumed that the weft yarn and the stitching warp yarn (stitched region) are made of different materials in the tapestry. Hence, if you assume so, number of materials should be two. If it is not, number of materials should be one i.e. the tapestry is a homogenous material.

- Once the analysis type has been selected, the **Material Behaviour** menu becomes active (see Figure 4)!

Step 4. Click on **Material Behaviour** menu and select how the fabric (tapestry) material behaves.

Currently, **Linear Elastic** and **Hyperelastic** materials properties are available. Enter the values of material properties in the dialog box that appears

Select how the fabric behaves

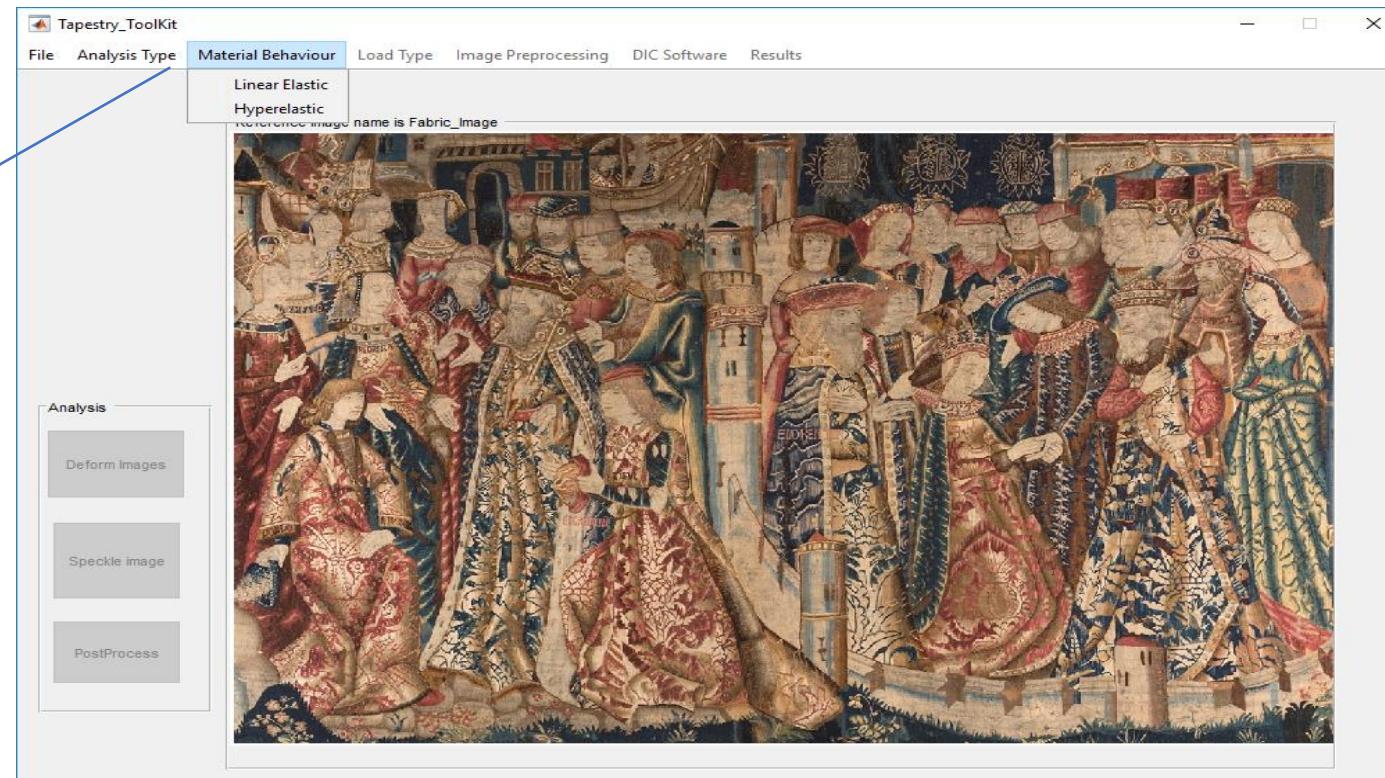


Figure 4

The material behaviour type is how your material (fabric/tapestry) behaves. A simple case is the linear elastic behaviour that obeys Hooke's law of elasticity. You need to know the Young's modulus and Poisson's ratio values for each of the materials in the tapestry image.

The hyperelastic behaviour implemented here is the isotropic Ogden model (Strain energy potential form). You need to have the mu, alpha and D values for each material in the image. The linear elastic analysis is faster in terms of the simulation run time than the hyperelastic behaviour.

- Once the Material behaviour has been selected and the values of the material properties entered, the **Load Type** menu becomes active (see Figure 5)!

Step 5. Click on **Load Type** menu and select the loading condition.

Currently, **Displacement (Stretching)** and **Self Weight (Gravity)** loading conditions are implemented. See info box 1 for more details

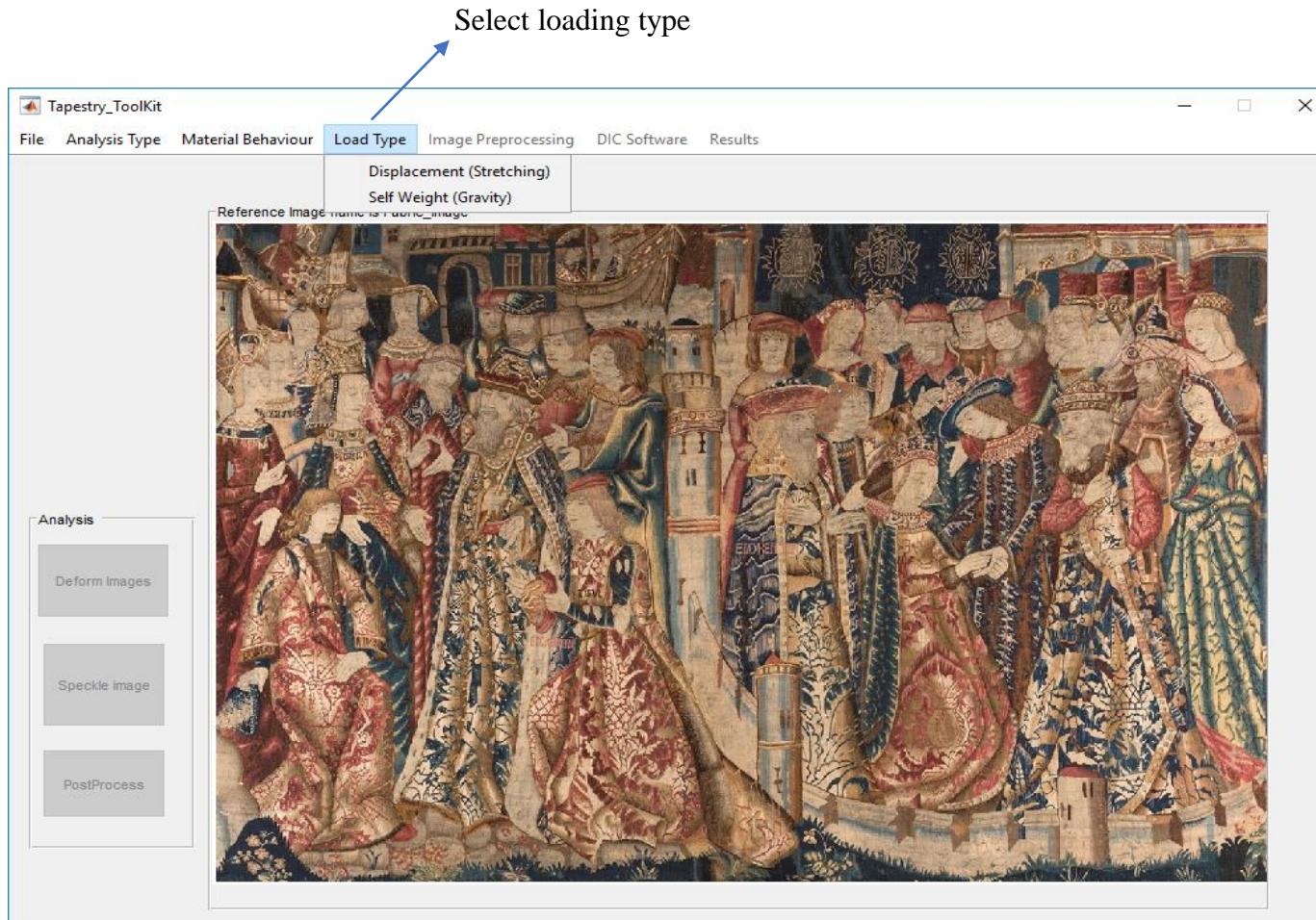


Figure 5

- The Displacement load requires applying a known displacement value. For example stretching the tapestry image to a known displacement value- say by 1% of its height.
- The Self Weight (Gravity) load is used to determine the strain distribution in the tapestry due to its own weight. This requires knowing the areal density value of the tapestry and the gravity value.
- When Load type has been selected, you are prompted to confirm if the loading is time dependent! If it is not time dependent, select No and enter the value of the Load (percent of expected stretching without the percent sign for displacement load or the value of gravity for self weight load). Be consistent with your units!
- The load can also be time dependent. For example the displacement varies over time or the weight changes due to humidity. This time dependent loading can be used in the analysis by entering the time and the corresponding load values in a table or reading the values from a table file. If the loading is time dependent, select Yes after selecting the load type. Use either of the two options to provide the time and load values.

Info box 1

- Once the loading type has been selected and the load values entered, the **Image Preprocessing** menu becomes active (see Figure 6)!

Step 6. Click on **Mesh Density** submenu to enter the ratio of finite element mesh to image pixel (see information box 2 for details)

Step 7. Click on **Scale Image** submenu to enter the image scaling value(see information box 2 for details)

Step 8. Click on **ROI** submenu select the region of interest ROI (see information box 2 for details)

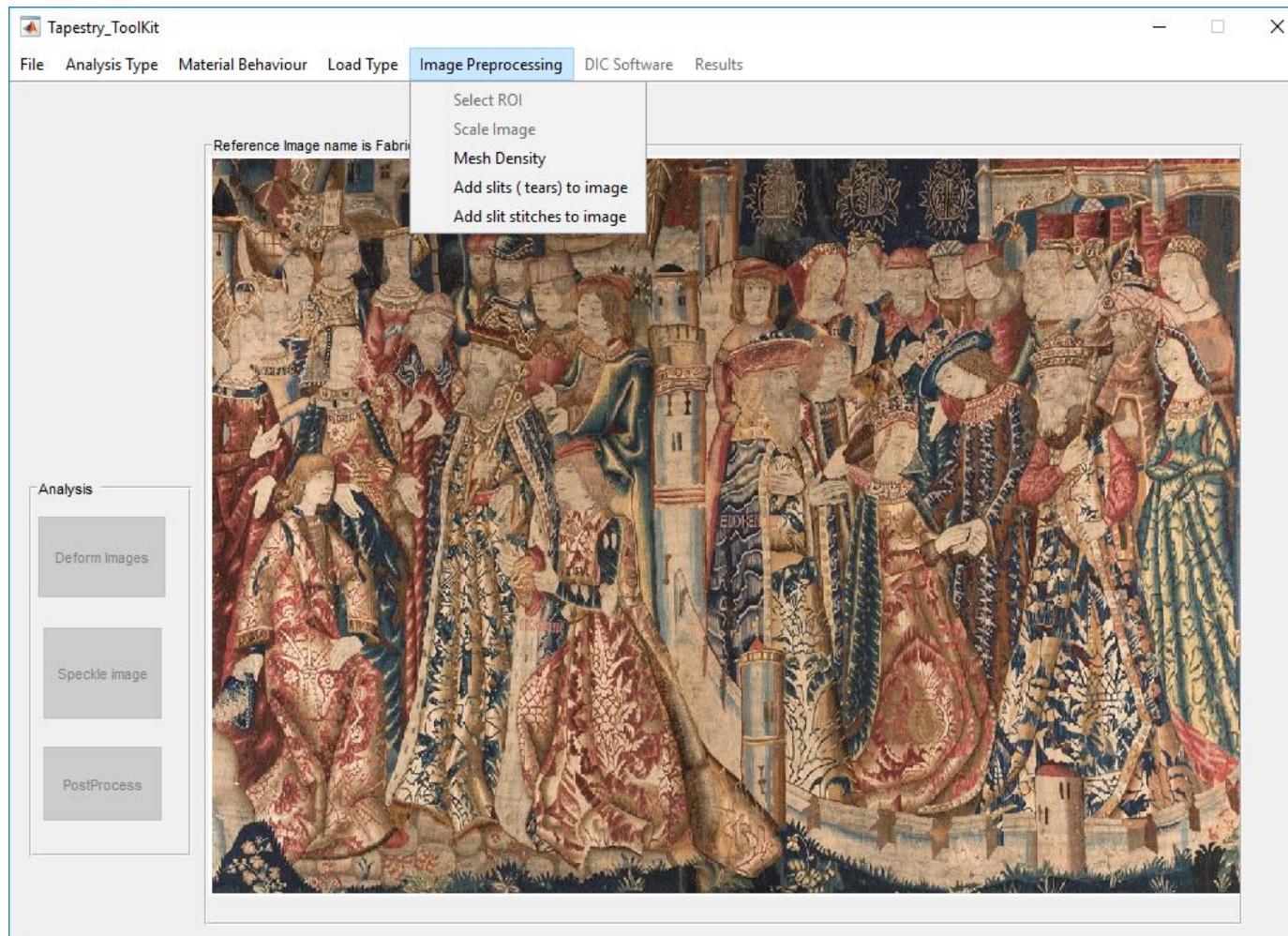
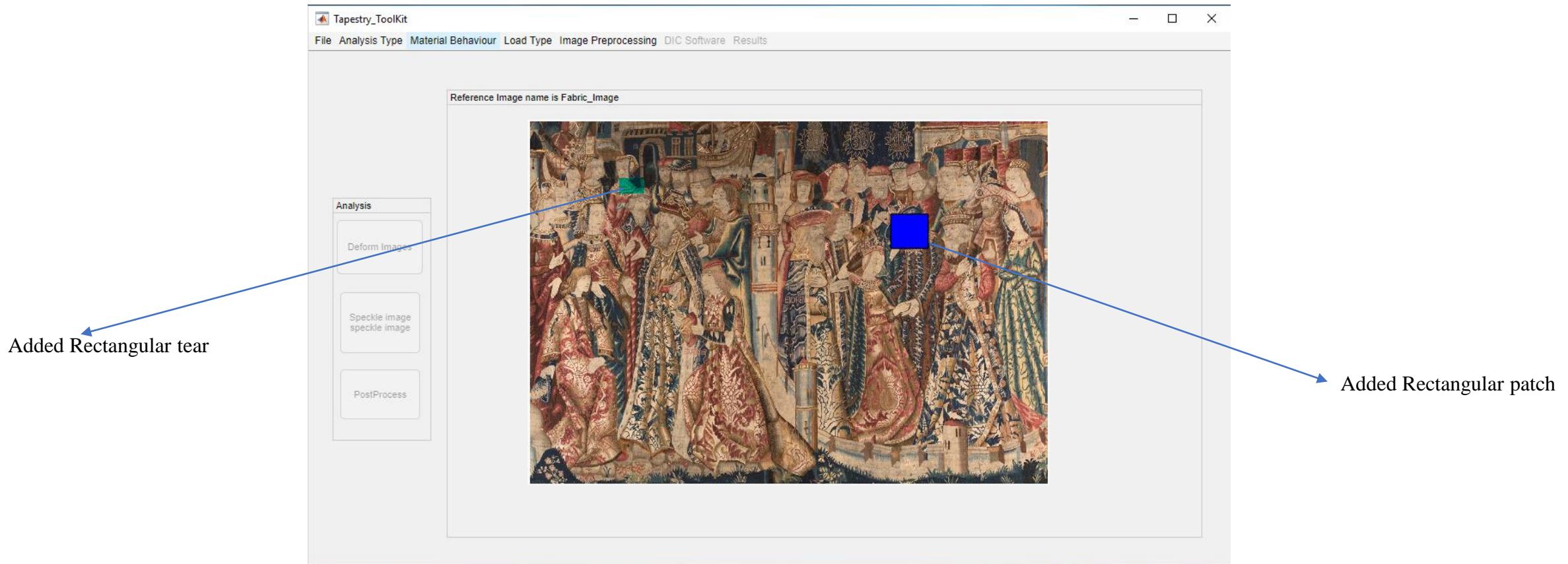


Figure 6

- The **Mesh Density** value determines how refined or coarse the finite element model is and must be a positive value. In the software, the number of elements in the finite element model is related to the number of pixels in the image through the mesh density value. It is the number of pixels per length of the 2D rectangular element. If the mesh density is 1, it means, the number of elements in the finite element model will be equal to the number of pixels in the image. If mesh density is greater than 1, the number of elements will be much less than the number of pixels. If the mesh density value is less than 1, it will increase the number of elements by 1 divided by the mesh density value. For example, if mesh density value is 0.5, the number of elements will be twice the number of pixels. The default and recommended value is 3. But higher values (10-20) are recommended for fast analysis time and if the inbuilt FEA is used.
- Sometimes, one may want to increase/decrease the reference image size due to resolution requirement or to zoom into a specific region of interest. The **Scale Image** value is the magnification factor to do this. If the value of the scale image is 2, the image size will be doubled. If it is 0.5, the image size will be reduced by 2. If it is 1, there is no resizing of the image. The default value is 1.
- The **Select ROI** submenu prompts the user to confirm if the whole reference image will be used to generate the deformed images or a specific region of interest is required. If the whole reference image is needed, click Yes. If a ROI is required from the reference image, select No. Then using the mouse draw a rectangle on the image making sure that your ROI is inside the rectangle. Double click on the rectangle to finish the selection.

Info box 2

- Adding tears and patches in the reference image
- The software can be used to model damage around tears or estimate the impact of slit patching on the tapestry structural integrity. To add tears or patches in the reference image, from the **Image Preprocessing** menu, click on the **Add slits (tears) to image** for tears or the **Add Slit stitches to image** for patches. Then enter the number of tears or patches as required. Use the pointer that appears to select (by clicking) the top and bottom corner locations of the tears or patches for a rectangular patch or tears. For line tears, use the pointer to click at the end points of the line location on the image. For more than one tears or patches, select the locations of the tears or patches as required. If you have added a patch in the image, you will be prompted to add the properties of the material used for the patching. This can be the same as the original tapestry materials or different material.



- Once the **Mesh Density** and **Scale Image** values have been entered and **ROI** selected, the **Deform Images** button becomes active (see Figure 7)!

Step 9. Click on **Deform Images** button to start the analysis (see information box 3 for more details)

Step 10. Enter the number of required deformed images(see information box 3 for details), click OK and wait for the analysis to complete

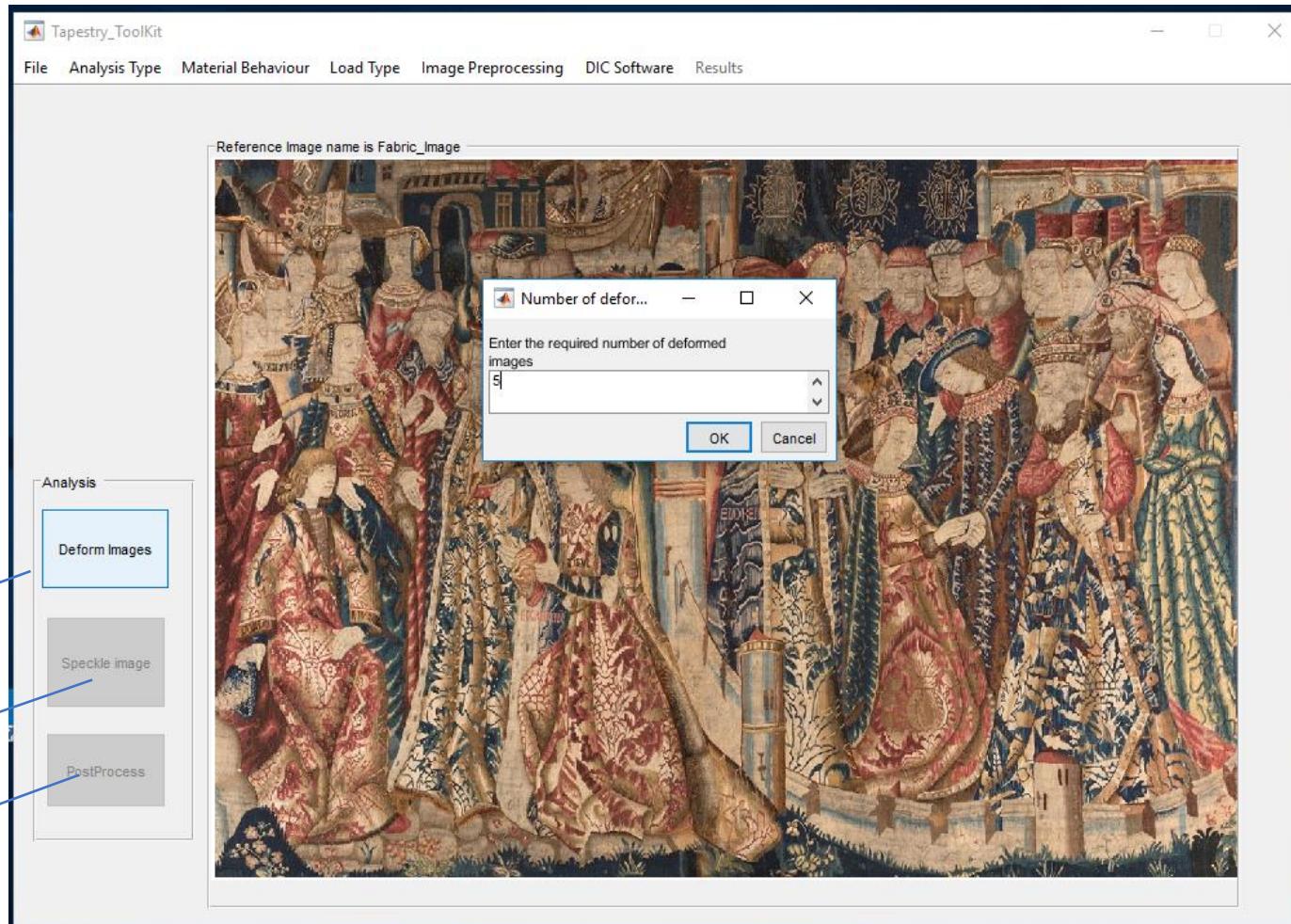


Figure 7

When you click on the **Deform Images** button:

1. You will be prompted to confirm if you want view the generated finite element mesh plotted on the reference image. If yes, select Yes else select No.
2. You will be prompted to confirm if you are using Abaqus software for the finite element analysis (FEA). If you are using Abaqus for the FEA, please see next page for options.
3. If you are using the in-built FEA function, select No and continue
4. If your loading is not time dependent, you will be prompted to enter the required number of deformed images. This depends on the user to specify the number of deformed images that the software will produce. It is similar to the number of images you would capture during deformation of the specimen in the DIC experiment. In the Software, the deformation magnitude will be divided into the number of images and gradually deform the images according to the deformation level.

Info box 3

Using Abaqus with the Software

- If you have selected to use Abaqus for FEA analysis, you have two options
 1. If you have Abaqus installed in the same PC as the Software and want the Abaqus simulation to run in the background
 - Select Yes to the question “Do you want to use Abaqus for the FEA” and select No to the question “Do you want to use external ABAQUS odb file for this analysis?”
 2. You can import Abaqus output data file (odb).
 - If this is the case, select Yes to the question “Do you want to use external ABAQUS odb file for this analysis?” and follow the steps below:
 - If you are running the ABAQUS FEA simulation on the same PC where the Toolkit is installed, select Yes to the prompt “**Is the external ABAQUS version same as in your PC?**”
 - If the ABAQUS software for the FEA simulation is on another PC, check the version of that ABAQUS:
 - If the version of that ABAQUS is the same as the version where the Toolkit is installed, select Yes as above.
 - If the versions of the ABAQUS are different (i.e. the version of ABAQUS in your PC and the version through which the odb file is produced), select No to the prompt “**Is the external ABAQUS version same as in your PC?**”
 - You will be informed to copy the Software (Tapestry_ToolKit) generated input text files (elements.txt, nodes .txt, TAPS_FEM.inp, El_Sets .txt and ND_Sets .txt) located in the **ABAQUS_SIMULATIONS** folder to your ABAQUS working directory (folder).
 - Then import the files (from ABAQUS Menu-File-Import- Model) and use them for the FEA simulation in ABAQUS. Edit and apply the loads, boundary conditions and material properties.
- ❖ Before submitting the ABAQUS job:
- Name the job as **JOB_TAPS**, if you are using the ABAQUS software on the same PC as the Toolkit or if the ABAQUS software from the other PC is of the same version as the ABAQUS on the PC with the ToolKit!
 - Name the job as **JOB_Ext** if the versions are different!
 - At the completion of the analysis, copy the odb file into the **ABAQUS_SIMULATIONS** folder and click OK to continue

Preparing for Postprocess

1. On completion of the FEA analysis, the software will inform you of this! Click OK to continue.
2. The deformed tapestry images will be generated, the software will inform you of this!
3. You will be prompted to confirm if you want to compare the Fabric (Tapestry) image with a speckle image (see information box 4 for more details).
4. If Yes, click the Speckle Image button (See Figure 7). Select your speckle image and press OK.
5. The software will generate a deformed speckle image.
6. The deformed speckle images will be saved in a folder named **Speckle_Images**, while the deformed fabric(tapestry) images will be saved in a folder called **Fabric_Images**.
7. The two folders containing the deformed images are located in your working directory (see Step 1)
8. If you do not wish to compare your analysis with a speckle image, only one folder containing the deformed fabric images will be created and saved in a folder called **Fabric_Images** in your working directory.
9. After generating the deformed images, the software will inform you to use the deformed images in the deformed image folder to perform DIC analysis.
10. You can locate the deformed image folder(s) by going to the **File** menu and selecting the **Deformed Image Folder** (See Figure 2) or by double clicking on your working directory.

Because the DIC analysis result is expected to be more accurate if the image has well distinct features such as a quality speckle patterned image.

One can use a speckle image or another fabric image to compare the accuracy of the DIC analysis based on the inherent fabric(tapestry) image. This helps to determine how the tapestry image inherent features affect the DIC accuracy

Perform DIC Analysis using Vic 2d following the steps in the next pages

- Once the deformed Images have been generated and you want to use Vic 2D software to perform the DIC analysis: follow these steps:
 - Open the Vic 2D software. The interface at start-up will look as shown in the Figure 8
 - If Vic 2D software is located on the same machine (PC) that you are running the software, there is no need to copy the deformed image folder(s). If the Vic-2D, is on another machine, copy the deformed image folders to that PC.

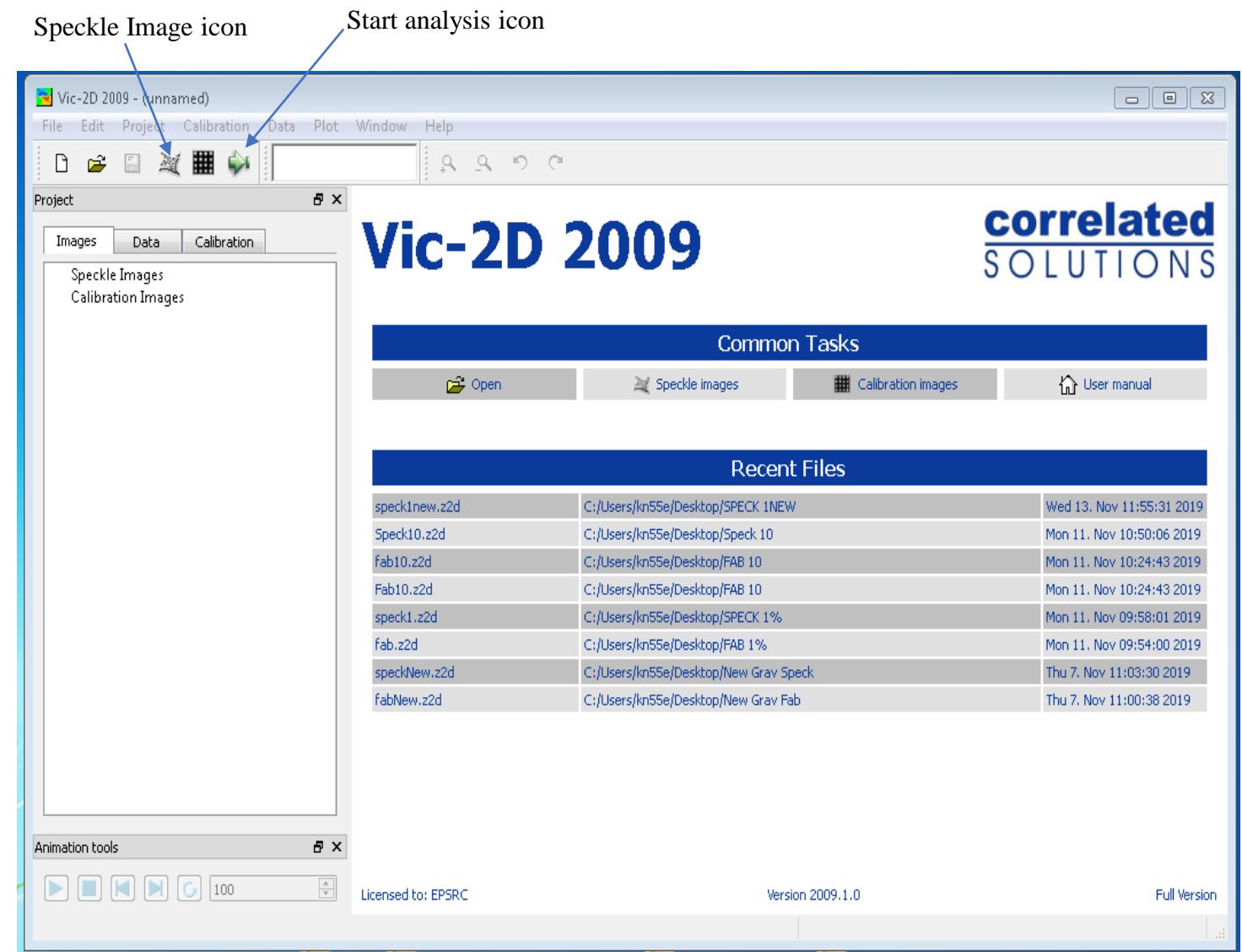


Figure 8

3. If you are comparing the tapestry image with a speckle pattern image, the DIC analysis should be performed separately for each image type. Add images to Vic software by clicking on the Speckle Image icon (see Figure 9). Locate the folder for image type and select all images in the folder (by pressing control and A buttons on the computer keyboard at the same time) and then click Open. The images are now in the Vic-2D software as shown in the Figure 9.

Please note the additional icons that appeared after opening the images in Vic 2D. Most important of these icons are labelled as shown in the Figure 9.

The Vic 2D software automatically predicts suitable Subset and Step size values as shown in the Figure 9. However, we can change them to our desired values after selecting the region of interest (ROI)

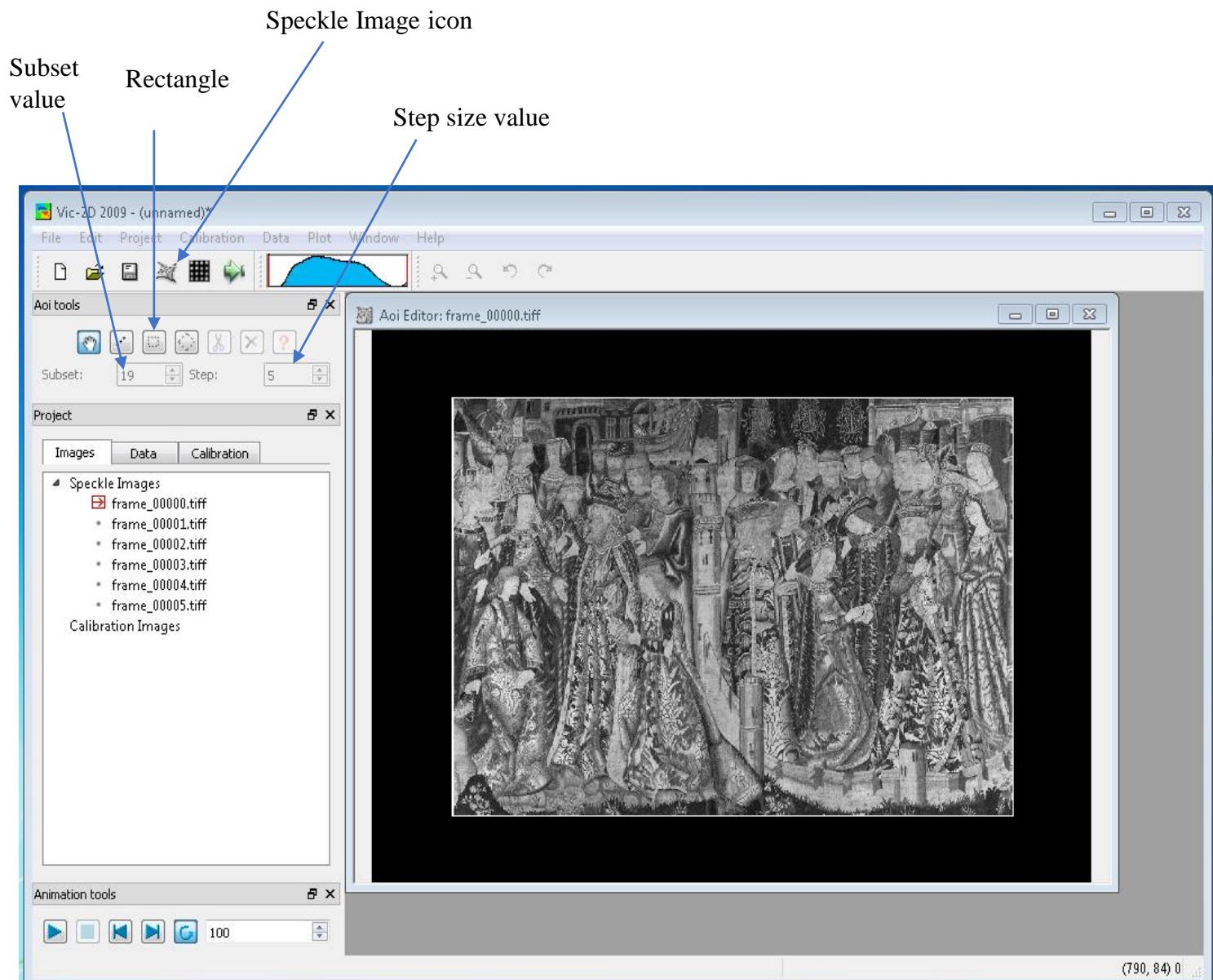
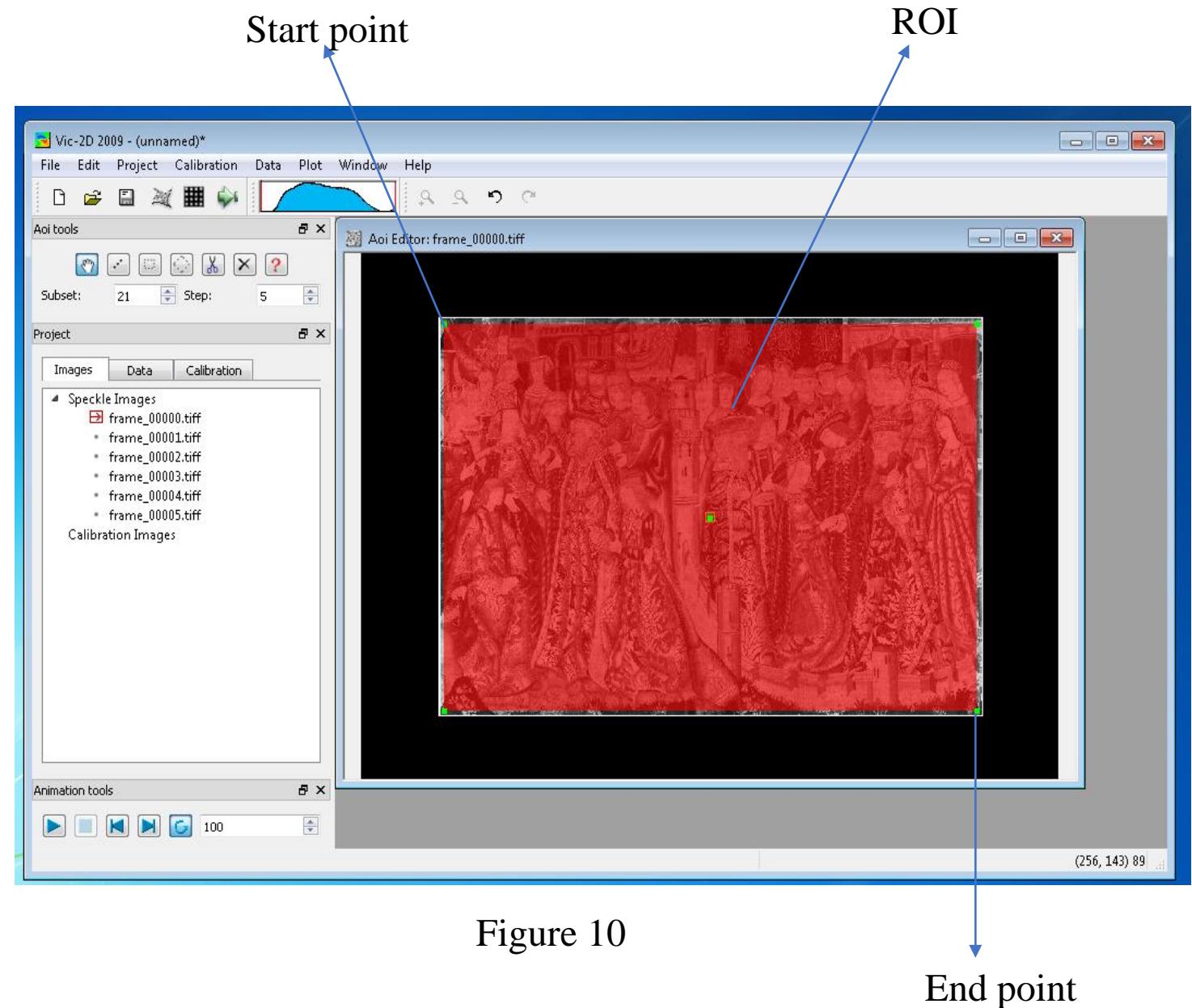


Figure 9

4. Use the Rectangle icon (see Figure 9) to select the region of interest (ROI) as shown in the Figure 10.

- To draw the ROI, click on the rectangle icon, place the cursor on the image and click at a start point as shown in the Figure 10. Move the cursor to the end point as shown in the Figure 10 and click on the image to complete the task.

5. Enter the values of the Subset and Step size in the text field as shown in the Figure 10



6. Run the analysis by first clicking on the Start analysis icon to open the Vic-2D Analysis settings box.

In the Vic-2D Analysis settings box, click on the Options button to select desired options such as Exhaustive search, low-pass filter images and Incremental correlation. For more accurate result, check all the three options and then click on the Run button as shown in the Figure 11.

Then wait for the analysis to run!

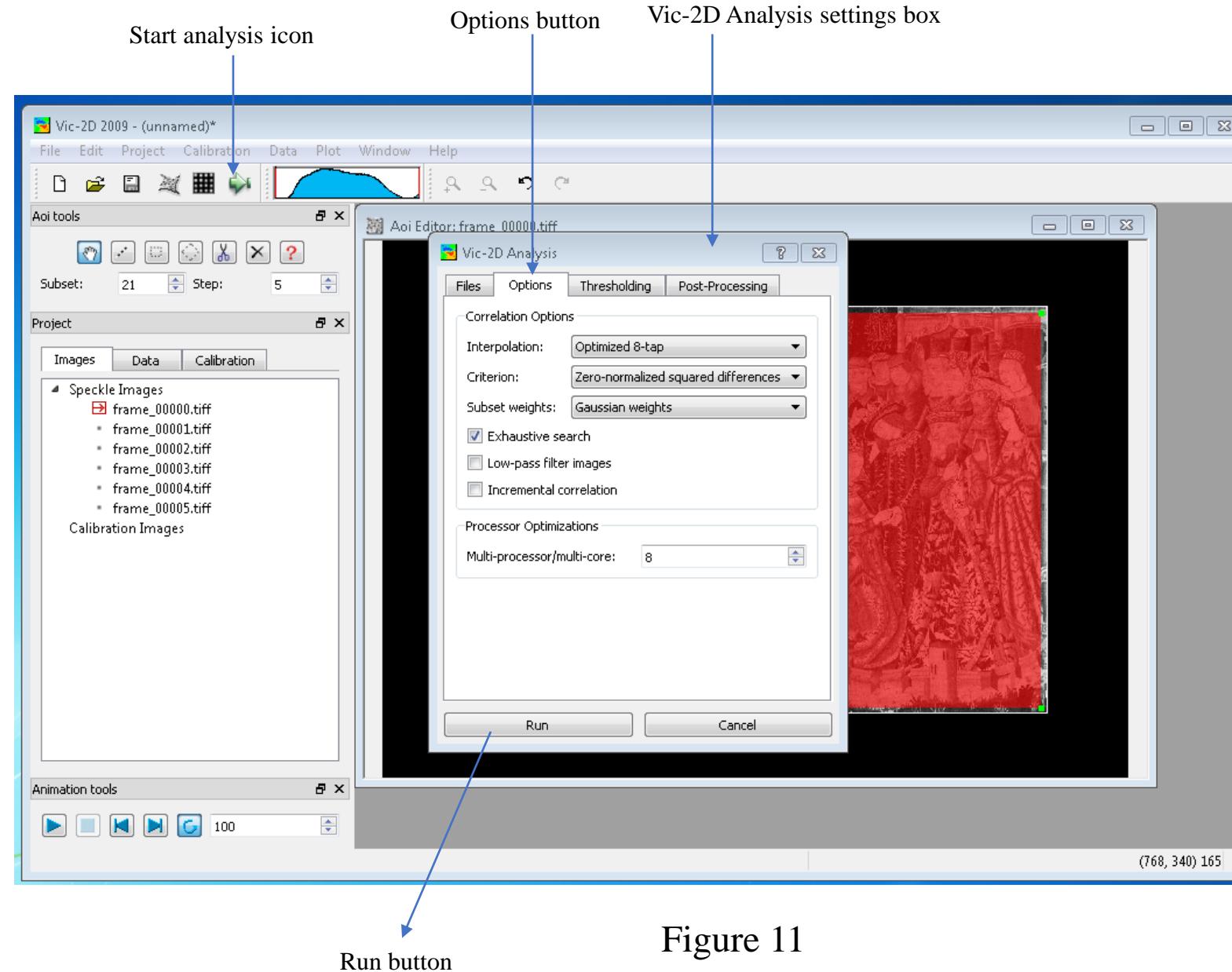


Figure 11

- Once the Run button has been pressed, the Analysis progress monitor appears as shown in the Figure 12.
- Vic-2D does not confirm the completion of the analysis, however, once the Close button becomes active (see Figure 12), it signifies the completion of the analysis.

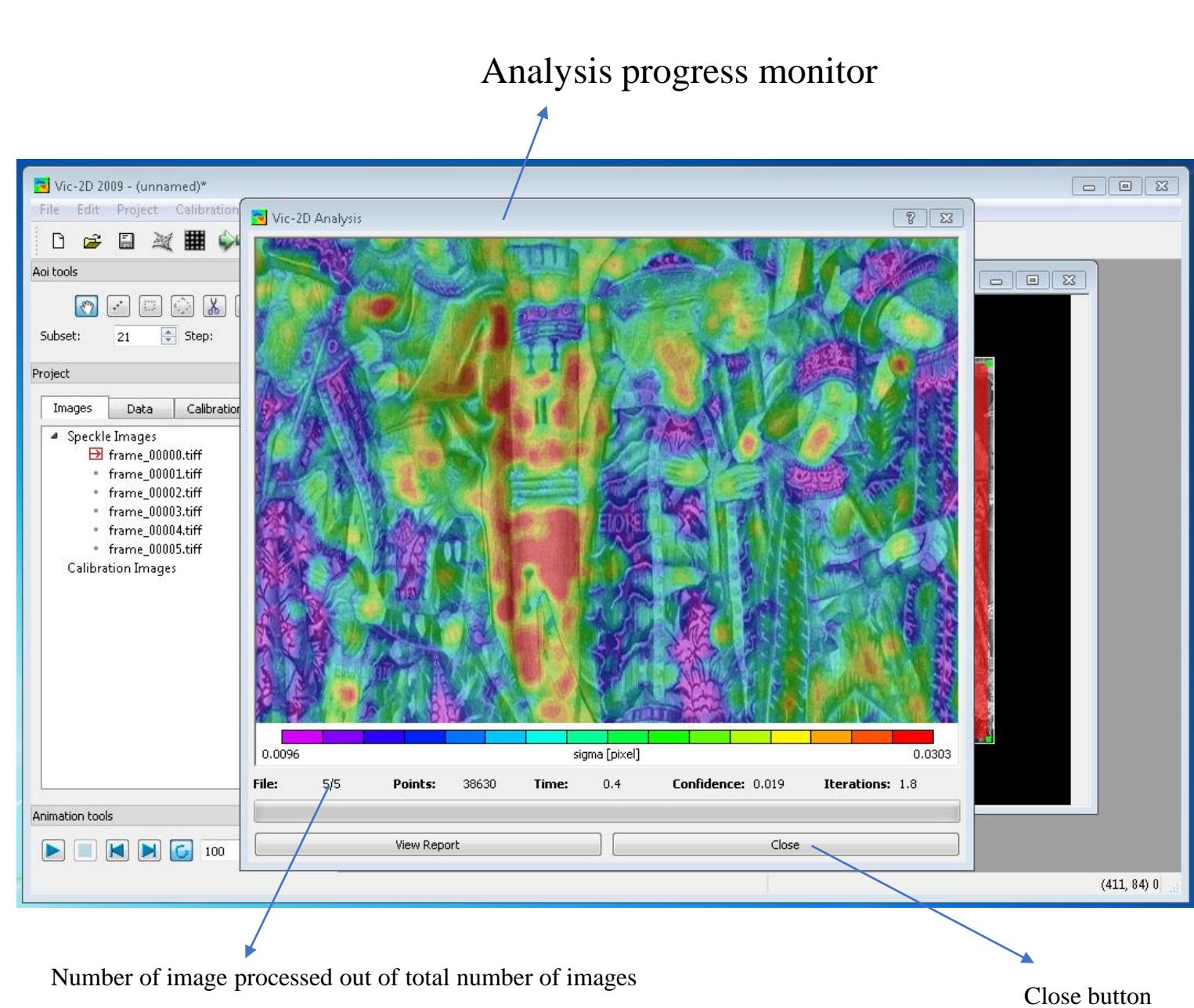


Figure 12

7. Compute the Hencky Strain. The Abaqus software computes Logarithmic strain (for large deformation) which is equivalent to Hencky strain.

- Vic 2D will compute strain in the Lagrange form. We need to convert the Lagrange to Hencky to compare like for like.
- To do this, first click on **Data** menu (see Figure 13), scroll to **Postprocessing options** and select **Calculate strain**. The **Strain Computation box** appears as shown in the Figure 13.
- Press the **Tensor Type** popup menu and select **Hencky (logarithmic)**
- You can change the **Filter size** to a value smaller or higher than the default value of 15. The Filter size is equivalent to strain window and affects the gradient of the strain distribution.
- Press **Start** button to compute the Hencky strain.
- Wait for the analysis to perform and then click close on the progress monitor

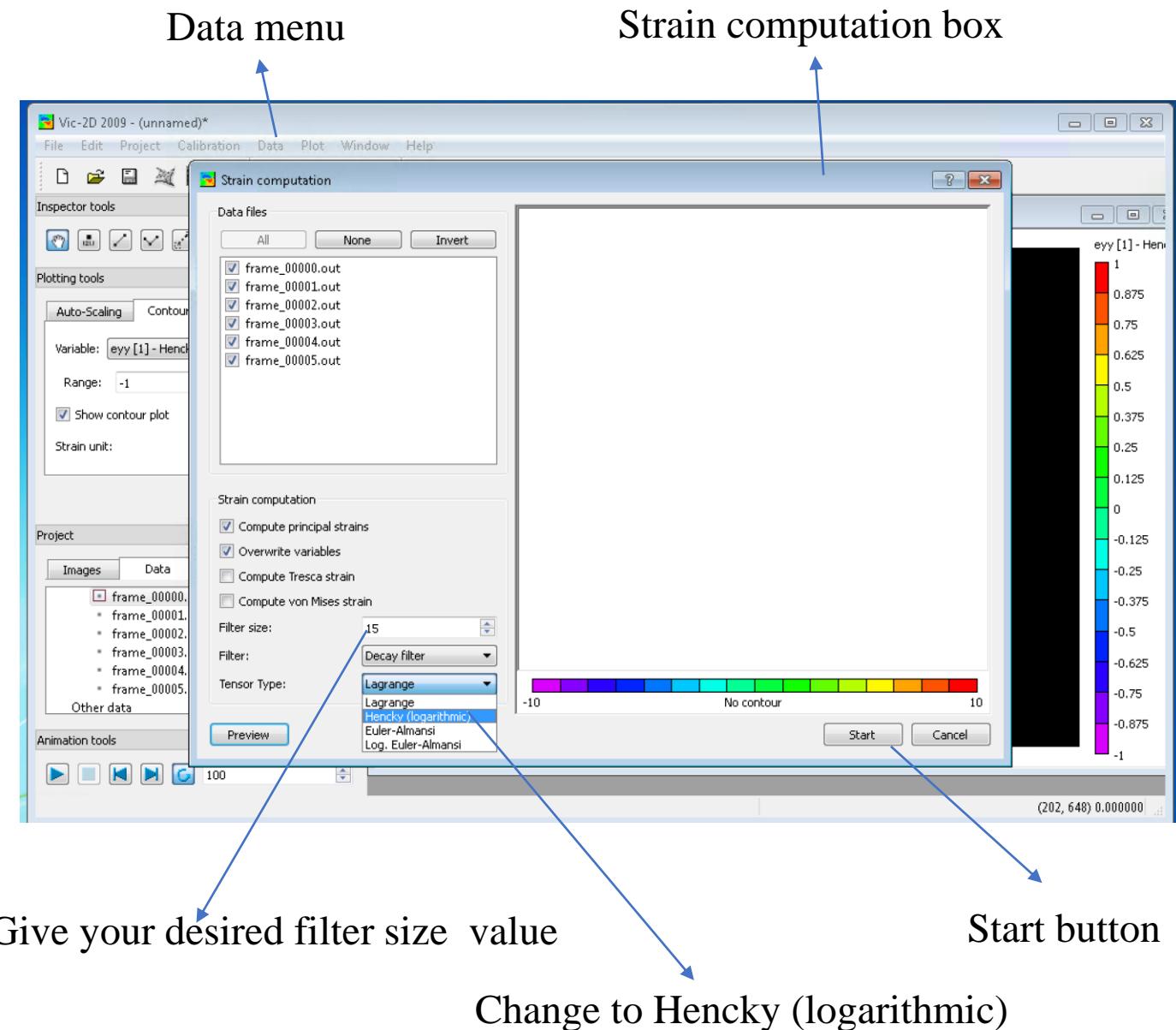


Figure 13

8. View and export result files.

To view the results first click on the Data menu under Project panel (see Figure 14). Then click on any of the file under the Current data. Right hand mouse click and select **Display** from the options.

The Vic-2D interface will change to Figure 15 in the next page

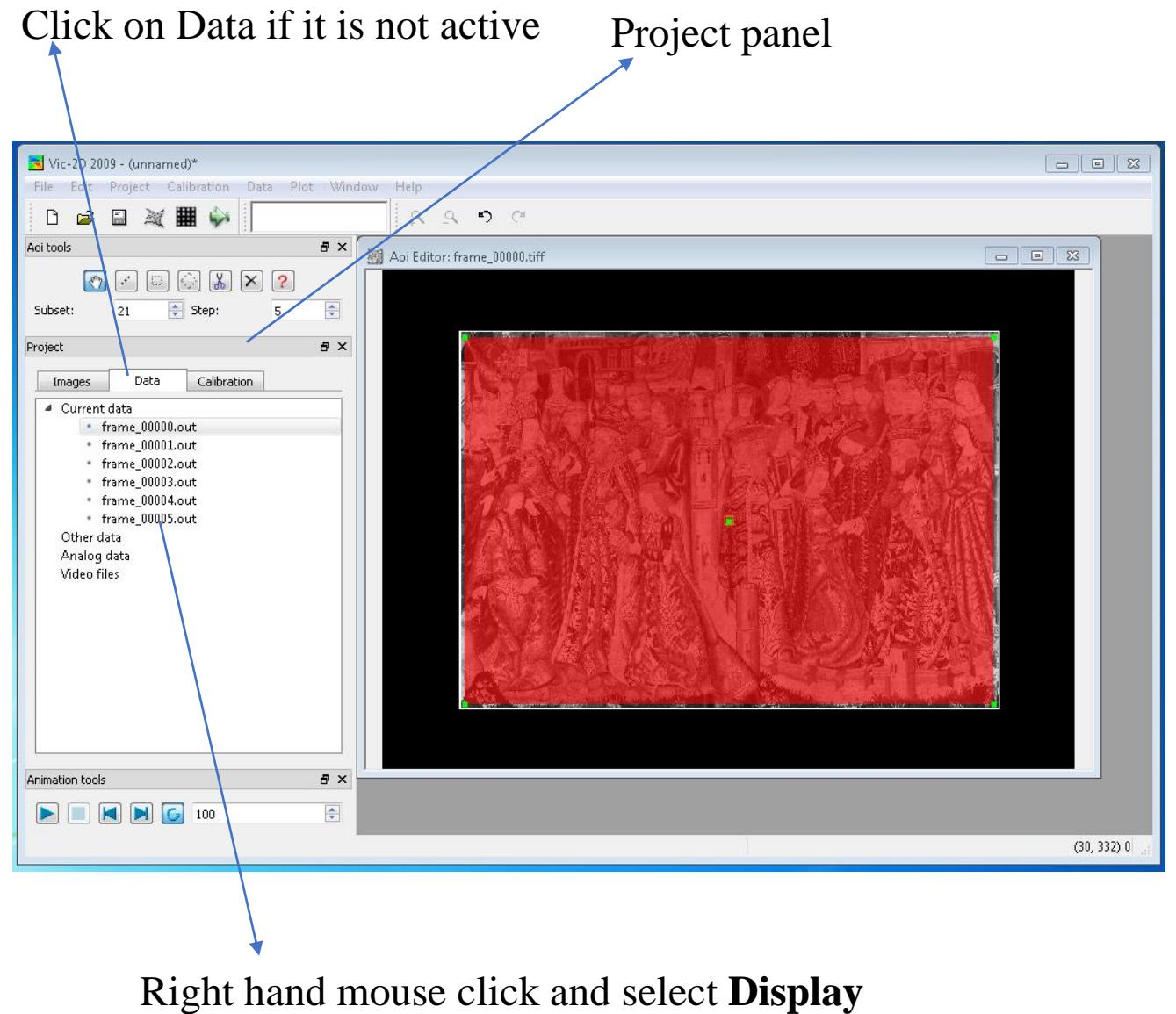
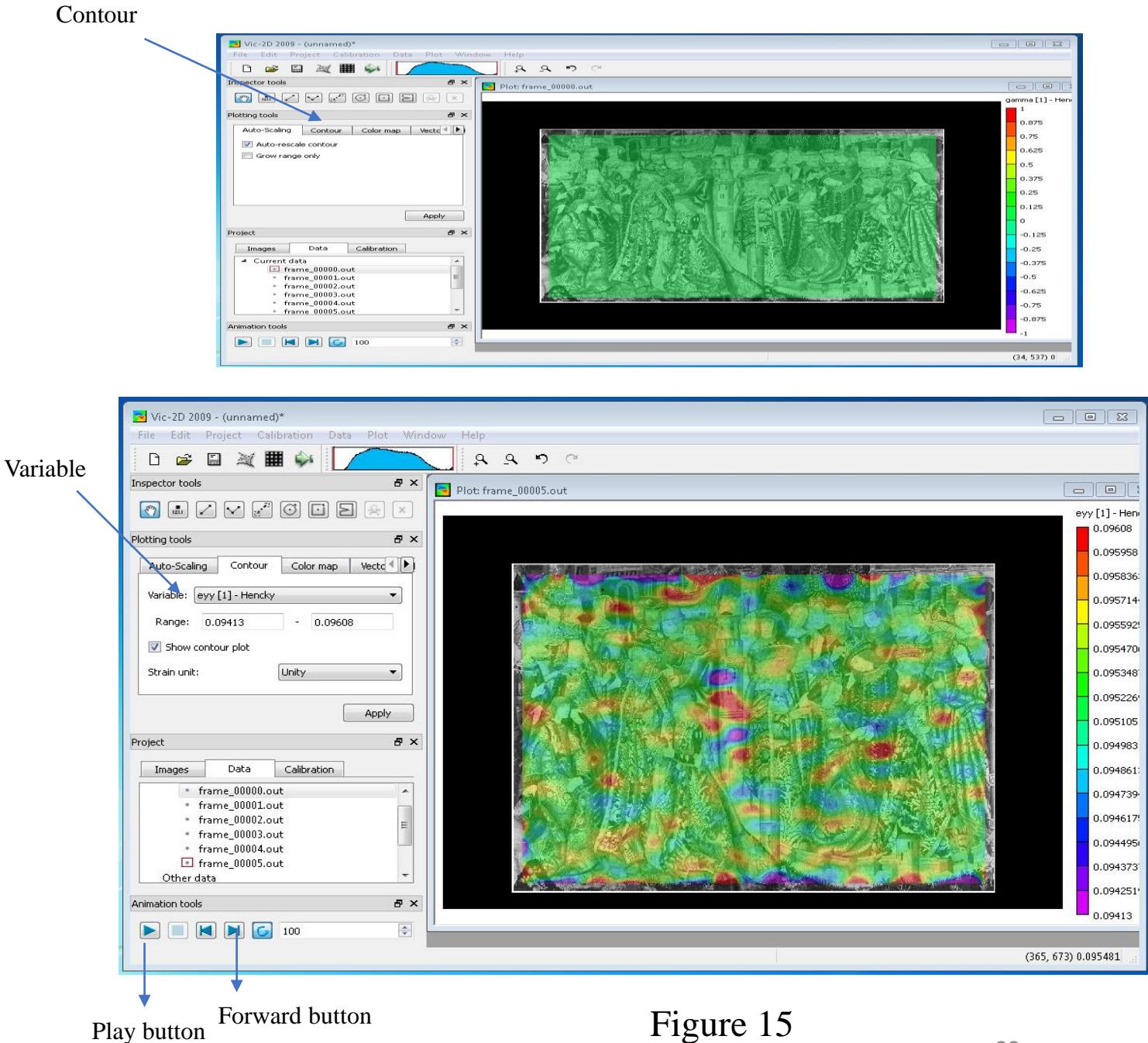


Figure 14

Click on Contour as shown in the Figure 15. Under Variable select result component desired.

Use the Play button, forward or backward buttons to navigate to results of other images



To export results in MATLAB format click on **Data** menu, and then select **Export data** as shown in the Figure 16.

The **Export data** box appears as shown in the next page

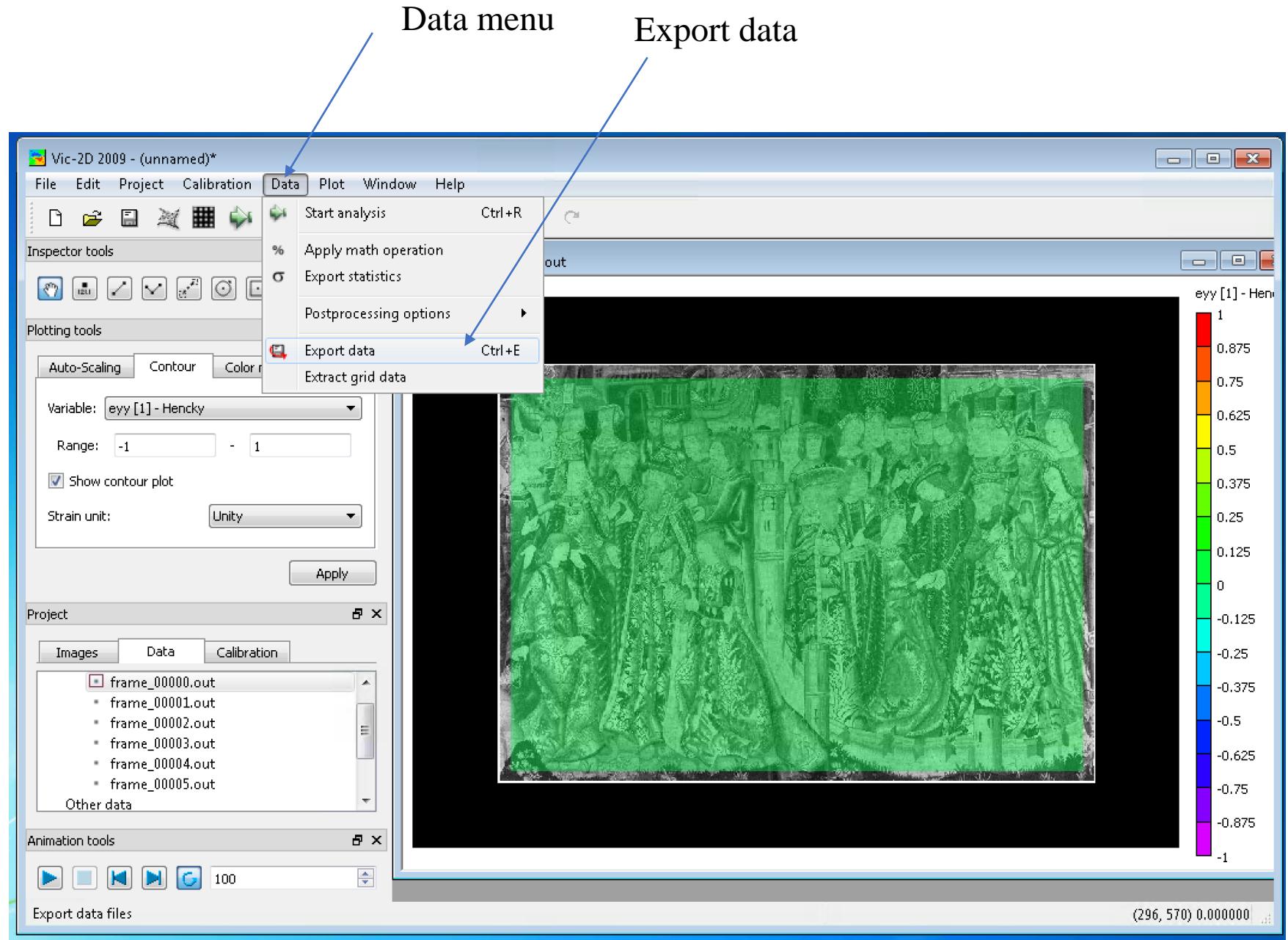


Figure 16

- Select **Matlab format v4** as shown in the Figure 17
- Click **Export**
- Now the results in MATLAB format are in the **Deformed image folder** as shown in the next page.
- If you are comparing the results with a speckle image, repeat the DIC analysis with the deformed speckle images and export the results for the speckle image following the DIC analysis steps outlined so far.

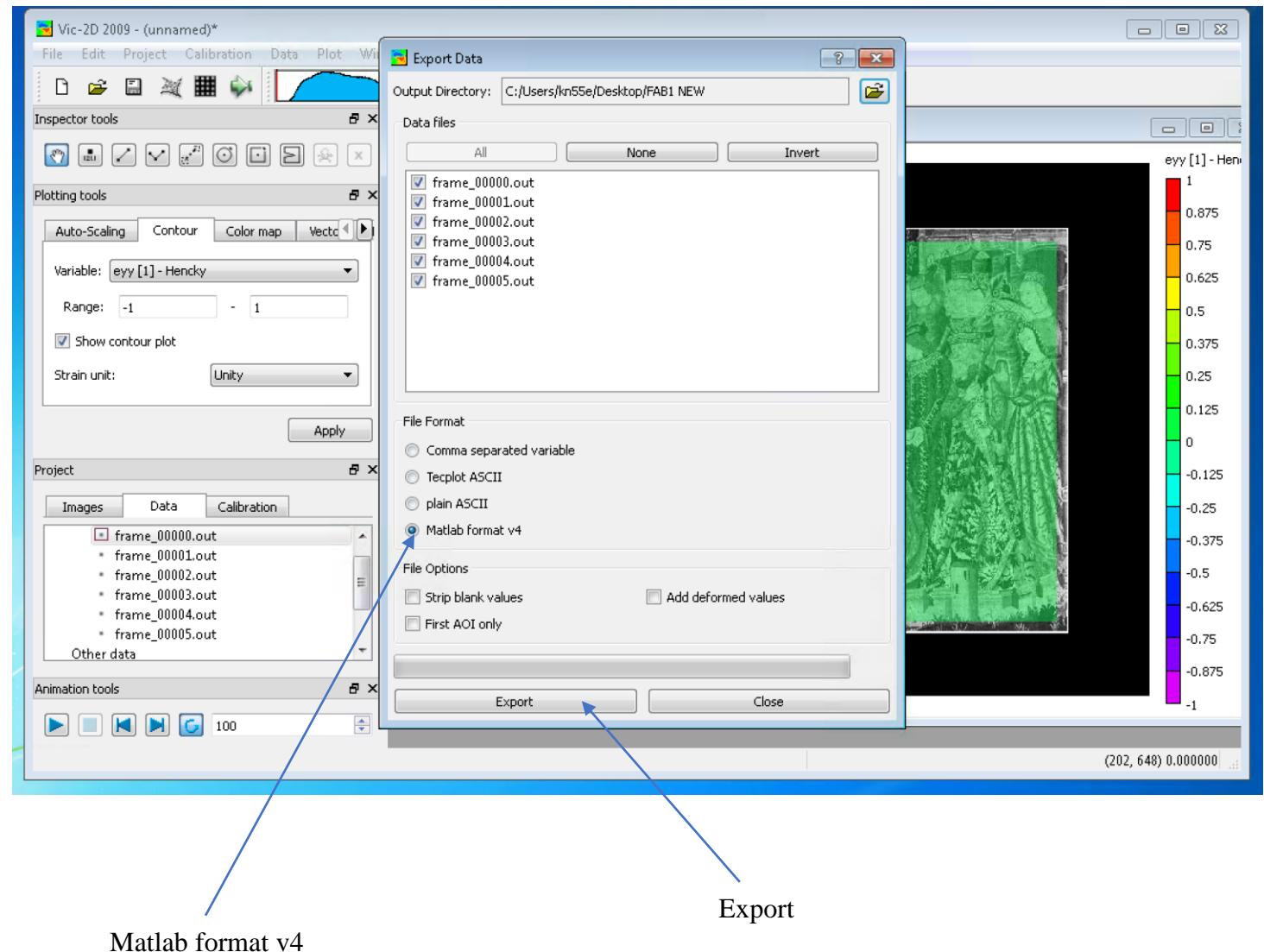
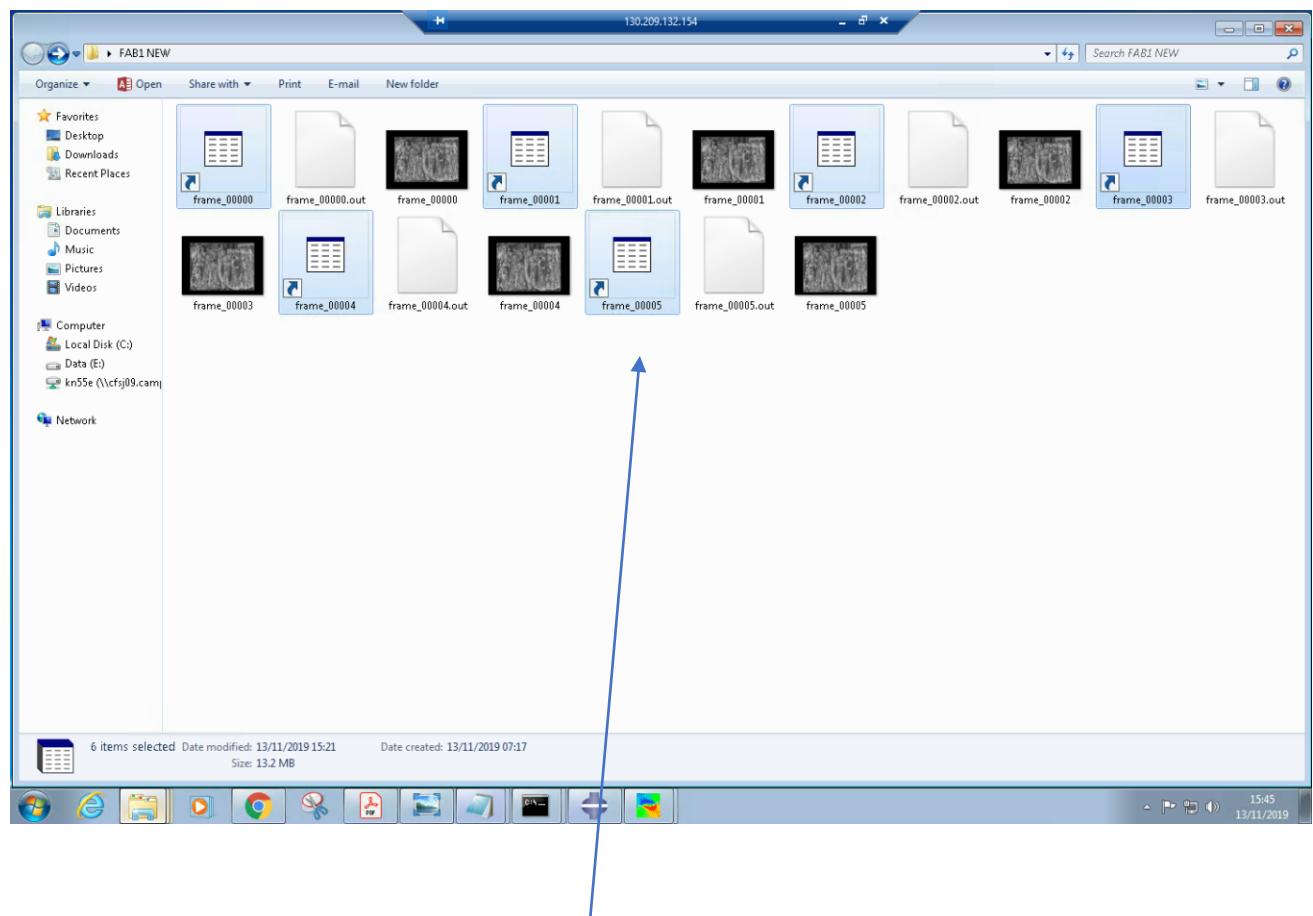


Figure 17

- If Vic-2D software is on the same computer as the Tapestry_ToolKit software, there is no need to copy the DIC results (in matlab format) to the deformed image folder(s). Just proceed to PostProcess in the Tapestry_ToolKit software by clicking the PostProcess button to continue.
- However, if the Vic-2D is on another PC, copy the exported DIC results (in matlab format) to the respective deformed image folder in the PC with the Tapestry_ToolKit software and then click Postprocess button to continue



The selected files are the exported DIC results in Matlab format for fabric (tapestry) image type

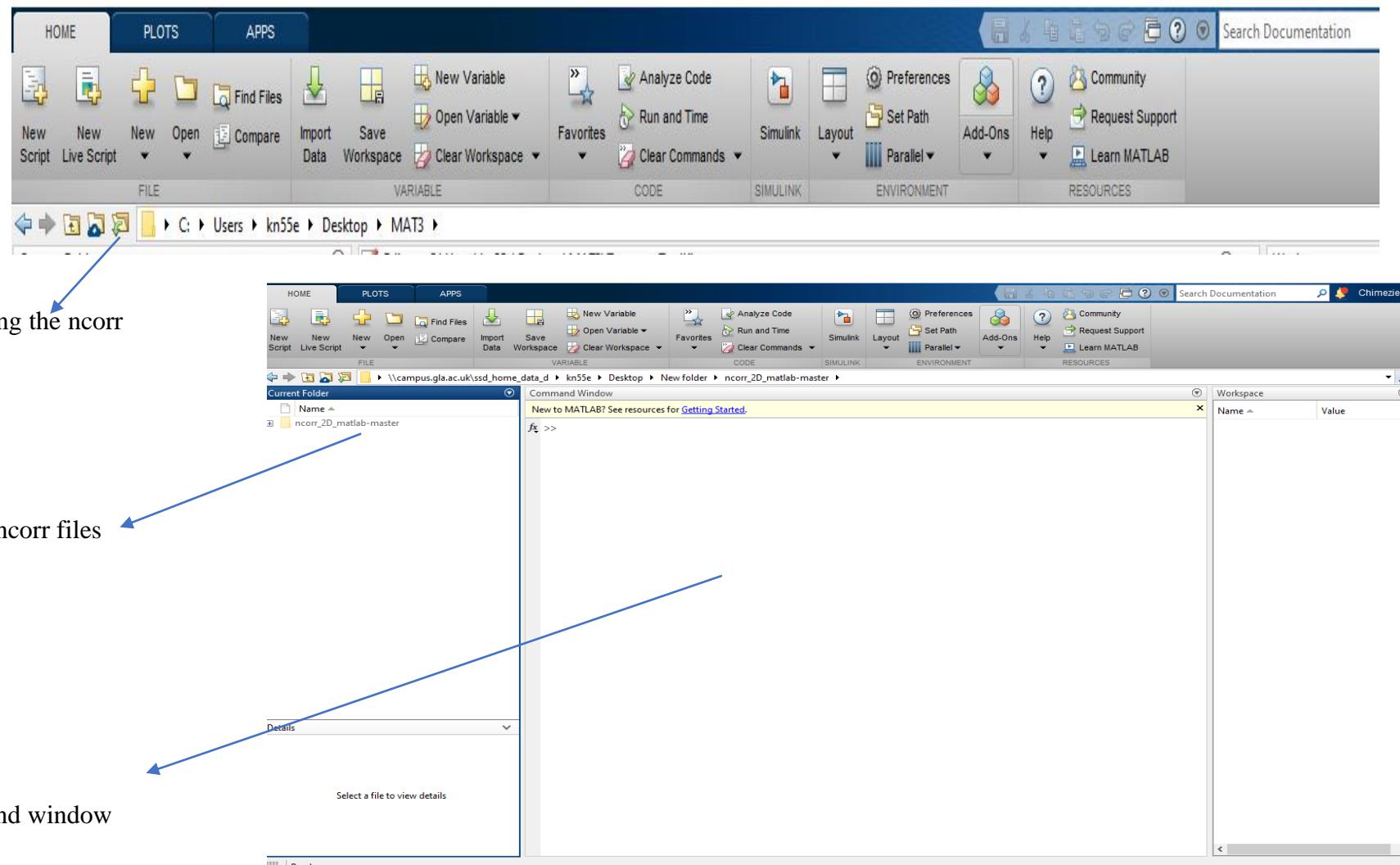
Figure 18

Perform DIC Analysis using Ncorr by following the steps in the next pages

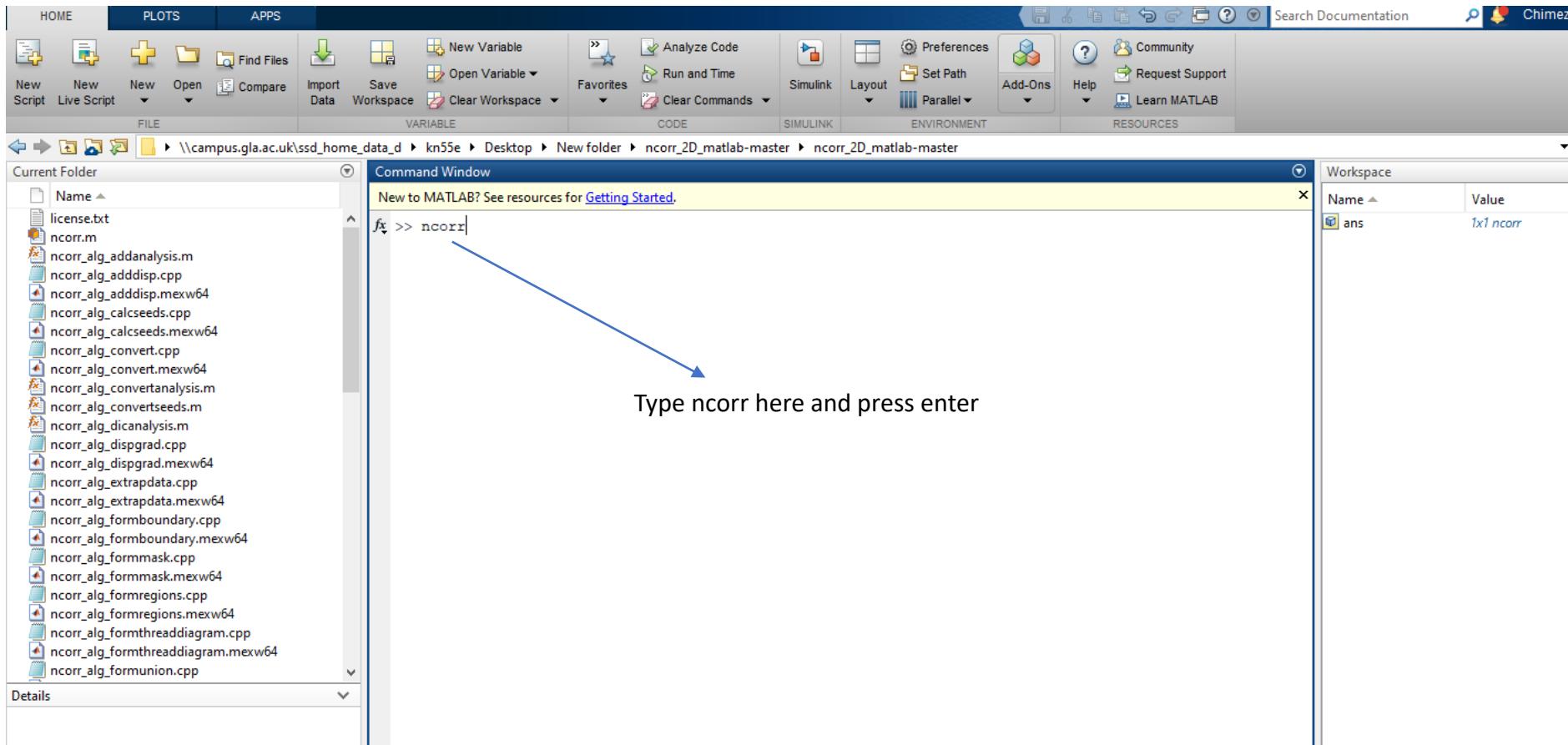
Ncorr: Download software, extract files, change MATLAB working directory and install ncorr

1. To use ncorr, you need a MATLAB software
2. Download Ncorr software from: www.ncorr.com/index.php/downloads: Under the **Program** section, click on []**ncorr-zip** link to download the files.
3. The files are stored in a zipped folder called **ncorr_2D_matlab-master.zip**.
4. Locate and copy the downloaded zipped folder to a directory (a location on your PC) that you have access.
5. Right hand mouse click on the zipped folder and select extract all to extract the files
6. A folder named **ncorr_2D_matlab-master** containing the files will be extracted in your chosen directory. You could change the folder name if you wish.

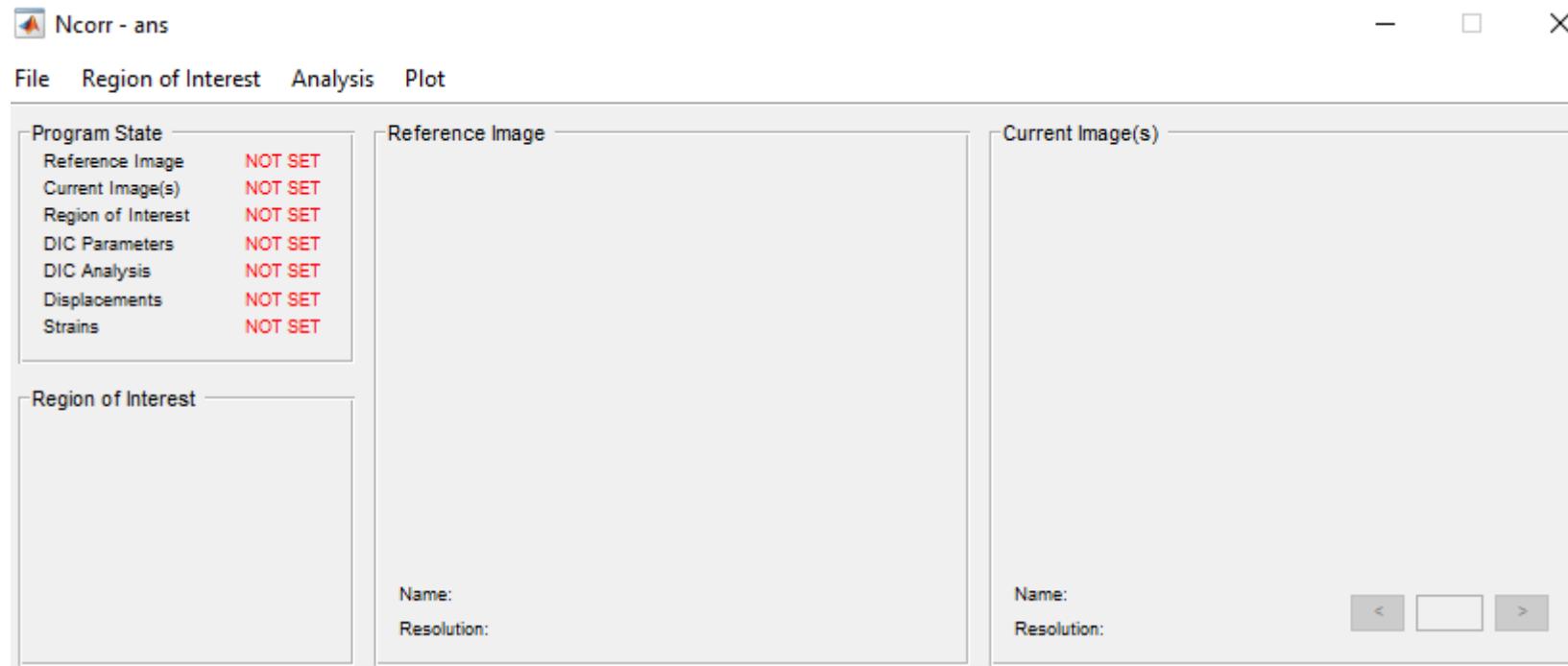
- Open MATLAB on your PC
- Change the working directory to be the folder containing the ncorr files as shown below



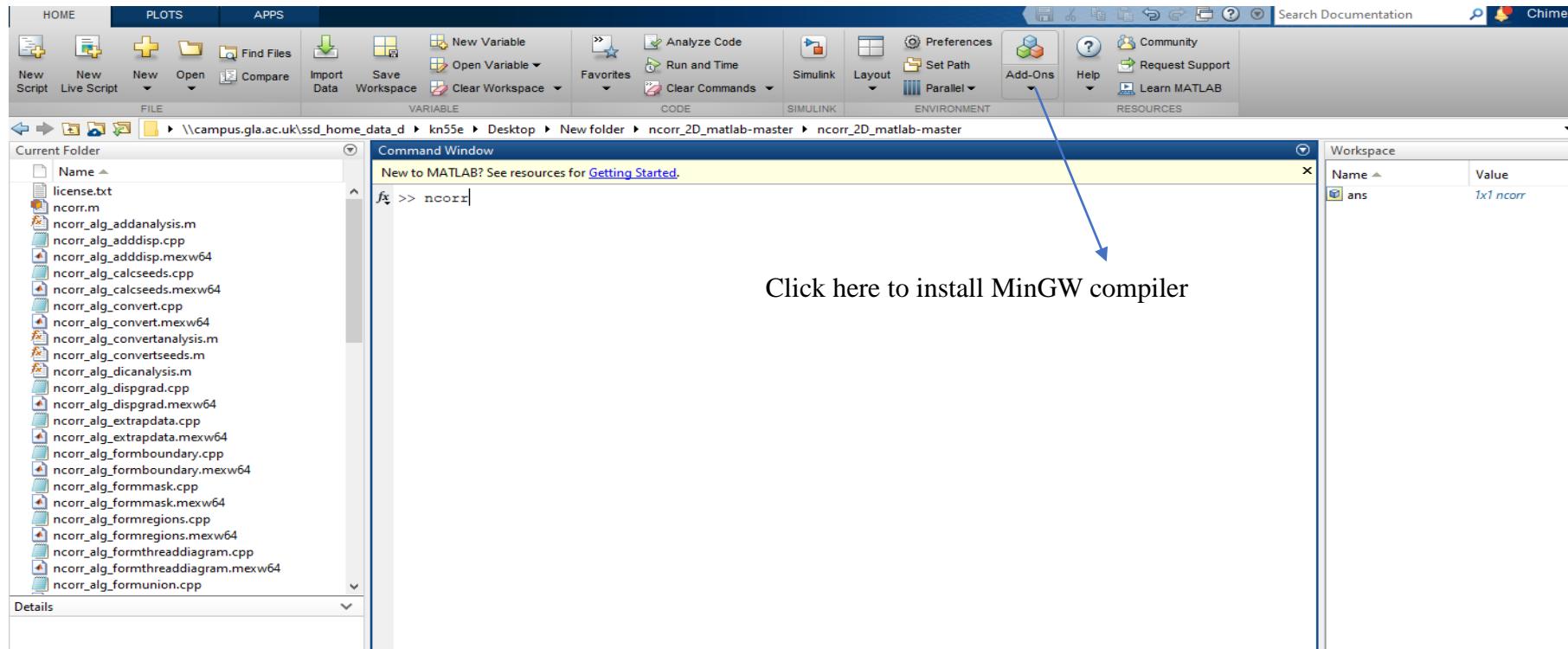
- From the MATLAB command window (see previous page) call ncorr by typing **ncorr** and then press enter as shown below



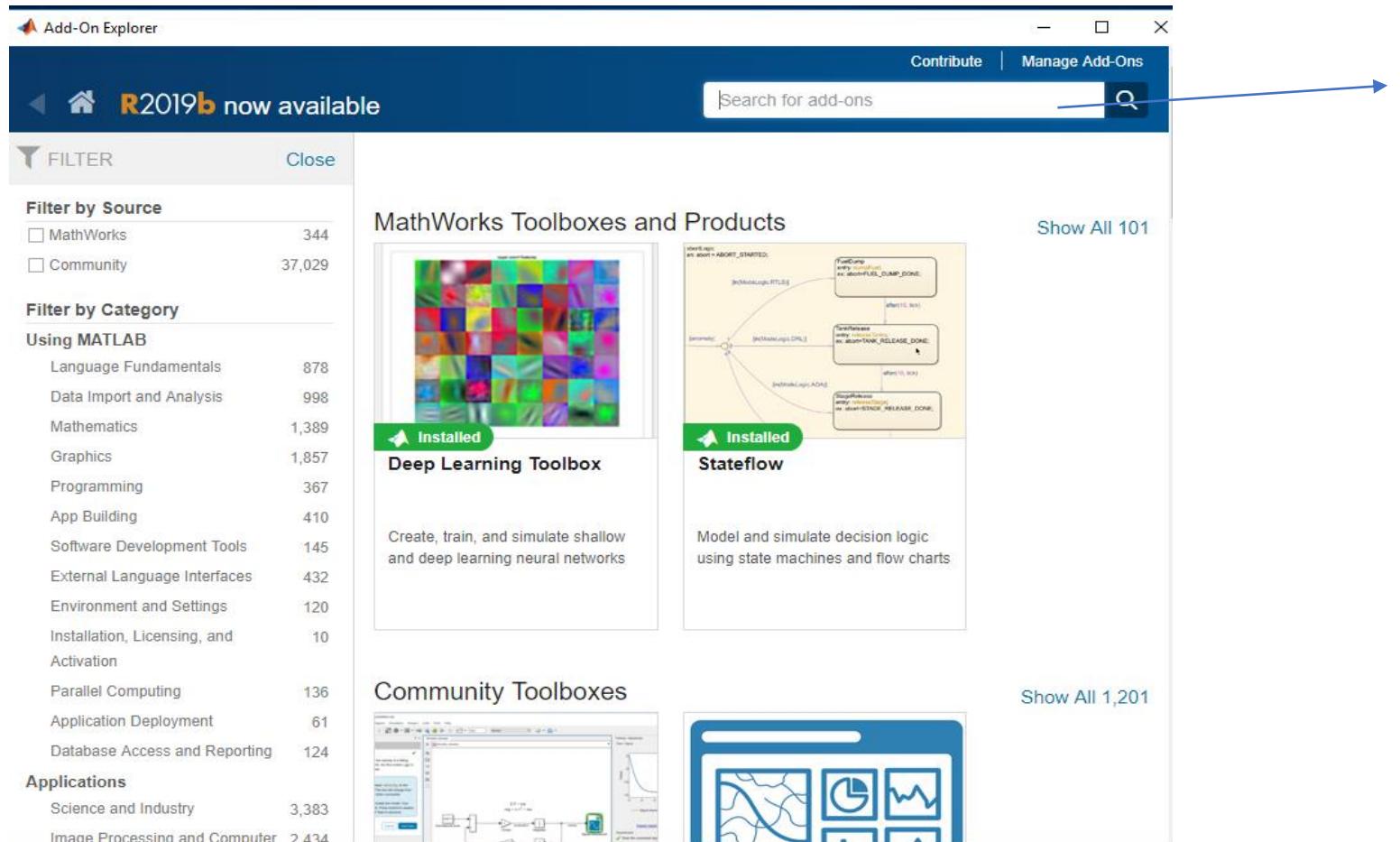
- The first time you call ncorr from your current working directory, it needs to compile the C++ files associated with the software.
- The C++ compiler MinGW 64 is needed for the compilation. After calling ncorr, a pop window appears, just click the **finish** button to continue. The C++ compilation will start and you need to wait for completion.
- After completion, the ncorr gui will appear and look as shown below.



- Compilation issues
- Most likely, your MATLAB does not have MinGW compiler. In this case the ncorr C++ files will not compile and MATLAB will give error/warning messages!
- You need to install MinGW compiler. To do this, click on the **Add-ons** button and wait for the Add-ons explorer to open

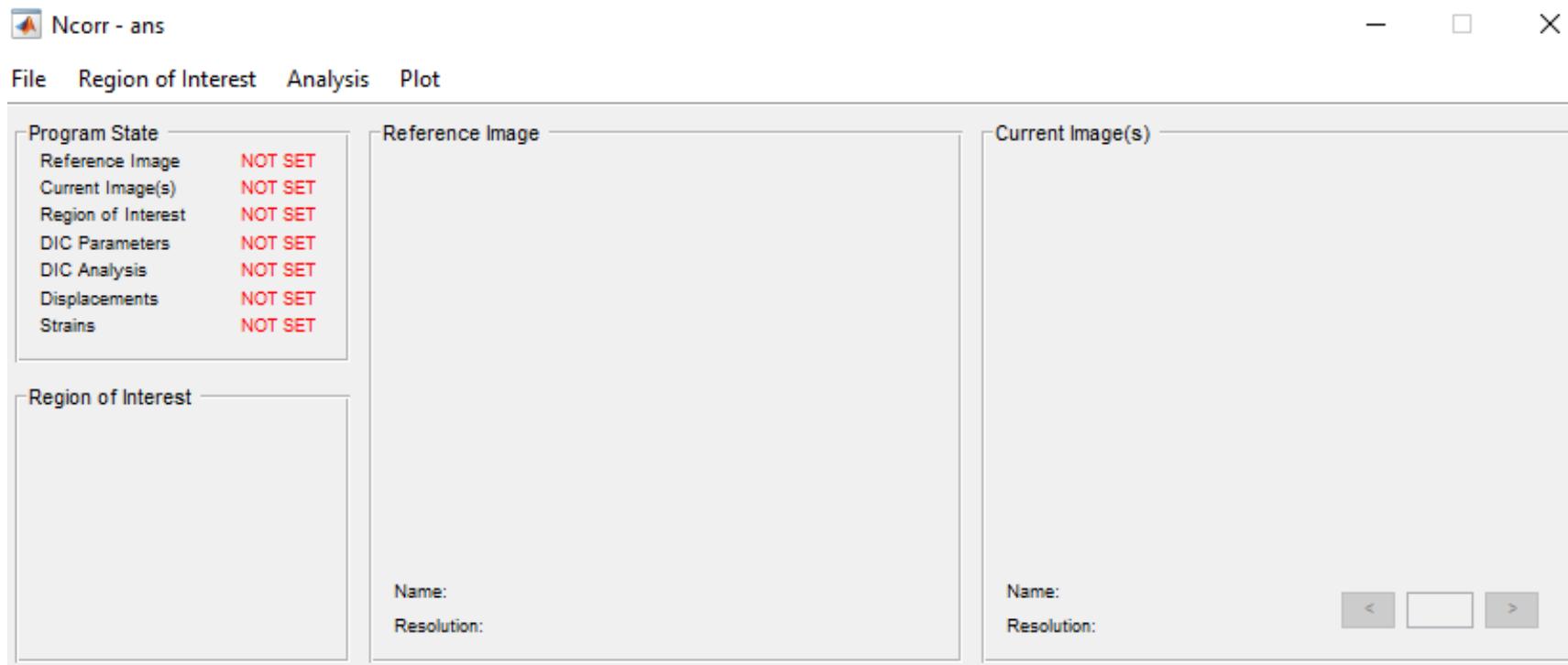


- In the Add-ons explorer type MinGW in the search for add-ons bar
- You will see MinGW-w64, click on install and wait for the installation to complete!.
- After installing the MinGW compiler, call ncorr again from the MATLAB command window to install ncorr as described previously.



Type MinGW here, find MinGW-w64 and click on install to install the compiler

Performing DIC Analysis with Ncorr

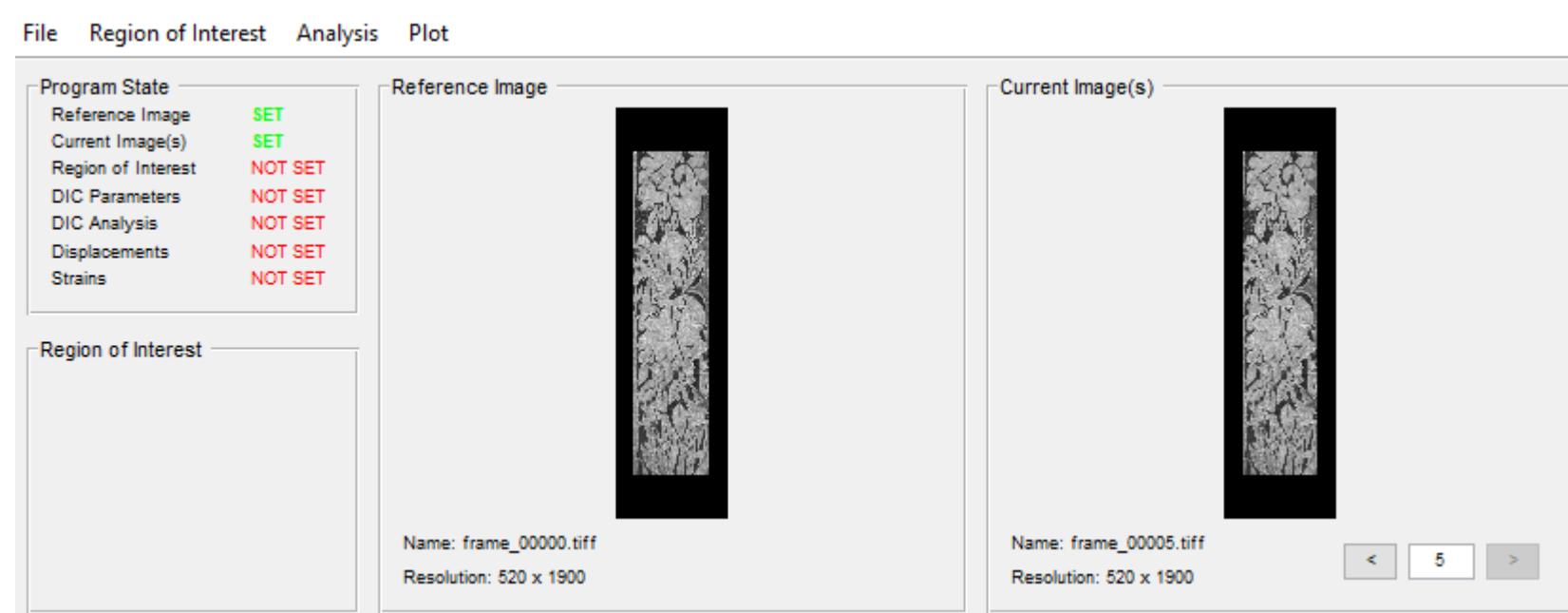


Ncorr graphical user interface (gui)

1. Click on **File** menu as shown in the gui above and select **Load Reference Image**: The reference image is the initial undeformed image. If you have generated the images with the Tapestry Toolkit, the reference image will be the image named frame_00000.tiff in the deformed image folder(s).

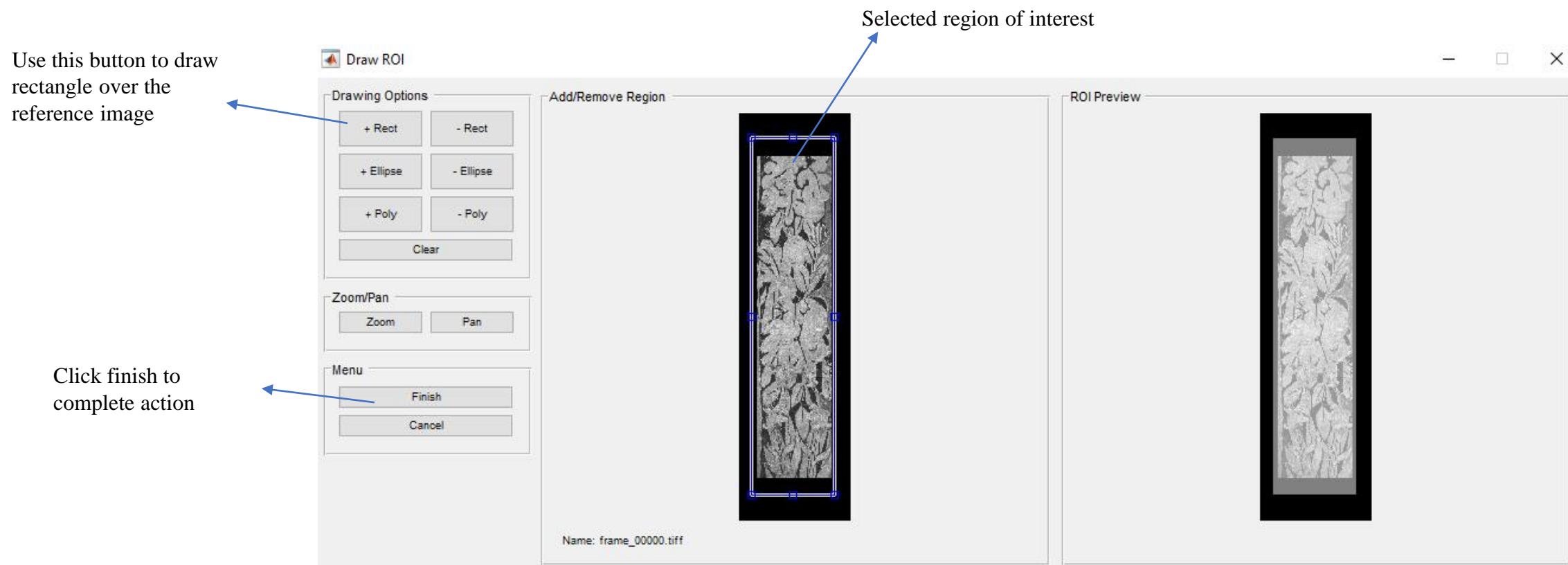
2. Click on the **File** menu and select **Load Current Images** to load current images using any of the options specified (**Load Lazy** is the preferred option). If you have generated the deformed images with Tapestry Toolkit, the current images will be all the deformed images in the deformed image folder (Fabric or Speckle) except the undeformed image file named **frame_00000.tif**.

The ncorr gui will look as shown below after loading reference and current images

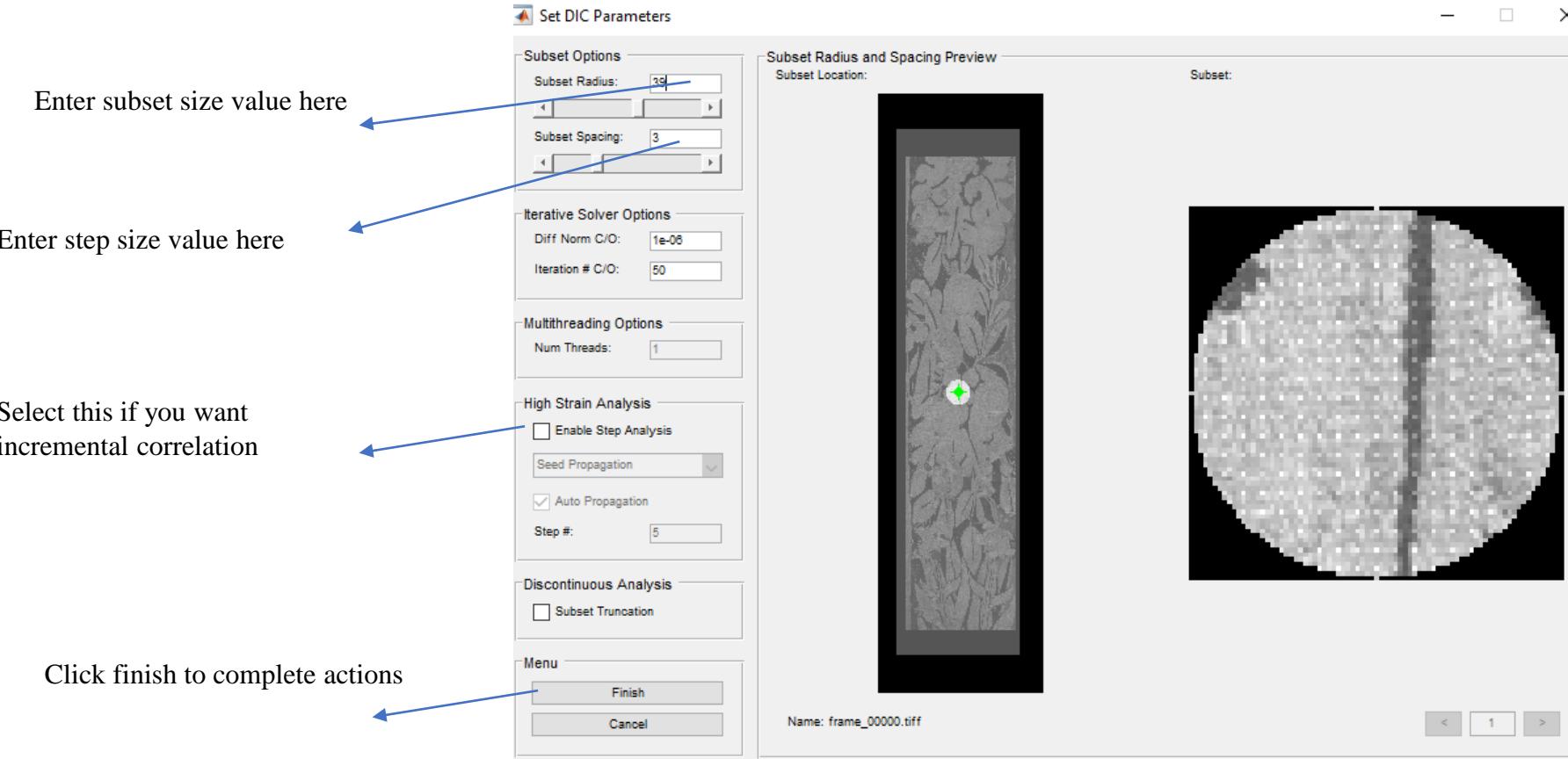


3. Click on the **Region of Interest** menu and select the **Set Reference ROI** option to select your desired region of interest (ROI). After clicking on the Set Reference ROI button, a new figure (named Draw ROI) will appear.

Click on the **Draw ROI** button in the figure, a new figure will appear shown below, then use the **+ Rect** button to draw a rectangular shape over the reference image. Click the **Finish** buttons on the two Draw ROI figures to complete action



4. Click on Analysis menu and select the **Set DIC Parameters** option to input DIC parameters

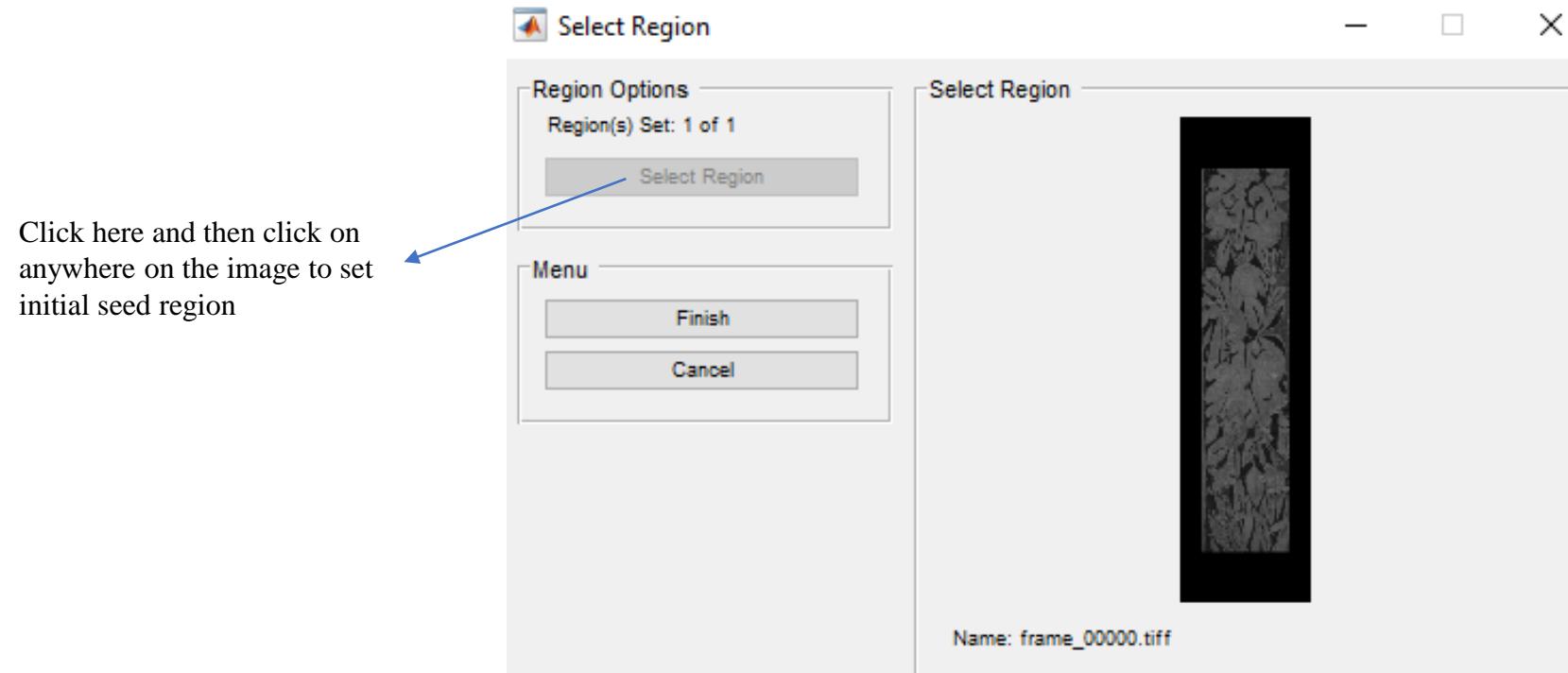


Review your input values and click **Yes** to the **Continue Op** window that will appear

5. Click **Analysis** menu and select **Perform DIC Analysis** option. From the **Select Region** figure that appears, first click on the **Select Region** button and click anywhere on the image (i.e. image on the Select Region figure).

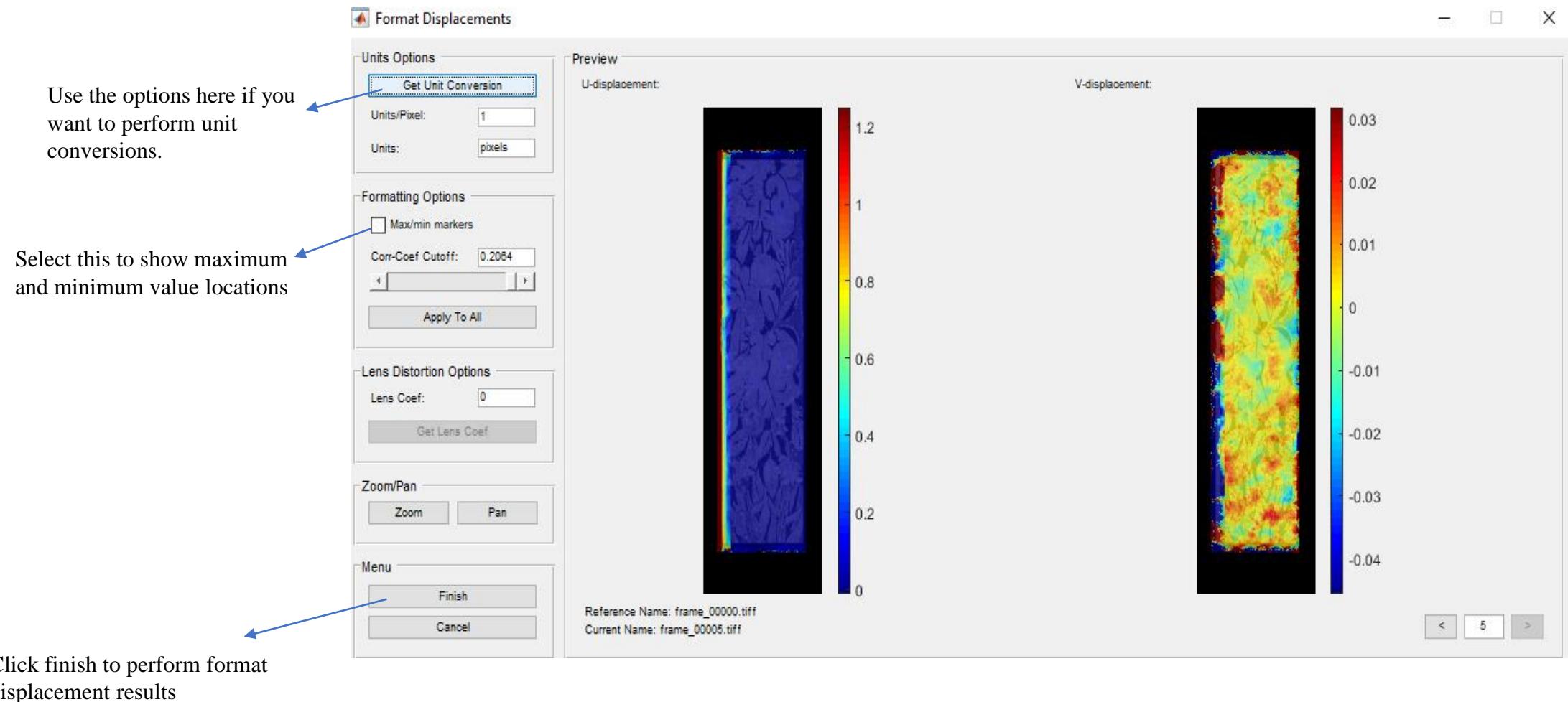
Then **Set Seeds** figure appears. Click on **Set seeds** button and click anywhere on the image (i.e. image on the Set Seeds figure) and click finish.

Wait for the seeding analysis to complete. Then click the **Finish** button on the **Seeding Preview** figure. Click the **Finish** button on the **Select Region** figure to complete actions. Wait for the DIC analysis to complete!. You will be informed on successful completion of the analysis. For more details on seeding for ROI and initialisation for DIC analysis using Ncorr, please see the Ncorr user manual at this site: <http://www.ncorr.com/index.php/downloads>

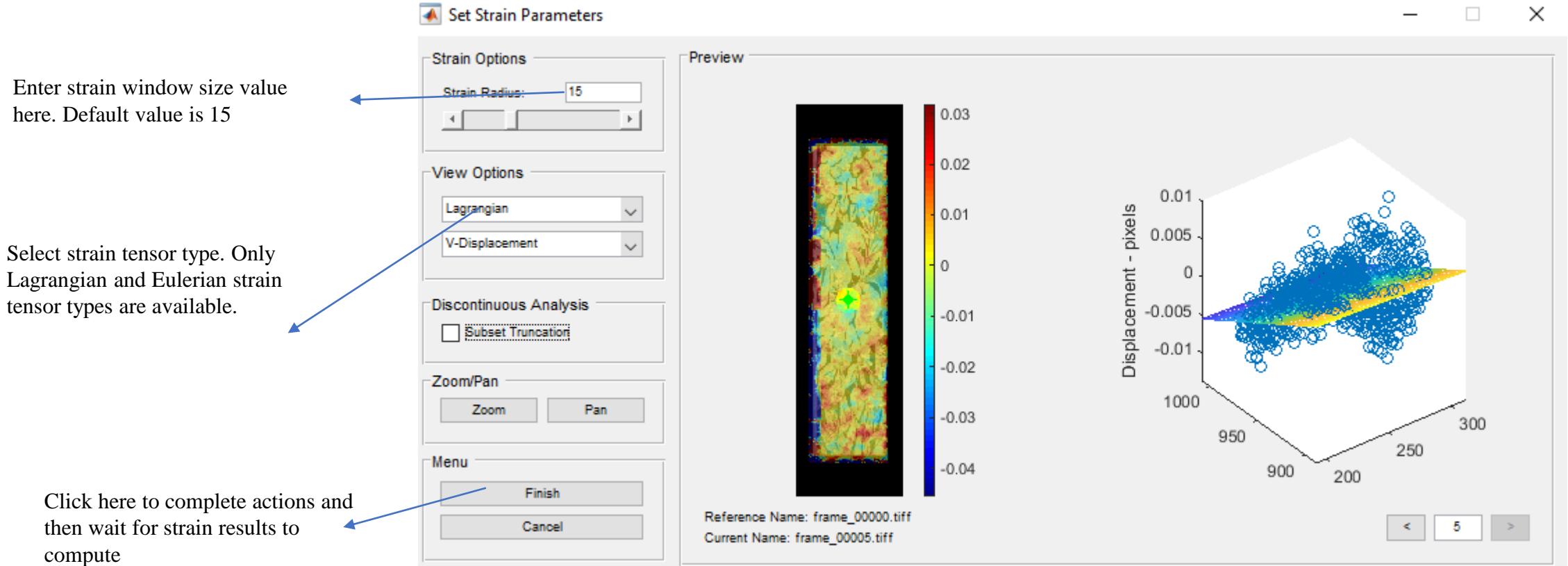


Select Region Figure

6. Click **Analysis** menu and select **Format Displacements** option.



7. Click **Analysis** menu and select **Calculate Strains** option.



8. Use **Plot** menu to plot and visualise strain and displacement results

❖ Save the results from Ncorr in the deformed image folder for each image type. To save results, go to **File** menu and select **Save Data**, locate the appropriate deformed image folder and save the data with your desired name.

Using Ncorr with the compiled version of the tool kit

- The compiled version of the tapestry toolkit cannot extract some specialised ncorr data type such as the values of the roi mask data. This data is required to estimate the position of data points for interpolation during post processing.
- To use the compile version of the toolkit with ncorr, the user need to manually extract the required values from the saved ncorr data (.mat file). To do this, please follow these steps:
 1. Save the ncorr DIC analysis results in correct deformed image folder (i.e. fabric or speckle deformed image folder)
 2. From MATLAB environment, change the working directory (see page 29 to see how to do this) to the each deformed image folder.
 3. Copy the following code to a Nnotepad or another text editor:

```
load('saved ncorr result.mat')

number_deformed_images=5  for num= 1:number_deformed_images
roi_mask{num,:}=data_dic_save.displacements(num).roi_dic.mask;
end

roi_mask= cell2struct(roi_mask,'val', number_deformed_images)

save('saved ncorr result.mat ','roi_mask','-append')
```

From the Notepad or another text editor,

In the first line of the code above, change the **saved ncorr result.mat** to the name of the ncorr result file in that deformed image folder ending with .mat. Ensure that it is in single quotes as above.

In the second line of the code above, change the value of **number_deformed_images** from 5 to your number of deformed images specified previously

In the last line of the code above, change the **saved ncorr result.mat** to the name of the ncorr result file in that folder ending with .mat. Ensure that it is in single quotes as above.

4. Copy each segment of the edited version of the code from Notepad and paste in the MATLAB Command Window (see page 30 for MATLAB Command Window)

5. After pasting each segment of the code, press enter for execution

Post Processing with Tapestry ToolKit

- Click on DIC Software menu and select DIC software used for the DIC analysis
- Postprocess with Tapestry_ToolKit: click on the Postprocess button (See Figure 7).
- You will be prompted to confirm if you want all displacement and strain components results. If yes, select Yes, if no, select the your desire result component.
- Then you will prompted to select if you want parallel program for the analysis. Select yes if you want to perform the postprocessing in parallel for the images or no, if you prefer serial analysis. See next page for more details.
- At completion, the **Results** menu becomes active as shown in the Figure 19
- To view the results click on **Results** menu and select the desired result type from the submenus
- Under Results menu are the following:
- **DIC and FEA Results:** Plots the DIC and FEA results for displacements and strain components
- **Percent Error:** Plots the percent difference between the FEA and DIC results at local level
- **Difference plots:** Shows the plots of the difference between the FEA and DIC results at local level
- **Global Average Plots:** Plots the global average of the displacement and strain components against global average error

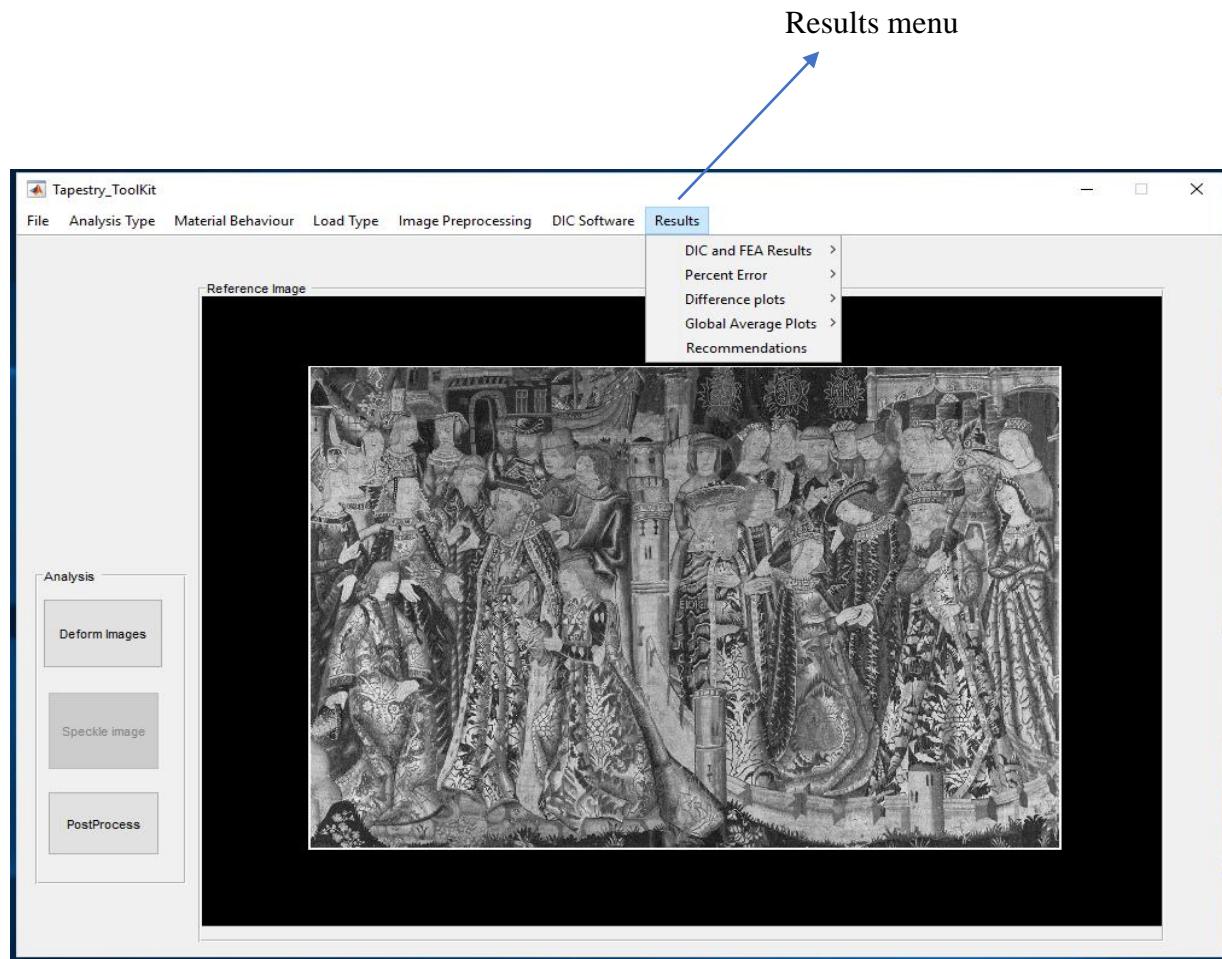


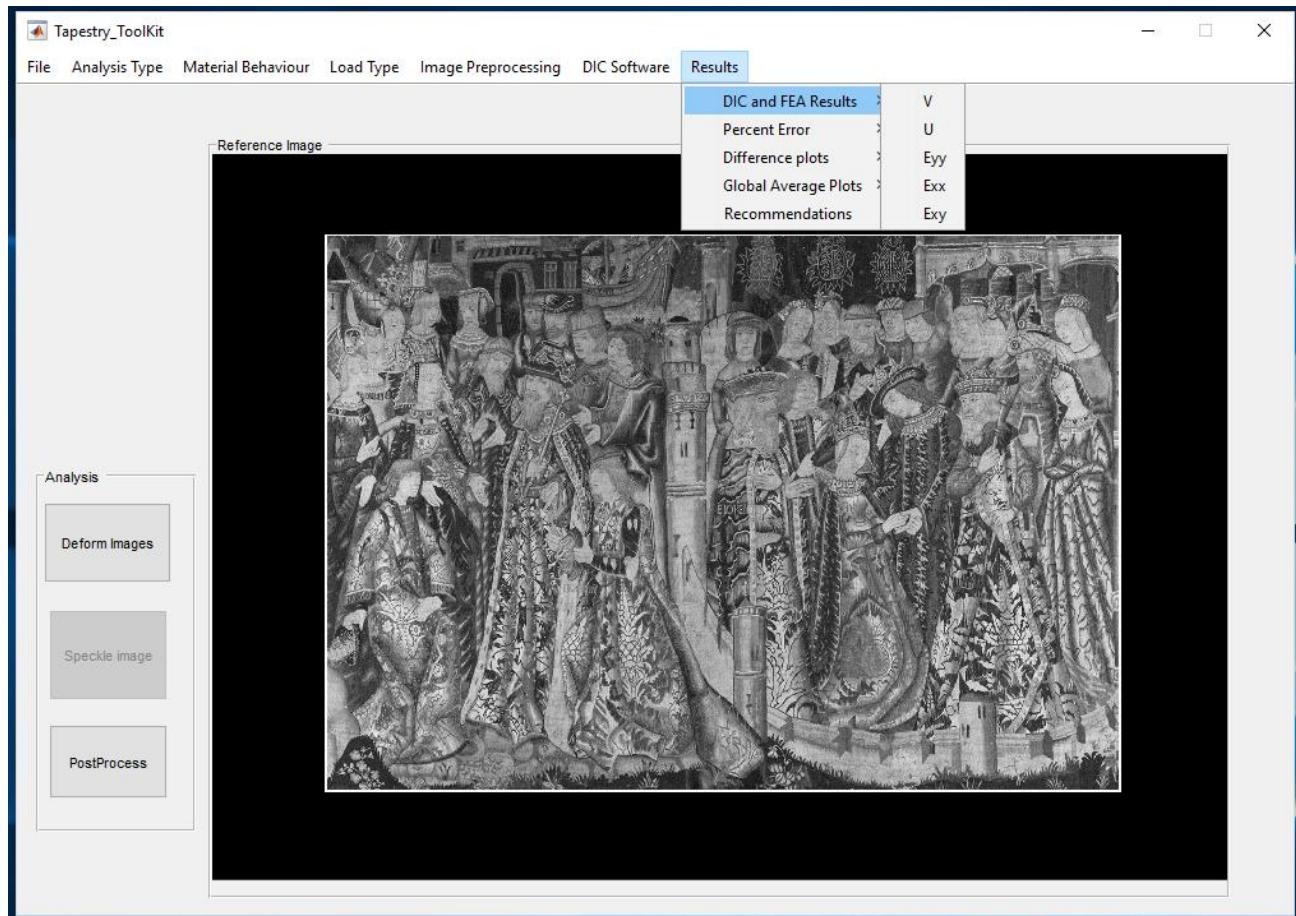
Figure 19

NOTES

- ❖ If you have used Ncorr for the DIC analysis, please make sure that only the saved result file (i.e. .mat file) from ncorr is in the deformed image folder(s) in addition to the deformed images. No additional .mat file should be in this folder!
- ❖ Selecting all results components will take longer for the postprocessing and more memory requirement. You can perform analysis for each result component (displacement components and strain components) sequentially to reduce memory requirement.
- ❖ Selecting parallel program for the postprocessing will use most of your PC computing power and slow other activities. But will reduce the time required to complete the postprocessing operation. If you select No to parallel program dialogue, the analysis for each image and result components will be performed in serial and will increase the processing time especially if all/many result components are requested.

Meaning of Results components

- Each of the submenu in the Results menu contains these symbols:
- V: is the vertical (Y) displacement
- U: is the horizontal (X) displacement
- Eyy: is the vertical (Y) strain
- Exx : is the horizontal (X) strain
- Exy: is the shear strain



- ❖ If you have used Ncorr for the DIC analysis, please note that the strain tensors available in Ncorr are Eulerian and Lagrangian! While ABAQUS strain tensor is Logarithmic. So be aware that two different strain tensors are being compared in this case! The strain field (in terms of distribution) will be similar in both software but the magnitude in difference between the two strain tensors will be higher if the deformation level is high. This will slightly increase the percent error values reported under large deformation analysis (greater 1% strain).

When a result component is pressed (except components under global average plot), the results are plotted in another figure and the software interface is as shown in the Figure 20.

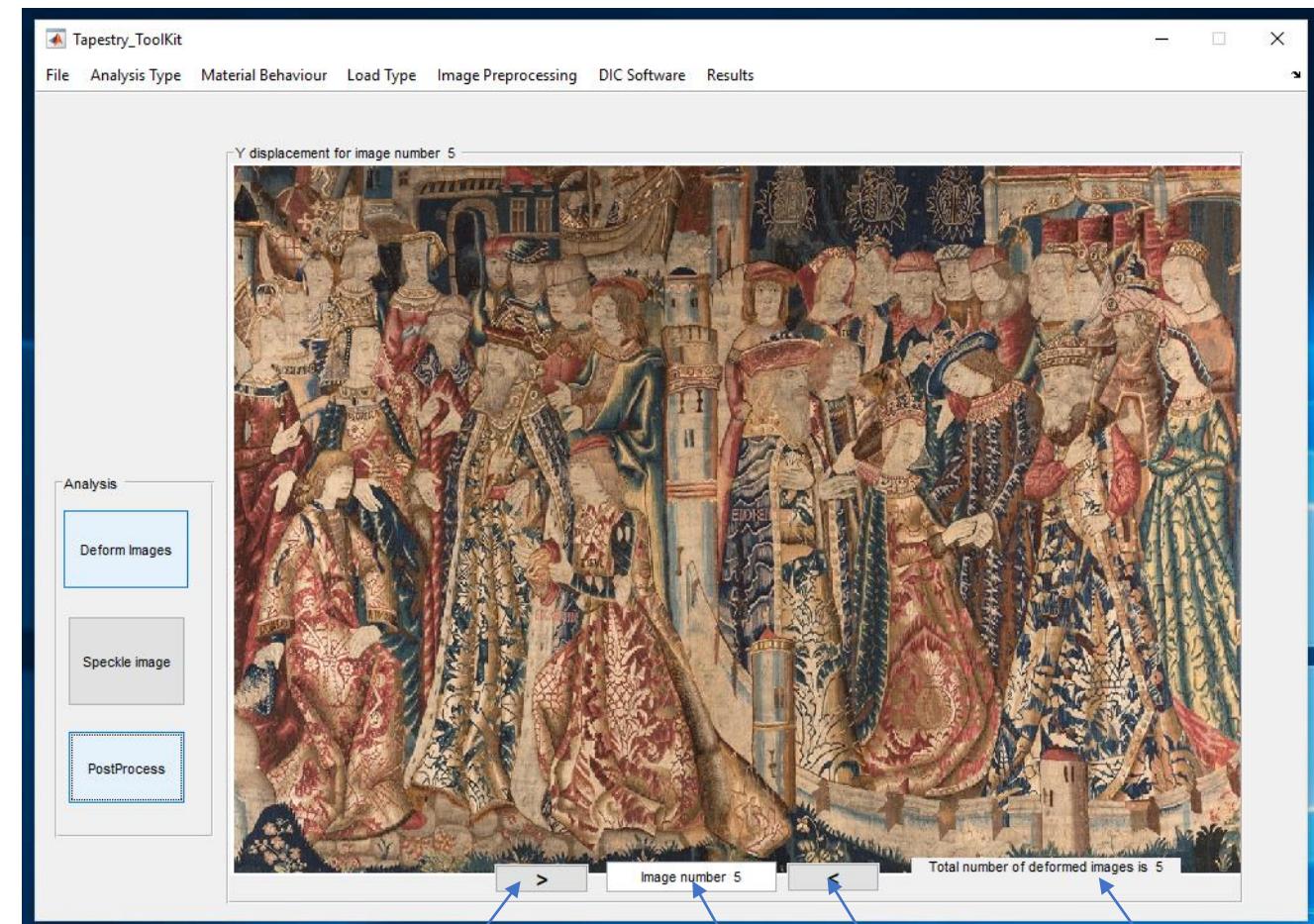


Figure 20

plot for another image number higher than current image

Current image number that it's results has been plotted

plot for another image less than current image

Total number of images used in the analysis

- When a result component under the global average plot has been clicked, the software plots the results in the software as shown in the Figure 21.
- To enlarge the plot, right hand mouse click on the plot and select **Open plot**

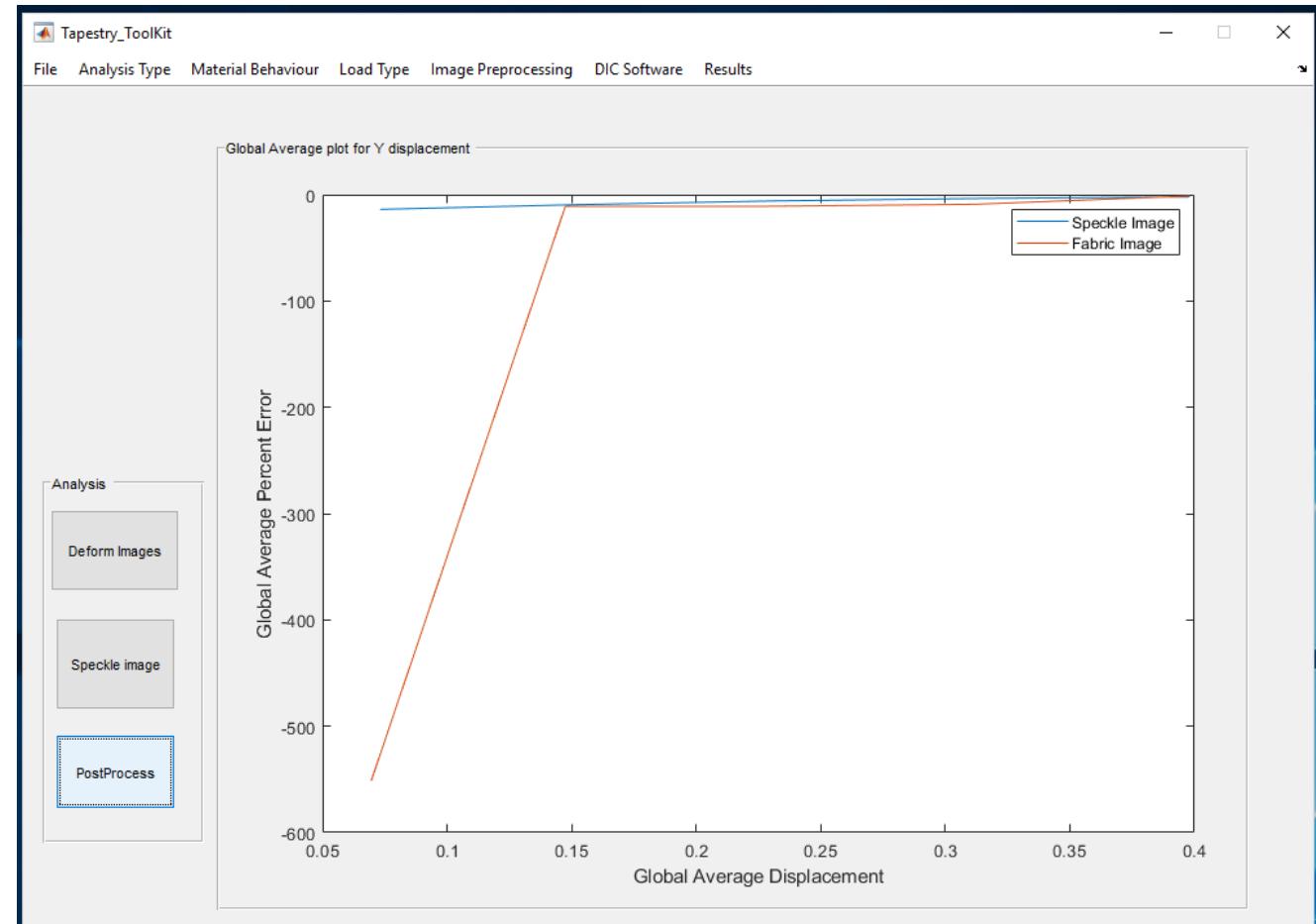
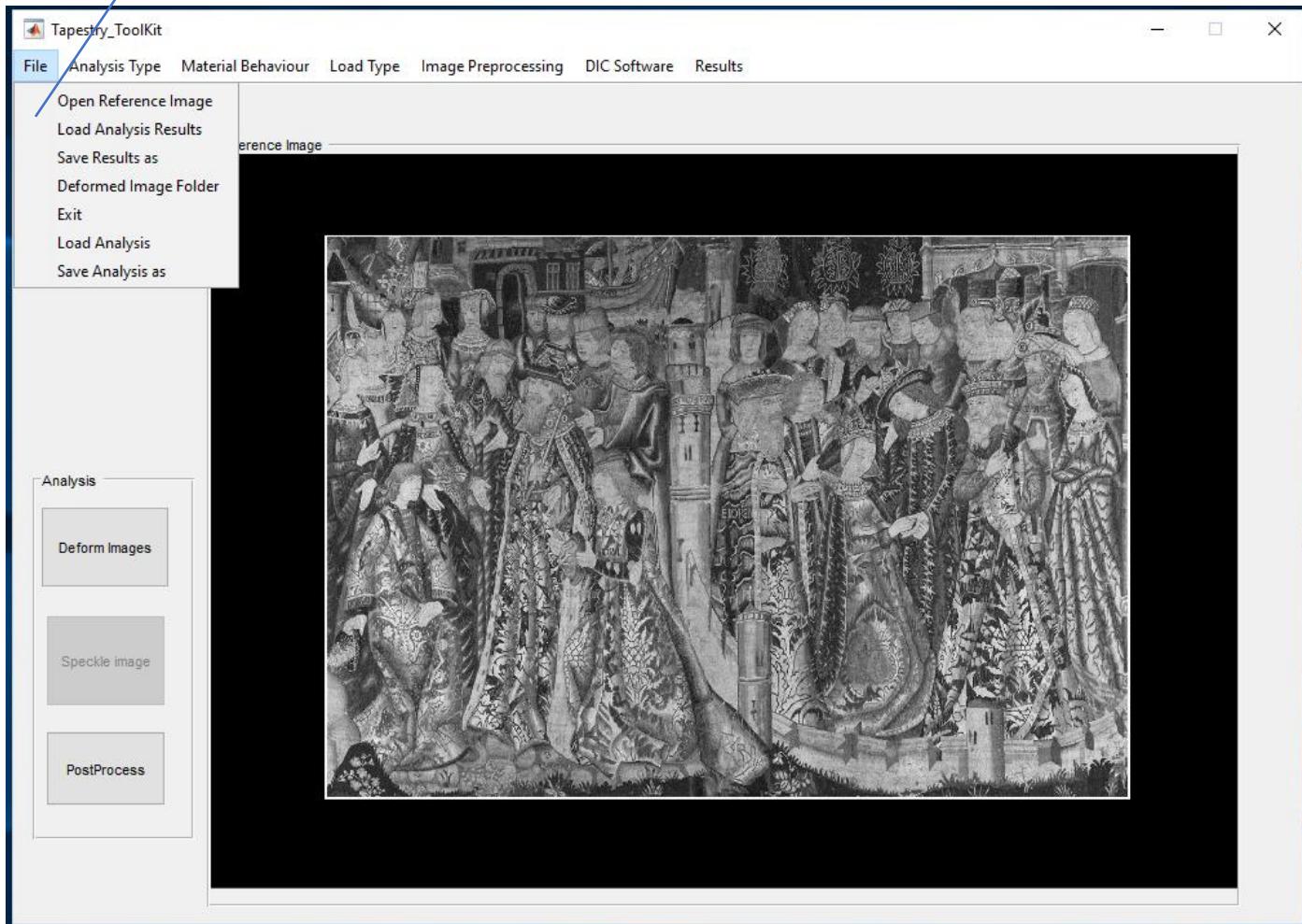


Figure 21

FILE SUBMENU FUNCTIONS

- Besides **Open Reference Image** under the **File** menu, other submenus and their functions include:
- **Load Analysis Results:** After **PostProcessing** step, the results generated are saved in a file named **Results.mat** in your working directory. You can view this results at a later time by going to **File** and selecting **Load Analysis Results**. You will be prompted to locate and select the Result file saved in your working directory.
- **Save Results as:** After **PostProcessing** step, the results generated are saved in a file named **Results.mat** in your working directory. If you perform another analysis with different parameters, the data in the **Results.mat** will be overwritten. To avoid this, change the name of the **Results.mat** file by going to **File** and selecting **Save Results as**. You will be prompted to enter a name of your choice and the **Results.mat** file will be changed to the name you entered. It is active only when results have been generated.
- **Deformed Image Folder:** Use this to locate the deformed image folders in your working directory. It is active only when deformed images have been generated.

File submenus



FILE SUBMENU FUNCTIONS continue

- **Exit:** Use this to exit and close the software.
- **Save Analysis as:** You can save parameters such as the reference image, material properties, Analysis type, load type and image preprocessing values used in a particular analysis for future use or to continue the analysis at a later time. To do so, use the **Save Analysis as** submenu. You will be prompted to enter a name that the analysis file be saved with. This becomes active once a reference image has been loaded into the software, i.e. after **Open Reference Image** task has been successfully completed.
- **Load Analysis:** To continue a saved analysis, use the **Load Analysis** submenu. You will be prompted to located the file containing the analysis data.

