# User manual
CTHarmonizer tool

Contents

1. General information

These instructions cover first the use of the software in MATLAB. At the end of the document, there are instructions for using the standalone versions of the tool. Please run the software in the location where the *kernelmatch.mat* file is located.

The software has been tested with MATLAB versions 9.10.0.1710957 (R2021a) Update 4 (macOS) and 9.6.0.1072779 (R2019a (Windows).

2. Basic Workflow

If the software does not automatically locate the folder containing the data, the user is prompted to identify this folder. Once identified, the directory to the data should be known by the software (excluding the standalone version, which requires the user to identify the folder each time the software is launched).
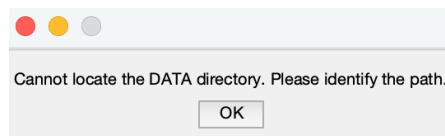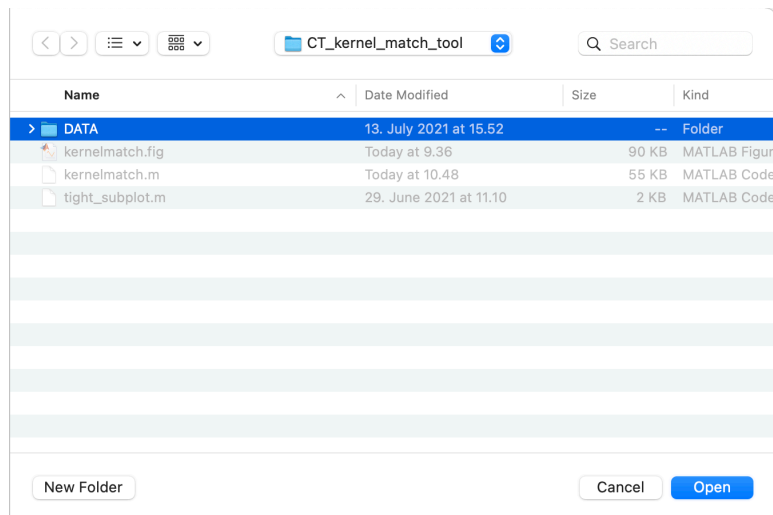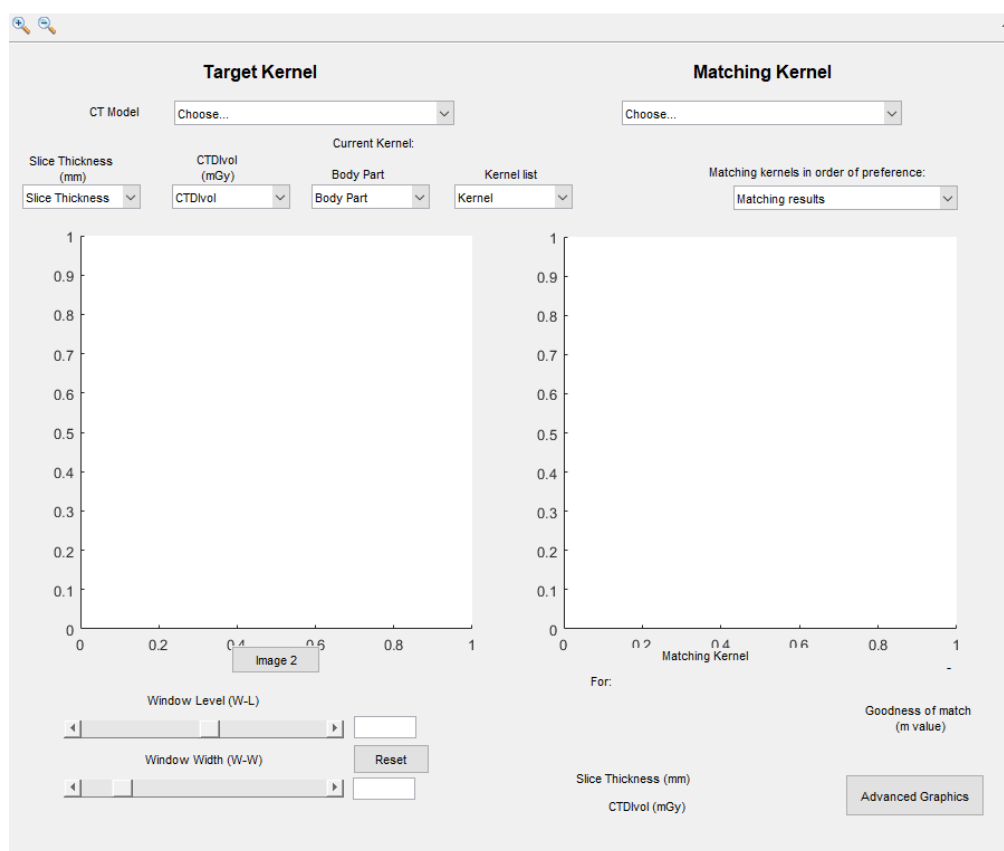
This directory should be given to the software (DATA-folder).

The tool launches to a user interface depicted below.

- Target Kernel defines the kernel with the desired image quality.
- Matching Kernel is the result of the matching algorithm, representing the best-matching reconstruction kernel and algorithm for the to-be-matched CT model.
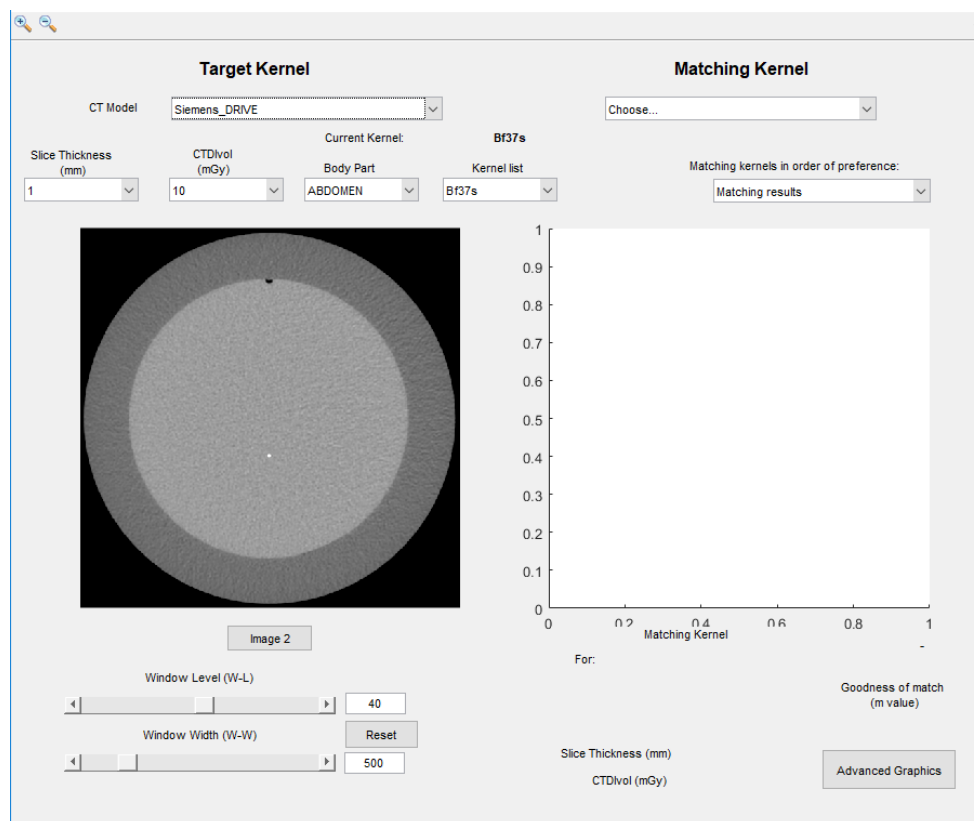

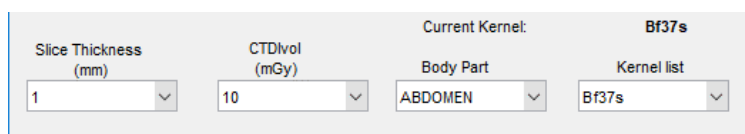First, the CT model for the target kernel needs to be chosen:
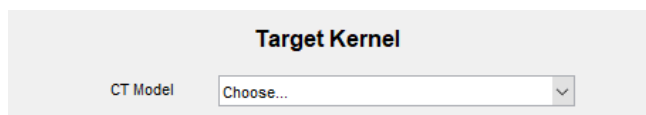
The list of available CT models is based on the database (results.mat-file) included with the tool. This file can be found in the *DATA* folder, identified by the user during startup.

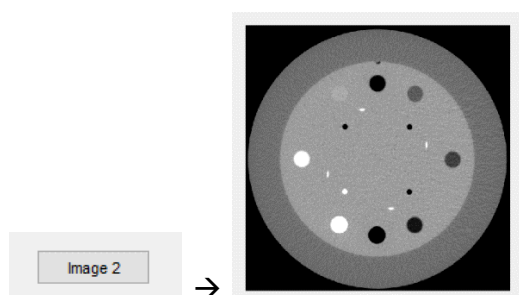When the target CT model is chosen, the tool will display a phantom image with default values.

You can choose the desired values for Slice Thickness (in mm), CTDIvol (in mGy), Body Part, and for the kernel from the dropdown menus:

The phantom image will change accordingly.

With the Image 2-button, you can check another phantom image, visualizing different contrast targets:

When the desired imaging parameters for the target kernel have been chosen, the CT model for the to-be-matched kernel should be picked from the dropdown menu:

Matching Kernel

Choose...

This will run the matching algorithm and present the results:

The parameters for the matching kernel are displayed below the matched image:

- CT model
- Body part/filter
- Kernel
- Slice Thickness (in mm)
- CTDIvol (in mGy)

The parameter called "Goodness of match" (or m-value) defines how good the match is. A value of 1 corresponds to an exact match, and a value of 0 indicates no match at all.

The best match is displayed as default. You can also check other matching kernels, in a descending matching function value order, from the dropdown list "Matching kernels in order of preference":

Matching kernels in order of preference:
DETAIL_AR70

Matching kernels in order of preference:
No match...
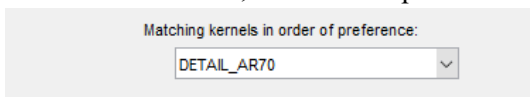
If no match is found, the list will display "No match":

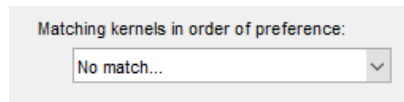In this case, please choose another CT model, or change the values for one or more of the following: Slice thickness, CTDIvol, Body part, and kernel.

The matching algorithm is automatically run every time any of the values is changed.

If the result of the match is poor (m-value is very low), the list will display "Bad result", and no sufficiently

Matching kernels in order of preference:
Bad result

matching kernel is found:
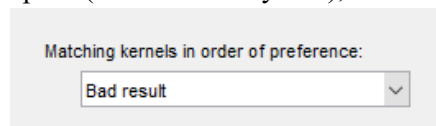
Changing the values for parameters (Slice thickness, CTDIvol, Body part, and kernel)

3. Adjusting images

You can adjust the window level (W-L) and window width (W-W) from the sliders or input the desired values to the text boxes:

Window Level (W-L)
◄ | ►   40
Window Width (W-W)   Reset
◄ | ►   500
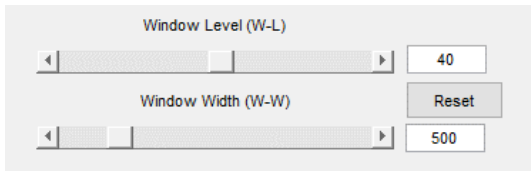
With the Reset button, you can reset the values back to the default values.

You can zoom the images with the buttons in the top-left corner:
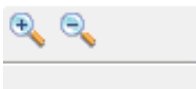
You can change between the two different phantom images with the Image 2/ Image 1 button:

Image 2   →
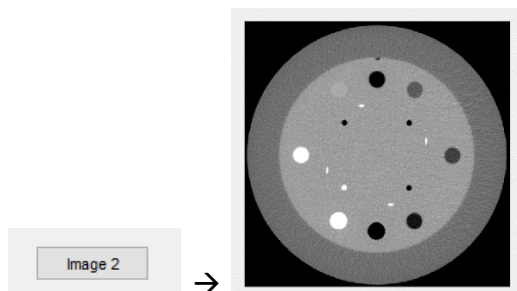
4. Advanced Graphics

With the Advanced Graphics button, you can display a graphic displaying more details (modulation transfer function and noise power spectrum) on the matching result:
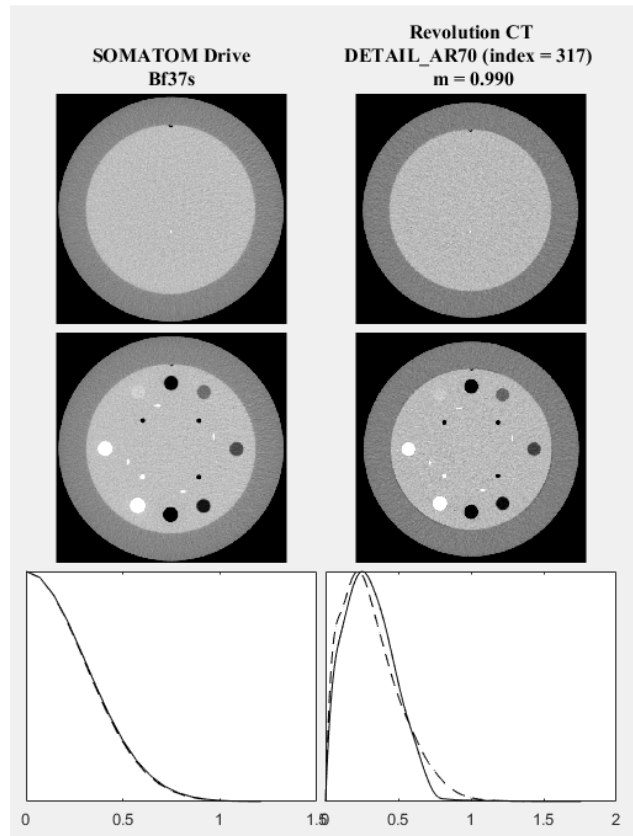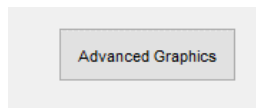
5. Description of the results structure

As discussed earlier, the *results.mat* file contains the data necessary to run the fitting. The structure itself contains several different parameters for one scanner:

```
results.GE_revolution   ✕

results.GE_revolution

Field ▲                        Value
{} Path                        1x1000 cell
ᶜₕ Manufacturer               'GE MEDICAL SYSTEMS'
ᶜₕ Model                      'Revolution CT'
{} Studies                     1x1000 cell
⊞ Slice_thickness             1x1000 double
{} Series_name                 1x1000 cell
{} Kernel_names                1x1000 cell
{} Recon_names                 1x1000 cell
{} Recon_filter                1x1000 cell
{} Body_part                   1x1000 cell
{} Recon_info                  1x1000 cell
{} Series_description          1x1000 cell
⊞ Width                        1x1000 uint16
⊞ CTDIvol                      1x1000 double
⊞ FR_NPS                       1x1000 double
⊞ FR_NPS_max                   1x1000 double
⊞ f_50                         1x1000 double
⊞ f_10                         1x1000 double
⊞ NPS                          1x1000 struct
⊞ MTF                          1x1000 struct
⊞ MTF_slice                    1x1000 double
```

In the above case for the GE Revolution CT scanner, the dataset contains 1000 different kernel combinations, CTDIvol, slice thickness. The different fields of the structure are described in Table 1.

*Table I*. *Description of the results structure fields.*

Field name	Description
Path	Describes the paths from which each of the original reconstructions were loaded. This can be used for debugging purposes.
Manufacturer	Dicom tag (0008,0070), containing the name of the CT manufacturer.
Model	Dicom tag (0008,1090), containing the model name of the CT scanner.
Studies	A cell array containing the study number for a specific kernel. This information is used when searching for the visualized slices.
Slice_thickness	Thickness of the slice for each reconstruction.
Series_name	A cell array containing the series number for a specific kernel. This information is used when searching for the visualized slices.
Kernel_names	Dicom tag (0018,1210) describing the convolution kernel.
Recon_names	For some of the scanners, the ConvolutionKernel-tag does not provide sufficient details regarding which algorithm and kernel combination is used. The Recon_names-field processes each scanner separately and combines the information provided in 'Kernel_names' with scanner-specific private tags.
Recon_filter	Describes the used reconstruction filter type (body, brain, …)
Body_part	Dicom tag (0018,0015) containing the examined body part.
Recon_info	Similar to Recon_names (further information in addition to the information included in the Dicom tag (0018,1210).
Series_description	Dicom tag (0008,103E).
Width	Width of the CT slice in pixels.
CTDIvol	Dicom tag (0018,9345) containing the volume CT dose index.
FR_NPS	The weighted average frequency of the noise power spectrum.
FR_NPS_max	The peak frequency of the NPS curve.

| f_50	The frequency at which the MTF is reduced to 50% of the maximum value.
f_10	The frequency at which the MTF is reduced to 10% of the maximum value.
NPS	The radially averaged one-dimensional NPS curves. This structure contains three different fields: freq = spatial frequencies of the sampled NPS (1/mm) NPS = The noise power for the sampled spatial frequencies NPS_SD = Noise standard deviation determined from the NPS.
MTF	Modulation transfer functions. This structure contains two different fields: freq = spatial frequencies of the sampled MTF (1/mm) MTF = The modulation transfer for the sampled spatial frequencies
MTF_slice	The slice used for determining the MTF.

6. Installing and running the standalone application

6.1.   Installation process

1. Download the correct standalone based on your operating system. Currently Windows and macOS are supported.
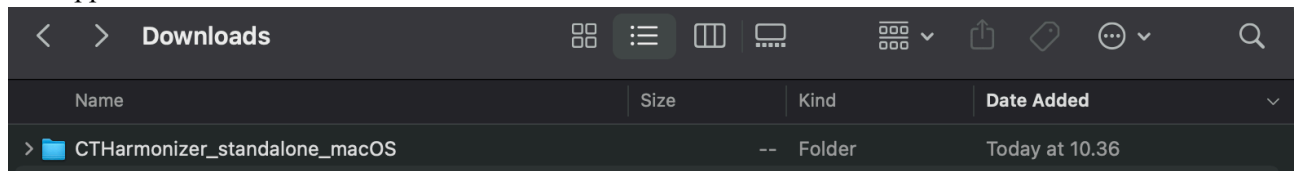
2. Run the installer and follow its instructions. Note that the standalone application requires Matlab runtime, and it will be installed automatically (https://se.mathworks.com/products/compiler/matlab-runtime.html).
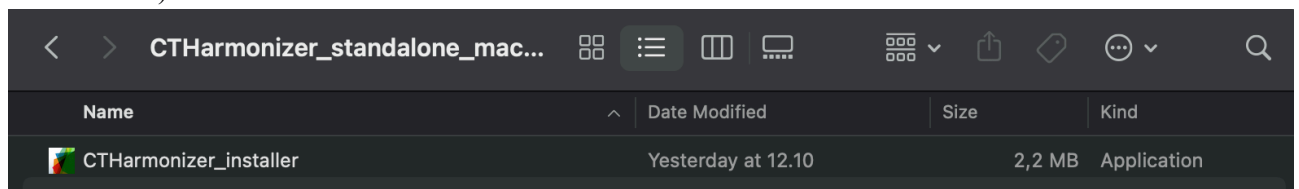
3. Pay attention to the plausible additional steps you may have to perform. For instance, for macOS, the DYLD_LIBRARY_PATH may require modifications (https://se.mathworks.com/help/matlab/matlab_external/set-run-time-library-path-on-mac-systems.html).
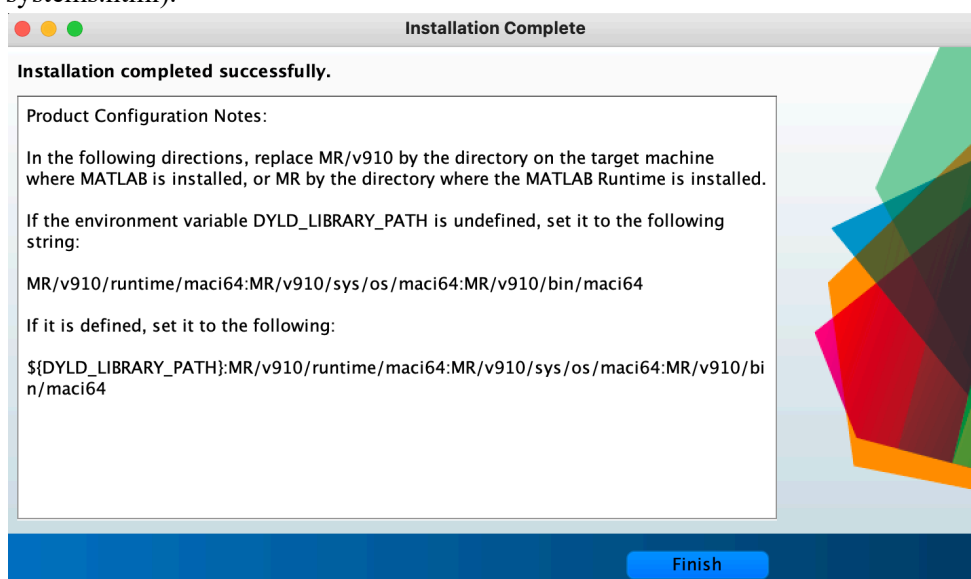
6.2. Running the software

Locate the CTHarmonizer-software. Each time the software is launched, the user is prompted to give the path to the DATA-folder. Once this is given, the software runs similar to the MATLAB-version, presented above.