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# **QMENTA Q-FiberMapper Manual**

*Release 1.0.3 for Q-FiberMapper 4.5*

**QMENTA Inc.**

**Mar 19, 2024**



## CONTENTS

<b>1</b>	<b>Contact</b>	<b>1</b>
<b>2</b>	<b>Q-FiberMapper</b>	<b>3</b>
<b>3</b>	<b>Copyrights</b>	<b>15</b>
<b>4</b>	<b>Document Changes</b>	<b>17</b>



## CONTACT

For assistance, contact QMENTA by sending an email to [support@qmenta.com](mailto:support@qmenta.com). For technical support please click on the support button in the sidebar to open a chat with our support engineer.

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**Note:** Please be aware that customer support is only available during office hours in Spain.

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### 1.1 Company

The company can be contacted at its European Office located in Barcelona:

QMENTA Imaging S.L.  
C/ Roger de Llúria 46, Pral. 1<sup>a</sup>  
08009 Barcelona, Spain  
Phone: +34 933 282 007

and in Boston:

Mint Labs, Inc., d/b/a. QMENTA  
One International Place, Suite 3700  
Boston, MA 02110  
USA



## Q-FIBERMAPPER

### 2.1 Certification

An extended explanation about the theory behind this algorithm can be found in the following paper, that details the competition organised by Bennett Landmann and held at the diffusion study group at ISMRM 2017 in which a number of teams competed to produce the most reproducible tractography on a set of specified white matter structures. QMENTA's entry was the 3rd most reproducible method:

Tractography Reproducibility Challenge with Empirical Data (TraCED): The 2017 ISMRM Diffusion Study Group Challenge Nath, V. Schilling, K. G., et al. (... , Rowe, M., Rodrigues, P., Prčková, V., ... ), & Landman, B. A. (2019). "Tractography Reproducibility Challenge with Empirical Data (TraCED): The 2017 ISMRM Diffusion Study Group Challenge". *Journal of Magnetic Resonance Imaging*.

### 2.2 Description

The Q-FiberMapper derives diffusion parameters for specific white matter fascicles in the brain using diffusion weighted magnetic resonance imaging (DW-MRI). 16 white matter fascicles are reconstructed by Q-FiberMapper. Q-FiberMapper reconstructs the left and right hemisphere counterparts of the following fascicles:

- Cortico-spinal tract
- Inferior fronto occipital fasciculus
- Inferior longitudinal fasciculus
- Uncinate fasciculus
- Superior longitudinal fasciculus
- Fornix
- Forceps major
- Forceps minor

For each fascicle, 7 diffusion parameters are derived and the mean and standard deviation over the volume of the fascicle is listed in the table below the visualization of the reconstructed fascicle. The diffusion parameters are derived from the diffusion tensor, a mathematical model that describes the mobility of water within the tissue.

- Fractional anisotropy (FA): a unitless parameter that describes the directional bias of the water diffusion pattern. FA scales between 0 and 1. A value near 1 indicates that the diffusion pattern is highly directionally biased such as in deep white matter, a value near 0 indicates that the diffusion pattern is more spherical, with water diffusing equally in every direction.

- Mean diffusivity (MD): this parameter describes the mean rate of diffusion in every direction, measured in  $10^{-3}$  mm<sup>2</sup>/s.
- Axial diffusivity (AD): this parameter describes the rate of diffusion along the axis of the white matter fibers, measured in  $10^{-3}$  mm<sup>2</sup>/s.
- Radial diffusivity (RD): this parameter describes the rate of diffusion perpendicular to the axis of the white matter fibers, measured in  $10^{-3}$  mm<sup>2</sup>/s.
- Coefficients of linearity (Cl), planarity (Cp) and sphericity (Cs): these unitless parameters describe the linearity, planarity and sphericity of the water diffusion pattern respectively.

When tissue changes occur at a cellular level, such as the breakdown of various cellular structures the diffusion pattern of water within the tissue changes. This will be reflected in the diffusion parameters FA, MD, AD and RD. Generally, pathological tissue changes tend to increase the mobility of water within the tissue, leading to increases in MD, AD or RD. FA can increase or decrease due to pathological tissue changes. Gradual changes in all parameters are expected in healthy aging, however, extreme changes could have a pathological cause.

## 2.2.1 Contralateral report

Our contralateral report provides a convenient way to compare the quantification outputs from our Q-FiberMapper of corresponding white matter fascicles of the same subject across opposing hemispheres (e.g: compare the properties of the left corticospinal tract with the right corticospinal tract). This can be useful in cases such as traumatic brain injury where trauma affects often only one of the hemispheres and changes to fascicle diffusion-derived properties can be more easily assessed using the non-affected counterpart as a baseline.

The report shows for each bilateral pair of fascicles the values corresponding to the main diffusion parameters indicated to each corresponding side of a central measuring axis. Below that axis, the absolute value of the difference between tracts is displayed.

## 2.3 Q-FiberMapper output description:

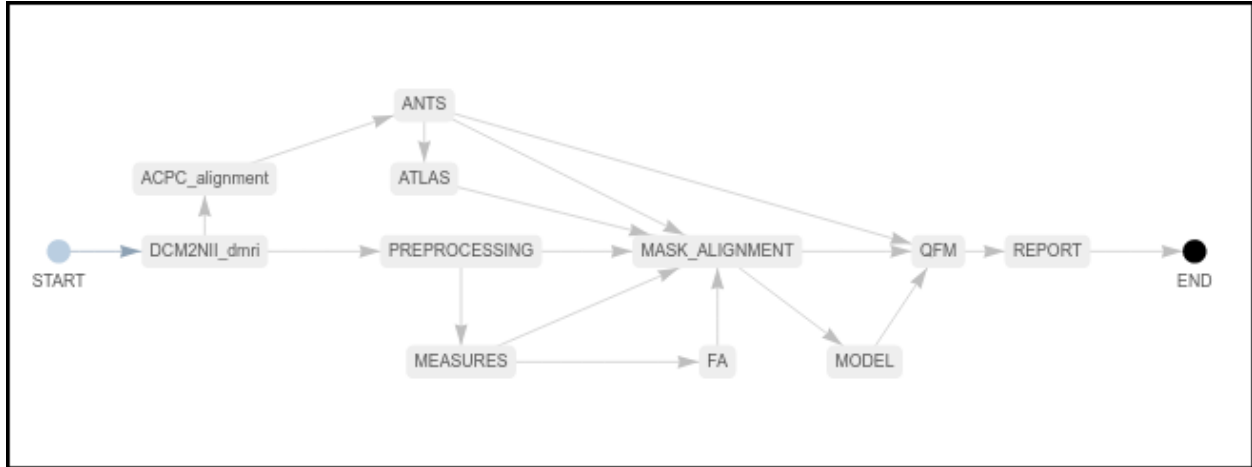
Visit <https://care.qmenta.com/> and provide your name and the email which you wish to use to access the platform.

The full workflow includes:

- DICOM files to NIfTI conversion and reorients to standard. The workflow file filter sends the DICOM or NIfTI files required for the workflow to run and the box converts the DICOM to NIfTI, extracts the necessary files (if possible) to do the dmri preprocessing step (eddy) and gradient tables. If NIfTI files or gradient tables are found in the input, it just does the reorient to standard step and outputs the files.
- dMRI preprocessing includes denoising, gibbs ringing correction, eddy correction, motion correction, bias field correction, distortion correction (if gradient field maps are available) and ACPC alignment.
- Gets the brain mask and computes the tensor from the diffusion image, plus derives different scalar measures: FA, AD, MD, RD, Cl, Cs, Cp.
- Runs ants cortical volumetry script over T1 image to extract the tissue segmentation file.
- Applies an atlas to the segmented mask of the cortex (gray matter + subcortical gray matter + brainstem + cerebellum)
- Align the diffusion image to the T1
- Estimate the diffusion model. Does nothing if the data is DTI. Runs constrained spherical deconvolution model.
- Perform probabilistic or deterministic tractography over the diffusion model.
- Extracts fascicles from tractography database, creates probabilistic maps of fascicle membership



- Outputs per fascicle mean diffusion metric fractional anisotropy (FA), mean/radial/axial diffusivity (MD, RD, AD), coefficient of linearity/planarity/sphericity (Cl, Cp, Cs)
- Contralateral report comparing fascicles and their diffusion metrics with their correspondent across hemispheres.
- Reports are presented in neurological and radiological orientations.



### 2.3.1 Required inputs:

- **T1:** anatomical 3D image. Isotropic resolution recommended. Must be labeled as ‘T1’ modality.
- **dMRI:** diffusion 4D image (DTI or HARDI). Isotropic resolution recommended. Must be labeled as ‘DTI’ or ‘HARDI’ modality.
- **Gradients:** gradient table (**optional** if dMRI is DICOM). MRtrix format supported: file must have ‘.b’ extension and be labeled as ‘gradient\_table’. FSL format supported: files must have ‘.bvec’ and ‘.bval’ extensions and be labeled ‘bvec’ and ‘bval’.

Minimum input requirements:

- Image must contain full brain DWI dataset.
- For optimal result reliability, an isotropic resolution is highly recommended
- T1 recommended resolution is 1 mm isotropic. T1 minimum reliable resolution is 2mm isotropic.
- dMRI recommended resolution is 2 mm isotropic. dMRI minimum reliable resolution is 3 mm isotropic.
- If DTI image must have at least 7 volumes (1 b0 and 6 diffusion volumes).
- If HARDI image must have at least 21 volumes (1 b0 and 20 diffusion volumes).
- For optimal preprocessing reliability, 1 b0 image is recommended every 10 gradient volumes.

Optional inputs:

- **GFMs:** Gradient field-maps, recommended (magnitude image and phase image). Same resolution and FOV as dMRI image recommended. Files must be labeled ‘gfm\_magnitude’ and ‘gfm\_phase’ respectively.

Description of the settings and the relevant outputs of each one of the steps of the workflow:

### 2.3.2 DICOM to NifTI (DCM2NII):

Preferred DICOM to NifTI conversion tool	<input type="text" value="dcm2niix"/>
<input checked="" type="checkbox"/> Reorient images to standard space	
<input checked="" type="checkbox"/> Delete ADC volume from Philips dMRI if detected	

**Settings:**

- Preferred DICOM to NIFTI conversion tool (drop-down selection). The selected tool will be tried first to convert DICOM to NIFTI. If the conversion fails, the other options will be tried sequentially until a successful conversion.
  - dcm2niix (Default)
  - Mrtrix
  - DCM2nii
  - diffunpack
  - MRIconvert (mcverter)

**Output files**

- T1 : T1 NifTI file
- HARDI / DTI : dMRI NIFTI file
- HARDI / DTI:
- HARDI / DTI ACQ\_PARAMS: acquisition parameter file for eddy preprocessing automatically extracted from DICOM file
- HARDI / DTI BVAL: BVAL file FSL format
- HARDI / DTI BVEC: BVEC file in FSL format
- HARDI / DTI GRADIENT\_TABLE: gradient table in mrtrix format
- HARDI / DTI INDEX: index file for eddy preprocessing automatically extracted from DICOM file

### 2.3.3 ACPC alignment and defacing (ACPC\_alignment):

<b>Do thickness</b>
<input type="checkbox"/> Compute thickness map

**Settings:**

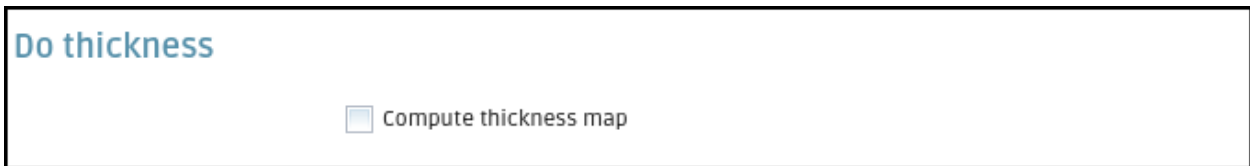
- T1 image is already skull strip (checkbox) (default, not checked)
- Change image resolution (checkbox) (default, checked)

- Voxel resolution value (in mm) (decimal) (default: 1mm)
- ACPC alignment and remove subject face (checkbox) (default, checked)
- Output transformation mat (checkbox) (default, not checked)

#### Output files

- T1 HEAD RESULT T1 acpc aligned and defaced image.
- IMAGE REPORT PNG from T1 result.
- MASK The binary mask used to deface the T1 image
- REPORT PDF.
- OUTPUT MAT the matrix used in the alignment will be shown in the output files if the setting is checked.

### 2.3.4 ANTs v2.3 (ANTS):



#### Settings:

- Perform additional cortical thickness on T1 (default unchecked)

#### Output files

- T1 HEAD Full T1 head image
- T1 BRAIN Skull stripped T1
- T1 MASK Binary skull stripped brain mask
- TISSUE\_SEGMENTATION 6-tissue segmentation image (1: CSF, 2: gray matter, 3: white matter, 4: deep gray matter, 5: brainstem, 6: cerebellum)
- CSV Volumetry information for ICV and each segmented tissue.
- REPORT PDF
- The full ANTs/ output.

### 2.3.5 Diffusion Preprocessing (PREPROCESSING):

#### Denoising step

Do denoising

#### Gibb ringing correction step

Do Gibb ringing correction

#### Gradient, Motion, Eddy & Distortion correction

**i** The following information about the sequence protocol is required for optimal pre-processing

- **Echo Spacing (s):** The time between echoes in an echo planar image (EPI).
- **Echo Factor:** also called Echo Train Length (ETL), the number of echoes acquired in a single repetition time (TR)
- **Acceleration factor:** the number of EPI lines acquired in parallel
- **Echo Difference (s):** (only needed if GFMs are provided), the difference in Echo Time (ET) between GFM acquisitions. Default value is typical for SIEMENS scanners

Do Eddy

Do Fugue

Use manual diffusion acquisition parameters

Echo Spacing (s)

Echo Factor

Acceleration Factor

Echo difference (s)

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#### Bias field correction step

Do bias field correction

#### Alignment

AC-PC alignment

#### Isotropic resampling

Resample dMRI image

dMRI isotropic resampling resolution (mm)

**Settings:**

- Do denoising (checkbox) (default checked)
- Do Gibb ringing correction (checkbox)(default checked)

- Do Eddy (checkbox)(default checked)
- Do Fugue (checkbox)(default checked)
- Use manual diffusion acquisition parameters (checkbox). If checked uses the parameters input manually in the following settings (Default unchecked).
- Echo Spacing (s) (float). The time between echoes in an echo planar image (EPI) (Default 0.0003ms)
- Echo Factor (integer). Also called Echo Train Length (ETL), the number of echoes acquired in a single repetition time (TR) (default 100)
- Acceleration Factor (integer). The number of EPI lines acquired in parallel (Default 1)
- Echo Difference (s) (float) (only needed if GFMs are provided), the difference in Echo Time (ET) between GFM acquisitions. (default 0.00246 for SIEMENS acquisitions)
- AC-PC alignment (checkbox) (default checked)
- Resample dMRI image (checkbox) (default checked)
- dMRI isotropic resampling resolution (mm) (float). Resamples the dMRI image to the indicated isotropic resolution in mm. (Default 2 mm)

#### Output files

- HARDI / DTI : dMRI NIfTI file processed with the steps selected in the settings
- GRADIENT\_TABLE: gradient table in mrtrix format
- AVERAGE\_B0S: Average b0s from the processed dMRI image
- PIS: Physically Implausible Signal for the diffusion image.
- REPORT: PDF report of the box

### 2.3.6 dMRI Measures (MEASURES):

**Settings:** This step has no settings.

#### Output files

- TENSOR: Diffusion tensor data
- AVERAGE\_B0S: Average b0s from the processed dMRI image
- MASK: dMRI binary brain mask

### 2.3.7 dMRI FA/Scalar Maps (FA):

**Settings:** This step has no settings.

#### Output files


- SCALAR AD: AD scalar file
- SCALAR CL: Cl scalar file
- SCALAR CP: Cp scalar file
- SCALAR CS: Cs scalar file
- SCALAR FA: FA scalar file
- SCALAR MD: MD scalar file

- SCALAR RD: RD scalar file
- VECTOR file.
- REPORT : PDF report of the box

### 2.3.8 dMRI Mask Alignment (MASK\_ALIGNMENT):

**Add non linear registration to the alignment.**

Compute non-linear registration EPI to T1 (FA input required) to correct for distortion when gradient field maps are not available. We strongly recommend to visually inspect the results when this is selected.

 Select which DWI-derived image has to be used to register the anatomical image to the diffusion weighted image. For more info, refer to [this paper](#).

Registration DWI-derived reference \*

#### Settings:

- Compute non-linear registration EPI to T1 (FA input required) (checkbox) (default not checked)

#### Output files

- HARDI / DTI : dMRI NIfTI file aligned to the anatomical image
- SCALAR AD: AD scalar file aligned to the anatomical image
- SCALAR CL: Cl scalar file aligned to the anatomical image
- SCALAR CP: Cp scalar file aligned to the anatomical image
- SCALAR CS: Cs scalar file aligned to the anatomical image
- SCALAR FA: FA scalar file aligned to the anatomical image
- SCALAR MD: MD scalar file aligned to the anatomical image
- SCALAR RD: RD scalar file aligned to the anatomical image
- AVERAGE\_B0S: Average b0s from the processed dMRI image aligned to the anatomical image
- GRADIENT\_TABLE: gradient table in mrtrix format
- MASK: dMRI binary brain mask aligned to the anatomical image
- TISSUE\_SEGMENTATION 6-tissue segmentation image for connectome
- ACT : ACT volume (5tt format) for connectome (not used in this workflow)
- LABELS : Labeled cortical brain for connectome (not used in this workflow)

### 2.3.9 Generate Labels from Atlas (ATLAS):

**Note:** This box is not used for the final tract segmentation but provides volumetric information on the T1-weighted input series.

Brain atlas for parcellation:

**Settings:** Brain atlas for parcellation (drop-down selection). The selected tool will be tried first to convert DICOM to NIFTI. If the conversion fails, the other options will be tried sequentially until a successful conversion.

- DKT40 (Mindboggle-101) (default)
- AAL

#### Output files

- ATLAS\_INFO : Text file with atlas information
- LABELS : Labeled cortical brain
- REPORT : PDF report of the box
- Vectorized data folder
- VECTOR : Volumetry information in a vector format

### 2.3.10 Diffusion Modelling (MODEL):

Tracking algorithm type

#### Settings:

- Tracking algorithm type (drop-down selection)
  - Constrained Spherical Deconvolution (CSD)
  - Tensor
  - Multi-tissue constrained spherical deconvolution (default)

#### Output files

- CSD / DTI models depending on the setting selected.

In the multi-tissue case we have:

- MSMT WM
- MSMT GM
- MSMT CSF
- RESPONSE

### 2.3.11 Q-FiberMapper Box (QFM):

**Settings:** This step has no settings.

#### Output files

The output bundles are:

- Cortico-spinal tract (LeftCST, RightCST)
- Inferior fronto occipital fasciculus (LeftIFOF, RightIFOF)
- Inferior longitudinal fasciculus (LeftILF, RightILF)
- Uncinate fasciculus (LeftUNC, RightUNC)
- Superior longitudinal fasciculus (LeftSLF, RightSLF)
- Fornix (LeftFornix, RightFornix)
- Forceps major (Fmajor)
- Forceps minor (Fminor)

There is a list of CSV files with the mean, standard deviation, minimum value and maximum value of the scalar measures per each bundle. The files with the *\_asym* prefix show a table with the mean value of the scalar measured comparing left and right sides.

- AD.csv, AD\_asym.csv
- Cl.csv, Cl\_asym.csv
- Cp.csv, Cp\_asym.csv
- Cs.csv, Cs\_asym.csv
- FA.csv, FA\_asym.csv
- MD.csv, MD\_asym.csv
- RD.csv, RD\_asym.csv
- FASCICLE\_INFO.csv shows other information about the fascicles (number of streamlines)
- SEG.nii.gz: All the fascicles together in a NIfTI file shown as an atlas.
- T1strip.nii.gz: T1 skull stripped.
- ANAT\_MAP/ Includes all the binary bundles from the segmentation in NIfTI format.
- DIFF\_MAP/ Includes all the probability weighted bundles from the segmentation in NIfTI format.
- IMAGE/ Includes all the bundles from the segmentation in PNG format.
- TRACK/ Includes all the bundles from the segmentation in .trk format.



### 2.3.12 Q-FiberMapper Report (REPORT):

**Settings:** - Report default orientation (drop-down selection)

- Neurological (default)
- Radiological

#### Output files

Same files as in the QFM box, plus:

- report.pdf: It would be the neurological or the radiological depending on the setting selected by the user.
- report\_neurological.pdf
- contralateral\_report\_neurological.pdf
- report\_radiological.pdf
- contralateral\_report\_radiological.pdf

## 2.4 REFERENCES:

- DWI gradient table check: [Ben Jeurissen et al. 2014]
- Subject motion & Eddy correction: [Andersson and Sotiropoulos 2016]
- Distortion correction: [Jezzard and Balaban 1995]
- ANTs registration: [Avants et al. 2008]
- MNI152 Atlas: [Grabner et al. 2006]
- FLIRT registration: [Jenkinson et al. 2002]
- MRtrix tools: [Tournier et al. 2012]
- Tensor estimation: [Veraart et al. 2013]
- Scalar measures: [Basser et al. 1994] , [Westin et al. 1997]
- ANTs script: [Tustison et al. 2014]
- ANTs registration: [Avants et al. 2008]
- Atropos tissue segmentation: [Avants et al. 2011]
- DiRECT cortical thickness: [Das et al. 2009]
- OASIS-30 tissue priors: [Landman and Warfield 2012]
- DKT40 Mindboggle 101 Atlas: [Klein and Tourville, 2012]
- AAL Atlas: [Tzourio-Mazoyer et al. 2002], [Rolls et al. 2015]
- MNI152 Atlas: [Grabner et al. 2006]
- msmt\_5tt: [Ben Jeurisen et al. 2014]
- CSD: [J-Donald Tournier et al. 2007]
- fod2dec: Two posters [T. Dhollander et al., 2015] [T. Dhollander et al. 2015]
- iFOD1 or SD\_STREAM: [J-Donald Tournier et al. 2012]
- iFOD2 poster: [J-Donald Tournier et al. 2010]

- Tensor\_Det: [Basser, P.J. et al. 2000]
- Tensor\_Prob: [Jones, D. et al. 2008]
- act, -backtrack, -seed\_gmwmi: [Robert E. Smith et al. 2012]

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## DOCUMENT CHANGES

Table 1: Releases

Version	Release Date	Description	Appoved by	Changed by	Document code
1.0	2022-05-18	First release	Tim Peeters	Marc Ramos	DOC-0006 - Q-FiberMapper IFU
1.0.1	2022-05-18	Remove blank page	Tim Peeters	Tim Peeters	DOC-0006 - Q-FiberMapper IFU
1.0.2	2022-08-31	Add USA company address	Tim Peeters	Tim Peeters	DOC-0006 - Q-FiberMapper IFU
1.0.3	2023-11-23	Updated QFM version	Alejandro Riera	Alejandro Riera	DOC-0006 - Q-FiberMapper IFU