**MRI QA hints regarding distortion correction**

**To correct for distortions one can either use Fieldmaps (Fugue) or ap/pa-Scans (Topup).**

**For Fugue:**

the dwell time (=echo spacing is the time between the center of two echos in k-space (distance between two k-space rows or time between PE-“blips”) is needed

<http://support.brainvoyager.com/functional-analysis-preparation/27-pre-processing/459-epi-distortion-correction-echo-spacing.html>

This can be found in the Siemens protocol of the scan (the actual echo spacing) or calculated from DICOM header (the effective echo spacing) as: ”effective” echo\_spacing=1/(BWinPE\*PixinPE)

**For Topup:**

the total readout time (defined as the time from the centre of the first echo to the centre of the last) in seconds) is needed.

It can be calculated from the actual number of echo spacings times the number of actual phase encoding lines -1, or as the number of reconstructed phase encodes times the effective echo spacing.

**In the case of GRAPPA/iPAT/partial fourier:**

First of all, if you want to estimate the echo spacing, partial Fourier must be neglected. Partial Fourier leaves out a complete junk of k-space (in contrast to GRAPPA where, e.g., every second line is skipped) without having an effect on the echo spacing of the remaining lines. Therefore, in order to calculate the number of phase-encoding lines which are relevant for estimating the echo spacing you need to divide the imaging matrix (in phase-encoding direction) by the iPAT factor --> Example: Imaging Matrix 128, iPAT = 2 --> 128 / 2 = 64. (Even though the actual number of phase encoding lines would be 48 if your partial Fourier is 6/8 —> 64 \* 0.75 = 48).

To finally obtain the total readout time, there are two possibilities:

Either you take the echo spacing from the syngo (or scan) protocol and divide it by the iPAT factor in order to get the effective echo spacing --> Example: 1 ms / 2 = 0.5 ms

Or you take "Bandwidth Per Pixel Phase Encode", stored in DICOM tag (0019, 1028), multiply with the number of reconstructed phase lines (here iPAT AND PF must NOT be taken into account!!!) and calculate the reciprocal --> Example: 1 / (15.625 Hz \* 128) = 0.5 ms

In both cases, the effective echo spacing would be 0.5 ms.

(If you did not use GRAPPA at all just use the number of phase encoding lines —> 128. The effective echo spacing should then be 1 ms. The "Bandwidth Per Pixel Phase Encode", stored in DICOM tag (0019, 1028) must also match your calculation and therefore should be around 7.8 Hz.)

**For calculating the total readout time, you have to distinguish between SPM and FSL correction:**

FSL:

Total readout time = (actual number of phase-encoding lines (which we calculated above) -1) \* echo spacing --> Example: (64 - 1) \* 1 ms = 63 ms (Or without GRAPPA: (128 - 1) \* 1 ms = 127 ms)

(or

Total readout time = (reconstructed number of phase-encoding lines - 1) \* effective echo spacing --> Example: (128 - 1) \* 0.5 ms = 63 ms (Without GRAPPA the calculation is identical: (128 - 1) \* 1 ms = 127 ms))

SPM:

Total readout time = 1/"Bandwidth Per Pixel Phase Encode", stored in DICOM tag (0019, 1028) --> Example: 1 / 15.625 Hz = 64 ms (Or without GRAPPA: 1 / 7.8 Hz = 128 ms)

It is important to notice that the "Bandwidth per Pixel" in the syngo (or scan) protocol is actually the bandwidth in readout direction. So do not use this bandwidth for your calculations! Instead use either the "Bandwidth Per Pixel Phase Encode", stored in DICOM tag (0019, 1028), which is not shown in the syngo (or scan) protocol, or the echo spacing from the syngo (or scan) protocol.

However, when using TOPUP to create field maps that are then given to EDDY for motion and distortion correction the exact number of the total readout time doesn’t matter as the two calculations cancel each other out (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/eddy/Faq>). Therefore, although for RSV 3T and 7T DWI data we put the wrong acquisition time (didn’t correct for GRAPPA factor 2) the result should still be valid.

Important: GRAPPA is parallel imaging: Most modern MR systems are built in a parallel architecture, consisting of a body transmit coil and set of local receiver coils that feed into parallel channels for signal amplification and processing. When operated in parallel imaging (PI) mode, information about coil positions and sensitivities can be used to reduce the number of phase-encoding steps and speed up imaging. This is quantified by the PI acceleration factor (R), a number typically between 2 and 6.

Important: multiband does not change anything about distortions!

For Philips Scanners:

other information from the DICOM header:

WaterFatShift & MagneticFieldStrength & EchoTrainLength (=Number of PE-steps/Parallelacceleration)

|  |
| --- |
| wfd\_ppm = 3.4 # water-fat diff in ppm |
| g\_ratio\_mhz\_t = 42.57 # gyromagnetic ratio for proton (1H) in MHz/T |
| wfs\_hz = MagneticFieldStrength \* wfd\_ppm \* g\_ratio\_mhz\_t = 434.21 |

Total readout time = WaterFatShift / (wfs\_hz )

effective echo spacing = WaterFatShift / (wfs\_hz \* EchoTrainLength )

according to [https://github.com/poldracklab/fmriprep/blob/260872273a1f4ef02de2cae20dd7d6948b531c4b/fmriprep/interfaces/fmap.py#L328](https://github.com/poldracklab/fmriprep/blob/260872273a1f4ef02de2cae20dd7d6948b531c4b/fmriprep/interfaces/fmap.py" \l "L328)

https://github.com/poldracklab/sdcflows/issues/5

**EXAMPLES:**

**Example (Philips scanner, 3 Tesla, Green-MED)**

WaterFatShift = 23.0209541 (from DICOM header)

Total readout time: 23.0209541/(434.21) = 0.05302 s

Example (LIFE resting state, without acceleration)

BW in PE=26.95 Hz/pix (DICOM-tag: (0019,1028)

Pix in PE=64, u.a. DICOM-tag: (0051,100b)

dwelltime = 1/(26.95\*64)=0.58ms

or from the protocol: echo spacing = 0.58 ms

total readout time = 0.03654 s = (0.58 ms \* (64 -1))

Example (LIFE MPIL DWI, with acceleration, partial Fourier=6/8, GRAPPA=2)

BW in PE= 16.446999999999999 Hz/pix (DICOM-tag: (0019,1028)

Pix in PE= 128, u.a. DICOM-tag: (0051,100b)

dwelltime = 1/(16.45\*128)=0.475ms

or from the protocol: echo spacing = 0.95 ms -> divide by acceleration factor=2 : effective spacing= 0.95ms/2 = 0.475 ms

total readout time = 0.95 ms \* (128/2-1) = 0.95\*63= 0.05985 s (seems less appropriate: 0.475 ms \* 127 = 0.0603 s OR)

Example (RSV 7T DWI, with acceleration, partial Fourier=6/8, GRAPPA=2)

BW in PE= 16.0259999999999998Hz/pix (DICOM-tag: (0019,1028)

Pix in PE= 160, u.a. DICOM-tag: (0051,100b)

dwelltime = 1/(16.45\*128)=0.389ms

from protocol: echo spacing -> 0.78 ms -> effective spacing = 0.39 ms

Total readout time = (actual number of phase-encoding lines (which we calculated above) -1) \* echo spacing = (80-1) \* 0.78 ms = 0.06162 s

Or reconstructed number of phase encodes -1 \* effective echo spacing = 0.06201 s

Example (RSV 3T resting state, with acceleration, partial Fourier=6/8, PAT=1, multiband=4)

dwell time of inv/norm scans = 0.00063 s, Nphase = 88

total readout time = 0.05481 s = 87\*63ms → for acquisition file

from protocol of actual restting state sequence: echo spacing -> 0.67 ms→ echo space given to fugue.. Sequence with GRAPPA = 4, PE = 88

Example (Agewell 3T resting state, with acceleration, partial Fourier=6/8, PAT=1, MB=3)

BW in PE= UNIMPLEMENTED Hz/pix (DICOM-tag: (0019,1028)

Pix in PE= 88, u.a. DICOM-tag: (0051,100b)

dwelltime = ?

from protocol: echo spacing -> 0.67 ms in norm/invpol scans and imaging sequence.

Total readout time = (actual number of phase-encoding lines (which we calculated above) -1) \* echo spacing = (88-1) \* 0.67 ms = 0.05829 s (NO acceleration, so effective echo spacing = echo spacing)

Example (Agewell 3T DWI, with acceleration, partial Fourier=6/8, PAT=2, MB=2)

BW in PE= UNIMPLEMENTED Hz/pix (DICOM-tag: (0019,1028)

Pix in PE= 128, u.a. DICOM-tag: (0051,100b)

PAT=2

dwelltime = ?

from protocol: echo spacing -> 0.95 ms in norm/invpol scans and imaging sequence.

**Total readout time = (actual number of phase-encoding lines (which we calculated above) -1) \* echo spacing = (64-1) \* 0.95ms = 0.05985 s (NO acceleration, so effective echo spacing = echo spacing)**