

FAST AND PERFECTLY REGISTERED MULTI-CONTRAST WHOLE BODY MRI IN A SINGLE RUN FOR PET/MR IMAGING

Benedicte MA Delattre^{1,2}, Peter Koken³, Christian Stehning³, Holger Eggers³, Susanne Heinzer², Giel Mens⁴, and Peter Börner³

¹Department of Radiology, Geneva University Hospitals, Geneva, Switzerland, ²Philips AG Healthcare, Zürich, Switzerland, ³Philips Research Laboratories, Hamburg, Germany, ⁴Philips, Best, Netherlands

Target audience: oncologists, clinical physicists, engineers

Purpose: With the recent introduction of hybrid modalities such as PET/MR, whole-body MRI reinforces its importance in the staging and follow-up of oncologic patients and shows its complementarity to FDG-PET imaging¹. A typical whole-body MRI exam contains T₂ and T₁ weighted imaging (with or without fat saturation) as well as diffusion weighted imaging with background suppression (DWIBS). The acquisition of these different contrasts requires several breath-holds for the patient (one per stack for T₁ and T₂) and several table movements. Moreover, images are potentially misregistered notably in the abdominal region, since the breath-hold position differs between multiple breath-holds. However, a good registration of the images is essential for PET/MR to reliably compare them and to support proper attenuation correction for the PET.

Our purpose is to propose a flexible whole-body MR protocol using an interleaved multi-station approach in which T₁ and T₂ weighted images are acquired during the same breath-hold and requiring a single table movement allowing a significant reduction in scan time and improvement in confidence in image interpretation.

Methods: A new framework was developed to interleave two or more different sequences at almost arbitrary granularity. Basically, the different sequence descriptions are stored on the data acquisition system in parallel tasks, allowing a very fast switching between them, and the preparation of all sequences is performed together at the beginning of the scan. Compared to the continuously moving table based 2D approach previously described², the sequences can be defined independently of each other in terms of all available scan parameters (contrast, geometry, resolution, etc.), which additionally simplifies the corresponding workflow. Experiments were performed with three different sequences, a 3D T₁-weighted mDixon sequence³, a single-shot T₂-weighted TSE sequence and a DWIBS sequence (b=800 s/mm²) (see Tab.1 for detailed scan parameters) using a Philips Ingenuity TF PET/MR. The acquisition was divided in one breath-hold of 22 sec for the acquisition of the mDixon and the T₂ TSE, and in 1 min 29 sec of free-breathing for the acquisition of the DWIBS (this time is also used for recovery of the patient between two breath-holds) (see Fig.1). Measurements were carried out on healthy volunteers and required 14 stacks (FH coverage ~1m with 12mm overlap between adjacent stacks) where only the ones located in the thoracic and abdominal area were performed under breath-hold. The integrated body coil was used for excitation and reception of the signal.

Results: The interleaved multi-station measurements were successfully performed and showed perfectly registered whole-body images (see Fig. 2), in particular of the mDixon and T₂-weighted in the abdomen. Total scan time for one stack was 22sec+1min29 = 1min51 where 100% of the time was used for imaging. In contrast, the conventional protocol requires 2 breath-holds for the mDixon and the T₂-weighted with recovery time between them (30 sec.), resulting in a total scan time of 11sec+30sec+11sec+1min29=2min21 (27% more compared to the proposed protocol, with only 80% of the time being used for imaging).

Discussion: The proposed interleaved multi-station protocol has the potential to greatly improve workflow of whole-body MR imaging, notably in the context of PET/MR investigations where optimizing patient comfort and reducing scan time is essential. The ability to perform mDixon and T₂-weighted TSE sequences in the same breath-hold gives inherently registered images and can improve confidence in image interpretation in presence of suspicious lesions. A combination with parallel imaging and suitable surface coils for signal reception could be desirable to improve signal to noise ratio and decrease scan time further.

Conclusion: The proposed framework greatly benefits to whole-body MR imaging for oncologic staging and follow-up of patients notably in the context of PET/MR where registration of images is crucial for interpretation and attenuation correction.

References: 1. Cibilerto M et al. Radiol Oncol 2013;47(3):206-218, 2. Sommer G et al. Magn Reson Med 2006; 55:918-922, 3. Eggers H et al. Magn Reson Med 2011;65(1):96-107.

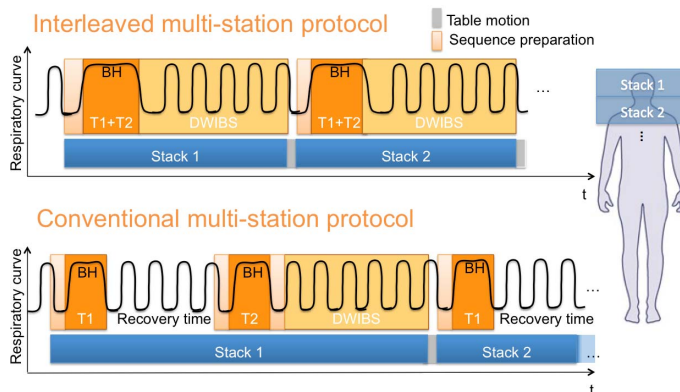


Fig.1: Scheme of the proposed interleaved multi-station protocol. T₁ and T₂ can be acquired during the same single breath-hold compared to the conventional protocol that requires 2 breath-holds with some dead time for patient recovery. The total acquisition time is reduced since all time is used for effective image acquisition.

Tab.1: Parameters of the 3 sequences used in the WB protocol.

Sequence	TE/TI/TR (ms)	Pixel size (mm)	FOV (RL x AP x FH mm)	Acq. time per stack
3D mDixon	TE1/TE2 1.1/2.1, TR 3.3	0.78 x 0.78 x 3	500 x 391 x 84	11 s.
T2 TSE	TE 80, TR 881	1.5 x 1.5 x 6	470 x 390 x 83	11 s.
DWIBS	TE 49, TI 230, TR 2619	1.45 x 1.45 x 6	375 x 296 x 83	1 min 29 s.

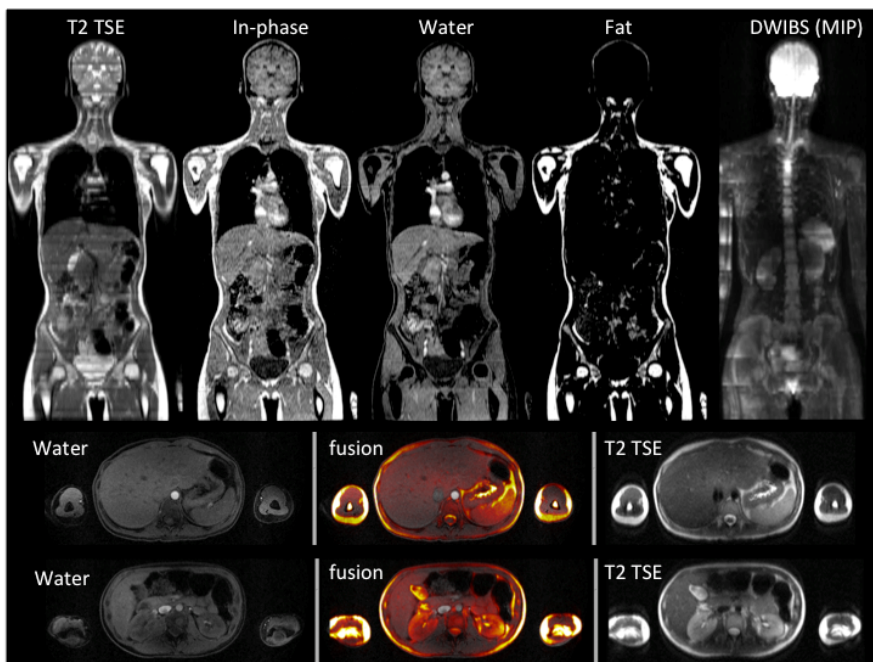


Fig.2: Coronal reformats of T₂-weighted, mDixon and DWIBS images (top). Fusions between water mDixon and T₂-weighted images at two different levels show perfect registration since the images were acquired during the same breath-hold. The entire scan is measured in a single run.