Whole-Body MRI Including DWI

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Background

National Institute for Health and Care Excellence (NICE) guidance (NG35) published in February 2016 [1] recommends to consider whole-body MRI (wbmri) as first-line imaging for patients with suspected or newly diagnosed Myeloma. The burden on the clinical MRI service is significant as these examinations can take approximately one hour and require special attention in order for favorable



image quality to be achieved. It is therefore important to optimize the workflow for maximum efficiency. Before embarking on wbmri, it is advisable to be familiar with articles such as Padhani et al. [2] and Koh et al. [3] in order to understand the aim of wbmri. The purpose of this article is to explain the technique of performing wbmri using particular features of the MR system and how to build a robust program rather than discuss clinical opinions or even to prescribe sequence parameters as these can be agreed locally.

Equipment

This article is based on using a MAGNETOM Aera / Skyra system with *syngo* MR E11 software. The following licenses are not mandatory, but do make the workflow more efficient: Tim Whole Body Suite (205 cm table movement), Tim Planning Suite (Set-n-Go) and Inline Composing.

Preparation

The referring clinician should be aware that the patients they send for this examination will be required to lie supine for approximately one hour and they will be covered from head to toe with receiver coils. It is not well tolerated by patients who will feel uncomfortable lying for this length of time or who may feel claustrophobic. It is also advisable that the patient empties their bladder prior to the examination.

Examination

The patient is positioned head first supine. If available, Head/Neck 20, Spine 32, Body 18 (x2) and peripheral angio 36 coils are arranged on the patient. Centre to the chin and move to isocentre.

It is helpful to use the Tim Planning User Interface (UI) (Top menu: *View > Tim Planning UI*), coupled graphics and Auto Coil Select (ACS). To ensure ACS is used, save each sequence with this switched on in local settings (*System > Miscellaneous > Coil Select Mode 'On-AutoCoilSelect'*). The imaging protocol will vary according to local agreements, but typically consists of:

Localizer		Whole body	
Sagittal	t2	Whole spine – 2 stations	Fig. 7A
Sagittal	t1	Whole spine – 2 stations	Fig. 7B
Coronal	tirm	Vertex to below knee joints	Fig. 7D
Coronal	t1	Vertex to below knee joints	Fig. 7E–G
Transverse	DWI	Vertex to mid femur	Fig. 7C

Localizer: Siemens > TimCT oncology > TimCT oncology > standard > FastView

FastView is preferred over multi step trufi as it has a shorter acquisition time and image quality is adequate to plan subsequent steps in the program. In *Geometry > Tim CT* (Fig. 1) the 'Range start' value of H 250 mm ensures the acquisition starts above the vertex when centred to the chin.

It is recommended to save this step before starting the examination with sufficient table movement in order to cover the required anatomy on the majority of patients. Suggested value for 'Total FoV H>>F' is 1700 mm. Allow the sequence to complete rather than stopping manually, otherwise it will re-acquire in the F>>H direction.

General	TA: 0:37 PM: ISO Voxel size: 5.0×5.0×5.0mm Rel. SNR: 1.00					₹ 1.00 : flct
Protocol Parameters	Routine Contrast Resol	ution Ge	ometrv	System Sea	uence	
Voice Commands	Comn	non Auto	Alian	Tim Planning Suit	e Tim CT	
Execution				g		
Image Management	Tim CT mode C	Dn 🦷	1000			
Auto Load	Range start H 🔹	250 📜	mm			
Copy References	Total FoV H >> F 🔹	1700 📜	mm			
	Slices	1	_			
	Slice thickness	5	mm			
	Dist. factor	100	%			
	FoV read	480	mm	Р	erform CTM adju	stments 🗹
	FoV phase	87.5	%		Table Speed	46 mm/s

Sagittal t2 whole spine: Siemens > c-spine > library > t2_tse_sag

These are acquired as a 2 subprotocol set-n-go protocol. Begin by opening a sagittal t2 and plan the cervical and upper thoracic spine off the Multi Planar Reconstruction (MPR) FastView localizer images. A field-of-view (FOV) of 400–420 mm for each subprotocol is suggested as this allows coverage of the whole spine, sacrum and coccyx in most patients. The use of integrated Parallel Acquisition Technique (iPAT) in order to achieve a short scan time is advisable. Once the upper subprotocol has been planned, add the second subprolocol by either the 'add sub-protocol' button in the Tim Planning UI (Fig. 2), or go to Geometry > Tim Planning Suite and tick 'Set-n-Go Protocol' (Fig. 3). Also tick 'Inline composing' at this stage. Select composing function 'adaptive'. Go to *Inline > composing* and type 'sag_t2' in series description for the composed series to be more obvious in the patient browser.





3									
	Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence	
		Com	mon Satura	ition Navig	ator Tim	Planning \$	Suite	Tim CT	
		Se	et-n-Go Protoc	ol 🗹	<				
			Step	2 🔹 + -					
	⊤able p	osition F	× 3	49 📜 mm					
	Table	position men	nory						
		In	line Composin	g	-				
		Norma	alize None						
	Con	nposing Fund	tion Spine						
	Figure 3:	Geometry	> Tim Planı	ning Suite					

Sagittal t1 whole spine:

Siemens > c-spine > library > t1_tse_sag

Ensure the FOV is 400 to 420 mm (as per sagittal t2). Create a copy reference to the t2_tse_sag of 'slices and saturation regions', and tick the boxes 'copy phase encoding direction' and 'steps'. Go to *Geometry* > *Tim Planning Suite* and tick 'Inline composing' Select composing function 'adaptive'. Go to *Inline* > *composing* and type 'sag_t1' in series description.

Coronal tirm:

Siemens > whole body oncology > head to pelvis > standard > headneck_t2_tirm_cor

(Or you can select a cor_tirm from the soft tissue neck program in the user tree as this is likely to contain local preferred parameters for tirm.)

Delete 'headneck' from the series description. Change FOV to 500 mm in order to visualize as much anatomy as possible in the X direction.

Prescribe as many slices as required in order to cover the patient's anatomy in the Y direction. It is accepted that the maximum FOV in the Z direction on MAGNETOM Aera and Skyra systems is 450 mm [5]. To avoid distortions being evident at the superior and inferior margins of the FOV (Fig. 4) degrading the original and composed images, it is suggested that the phase encoding direction is F>>H and to use 68.8% FOV phase. Subsequent subprotocols will then be acquired with a smaller table movement. Use 70% phase oversampling to avoid wrap. Position the first subprotocol so that the superior margin of the FOV is above the vertex. Add further subprotocols by using the 'add subprotocol'



Figure 4: Z axis distortions represented by orange circles on a 500 mm FOV image

button in the Tim Planning UI. This will position the next subprotocol displaced inferiorly by a distance of the FOV -50 mm i.e. 450 mm. With a 100% FOV phase, there would be adequate overlap, but using 68.8% means that there is a gap between the rectangular FOV's. After adding sufficient subprotocols to cover the anatomy, click on the first subprotocol in the Graphic Slice Position (GSP). It will appear yellow. Click 'Align FOV' (Fig. 5). This will result in all subprotocols being aligned and overlapping sufficiently. Tick 'Inline composing' at this stage. Select composing function 'adaptive'. Go to *Inline > composing* and type 'cor_tirm' in series description.



Figure 5: Tim Planning UI: 'Align FOV'

Coronal t1:

Siemens > abdomen > library > 3D > t1_vibe_dixon_cor

A turbo spin echo (TSE) pulse sequence could be considered for this acquisition, however volume interpolated breathhold acquisition (VIBE) has some advantages. VIBE is faster and this is important in an examination that is already lengthy. It is possible to acquire on breath-hold (Dot Cockpit: double click on sequence, or in the queue: right mouse button > Edit Properties > Voice Commands) which results in less movement artifact particularly on the thorax and abdominal sub-protocols. The use of auto voice commands results in a more efficient workflow. It is also possible to re-construct up to 4 contrasts. Go to *Contrast* > *Common* and click on the 3 dots next to Dixon. Ensure in phase, out of phase, fat and water images boxes are ticked.

Change FOV to 500 mm and phase encoding direction F>>H. 68.8% FOV phase and 70% phase oversampling. Manipulate slice thickness and number of slices to ensure adequate coverage in the A-P direction. Create a copy reference to the cor tirm of 'centre of slice groups and saturation regions', and tick the boxes 'copy phase encoding direction' and 'steps'. Go to *Geometry* > *Tim Planning Suite* and tick 'Inline composing'. Select composing function 'adaptive'. Go to *Inline* > *composing* and type 'cor_t1' in series description.

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Transverse DWI:

Siemens > whole body diffusion > general > standard > ep2d_diff_stir

For robust nulling of fat signal over a large FOV, a short tau inversion recovery (STIR) pulse is preferred over spectral adiabatic inversion recovery (SPAIR). As there are multiple

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modifications to make, it is more efficient to do this to step 1 first and then add subprotocols rather than modifying every subprotocol. Therefore, go to *Geometry* > *Tim Planning Suite* and un-tick 'Set-n-Go Protocol' in order to reduce the number of steps to 1. Change FOV to 500 mm. It is optional to reduce the number of slices from 50 to 40. This results in a 200 mm (assuming 5 mm slice thickness with 0% distance factor) scan range in the Z direction per subprotocol resulting in the first and last slices being less distorted. Naturally, more subprotocols will be required to cover the same range in the slice direction, but this is offset by each subprotocol containing fewer slices and a lower minimum TR possible which reduces the acquisition time of each subprotocol. Crucially, the Maximum Intensity Projection (MIP) of the composed high b-value inverted window series will contain less step artefact. A bipolar double refocused spin echo diffusion encoding can be used rather than monopolar. Although bipolar will lead to a higher minimum TE and therefore lower signal-to-noise ratio (SNR) and longer TR (therefore increased acquisition time) distortions will be reduced [6].



In the *Diff>Body card* (Fig. 6), it is possible to define the required number of diffusion weightings and b-values. This is to be decided locally, but typically 2 diffusion weightings are acquired, for example b=50 and b=900 [7]. As the b-value increases, SNR is reduced. It is therefore advantageous to employ more averages on higher b-value images than lower b-value images. Ensure the boxes 'Trace-weighted images' and 'ADC Maps' are ticked. If a calculated b-value is required, tick the 'Calculated Image' box. The default calculated b-value is 1400 s/mm² but up to 1600 s/mm² can be calculated inline. Ensure 'Invert Gray Scale' is ticked. This will allow you to produce inverted MIP radial ranges from the composed high b-value images.

In resolution>filter image there is an option: dynamic field correction. This can be selected using 'direct' mode (click on the 3 dots next to the parameter option) in order to reduce eddy current induced distortions in diffusion-weighted images. There will be a small time penalty if this feature is used. After modifying the sequence parameters, position the first subprotocol either above the vertex or at the level of the eyes. Click 'Add Subprotocol'. The subsequent subprotocol is positioned with an inferior offset which corresponds to the slice range -50 mm which ensures adequate overlap in the slice direction. Continue to 'Add Subprotocols' until the desired coverage has been achieved. Go to *Geometry* > *Tim Planning Suite* and ensure that 'Inline composing' is ticked and composing function is set to 'Diffusion'. Go to *Inline* > *composing* and type 'tra_DWI' in series description.

A wbmri Dot program can then be saved in the user tree by dragging and dropping the steps from the queue into a new program in the Dot Cockpit. In the patient view go to *Dot Add-In Configurator > GSP* and ensure GSP layout is set to Tim Planning UI and coupled graphics are on. This results in these settings being default every time the wbmri Dot program is used. The sequences should contain the required number of subprotocols and 'copy references' applied where appropriate. Although the initial program building can be intensive, the workflow for future examinations should be straightforward.



Results and post processing

The source images as well as the Inline composed images for all series must be available to the radiologist for reporting.

Select the composed transverse high b-value images from the patient browser or the viewing card. Load to 3D MIP and select the transverse image. Use 'radial ranges' to reconstruct a MIP series of images rotating around the Z axis. See Fig. 7C for example images.

The syngo.MR OncoCare package offers a histogram tool. It is possible to define a region-of-interest (ROI) around the spine. Then right click on the ROI and create the histogram. A threshold can then be set of what is accepted as pathology and what is accepted as normal tissue in order to predict metastatic load. This can then be mapped as a color overlay onto the tissue. This process can also be performed with the gray-scale images from the morphology scans and the ADC levels from the whole-body images.

Limitations

Some patients will be excluded on safety grounds e.g. implanted devices.

A proportion of patients will be unable to tolerate the procedure due to claustrophobia or discomfort.

It can be challenging to achieve adequate quality images of the humeri due to these structures being situated outside of the maximum 500 mm range in the X axis when the patient is positioned. It is possible to position the patient's arms anterior to the chest so they are not out of range in the X axis or to use an immobilisation device (e.g. velcro strap) to ensure that the patient's arms are as central as possible. However, patient comfort must also be considered and most examinations are performed with the patient in a comfortable position that they can maintain for the duration of the examination.

Conclusion

Inevitably whole-body MRI requests to the clinical MRI department will increase and therefore so will the pressure with regards to throughput. By building a wbmri program which employs Tim Whole Body Suite, Tim Planning Suite, Inline Composing and utilizing *syngo*.via for image reading it is possible to create an effective workflow for every step of the patient journey in order to maximize efficiency.

References

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