

# Whole-Body MRI at 1.5T in the Era of Deep Resolve

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Until recently it could take up to an hour to perform a whole-body MRI (WB-MRI). But what if you could cut that in half and make it better? Buckle up.

Around six years ago we shared a how-to guide hosted on the Siemens Healthineers *WB-MRI website*. Hopefully, many of you found this helpful in designing and refining your protocols to meet the increasing demand for WB-MRI for clinical indications including the diagnosis of multiple myeloma, the surveillance of patients with cancer predisposition syndromes, and for patients with bone predominant metastatic disease from prostate and breast cancer. Over the past few years several technological and software developments have improved access to this technique by significantly reducing scan times (TA) while maintaining (and in many cases improving) image quality.

In this article, we share our experience in developing WB-MRI protocols on the 1.5T MAGNETOM Sola emphasising how we have harnessed the power of Deep Resolve and the XA platform. For reference, previous guides and resources remain available online and as such we won't touch on the older software platforms and instead focus on how things have changed.

## XA platform

The latest generation MAGNETOM scanners feature the new XA-platform scanner software. Previous-generation systems may also be offered upgrades (dependent on individual support agreements) enabling access to the library of the latest scanning techniques.

Sequence/ stations	TR (ms)	TE (ms)	FOV (mm)	Phase FOV (%)	Slice	Slice thick- ness (mm)	Gap (%)	Matrix (inter- polation)	Phase enc. direction (over- sampling)	iPAT / DRB / DRS / DRG	b- values (s/mm <sup>2</sup> )	Aver- ages	TA (min:sec)
FastView	n/a	n/a	n/a	n/a	Range 1350 mm	n/a	n/a	n/a	n/a	n/a	n/a	n/a	00:38
STIR spine sag (x2)	3500	89	380	100	15	4	20	272×218 (on)	H>F (80%)	2 / off / on / on	n/a	1	02:24 total
T1 spine sag (x2)	266	8.6	380	100	15	4	20	256×204 (on)	H>F (80%)	0 / off / on / on	n/a	1	02:08 total
T1 Dixon VIBE axial (x6)	6.8	2.39 / 4.77	430	93.8	44	5	0	256×204 (off)	A>P (PE – 0% SL – 45.5%)	CAIPI 4 (2×PE2×SL)	n/a	1	01:36 total
DWI axial (x6)	5370	63	430	90.6	40	5	0	128×128 (on)	A>P (0%)	2 / on / on / off	50, 900	3D diagonal 3, 8	07:42 total
T2 HASTIRM cor (x4)	1000	95	450	100	38	6	10	384×346 (off)	R>L (50%)	3	n/a	1	02:32
T2 HASTE axial (x6)	1000	96	430	93.8	40	5	0	320×240 (off)	A>P (0%)	3	n/a	1	02:48
Total measurement time													19:48

**Table 1:** Key sequence parameters for MET-RADS [1] core sequences on 1.5T MAGNETOM Sola – excluding adjustment times.

## Evolution, not revolution

This updated protocol relies heavily on the utilization of **Deep Resolve Boost (DRB)**, **Gain (DRG)** and **Sharp (DRS)** which are available to current owners and new purchasers of the various Deep Resolve packages. DRB for DWI<sup>1</sup> will become available upon future upgrades to syngo MR XA60/61 – contact your local product specialist for details. Cases demonstrating the clinical use of DRB in whole-body DWI can be found in the article “*Initial experiences using DRB to accelerate whole-body diffusion MRI*” presented in this edition of MAGNETOM Flash.

Procedurally, many aspects of executing a whole-body examination remain the same as were set out in the previous guide – Table 1, detailing parameter selections, shows the familiar structure of the examination.

### Software compatibility

A downloadable \*.exar1 file from the syngo MR XA51 platform is available at [www.siemens.com/wb-mri](http://www.siemens.com/wb-mri). Due to the inability to perform sequence conversion to an older software platform, \*.pdf files are also available. Please note that, at the time of publishing, these files do not include the DRB DWI sequence – updates will be posted online as this becomes available.

<sup>1</sup>Work in progress. The product is still under development and not commercially available. Its future availability cannot be ensured.

## Managing changes

As changes in quantitative measurements such as ADC values and bone marrow fat fraction are increasingly relied on by radiologists to assess the success of anticancer treatments [1], scan parameters must remain as consistent as possible between patient visits – we recommend this should include ensuring patients are scanned on the same hardware each time. Those managing a fleet of different scanner models will be familiar with the difficulties around standardization of acquisition in this context. Naturally, as scanners are replaced and upgrades are performed,

it can be difficult to match exactly what was done before and this may mean the advantages of new techniques are overlooked in the pursuit of reproducibility.

Utilize the resources available to you, whether that be through the expertise of the Siemens Healthineers MR Applications team or via assistance from expert colleagues. You should ensure that whatever changes to image appearance manifest as a result of system upgrades, everyone in the team knows how to identify and interpret the effect of those changes.

You may find **teamplay Protocols** useful if managing more than one Siemens Healthineers MR system. This service allows you to distribute protocol changes remotely.

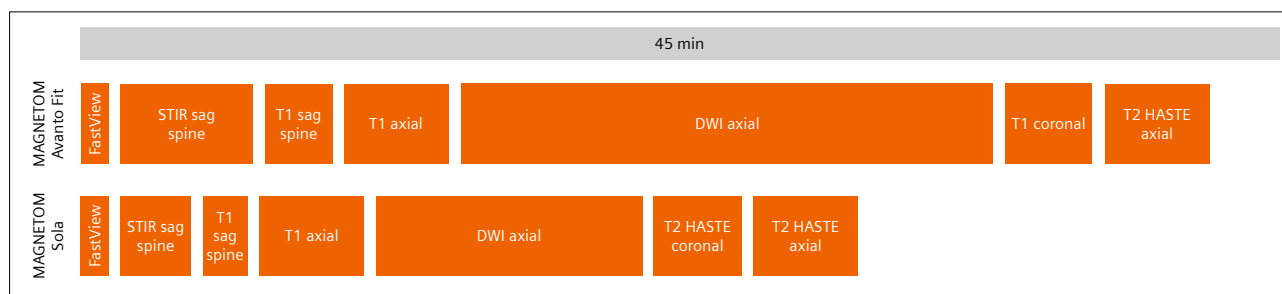
### Minimum equipment requirements

- Spine 32
- BioMatrix Head/Neck 20
- Body 18 coils as required for coverage to knees (3× recommended)
- Optional: Peripheral Angio 36 if full-leg coverage is required without patient repositioning

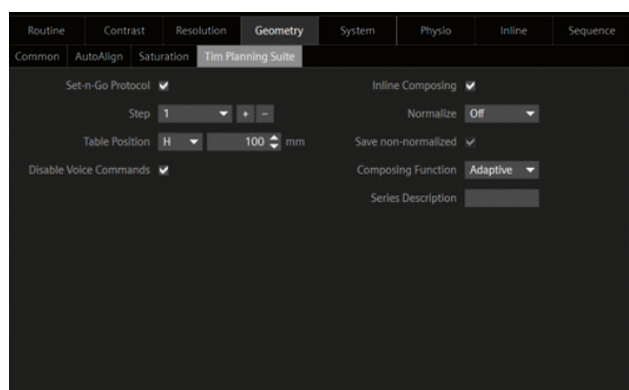
## Protocol set-up

As pointed out in the introduction, little has changed in the set-up for whole-body MRI examinations. However, as acquisition times become shorter, inefficient workflows can have a greater impact on the total examination time. Some sites will find the features of **MyExam Whole-Body Assist** useful particularly when designing user friendly protocols for less experienced operators.

The sequences presented here are ordered in such a way that ensures any post-processing (MIPs, MPRs) can be completed while the patient is being examined. Due to the decreased TAs, adjustments can occupy a greater proportion of the examination length (Fig. 1). Use the shim mode “Tune up” where appropriate for spine and HASTE sequences that do not require a comprehensive adjustment strategy to reduce the impact on examination duration.



**1** Comparison of example examination times on the MAGNETOM Avanto Fit (top) versus MAGNETOM Sola (bottom) scanners with approximate adjustment times included.



**2** Location of disable voice commands tick box – this can be set on a per-step basis.



**3** A colleague demonstrating vertex to knee coil coverage with three Body 18 coils.

During initial protocol setup, disable breath-hold instructions on slice groups positioned in the head, lower body and leg regions as there are minimal breathing artifacts in these anatomical regions (**Geometry: Tim Planning Suite: Disable Voice Commands** tick box, Fig. 2).

You may choose to have the T2 HASTE/HASTIRM sequences run without breath-holds as standard – the single-shot nature of the acquisition effectively eliminates motion artifact, however, there may be some slice-to-slice positional mismatch if this approach is selected. Including extras such as a fast FLAIR brain sequence using Deep Resolve is optional but can serve as early asymptomatic lesion detection for some patient groups.

## Patient and equipment set-up

It is important to ensure patients are as comfortable as possible so that they can tolerate the full examination without interruption. Use foam pads, pillows and knee supports where required for comfort and to protect patients from possible injury from a conductive loop or RF proximity burns. Changing patients into hospital gowns or other suitable clothing can help reduce the likelihood of discovering non-implanted metallic objects once the scan has begun.

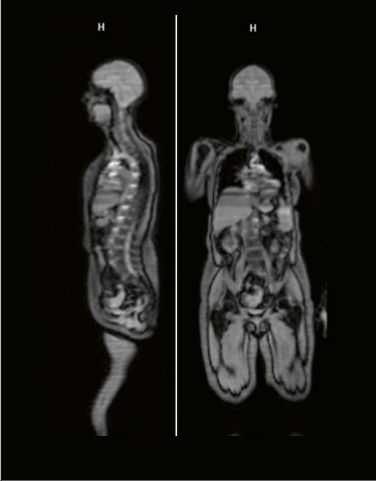
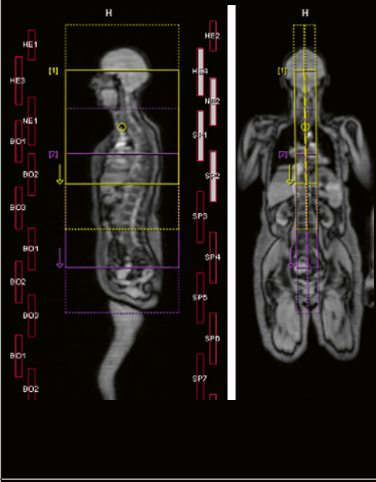
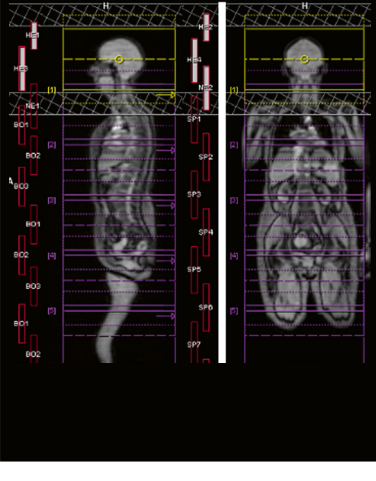
Use of the anterior part of the Head/Neck 20 will improve image quality in the anterior head and neck region. All of the sequences in this protocol are fairly tolerant to the removal of these coil elements, so you can afford to be led by patient preference. Remember

that BioMatrix Head/Neck 20 coil can be tilted to 9 or 18 degrees, enabling closer posterior coil positioning for kyphotic patients and thus greatly improving both patient comfort and image quality in the head and neck region. Place Body 18 and/or Peripheral Angio 36 coils as required to cover the desired length of scan (Fig. 3) – ensure the first Body 18 coil is positioned to cover the patient's shoulders superiorly.

If regularly used together you can prepare two of your Body 18 coils for whole-body placement using loosely connected Velcro straps – being careful not to damage the coils.

Depending on the height of the patient and the range of motion of your scanner table you may be able to achieve full head-to-toe coverage with the Peripheral Angio 36 coil. With this coil you may notice signal drop posteriorly which can be countered by positioning an upside-down Body 18 coil longways in the recess the removable table padding occupies. Ensure that excess pressure is not placed on this Body 18 coil by strategic placement of the foam pads supplied with your system.

AutoCoilSelect is now managed on a per-sequence basis (further details in Table 2) and you should set group graphics to ON before you start. If patients are unable to hold their breath remember to disable any automatic voice commands. Using the positioning laser, set the start position to a patient's chin and the FastView localizer will begin acquisition from above the skull vertex. You're now ready to scan – read on for sequence-specific tips and follow along with the video at [www.siemens.com/wb-mri](http://www.siemens.com/wb-mri).

Sequence details	Positioning and ranges	Acquisition tips	Adjustable parameters	Notes
<b>Step 1</b>  <b>FastView localizer</b>  <b>Range:</b> Vertex to knees  <b>Plane:</b> Axial (MPRs are generated automatically)		Set the acquisition range required for your study – the maximum range will vary depending on the table movement limits of your scanner		As before you should allow this localizer to fully complete before planning further. When complete your anterior elements will display on screen
<b>Step 2</b>  <b>STIR and T1 spine</b>  <b>Range:</b> Whole spine  <b>Plane:</b> Sagittal to patient's anatomy  <b>Method:</b> Set-n-Go		Enable spine or adaptive composing in the <b>Geometry: Tim Planning Suite</b> tab  Ensure H>F coverage from skull base to at least S3  Angle to cover all vertebral bodies R>L for best fit  Reduce artifact by setting AutoCoilSelect to "Restricted" and allowing only posterior elements to be used	Increase the number of slices to cover vertebral bodies R>L  Increase phase FOV to a maximum of 120% to accommodate taller patients while maintaining resolution  If this is still insufficient, add an additional slice group	Experiment with the amount of overlap required to maintain the quality of the composed images – be mindful that shorter bore scanners may have a more limited region of homogeneity
<b>Step 3</b>  <b>T1 Dixon CAIPI VIBE</b>  <b>Range:</b> Vertex to knees  <b>Plane:</b> Axial  <b>Method:</b> Set-n-Go with automated breath-hold instructions		Position the Set-n-Go stack so that the first step has "spare" slices proud of the vertex – this ensures the DWI and HASTE axial series have the correct coverage  Disabling breath-holds on those steps not affected by breathing motion can reduce TA and improve the patient experience	Add further steps if required for taller patients  You may increase FOV for larger patients but be aware you will gain little additional anatomical coverage R>L due to edge-of-field artifact	Stacked 3D VIBE images benefit from a small amount of overlap – this is why the VIBE has 44 slices versus the 40 for DWI/HASTE which do not require overlap

**Table 2:** Step-by-step sequence positioning and acquisition tips (steps 4–6 on the next page).

Sequence details	Positioning and ranges	Acquisition tips	Adjustable parameters	Notes
<b>Step 4</b>  <b>DWI</b>  <b>Range:</b> Vertex to knees  <b>Plane:</b> Axial  <b>Method:</b> Set-n-Go		<p>Applying copy reference functions to the DWI and HASTE axial sequences will ensure slice position match between series</p> <p>Experiment with setting the AutoCoilSelect range to “Generous” – you may find this improves SNR by activating additional receiver elements</p>	<p>Limit parameter changes to this sequence as the ADC values produced are increasingly relied on for quantitative response assessment – altering acquisition parameters may impact the ADC and make serial comparison more challenging</p>	<p>Removing b900 averages from the signal-rich head step and adding them to the abdomen steps can reduce stepping artifacts through the liver and spleen</p>
<b>Step 5</b>  <b>T2 HASTIRM</b>  <b>Range:</b> Vertex to knees  <b>Plane:</b> Coronal  <b>Method:</b> Set-n-Go		<p>Leave some space above the level of the vertex – without this, the head will be affected by edge-of-field artifact</p> <p>If desired this sequence can be performed with breath-holds but typically motion artifact is not significant using this single-shot technique</p>	<p>Vary the inversion time (TI) to achieve the desired level of fat suppression</p> <p>For a HASTE, TR controls the spacing between shots rather than having a significant impact on image contrast – be wary of going too fast however as you can increase SAR issues and introduce artifact if the TR is too short</p>	<p>Where available, applying DRB will compensate for noise introduced by using an increased GRAPPA factor – this shortens the echo train and sharpens HASTE images</p>
<b>Step 6</b>  <b>T2 HASTE</b>  <b>Range:</b> Vertex to knees  <b>Plane:</b> Axial  <b>Method:</b> Set-n-Go		<p>Use the copy reference function to ensure slice positions match with the DWI and T1 VIBE axial images</p> <p>As with step 5, this sequence can be performed with breath-holds if required</p>	<p>As above</p>	<p>In addition to the above, where available increase the interleaving step size to reduce any artifact from shorter TRs on image quality</p>

Table 2: Step-by-step sequence positioning and acquisition tips.



## Spine sequences (STIR and T1-weighted)

These sequences are used to evaluate bone lesions and reveal any lesions threatening the spinal canal. STIR remains the recommended approach for fat-suppressed whole-spine imaging due to its robustness against artifacts, and ability to tailor the degree of fat suppression by varying the inversion time (TI). The CoilShim feature, integrated into the BioMatrix Head/Neck 20 coil, improves local field homogeneity and has a role to play where spectral fat-suppression techniques are preferred, reducing or eliminating bright-fat artifact in the cervical and upper thoracic spine.

For T1-weighted imaging, setting a low TR can improve the contrast between normal and tumour-infiltrated bone marrow, spinal cord, and cerebrospinal fluid. When set to only activate posterior elements, the new per-sequence AutoCoilSelect setting "Restricted" allows operators the freedom to move scan volumes without inadvertent activation of anterior artifact-creating elements during spinal imaging.



**4** STIR and T1 sagittal composed whole-spine images demonstrating improvements in image quality between conventional (**4A, 4C**) and DRG+DRS (**4B, 4D**) sequences.

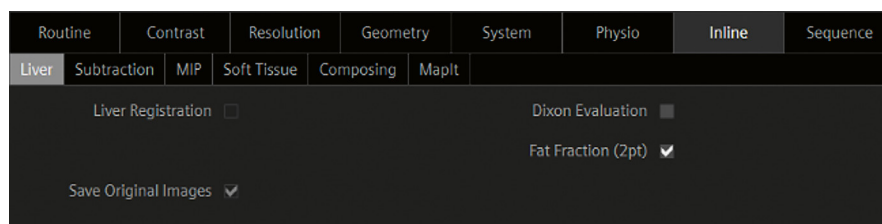
Deep Resolve for TSE can facilitate marked reductions in TA while maintaining or improving image quality (Fig. 4). You may find DRB less useful for spine imaging due to infolding (SENSE) artifacts when an H>F phase encoding direction is selected. This protocol uses the image-based denoising technique DRG which (while less effective at denoising) avoids such infolding artifacts. DRG has several settings which require trialling using the retro-recon function to find the best balance for your readers. DRS permits a lower base resolution to be selected for equivalent or better reconstructed image resolution.

Utilizing simultaneous multi-slice (SMS) can allow you to quickly acquire large volume T1 and T2 TSE axial spine series in regions of concern (for example if impending cord compression is seen). If thinner slice resolution is required you might consider using Compressed Sensing (CS) on a SPACE axial sequence to reduce the comparatively lengthy TA.

## Whole-body sequences (T1 Dixon, T2 HASTE, and HASTIRM)

T1 Dixon imaging allows the creation of quantitative fat-fraction images which are used to assess tumor response or progression. Previously, the creation of these images was a manual procedure involving the addition and division of image series but can now be generated inline (**Inline: Liver: Fat Fraction (2pt)** tick box, Fig. 5) and will be composed along with the chosen Dixon contrasts.

If enabled, DRB can improve the sharpness of HASTE images by compensating for noise introduced with the use of higher acceleration factors, reducing the echo train length and thus reducing blurring.



**5** Tick box for automatic fat-fraction reconstruction.

## Diffusion-weighted imaging

Previously, WB diffusion sequences were affected by broken spine artifacts, which were countered with awkward manual frequency-fixing techniques. This is now a thing of the past with the advent of SliceAdjust – a slice-by-slice shimming technique available on BioMatrix scanners. SliceAdjust should be used when acquiring and composing multiple large-volume DWI blocks.

Acquiring liver-lesion sensitive b-value images (between b500-b600 s/mm<sup>2</sup>) was previously recommended by the MET-RADS and MY-RADS guidelines. However, improvements in the signal-to-noise ratio enabled by the XA platform now allow good-quality b500-b600 s/mm<sup>2</sup> to be calculated rather than acquired, saving you time. Setting a calculated b value is straightforward – simply enable it in the **Diff**: tab on each DWI step.

DWI-SNR can be optimized by setting the bandwidth to allow minimum echo spacing, permitting the selection of an optimally minimized TE.

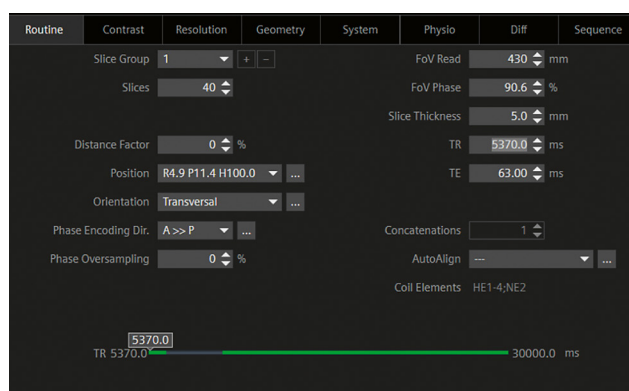
The diffusion parameters should be set to your team's preferred balance of SNR versus geometric distortion. Typically a 3D diagonal acquisition maximizes gradient performance resulting in greater SNR compared to the 3-scan-trace method. It's important to note that if the single-diffusion-direction 3D diagonal mode is selected, averages should be multiplied by 3 to reach an equivalent number of averages to a 3-directional 3-scan-trace. Additionally, the selection of a monopolar diffusion scheme will allow a shorter TE (and thus increased SNR) at the cost of increased geometric distortion.

When optimizing the sequence you may find a TR gap between a range of shorter, more SAR-intensive TRs and the next selectable TR (Fig. 6). Usually it is optimal

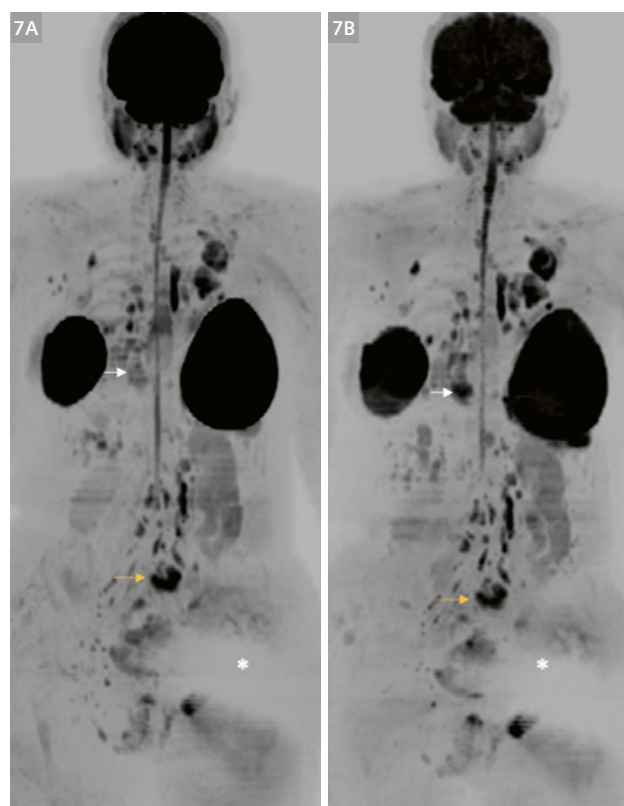
to select the lowest TR however if SAR is an issue (e.g., if you are attempting to replicate this technique at 3T) an effective tactic is to select the minimum TR of the second “window” – reducing heating while minimizing TA.

Currently, SMS is an ineffective acceleration technique for WB-DWI. To maximize time-saving, one must either select a much shorter TR (which may have a significant negative impact on image contrast / DWI-SNR) or acquire more slices per step risking straying into the region of ADC drop-off as demonstrated by Winfield et al. [2]. SMS may however have a role to play in addressing the TA implications of a large TR “gap” as discussed above.

Deep Resolve Boost performs excellent denoising, enabling the selection of fewer averages per b-value resulting in a much shorter total TA versus conventional DWI (Fig. 7). Asymmetric averaging ensures the majority of time is spent acquiring high b-value data. Additionally, step-based averaging (e.g., more on the liver, fewer on the brain) helps to reduce the more conspicuous stepping artifact which can be seen in the liver and spleen with these shorter duration/fewer average sequences.



**6** TR selection demonstrating interval between selectable TRs.



**7** b900 inverted coronal MIP projections of conventional (7A) and DRB (7B) DWI.

## Embrace the potential

Re-learning the relationships between SNR, scan time, and sequence parameters in the era of Deep Resolve has been a fascinating journey. Ultimately, you'll need to take that journey yourself to find what works best for you and your team.

By leveraging the power of these acceleration techniques, we've seen that patients' experience and image quality can be improved while allowing greater utilization of these often-limited resources.

While we'll always have fond memories of the MAGNETOM Avanto Fit, we've aimed to show that you too can make a huge impact for your patients by embracing the future of MRI. Good luck!

Visit [www.siemens.com/wb-mri](http://www.siemens.com/wb-mri) to watch the video tutorial.

## References

- 1 Padhani AR, Lecouvet FE, Tunariu N, et al. METastasis Reporting and Data System for Prostate Cancer: Practical Guidelines for Acquisition, Interpretation, and Reporting of Whole-body Magnetic Resonance Imaging-based Evaluations of Multiorgan Involvement in Advanced Prostate Cancer. *Eur Urol*. European Association of Urology; 2017;71:81–92.
- 2 Winfield JM, Collins DJ, Priest AN, et al. A framework for optimization of diffusion-weighted MRI protocols for large field-of-view abdominal-pelvic imaging in multicenter studies. *Med. Phys*; 2016;43:95–110.

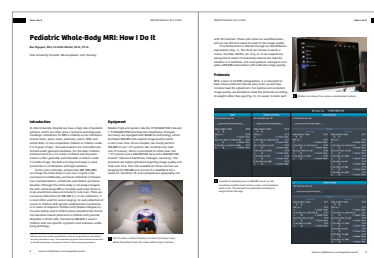
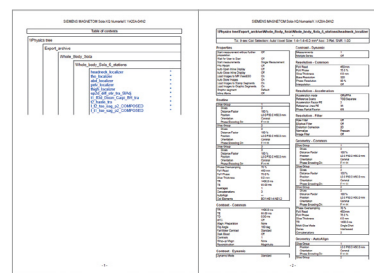
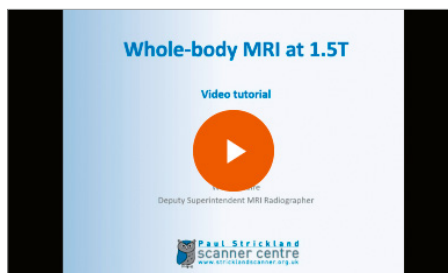


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