Clinical User Perspective of Deep Learning Image Reconstruction Techniques (Deep Resolve) for Improved MRI Capabilities

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Abstract

Decreased acquisition time and increased image quality during magnetic resonance imaging (MRI) exams are important diagnostic imaging considerations. MRI scan times are highly variable depending on the body area being imaged, patient compliance, and the radiologist's preferred imaging protocols. Attempts to reduce imaging time and increase resolution are becoming increasingly important, due to the time required to complete a high-quality MRI exam while keeping patient comfort in mind. Advanced imaging methods using deep learning (DL) algorithms offer unique advantages for demonstrating human anatomy, physiology, and pathology in a variety of ways.

In this paper, we review initial user experience with a combination of the DL algorithms Deep Resolve Boost (DRB) and Deep Resolve Sharp (DRS). Deep Resolve Boost is a denoising algorithm applied after collection of *k*-space data. How does it work? Deep Resolve Boost uses raw data from a data-reduced fast scan and applies an iterative process which uses multiple applications of a deep neural network to produce a final image with significantly reduced noise and a high apparent signal-to-noise ratio (SNR) in a shortened acquisition time. In the remainder of this manuscript, we will refer to the simultaneous application of Deep Resolve Boost and Deep Resolve Sharp simply as "Deep Resolve" since the combined application of both DL tools leads to the best results.

Introduction

Increasing demand for diagnostic testing, specifically MRI, has outpaced the provincial capacity in British Columbia. Wait lists for access to MRI technology are long, and attempts to increase capacity and streamline patient flow are required to ensure future sustainability. Patient flow through the MRI department can be improved by using quick imaging protocols that are standardized and optimized. Vendors are supporting frontline users by developing methods to improve imaging quality and reduce scan time through the use of deep learning algorithms. To build capacity and improve access to magnetic resonance imaging (MRI), artificial intelligence (AI) and machine learning (ML) technology can be advantageous in reducing MRI scan times. Deep learning (DL) methods with new algorithms for gathering high-quality data in shorter acquisition times are now routinely being employed in medical imaging departments in Canada. Deep learning can optimize and streamline imaging protocols by reducing the time spent acquiring image data, or it can be used to improve resolution and enhance image quality.

Background

AI and deep neural networks or DL are rapidly expanding in medical imaging departments. Several factors that are under direct control of the MR technologist can determine quality in MR imaging. The quality tradeoffs aim to balance scan time, image resolution, and signal-to-noise ratio (SNR) while minimizing image artifacts. The focus is to reduce the amount of time spent in the MR system while contributing to patient comfort and tolerance. In an ideal MRI world, images would be acquired with short acquisition times, high spatial resolution, and adequate SNR to produce a high-quality image. If DL algorithms can accurately improve image quality, MRI departments can make steady gains in decreasing the time the patient spends in the scanner.

Siemens Healthineers has introduced advanced DL imaging technologies to denoise images and increase sharpness. These DL reconstruction techniques allow for improved resolution and increased SNR while potentially decreasing acquisition times. Currently Deep Resolve Boost can be applied to TSE sequences. Nanaimo Regional General Hospital (NRGH) is a test site for the new Deep Resolve reconstruction algorithm and was granted a trial license in 2023.

Methods

Clinical applications of Deep Resolve

NRGH opted to assess the Deep Resolve technology in a variety of body areas that relied heavily on TSE acquisitions. Between February and August 2023, frontline user input was compiled, and clinical examples were shared with Siemens Healthineers in an early review of the technology. The body areas where we tested Deep Resolve technology include:

- Knee and shoulder, including arthrogram
- Wrist and ankle
- Brain, pituitary gland
- Cervical, thoracic, and lumbar spine
- Pelvis (prostate, female pelvis, rectum)
- Heart

This is by no means an exhaustive list, but we felt these were the most important areas to focus on for our site. Additionally, routine protocols for areas such as the internal auditory canal (IAC) and musculoskeletal (MSK) mass protocols, might be more easily implemented if imaging protocols are TSE-based. NRGH uses 3D SPACE and MPRAGE sequences for IAC protocols, and Dixon for orbit and small-part mass protocols.

Assessments and measures

In early discussions, it was felt that NRGH would attempt to use Deep Resolve in both small and large MSK studies. Small field-of-view (FOV) MSK imaging can be prone to signal loss due to the size of the FOV, especially in finger and wrist imaging, where the FOV ranges from 80 to 100 mm. Deep Resolve was used in a variety of ways to ensure the technology directly aided protocol optimization. The intent was to gather data about the technology in use and then observe the resultant images to ensure no major differences existed in the final image quality, such as loss of contrast or an increase in image artifacts or noise. Several of our MRI technologists were involved in using the technology and were consulted on patient response to scan time, patient movement, and the protocols best suited to Deep Resolve. The radiologists visually assessed the images for contrast and spatial differentiation and clinical significance. The technology was implemented into existing imaging protocols using a triangulated assessment approach in the following categories:

- Pure comparative analysis
- Optimized Deep Resolve pulse sequence
- Resolution enhancement
- Speed enhancement

Comparative analysis

Comparative analysis was performed when the Deep Resolve option was rerun as a second acquisition with identical parameters, or as close to identical parameters as possible. When Deep Resolve is applied in the resolution card, interpolation and generalized autocalibrating partially parallel acquisition (GRAPPA) with a parallel acquisition technique (PAT) factor of 2 is automatically applied to the sequence in the *k*-space domain. No change in time is noted when Deep Resolve is applied, but significant inherent signal is gained from the technology. Our site used the inherent signal gain in a variety of ways while preserving or improving image quality.

Deep Resolve was initially applied in the knee and shoulder trials. The department did not purchase new coils for the Deep Resolve technology: We used our 15-channel transmit/receive knee coil and our single (large) 16-channel receive shoulder coil. If the original sequence did not have parallel imaging, the *k*-space-based GRAPPA with a PAT factor of 2 was automatically applied with Deep Resolve. Depending on the number of averages in the original sequence, and if GRAPPA was selected, we used this as a starting point to either increase the PAT factor, decrease averages, or decrease acquired resolution.

Initial consultations from the radiologists indicated which exams/sequences required higher resolution or when faster scanning was acceptable. When the department first started using Deep Resolve, our approach was overly aggressive: We increased two resolution steps, increased the PAT factor, and decreased an average without adding any oversampling. While the approach seemed to work for most small adults, the images could be signal-starved on large or bariatric subjects. With time and experience, we developed a nuanced approach. We learned we could be quite aggressive with PAT factors and resolution, as long as sufficient phase oversampling was present.

Optimized Deep Resolve pulse sequence

Optimized Deep Resolve versions of pulse sequences, with several modified parameters, were created to compare with NRGH's standard sequences. This will be discussed in detail in the individual clinical examples with an accompanying image to demonstrate the potential benefits. Parameter changes include TR, TE, concatenation, base matrix, bandwidth, echo train length, motion compensation, slice thickness, gap, phase oversampling and direction, number of signal averages, and FOV. Some of the current standard spine sequences employ simultaneous multi-slice (SMS), and despite the thinner slices, an optimized Deep Resolve acquisition only with in-plane parallel imaging is felt to be superior in image quality. Overall, we found removing SMS and using Deep Resolve with in-plane parallel imaging provided better image quality in most applications. The combination of changes will be looked at when continuing to develop new protocols for NRGH.

Resolution enhancement

With new advances in Deep Resolve, the primary two foci are resolution or speed enhancement. Resolution enhancement was the early focus at NRGH for specific protocols. Attempts were made to keep the pixel aspect ratio as close to square as possible to optimize resolution, or at least to keep the ratio at 80% of the base matrix or higher, e.g., 80% of 256, 320, or 384. This equates to 204 × 256, 256 × 320, and 307 × 384 matrices. For most MSK areas, we found the optimal resolution/time balance was between 80% and 85% phase resolution. Clinical decisions were made to reduce the phase resolution for certain sequences (i.e., anatomic information), while higher resolution was applied to critical 'money-shot' sequences. Resolution enhancement can also be performed in the slice direction with a reduction in slice thickness. In brain imaging, the standard seems to traditionally be 5 mm slice thickness. However with the continued advances in pulse sequences, sites can strive for thicknesses of 3 to 4 mm. Spinal imaging also seems to be in the 3 to 4 mm range. At NRGH, the slice gap is consistently above 20%, and attempts to reduce this below 10% were employed, especially when covering neurological and musculoskeletal anatomy. We found an increased susceptibility to artifacts in areas which are subject to motion, such as the bowel (peristalsis) which can be explained by the fact that Deep Resolve protocols usually contain less averages and may be balanced by increasing the number of averages to benefit from motion averaging (of cause giving up on some of the scan time reduction gained with Deep Resolve).

Speed enhancement

With the paucity of MR resources in Canada, doing more scans in less time is an important focus. NRGH decided that quick imaging attempts and scans at very low base matrix settings of 256 or below might also be an interesting way to use Deep Resolve. Reducing the cycle time of a patient through the system, without altering the diagnostic quality of the final image, has the potential to drastically improve access to limited MR resources in Canada. There are several applications where a quick scan is beneficial, namely in patients who are:

- Claustrophobic
- In extreme pain
- Pediatric
- Geriatric
- Unable to hold still for long periods of time
- High risk (patients under sedation or ICU patients)
- Fitted with implants[1] requiring restrictive SAR deposition, e.g., neurostimulators

The method employed was to drop the base matrix, e.g., 256 or lower in cardiac or pelvic TSE imaging, and reduce a signal average. This typically shortens the time drastically by a factor of 2, which can be useful when imaging patients in the aforementioned categories. The image findings (outlined below) are very exciting and potentially far reaching for one of the traditional challenges in MR: total imaging time.

[1] *The MRI restrictions (if any) of the metal implant must be considered prior to patient undergoing MRI exam. MR imaging of patients with metallic implants brings specific risks. However, certain implants are approved by the governing regulatory bodies to be MR conditionally safe. For such implants, the previously mentioned warning may not be applicable. Please contact the implant manufacturer for the specific conditional information. The conditions for MR safety are the responsibility of the implant manufacturer, not of Siemens Healthineers.*

Musculoskeletal imaging focus
Wrist imaging

Prior to Deep Resolve, the wrist protocol was run with an FOV between 90 and 100 mm, depending on slice orientation, and took 12.5 minutes. The wrist protocol has been converted to Deep Resolve and is now 8 minutes with significantly better resolution, including an overall smaller FOV between 80 and 85 mm. The 16-channel hand/wrist coil is used for routine image acquisition. For the routine wrist protocol, NRGH runs the following Deep Resolve TSE sequences:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
ax Deep Resolve PD FS TSE	2.5	0.25	2:11
cor Deep Resolve T1 TSE	2.0	0.2	2:00
cor Deep Resolve PD FS TSE	2.0	0.2	2:00
sag Deep Resolve PD FS TSE	2.5	0.25	2:25

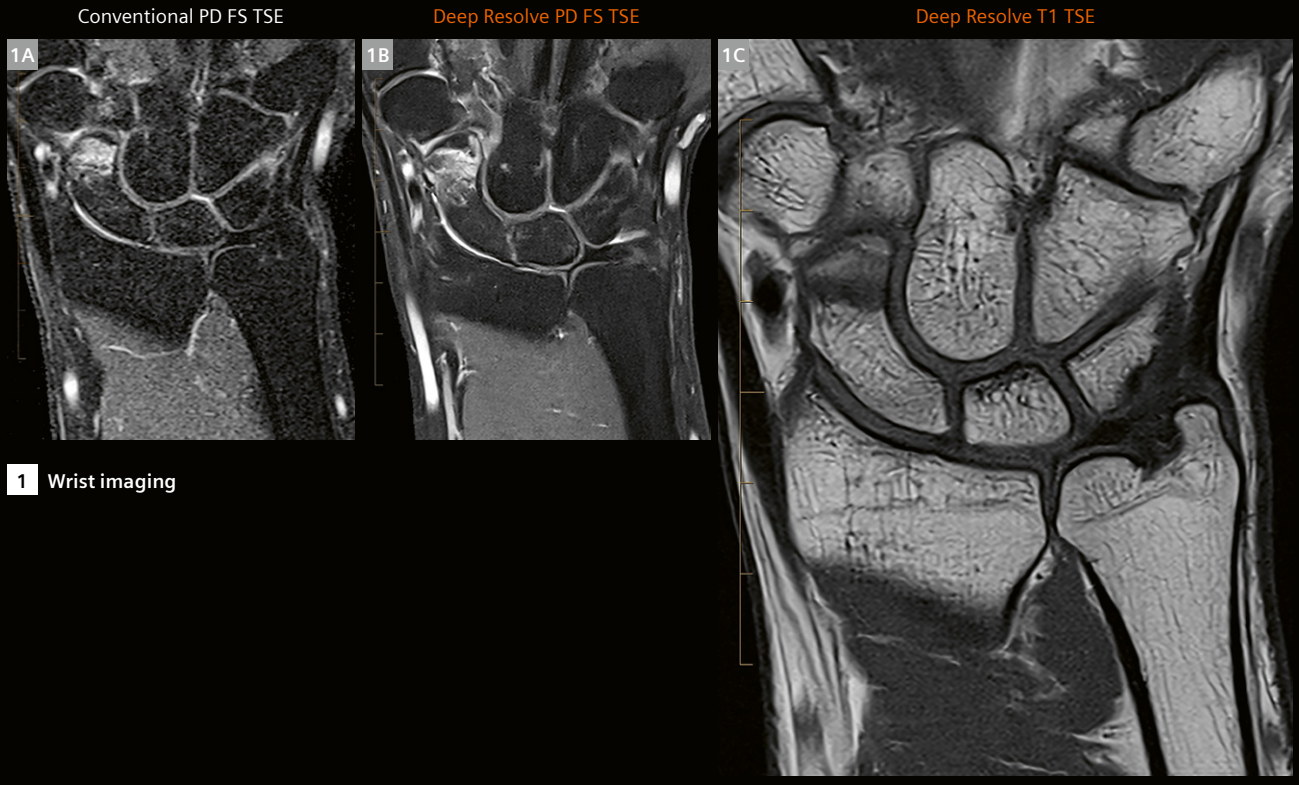
Table 1: Wrist imaging

Coronal wrist (Figure 1)
(1A) is the standard coronal PD FS TSE wrist image with a base matrix of 230 × 288, a FOV of 100 mm, and was acquired in 3:03 minutes. Two averages were used with a GRAPPA acceleration of 2.

(1B) is the Deep Resolve sequence, with an acquisition time of 2:48 minutes, a base matrix of 220 × 256, and a FOV of 85 mm. Three averages were used with a PAT acceleration factor of 4.

(1B) shows a significant improvement in image quality with Deep Resolve for the coronal PD FS TSE sequence. It improves the depiction of articular cartilage, scaphoid edema, and the triangular fibrocartilage complex (TFCC). Also note the improved assessment of the scapholunate ligament.

(1C) is the Deep Resolve T1 TSE sequence with a base matrix of 216 × 288, a FOV of 85 mm, acquired in 2:04 minutes. Three averages were used with a PAT acceleration factor of 4. The acquired voxel size is $0.39 \times 0.29 \times 2.0$ mm^3, compared to the reconstructed voxel size of $0.15 \times 0.15 \times 2.0$ mm^3. The coronal Deep Resolve T1 TSE demonstrates excellent cortical and trabecular detail.



1 Wrist imaging

Knee imaging

At NRGH, the knee protocol is run with a FOV of around 150 mm, depending on slice orientation, with a 15-channel transmit/receive coil. We have adopted Deep Resolve for our routine knee protocol, as imaging time has decreased to 9 minutes from 15 minutes with an overall improvement in image resolution.

Coronal knee (Figure 2)
(2A) and (2B) demonstrate a displaced osteochondral fragment within the medial compartment. Image quality is almost equivalent between conventional and Deep Resolve imaging, with slightly better edge sharpness of the menisci and articular cartilage definition on the Deep Resolve image. The acquisition time and parameters of (2A) are: 4:15 minutes, matrix 246 × 352, SMS 2, GRAPPA acceleration 2, and 3 averages, compared to (2B) with an acquisition time of 1:55 minute. Sequence time is less than half the original due to lower base resolution, an SMS acceleration factor of 3, and dropping the averages to 2. Figures (2C) and (2D) demonstrate improved delineation of menisci and articular cartilage using Deep Resolve. Scan time: 4:15 minutes vs. 1:55 minute.

Elbow imaging

The current elbow protocol at NRGH includes coronal and axial T1 with axial, sagittal, and coronal PD FS. We have converted our elbow protocol to Deep Resolve and while our time has remained relatively constant (9:50 compared to 9:00 minutes with Deep Resolve), image quality has significantly improved. Due to positioning requirements, patients with elbow pathology often have difficulty remaining motionless as a result of pain. In patients who have difficulty with positioning, the excellent SNR with Deep Resolve means NRGH could have sacrificed resolution to allow for shorter scan times. However, as our previous elbow routine was already short, we were able to significantly improve image quality while still decreasing overall scan time.

Coronal and axial elbow (Figure 3)
(3A) and (3B) show a significantly improved depiction of cortical bone, trabecular pattern, and articular cartilage using Deep Resolve. Scan time is 1:42 minute (conventional) compared to 1:29 minute (Deep Resolve). Both sequences have 1 average, but the conventional sequence uses SMS acceleration 3 and the Deep Resolve sequence uses GRAPPA 4.

In (3C) and (3D), DL allows for improved contrast, sharpness, and resolution. Scan time: conventional 2:34 minutes, Deep Resolve 2:29 minutes. The reconstructed voxel size was $0.51 \times 0.51 \times 2.5$ mm^3 on the conventional scan, and decreased to $0.18 \times 0.18 \times 2.5$ mm^3 using Deep Resolve. Both sequences use 1 average but (3C) uses SMS acceleration 2 while (3D) uses GRAPPA 4.

Hand imaging

Imaging of the fingers can be challenging due to the small anatomic structures. This necessitates thinner slices, which increases scan time. Our current finger protocol consists of the following sequences, and acquisition time has decreased from 15 minutes to 9 minutes:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
ax Deep Resolve T2 TSE	2.0	0	2:18
cor Deep Resolve PD FS TSE	2.0	0.1	1:52
cor Deep Resolve PD FS TSE	2.0	0.1	1:33
cor Deep Resolve T2 TSE	2.0	0.1	2:27

Table 2: Hand imaging

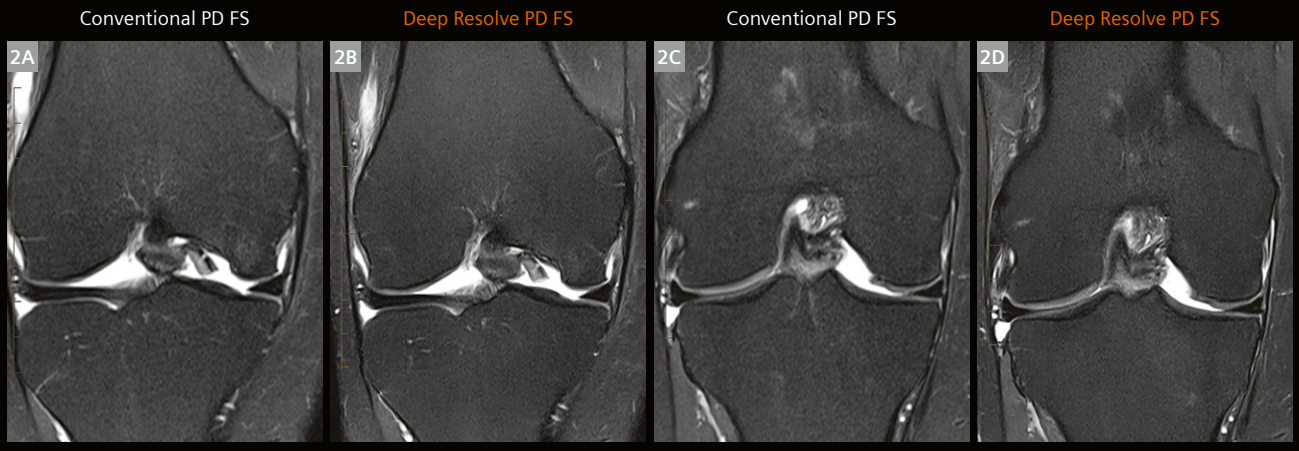
Sagittal and coronal thumb (Figure 4)
(4A) and (4B) show improved signal and contrast on the Deep Resolve image. There are also significant time savings. Scan time: conventional 3:39 minutes, Deep Resolve 1:22 minute.

(4C) and (4D) are from the same patient. Tear and retraction of the ulnar collateral ligament are shown nicely with both techniques. There is improved delineation of the adductor aponeurosis and articular cartilage using Deep Resolve. Scan time: conventional 2:53 minutes, Deep Resolve 2:07 minutes.

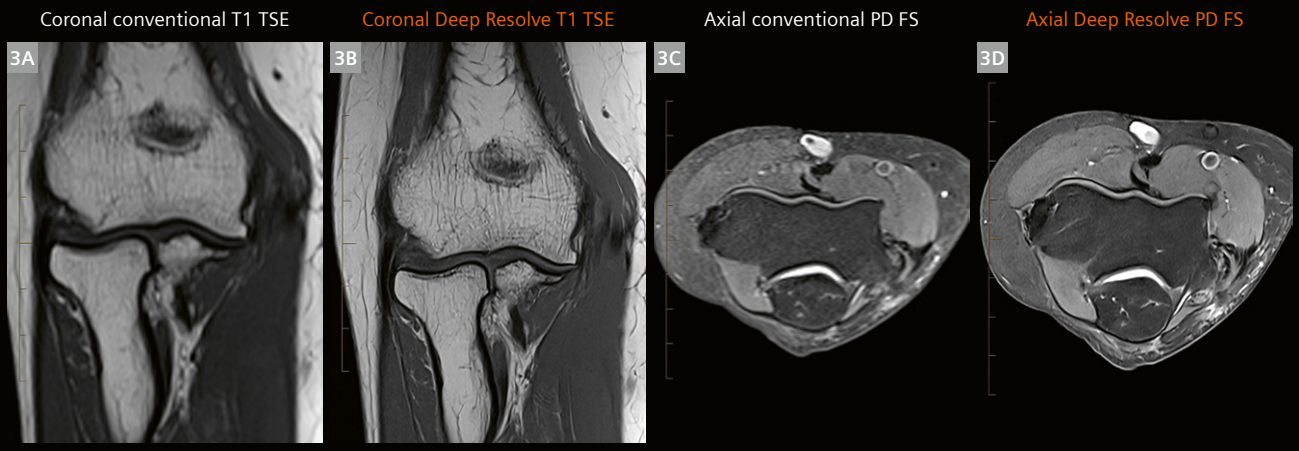
Shoulder imaging

The shoulder arthrogram protocol is run with a FOV of around 150 mm, depending on slice orientation and the size of the patient. A 16-channel dedicated shoulder coil is used for image acquisition. Shoulder imaging is known to be full of motion artifacts due to patient discomfort and respiratory motion. Shorter scan times can be helpful when scanning claustrophobic, elderly, or pediatric[2] patients, or patients in significant discomfort. Optimized shoulder imaging involves high-quality images with minimal other troublesome artifacts, such as magic angle artifacts. Both our routine shoulder and shoulder arthrogram protocols have been converted to Deep Resolve, with significant time savings.

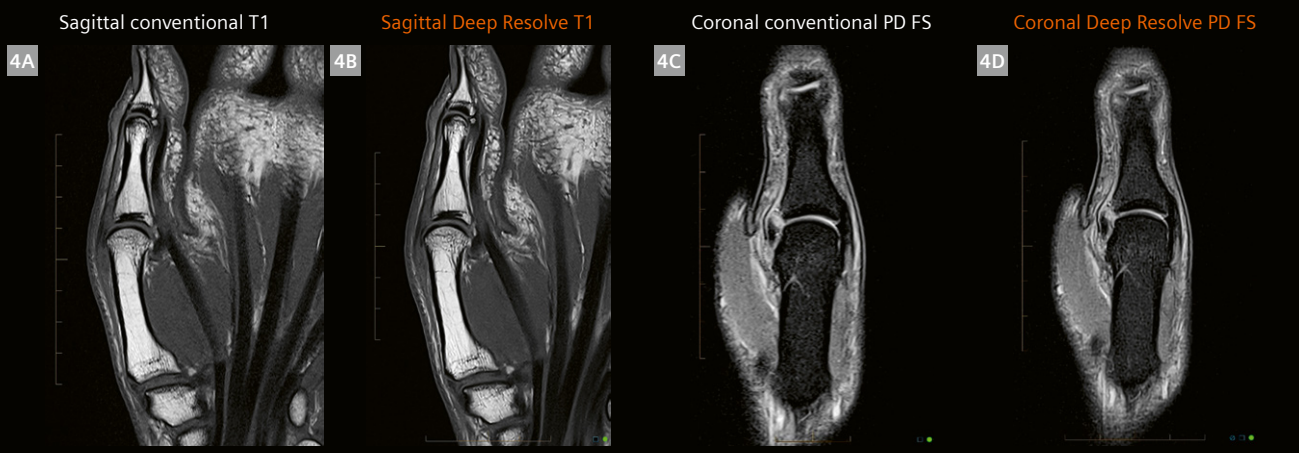
[2]MR scanning has not been established as safe for imaging fetuses and infants less than two years of age. The responsible physician must evaluate the benefits of the MR examination compared to those of other imaging procedures. Note: This disclaimer does not represent the opinion of the authors.



2 Knee imaging



3 Elbow imaging



4 Thumb imaging

For the routine shoulder protocol, our acquisition time is around 9 minutes, down from 15 minutes. NRGH runs the following sequences:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
ax Deep Resolve PD FS TSE	3.0	0.3	1:36
cor Deep Resolve PD FS TSE	3.0	0.3	1:21
sag Deep Resolve PD FS	3.0	0.3	1:20
cor Deep Resolve T1 FS TSE	3.0	0.3	1:24
ax 3D T1 VIBE	0.6		

Table 3: Shoulder imaging

For the routine shoulder arthrogram protocol, our acquisition time is 9 minutes, down from 15 minutes. NRGH runs the following sequences:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
ax Deep Resolve T1 FS TSE	3.0	0.3	1:22
cor Deep Resolve T1 FS TSE	2.5	0.1	1:24
cor Deep Resolve PD FS TSE	3.0	0.3	1:05
sag Deep Resolve T1 FS TSE	3.0	0.3	1:28
ax 3D T1 VIBE	0.6		

Table 4: Shoulder arthrogram

Axial and coronal shoulder arthrogram (Figure 5)
(5A, 5B) Note the improved edge sharpness of the cortical bone and labrum, and the improved depiction of articular cartilage. We do not routinely use abduction and external rotation (ABER) positioning, although a faster sequence would make scanning in the ABER position more attractive. (5A) has a base matrix of 212 × 304. The image was acquired with a voxel size of 0.75 × 0.53 × 3.0 mm^3 and interpolated to 0.26 × 0.26 × 3.0 mm^3, with 2 averages, 3 concatenations, GRAPPA 3, and an echo spacing of 10.9 ms.

(5B) is from the same patient with medium denoising and Deep Resolve Sharp options, interpolated to a reconstructed voxel of 0.28 × 0.28 × 3.0 mm^3 with a base matrix of 201 × 288. The image was acquired with a voxel size of 0.79 × 0.53 × 3.0 mm^3, 2 averages, 3 concatenations, GRAPPA 3, and an echo spacing of 10.9 ms. Both sequences have a TR of 635 ms and a TE of 11 ms. Scan time: conventional 3:32 minutes, Deep Resolve 2:18 minutes.

(5C) and (5D) include coronal PD FS TSE arthrographic images. The images demonstrate a full-thickness supraspinatus tendon tear with fraying and delamination of the tendon. The membranes within the bursa are better demonstrated with Deep Resolve. (5C) has a base matrix of 224 × 320 acquired in 3 minutes. The image was acquired with a voxel size of 0.71 × 0.71 × 3.0 mm^3 reconstructed to 0.25 × 0.25 × 3.0 mm^3, with 2 averages, 1 concatenation, GRAPPA 3, and an echo spacing of 10.2 ms.

(5D) was acquired from the same patient with medium denoising and sharp edge options, interpolation, and a reconstructed voxel of 0.26 × 0.26 × 3.0 mm^3 with a base matrix of 213 × 304. The sequence was acquired with a voxel size of 0.75 × 0.53 × 3.0 mm^3, 2 averages, 1 concatenation, GRAPPA 3, and an echo spacing of 10.2 ms. Both sequences have a TR of 2750 ms and a TE of 41 ms. Scan time: conventional 3:00 minutes, Deep Resolve 2:02 minutes.

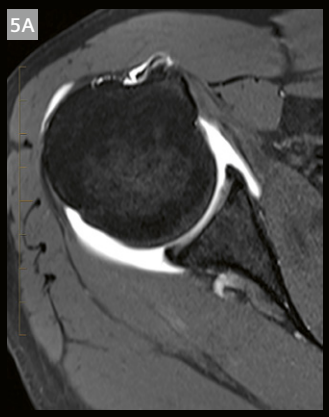
(5E) and (5F) show coronal T1 FS images from the same patient. Again, the tear and membranes are better graded using Deep Resolve. Also note the improved delineation of articular cartilage with Deep Resolve. Scan time: conventional 2:56 minutes, Deep Resolve 1:58 minute.

(5E) was acquired with a base matrix of 212 × 304. The image was acquired with a voxel size of 0.75 × 0.53 × 2.5 mm^3 and reconstructed to 0.26 × 0.26 × 2.5 mm^3; 2 averages, 3 concatenations, GRAPPA 2, and an echo spacing of 9.7 ms. (5F) was collected with medium denoising and sharp edge options, interpolation, and a reconstructed voxel of 0.28 × 0.28 × 2.5 mm^3 with a base matrix of 201 × 288, acquired in 1:58 minute. The sequence was acquired with a voxel size of 0.79 × 0.56 × 2.5 mm^3, 2 averages, 3 concatenations, GRAPPA 3, and an echo spacing of 9.6 ms. Both sequences have a TR of 580 ms and a TE of 9 ms.

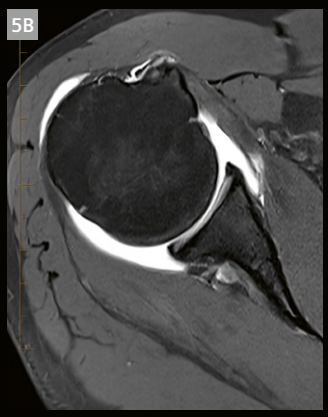
Axial shoulder (Figure 6)
(6A, 6B) The subscapularis tendon and posterior labral tear are equally assessed. There is improved depiction of articular cartilage and cortical bone on the Deep Resolve image. There is an overall improvement in signal and resolution on the Deep Resolve image.

(6A) and (6B) are identical with the same imaging parameters, but Deep Resolve was applied in (6B). Both are acquired with a base matrix of 256 × 256 and an acquired voxel size of 0.63 × 0.63 × 3.0 mm^3. Both sequences have 1 average and 1 concatenation, a turbo factor of 7, and echo spacing of 11.6 ms. (6A) is our conventional sequence with no acceleration and no interpolation. (6B) has an acceleration factor of GRAPPA 3, Deep Resolve Boost with medium denoising and sharp edge options. The conventional sequence took 3:59 minutes. The Deep Resolve sequence took 1:36 minute, and is now part of our routine shoulder protocol.

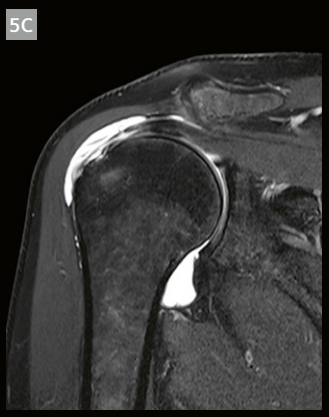
Axial conventional T1 FS



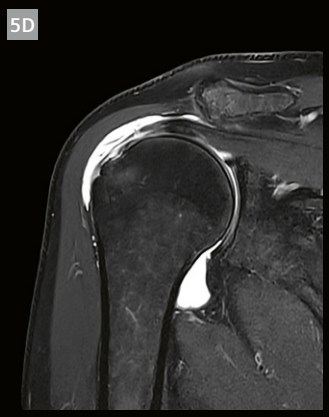
Axial Deep Resolve T1 FS



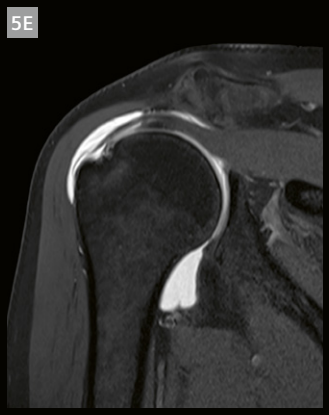
Coronal conventional PD FS



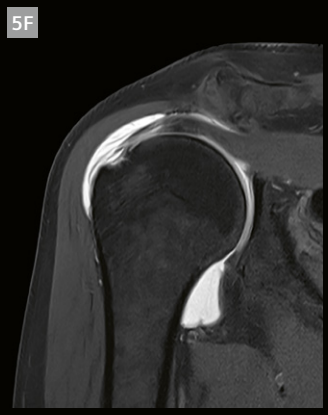
Coronal Deep Resolve PD FS



Coronal conventional T1 FS TSE

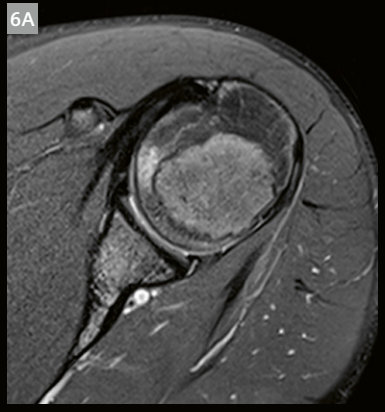


Coronal Deep Resolve T1 FS

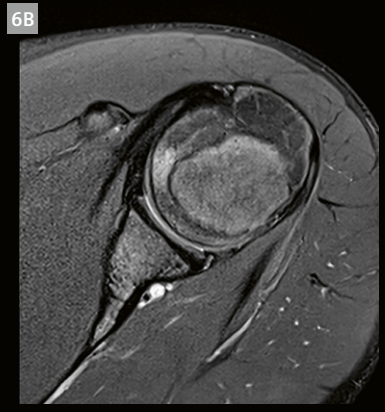


5 Shoulder arthrogram

Axial conventional PD FS TSE



Axial Deep Resolve PD FS TSE



6 Shoulder imaging

Foot imaging

Imaging of the feet and toes can be challenging due to the small structures being assessed. Evaluating the phalanges and metatarsophalangeal (MTP) joints in particular demands both high-resolution and high-contrast images. Our routine foot protocol varies depending on the clinical reason for referral, but generally consists of multiplanar PD FS with at least a single plane T1-weighted sequence. Scanning of the toes and MTP joints requires thinner slices, generally 2 to 3 mm.

The 16-channel receive foot/ankle coil is used for routine image acquisition. We have adopted Deep Resolve sequences for routine foot sequences. At NRGH, the routine foot protocol consists of the following TSE sequences, and the acquisition time is down from 17 minutes to 10 minutes with Deep Resolve:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
sag Deep Resolve PD FS TSE	3.0	0.3	1:56
cor Deep Resolve PD FS TSE	3.0	0.3	1:58
ax Deep Resolve PD FS TSE	2.0	0.2	2:06
ax Deep Resolve T1 TSE	2.0	0.2	2:05
cor Deep Resolve T1 TSE	3.0	0.3	1:45

Table 5: Foot imaging

Sagittal and axial foot (Figure 7)

(7A) is a sagittal conventional PD FS and (7B) is a sagittal Deep Resolve PD FS of the first MTP joint. The Deep Resolve image demonstrates improved image resolution. Scan time: 2:50 minutes for (7A) and 1:56 minute for (7B). Slice thickness is 3 mm. Both have a reconstructed voxel size of $0.2 \times 0.2 \times 3.0$ mm^3 but differ in the acquired matrix (307×384 for conventional; 294×368 for the Deep Resolve sequence). The acceleration factor on the conventional sequence is GRAPPA 2, vs. GRAPPA 3 on the Deep Resolve sequence.

(7C) is an axial conventional T1 TSE and (7D) is an axial Deep Resolve T1 of the forefoot. Note the improved assessment of muscles, trabecular pattern, and cortical bone. The components of the Lisfranc ligament complex are also better seen using Deep Resolve.

(7C) and (7D) are the same sequence but with Deep Resolve applied to (7D). Imaging parameters are as follows: a fairly close reconstructed voxel size ($0.2 \times 0.2 \times 2.0$ mm^3 for the conventional versus $0.21 \times 0.21 \times 2.0$ mm^3 for the Deep Resolve sequence); a lower acquisition matrix for Deep Resolve (336 versus 352 for the conventional), and a higher acceleration for Deep Resolve (GRAPPA 3 versus GRAPPA 2 for the conventional sequence). Scan time: conventional 3:06 minutes, Deep Resolve 2:03 minutes. The images nicely demonstrate the benefits of AI technology: the Deep Resolve sequences use raw data from a data-reduced scan. Through iterative processes, they produce a final image with significantly reduced noise and high SNR in a shortened acquisition time.

Neurological imaging focus
Pituitary imaging

The pituitary gland examination is one area where the NRGH radiologists have made it a priority to attain high resolution scans. For the Deep Resolve images currently in our pituitary protocol, we have aimed to use as square a voxel as possible (90%–100%) and the improved signal from the AI sequences helps to facilitate the improved phase resolution without adding a time penalty. The Deep Resolve sequence shown below has a 90% phase resolution compared to the 75% phase resolution in the conventional sequence.

We used Deep Resolve with success for both pre-contrast T1 and T2, as well as post-contrast T1 imaging. We have adopted Deep Resolve sequences for our routine pituitary sequences. The total time with Deep Resolve sequences is 13:51 minutes compared to 13:32 minutes with our conventional sequences, and the image quality has significantly improved, as illustrated in the following examples. Our routine pituitary protocol consists of:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
sag Deep Resolve T1 TSE	2.0	0.2	2:43
cor Deep Resolve T1 TSE	2.0	0.2	2:38
cor Deep Resolve T2 TSE	2.0	0.2	2:10
cor Dynamic T1 TSE			
sag Deep Resolve T1 TSE post contrast	2.0	0.2	2:43
cor Deep Resolve T1 TSE post contrast	2.0	0.2	2:38

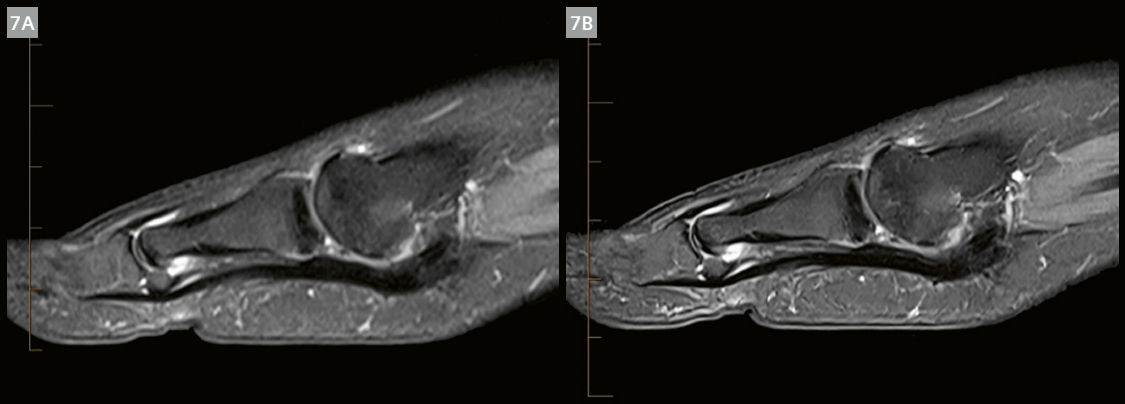
Table 6: Pituitary imaging

Pituitary imaging (Figure 8)

(8A) sagittal conventional T1 pre-contrast and (8B) sagittal Deep Resolve T1 pre-contrast imaging of the sella demonstrates improved edge sharpness but also exposes higher noise levels due to shorter scan time and increased resolution of Deep Resolve. Improved depiction of the infundibulum is apparent with Deep Resolve. Both images are acquired with a matrix of 192×256 and 2 averages.

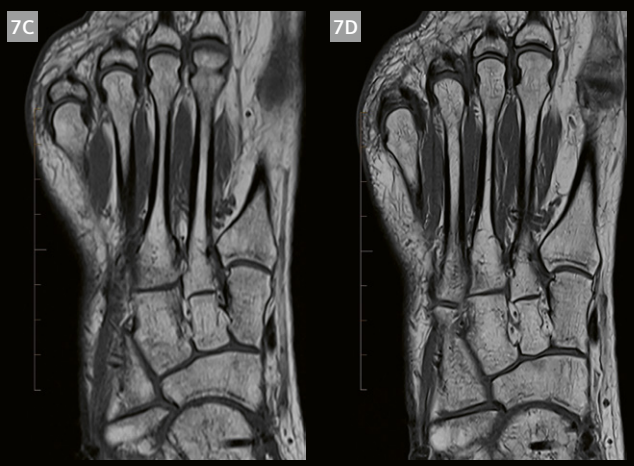
Sagittal conventional PD FS TSE

Sagittal Deep Resolve PD FS TSE



Axial conventional T1 TSE

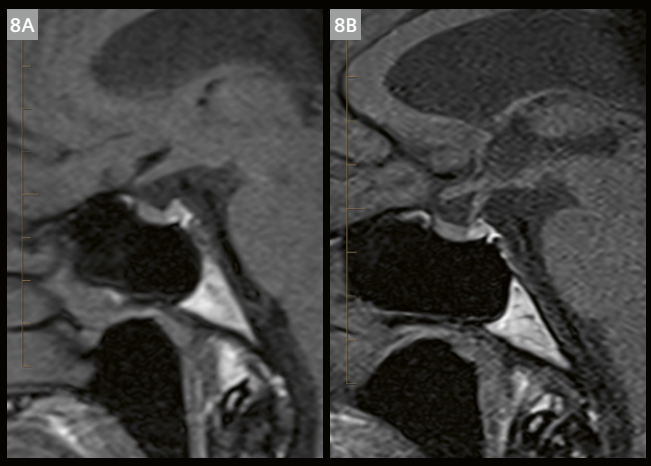
Axial Deep Resolve T1 TSE



7 Foot imaging

Sagittal conventional T1 TSE

Sagittal Deep Resolve T1 TSE



8 Pituitary gland imaging

An acceleration factor of GRAPPA 2 was used on the Deep Resolve image, and no acceleration on the conventional image. Scan time: 3:29 minutes for the conventional image and 1:49 minute for the Deep Resolve image.

The Deep Resolve image is noisier than what we currently use in our Deep Resolve protocol because it is highly resolved. This resolution and speed would not be possible without Deep Resolve.

Coronal and sagittal pituitary gland (Figure 9)
(9A, 9B) are from the same patient. The Deep Resolve image demonstrates improved delineation of the pituitary adenoma with overall higher resolution. Note the exquisite detail of cranial nerves within the left cavernous sinus.

(9A) has a base matrix of 192 × 256 (75% phase) acquired in 2:26 minutes. The sequence was acquired with a voxel size of 0.94 × 0.7 × 2.0 mm^3 and interpolated to 0.35 × 0.35 × 2.0 mm^3. Four averages, 1 concatenation, and GRAPPA 2 were used. Both sequences have a 2 mm slice thickness, a FOV of 180 mm, echo spacing of 10.9 ms, and a TE of 11 ms. The conventional sequence has a TR of 741 ms and the Deep Resolve sequence has a TR of 622 ms.

(9B) is the Deep Resolve Boost sequence with medium denoising and sharp edge options on, a 272 × 304 acquired matrix (90% phase), and a reconstructed voxel of 0.3 × 0.3 × 2.0 mm^3 collected over 2:20 minutes. The sequence has an acquired voxel size of 0.66 × 0.59 × 2.0 mm^3, 3 averages, 1 concatenation, and GRAPPA 2.

(9C, 9D) were acquired in the same patient. There is much better definition of the margins of the pituitary gland, adenoma, and infundibulum using Deep Resolve. Also note the cystic change within the adenoma, which is not apparent on the conventional sequence.

(9C) is a conventional sagittal T1 TSE post-contrast sequence with a base matrix of 192 × 256 (75% phase) acquired in 3:12 minutes. The sequence was acquired with a voxel size of 0.97 × 0.74 × 2.0 mm^3 and interpolated to 0.4 × 0.4 × 2.0 mm^3 with 2 averages, 1 concatenation, and no acceleration factor. Both sequences have a FOV of 190 mm, a TR of 550 ms, a TE of 11 ms, and echo spacing of 10.9 ms.

(9D), which is the Deep Resolve sequence, has medium denoising and sharp edge options, a 259 × 288 matrix (90% phase), and a reconstructed voxel size of 0.3 × 0.3 × 2.0 mm^3. It runs for 2:43 minutes. The sequence was acquired with a voxel size of 0.73 × 0.76 × 2.0 mm^3 with 2 averages and 1 concatenation. The Deep Resolve sequence required 120% phase oversampling, compared to 80% phase oversampling with the conventional sequence. The Deep Resolve sequence was acquired with a 90% phase resolution, compared to 75% phase resolution in the conventional sequence.

(9E) Is from the same patient as in the example above. (9E) used medium denoising and sharp edge options, a reconstructed voxel size of 0.3 × 0.3 × 2.0 mm^3, with a base matrix of 259 × 288 (90% phase), an acquired voxel size of 0.69 × 0.63 × 2.0 mm^3, and a scan time of 2:10 minutes. The sequence also has 2 averages, 1 concatenation, a FOV of 180 mm, GRAPPA 2, a TR of 3800 ms, a TE of 82 ms, a turbo factor of 17, and echo spacing of 10.3 ms.

Whole-brain imaging

At NRGH, our previous standard axial was a 5 mm BLADE sequence, acquiring 26 slices with a 30% gap (1.5 mm) over 1:51 minute. The sequence is lacking spatial resolution, although it had a fairly high-resolution matrix of 320 × 320 and a FOV of 230 mm (which was not rectangular due to the BLADE option).

The results of the optimized axial Deep Resolve T2 TSE sequence are stunning and shown in Figures 10B and 10D. In a scan time of 2:39 minutes, a very high-resolution square voxel sequence is acquired with 46 slices of 3 mm thickness with a 20% gap (0.6 mm). Spatial resolution is increased as slice thickness is 3 mm instead of 5 mm, the acquisition matrix has increased to 400 × 400 from 320 × 320, and the slice gap has decreased by over 50%, so more of the brain tissue is being imaged. The resolution advantage can be demonstrated in cranial nerves 7 and 8, with the individual nerves clearly resolved in Figure 10B. The normal flow voids appear similar in both the standard and Deep Resolve versions of the axial T2 TSE sequence. We first adopted the sequence as part of our seizure protocol, and the slightly shorter axial Deep Resolve T2 TSE is now part of our routine brain imaging.

Axial T2 TSE brain (Figure 10)
In Figure 10, we see axial T2 images of the posterior fossa from a whole-brain exam. (10A) is conventional BLADE, while (10B) is a Deep Resolve image from the seizure protocol. Scan time: 1:51 minute for the BLADE sequence and 2:59 minutes for the Deep Resolve sequence. Both sequences have a TR of 4500 ms, and a TE of 88 and 95 ms respectively. (10A) is an axial T2 TSE BLADE with a base matrix of 320 × 320, an acquired voxel size of 0.72 × 0.72 × 5.0 mm^3 with no interpolation, 2 concatenations, GRAPPA 2, 26 slices with a 30% gap (1.5 mm), and an echo spacing of 5.5 ms.

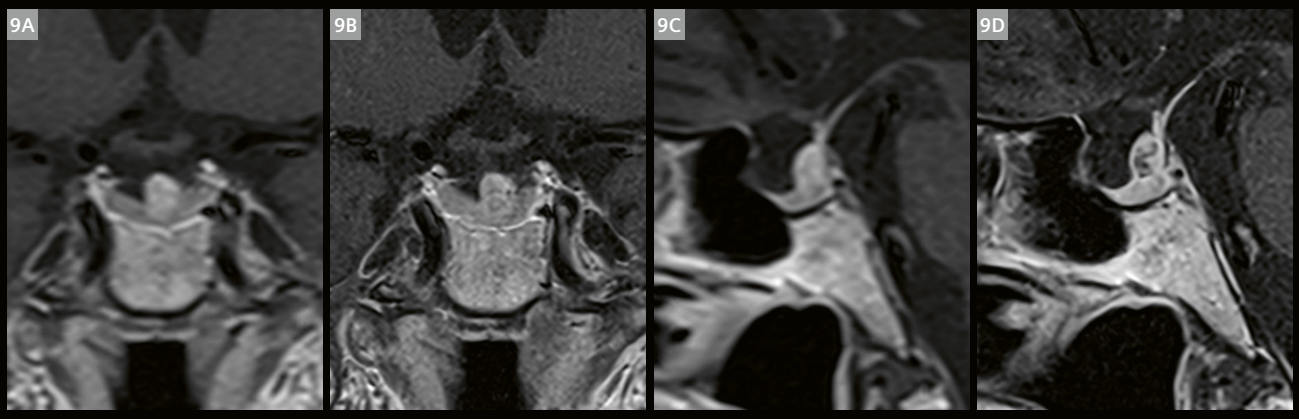
(10B) is the axial Deep Resolve T2 sequence and part of the seizure protocol. 46 slices of 3 mm thickness are collected over 2:59 minutes with medium denoising and sharp edge options. The base matrix is square at 400 × 400, the acquired voxel is 0.57 × 0.57 × 3.0 mm^3 and is reconstructed to 0.29 × 0.29 × 3.0 mm^3. The slice gap is 20% (0.6 mm), and 1 average, 2 concatenations,

Coronal conventional T1 post-contrast

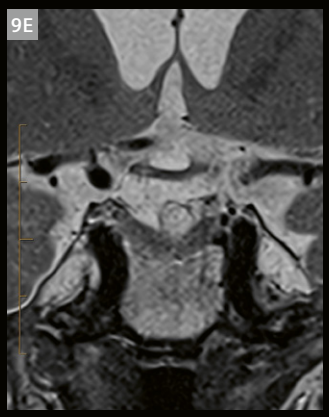
Coronal Deep Resolve T1 post-contrast

Sagittal conventional T1 post-contrast

Sagittal Deep Resolve T1 post-contrast



Coronal Deep Resolve T2 TSE



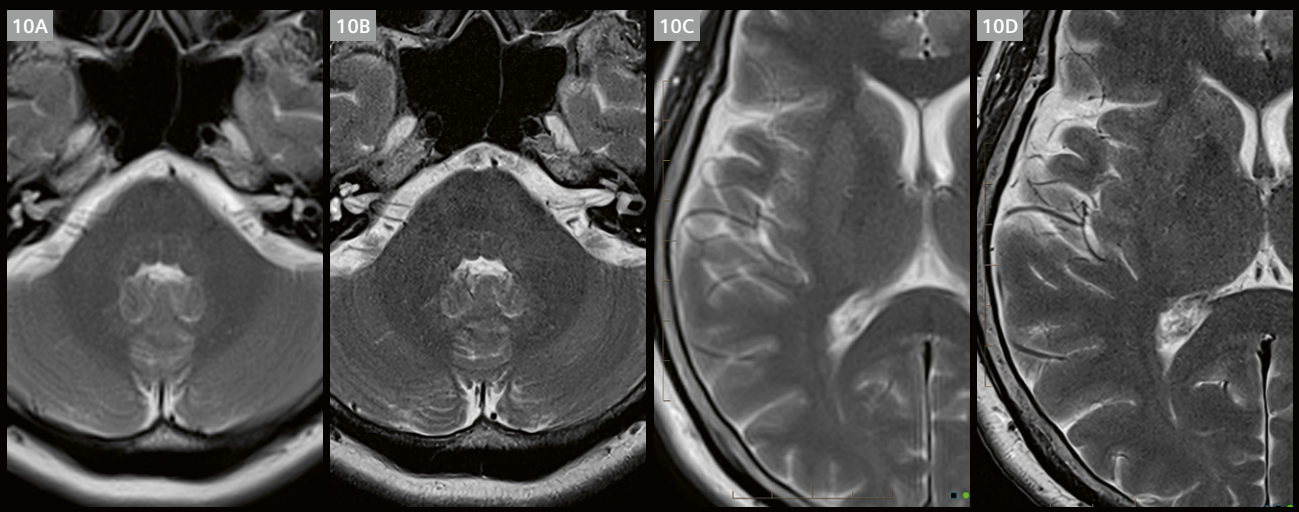
9 **Pituitary gland imaging**

Axial conventional T2 TSE BLADE

Axial Deep Resolve T2 TSE

Axial conventional T2 TSE BLADE

Axial Deep Resolve T2 TSE



10 **Brain imaging**

GRAPPA 2, 50% phase oversampling, and an echo spacing of 10.6 ms are used. Note the significantly improved resolution on the Deep Resolve image with excellent delineation of cranial nerves 7 and 8, the inner ear structures, and the cerebrospinal fluid (CSF)/parenchymal interfaces. Improved assessment of the basilar artery is seen. (Another axial Deep Resolve T2 sequence, now part of the routine brain protocol, takes 2:39 minutes, uses 3 concatenations, and a higher TR. All other parameters are the same as the Deep Resolve seizure sequence above.)

(10C, 10D) are from the same patient and sequence as above. Both images are zoomed to illustrate the significant improvement in spatial resolution. Note the improved grey/white matter differentiation and depiction of the CSF/parenchymal interfaces, and that the preservation of the normal vascular flow voids is apparent.

Our previous standard axial FLAIR at NRGH was a 5 mm sequence, acquiring 26 slices with a 30% gap (1.5 mm) over 3:54 minutes. The sequence had a spatial resolution of 240 × 320 (70% phase), was not interpolated, and yielded a 0.7 × 0.7 × 5.0 mm^3 voxel size. The sequence was adequate but long and the phase resolution was not near the 90% to 100% we are aiming for in neuro imaging. Our routine brain protocol now includes a 3 mm Deep Resolve FLAIR sequence. We illustrate two Deep Resolve options below and compare them to our conventional FLAIR sequence. The first is a 5 mm Deep Resolve FLAIR sequence and the second is a 3 mm Deep Resolve FLAIR sequence. The 5 mm Deep Resolve FLAIR has a scan time of 2:42 minutes and the 3 mm Deep Resolve FLAIR is taken directly from the protocol tree of Siemens Healthineers and has a scan time of 2:39 minutes. We have added the 3 mm Deep Resolve FLAIR to our routine brain protocol, but please note that we do see CSF-related flow artifact in the ventricles with the thin slice sequence.

Axial FLAIR brain (Figure 11)

(11A) is a conventional axial FLAIR with a base matrix of 240 × 320 (70% phase) and acquired in 3:56 minutes. The image was acquired with a voxel size of 0.7 × 0.7 × 5.0 mm^3, 1 average, 2 concatenations, and GRAPPA 2 with no interpolation.

(11B) is an axial Deep Resolve FLAIR sequence with medium denoising and sharp edge options, an acquired voxel size of 1.2 × 0.9 × 5.0 mm^3 reconstructed to 0.4 × 0.4 × 5.0 mm^3, and acquired in 2:26 minutes. The matrix is 192 × 256 (75% phase) and was acquired with 1 average, 2 concatenations, and an increased GRAPPA factor of 3. Both (11A) and (11B) have a slice thickness of 5 mm, a TR of 9000 ms, a TE of 86 ms, and 40% phase oversampling.

In (11A) and (11B), there is minor ischemic change within the periventricular region. Resolution is improved on the Deep Resolve image, with improved edge definition and grey/white matter differentiation.

(11C) is the 3 mm Deep Resolve FLAIR sequence that is now part of our routine brain imaging. The sequence collects 50 slices of 3 mm thickness, has a 10% slice gap (0.3 mm), a base matrix of 272 × 272 (100% phase), a reconstructed voxel size of 0.4 × 0.4 × 3.0 mm^3, and is acquired in 2:39 minutes. The sequence has Deep Resolve high denoising and sharp edge options, 1 average, 2 concatenations, and GRAPPA 2. The image demonstrates flow void artifact within the ventricle seen with this 3 mm Deep Resolve FLAIR sequence. The sequence replaced our previous FLAIR sequence, which had 5 mm slice thickness and took 3:54 minutes (shown in (11A)).

The combination of Deep Resolve sequences, a slightly longer axial T2 TSE, and a shorter axial FLAIR allows the department to perform highly resolved brain imaging. In our previous protocol, the conventional 5 mm axial T2 TSE BLADE and the 5 mm axial FLAIR had a cumulative acquisition time of 4:55 minutes. With the Deep Resolve sequences, the protocol has a cumulative acquisition time of 5:19 minutes, however, with thinner 3 mm slices for both the axial Deep Resolve T2 TSE and the axial Deep Resolve FLAIR sequences.

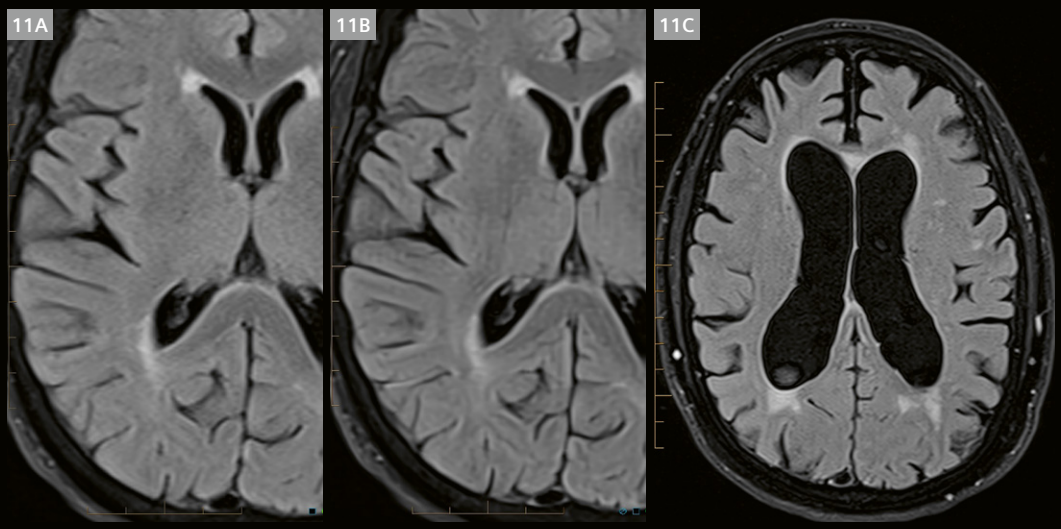
Cervical spine imaging

In the first example of the cervical spine, we compare the standard SMS protocol to Deep Resolve sequences, for which different percentages of phase data are acquired. The Deep Resolve option, with its inherent SNR advantage from AI technology, was used to decrease acquisition time while improving contrast and spatial resolution. The routine sagittal T2 TSE sequence is run with a resolution of 240 × 320 with 75% of the base matrix in the phase direction, a slice thickness of 2.5 mm, a 10% gap (0.25 mm), and is acquired in 3:05 minutes. The sagittal Deep Resolve T2 cervical spine images demonstrate a two-step decrease in base resolution, decreased averages (from 5 to 2), in-plane parallel imaging GRAPPA (instead of SMS acquisition), and an increase in phase oversampling from 100% to 140% to prevent phase-wrapping artifact from the higher PAT factor. We ran the Deep Resolve sequences with 75% and 85% phase resolution and compared the results with our routine sequence. The results were improved contrast, higher reconstructed resolution, less flow artifact, and acquisition times for the Deep Resolve sequences that were 38% less than the conventional sequence for the sagittal T2 TSE.

Sagittal cervical spine (Figure 12)

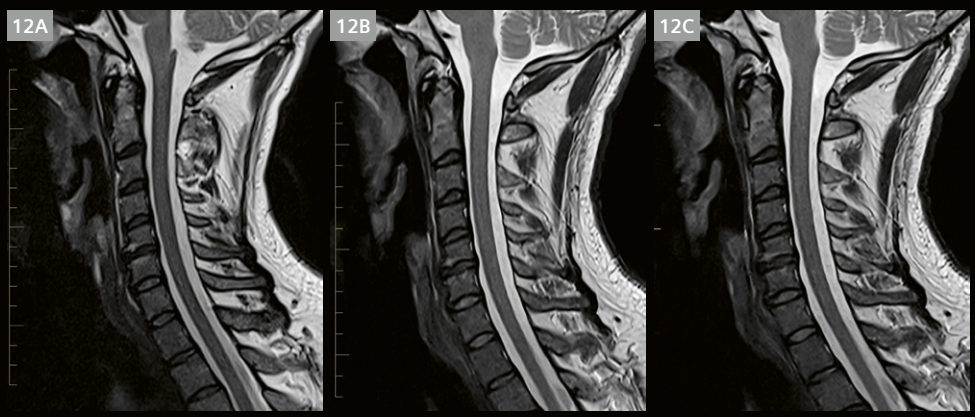
(12A–12C) show images of the cervical spine from the same patient. There is improved resolution and contrast on the Deep Resolve images. There is slightly improved

Axial conventional FLAIR 5 mm | Axial Deep Resolve FLAIR 5 mm | Axial Deep Resolve FLAIR 3 mm

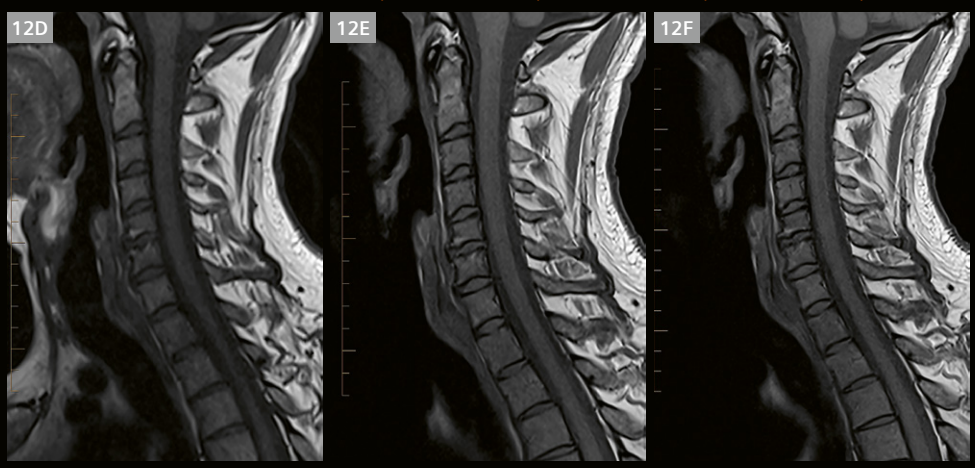


11 FLAIR brain imaging

Routine sagittal conventional T2 TSE | Deep Resolve T2 TSE 75% phase | Deep Resolve T2 TSE 85% phase



Conventional T1 TSE | Deep Resolve T1 TSE, phase 80% | Deep Resolve T1 TSE, phase 90%



12 Cervical spine imaging

sharpness on the sagittal Deep Resolve T2 TSE 85% phase image. Scan time: conventional sagittal T2 acquired in 3:05 minutes, sagittal Deep Resolve T2 TSE 75% phase resolution acquired in 1:56 minutes, and sagittal Deep Resolve T2 TSE 85% phase resolution acquired in 2:05 minutes.

Increasing the number of phase steps collected (from 75% to 85%) raised image resolution slightly and the penalty was an increased data collection time of 9 seconds. Both Deep Resolve sequences have 140% phase oversampling, GRAPPA 3, a TR of 4630 ms, a TE of 81 ms, medium denoising, and sharp edge enhancement. All three of the sagittal T2 sequences have a FOV of 240 mm, an echo time of 11.5 ms, and a turbo factor of 16.

(12A) is a conventional sagittal T2 TSE with a base matrix of 240 × 320 (75% phase), an acquired voxel size of 1.0 × 0.75 × 2.5 mm^3 interpolated to 0.75 × 0.75 × 2.5 mm^3, 5 averages, 1 concatenation, an SMS factor of 2, a TR of 2310 ms, a TE of 81 ms, and an acquisition time of 3:05 minutes.

(12B) is a sagittal Deep Resolve T2 TSE with 75% phase collection that was acquired with a voxel size of 1.18 × 0.88 × 2.5 mm^3 reconstructed to 0.44 × 0.44 × 2.5 mm^3. (12C) is a sagittal Deep Resolve T2 TSE with 85% phase collection. It has a slightly smaller acquired voxel at 1.04 × 0.88 × 2.5 mm^3, reconstructed to 0.44 × 0.44 × 2.5 mm^3. The reconstructed data from the Deep Resolve sequences have almost twice the resolution compared to our routine sequence, and were collected in significantly less time. The slightly improved detail and signal seen in (12C) is due to the higher percentage of phase data collected.

In the next cervical spine example, we again compare the standard SMS protocol to Deep Resolve sequences with different percentages of phase data acquired in the pursuit of improving resolution while decreasing scan time. (12D) shows a conventional sagittal T1 TSE with 80% phase resolution, (12E) is a sagittal Deep Resolve T1 TSE with 80% phase resolution, and (12F) is a sagittal Deep Resolve T1 TSE with 90% phase resolution of the cervical spine. They were all collected from the same patient. The Deep Resolve images demonstrate improved resolution and contrast. There is slightly improved sharpness and signal on the Deep Resolve image with more phase data collected (12F, 90% phase). In terms of scan time, the conventional sagittal T1 is acquired in 2:32 minutes, while the sagittal Deep Resolve T1 with 80% phase is acquired in 2:32 minutes, and the sagittal Deep Resolve T1 TSE with 90% phase is acquired in 2:51 minutes. Increasing the number of phase steps (from 80% to 90%) slightly decreased SNR and improved the image resolution minimally, although the time penalty was 20 seconds. The interpolated data for (12D) and (12E) are the same voxel size (0.47 × 0.47 × 2.5 mm^3), demonstrating significant improvement in spatial and contrast resolution when moving from a conventional sequence to a sequence with AI technology.

(12D) is a conventional sagittal T1 TSE with a base matrix of 205 × 256 (80% phase resolution), an acquired voxel size of 1.17 × 0.94 × 2.5 mm^3 interpolated to 0.47 × 0.47 × 2.5 mm^3, with 5 averages, 1 concatenation, an SMS factor of 2, a TR of 412 ms, and a TE of 9.9 ms. The acquisition time is 2:32 minutes.

(12F) is a sagittal Deep Resolve T1 TSE with 90% phase resolution, with a base resolution of 230 × 256, a slightly smaller acquired voxel at 1.04 × 0.94 × 2.5 mm^3 reconstructed to 0.47 × 0.47 × 2.5 mm^3, and a scan time of 2:51 minutes. Both Deep Resolve sequences have 140% phase oversampling, GRAPPA 3, a TR of 645 ms, a TE of 12 ms, medium denoising, and sharp edge enhancement. All of the sagittal T1 sequences have a FOV of 240 mm, an echo time of 9.9 ms, and a turbo factor of 3.

(12D–12F) demonstrate findings similar to the previous example. There is improved resolution and contrast on the Deep Resolve images, and increased signal on the Deep Resolve sequence with the highest phase resolution (most square voxel imaging). Increasing the number of phase steps (from 80% to 90%) increases image resolution but the penalty is a longer data collection time and reduced SNR. Images acquired with a square or 100% phase would have more resolution but would suffer a higher time penalty and reduced SNR. Clinical decisions are used to justify the tradeoffs of added time, SNR, and resolution. We can see from the images above that there is only minor benefit when moving from a phase of 80% to 90%.

Thoracic spine imaging

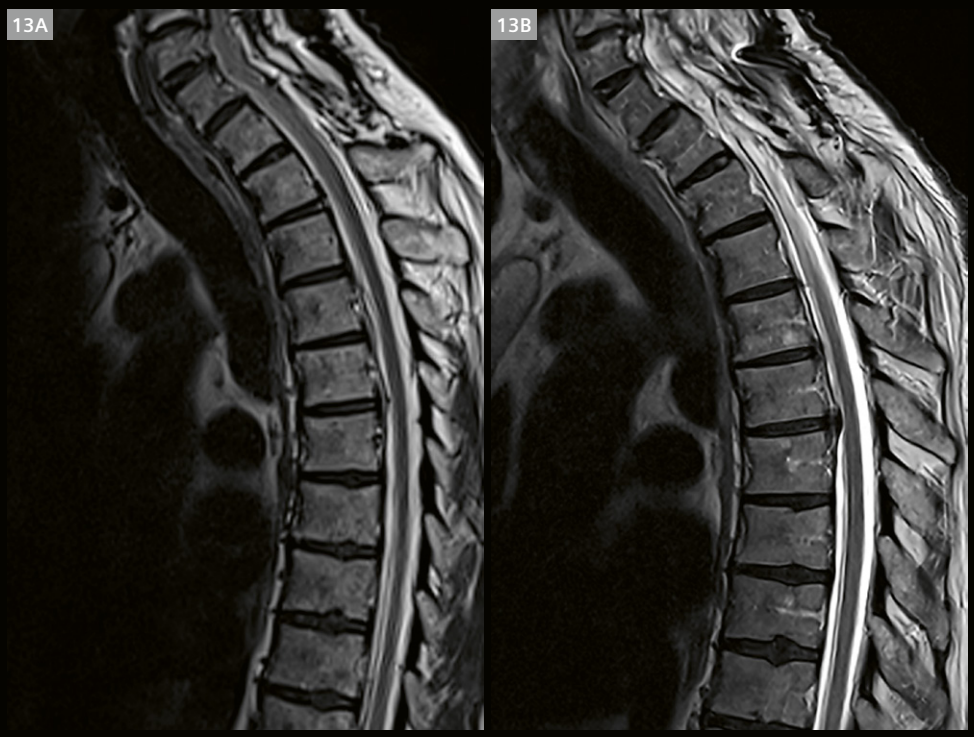
High-quality imaging of the thoracic spine can at times be challenging due to respiratory motion and CSF flow artifact. Deep Resolve was used to decrease scan times and improve SNR, spatial resolution, and contrast resolution. Imaging of the thoracic spine was challenging with Deep Resolve, yet we achieved acceptable thoracic spine images when increased phase FOV was used in combination with phase oversampling. The sagittal Deep Resolve T2 sequence is now part of our routine thoracic spine protocol.

Sagittal and axial thoracic spine (Figure 13)
(13A, 13B) Demonstrate improved contrast and SNR, decreased artifact, and increased conspicuity of the thoracic disc with Deep Resolve. Scan time: routine sagittal T2 acquired in 2:29 minutes; sagittal Deep Resolve T2 acquired in 2:16 minutes.

(13A) is a conventional sagittal T2 TSE with a base matrix of 307 × 384 (80% phase resolution) and an acquired voxel size of 1.14 × 0.9 × 3.0 mm^3 interpolated to 0.91 × 0.91 × 3.0 mm^3, with 3 averages, 1 concatenation, an SMS factor of 2, a TR of 2110 ms, a TE of 86 ms, and an acquisition time of 2:29 minutes.

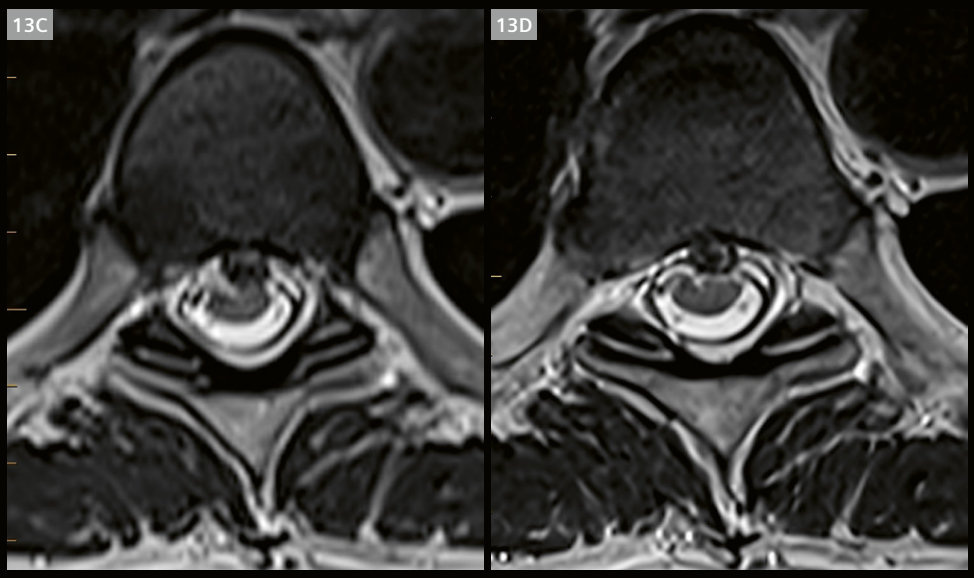
Sagittal conventional T2 TSE

Sagittal Deep Resolve T2 TSE



Axial conventional T2 TSE

Axial Deep Resolve T2 TSE



13 **Thoracic spine imaging**

(13B) is a sagittal Deep Resolve T2 TSE sequence acquired in 2:16 minutes. The sequence is a rectangular FOV with 150% FOV phase, an FOV of 230 mm, and 150% phase oversampling. The base resolution is 346 × 256 (90% phase resolution) and the acquired voxel is 1.0 × 0.9 × 3.0 mm^3, reconstructed to 0.45 × 0.45 × 3.0 mm^3. A GRAPPA 2 acceleration was used with high denoising and sharp edge enhancement. The base matrices of both sequences are similar, but the Deep Resolve produces a sequence with twice the spatial resolution when reconstructed.

(13C, 13D) demonstrate similar findings in the axial plane (improved contrast and SNR, decreased artifact) and increased conspicuity of the thoracic disc with Deep Resolve, with improved depiction of the disc protrusion. Scan time: routine axial T2 acquired in 4:08 minutes; axial Deep Resolve T2 acquired in 3:13 minutes.

Both sequences have a FOV of 190 mm, 36 slices, a 15% gap, and a slice thickness of 3.5 mm. (13C) has a base matrix of 202 × 288 (70% phase resolution), an acquired voxel size of 0.94 × 0.66 × 3.5 mm^3, 3 averages, GRAPPA 2, and 30% phase oversampling. (13D) has a base matrix of 205 × 256 (80% phase resolution) and an acquired voxel size of 0.93 × 0.74 × 3.5 mm^3 reconstructed to 0.37 × 0.37 × 3.5 mm^3. It used GRAPPA 2, as well as 2 averages and 70% phase oversampling.

Axial upper thoracic spine imaging can often be suboptimal due to the changing spinal curvature in the area and the inability of the block of slices to be perpendicular to each disc. Depending on the curvature of the spine, data can be collected at acute angles to the vertebrae, which yields suboptimal images. In our experience, axial Deep Resolve imaging seems to resolve this problem somewhat and can produce improved axial imaging in the upper thoracic spine when block axial acquisitions are collected.

Lumbar spine imaging

Similar to the imaging attempts in the cervical and thoracic spine areas, Deep Resolve was used to optimize imaging in the lumbar spine. Imaging of the spine was challenging and rewarding with Deep Resolve. We experienced acceptable sagittal thoracic and lumbar spine images when extended phase FOV was used in combination with phase oversampling. The sagittal Deep Resolve T2 and T1 TSE sequences and the axial Deep Resolve T2 TSE sequences are now part of our routine protocol for both the thoracic and lumbar spine. Based on the findings and optimization of Deep Resolve sequences, NRGH has done the following:

- Implemented a 13-minute T-spine protocol, which took almost 18 minutes without Deep Resolve
- Implemented a 9-minute L-spine protocol, which took 13 minutes without Deep Resolve

Lumbar spine imaging (Figure 14)

(14A) Is a conventional sagittal T2 TSE sequence with a FOV of 280 mm and 100% oversampling. The sequence uses a base matrix of 280 × 400, has an acquired voxel size of 1.0 × 0.7 × 3.0 mm^3 reconstructed to 0.7 × 0.7 × 3.0 mm^3, 2 averages, and 1 concatenation.

(14B) Is a sagittal Deep Resolve T2 TSE sequence with a rectangular FOV of 190 mm with a 150% FOV, and 150% phase oversampling. The base resolution is 280 × 208 (90% phase) with an acquired voxel size of 1.0 × 0.9 × 3.0 mm^3, reconstructed to 0.46 × 0.46 × 3.0 mm^3. GRAPPA 2 acceleration was used with high denoising and sharp edge enhancement.

The Deep Resolve images demonstrate increased signal with improved delineation of vertebral endplates and nerve roots, with decreased motion and pulsation artifact. Scan time: conventional sagittal T2 TSE acquired in 2:59 minutes; sagittal Deep Resolve T2 TSE acquired in 1:12 minute.

(14C, 14D) Illustrate improved resolution and contrast with decreased artifact using Deep Resolve. Scan time: conventional sagittal T1 TSE acquired in 2:36 minutes; sagittal Deep Resolve T1 TSE acquired in 1:57 minute.

(14C) A conventional sagittal T1 TSE sequence with an FOV of 280 mm and 70% oversampling. The sequence uses a base matrix of 268 × 384, an acquired voxel size of 1.0 × 0.7 × 3.0 mm^3 reconstructed to 0.7 × 0.7 × 3.0 mm^3, with 2 averages and 2 concatenations.

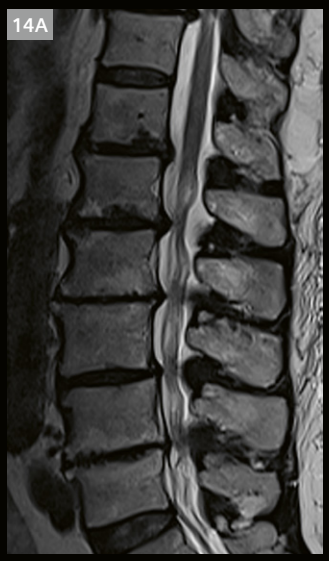
(14D) A sagittal Deep Resolve T1 TSE sequence that uses a rectangular FOV of 190 mm with a 150% FOV phase and 120% phase oversampling. The base resolution is 270 × 208 (90% phase) with an acquired voxel of 1.01 × 0.91 × 3.0 mm^3 reconstructed to 0.46 × 0.46 × 3.0 mm^3. Deep Resolve with high denoising and sharp edge enhancement was used, as well as 1 average and 1 concatenation.

The axial Deep Resolve T2 TSE sequence had a base resolution of 205 × 256 (80% phase resolution) with an acquired voxel of 0.93 × 0.74 × 3.5 mm^3, reconstructed to 0.37 × 0.37 × 3.5 mm^3. Two averages, 1 concatenation, medium denoising, and sharp edge enhancement were also used. The reconstructed spatial resolution in the Deep Resolve imaging has doubled, as seen in the image comparison below.

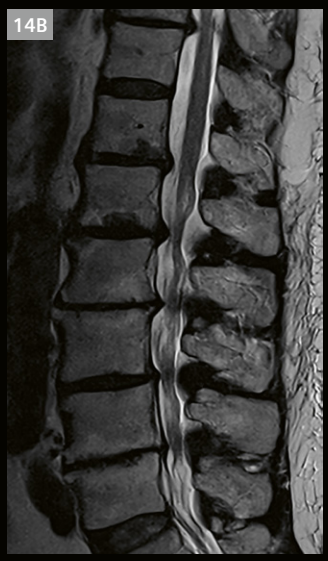
Both sequences collect 3 mm slices and use an acceleration factor of GRAPPA 2. (14E) and (14F) demonstrate increased signal and sharpness of visualized nerve roots. Scan time: 4:08 minutes for (14E) and 3:13 minutes for (14F).

Both sequences collected 36 slices at 3.5 mm slice thickness using a FOV of 190 mm. On the conventional axial T2 TSE sequence, the base resolution was 202 × 288 (70% phase resolution) with an acquired voxel of 0.94 × 0.66 × 3.5 mm^3. The images are not interpolated. Three averages, 1 concatenation and an acceleration factor of GRAPPA 2 were also used.

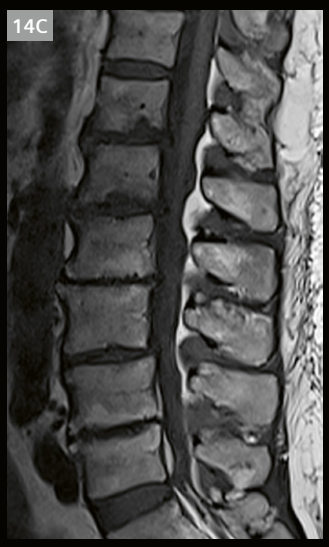
Conventional sagittal T2 TSE



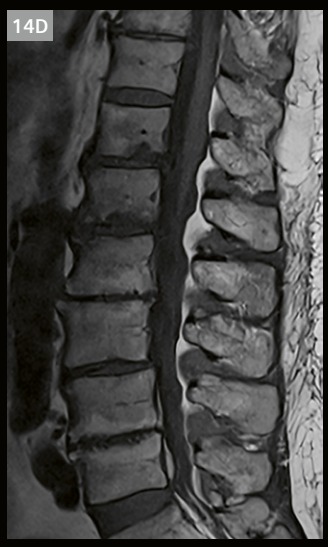
Sagittal Deep Resolve T2 TSE



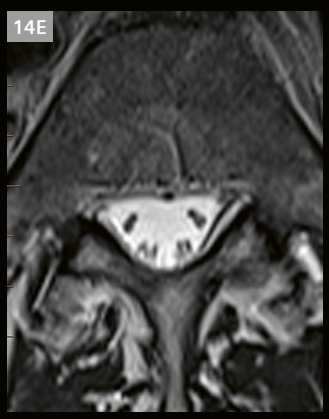
Sagittal conventional T1 TSE



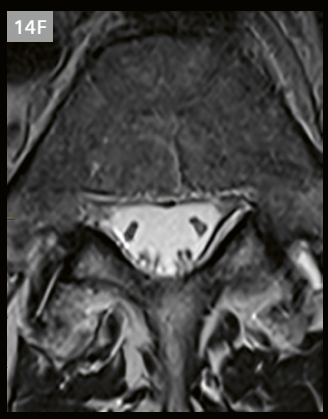
Sagittal Deep Resolve T1 TSE



Axial conventional T2 TSE



Axial Deep Resolve T2 TSE



14 Lumbar spine imaging

Body imaging focus
Pelvis imaging

Early on, a decision was made to optimize prostate imaging with Deep Resolve. The standard prostate protocol at NRGH consists of the following sequences:

Sequence	Slice thick-ness (mm)	Gap (mm)	FOV	Time (min:s)
cor T2 TSE prostate	3.0	0	200	3:58
sag T2 TSE prostate	3.0	0	200	3:22
ax T2 TSE prostate and entire pelvis	3.0	0	200	2:49
ax T1 TSE entire pelvis	6.0	1.2	300	2:00
ax T1 GRASP pre- and post-contrast (dynamic)				
ax DWI ZOOMit, small FOV prostate				

Table 7: Prostate imaging

The standard rectal cancer protocol is:

Sequence	Slice thick-ness (mm)	Gap (mm)	FOV	Time (min:s)
ax T2 TSE	5.0	0.5	230	3:23
sag T2 TSE	3.0	0	200	2:59
cor T2 TSE	3.0	0	200	3:40
ax oblique T2 TSE	3.0	0	200	3:02
ax T1 TSE	5.0	0.5	230	2:23

Table 8: Rectal cancer imaging

As a result of previous success with Deep Resolve for rectal and prostate imaging, it was felt that using Deep Resolve would offer even more advantages. One of the challenges we observed with Deep Resolve, however, is the susceptibility to peristaltic motion artifacts, which can be explained by the reduced motion averaging effect with the lower number of averages acquired in Deep Resolve protocols.

As we do not use antiperistaltics routinely we were not able to consistently obtain high quality, high-resolution images required for these anatomic regions and consequently have not adopted Deep Resolve for our default protocol. Sites that routinely use antiperistaltics for rectal imaging may have a different experience: Image quality may be improved and scan time shortened with the application of Deep Resolve. Another countermeasure may be to balance out motion with more averages, which partially counteracts the time savings gained with Deep Resolve and has not been systematically tested in our setting.

One other area where Deep Resolve may be of benefit is in the evaluation of organ-at-risk (OAR) prostate spacer gel prior to radiation therapy in prostate cancer. These exams do not require high-resolution imaging.

Sagittal and axial prostate (Figure 15)

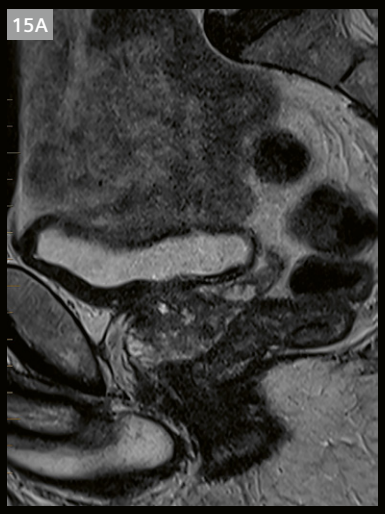
Figures (15A) and (15B) from a prostate exam demonstrate less motion and improved delineation of the rectal and bladder wall with Deep Resolve. However, the posterior peripheral zone cancer is slightly less conspicuous on Deep Resolve imaging.

(15C) and (15D) from a different patient show the following: While the margins of the prostate are more distinct on the Deep Resolve image, the apical cancer is more conspicuous and better defined on the conventional sequence in this particular case, potentially caused by motion effects as described before.

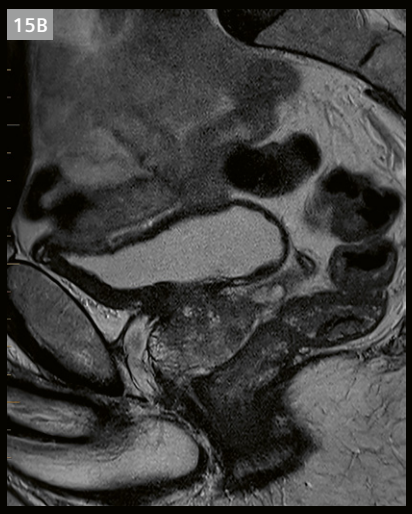
One area in prostate imaging that may benefit from Deep Resolve is in the evaluation of OARS spacer gel. The exam is performed to document the position of the gel spacer relative to the prostate and does not require high resolution. A shorter scan time would be attractive in these patients. Figures (15E) and (15F) show the position of the gel spacer, with improved signal on the Deep Resolve image. Scan time: (15E) conventional is 3:09 minutes and (15F) Deep Resolve is 2:40 minutes.

(15E) has a base resolution of 336, and (15F) has a base resolution of 320. Both sets of images reconstruct to $0.31 \times 0.31 \times 3.0$ mm^3 voxel size. The Deep Resolve image demonstrates the power of AI when voxel sizes are directly compared.

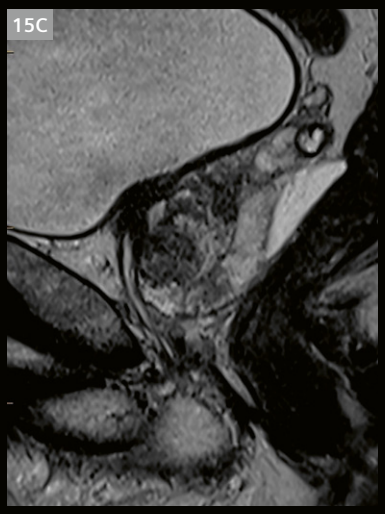
Sagittal conventional T2 TSE



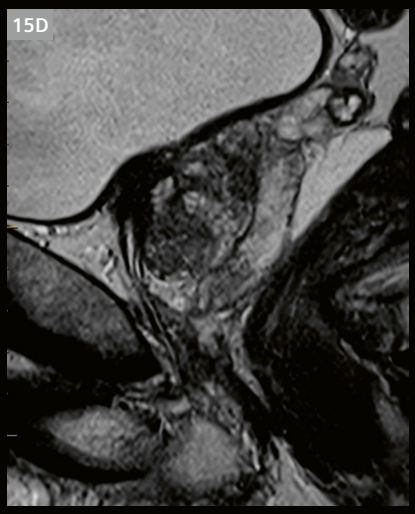
Sagittal Deep Resolve T2 TSE



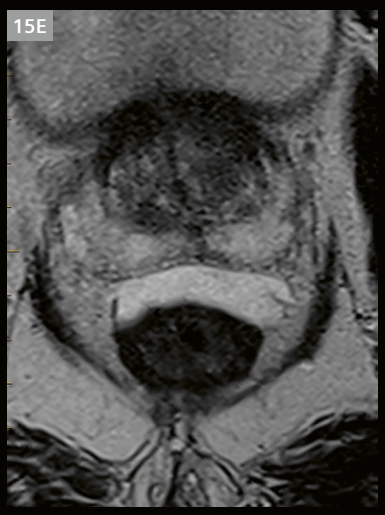
Sagittal conventional T2 TSE



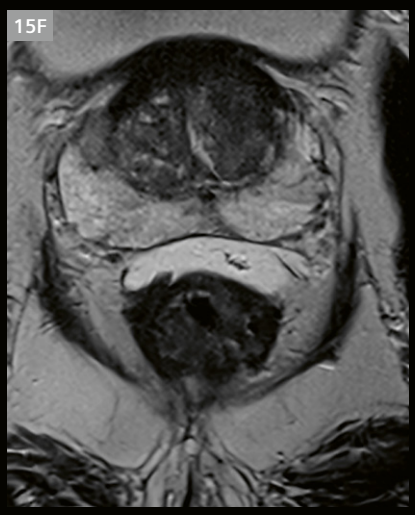
Sagittal Deep Resolve T2 TSE



Axial conventional T2 TSE



Axial Deep Resolve T2 TSE



15 Prostate imaging

Female pelvis imaging

The standard female pelvis protocol at NRGH consists of the following sequences:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
cor Deep Resolve STIR Pelvis	4.0	0.8	1:11
sag T2 TSE uterus	4.0	0.4	2:58
ax T2 TSE pelvis	5.0	0.5	3:10
ax T1 TSE pelvis	5.0	0.5	2:23
ax T1 FS TSE pelvis	5.0	0.5	3:20
sag Deep Resolve T1 FS TSE	4.0	0.4	2:22
ax T1 TSE FS pre- and post-contrast	5.0	0.5	3:20
ax DWI pelvis	5.0	0.5	3:15

Table 9: Female pelvis

Coronal, axial, and sagittal pelvic imaging (Figure 16)
(16A) and (16B) demonstrate similar conspicuity of the uterine fibroids on Deep Resolve and conventional images. The scan time for the conventional sequence was 2:27 minutes and for the Deep Resolve sequence it was 1:11 minute. Fat saturation is uniform and equivalent. Note the improved edge definition of the hip joints and the bladder wall with Deep Resolve.

(16A) is a conventional coronal STIR with a base matrix of 288 × 384, a 380 mm FOV, and a scan time of 2:27 minutes. The image was acquired with a voxel size of 0.99 × 0.99 × 4.0 mm^3, no interpolation, 1 average, 1 concatenation, and GRAPPA 2. (16B) is the Deep Resolve sequence with medium denoising and sharp edge enhancement options, interpolation, a reconstructed voxel of 0.59 × 0.59 × 4.0 mm^3, a 380 mm FOV acquired in 1:11 minute. The image was acquired with a voxel size of 1.58 × 1.19 × 4.0 mm^3, 1 average, 1 concatenation, and GRAPPA 4. The 1-minute coronal STIR is now part of the routine protocol for female pelvic imaging.

(16C) and (16D) also demonstrate equivalent image quality on axial T2 TSE. (16C) was acquired with a base matrix of 256 × 320 and a 230 mm FOV in 3:10 minutes. The image was acquired with a voxel size of 0.7 × 0.7 × 5.0 mm^3, no interpolation, 1 average, and 1 concatenation.

(16D) is the axial Deep Resolve T2 TSE sequence with medium denoising and sharp edge enhancement options, interpolation, a reconstructed voxel of 0.42 × 0.42 × 5.0 mm^3, and a 230 mm FOV acquired in 2:25 minutes. The image was acquired with a voxel size of 0.94 × 0.85 × 5.0 mm^3, 1 average, 2 concatenations, and GRAPPA 2. The conventional sequence had a TR of 3940 ms and a TE of 101 ms, and the Deep Resolve sequence had a TR of 3580 ms with a TE of 103 ms.

(16E, 16F) The Deep Resolve image demonstrates slightly improved edge definition. Note the improved conspicuity of the right ovarian T1 hyperintensity with Deep Resolve. (16E) was acquired with a base matrix of 240 × 320 and a 230 mm FOV in 2:23 minutes. The image was acquired with a voxel size of 0.7 × 0.7 × 5.0 mm^3, no interpolation, 1 average, and 3 concatenations.

(16F) is the axial Deep Resolve T1 TSE sequence with medium denoising and sharp edge enhancement options, interpolation, a reconstructed voxel of 0.4 × 0.4 × 5.0 mm^3, and a 230 mm FOV acquired in 2:38 minutes. The image was acquired with 1 average, 3 concatenations, GRAPPA 2, and 120% phase oversampling. The conventional sequence had a TR of 555 ms and a TE of 19. The Deep Resolve sequence had a TR of 578 ms and a TE of 20 TE ms.

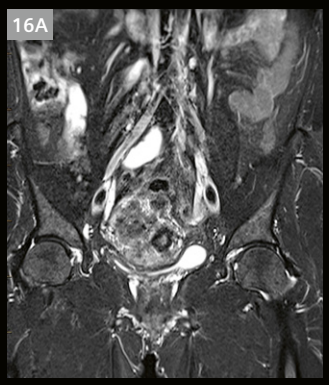
(16G, 16H) demonstrate improved resolution and diminished motion artifact related to vascular pulsation and peristalsis using Deep Resolve. Note the improved delineation of the left ovary, as well as increased conspicuity of the right ovarian hyperintensity.

(16G) is the conventional axial T1 TSE FS post-contrast with a base matrix of 240 × 320 acquired in 3:20 minutes. The image was acquired with a voxel size of 0.7 × 0.7 × 5.0 mm^3, no interpolation, 1 average, and 4 concatenations.

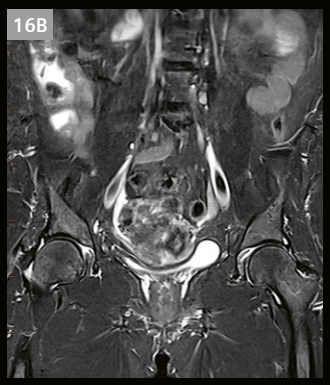
(16H) is the axial post-contrast Deep Resolve T1 TSE FS with high denoising and sharp edge options, interpolation, a reconstructed voxel of 0.4 × 0.4 × 4.0 mm^3 with a base matrix of 288 × 320. The image was acquired with 1 average, 5 concatenations, GRAPPA 4, and 140% phase oversampling. Extended phase oversampling was required to ameliorate the aliasing effects of a higher acceleration GRAPPA. A TR of 576 ms, a TE of 19 ms, and 40 slices of 5 mm thickness were used on the conventional sequence, compared to a TR of 611 ms, a TE of 8.4 ms, and 50 slices at 4 mm thickness for the Deep Resolve sequence.

Figure (16I) illustrates the lack of motion artifact and excellent fat saturation on the sagittal Deep Resolve T1 FS. This is a reliable and robust sequence, which has been adopted as part of our endometriosis protocol. The sagittal Deep Resolve T1 FS was acquired with high denoising and sharp edge enhancement options, interpolation, a reconstructed voxel of 0.4 × 0.4 × 4.0 mm^3 with a base matrix of 288 × 320. The image was acquired with a voxel size of 0.8 × 0.7 × 4.0 mm^3, 1 average, 4 concatenations, GRAPPA 4, and 140% phase oversampling. A TR of 550 ms and a TE of 8.4 ms were used.

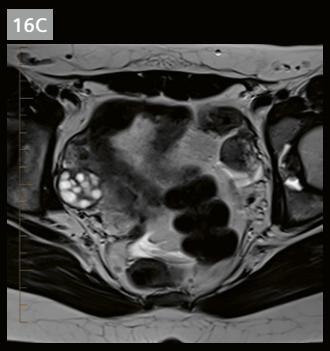
Coronal conventional STIR



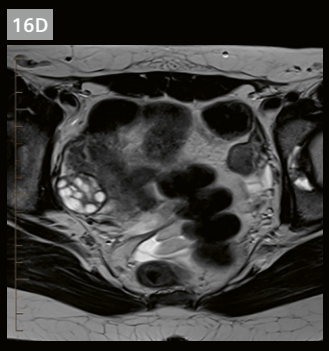
Coronal Deep Resolve STIR



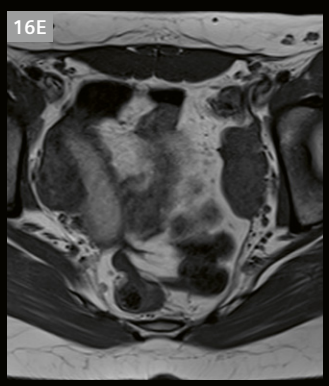
Axial conventional T2 TSE



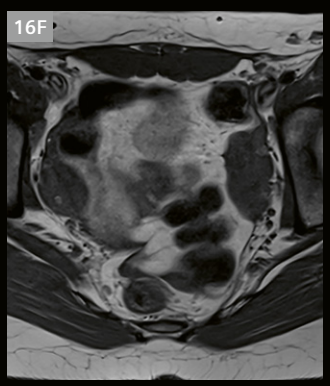
Axial Deep Resolve T2 TSE



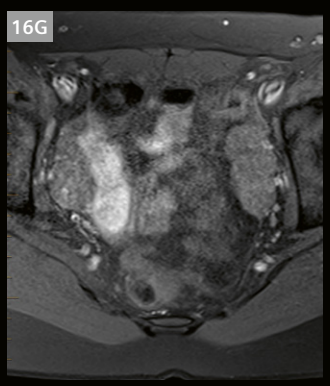
Axial conventional T1 TSE



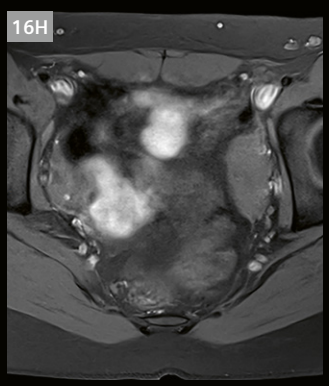
Axial Deep Resolve T1 TSE



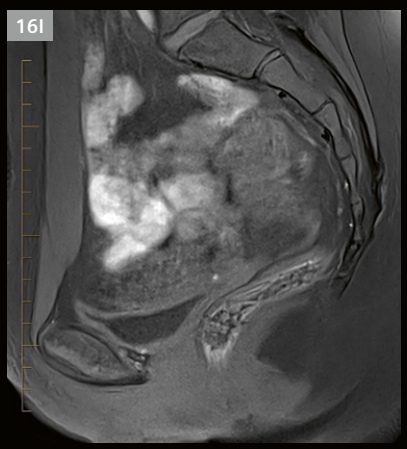
Axial conventional T1 FS post-contrast



Axial Deep Resolve T1 FS post-contrast



Sagittal Deep Resolve T1 FS TSE



16 Pelvic imaging

Cardiac imaging

Our final assessment of Deep Resolve was for TSE imaging of the heart. This is a common technique for turbo inversion recovery magnitude (TIRM) and TSE anatomical and morphologic assessment of the cardiac muscle. TIRM is commonly employed in the arrhythmogenic right ventricular cardiomyopathy (ARVC) protocol, the myocarditis protocol, and in the cardiac mass protocol.

Deep Resolve performance was compared to standard TIRM in the short axis. TIRM is a common sequence for assessment of myocardial edema in myocarditis. Figures (17A) and (17B) show that the Deep Resolve image has significantly improved resolution and signal. Motion artifacts are minimized. Deep Resolve also allows for a shorter breath-hold, approximately 13 seconds compared to 19 seconds for the conventional sequence. Since changing our default protocol to Deep Resolve, we feel that Deep Resolve facilitates improved detection of myocardial edema.

Short-axis dark-blood cardiac imaging (Figure 17)
(17A) is the conventional T2 short-axis dark-blood (DB) inversion recovery with a base matrix of 154 × 192 and an FOV of 360 mm acquired in a 19-second breath-hold. The image was acquired with a voxel size of 1.8 × 1.8 × 10 mm^3, no interpolation, 1 average, and no acceleration. (17B) is the Deep Resolve sequence with medium denoising and sharp edge options, a reconstructed voxel of 0.63 × 0.63 × 6.0 mm^3, and a 400 mm FOV (with an 84% phase FOV) acquired in a 13-second breath-hold. The image was acquired with a voxel size of 1.67 × 1.25 × 6.0 mm^3, 1 average, and GRAPPA 3.

Ultrafast imaging

Scanner efficiency and patient care can be improved by using ultrafast sequences on selected populations, such as pediatric, anesthetized, or claustrophobic patients. We provide two examples of ultrafast imaging performed with Deep Resolve at our site: head and knee imaging.

Ultrafast brain and knee imaging (Figure 18)
(18A) is the 3 mm Deep Resolve FLAIR sequence now part of our routine brain imaging. Scan time is 2:39 minutes compared to 1:06 minute for (18B), which is the ultrafast 3 mm FLAIR. Gibbs (or truncation) artifact is evident on the ultrafast image and can be corrected by increasing the matrix, but that would also increase the acquisition time.

Both sequences collect 50 slices of 3 mm thickness, have a 10% slice gap (0.3 mm), and use high denoising and sharp edge options. (18A) has a base matrix of 272 × 272 (100% phase) compared to a matrix of 141 ×176 (80% phase) in (18B). (18B) uses the highest possible acceleration factor of GRAPPA 4 while (18A) uses GRAPPA 2.(18C) is the axial Deep Resolve T2 TSE 3 mm sequence now part of our routine brain imaging. Scan time is 2:39 minutes compared to 1:03 minute for (18D), the ultrafast 3 mm axial Deep Resolve T2.

Both axial T2 TSE 3 mm sequences collect 50 slices of 3 mm thickness, have a 10% slice gap (0.3 mm), with high-level denoising and sharp edge options. (18C) has a base matrix of 400 × 400 (100% phase) compared to a matrix of 212 × 352 (60% phase) with the ultrafast scan in (18D). (18C) uses the highest possible acceleration factor of GRAPPA 4, while (18D) uses GRAPPA 2. Note the resolved detail in the ultrafast minute-long sequence.

Using ultrafast sequences, a complete knee exam can be acquired in 4:31 minutes. The approach was to take the Deep Resolve sequences in our current protocol and maximize the acceleration factor, decrease the frequency matrix, and use a reduced-phase FOV where possible with as little phase oversampling as possible. Parameters of the ultrafast knee protocol are:

Sequence	Slice thickness (mm)	Gap (mm)	Time (min:s)
sag Deep Resolve PD FS ultrafast	2.5	0.3	1:07
cor Deep Resolve PD FS ultrafast	2.5	0.3	0:59
cor Deep Resolve T1 ultrafast	2.5	0.3	1:16
ax Deep Resolve T2 FS ultrafast	2.5	0.3	1:08

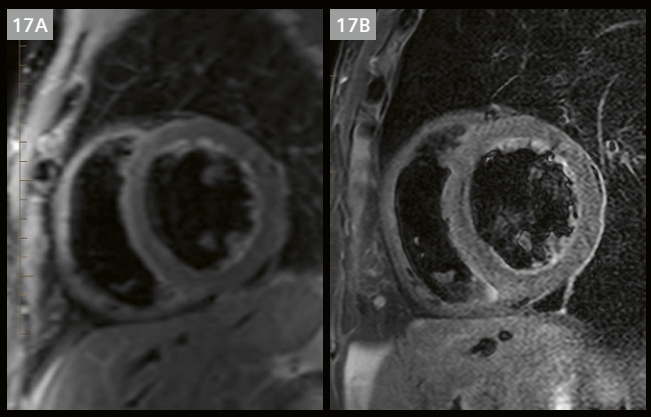
Table 10: Ultrafast knee imaging

Images (18E–18H) demonstrate the difference in time and image quality between the sagittal Deep Resolve PD FS sequence in our routine Deep Resolve protocol and the ultrafast sagittal Deep Resolve PD FS sequence. Image quality is clearly superior using standard Deep Resolve parameters, although the ultrafast scan is deemed diagnostic.

Images (18E) and (18F) demonstrate a partially torn meniscus. (18G) and (18H) demonstrate the ACL surrounded by fluid. Both sequences collected 38 slices of 2.5 mm thickness, with a 10% gap (0.3 mm) and used 90% phase oversampling; medium denoising and sharp edges were applied to both sequences. The Deep Resolve PD FS sequence used a matrix of 202 × 288, SMS 2, and 2 averages. The ultrafast Deep Resolve PD FS sequence used a matrix of 134 × 192, GRAPPA 4, and one average. Scan time: Deep Resolve PD FS was 1:55 minute, and the ultrafast Deep Resolve PD FS was 1:07 minute.

Conventional SA TIRM DB

Deep Resolve SA STIR DB



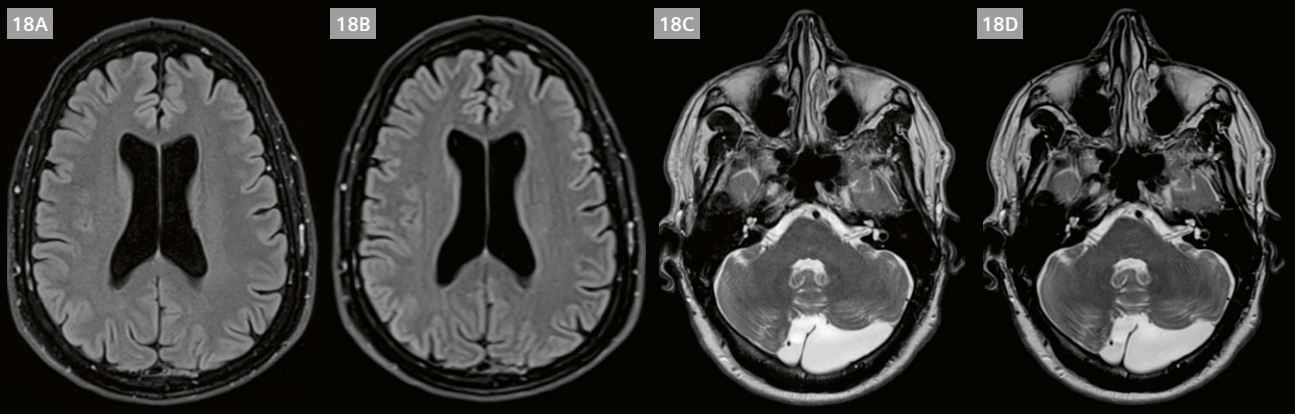
17 **Short-axis dark-blood cardiac imaging**

Axial Deep Resolve FLAIR 3 mm

Axial Deep Resolve FLAIR ultrafast 3 mm

Axial Deep Resolve T2 TSE 3 mm

Axial Deep Resolve T2 TSE ultrafast

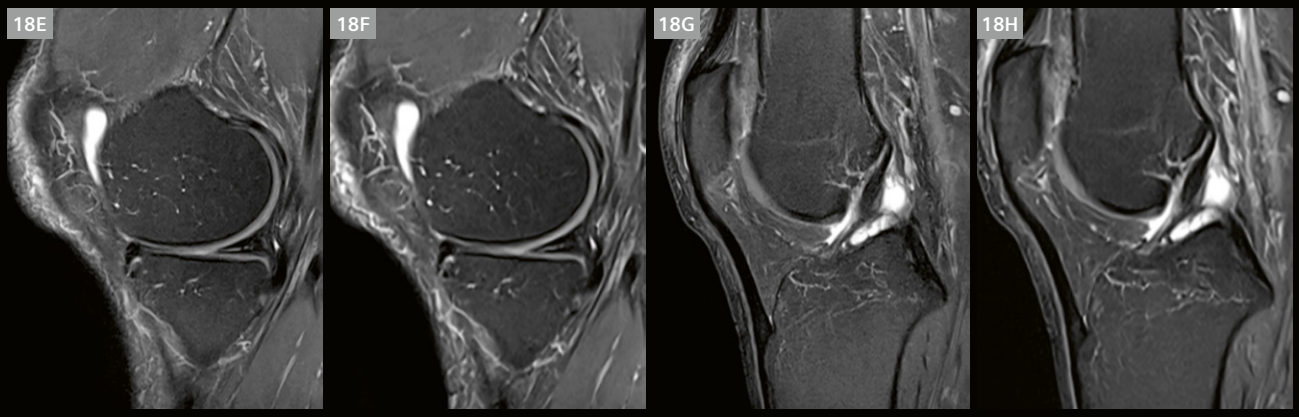


Sagittal Deep Resolve PD FS TSE

Sagittal Deep Resolve PD FS TSE ultrafast

Sagittal Deep Resolve PD FS TSE

Sagittal Deep Resolve PD FS TSE ultrafast



18 **Ultrafast brain and knee imaging**

Aside from being advantageous in sedated, pediatric, and claustrophobic patients, ultrafast techniques might be usefully applied in exams requiring lower resolution, such as in patients deemed nonsurgical due to underlying arthritis. Ultrafast sequences might also allow for limited dynamic imaging in certain orthopedic applications.

Observations

The most obvious benefits of Deep Resolve are the resolution enhancement, decreased acquisition time, and apparent SNR boost. Application to virtually all MSK imaging was fairly easy. Spine imaging and body imaging were more challenging as fold-over artifacts may occur in regions with large anatomies and small FOVs, in particular when applying higher PAT factors. To avoid such, an increase of phase oversampling was required for many sequences to compensate for the higher GRAPPA values. When first using Deep Resolve, we were very aggressive with increasing the matrix and averages while increasing GRAPPA, and learned to provide enough phase oversampling to prevent aliasing artifacts, at times up to 200%. After making adjustments and working to optimize the sequences, many of these issues were resolved. The presence of motion poses challenges to MRI, and Deep Resolve acquisitions are no exception, but many of the challenges can be ameliorated with shorter acquisitions or patient coaching. The issue with the phase oversampling requirements being more sensitive to wrap and phase aliasing were resolved by keeping the oversampling at acceptable levels, specific to the area being imaged.

The images included in this report are a sample of the variety of applications that we trialed with the Deep Resolve technology. It appears that more can be achieved in other areas of the body, such as the orbits, IACs, cranial nerves, and other small structures. Vessel wall imaging may also be an interesting area to focus on for future efforts.

Clinical results

In our opinion, Deep Resolve excels the most at musculoskeletal imaging. AI and deep learning generate opportunities that allow for a quantum shift in scheduling and can potentially increase throughput of MSK exams. Decreasing scan times by up to 50% will allow new booking models to increase capacity, which is particularly important in the Canadian system, where limited access is an issue. Future projects could evaluate these changes and how application might affect volumes, efficiency, and wait times. Shorter scan times will also translate into a more satisfactory patient experience, particularly for claustrophobic and pediatric patients.

As we have seen, Deep Resolve technology allows for a significant increase in spatial resolution and contrast, which is particularly important in small joints. Slice thickness can be reduced while maintaining signal without a significant time penalty, particularly when evaluating fingers, toes, and potentially the temporomandibular joint (TMJ).

Deep Resolve performs well with TSE sequences in the brain. In regard to T2 and FLAIR whole-brain imaging, there is a modest decrease in scan time with an overall improvement in image quality. However, it is particularly advantageous in pituitary imaging, allowing for a decrease in acquisition time and a significant improvement in resolution. Potential future applications might include imaging of the globe and for diagnosis of vasculitis.

Advantages are seen in spinal imaging. Again, these concern shorter scan times, and improved SNR and resolution. An attractive future development would be a Deep Resolve sequence compatible with the Dixon technique for pre- and post-contrast spine work.[3]

In view of our experience with Deep Resolve, we anticipated that Deep Resolve would excel at pelvic work. Though significant improvements in terms of image quality and time savings were reported in the literature [3] we, unfortunately, were not able to reproduce this in our practice due to the waiver of antiperistaltics. Accordingly, exams requiring high-resolution, small-FOV sequences such a prostate, rectal, and cervical exams were very susceptible to motion, particularly peristalsis but also bladder filling. At this time we have not adopted Deep Resolve protocols in these applications. We do not routinely administer antiperistaltics in these cases, but sites that do would likely have more success. However, full FOV STIR in the pelvis performed well, both for MSK and intrapelvic pathology. In addition, T1 FS was very robust, with excellent fat saturation and a decrease in both motion and flow artifacts compared to conventional T1 FS. The Deep Resolve T1 FS has become our default sequence for evaluation of endometriosis and post-contrast imaging in the pelvis.

There are a few niche situations where Deep Resolve might be advantageous. In pre-radiation MR of the prostate to confirm OARS gel spacer position, high-resolution scanning is not required. Deep Resolve technology also results in very short examinations, so another application is in the use of ultrafast MSK protocols. The ability to perform exams in scan times of less than 5 minutes provides obvious benefits for pediatric and claustrophobic patients.

[3] *Work in progress. Available as a research sequence.*

However, while higher resolution images as provided by routine Deep Resolve would be preferred for most patients, a lower resolved but diagnostic scan may be advantageous in selected patients. This technique might be applied in older patients undergoing knee MRI who are unlikely to be surgical candidates. With scan times of approximately a minute, there might be opportunity to perform dynamic imaging through a limited range of motion. Ultrafast techniques requiring lower resolution could be developed for non-MSK applications, such as for documenting cord compression prior to radiation therapy.

Overall, we have been very happy with the performance of Deep Resolve. It has become our method of choice for essentially all MSK protocols, small-FOV neurological brain, spine, and selected body applications. While Deep Resolve for TSE sequences already covers a huge scope of applications and clinical use-cases we are excited to evaluate and clinically implement new and upcoming deep learning algorithms for more sequences in the very near future.

Conclusion

NRGH spent a great deal of time carefully optimizing and refining the protocols with the Deep Resolve sequences on clinical patients. Many of the improvements were made on the fly with clinical patients presenting with a range of common concerns and imaging challenges. Frontline MRI departments face a variety of scenarios and challenges in clinical imaging protocols. Building capacity and improving access to MRI for the future in a sustainable way is critical. The use of deep learning methods with new algorithms to gather high-quality data in shortened acquisition times will be a way forward. Deep learning can optimize and streamline imaging protocols to enhance patient care and reduce the cycle time spent acquiring image data.

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