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# The TwinsUK MR Imaging study protocol: Brain and spine at 3T and cardiac plus whole-body at 0.55T

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## Synopsis

**Keywords:** Low-Field MRI, Aging, Neuro, Cardiovascular, Lung, Body composition

**Motivation:** TwinsUK hosts 30 years of biological data, linked with imaging this can be used to understand how lifestyle, environment and infection exposures influence organ-specific ageing and disease.

**Goal(s):** To develop MRI protocols at 0.55T and 3T covering the whole body, and specifically the brain, heart and liver.

**Approach:** A protocol, consisting of two ~45 minute sessions, was developed that was inspired by the UK Biobank but optimised to suit technological advancements, and an ultra-wide bore low-field system.

**Results:** Data collection is underway with >300 participants scanned so far and ~2500 participants to be scanned over five years. Dedicated analysis pipelines are under development.

**Impact:** This study will generate a comprehensive MRI resource in a twin cohort of ~2500 participants. Combined with biological data, this facilitates the study of ageing and has potential to lead to more personalised approaches to managing health as we age.

## Introduction

The TwinsUK[1] MRI study aims to create a data repository from ~2500 participants, comprising a mixed cohort of monozygotic and dizygotic twin pairs. Data collection began in January 2024 and will run for five years. When linked with other TwinsUK datasets, including biochemical, physical and self-reported measures, this data can be used to generate organ specific biomarkers and understand how infection, lifestyle and environment exposures influence ageing and disease. Here we present the imaging protocol for this study developed on two scanners at 3T and 0.55T.

## Methods

Participants are recruited from the TwinsUK cohort, age range 50+ years, with twin pairs scanned on the same day. There are two sessions of ~45 minutes each; neurology at 3T and cardiac plus body at 0.55T (MAGNETOM Vida and Free.Max systems, Siemens, Erlangen, Germany). Each component of the acquisition was individually optimised.

The protocol was inspired by the UK Biobank imaging study[2] but adapted to benefit from recent advancements in hardware and software. Significant changes were required to accommodate the lower field system, utilising a wider bore (80 cm), but lower gradient specification (26 mT/m and 45 T/m/s per axis) compared to the current clinical standard. Imaging parameters are given in Tables 1-2.

At 3T, subjects are scanned head-first-supine, using a 64-channel Head/Neck coil, in combination with the 32-channel Spine array, accommodating higher acceleration factors and providing appropriate coverage for neck and whole spine imaging. For brain imaging, structural T1w (MPRAGE), T2w (2D-TSE), FLAIR (3D-SPACE), susceptibility weighted imaging (SWI), diffusion weighted imaging (DWI), and head-neck time-of-flight (TOF) angiography are acquired. T1w, DWI and SWI closely align with UK Biobank. Additionally, the T1w MPRAGE utilises the DISORDER framework for motion correction[3], implemented on the Gadgetron platform[4] to achieve inline reconstruction and PACS archiving. Structural T2w data (2D-TSE) is collected in three sagittal stations covering the whole spine.

At 0.55T, subjects are scanned head-first-supine using the 9-element Spine coil and two 6-element Contour coils. Two-point Dixon imaging is acquired over 9 stations utilising the full range of table movement, yielding neck-to-knee coverage. Structural T2w imaging is acquired of the abdomen and thorax. In the liver, modified Look-Locker inversion recovery (MOLLI) and multi-echo gradient-echo (MEGE) sequences are collected. Optimisation of the Dixon, MOLLI and MEGE data previously described for 0.55T[5] is now being validated against comparable 1.5T data, using the UK Biobank protocol, in a small cohort. A respiratory navigated fast-BLADE is acquired of the thorax, as well as a free-breathing balanced steady-state free precession (bSSFP) sequence in three orientations. For the cardiac section, compressed sensing bSSFP cines are acquired in 2-chamber, 3-chamber, 4-chamber, short-axis and left-ventricular outflow tract views. An axial cine series is also acquired of the thoracic aorta, with blood pressure measured before and after the acquisition for calculation of aortic distensibility. Native cardiac T1 mapping (MOLLI) is acquired at basal, mid-ventricular and apical slices for tissue characterisation. Aortic flow is assessed with a phase-contrast sequence. Cardiac sequences were specifically developed at 0.55T and have been validated and compared to 1.5T previously[6-8].

## Results and Discussion

Data collection is underway, with over 300 participants scanned so far. Preliminary analysis has been performed for the initial 232 participants, of which 17 were male, 120 were monozygotic twins, 110 were dizygotic twins and two had unknown zygosity. Mean age and BMI in this initial data set were 67 years [IQR 60;70] and 26.26 kg/m2 [IQR 22.6;29.4].

Automated quality control (QC) and dedicated analysis pipelines are being developed for feature extraction of neuro data (example images shown in Figure 3), with plans to extend to all body parts. Qualitative QC checks have been performed on an initial portion of the cardiac data with images being scored based on orientation and artefacts, example images shown in Figure 4.

Figure 5 demonstrates example images of the whole-body, liver and lung. Dixon data can be used for measurement of adipose tissue and muscle distribution and segmentation of all abdominal organ volumes. MOLLI and MEGE data allows liver T1[9], T2* and proton-density fat-fraction quantification. Visualisation of the lung parenchyma is possible with fast-BLADE data.

## Conclusion

The TwinsUK MR Imaging study protocol has been set up and optimised to enable analysis of structural changes across multiple organs in adult twins. The protocol took inspiration from UK Biobank, making appropriate adjustments given the advancement in technology and lower field strength of the MAGNETOM Free.Max scanner for wide bore body imaging. The intention is that this data can be used as stand-alone, or in conjunction with the wider TwinsUK resource, by researchers worldwide to study health, disease and ageing.

## Acknowledgements

## Figures

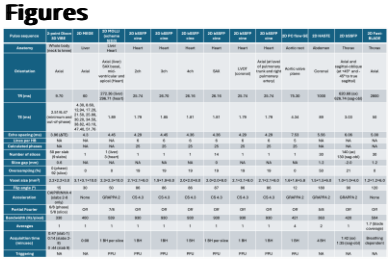

Figure 1: Sequence parameters for cardiac plus body protocol acquired at 0.55T. AD = aortic distensibility, CAIPIRINHA = controlled aliasing in parallel imaging results in higher acceleration, CS = compressed sensing, GE = gradient echo, GRAPPA = generalised autocalibrating partially parallel acquisitions, HASTE = half Fourier single-shot turbo spin-echo, LVOT = left-ventricular outflow tract, PC = phase contrast, SAX = short axis, VIBE = volumetric interpolated breath-hold examination.

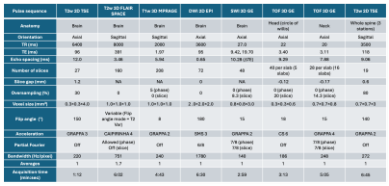

Figure 2: Sequence parameters for neurology protocol acquired at 3T. CAIPIRINHA = controlled aliasing in parallel imaging results in higher acceleration, EPI = echo planar imaging, FLAIR = fluid attenuated inversion recovery, GE = gradient echo, GRAPPA = generalised autocalibrating partially parallel acquisitions, MPRAGE = magnetisation-prepared rapid gradient echo, SPACE = sampling perfection with application optimised contrast using different flip-angle evolution, TOF = time of flight, TSE = turbo spin echo.

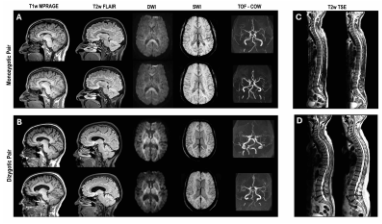


Figure 3: Brain and spine images for example pairs of monozygotic (A, C) and dizygotic (B, D) twins. COW = circle of Willis, DWI = diffusion weighted image, FLAIR = fluid attenuated inversion recovery, MPRAGE = magnetisation-prepared rapid gradient echo, SWI = susceptibility weighted imaging, TOF = time of flight, TSE = turbo spin echo.

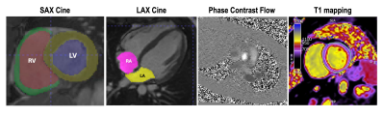


Figure 4: Cardiac images for an example participant. LAX = long axis, LA = left atrium, LV = left ventricle, RA = right atrium, RV = right ventricle, SAX = short axis. cvi42[10] software was used for region segmentation.

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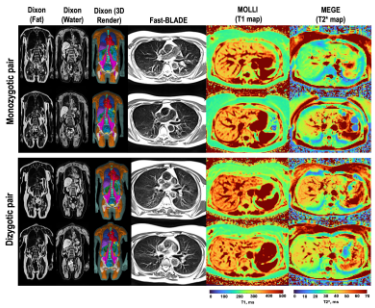


Figure 5: Cardiac and body images for example monozygotic and dizygotic twin pairs. Image derived phenotype 3D renders were obtained after preprocessing and application of segmentation pipelines. 3D segmentations: Liver (purple), lungs (dark blue), spleen (yellow), kidneys (green), subcutaneous adipose tissue (teal), visceral adipose tissue (blue), iliopsoas muscles (pink), total muscle (orange), pelvic bones (white), vertebrae (light blue) and the intervertebral disks (white), bladder (light yellow), heart (red), aorta (deep pink).