Porting UK Biobank Diffusion Protocol to New Scanners

Summary.

The UK Biobank diffusion protocol was designed to make maximal usage of the gradient hardware available on the Siemens Skyra platform. The protocol uses the minimal echo time (TE) that could be robustly achieved on the pilot scanner, which maximizes SNR, but also means that the protocol runs close to hardware limits.

Subsequent porting to other Skyra scanners has revealed an interaction between the shim settings on a particular scanner and the diffusion-encoding gradients, as described below. On some scanners, the result is that the scanner will stop partway through the scan on many subjects. Fortunately, a straightforward modification to the diffusion direction set has been demonstrated to fix this problem with no anticipated compromise to the protocol or data, including compatibility with the unmodified protocol.

Gradient hardware.

MRI scanners include electrical coils that dynamically impose gradients in the magnetic field along 3 independent spatial axes, with each axis limited to some maximum gradient (Skyra platform: ~40mT/m).

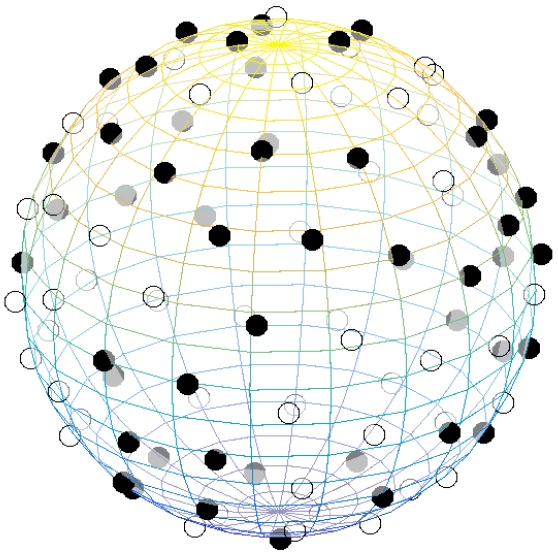
These gradients have two purposes that are relevant to this discussion:

- to impart diffusion contrast along a particular direction
- to homogenize the overall magnetic field (i.e. the linear "shims")

The same hardware is used for both purposes. The linear shims remain constant during the scan, while the diffusion gradients are turned on and off transiently. The amplitude of the diffusion gradients is a fixed aspect of the acquisition protocol, while the linear shims depend on both the scanner (the intrinsic homogeneity of the magnetic field) and the subject (whose body slightly alters that field).

Diffusion directions on a sphere.

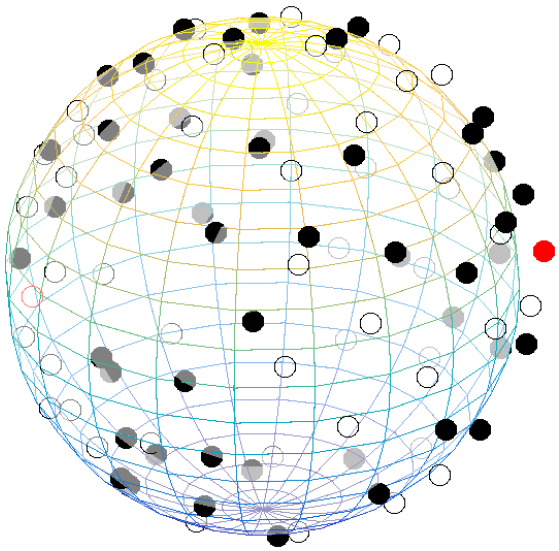
The diffusion gradients for the Biobank protocol are illustrated below, showing the 50 directions for one of the two acquired "shells" (b-value). Solid points are the diffusion directions that are actually acquired, each of which is paired by a point on the opposite side of the sphere, indicated by an open circle. Diffusion contrast is "symmetric" about the centre of the sphere, meaning that either point could be acquired and would impart the same information.



Above, the coloured reference sphere indicates a constant gradient demand, independent of direction. The protocol runs close to hardware limits whenever a given direction is primarily oriented along one of these axes, while directions that are far from any single axis "share the load".

Problem description.

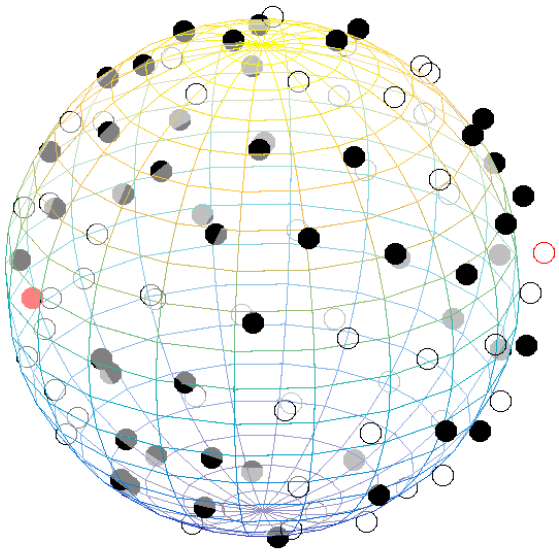
If the scanner needs to achieve a significant linear shim in order to homogenize the field, this leads to an offset in the gradient demand. The example below assumes that an additional, positive gradient is required along the x-axis to achieve the desired linear shim. In this case, the total necessary gradient is shifted to the right for all points, and the point in red has exceeded the total available gradient indicated by the colored sphere.



The overall field inhomogeneity that the linear shims attempt to compensate for is dictated by an interaction between the scanner-specific field homogeneity and the disruption of this field by the subject's head. Thus, the required linear shims will vary to some degree from subject-to-subject, but will be fairly similar on a given scanner. For this reason, a direction that can readily be achieved on one scanner may consistently exceed the maximum gradient available on another scanner.

Solution.

If this behaviour is observed on a given scanner, we can take advantage of the symmetric nature of the diffusion signal. Because the original points in Fig 1 all lie on the sphere, the shift in all points imposed by the linear gradients mean that if one acquired direction (solid circle) has shifted outside the sphere of achievable gradients, its reflection (open circle) will lie inside it. Thus, the problematic direction(s) can simply be replaced with their reflection to the opposite side of the sphere, as described below.



Implementing proposed solution.

The solution described above can be achieved in two straightforward steps. This assumes some familiarity with the diffusion sequences, including the installation of diffusion vectors files (that should have been done when setting up the Biobank protocol).

1. Identify the problematic direction(s). This can typically be achieved by simply running the protocol on a phantom. The scanner will stop when it reaches a direction that exceeds the gradient maximum.
2. Check the corresponding direction in the directions file. This should correspond to a direction that is heavily weighted on one axis. For example, direction 49 below is dominated by the x axis:

```
…
Vector[47] = ( 0.577, 0.725, 0.376 )
Vector[48] = ( 0.290, 0.296, 0.573 )
Vector[49] = ( 0.966, 0.257, -0.006 )
Vector[50] = ( -0.478, -0.508, -0.114 )
Vector[51] = ( 0.892, -0.208, 0.402 )

…
```

3. The problematic direction can be inverted by simply negating all three (x,y,z) coordinates in the directions file.

```
…
Vector[47] = ( 0.577, 0.725, 0.376 )
Vector[48] = ( 0.290, 0.296, 0.573 )
Vector[49] = ( -0.966, -0.257, 0.006 )
Vector[50] = ( -0.478, -0.508, -0.114 )
Vector[51] = ( 0.892, -0.208, 0.402 )

…
```

4. You may find that the scanner fails on more than one direction, which may require iterating the process above until the scan runs to completion.

18 July 2017
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