This file provides information about the dynamic image sets in the B1_Correction QIBA series (version 13).

This data set is similar to version 5, except that it simulates B1 inhomogeneity correction.

There are several different schemes used to correct for B1 inhomogeneity. We simulate two double-angle correction schemes: (60-120 and 120-240) and (60-180 and 120-180). The output of these images is the B1 correction images. Four sets of T1 Mapping and dynamic images were made by adjusting the nominal flip angle by ±10% and ±20% to give the actual flip angle.

Two sets of images are provided for each series. DICOM part 10 format images are in the DICOM directory. XML files are in the XML directory. The XML images allow the values for the DICOM tags to be altered using a text editor, and new DICOM images can then be generated using dcm4che's tool called "xml2dcm," available at http://www.dcm4che.org/confluence/display/d2/dcm4che2+DICOM+Toolkit.

The parameters used to generate the data are:

Nominal dynamic flip angle = 25 degrees
Actual dynamic flip angle = Nominal flip angle X Correction factor
Repetition Time = 5 msecs
Time interval between the DCE images = 0.5 seconds
Assumed T1 (in tissue) = 1000 msecs
Assumed equilibrium magnetization (in tissue) = 50000
Assumed T1 (in blood vessel) = 1440 msecs
Assumed equilibrium magnetization (in blood vessel) = 50000

The correction factors used are {0.8, 0.9, 1.1, 1.2} (i.e. {-20%, -10%, +10%, +20%}).

GE timing information is included in the DICOM headers at fields 0008,0032 (Acquisition Time) and 0018,1060 (Trigger Time).

The input function was derived from the JSim model ToftsKermode_two_parameter_B1_20150701.proj, which is available on the QIBA page of our website. A link to the JSim website is also provided. This function representing a blood concentration time curve was converted to a plasma concentration time curve assuming a blood hematocrit of 45%. The relaxivity of the gadolinium contrast agent at 1.5 T was assumed to be 0.0045 $mmol^{-1}$ $msec^{-1}$ (Stanisz GJ, Henkelman RM. Gd-DTPA relaxivity depends on macromolecular content. Magn Reson Med. 2000 Nov;44(5):665-7. PubMed PMID: 11064398).

The data sets are organized as follows: Each correction factor is in its own folder, with the dynamic, T1 Mapping, and EPI_SEG images contained in subfolders within these correction factor folders. The naming convention for the correction factor folders is “B1_Correction_<CF>Percent_<Creation date>” where <CF> is the correction factor and <Creation date> is the date when the images were created. Thus, the folder “B1_Correction_+10Percent_20150721” has a correction factor of +10% (1.1) and was created on July 21, 2015.

The folders with the dynamic images are titled “QIBA_Dyn_<Creation date>”.

The data in the dynamic test images is organized as follows:

The test data is generated using several combinations of Ktrans and Ve, using the modified Tofts Kermode 2-parameter model. The Ktrans takes values {0.01, 0.02, 0.05, 0.1, 0.2, 0.35}. The Ve takes values {0.01, 0.05, 0.1, 0.2, 0.5}.

The test data contains 10*10 pixels patches of each Ktrans and Ve combination. While generating the test data, the Ve values {0.01, 0.05, 0.1, 0.2,0.5} vary along the x direction. Ktrans values {0.01, 0.02, 0.05, 0.1, 0.2, 0.35} vary along the y direction.

The Vascular region of interest is the bottom 50*10 pixels strip of the image. The peak of the Vascular region is the top-left 25*10 pixels strip of the image. This strip also contains time point labels given in seconds. The Zero patch (Ktrans=0.0, Ve=0.5) is the top-right 25*10 pixels strip of the image.
The following is a detailed list giving the specific Ktrans,Ve combination used to generate each 10*10 pixel patch. The x,y location specifies the upper-left corner of each 10*10 pixel patch containing a specific Ktrans,Ve combination.

x	y	Ktrans	Ve
0	10	0.01	0.01
0	20	0.02	0.01
0	30	0.05	0.01
0	40	0.1	0.01
0	50	0.2	0.01
0	60	0.35	0.01
10	10	0.01	0.05
10	20	0.02	0.05
10	30	0.05	0.05
10	40	0.1	0.05
10	50	0.2	0.05
10	60	0.35	0.05
20	10	0.01	0.1
20	20	0.02	0.1
20	30	0.05	0.1
20	40	0.1	0.1
20	50	0.2	0.1
20	60	0.35	0.1
30	10	0.01	0.2
30	20	0.02	0.2
30	30	0.05	0.2
30	40	0.1	0.2
30	50	0.2	0.2
30	60	0.35	0.2
40	10	0.01	0.5
40	20	0.02	0.5
40	30	0.05	0.5
40	40	0.1	0.5
40	50	0.2	0.5
40	60	0.35	0.5