This file provides information about the data set in the folders QIBA_v6_Tofts_GE and QIBA_v6_Tofts_Siemens.

The image data for the GE and Siemens sets are identical. The only difference is that the GE series contains DICOM headers that a GE machine would generate, while the Siemens series contains DICOM headers from a simulated Siemens machine.

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 this data are:

Flip angle = 30 degrees
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

GE timing information is included in the DICOM headers at fields 0008,0032 (Acquisition Time) and 0018,1060 (Trigger Time). The imaging start time for Siemens machines is given in the DICOM headers at fields 0008,0030 (Study Time) and 0008,0031 (Series Time), and acquisition time for each image is given in the DICOM headers at fields 0008,0032 (Acquisition Time) and 0008,0033 (Image Time).

A 10 minute study is simulated, with injection of contrast agent occurring at 60 seconds. Thus, the total duration of imaging is 660 seconds.

The input function was derived from the JSim model ToftsKermode_two_parameter_20120103.proj (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 in the test image 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