To access and download the data (located in the "Test-retest Clinical Study" directory) refer to: http://www.qi-bench.org/wiki/index.php/Manually_access_data.

In the "Test-retest Clinical Study" directory there are 31 sub directories, one per subject, and one excel file "Test-retest-Clinical-Study-Summary-Lesion-Position.xls", which summarizes the location of the lesions for all subjects. Note that for the 3A-Second Challenge we are using the coordinates highlighted in the yellow area. The coordinates in the purple area are the ones used for the 1B and can be used as a reference if needed.

In **each** subject folder there are 6 files:

dcm_RIDER-#_0_0_CT: set of dicoms acquired at acqrep=0 (i.e. The first scan)
dcm_RIDER-#_0_1_CT: set of dicoms acquired at acqrep=1 (i.e. The second scan)

loc_RIDER-#_0_0.csv: file that contains the location of the lesion to segment for acqrep=0 (pertinent to the first scan)
loc_RIDER-#_0_1.csv: file that contains the location of the lesion to segment for acqrep=1 (pertinent to the second scan)

Example of a loc file:

SUBJID	TPINDEX	ACQREP	TARGET	LOCRDR	LOCTOOL	LOCREP	LOCX	LOCY	LOCZ	BBX0	BBX1	BBY0	BBY1	BBZ0	BBZ1
RIDER-#	0	0					-57.97	56.16	-125	-90.24	-14.18	5.452	84.39	-148.8	-86.25

Where LOCX, LOCY, LOCZ are the coordinates of a point approximately in the center of the lesion and BBX0, BBX1, BBY0, BBY1, BBZ0, BBZ1 are the coordinates of a box containing the lesion.

rdg_RIDER-#_0_0.csv: this is the file that the participant needs to fill out with his/her results from the **first** scan
rdg_RIDER-#_0_1.csv: this is the file that the participant needs to fill out with his/her results from the **second** scan

Example:

SUBJID	TPINDEX	ACQREP	LOCRDR	LOCTOOL	LOCREP	TARGET	SEGRDR	SEGTOOL	SEGREP	SERIESTYPE	READINGTYPE	READING	UNITS
RIDER-#	0	0/1											

The participant needs to fill out the following fields in the rdg files:
SEGRDR: anonymized Participant ID given at time of registration
SEGTOOL: segmentation tool or algorithm ID. This field value is chosen by the participant to identify his/her algorithm
SEGREP: segmentation repetition (zero based). It is relative to the number of readings performed by the algorithm in SEGTOOL.
READING: the actual volume measurement
UNITS: units of the volume measurement

Note: The participant needs to fill out one line per measurement. Use SEGTOOL to differentiate measurements performed by multiple algorithms and SEGREP to differentiate measurements done by the same algorithm multiple times. If only one algorithm is used to perform one reading, the rdg file will have one line with SEGREP=0.
Segmentation objects, if provided, should preferably be in Nifti format (.nii).

Any questions, please email: jovanna.danagoulian@bbmsc.com