# ACRIN 6698 / I-SPY 2 Public Data Description – TCIA Data Collection

| MODIFICATION/REVIEW ACTIONS | |
|---|---|
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| 9/22/2014 | Created by: David Newitt |
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# Data Dictionary and Object Descriptions

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## Scope

This document contains definitions for the DICOM objects and attributes specific to the ACRIN 6698/I-SPY 2 MRI image data collections, and descriptions of associated derived data objects provided with this image data set.

## Patient and study identification

All patients and studies are identified through standardized, deidentified attributes as shown in Table 1.

- Patient unique identification is provided through a 6-digit identifier set by the I-SPY 2 TRIAL

- Study time-point is identified through the Clinical Trial Visit Codes: T0, T1, T2, and T3
- Imaging center discrimination has been retained (Clinical Trial Site ID) to allow for center-based analysis, but has been anonymized as codes “SITE AAA”, “SITE AAB”, etc…
- In general, all private DICOM attributes considered HIPAA compliant by TCIA have been retained in the image sharing submission process; but it should be noted that some studies may have been anonymized prior to submission to the analysis and archiving centers, so the presence of scanner manufacturer private attributes that may be required for some analyses cannot be guaranteed.

All objects have been deidentified to preserve patient privacy. If any evidence of non-HIPAA compliant patient PHI is found please notify the UCSF Breast Imaging Research Program core lab: ispy imaging lab .

Table 1: Patient and study identification attributes included in all DICOM objects

| Variable Name | Variable Description | Format | DICOM Tag |
|---|---|---|---|
| Patient Name | Patient ID (pppppp), Site ID(sss) and Trial | Text:<br>ACRIN-6698-<pppppp>^Site<br><sss>^ISPY2 | (0010,0010) |
| Patient ID | Study name and patient ID number | Text:<br>ACRIN-6698-<pppppp> | (0010,0020) |
| Clinical Trial Patient ID | Unique identification number for patient in the trial | Text encoded number:<br><pppppp> | (0012,0040) |
| Clinical Trial Site ID | 3 letter code of the imaging site:<br>“SITE sss” | Text:<br><sss> | (0012,0030) |
| Clinical Trial Visit Code | ID code for the trial visit<br>T0 baseline<br>T1-n follow-ups | Text:<br>T<n> | (0012,0050) |
| Clinical Trial Visit Description | Description for the trial visit given in (0012,0050) | Text: defined terms:<br>baseline<br>early-treatment<br>inter-regimen<br>pre-surgery | (0012,0051) |

## DICOM Objects

Wherever possible, all original DICOM image objects from the initial scout series, the T2 weighted (T2w) series, the diffusion weighted (DWI, ACRIN-6698 sub-study only) series, and the dynamic contrast enhanced (DCE) series, are included in the collection. These original image objects are unprocessed except for necessary alterations of the DICOM metadata for deidentification. In addition, derived objects calculated by the UCSF imaging lab for primary analyses on the DWI and DCE data are included. Table 2 details identification by series number (0020,0011) and series description (0008,103e) of the derived DICOM objects provided in the shared data collection on TCIA. Not all objects will be present in all cases due to unanalyzable studies.

DWI derived image objects include a set of series based on the full DWI acquisition. For ACRIN-6698 subjects, this was a four b-value protocol optimized across platforms for the trial and was a required acquisition for all studies. For I-SPY 2 subjects *not* in the 6698 sub-study, DWI series are not currently included but will be added at a future time subject to further quality review. These may be either the optimized four b-value protocol or a site-specified two b-value protocol. The DWI derived series set consists of: 1) TRACE images, 2) mono-exponential ADC maps, and 3) manually defined whole-tumor segmentations stored as DICOM MRI objects and as a DICOM segmentation object. One ACRIN-6698 site did not have multi-b-value capabilities on their MRI scanners at the time of this study, and instead acquired three series with 2 b-values each [(0,800), (0,600) and (0,100) s/mm$^2$]. For these studies, a combined multi-series multi-b-value (MSMB) series was created, consisting of all non-0 b-value images plus a single averaged b=0 image. DICOM metadata fields were adjusted in this MSMB series to permit reading as a standard multi-b-value acquisition.

DCE derived image objects include a set of series based on an image cropped to include the breast with the primary tumor per I-SPY 2 analysis. These series include early and late time-point percent enhancement maps ($PE_{early}$, nom. 2'30" seconds post injection, $PE_{late}$, nom. 7'30" post injection) and a signal enhancement ratio map (SER = $PE_{early}/PE_{late}$). In addition, a functional tumor volume (FTV) analysis mask is provided as a DICOM segmentation object, as described in a separate document which may be downloaded from the TCIA wiki page for this collection.

Table 3 lists the series numbers and descriptions for an example MRI study. ADC calculation values, FTV calculation parameters and FTV results are stored in DICOM private group attributes in each object as described in the following section.

Table 2. Series identification for derived DWI and DCE objects. Root series number for derived objects was determined as indicated for the different scanner manufacturers.

| Data type | Series number | Series Description Match |
|---|---|---|
| DWI | Siemens, GE: <root> = 1st original DWI series number<br>Philips: <root> = Original DWI series number / 100 | |
| TRACE Images | <root>0100 | ACRIN-6698: *DWI TRACE* |
| ADC Maps | <root>0200 | ACRIN-6698: *ADC* |
| Whole tumor mask | <root>9000 | ACRIN-6698: *DWI MASK* |
| Whole tumor segmentation | <root>9100 | ACRIN-6698: *DWI SEG* |
| Combined multi-series | <root>28 | ACRIN-6698: MergedMSMB* |
| DCE | Siemens, GE: <root> = 1st original DCE series number<br>GE resaved <root> = 1st resaved DCE series number / 100 [a]<br>Philips: <root> = Original DCE series number / 100 | |
| SER | <root>1000 | ISPY2: VOLSER: unilateral cropped: SER |
| PE phase <n> | <root>100<n> | ISPY2: VOLSER: unilateral cropped: PE<n> |
| Ipsilateral cropped Original | <root>1800 | ISPY2: VOLSER: unilateral cropped: original DCE |
| FTV Analysis Mask | <root>1900 | ISPY2: VOLSER: unilateral cropped: Analysis Mask |

[a] DCE scans on the GE scanner studies may be stored either with all phases in a single series (series number < 100) or as a set of single-phase series starting with number:
100 * <acquired series number>.

Table 3. Example series descriptions for a case with three 2 b-value DWI acquisitions.

| Series # | DICOM Series Description | Description |
|---|---|---|
| 1 | ISPY2: LOCALIZER | |
| 2 | ISPY2: LOCALIZER | |
| 6 | ISPY2: Ax T2 FSE FS | Original I-SPY 2 required T2w acquisition |
| 7 | ACRIN-6698: AX DWI 800 | Original DWI, b-values = 0, 800 s/mm$^2$ |
| 8 | ACRIN-6698: AX DWI 600 | Original DWI, b-values = 0, 600 s/mm$^2$ |
| 9 | ACRIN-6698: AX DWI 100 | Original DWI, b-values = 0, 100 s/mm$^2$ |
| 728 | ACRIN-6698: MergedMSMB: AX DWI 100 | 4 b-value image set created by merging the three 2 b-value acquisitions. |
| 7280100 | ACRIN-6698: DWI TRACE: from S728: bVals=0,100,600,800 | DWI trace images for all b-values. May or may not be identical to the original data depending on whether directional data was saved in the acquisition. |
| 7280200 | ACRIN-6698: ADC: from S728: bVals=0,100,600,800 | ADC map, mono-exponential, linear fit to the log of the pixel values for all b-values. |
| 7289000 | ACRIN-6698: DWI MASK: from S728: Whole Tumor Manual | Whole tumor segmentation created for the ACRIN-6698 primary analysis or later I-SPY 2 analyses. Stored as 2D DICOM MRI objects. |
| 7289001 | ACRIN-6698: DWI SEG: from S728: Whole Tumor Manual | Whole tumor segmentation stored as single DICOM SEG object |
| 10 | ISPY2: Ax Vibrant PRE/POST | Original single-series DCE acquisition, 80-100s phase time, generally 1 pre- and 5-8 post-contrast phases |

| | | |
|---|---|---|
| 101800 | ISPY2: VOLSER: uni-lateral cropped: original DCE | Original DCE images cropped to focus on the breast with the I-SPY 2 primary tumor. Used for FTV calculation in the trial. [No cropping done if the images have < 384 pixel columns.] |
| 101000 | ISPY2: VOLSER: uni-lateral cropped: SER | Signal enhancement ratio map; masked to only include pixels passing all filtering steps. |
| 101002 | ISPY2: VOLSER: uni-lateral cropped: PE2 | $PE_{early}$ map masked to only include voxels passing the background intensity filter. |
| 101006 | ISPY2: VOLSER: uni-lateral cropped: PE6 | $PE_{late}$ map masked to only include voxels passing the background intensity filter. |
| 101900 | ISPY2: VOLSER: uni-lateral cropped: Analysis Mask | DICOM FRACTIONAL Segmentation object encoding all filtering steps in the I-SPY 2 primary FTV analysis. |

## Private attribute tables

### Overview

The following information has been added to some of the derived DICOM objects in the data collection:

- DCE Timing information
- DCE Tumor volume of interest (VOI)
- SER analysis parameters
- Functional tumor volume (FTV) results
- DWI acquisition information and ADC map calculation

All are contained in DICOM group 0117x, labeled with a private creator field:

(0117,0010) UCSF BIRP PRIVATE CREATOR 011710xx

### Timing information

WARNING: Timing information was determined to the best of the core lab's ability based on the DICOM meta data in the original images submitted. **Accuracy of the timing information cannot be guaranteed**. In particular, all post-contrast times are based on the assumption that the injection and the start of the 1st post-contrast scan were simultaneous, which could not be confirmed.

Timing information fields are shown in Table 4. Timing information was added to all DCE derived image and segmentation objects.

Table 4: Scan timing information fields for dynamic contrast-enhanced (DCE) MRI

| Name | Description | VR (VM) | DICOM Tag |
|---|---|---|---|
| Total phases | Number of acquired time points (phases) including a single pre-contrast acquisition | IS | (0117,1030) |
| Acquisition duration | Single phase acquisition duration | DS | (0117,1031) |
| Acquisition start times | Starting time delay in seconds for each acquisition relative to the start of the 1st post-contrast acquisition | DS (1-n) | (0117,1032) |
| Injection time | Assumed injection time per scanner clock | TM | (0117,1033) |
| Effective acquisition delay | Effective post-injection delay for each acquisition. Non-centric phase encoding is assumed, placing the effective time half way through the acquisition | DS (1-n) | (0117,1034) |
| SER timing indices | Indices (0-origin) of the 3 acquisitions used in the SER calculation | IS (3) | (0117,1035) |
| Timing information method | Method used to determine the timing acquisition. Defined terms:<br>AUTO: Automatic based on original image meta data<br>MANUAL: Manually input "best-guess" timing information | LO | (0117,103A) |
| Timing information comments | Comments on determination of timing information | LT | (0117,103B) |

### Tumor volume of interest (VOI)

A 3D rectangular VOI enclosing the enhancing tumor region was defined on all cases with acceptable quality and compliance for volume SER analysis. VOI are defined in the DICOM standard patient coordinate system, as defined by the Image Position Patient (0020,0032) and Image Orientation Patient (0020,0037) fields in the original DICOM image objects. Tumor VOI attributes are described in Table 5 and are included in all DCE derived image and segmentation objects. While the VOI definition allows for oblique analysis regions this is not used in the I-SPY 2 analysis procedures. Therefore, all analysis and OMIT VOIs are aligned with the DCE image axes.

In cases where significant regions of non-tumor enhancement could not be excluded from the VOI without also excluding tumor areas, "OMIT" regions of interest (ROI) were defined to mask out these regions. OMIT ROIs were defined either as 3D rectangular VOI analogous to the analysis VOI, or as 2D irregularly shaped ROIs which were projected across the 3D image

along one of the 3 orthogonal image axes. The projected OMIT ROIs were defined using one of three orthogonal maximum intensity projection (MIP) images that had been interpolated to have isotropic voxel dimensions and were transposed where necessary to display in the standard radiologic orientations. Therefore, except for ROIs projected along the slice-axis [projection axis (0117,1051) = 2] the stored X- and Y- vertices cannot be directly applied to the original images. The ACRIN-6698 collection includes 1110 studies with derived SER maps, of which 150 have OMIT regions defined. 58 of these are of the projection type, so correct implementation of these features effects a not-insignificant number of cases. Researchers wishing to use the primary FTV segmentations may prefer to utilize the "FTV Analysis Masks" also provided with the collections. These DICOM segmentation objects encode all the FTV filtering steps, including VOI selection and OMIT regions, on a pixel-by-pixel basis for the cropped analysis images. Download the file "*Analysis mask files description.docx*" available on the TCIA wiki page for this collection for more information.

OMIT regions are defined in the DCE derived maps in private attributes detailed in Table 6.

Table 5: DICOM Fields for rectangular VOI

| Name | Description | VR (VM) | DICOM Tag |
|---|---|---|---|
| VOILPS | Patient coordinate system specified rectangular VOI Sequence | SQ | (0117,1020) |
| > VOILPS Center | Center of the VOI | DS (3) | (0117,1042) |
| > VOILPS HalfWidth | 1st half dimension vector of the VOI | DS (3) | (0117,1043) |
| > VOILPS HalfHeight | 2nd half dimension vector of the VOI | DS (3) | (0117,1044) |
| > VOILPS HalfDepth | 3rd half dimension vector of the VOI | DS (3) | (0117,1045) |
| > VOILPS Type | Use for the specified region. Defined terms:<br>VOI Region to be analyzed<br>OMIT Region to be excluded from the analysis | CS | (0117,1046) |
| VOI_pixel_start * | (x,y,z) coordinates of the first voxel in the VOI | US (3) | (0117, 10A1) |
| VOI_pixel_end * | (x,y,z) coordinates of the last voxel in the VOI | US (3) | (0117, 10A2) |

* VOI_pixel_start and VOI_pixel_end are defined in reference to the cropped analysis image and assume slices are read in original acquisition order as given by the instance number value (0020,0013). Since this may not be the standard DICOM reading order, care must be taken in interpreting these values. Use of the patient coordinate system VOI definitions is recommended.

Table 6: DICOM Fields for description of OMIT regions: rectangular VOI and irregular projected 2D ROIs

| Name | Description | VR (VM) | DICOM Tag |
|---|---|---|---|
| OMIT regions | OMIT region sequence. Each item contains either a 3D patient-coordinate system rectangular VOI or a 2D pixel-coordinate projection ROI | SQ | (0117,1022) |
| > VOILPS ROI flag | Type of VOI: enumerated values:<br>0 rectangular VOI<br>1 irregular projected pixel-coordinate ROI | IS | (0117,1041) |
| > VOILPS item | See Table 5 for attributes for rectangular VOI | | |
| > ProjectedROI npixels | Number of pixels for image used for ROI definition | US | (0117,1050) |
| > Projection axis | Image pixel axis of projection for the 2D ROI. Enumerated values: 0=x-axis, 1=y-axis, 2=z-axis | IS | (0117,1051) |
| > ProjectedROI transpose flag | Flag indicating ROI coordinates are defined on a transposed image | IS | (0117,1052) |
| > ProjectedROI X vertices * | X-axis pixel coordinates defining the irregular ROI | US (3-n) | (0117,1053) |
| > ProjectedROI Y vertices * | Y-axis pixel coordinates defining the irregular ROI | US (3-n) | (0117,1054) |
| > ProjectedROI Z range * | Z-axis (plane) range of projection of the ROI. If not present the ROI was projected across all planes in the image. | US (2) | (0117,1055) |
| > ProjectedROI type | Type (usage) of ROI. Defined terms:<br>OMIT region to be excluded from the analysis | CS | (0117,1056) |
| > ProjectedROI label | Label for display with the ROI | LO | (0117,1057) |

* ROI vertices are defined on the images that were used for the volume SER calculation. For all ROIs with projection axis 0 or 1 the transpose flag and npixels values must be used to convert the stored vertices into the original image coordinate system. Use of the provided analysis masks

### SER analysis parameters

Parameters used to specify the Volume SER calculation are stored in a DICOM sequence (0117,1010) described in Table 7. Table 8 lists the parameters used, with each parameter being described in one item in the sequence. See Appendix A for a description of the Volume SER calculation.

Table 7: DICOM sequence for storing analysis parameters

| Name | Description | VR (VM) | DICOM Tag |
|---|---|---|---|
| Parameter sequence | | SQ (1-n) | (0117,1010) |
| > Parameter type | Parameter type. Enumerated values: FLOAT, INTEGER, STRING | CS | (0117,1012) |
| > Parameter name | Identifies parameter | LO | (0117,1014) |
| > Parameter description | Description of parameter | LT | (0117,1016) |
| > Floating parameter value | Value of floating-point parameter<br>required for type (0117,1012) FLOAT | DS (1-n) | (0117,1018) |
| > Integer parameter value | Value of integer parameter<br>required for type (0117,1012) INTEGER | IS (1-n) | (0117,1019) |
| > String parameter value | Value of string parameter<br>required for type (0117,1012) STRING | LO (1-n) | (0117,101A) |

Table 8: Parameters for Volumetric Signal Enhancement Ratio (VOLSER) Analysis of Dynamic Contrast-enhanced (DCE) MRI stored in Parameter sequence (0117,1010). Each item in the sequence describes one parameter.

| Name (0117,1014) | Description | Type (0117,1012) |
|---|---|---|
| tissue_masking_method | Method used for pre-contrast selection of breast fibroglandular tissue regions.<br>Defined terms:<br>NONE — No pre-contrast T1 masking employed<br>MANUAL — Operator set pre-contrast T1 intensity threshold<br>PERCENT_MAX — Pre-contrast T1 intensity threshold set to percentage of 95$^{th}$ percentile intensity in VOI<br>FCM — Tissue mask defined by fuzzy C-means analysis | STRING |
| pre_contrast_threshold | Intensity threshold applied to pre-contrast T1 image to select fibroglandular tissue regions.<br>Required if tissue_masking_method is MANUAL or PERCENT_MAX | INTEGER |
| PCT_background_threshold | Background masking level percentage<br>Required if tissue_masking_method is PERCENT_MAX | INTEGER |
| PE_threshold | $PE_{thresh}$: early percent enhancement threshold | INTEGER |
| minimum_neighbor_count | Kernel size for a minimum connectivity filter for SER analysis: voxels with fewer than this number of immediate neighbors passing the pre-contrast intensity and PE threshold tests were not included in the SER volume. | INTEGER |
| ser_time_correct | Flag indicating that SER values were adjusted for scan timing. | INTEGER |
| target_time_1<br>target_time_2<br>time_tolerance<br>ser_correct_amp_1<br>ser_correct_amp_2<br>ser_correct_exp_1<br>ser_correct_exp_2 | Parameters used for correction of SER values for acquisitions with significant protocol timing errors. Present if and only if ser_time_correct is present and equal to 1.<br>For a full description see<br>Ka-Loh Li et al, Radiology, 248 (1), July 2008, pages 79-87<br>NOTE: This correction is not currently employed in I-SPY 2 processing | FLOAT |

### Functional tumor volume (FTV) results

Functional tumor volume [FTV = FTV($PE_{thresh}$, $SER_{min}$) ] is defined as the volume of tissue within the specified VOI (or otherwise segmented breast tissue region) with a PE greater than or equal to the early PE enhancement threshold ($PE_{thresh}$) and an SER greater than a specified minimum $SER_{min}$ . Calculated FTV values are stored in the SER map DICOM objects using the sequence described in Table 9. For the I-SPY 2 / ACRIN 6698 data set two FTVs are reported: $FTV_{PE}$ ($PE_{thresh}$, $SER_{min}$=0.0) and $FTV_{SER}$ ($PE_{thresh}$, $SER_{min}$=0.9). $PE_{thresh}$ is generally set at 70% but was set empirically to other values for some patients in the study based on visual assessment of the tumor segmentation at the baseline (T0) MRI study. For these patients the selected value of $PE_{thresh}$ was used for all subsequent MRI studies. $FTV_{PE}$ corresponds to the FTV value used in the I-SPY 2 trial.

Table 9: DICOM sequence for storing functional tumor volume (FTV) results

| Name | Description | VR (VM) | DICOM Tag |
|---|---|---|---|
| FTV Sequence | MRI SER FTV results | SQ (1-n) | (0117,10B0) |
| > SER Minimum | Minimum value of SER | DS | (0117,10B1) |
| > SER Maximum | Maximum value of SER: assumed to be infinite if not specified | DS | (0117,10B2) |
| > Voxel count | FTV number of voxels | IS | (0117,10B3) |
| > Volume | FTV in cc | DS | (0117,10B4) |
| > Label | Display label for FTV result | LO | (0117,10B5) |

### DWI and ADC calculation

B-values were determined automatically from appropriate private attributes using custom manufacturer-specific code for all DWI acquisitions. For consistency in the derived objects these values were all stored in the DICOM field (0018, 9087) in the TRACE images (Series numbers <root>0900).

Programs and parameters used for creating the ADC maps are stored in the ADC map objects, in sequence (0119,1180). Details are given in Table 10.

Table 10: DICOM sequence for storing functional tumor volume (FTV) results

| Name | Description | VR (VM=1) | DICOM Tag |
|---|---|---|---|
| b-value | DW b-value for image | FD | (0018,9087) |
| ADC Sequence | Single item SQ with parameter settings for calculated ADC maps | SQ | (0119,1180) |
| > FitMap Version | Fitting program version number | IS | (0119,1100) |
| >Source Indices | Indices of acquisition volumes used for ADC map | IS | (0119,1102) |
| >Parameter Values | b-values for each acquisition volume used | DS | (0119,1103) |
| >Smoothing Kernel | Kernel size for smoothing data (not used in I-SPY 2/ 6698) | IS | (0119,1109) |
| >Fit Parameter Name | "ADC" | LO | (0119,110a) |
| >Fit IC Function | Function name for any initial conditions calculation | LO | (0119,110c) |
| >Fit Formula Procedure | Fitting procedure. "regression" for linear regression | LO | (0119,110d) |
| >Fitting Program | "adcmap": UCSF core lab fitting program | LO | (0119,110e) |
| > Fitting Program Version | Version number of the fitting program | IS | (0119,110f) |
| >Fit Type | "DIFF_EXP" for mono-exponential diffusion decay fit using linear regression fit to log(signal intensity) | CS | (0119,1110) |
| >Set IC Flag | "0": No initial conditions used in the fitting process | IS | (0119,1111) |
| >Threshold flag | Indicates what thresholding method was used. Defined terms:<br>0: No masking<br>1: Simple masking on all images<br>3: Point-threshold (fit with all values exceeding thresh)<br>5: Simple masking on b=0 image only – I-SPY 2 / 6698 method | IS | (0119,1120) |
| >Threshold | Intensity threshold used to mask out background noise | DS | (0119,1121) |
| >Upper Fit Limit | Maximum allowed value for the fit parameter | DS | (0119,1130) |

## Appendix A: *Functional Tumor Volume (FTV)* [1,2,3]

Signal Enhancement Ratio (SER) is a combined enhancement/washout measure derived from dynamic contrast enhanced MRI scans. Three time-points are used: pre-contrast injection, early post-contrast, and late post-contrast. Each acquisition is a high spatial resolution, 3D, T1-weighted scan. Sequential (non-centric) phase encoding is used to ensure that the effective acquisition time for time-points 2 and 3 can be taken as the time from contrast injection to the midpoint of the MRI scan. This time is generally approximately 2.5 minutes after injection for the early time-point, and 7.5 minutes or greater for the late time-point. Initial validation studies of the ACRIN 6657 protocol were done with MRI acquisition duration of 5 minutes, with post-contrast scan timings of 2.5 and 7.5 minutes.

Tumor vascularity can be characterized by the percent enhancement (PE) of a post-contrast time-point $S_1$, from the pre-contrast time-point $S_0$, which reflects contrast uptake in the tissue and is given by

$$PE_1 = \frac{S_1 - S_0}{S_0} * 100\% .$$

SER, given by the ratio of the PE at the early post-contrast time to the PE at the late post-contrast time, adds a measure of the washout rate in the tissue. SER is given by:

$$SER = \frac{PE_{early}}{PE_{late}} = \frac{S_{early} - S_0}{S_{late} - S_0} .$$

SER is a three-point approximation of the contrast-enhancement curve that has previously been shown to correlate well with tumor microvessel density and tumor grade, with promising prognostic value for breast cancer. Both PE and SER are calculated on a per-pixel basis.

We calculate functional tumor volume (FTV) using a semi-automated tumor segmentation algorithm based on the PE and SER maps. To avoid including skin and chest wall enhancement and imaging artifacts, analysis is limited to an operator selected rectangular volume of interest (VOI). The VOI is usually drawn on a set of orthogonal maximal intensity projection (MIP) images taken either from the early post-contrast image or from a subtraction image $S_{early}$ -$S_0$. For a subset of cases, it is also necessary for the operator to draw one or more exclusion regions ("OMIT ROIs") to eliminate enhancing non-tumor regions that cannot be excluded by placement of the primary analysis VOI. All further processing is fully automatic. A map consisting of the SER of each voxel is calculated after 3 levels of masking of the DCE images: a pre-contrast background intensity mask level set to 60% of the 95$^{th}$ percentile intensity of the VOI is used to reduce spurious noise and to exclude low signal regions such as suppressed adipose tissue and strongly enhancing vessels; a PE threshold, typically 70%, at the early post-contrast time point is applied to segment malignant tissue from normal appearing tissue; and a connectivity test is applied to the combined

background and PE threshold mask, requiring a minimal number of connected neighboring voxels, to eliminate speckle noise. An SER color map is generated for qualitative assessment, showing areas of strong enhancement and washout (SER>0.9) in a gradation of colors from white to green, while enhancing but non-washing out tissue (SER<0.9) is shown in blue. $FTV_{PE}$ is calculated by summing the volumes of all voxels within the VOI passing all the filtering steps and having a positive SER. Inclusion of the low SER component of the map was found to be beneficial to getting a useable FTV measure in post-chemotherapy pre-surgery examinations where enhancement values are significantly depressed relative to pre-treatment values. $FTV_{SER}$, measured similarly but with a lower limit of SER > 0.9, giving a volume measure of the washout regions of the lesions, was also investigated.

For further information see:


1. Partridge SC, Gibbs JE, Lu Y, et al: Accuracy of MR imaging for revealing residual breast cancer in patients who have undergone neoadjuvant chemotherapy. AJR Am J Roentgenol 179:1193-9, 2002
2. Hylton NM, Blume JD, Bernreuter WK, et al: Locally advanced breast cancer: MR imaging for prediction of response to neoadjuvant chemotherapy--results from ACRIN 6657/I-SPY TRIAL. Radiology 263:663-72, 2012
3. ACRIN PROTOCOL 6657 / CALGB 150007 http://www.acrin.org/6657_protocol.aspx
   *Contrast-Enhanced Breast MRI for Evaluation of Patients Undergoing Neoadjuvant Treatment for Locally Advanced Breast Cancer*