Recommendations for Submission of Auxiliary Information

Summary

When sharing any kind of scientific data it is of great utility to provide as much information as possible to aid researchers in their understanding of that data. This is especially true with imaging since there are many important details that are required to perform common types of analysis which are not part of the DICOM header information. As a result TCIA strives to include this missing information on the associated wiki page for each Collection. What follows is a series of recommendations to data providers which will help them provide all of the context necessary to maximize the value of their data contribution to the TCIA research community.

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- Matthew Oborski, University of Pittsburgh
- Charles Laymon, University of Pittsburgh
- Mark Muzi, University of Washington
- John Sunderland, University of Iowa

Clinical Data

Supporting clinical information such as patient demographics, treatment details, and outcomes can significantly increase the utility of datasets shared on TCIA. The NCI Genomic Data Commons has established a data dictionary viewer and templates which TCIA recommends as a good model for sharing clinical data in a standardized fashion.

General Description Information for Cancer Imaging Studies

1. ***Patient therapy regimen***
    a. Describe the **entire** current therapy protocol, any previous therapies and **dates of treatment** including RT, chemotherapy and surgery.
    b. If RT was performed, describe the method (e.g., IMRT), dose in Gy and fractionation schedule, if any.
    c. If chemotherapy, identify the treatment agent(s) and delivery protocol.
2. ***Cancer type and site of neoplasm***
    a. Type of cancer (cell origin) for the primary lesion(s) and anatomical location Date of pathological confirmation of the cancer (from biopsy or surgical resection).
    b. Is this a newly diagnosed neoplasm or recurrence?
    c. If metastases are present, describe anatomical location(s).
3. ***Imaging time-point with respect to therapy***
    a. Is this a baseline scan (prior to therapy initiation) or a follow-up scan after the onset of therapy? Follow-up scans include scans performed during therapy, post-therapy, or at the time of recurrence. The following definitions will be helpful:
        i. Visit 1: Baseline scan prior to any therapy (including surgery).
        ii. Visit 1a: Repeat scan for examining reproducibility.
        iii. Visit 2: If the initial therapy is surgery, scan following surgical resection and prior to other therapies.
        iv. Visit 3: Scan during therapy (e.g., early therapy after 1 cycle of ChX)
        v. Visit 4: Scan after completion of therapy.
        vi. Visit 5: Scan at the time of suspected recurrence, usually much later than Visit 4.
    b. Specify date of scan and Visit # (if the scan circumstances are not adequately characterized by any of the above Visit definitions, please describe here).

Information Regarding Dynamic PET Imaging for Cancer Studies

1. ***For the dynamic PET data set you are submitting, is there corresponding structural/anatomical imaging (e.g. MRI, CT) being submitted to TCIA?***
    a. If yes, specify
        i. the date(s) of the anatomical image scans and
        ii. TCIA identifiers (how are they listed in TCIA?).
2. ***Identify the imaging agent (e.g., ^{18}F-FLT) and describe the injection protocol for the dynamic PET data set you are submitting.***
    a. Specify the time difference between start-of-injection and start-of-scan (positive values indicate that PET acquisition started after injection).
    b. If an infusion pump was used for tracer delivery, specify the volume of the injection and the delivery rate and/or time period of infusion (e.g., 5 mL bolus or 10 mL over a 1 min period).
3. ***Reconstruction Method (assuming 3D acquisition):***
    a. As appropriate, specify rebinning and reconstruction methods (e.g. FORE/OSEM)
        i. If an iterative reconstruction, specify the number of subsets and number of iterations.
        ii. Describe any post-reconstruction treatment of the imaging data, such as type of filter and size /width; for Philips scanners add parameters such as speed and sharpness.
4. ***Dynamic Framing Information:***
    a. Was the dynamic image sequence collected using a list mode acquisition? [If so, reconstruction of alternate frame timing could be requested from the submitting site, providing an alternate set of dynamic image data to TCIA].
    b. Please specify frame timing in chronological order using the format: (number of frames)x(frame length in seconds). For example, if a total of 20-frames of data were acquired for a dynamic PET scan, in which the first 5-frames are 5 seconds long, the next 5-frames were 30seconds long and the last 10 frames were 300 seconds long, then the framing description would look like: 5x5sec, 5x30sec, 10x300sec. Alternatively, please provide a file describing the frame timing, such as the .acqtimes file in PMOD or an Excel matrix of start times and frame duration.
5. ***The Arterial Input Function (AIF): Is an AIF supplied with the data, such as an externally counted blood time activity curve?***
    a. If yes, please describe the source of the AIF as
        i. Actual drawn blood samples counted in a cross calibrated counting system for the determination of the time radioactivity concentration profile and/or tracer metabolite determination.
            1. Please provide the following information in table format, if available
                a. Arterial or venous sampling
                b. The number and volume of samples taken
                c. The time the samples were taken relative to the onset of injection[JS1][MM2] .
                d. Activity concentration of each blood sample (uCi/mL or MBq/mL).
                e. Metabolite Correction Data (fraction of the parent molecule and subsequent metabolites in each measured sample).
    b. A population curve based on historical data for this tracer.
    c. A computed curve based on previous reports (e.g., 3 exponential curve)
    d. A mathematically segmented curve from the dynamic emission data
    e. A curve extracted from the dynamic emission data using a region of interest over a blood pool in the image.
    f. Other, please explain_____

6. ***Specify max voxel activity (kBq/cc) and the PET slice number in the primary tumor from the last frame of the dynamic data set to help in the location of the primary tumor.***

Tracer Specific Biological Information

Please add any measured biological parameters pertinent to the quantification of tracer uptake and values with units

Blood Glucose _____ mg/dL

Hematocrit _____

Blood Estradiol _____ µM/mL

Blood O2 _____ Psat, torr

_____ _____

Optional Patient Characterization Information

1. Prognostic blood/tissue biomarkers (e.g. histochemical assay of Ki-67, VEGF, HIF1a; promoter methylation status (MGMT); a characteristic chromosomal deletion/amplification; ER, HER2 or PR status).
2. Molecular blood/tissue biomarkers that are predicative of therapy response (e.g., PSA blood levels)
3. Example kinetic analysis of dynamic data set or parameter output file for the primary tumor and a control/normal region.