

Where's my scan data?

Introduction

Beginning with the 3T we are implementing a more integrated scan data system. The purpose is to automate radiological reads and processing pipelines as well as to hook into new file system security configurations.

How does it work?

Under normal operation each sequence on the 3T will automatically be transferred to archive storage. During a transfer the dicom header is examined and a database record of the scan is entered into our research data database. A record for radiological review is then also created.

What is “lost and found” and how can my scan data end up there?

When the dicom header is examined its information is checked against the database. Some information in the header will cause the system to send your data into an inaccessible lost and found storage area.

- a) The scan must be conducted under a valid PI account already registered in the database.
- b) The study under which the scan is performed must be a valid study in the database with the correct IRB number.
- c) The study must also be registered under the correct PI.
- d) The URSI/Subject ID must already be registered in the database.
- e) The URSI must be enrolled in the study for which you are scanning.

Before you scan check the following:

- 1) Is your study entered in MICIS with the correct PI?
- 2) Has the correct information been created for your study in the Exam Explorer of the 3T console? See the document “How to setup a Study” for help on this.
- 3) Do you have an URSI for your subject?
- 4) Is the URSI enrolled in your study? In MICIS click on “Look up a subject”. Enter the URSI. When the subject record comes up click on “Study Enrollment”. Check the list and see if the subject is enrolled in the study.

How can I check on my scan data?

After you run the localizer the run should be automatically transferred to the archive system. At this time you can check that your data has been properly register by clicking on “Look up a subject” in MICIS. Enter the URSI. When the subject record comes up click on “Scans”. You should see an entry for your current scan in that listing. You may also look up a scan session by clicking “List Scans” on the main menu and filtering the list by URSI.

What are all these “*.nii” files doing with my dicom images?

Is phantom data processed differently?

Yes. There is an existing naming convention that says that all phantom subject IDs shall begin with the word “phantom”. Using that subject ID your phantom data is routed to a slightly different archive location at “/export/research/archive/phantom”. Essentially the archive trees for phantom and human data differ only at that one level.

Note that Nifti data generated by a sequence for a phantom subject will not be processed. It will be deleted from the console without being stored in the archive.