

Recommendations for Processing Head CT Data

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Abstract

Many research applications of neuroimaging use magnetic resonance imaging (MRI). As such, recommendations for image analysis and standardized imaging pipelines exist. Clinical imaging, however, relies heavily on X-ray computed tomography (CT) scans for diagnosis and prognosis. We present tools and recommendations for processing CT data, with emphasis on head CT scans and focusing on open-source solutions. We describe going from raw DICOM data to a spatially normalized brain within CT and present a full example with code.

1. Introduction

Many research applications of neuroimaging use magnetic resonance imaging (MRI). MRI allows researchers to study a multitude of applications and diseases, including studying healthy volunteers. Clinical imaging, however, relies heavily on X-ray computed tomography (CT) scans for diagnosis and prognosis. Studies using CT scans cannot generally recruit healthy volunteers or large non-clinical populations due to the radiation exposure and lack of substantial benefit. As such, much of head CT data is gathered from prospective clinical trials or retrospective studies based on health medical record data and hospital picture archiving and communication system (PACS). We discuss transforming this data from clinical to research data and provide some recommendations and guidelines from our experience with CT data similar insights from working with MRI studies. We will discuss existing software options, focusing on open-source tools, for neuroimaging in general and those that are specific to CT throughout the paper.

We will focus on aspects of quantitatively analyzing the CT data and getting the data into a format familiar to most MRI neuroimaging researchers. Therefore, we will not go into detail of DICOM reading tools or imaging suites designed for radiologists, which may be proprietary and quite costly. Moreover, we will be focusing specifically on non-contrast head CT data, though many of the recommendations and software is applicable to images of other areas of the body.

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2. Data Organization

Most of the data coming from a PACS is in DICOM (Digital Imaging and Communications in Medicine) format. Generally, DICOM files are a combination of metadata (i.e. a header) about an image and the individual pixel data, many times embedded in a JPEG format. The header has a collection of information, usually referred to as fields or tags. Tags are usually defined by a set of 2 hexadecimal numbers, which are embedded as 4 alphanumeric characters. For example, (0008,103E) denotes the **SeriesDescription** tag for a DICOM file. Most DICOM readers extract and use these tags for filtering and organizing the files.

We will use the phrase scanning session (as opposed to “study” and reserve study to denote a trial or analysis), a series for an individual scan, and a slice for an individual picture of the brain. Each series (**Series Instance UID** tag) and scanning session (**Study Instance UID** tag) should have a unique value in the DICOM header that allows DICOM readers to organize the data by scanning session and series. The following sections will discuss data organization and data formats.

2.1. DICOM Anonymization

One of the common issues with DICOM data is that a large amount of protected health information (PHI) can be contained in the header. DICOM is a standard where individual fields in the header are to contain the same values across different scanners and sites, but only if that manufacturer and site are diligent to ascribing to the DICOM standard. Though many DICOM header fields are consistent across neuroimaging studies, many fields may be required to obtain the full amount of data required for analysis. Moreover, different scanning manufacturers can embed information in non-standard fields. The goal is to remove these fields if they contain PHI, but retain these fields if they embed relevant information of the scan for analysis. These fields then represent a challenge to a lossless anonymization if the data do not conform to a standard across scanning sites, manufacturers, or protocols.

We will discuss reading in DICOM data and DICOM header fields in the next section. Though these steps can be crucial for extracting information from the data, many times the data must be shared or transferred before analysis. Depending on the parties receiving the data, anonymization of the data must be done first. Aryanto, Oudkerk, and Ooijen (2015) provides a look at a multitude of options for DICOM anonymization and recommend the RSNA MIRC Clinical Trials Processor (CTP, <https://www.rsna.org/research/imaging-research-tools>) cross-platform Java software as well as the DICOM library (<https://www.dicomlibrary.com/>) upload service. We also recommend the DicomCleaner cross-platform Java program as it has fit many of our needs. Bespoke solutions can be generated using **dcm4che** (such as **dcm4che-deident**) and other DICOM reading tools (discussed below), but many of these tools have built-in capabilities that are difficult to add (such as removing PHI embedded in the pixel data, aka “burned in”).

2.1.1. A note on de-identification: time between scans

Although most of the presented solutions are good at anonymization and de-identification of the header information, only a few such as CTP, have the utilities required for longitudinal preservation of date differences. Though it can be debated whether dates are identifiable information, some clinical trials and other studies rely on serial CT imaging data, and the differences between times are crucial to determine when events occur.

2.1.2. Reading DICOM data

We will focus on 2 analysis platforms for statistical analysis, including **R** (CITE) and **Python** as well as standalone software. The main reasons are that **R** and **Python** are free, open source, and popular in the neuroimaging analysis community. We are also lead the Neuroconductor project (<https://neuroconductor.org/>) (Muschelli et al. 2018), which is a repository of **R** packages for medical image analysis. Other imaging platforms such as the Insight Segmentation and Registration Toolkit (ITK) are well-maintained, useful pieces of software that can perform many of the operations that we will be discussing. Moreover, **MATLAB** has an extensive general imaging suite, as well as large neuroimaging platforms such as SPM (CITE). We will touch on some of this software with varying levels. We aim to present software that we have had used directly for analysis or preprocessing. Also, other papers and tutorials discuss their use (CITE).

For reading DICOM data, there are multiple options. The **MATLAB** imaging toolbox, `oro.dicom` **R** package, `pydicom`, and **ITK** interfaces can read DICOM data amongst others. The DICOM toolkit `dcm2tk` has multiple DICOM manipulation tools, including `dcmconv` to convert DICOM files to other imaging formats.

Though most imaging analysis tools can read in DICOM data, there are downsides to using the DICOM format. In most cases, a DICOM file is a single slice of the full 3D image series. This separation can be cumbersome on data organization if using folder structures. As noted above, these files also can contain a large amount of PHI. Some formats may be compressed using proprietary compression such as JPEG2000. Alternatively, if data are not compressed, file storage is inefficient. Most importantly though, many imaging analyses perform 3-dimensional operations, such as smoothing. Thus, putting the data into a different format that handles 3D images as 1 compressed file is desirable.

2.2. Converting DICOM to NIfTI

Many different general 3D medical imaging formats exist, such as **ANALYZE**, **NIfTI**, **NRRD**, and **MNC**. We recommend the **NIfTI** format, as it can be read by nearly all medical imaging platforms, has been widely used, has a format standard, can be stored in a compressed format, and is how much of the data is released online. Moreover, we will present specific software to convert DICOM data and the recommended software (`dcm2nii`) outputs data in a **NIfTI** file.

Although we recommend this software, many good and complete solutions exist. Examples include `dicom2nifti` in the `oro.dicom` **R** package, `pydicom`,

`dicom2nifti` in MATLAB, and using large imaging suites such as using ITK image reading functions for DICOM files and then write NIfTI outputs. We recommend the `dcm2niix` (<https://github.com/rordenlab/dcm2niix>) (Li et al. 2016) function from Chris Rorden for CT data for the following reasons: 1) it works with all major scanners, 2) incorporates gantry-tilt correction for CT data, 3) can handle variable slice thickness, 4) is open-source, 5) is fast, 6) has responsive developers, and 7) works on all 3 major operating systems (Linux/OSX/Windows). Moreover, the popular AFNI neuroimaging suite includes a `dcm2niir` program with its distribution. Interfaces exist, such as the `dcm2niir` package in R and `nipype` Python module. Moreover, the `divest` package (LINK) wraps the underlying code for `dcm2niix` to provide the same functionality of `dcm2niix`, along with the ability to manipulate the data for more versatility.

We will describe a few of the features above. In some head CT scans, the gantry is tilted to reduce radiation exposure to non-brain areas, such as the eyes. Thus, the slices of the image are at an oblique angle. If slice-based analyses are done or an affine registration (as this tilting is a shearing) are applied to the 3D data, this tilting is not an issue. This tilting does cause issues for 3D operations as the distance of the voxels between slices is not correct and especially can show odd visualizations. The `dcm2niix` output returns both the corrected and non-corrected image (Figure 1). As the correction moves the slices to a different area, `dcm2niix` may pad the image so that the entire head is still inside the field of view. As such, this may cause issues with algorithms that require the 512x512 axial slice dimensions. Though less common, variable slice thickness can occur in reconstructions where only a specific area of the head is of interest. For example, an image may have 5mm slice thicknesses throughout the image, except for areas near the third ventricle, where slices are 2.5mm thick. To correct for this, `dcm2niix` interpolates between slices to ensure each image has a consistent voxel size. Again, `dcm2niix` returns both the corrected and non-corrected image.

Once converted to NIfTI format, one should ensure the scale of the data. Most CT data is between -1024 and 3071 Hounsfield Units (HU). Values less than -1024 HU are commonly found due to areas of the image outside the field of view that were not actually imaged. One first processing step would be to Winsorize the data to the $[-1024, 3071]$ range. After this step, the header elements `scl_slope` and `scl_inter` elements of the NIfTI image should be set to 1 and 0, respectively, to ensure no data rescaling is done in other software. Though HU is the standard format used in CT analysis, negative HU values may causes issues with standard imaging pipelines built for MRI, which typically have positive values. Rorden (CITE) proposed a lossless transformation, called Cormack units, which have a minimum value of 0. The goal of the transformation is to increase the range of the data that is usually of interest, from -100 to 100 HU.

2.3. Convolution Kernel

Though we discuss CT as having more standardized Hounsfield unit values, this does not imply CT scans cannot have vastly different properties depending on parameters of scanning. One notable parameter in image reconstruction is the

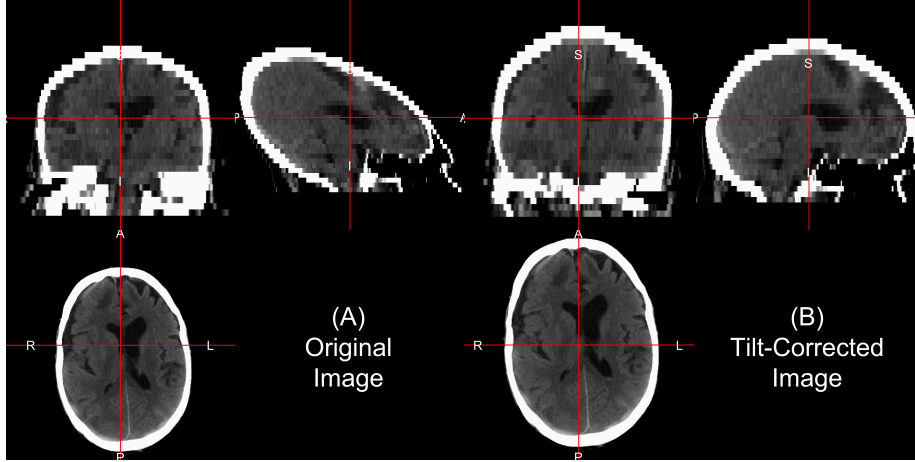


Figure 1: Example of Gantry-tilt Correction. Using ‘dcm2niix’, we converted the DICOM files to a NIFTI file, which had a 30 degree tilt. The output provides the uncorrected image (A) and the tilt-corrected image (B). We see that the reconstructed image without correction appears fine within the axial plane, but out of plane has an odd 3D shape. This shape will be corrected with an affine transformation, which is done in the conversion, correcting the image as seen in (B).

covolution kernel (i.e. filter, DICOM field (0018,1210)) used for reconstruction. We present slices from an individual subject from the CQ500 (Chilamkurthy et al. 2018) dataset (described below) in Figure 2. Information on which kernel was used, and other reconstruction parameter information can be found in the DICOM header (e.g. field (0018,1210)). The kernel is described usually by the letter “H” (for head kernel), a number indicating image sharpness (e.g. the higher the number, the sharper the image, the lower the number, the smoother the image), and an ending of “s” (standard), “f” fast, “h” for high resolution modes (Siemens <http://docshare01.docshare.tips/files/24454/244544233.pdf>), though some protocols simply name them “soft-tissue”, “standard”, “bone”, “head”, or “blood”, amongst others. The image contrast can depend highly on the kernel, and “medium smooth” kernels (e.g. H30f, H30s) can provide good contrast in brain tissue (Figure 2E). Others, such as “medium” kernels (e.g. H30f, H30s) provide contrast in high values of the image, such as bone for detecting fractures (Figure 2A), but not as good contrast in brain tissue (Figure 2B). Thus, when combining data from multiple sources, the convolution kernel may be used to filter, stratify, or exclude data.

Moreover, the noise and image contrast can be different depending on the image resolution of the reconstruction. Most standard head CT scans have high resolution within the axial plane (e.g. 0.5mm^2). Image reconstructions can have resolution in the interior-superior plane (e.g. slice thickness) anywhere from 0.5mm (aka ‘thin-slice’, Figure 2F)) to 2.5mm , to 5mm , where 5mm is fairly common. The larger the slice thicknesses are, the smoother the reconstruction (as areas are averaged). Also, the added benefit for radiologists and clinicians are

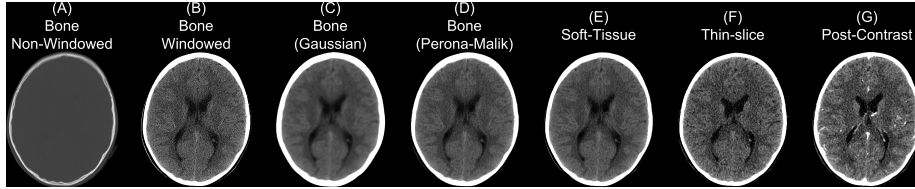


Figure 2: Different Series for a Scanning Study. Here we present different non-contrast head CT exported from a PACS. We display a reconstructed scan with a bone convolution kernel (A), showing bright areas of the skull, which can be investigated for breaks or fractures. When applying a window of 0 - 100 Hounsfield units (HU) of this image, we see the image resolution (B). Using a Gaussian (C) or Perona-Malik (D) smoother, we see we get smoother images, similar to the image reconstructed with a soft-tissue convolution kernel (E). Images (A-E) had a slice thickness of 5mm. The thin-slice scan (F) had a slice thickness of 0.62mm and a soft-tissue convolution kernel.

that fewer slices are needed to be reviewed for pathology or to get a comprehensive view of the head. In research, however, these thin-slice scans can get better estimates of volumes of pathology, such as a hemorrhage (CITE), or other brain regions. Moreover, when performing operations across images, algorithms may need to take this differing resolution, and therefore image dimensions, into account. We will discuss image registration in the data preprocessing as one way to harmonize the data dimensions, but registration does not change the inherent smoothness or resolution of the original data.

In some instances, only certain images are available for certain subjects. For example, most of the subjects have a non-contrast head CT with a soft-tissue convolution kernel, whereas some only have a bone convolution kernel. Post-processing smoothing can be done, such as 3D Gaussian or anisotropic (Perona-Malik) smoothing (Perona and Malik 1990) (Figure 2C-D). This process changes the smoothness of the data, contrast of certain areas, can cause artifacts in segmentation, but can make the within-plane properties similar for scans with bone convolution kernel reconstructions compared to soft-tissue kernels in areas of the brain.

2.4. Contrast Agent

Though we are discussing non-contrast scans, head CT scans with contrast agent are common. The contrast/bolus agent again should be identified in the DICOM header field (0018,0010), but may be omitted. The contrast changes CT images, especially where agent is delivered, notably the vascular system of the brain. These changes may affect the steps recommended in the next section of data preprocessing, where thresholds may need to be adjusted to include areas with with contrast which can have higher values than the rest of the tissue (e.g. $> 100\text{HU}$). (FIGURE)

3. Data Preprocessing

Now that the data is in a standard file format, we can discuss data preprocessing. As the data are in NIFTI format, most software built for MRI should work, but adaptations and other considerations may be necessary.

3.1. *Bias-field/Inhomogeneity Correction*

In MRI, the scan may be contaminated by a bias field or set of inhomogeneities. This field is generally due to inhomogeneities/inconsistencies in the MRI coils or can be generated by non-uniform physical effects on the coils, such as heating. One of the most common processing steps done first is to remove this bias field. In many cases, these differences can more general be considered non-uniformities, in the sense that the same area with the same physical composition and behavior may take on a different value if it were in a different spatial location of the image. Though CT data has no coil or assumed bias field due to the nature of the data, one can test if trying to harmonize the data spatially with one of these correction procedures improves performance of a method. Though we do not recommend this procedure generally, as it may reduce contrasts between areas of interest, such as hemorrhages in the brain, we would like to discuss methods.

Overall, the assumptions of this bias field are that it is multiplicative and is smoothly varying. One of the most popular inhomogeneity corrections are the N3 (CITE N3) and its updated improvement N4 (CITE N4) in ANTs, though other methods exist in FSL (CITE zhang) and other software (CITE, SPM, AFNI versions, and others). Given the assumption of the multiplicative nature of the field, N4 performs an expectation–maximization (EM) algorithm on the log-transformed image, assuming a noise-free system. As CT data in HU has negative values, the log transform is inappropriate. Pre-transforming or shifting the data values may be necessary to perform this algorithm, though these transforms may affect performance. Moreover, artifacts or objects that are not the subject (described below) may largely effect the estimation of the field and segmentation may be appropriate before running these corrections, such as brain extraction or extracting only subject-related data and not imaged hardware. The ANTsR package (CITE ANTsR) provides the `n4BiasFieldCorrection` function in R.

3.2. *Brain Extraction in CT*

Head CT data typically contains the subject’s head, face, and maybe neck and other lower structures, depending on the field of view. Additionally, other artifacts are typically present, such as the pillow the subject’s head was on, the bed/gurney, and any instruments in the field of view. We do not provide a general framework to extract the subject from the artifact data, but provide some recommendations for working heuristics. Typically the range of data for the brain and facial tissues are within -100 to 300 HU, excluding the skull, other bones, and calcifications. Creating a mask from this data range tends to remove the bed/gurney, most instruments, the pillow, and the background. Retaining the largest connected component, filling holes (to include the skull), and masking the original data with this resulting mask will return the subject. Note, care

must be taken whenever a masking procedure is used as one standard way is to set values outside an area of interest to 0. With CT data 0 HU is a real value of interest: if all values are set to 0 outside the mask, the value of 0 is aliased to both 0 HU and outside of mask. Either transforming the data into Cormack units, adding a value to the data (such as 1025) then setting values to 0, or using NaN are recommended in values not of interest.

One of the most common steps in processing imaging of the brain is to remove non-brain structures from the image. We have published a method that uses the brain extraction tool (BET) from FSL, originally built for MRI, to perform brain extraction (CITE) with code provided (http://bit.ly/CTBET_BASH). Many papers present brain extracted CT images, but do not always disclose the method of extraction. Recently, convolutional neural networks and shape propagation techniques have been quite successful in this task (Akkus et al. 2018) and models have been released (https://github.com/aqqush/CT_BET). Overall, much research can still be done in this area as conditions such as traumatic brain injury (TBI) and surgery, such as craniotomies or craniectomies can cause these methods to potentially fail. Overall, however, large contrast between the skull and brain tissue and the standardized nature of Hounsfield Units can make brain segmentation more straightforward than in MRI.

3.3. Registration to a CT template

Though many analyses in clinical data may be subject-specific, population-level analyses are still of interest. In some cases, registration from a template space to a subject space can provide information that can be aggregated across people for analysis. For example, one can perform a label fusion approach to CT data to infer the size of the hippocampus and then analyze hippocampi sizes across the population. One issue with these approaches is that most templates and approaches rely on an MRI template. These templates were developed by taking MRI scans of volunteers, which again is likely unethical with CT due to the radiation exposure risk without other benefits. To create templates, retrospective searches through medical records can provide patients who came in with symptoms warranting a CT scan, such as a migraine, but had a diagnosis of no pathology or damage. Thus, these neuro-normal scans are similar to that of those collected those in MRI research studies, but with some important differences. As these are retrospective, inclusion criteria information may not be easily obtainable if not clinically collected, scanning protocols and parameters may vary, even within hospital and especially over time, and these patients still have neurological symptoms. Though these challenges exist, with a large enough patient population and a research consent at an institution, these scans can be used to create templates and atlases based on CT. To our knowledge, the first publicly available head CT template exists was released by Rorden et al. (2012), for the purpose of spatial normalization/registration.

One interesting aspect of CT image registration is again that CT data has units within the same range. To say they are uniformly standardized is a bit too strong as tomography and other confounds can impact units. Thus, it is our practice to think of them as more standardized than MRI. This standardization

may warrant or allow the user different search and evaluation cost functions for registration, such as least squares. We have found though that normalized mutual information (NMI) still performs well in CT-to-CT registration and should be at least considered when using CT-to-MRI or CT-to-PET registration. Along with the template above, Rorden et al. (2012) released the clinical toolbox (<https://github.com/neurolabusc/Clinical>) for SPM [CITE] to allow researchers to register head CT data to a standard space. However, as the data are in the NIfTI format, almost all image registration software should work, though one should consider transforming the units using Cormack units or other transformations as negative values may implicitly be excluded in some software built for MRI registration. We have found using diffeomorphic registrations such as symmetric normalization (SyN) from ANTs and ANTsR with NMI cost functions to perform well.

3.4. Intensity Normalization

4. Publicly Available Data

With the issues of PHI above coupled with the fact that most CT data is acquired clinically and not in a research setting, there is a dearth of publicly available data for head CT compared to head MRI. Sites for radiological training such as Radiopedia (<https://radiopaedia.org/>) have many cases of head CT data, but these are converted from DICOM to standard image formats (e.g. JPEG) so crucial information, such as Hounsfield Units and pixel dimensions, are lost.

Large repositories of head CT data do exist, though, and many in DICOM format, with varying licenses and uses. The CQ500 (Chilamkurthy et al. 2018) dataset provides approximately 500 head CT scans with different clinical pathologies and diagnoses, with a non-commercial license. The Cancer Imaging Archive (TCIA) has hundreds of CT scans, many cases with brain cancer. TCIA also has a RESTful API, which allows cases to be downloaded in a scripted way; for example, the `TCIApathfinder` R package (Russell 2018) and Python `tciaclient` module provide an interface. The Stroke Imaging Repository Consortium (<http://stir.dellmed.utexas.edu/>) also has head CT data available for stroke. The National Biomedical Imaging Archive (NBIA, <https://imaging.nci.nih.gov>) demo provides some head CT data, but are duplicated from TCIA. The NeuroImaging Tools & Resources Collaboratory (NITRC, <https://www.nitrc.org/>) provides links to many data sets and tools, but no head CT data at this time. The RIRE (Retrospective Image Registration Evaluation, <http://www.insight-journal.org/rire/>) and MIDAS (<http://www.insight-journal.org/midas>) projects have small set of publicly available head CT.

4.1. Pipeline

Overall, our recommended pipeline is as follows:

1. Use CTP to organize and anonymize the DICOM data from a PACS.
2. Extract relevant header information for each DICOM, using software such as `dcmdump` from `dcmtk` and store, excluding PHI.

3. Convert DICOM to NIfTI using `dcm2nii`, which can create brain imaging data structure (BIDS) formatted data. Use the tilt-corrected and data with uniform voxel size.

After, depending on the purpose of the analysis, you may do registration then brain extraction, brain extraction then registration, or not do registration at all. If you are doing analysis of the skull, you can also use brain extraction as a first step to identify areas to be removed.

For brain extraction, run `BET` for CT or `CT_BET` (especially if you have GPUs for the neural network).

4.2. Concurrent MRI

Additionally, the spatial contrast is much lower than T1-weighted MRI for image segmentation. Therefore, concurrent MRI can be useful. One large issue is that any data gathered with concurrent MRI the high variability in MRI protocol done if it is not standardized within or across institution. Data is not guaranteed to be even the same type of sequence, let alone the sequence parameters and order. As many studies have shown (CITE), this variability limits the comparability or aggregation of data.

5. Conclusions

We present a simple pipeline for preprocessing of head CT data, along with software options of reading and transforming the data. We have found that though many tools exist for MRI and are applicable to CT data. Noticeable differences exist between the data in large part due to the collection setting (research vs. clinical), data access, data organization, and population-level data. As CT scans provide fast and clinically relevant information and with the increased interest in machine learning in medical imaging data, particularly deep learning using convolutional neural networks, research and quantitative analysis of head CT data is bound to increase. We believe this presents an overview of a useful set of tools and data for research in head CT.

For research using head CT scans to have the level of interest and success as MRI, additional publicly available data needs to be released. We saw the explosion of research in MRI, particularly functional MRI, as additional data were released and consortia created truly large-scale studies. This collaboration is possible at an individual institution, but requires scans to be released from a clinical population, where consent must be first obtained, and upholding patient privacy must be a top priority. Large internal data sets likely exist, but institutions need incentives to release these data sets to the public. Also, though institutions have large amounts of rich data, general methods and applications require data from multiple institutions as parameters, protocols, and population characteristics can vary widely.

One of the large hurdles after creating automated analysis tools or supportive tools to help radiologists and clinicians is the reintegration of this information into the healthcare system. We do not present answers to this difficult issue,

but note that these tools first need to be created to show cases where this reintegration can improve patient care, outcomes, and other performance metrics. We hope the tools and discussion we have provided advances those efforts for researchers starting in this area.

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