
SOLVING THE PERVASIVE PROBLEM OF PROTOCOL NON-COMPLIANCE IN MRI USING AN OPEN-SOURCE TOOL

mrQA

A PREPRINT

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ABSTRACT

The neuroimaging community is steering towards increasingly large and diverse datasets acquired by multisite consortia. Pooling data across diverse sources requires consistency and compliance with the acquisition protocols *i.e.*, ensuring different sites and scanners for a given project have used identical or compatible MR physics parameter values. Conventionally, protocol compliance has been an ad-hoc and manual process that is easily error-prone. Moreover, this is often overlooked for lack of realization that parameter values are routinely improvised locally at various sites in different ways. Ensuring compliance is an arduous process for many reasons, including difficulties in working with the complicated DICOM standard and lack of resources allocated towards protocol compliance and data management. The overlooked inconsistencies across acquisition protocols can reduce SNR, statistical power, and in the worst case, may invalidate the results altogether due to incompatible values. To address this issue, we developed an assistive tool to interface with multiple dataset formats (DICOM, BIDS) and automatically generate protocol compliance reports. In this paper, we describe the origins of the issue and demonstrate its prevalence based on our analysis of the ABCD dataset and, over 20 open neuroimaging datasets. We found that many of these datasets exhibit non-compliance in acquisition parameters. We propose a practical quality assurance (QA) solution to address the issue and offer an open-source tool *mrQA* to monitor protocol compliance in neuroimaging datasets.

Keywords neuroimaging · quality assurance · dataset integrity · protocol compliance · DICOM · open data

1 Introduction

Large-scale neuroimaging datasets play an essential role in predicting brain-behavior relationships. The average sample size of neuroimaging studies has grown tremendously over the past two decades [1, 2]. Open datasets like the Alzheimer’s Disease Neuroimaging Initiative (ADNI) consists of 800 subjects from 50 sites across the United States collected over 2-3 years [3], the Human Connectome Project (HCP) [4] contains 1200 participants, the Adolescent Brain Cognitive Development (ABCD) study [5] includes over 12000 youth participants at 21 sites, the Autism Brain Imaging Data Exchange (ABIDE) provides a dataset of 1000 individuals at 16 international sites, and the UK Biobank is following about 500,000 participants in the UK. Often these large-scale datasets are acquired over several years that involve multiple sites, with several vendor-specific models.

A typical MR study consists of field maps, localizers, head scouts, and multiple other modalities (including but not limited to anatomical, functional, and diffusion MRI) for each subject. Each of these modalities provides complementary information about the structural and functional organization. The electronic protocol files (*i.e.*, Exam Card, Protocol

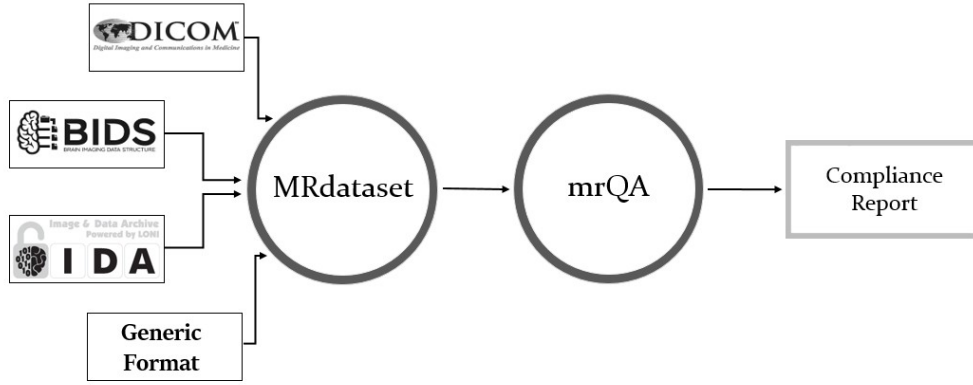


Figure 1: *MRdataset* offers a unified interface to parse & traverse different dataset formats and access acquisition information and metadata *e.g.*, various modalities, subjects, and sessions. This interface is used for generating protocol compliance reports via *mrQA*.

Exchange, or .exar files) include thousands of parameter values for a single session. To use these distinct modalities effectively, it is important to validate the combinations of protocols used for acquisition *i.e.*, evaluating the reliability of chosen imaging sequences and ensuring that the imaging data is acquired accurately for each subject across all sites and scanners. Neither is it a recommended scientific practice nor is it practical to “hope” for data integrity by manual compliance checks across numerous parameters, given the ever-increasing size of neuroimaging studies, cross-site evaluations, multiple scanners, and varied environments.

As maintenance of imaging protocols in MRI centers is typically an ad-hoc and error-prone process, it often leads to variations in acquisition parameters across different subjects and sessions. For instance, protocol configurations are manually uploaded on each scanner which impacts consistency. Inconsistencies arising from software updates and hardware upgrades which alter the default behavior of the scanning interface should be promptly addressed before the acquisition. Even subtle deviations in acquisition parameters have the potential to affect reproducibility of MRI-based brain-behavior studies [6]. Prior works have focused on developing post-processing techniques to reduce the impact of such deviations on neuroanatomical estimates [7, 8, 9, 10, 11, 12]. Such post-processing techniques often rely on large sample-size per site to estimate site-specific effects. Recent work by George *et al.* [13] used power analysis techniques to demonstrate that using standardized protocols yield over a two-fold decrease in variability for cortical thickness estimates when compared against non-standardized acquisitions. Therefore, adherence to standardized image acquisition protocols at the scanner is an essential pre-requisite for ensuring quality of MRI-based neuroimaging studies [14, 15]. Otherwise, some subject-specific scans might have to be discarded due to a flawed data collection process, thus reducing the sample size, and consequently the power of statistical analysis [16]. Yet not much effort has been devoted to eliminating these inconsistencies in image acquisition protocol. Insufficient monitoring can lead to non-compliance in imaging acquisition parameters, including but not limited to flip angle (FA), repetition time (TR), phase encoding direction (PED), sampling bandwidth, and echo time (TE). This problem becomes particularly relevant for analyses from T1/T2 weighted images, which are known to be sensitive to acquisition parameters [17]. In EPI, co-registration with its structural counterpart becomes difficult if EPI is non-compliant with the field map regarding field-of-view, pixel bandwidth, and multi-slice mode [18, 19]. In DTI, the images acquired with different polarities of PED cannot be used synonymously as they differ in fractional anisotropy estimates [20]. Inconsistencies in image acquisition parameters may implicitly bias the texture in brain images, confounding brain-behavior prediction or phenotypes from brain images [21]. Thus, any analyses conducted without eliminating sources of error in acquisition metadata may reduce statistical power and, in the worst case, may invalidate results altogether, hindering widespread clinical adoption of the experimental results.

To mitigate these challenges, it is important to embrace a mindset of proactive quality assurance *i.e.*, validating the acquired data as soon as possible to suppress any inconsistencies in acquisition. For instance, if the data is reformatted to BIDS (NIfTI) format, a major part of acquisition metadata is lost. This is because the NIfTI format has limited scope for adding important acquisition parameters to the header. The limited space in the header is taken up by fields that play a crucial role in describing a volume [22] while the acquisition metadata is exported to a JSON sidecar which is not standardized and hence often prone to manual tinkering. In contrast, DICOM images contain almost all the acquisition metadata with standard tags and can thus act as a crucial step in quality assurance. We advocate that if imaging acquisition parameters could be checked for compliance in DICOM files, they could be fixed as soon as possible, right

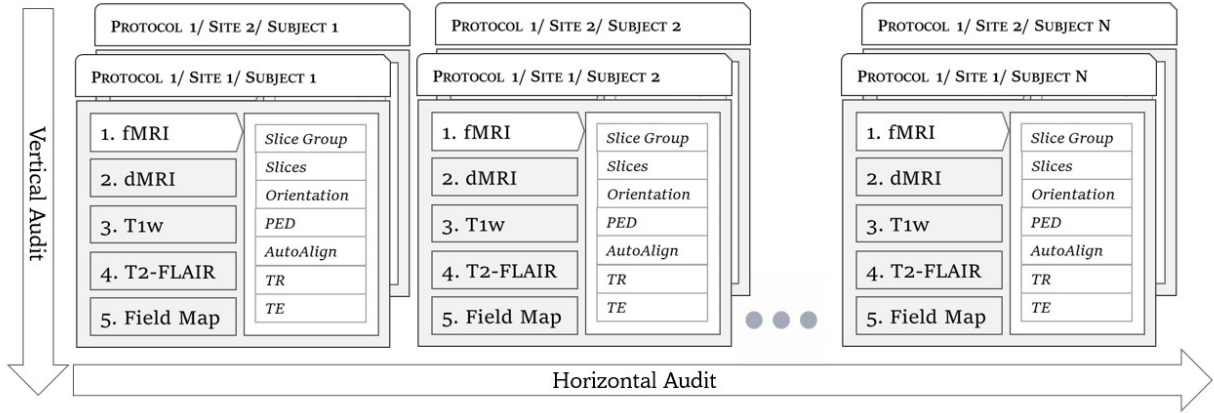


Figure 2: Overview of the relationship between various levels relevant to protocol compliance checks such as subject, modality, site, etc. We define a horizontal audit to be across different subjects in a given modality (compliant w.r.t a predefined protocol), whereas vertical audit checks if a single subject is compliant across all the acquired modalities.

at the scanner itself. Analyzing non-compliance in acquisition metadata (via JSON sidecars) after organizing files in a suitable directory structure (*e.g.*, BIDS) is very useful for data analysis, but the source of inconsistencies in the scanning interface is not fully addressed. It might be possible that the default acquisition parameters in the scanner user interface might be inconsistent with the recommended protocol. Addressing the non-compliance as early as possible at the scanner can save a lot of effort and valuable time. The focus must shift from addressing quality control via image post-processing to preventing non-compliance.

To summarize, a critical aspect of MR imaging is adherence to recommended protocol which would enhance the consistency of acquired images, ensuring that the results are reproducible. Secondly, inconsistencies should be checked promptly so that corrective measures can be taken to minimize differences in acquisition parameters. Finally, checking for compliance would make us much more familiar with our own data, enabling us to draw meaningful conclusions while considering potential biases or anomalies that impact the quality of statistical analysis.

Therefore, we present *mrQA*, a software platform to ensure data integrity in MRI datasets. *mrQA* is designed to aggregate and summarize compliance checks on DICOM images at the MRI scanner itself. Automating the compliance check process *mrQA* can help reduce the risk of errors and omissions in handling and use of DICOM images, thus improving patient healthcare. DICOM images have an inherent complex structure, and relying on manual interpretation of DICOM fields is prone to error. For instance, left-right flips are not easy to spot visually, but they can be checked for consistency using automated checks [23]. Such subtle errors can have serious consequences, especially for brain surgery. The long-term goal of *mrQA* is to enable healthcare organizations to operate efficiently by saving valuable time and effort for essential tasks rather than being dissipated in reviewing MR images for protocol compliance manually. Large healthcare organizations generate thousands of images on a daily basis, and *mrQA* can serve as a continuous monitoring service (daily, hourly, or real-time) for aggregating compliance checks on DICOM images.

Prior works [24] have proposed validation of acquisition parameters for BIDS datasets. Their work is focused on the execution of BIDS-apps by identifying variations in acquisition metadata. In contrast, *mrQA* focuses on enunciating variation in acquisition parameters for DICOM images. Even though the DICOM format suffers from storage overhead, with complex specifications, DICOM contains complete acquisition metadata with standardized tags. Therefore it has been the established output format for medical images. In contrast, NIFTI has limited scope for adding important acquisition metadata rather it relies on JSON sidecars. *mrQA* can discover variations in acquisition parameters in the rawest data format available, *i.e.*, DICOM format. Moreover, *mrQA* doesn't impose a predefined file directory structure for metadata evaluation of a neuroimaging study. *mrQA* has been developed primarily for DICOM-based datasets, but it also expands its functionality to NIFTI-based BIDS datasets. In the broader scope, *mrQA* would enable users to enforce strict acquisition protocols that will alleviate unintended sources of error at the first step of acquisition pipeline by creating laboratory-specific plugins.

In addition, we provide a critical perspective on the wide diversity of acquisition metadata in open neuroimaging datasets. The motivation behind this exploration is to identify the common parameters which are prone to change. By understanding common issues, we can be more attentive to these parameters during the acquisition. Its important to note that the exploration of common issues in acquisition is not about finger-pointing for mistakes. Rather, it is

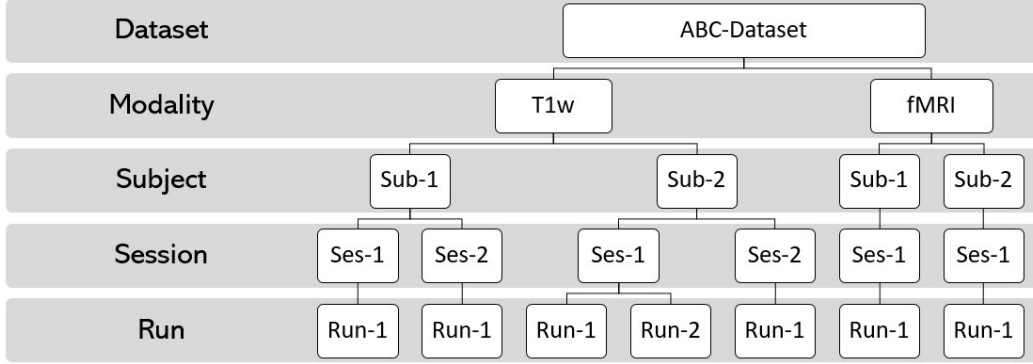


Figure 3: Illustration of hierarchical structure for representing elements of neuroimaging dataset, namely modalities, subjects, sessions, and runs. The structure is important for the representation, rearrangement, and extraction of subsets. *MRdataset* infers the information directly from DICOM headers. Neither does it depend on filename hierarchy nor it expects a particular file organization on disk to accomodate varied configurations in MRI datasets.

about recognizing common issues and working collaboratively to address such issues to create an effective research community. Towards this end, we assess protocol compliance, or lack thereof, in the ABCD dataset [25], over 20 datasets on OpenNeuro [26] and public DICOM datasets on TCIA [27]. We also discuss common sources of non-compliance and their impact on image quality and downstream statistical analyses.

2 Materials and Methods

The proposed framework aims to help researchers track compliance in neuroimaging datasets by summarizing the dataset’s acquisition metadata. This would enable the researchers to discover variations in scanning parameters and fix critical errors as per their feasibility. The execution of the entire framework is depicted in two stages, as shown in Figure 1. First, the input dataset directory is parsed to create a unified interface to access modalities, subjects, and sessions of a neuroimaging study (*MRdataset*), which is in turn used for generating a protocol compliance report (*mrQA*). In this section, we include a detailed description of the methods, along with the design and API specifications.

2.1 Design Considerations

Experimental neuroimaging data is hugely diverse and may be structured differently according to study design or clinical protocol, especially the stimulus, behavioral response, and interventions. Thus, any tool must address the fundamental capability of representing and manipulating any neuroimaging dataset format. *MRdataset* is designed to contain specific classes for representing elements of a neuroimaging experiment, such as modalities, subjects, sessions and runs [28] as shown in Figure 3. The *MRdataset* model allows a hierarchical structure between these elements, which is essential to represent the organization of neuroimaging experiments. It also enables reading from multiple formats (such as BIDS, and DICOM) to a common structure. Moreover, definitive functionality representing the elements (subjects, modalities, sessions) would also allow the rearrangement and extraction of subsets. *MRdataset* infers information about the hierarchical structure directly from the DICOM headers. For example - there might be several subjects for a modality *rs-fMRI*, and each of these subjects may have several sessions. *MRdataset* doesn’t rely on filename hierarchy or expect a particular idiosyncratic organization of files to cope with various configurations. *MRdataset* provides a simple container interface to improve the use, accessibility, and reproducibility of research in neuroimaging. As the immediate objective is to achieve protocol compliance, the framework excludes any visualization methods for brain image data, making *MRdataset* as lightweight as possible. In the future, we expect to extend the *MRdataset* dataset class to support other data formats, such as LONI IDA, but these were not included in the initial design. Keeping these considerations in mind, the package is written in Python and it uses *pydicom* [29] for reading DICOM images. Python is becoming the de facto standard for scientific applications as it provides community support and easy extensibility for the future.

Table 1: An example of the reference protocol. Note that the reference values are either be pre-defined or inferred by searching for most frequent values for each parameter.

Scanning Sequence	Echo Train Length	Phase Encoding Direction	Magnetic Field Strength	Phase Encoding Direction	Multi Slice Mode	Pixel Bandwidth	Flip Angle	MR Acquisition Type
GR	1	j	3	ROW	interleaved	350	40	2D

is3D	Phase Encoding Steps	Shim	Repetition Time	iPAT	Manufacture	Sequence Variant	Body Part Examined	Echo Time
False	448	Standard	465	Grappa	SIEMENS	MTC_SS	BRAIN	3.73

2.2 Creating a unified interface (*MRdataset*)

MRdataset is designed to be as interoperable as possible with the existing neuroimaging formats considering that it should be easy to build, install and use on various platforms. *MRdataset* was created to provide a unified interface to various data formats in a neuroimaging pipeline, primarily focusing on DICOM image datasets. *MRdataset* organizes all the files hierarchically as per the DICOM header information regarding the acquired modalities, subjects, sessions, and runs. This allows the data structure to be independent of the folder organization on disk. Currently, *MRdataset* supports DICOM and BIDS data formats. However, it is completely extensible to any new format, using the CLI option `--style`. While writing scripts, the user doesn't need to invoke different functions for corresponding neuroimaging formats. The same function (`import_dataset`) can read various neuroimaging data formats. An example source code is provided in Listing 1.

In addition to conforming to a unified interface, *MRdataset* performs validation to reject localizers, head scouts, and phantoms. If required, the user can pass a flag `--include-phantom` to include them instead. To extract values for image acquisition parameters (*e.g.*, repetition time, echo time), *MRdataset* uses metadata information in DICOM headers. However, these values are absent in NIFTI headers. Therefore, *MRdataset* depends on the information in the JSON sidecar associated with each NIFTI file in a BIDS dataset. If required, it is possible to include parameters such as obliquity, voxel sizes, and matrix dimensions from the NIFTI header using a flag `--include-nifti-header`.

The inclusion of support for multiple neuroimaging formats in the *MRdataset* package has several benefits: Firstly, it exemplifies the *MRdataset*'s flexibility, by which it can create a unified interface to represent the data from different formats such as BIDS and DICOM. Secondly, it is a crucial step towards achieving interoperability and ease of data sharing data between various labs. Finally, it benefits a diverse set of users who can take advantage of *MRdataset*'s unified interface, saving valuable time wasted in redundant implementations.

2.3 Generating a compliance report (mrQA)

In this section, we describe the considerations and the procedure used for evaluating protocol compliance of a MR imaging dataset. There can be two kinds of compliance evaluations - a *horizontal audit* and a *vertical audit*. Both of these processes are important to establish data integrity.

```
from MRdataset import import_dataset

dicom_ds = import_dataset(data_source='/path/to/data', name='abc', style='dicom')
bids_ds = import_dataset(data_source='/path/to/data', name='xyz', style='bids')
```

```
$ mrds --data-source /path/to/dataset --style bids --name my_bids_dataset
```

Listing 1: An example using *MRdataset* (above: Python API, below: CLI) for importing DICOM/BIDS dataset. An identifier (name) can be used for persistent data, and the `style` argument is used to specify the dataset format.

Table 2: An example report for a neuroimaging dataset. Observe that the project has 7 modalities across 5 subjects. Subjects sub-566 and sub-879 are non-compliant w.r.t Pixel Bandwidth and Phase Encoding Direction respectively.

Modality	Non-compliant		Non-compliant subjects	Reasons	Compliant		Total subjects
rsfMRI	0	0.00 %			5	100.00 %	5
GRE	1	20.00 %	sub-566	Pixel Bandwidth	4	80.00 %	5
T2-FLAIR	0	0.00 %			5	100.00 %	5
DTI	1	20.00 %	sub-879	Phase Encoding Direction	4	80.00 %	5
T1-weighted	0	0.00 %			5	100.00 %	5
SWI	0	0.00 %			5	100.00 %	5

A *horizontal audit* is focused on investigating parameters on various levels (e.g., subject, modality) of a neuroimaging study. In a *horizontal audit*, a run is said to be *compliant* if the acquisition parameters for the run are the same as the reference protocol. A reference protocol is a pre-defined set of recommended values for each of the acquisition parameters. As shown in Figure 3, a subject may have one or more sessions for each modality (e.g., T1, T2) and each session has multiple runs. A subject is said to be *compliant* for a given modality if all the sessions for the subject are *compliant* with the reference protocol. Therefore, a subject can be *compliant* for one modality (say T1w), but it might be *non-compliant* for another modality (say T2w). A subject is tagged as *non-compliant* even if a single run is found to be non-compliant for a given modality. This means there might be some datasets where none of the subjects are compliant. Similarly, a modality is said to be *compliant* if all the subjects in this modality are *compliant*.

Horizontal audits can be a great tool to examine whether the acquisitions across sessions were performed correctly. A *horizontal audit* is a vital aspect for identifying common pitfalls in data integrity. However, a *horizontal audit* does not address the interaction between different modalities in a given session. In contrast, a *vertical audit* checks for compliance issues across all the modalities for a single subject. For example, given a subject, all field maps must be set up with the same field-of-view, pixel bandwidth, and multi-slice mode as the probe [18]. Similarly, optimization of homogeneity for the magnetic field, known as shimming, is specific to a subject. The shim method should not vary across modalities for a single subject. It is ideal to have consistent shimming especially for spectroscopic experiments [?]. As MRI scans are structured specifically as per requirements of the study, subtle deviations in shimming might not pose a critical problem for some studies. In addition, vertical audits are also helpful in revealing specific scans which are found to be non-compliant across multiple modalities. It might be possible that a navigator slices which might also have been erroneously uploaded along with scan for a subject. We recommend that both *horizontal audit* and *vertical audit* must be enforced to eliminate subtle errors in acquisition protocols.

```

from MRdataset import import_dataset
from mrQA import check_compliance

dicom_ds = import_dataset(data_source='/path/to/data', style='dicom', name='abc')
check_compliance(dicom_dataset)
# In [1]: In abc dataset, modalities "GRE, DTI, rsfMRI" are non-compliant. See
→ abc_09_07_2022_17_07.html for report

bids_ds = import_dataset(data_source='/path/to/data', style='bids', name='xyz')
check_compliance(bids_dataset)
# In [2]: In xyz dataset, modalities "func" are non-compliant. See
→ xyz_09_07_2022_17_07.html for report

```

```
$ mrqa --data-source /path/to/dataset --style bids --name my_bids_dataset
```

Listing 2: An example using mrQA (above: Python API, below: CLI) for generating a compliance report.

Table 3: An example of a detailed report for non-compliance in Gradient Echo (GRE) modality. Subject *sub-566* has a non-compliant pixel bandwidth in sessions 6, 7, 8, 9 & 10

Parameter	Ref. Value	Found	Subject_Session
PixelBandwidth	350	485	sub-566_6, sub-566_7, sub-566_8, sub-566_9, sub-566_10

Table 4: An example of a detailed report for non-compliance in Diffusion Tensor Imaging (DTI) modality. Subject *sub-879* has a non-compliant phase encoding direction in session 1.

Parameter	Ref. Value	Found	Subject_Session
Phase Encoding Direction	COL	ROW	sub-879_1

Further, we advocate a two-pronged approach for checking compliance against a reference protocol. The first is *pre-acquisition* compliance, where the parameters will be checked for compliance against a reference protocol before a scan is performed. And the second approach is *post-acquisition* compliance, where the parameters are checked after complete data acquisition across all subjects, validating the *acquired* dataset for compliance. Ideally, both of these two prongs should be performed to maximize data integrity and minimize loss *i.e.*, carrying out pre-acquisition compliance checks at initial setup to prevent bad acquisitions in the first place and validating the acquired images with post-acquisition compliance checks to remove any accidental or unknown sources of non-compliance.

In this work, we focus on the horizontal audit via post-acquisition protocol compliance to explore neuroimaging datasets. Towards this end, we propose *mrQA*, which focuses on capturing protocols across the dataset. *mrQA* infers the most frequent values for each acquisition parameter across all runs in the directory. In case a reference protocol is not provided, we define the reference protocol to be the set of most frequent values for each parameter. The parameter values of individual runs are checked for consistency against the reference protocol. Note that each modality can have a reference protocol with multiple echo times. This feature is required to accommodate modalities with multi-echo times. If the reference protocol is not provided for evaluation, the runs in a modality are stratified by echo time before inferring the most frequent values for each parameter. Each modality is indicated with scores of non-compliance and compliance percentage.

$$\begin{aligned} \text{non-compliant \%} &= \frac{\text{Number of non-compliant subjects in modality}}{\text{Total number of subjects in modality}} \times 100 \\ \text{compliant \%} &= 100 - \text{non-compliant \%} \end{aligned} \quad (1)$$

A complete report is generated for the neuroimaging study that presents complete information in a concise manner, and exported as an HTML file to disk. The report has two parts - a summary view (as shown in Table 2) which gives a brief assessment of protocol compliance for all the modalities. Following the summary, each modality is accompanied by a detailed view (as shown in Table 3 and Table 4).

Table 2 shows that there are two non-compliant subjects, *sub-566* and *sub-879*, for the modalities GRE and DTI. Subject *sub-566* has inconsistent pixel bandwidth, while subject *sub-879* has an inconsistent phase encoding direction (PED). In this example, two modalities are non-compliant - GRE and DTI. The full report contains reference protocols for each modality and corresponding details about sources of error in acquisition parameters. Table 3 shows that the Pixel Bandwidth in the reference protocol is 350, but subject *sub-566* has a pixel bandwidth of 485 in sessions 6, 7, 8, 9, and 10. Similarly, Table 4 shows subject *sub-879* has a non-compliant PED, ROW in session 1, compared to reference value - COL.

2.4 Data and Code Availability Statement

We tested *mrQA* against ABCD dataset [25], and 20 large BIDS datasets publicly available on OpenNeuro [26]. These datasets on OpenNeuro were chosen based on their large size and availability of JSON sidecar files. The software was tested with public DICOM datasets available on TCIA [27]. Finally, *mrQA* was tested on ABCD FastTrack Ongoing Series which provides a unique opportunity to test on a large and diverse sample of over 11,000 subjects across multiple sites and various scanner models. The source code is publicly available at <https://github.com/Open-Minds-Lab/mrQA> and <https://github.com/Open-Minds-Lab/MRdataset>, the documentation of the software is available at

Table 5: The table summarizes the compliance report for DICOM images from ABCD-baseline FastTrack Ongoing series. For each of the modality (*i.e.*, T1, T2 and field maps), the table shows the number of distinct echo times, percentage of non-compliant & compliant subjects, and the parameters which were found to be non-compliant *i.e.*, Repetition Time (TR), Echo Time (TE), Flip Angle (FA) and Pixel Bandwidth (PB). Some minor cases were observed in Phase Encoding Direction (PED), Phase Encoding Steps (PES), Echo Train Length (ETL), and Shim. In contrast to scans acquired with Philips and GE, images scanned with Siemens exhibit minimal non-compliance across all the modalities. Ensuring compliance in acquisition parameters manually is non-trivial for large-scale multi-site datasets such as ABCD. Automated tools like mrQA can help researchers achieve protocol compliance in a practical manner.

Modality	Vendor	#Distinct Echo Times	#Non-compliant Subjects		Parameters	#Compliant Subjects		Total Subjects
T1	GE	4	620	22.26 %	TE, FA, PB	2165	77.73 %	2785
	Philips	13	434	28.53 %	TE, ETL, PED, PES, PB, TR	1087	71.46 %	1521
	Siemens	2	30	0.41 %	Shim	7184	99.58 %	7214
T2	GE	19	717	25.45 %	TE, TR, PB	2100	74.54 %	2817
	Philips	33	33	2.26 %	TE, PB	1425	97.73 %	1458
	Siemens	1	6	0.08 %	PED, Shim	7024	99.91 %	7030
Diffusion Fmap	GE	3	620	22.26 %	TE, FA, PB	2165	77.73 %	2785
Diffusion Fmap A>>P	Philips	2	3	0.20 %	PB	1438	99.79 %	1441
	Siemens	2	128	1.81 %	PED, TR, Shim	6820	96.69 %	7057
Diffusion Fmap P>>A	Philips	2	4	0.27 %	PB	1435	99.72 %	1439
	Siemens	2	233	3.30 %	PED, TR, Shim	6820	96.69 %	7053
fMRI Fmap	GE	1	0	0.00 %		2862	100.00 %	2862
fMRI Fmap A>>P	Philips	1	873	58.70 %	FA, PB	614	41.29 %	1487
	Siemens	2	1	0.01 %	Shim	7199	99.98 %	7200
fMRI Fmap P>>A	Philips	1	876	58.83 %	FA, PB, TR	613	41.16 %	1489
	Siemens	2	0	0.00 %		7202	100.00 %	7202

<https://open-minds-lab.github.io/mrQA/> and <https://open-minds-lab.github.io/MRdataset/>. The binary package is available on the Python Package Manager (PyPI) <https://pypi.org/project/mrQA>

2.5 Ethics Statement

No new data were collected specifically for this paper. The datasets used are publicly available at NIMH Data Archive [25], OpenNeuro [26] and TCIA [27].

3 Results

We focused on evaluating public datasets as they often serve as a benchmark for neuroimaging analyses. The exploration is not meant to be a finger-pointing exercise, rather the availability of these datasets has made it possible to discover common pitfalls in an acquisition. By understanding these common issues, we can be more attentive to these parameters during acquisition. Assuming that acquisition for most subjects in a given study follows a predefined standardized protocol, the most frequent value for each parameter is taken as the reference value. Table 5 and Table 6 summarize the results for ABCD and OpenNeuro datasets, respectively. Frequent sources of non-compliance includes the Phase Encoding Direction (PED), Repetition Time (TR), Echo Time (TE), Flip Angle (FA) and Pixel Bandwidth (PB).

Table 6: The table summarizes compliance report for some OpenNeuro datasets that exhibit deviations in acquisition protocol. For each of these datasets, the table shows the number of distinct echo times, percentage of non-compliant & compliant subjects for each modality, and the parameters which were found to be non-compliant *i.e.*, Repetition Time (TR), Echo Time (TE), Flip Angle (FA) and Magnetic Field Strength (MFS). Some minor cases were observed in Phase Encoding Direction (PED), Phase Encoding Steps (PES), Sequence Variant and Pixel Bandwidth (PB). Thus, mrQA provides the ability to automatically discover scanner-related variance in MR datasets. Automatic compliance checks are especially important for large datasets such as ds004169 which exhibit non-compliance% of less than 1%.

Dataset	Modality	Suffix	Vendor	#Non-Compliant Subjects		Parameters	#Compliant Subjects		Total Subjects
ds000201	dwi		GE	21	27.63%	PB	55	72.36%	76
	fmap		GE	24	28.23%	PED, PB, TR	61	71.76%	85
ds003826	anat	t1w	Siemens	2	1.47%	PES, SV	134	98.52%	136
ds004215	anat	acq-cube_t2w	GE	39	25.49%	TE, TR	114	74.50%	153
	dwi	dir-unflipped	GE	2	1.39%	PB	141	98.60%	143
	fmap	acq-bold	GE	1	1.69%	PED	58	98.30%	59
	fmap	acq-dwi	GE	2	3.03%	PED, PB	64	96.96%	66
	func	task-rest_dir-forward	GE	6	4.61%	FA, PED	124	95.38%	130
	func	task-rest_dir-reverse	GE	40	31.00%	FA, PED	89	68.99%	129
	perf	asl	GE	1	0.70%	TR	141	99.29%	142
ds000030	anat	t1w	Siemens	92	34.71%	PES, PB	173	65.28%	265
	dwi		Siemens	112	42.74%	PB, TR	150	57.25%	262
	func	task-bart	Siemens	7	2.66%	PED	256	97.33%	263
	func	task-bht	Siemens	8	3.10%	PED	250	96.89%	258
	func	task-pamnec	Siemens	5	2.41%	PED	202	97.58%	207
	func	task-pamret	Siemens	6	2.88%	PED	202	97.11%	208
	func	task-rest	Siemens	9	3.35%	PED	259	96.64%	268
	func	task-scaph	Siemens	9	3.35%	PED	259	96.64%	268
	func	task-stopsignal	Siemens	9	3.38%	PED	257	96.61%	266
	func	task-taskswitch	Siemens	9	3.38%	PED	257	96.61%	266
ds000221	fmap	acq-GE	Siemens	1	0.31%	PED	316	99.68%	317
	fmap	acq-SE	Siemens	1	0.44%	PED	226	99.55%	227
	func	task-rest_acq-PA	Siemens	14	7.07%	TE	184	92.92 %	198
ds002345	func	task-milkway	Siemens	17	32.07%	TR	36	67.92 %	53
ds000228	func	task-pixar	Siemens	3	1.93%	FA	152	98.06 %	155
ds000258	func	task-rest	Siemens	4	4.49%	TR	85	95.50%	85
ds002785	dwi		Philips	33	15.63%	TR	178	84.36%	211

3.1 Evaluation of FastTrack Images for ABCD

The Adolescent Brain Cognitive Development (ABCD) [25] is a multi-site longitudinal study focused on understanding the development of the brain in adolescents over a diverse set of socio-demographic features. We analyzed ABCD-baseline scans for three modalities, namely T1-weighted, T2-weighted, and field maps as shown in Table 5. As the

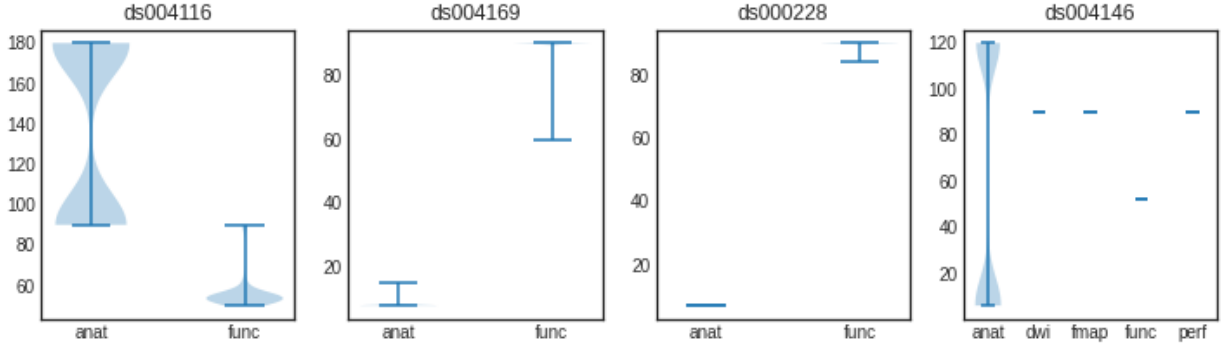


Figure 4: Violin plot shows the variance in flip angle across various datasets and modalities. Flip angles affect image contrast for both anatomical and functional MRI. Flip angle for *anat* in datasets ds004116 and ds004146 exhibit considerable variance which would require explicit standardization before morphometric analyses.

objective for mrQA is to achieve real-time protocol compliance, we analyze DICOM images from the FastTrack Ongoing Active Series for each modality.

For T1w images, we observe that MRI scans from GE and Philips scanners exhibit non-compliance in acquisition parameters, especially for TE, TR, and PB. We also observe some minor issues in FA, PED, Echo Train Length (ETL), and Phase Encoding Steps (PES). For T2w images, we observe that MRI scans from GE scanners have issues of non-compliance in TE, TR, and PB. For Philips, T1w scans have a non-compliance percentage of 28.53%, while T2w scans exhibit only 2.26% non-compliance. In contrast, scans from Siemens scanners exhibit only some minor issues in shimming (T1w, T2w) and in PED (T2w).

Table 5 also shows the assessment of field maps in the ABCD dataset for protocol compliance. The subjects are stratified into vendor and PED-specific groups as per information in the DICOM header. Often neuroimaging experiments consists of both $A \gg P$ and $P \gg A$ scans to reduce artifacts like eddy current effects, and susceptibility artifacts [30]. Therefore, the scans will not have a unique PED across all scans. To avoid misinterpretation the compliance checks should be performed within these sub-groups of $A \gg P$ and $P \gg A$ scans. Similarly, the field maps intended for Diffusion Images should not be compared to the field maps intended for fMRI images. This information is not automatically captured in DICOM images and should be annotated manually after acquisition. Similarly, BIDS JSON sidecar have IntendedFor parameter which is not automatically exported by *dcm2niix* but can be manually annotated by dataset-specific scripts. We observe that field maps for Diffusion images from GE scanners have a 22.26 % non-compliance due to two distinct values of flip angles *i.e.*, 77 and 90 respectively. Similarly, Philips scanners exhibit non-compliance in flip angle for fMRI field maps. We observe that a lot of subjects have two sessions with flip angle values 52 and 90, respectively. The report indicates that these subjects don't comply with a single predefined value for flip angle. We choose to flag this issue, however whether it is an issue or a study requirement would be best judged by the investigators of the study. We also observe some minor issues in TR and TE. In contrast, MRI scans acquired with Siemens scanner have a unique flip angle of 90, and some minor issues in Shim, PED, and TR.

As compared to Philips and GE scanners, MRI scans acquired with Siemens scanner are observed to be consistent and compliant achieving more than 99% compliance over seven thousand subjects both in T1w, T2w and field maps. This might be because the Siemens scans were performed only on Prisma scanners with consistent software version (*syngo MR E11*). In contrast, scans for Philips were performed on Achieva dStream and Ingenia models, and the GE scans were executed on MR750 and DV25-26. Furthermore, both GE and Philips scans had differences in software versions.

3.2 Evaluation of BIDS datasets on OpenNeuro

OpenNeuro [26] is a data archive dedicated to open neuroscience data sharing based on FAIR principles. We analyze over 20 open datasets available on OpenNeuro accessible in BIDS format. Table 6 presents some of the datasets which exhibit a lack of protocol compliance. Due to the absence of standard acquisition metadata in NIfTI files, we rely on associated JSON sidecar files for evaluating protocol compliance on NIfTI-based datasets. The most common image acquisition parameters which suffer from variation are repetition time (TR), echo time (TE), phase encoding direction (PED), flip angle (FA), and magnetic field strength (MFS). Some datasets had distinct data clusters under the same project name. These data clusters can be repeat experiments with varying acquisition parameters for each subject *e.g.*, scans with different PED ($A \gg P$, $P \gg A$) for DTI or separate cognitive or behavioral tasks captured with

different acquisition protocols in an fMRI study. In such cases, none of the subjects would be seen to comply with a single predefined protocol and compliance checks should be performed after stratification into coherent clusters to avoid misinterpretation.

3.3 Evaluation of DICOM datasets on TCIA

We also analyze three public DICOM datasets available on The Cancer Imaging Archive (TCIA) [27], namely Rembrandt [31], TCGA-GBM [32] and TCGA-LGG [33]. For Rembrandt, we observe issues of non-compliance in TR. Many volumes had missing values for crucial parameters like magnetic field strength, pixel bandwidth, PED for FLAIR, and diffusion images. We observe issues in repetition time, pixel bandwidth, and magnetic field strength for TCGA-LGG and TCGA-GBM datasets.

4 Discussion

To obtain better insight into the impact of variation in acquisition parameters on image quality, statistical analyses and the issue of non-conformance among different vendors in terms of MRI physics parameters. We discuss these issues contextualizing them within the broader literature and exploring their implications for future research.

4.1 Effect on image quality

In this section, we look deeper at acquisition parameters that exhibit greater variation. We discuss the impact of these existing variations in open datasets. However, empirical quantification of the effect on image quality due to variation in these parameters is out of the scope for this work.

The flip angle affects the net magnetization relative to the primary magnetic field as it controls the amount of longitudinal magnetization converted to transverse magnetization. Thus, the flip angle affects the RF signal of the cycle, thereby affecting the signal intensity. For instance, large flip angles produce T1 contrast, low flip angles produce PD (proton-density) contrast, and the T1 and PD contrast can cancel each other for intermediate flip angles [34, 35, 36]. Apart from anatomical MRI, flip angle also affect functional MRI. Large flip angles deteriorates the spatial contrast between cerebrospinal fluid (CSF), gray matter (GM) and white matter (WM), which makes it difficult to align EPI to its structural counterpart [37]. The impact on signal intensity and its significance for pattern discrimination would be governed by specific tissue in context. Yet, it is important to understand that flip angles have a direct effect on image contrast. Figure 4 shows variation in flip angle for some of the datasets available in OpenNeuro. Flip angle for *anat* in datasets ds004116 and ds004146 exhibit variance which would require explicit standardization before morphometric analyses.

A correct choice for echo time (TE) and repetition time (TR) is important for T2-weighted images. Acquisition parameters like TR and TE can influence the tissue-specific response as different tissues vary in their respective T1 and T2 times. For instance, to generate a valid T1-weighted image, it is important that the repetition time & echo time is less than tissue-specific T1 & T2 times, respectively. In contrast, repetition time & echo time should be much greater than tissue-specific T1 time & T2 time, respectively to generate T2 weighted images. However, if repetition time is much greater than tissue-specific T1 time but echo time is less than tissue-specific T2 time, the result is a proton density-weighted image. Thus, variations in repetition time and echo time can dictate image contrast characteristics [17].

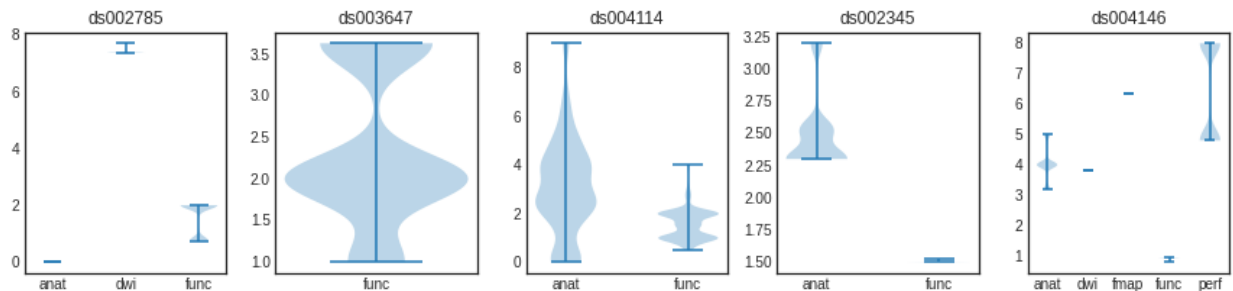


Figure 5: Violin plot shows the variance in Repetition Time across various datasets and modalities. Datasets ds004114 and ds004146 have significant variance in repetition time for modalities *anat* and *perf*, respectively.

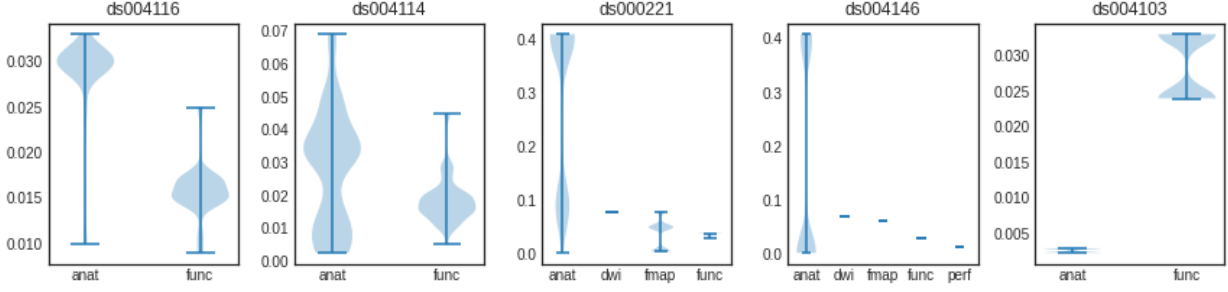


Figure 6: Violin plot shows the variance in Echo Time across various datasets and modalities.

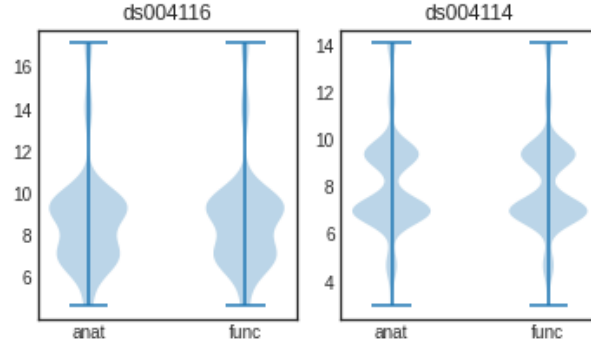


Figure 7: Violin plot shows the variance in Magnetic Field Strength across various datasets and modalities. It is rare to observe significant variances in magnetic field for scans in a single dataset. However, both of these datasets are multi-center rat fMRI datasets.

Figure 5 and 6 show the variance of repetition time and echo time in open datasets respectively. Datasets ds004114 and ds004146 have significant variance in repetition time for modalities *anat* and *perf*, respectively.

Variation in magnetic field strength has a strong influence on texture features. Ammari *et al.* [38] show a comprehensive analysis studying the impact of magnetic field strength on various texture features. The study evaluates 38 texture features of which 15 features in healthy volunteers were sensitive to variations in magnetic field strength. Visually, images from various field strengths may have the same visual diagnostic accuracy [39], but in context to texture features, images with varying magnetic field strength cannot be used interchangeably [38]. Figure 7 shows the variance of magnetic field strength in open datasets such as ds004116 and ds004114. Both of these datasets are multi-center rat fMRI datasets. Distinct data clusters were pooled across 10 different labs for a multi-center comparative study of functional connectivity in rats.

PED plays a crucial role in EPI sequences. A common issue in EPI sequences is their vulnerability to artifacts like eddy current effects, off-resonance, and susceptibility artifacts. These artifacts are apparent, especially when the bandwidth is low [40, 41]. To diminish the effect of these distortions, the collection of additional scans with varying PED is very helpful [30]. Although it is important to eliminate these artifacts to improve image quality in DTI sequences, varying the phase encoding direction is known to affect fractional anisotropy estimates. Kennis *et al.* [20] utilize Freesurfer to show that magnitude of fractional anisotropy magnitude between $P \gg A$ and $A \gg P$ scans can range from 0.4% to 30% even after correction for subject motion, eddy currents effects, and susceptibility artifacts. It is possible that these differences are arising due to signal intensities from $P \gg A$ and $A \gg P$ scans that can confound DTI neuroanatomical studies. Similarly, Tudela *et al.* [42] show that misalignment in PED from the main magnetic field can lead to much more artifacts reflected by lower fractional anisotropy values. Figure 8 shows a stacked column chart to visualize the apportionment of PED across various datasets and modalities. It is not always feasible to use an equal number of scans for each PED direction. The PED should be defined on specific imaging needs of the patient and radiation exposure risks. However, consistency of PED across subjects can help improve the reliability and accuracy of downstream analyses.

4.2 Effect on statistical analyses

Prior works have measured the effect of various acquisition protocols on texture analysis [43, 44, 45], to evaluate which features are stable against changes in acquisition protocols. Some parameters such as TR and TE do not affect the shape and size of the image, but they affect uniformity in grayscale intensity [21]. It is evident that different acquisition protocols can affect data distribution, reducing the reliability of the extracted features and consequently increasing the bias of downstream statistical analyses [46]. Thus, special attention must be attributed to image preprocessing before any feature extraction [47]. Harmonization is possible only if we know that the data exhibits heterogeneity in imaging acquisition protocol. In cases when sources of non-compliance is not known, data cannot be categorized into clusters and it would be difficult to perform data harmonization. Thus, *mrQA* can play a pivotal role in establishing data integrity by discovering sources of non-compliance allowing the investigators to perform harmonization, if required. As we progress towards algorithms that are able to learn features automatically pivoted at a particular task (*e.g.*, deep learning), it is even more important to ensure that the derived features are stable with respect to variations in acquisition parameters. Without acknowledging these sources of variation in acquisition parameters, the statistical results might be subject to confounding which can obscure or exaggerate the effects of interest, leading to misinterpretation of neural correlates for behavior and cognition.

4.3 Impact of scanner vendor heterogeneity

Although MRI scanners from different vendors function on the same underlying principles, image sequences can have significant differences in gradient strengths, RF pulse sequences and timing parameters. In addition, different vendors use specific software to reconstruct the images from k -space. Therefore, these sequences are denoted with specific names and abbreviations. For example, Siemens scanners provide an MPRAGE imaging sequence, while Philips scanners provide SPACE imaging sequence. Even though both these sequences are T1-weighted images, the significant differences in hardware and software makes it non-trivial to compare scans across vendors. Even if the modality is same (say T1w), the resulting images can be different due to vendor-specific differences in image quality and appearance [48]. It is better to stratify scans w.r.t. vendor to avoid any misinterpretations. This problem becomes particularly relevant for studies that analyze images collected with different imaging acquisition protocols (multi-site studies).

Therefore, the subjects are stratified into different vendor-specific sub-groups in Table 5 as per the information in the DICOM header. We observed that scanners from various vendors (*e.g.*, Siemens, GE, Philips) differ in terms of units of measurement even for the same parameter. For example, in a Siemens scanner, TR is typically in the range of 2000-4000, while the range is typically 6-7.5 for a GE scanner. It might be possible that GE/Philips scanners express TR for a single sweep in the k -space while Siemens scanner stores TR for the entire volume. The precise details of these differences are stored in Exam Card (Philips), Protocol Exchange (GE), or .exar file (Siemens) generated by corresponding software. These electronic protocol files can be loaded into the corresponding scanner to achieve uniformity of imaging protocol. However, automatic cross-vendor compliance is not possible.

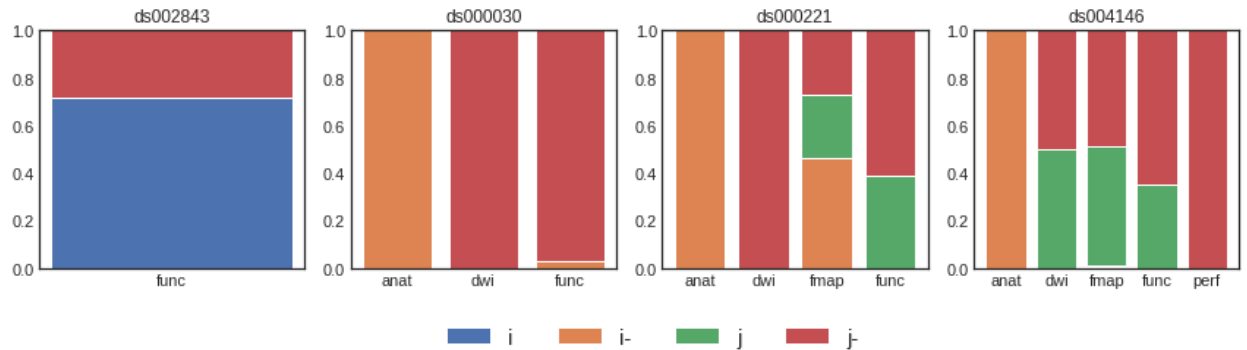


Figure 8: Stacked column chart shows the variance in Phase Encoding Direction across various datasets and modalities. i and j correspond to the first and second axes of the corresponding image, $i-$ and $j-$ correspond to reversed axes, respectively.

5 Limitations

Although variation in image acquisition parameters can be a source of inconsistencies, an adjustment might be necessary for clinical diagnosis. For instance, sequences for adolescents may be acquired with a slower acquisition time to reduce discomfort. Similarly, TR is increased and flip angle is reduced incase the SAR limits are exceeded for high SAR sequences such as FLAIR [49]. Furthermore, multiple scans with varying PEDs might be acquired to alleviate susceptibility artifacts [40], or shimming method might be adjusted specifically for a subject to obtain high-quality MRI images [50]. Nevertheless, these variations lead to issues in morphometric estimates [46]. It is possible to include such requirements before analyzing data for protocol compliance by skipping particular parameters known to exhibit high variance. However, the current framework doesn't include this functionality explicitly.

mrQA checks for absolute equivalence for parameter values. However, compliance to a pre-defined standard is often determined by design of a neuroimaging study. *mrQA* allows us to discover sources of non-compliance in acquisition but, this may not necessarily be a part of inclusion/exclusion criteria for a subject. For example, *mrQA* marks a subject as non-compliant if it deviates from the reference protocol in any of its runs even in a single parameter. However, a subject cannot be tagged as *non-compliant* if a parameter varies due to differences in precision. Given some context about the neuroimaging study, it might be possible to include certain tolerance in a variation of these parameters. The standard for acquisition can be best judged by investigators [51, 52] and hence, cannot be attributed prematurely in the software.

The DICOM format suffers from storage overhead, with complex specifications for multi-frame MRI and spatial registration. *mrQA* extracts certain acquisition parameters such as shim method, effective echo spacing, iPAT, PED, and multi-slice mode from Siemens private headers. All other parameters were extracted from the official DICOM standard set of elements. The current framework skips the private header while reading DICOM images from other scanners such as GE and Philips. Therefore, *mrQA* at its current stage of development cannot discover discrepancies in parameters present in private headers for GE and Philips scanners.

mrQA checks for compliance in the acquisition parameters captured by the DICOM header. However, this may not be sufficient to achieve consistent acquisition across multiple sites. For instance, in fMRI analysis stimuli is used to elicit specific neural responses from various parts of brain. The presentation of stimuli can vary across scanners due to differences in their duration, and intensity; that may in-turn affect the measurement of neural responses. Consequently, differences in neural responses would make it difficult to pool and interpret data across scanners.

6 Conclusions

We demonstrate the pervasive problem of protocol non-compliance based on analyses of many open datasets from OpenNeuro and the ABCD dataset. It is non-trivial to maintain protocol compliance in imaging acquisition parameters, especially for large-scale multi-site studies. Insufficient monitoring can lead to non-compliance in MR physics parameters which may confound downstream statistical analyses. Therefore, we propose a practical solution towards achieving quality assurance in neuroimaging experiments. We propose open source tool, *mrQA* (and *MRdataset*) which aims to help researchers summarize and aggregate image acquisition metadata to discover any issues of protocol compliance. We also believe that it is important to embrace a mindset of pre-emptive, preventive, and proactive quality assurance to weed out any source of inconsistencies at the scanning interface itself rather than waiting for the end-of-analyses to catch confounding. Adopting such an approach before organizing files in a suitable directory structure (e.g., BIDS) will save time and effort. *mrQA* can discover subtle deviations in acquisition parameters in the rawest data format available, i.e., DICOM format. A thorough investigation of image acquisition metadata is a key step toward achieving compliance (intra- and inter-site), thereby contributing to the validation and integrity of statistical analyses. In the future, more resources like *mrQA* should be made available to MR research labs for removing issues in a real-time, efficient and practical manner.

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