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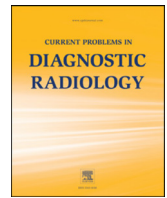
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## Correlating the Radiological Assessment of Patient Motion with the Incidence of Repeat Sequences Documented by Log Files

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### ABSTRACT

**Objective:** To correlate a radiological assessment of MR motion artifacts with the incidence of repeated sequences and delays derived from modality log files (MLFs) and investigate the suitability of log files for quantifying the operational impact of patient motion.

**Materials and methods:** An experienced, blinded neuroradiologist retrospectively evaluated one full calendar month of sequentially obtained clinical MR exams of the head and/or brain for the presence of motion artifacts using a previously defined clinical grading scale. MLF data were analyzed to extract the occurrence of repeated sequences during the examinations. Statistical analysis included the determination of 95% confidence intervals for repetition ratios, and Welch's t-test to exclude the hypothesis of equal means for different groups of sequences.

**Results:** A total of 213 examinations were evaluated, comprising 1681 MLF-documented sequences, from which 1580 were archived. Radiological motion assessment scores (0, none to 4, severe) were assigned to each archived sequence. Higher motion scores correlated with a higher MLF-derived repetition probability, reflected by the average motion scores assigned to sequences that would be repeated (group 1, mean=2.5), those that are a repeat (group 2, mean=1.9), and those that are not repeated (group 3, mean=1.1) within an exam. The hypothesis of equal means was rejected with  $P = 5.9 \times 10^{-5}$  for groups 1 and 2,  $P = 9.39 \times 10^{-16}$  for groups 1 and 3, and  $P = 1.55 \times 10^{-12}$  for groups 2 and 3. The repetition probability and associated time loss could be quantified for individual sequence types. The total time loss due to repeat sequence acquisition derived from MLFs was greater than four hours.

**Conclusion:** Log file data may help assess patterns of scanner and exam performance and may be useful in identifying pitfalls to diagnostic imaging in a clinical environment, particularly with respect to patient motion.

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### Introduction

Patient motion during clinical MR examinations is a frequent cause of image degradation. Prior studies have reported that patient motion impacts image quality in 10%–42% of examinations of the head,<sup>1,2</sup> and necessitates repeated MR sequences in nearly 20% of MR examinations.<sup>2</sup> In abdominal imaging, extra sequences have been identified in 30%–40% of examinations, and more than 30% of added sequences were repeats due to motion.<sup>3</sup> Moreover, image degradation due to motion artifacts impairs radiological interpretation,<sup>1,2,4</sup> particularly when using advanced MR techniques.<sup>15–10</sup> The additional scan time required for the repetition of motion-corrupted images also leads to increased operational cost.<sup>2,11</sup>

Conflict of interest: Jalal B. Andre is a consultant for Hobbitview, Inc. Thomas Amthor is an employee of Philips GmbH, Germany. Christopher S. Hall was employed by Philips Health Care, Bothell, WA at the time this research was performed.

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The rate of motion-degraded and repeated sequences may be underestimated for several reasons. MR technologists are usually the first to identify and react to patient motion, which may leave the radiologist unaware of the motion, and excluded from the decision-making process. Furthermore, the initial, motion-degraded sequence may not be archived to the picture archiving and communication system (PACS) when a subsequent similarly-weighted, more motion-robust sequence was acquired successfully, leaving the radiologist unaware that a motion degraded sequence was acquired initially. This observation underscores the need for a more accurate method to determine the rate of MR sequence repetition; one that reliably captures all image-acquisition data and is independent of human factors including technologists' choice to send or not to send sequences to PACS.

In this context, modality log file (MLF) data represent an attractive opportunity to more accurately document the prevalence of repeated sequences and their associated temporal footprint. MLF data, which are generated during scanner use and track several metrics of scanner efficiency, act much like a "black box" used in modern-day aircraft.<sup>12</sup> The log files are stored locally on the MR system and include granular data describing system utilization and detailed information about interactions between the user and the system, including repeated and terminated sequences and scanner table position.<sup>12</sup> In recent

studies, log files have been used to accurately measure MR system utilization and table times.<sup>13–15</sup> The purpose of this study was to compare a radiologist's qualitative, independent assessment of the presence, rate and severity of motion artifacts to the rate of repeated sequences documented by MR scanner MLF data. In this way, we sought to investigate the suitability of MLFs for the quantification of the impact of patient motion on the radiologic workflow.

## Materials and methods

In this institutional review board approved retrospective study, one full calendar month of sequential clinical MR examinations of the head and/or brain, acquired on two 3T MR systems (Ingenia, Philips Healthcare, Best, The Netherlands), were evaluated for the presence of motion artifacts (on a per-sequence basis) using a previously defined 5-point clinical grading scale.<sup>2</sup> The evaluation was performed on available images archived in PACS of a clinical population at an academic medical center, with inclusion criteria limited to only examinations performed both without and with administration of a gadolinium-based contrast agent (GBCA). Technologists were instructed to send all acquired images to the PACS during this month to allow capture of motion degraded imaging studies.

A neuroradiologist with 11 years of radiological experience served as an expert reader and was blinded to all patient history and log file data. Radiological motion assessment scores, ranging from 0 (none) to 4 (severe),<sup>2</sup> were retrospectively assigned to all sequences within each MR examination, and correlated with the MLF documentation of repeated sequences, on a per-sequence basis. Planning, survey, and/or localizer sequences were not evaluated for the presence of motion artifacts. Thus, only those sequences archived in PACS and used to generate a medical diagnosis (ie, diagnostic sequences) were evaluated.

Matching MLF data, collected for the same time period, were retrospectively evaluated and analyzed using in-house Python scripts. Repeat sequences were identified automatically, using MLF data, even when the first acquired sequence had not been archived in the PACS. Sequences were subsequently grouped with respect to observed sequence repetition status, as follows: “will be repeated” was used to denote the initial occurrence of a sequence for which a subsequent sequence was obtained (repeated) within the same examination; “is a repeat” was used to classify those sequences that represented a repeat of a previously acquired sequence within the same examination; “not repeated” was used to denote those sequences that do not belong to either of the aforementioned groups. The category “is a repeat” was further divided into two categories; “exact” was used to denote repeated sequences that were obtained with sequence parameters identical to those of the original “will be repeated” sequence, whereas “non-exact” was used to denote those obtained with identical weighting (ie, T1, T2, FLAIR, etc.), albeit with software and/or parameter optimization to reduce sensitivity to motion artifacts.

The reader-derived motion score was correlated with MLF data on a per-sequence basis. Sequences with identical weighting and readout (ie, T1-weighted, FLAIR, etc.) were grouped, irrespective of GBCA administration status. Recognizing that the acquisition of suboptimal quality (aka. “non-diagnostic”) imaging data is of limited radiological value, the time expended in acquiring a “will be repeated” sequence was used to define a “Time Lost” parameter, regardless of whether the subsequently repeated sequence was “exact” (same acquisition time) or “non-exact” (potentially shorter or longer acquisition time, depending on selected parameters and sequence readout). Thus, “Time Lost” was always defined by the acquisition time of the “will be repeated” sequence, rather than that of the “is a repeat” sequence.

Repetition ratios derived from the MLF data can be used as an estimate for repetition probabilities, when binomial proportion intervals are used as confidence intervals. For this, we calculated the Wilson score, which has been found to be a reliable, correlative method for

small sample sizes;<sup>16</sup> the corresponding 95% confidence intervals are depicted by asymmetric error bars for all repetition ratios. Alternatively, when average motion scores are displayed, error bars specify the standard deviation. To compare average motion scores of different groups of sequences, Welch's t-test was employed to exclude the hypothesis of equal means. All statistical calculations were performed in Python.

## Results

We evaluated 213 examinations of the head and/or brain on a per sequence basis for the presence of motion artifacts. Within these 213 examinations, 1580 of the 1681 acquired diagnostic sequences (94.0%) were available in PACS for image review, despite requests that all sequences be sent to PACS. MLF data utilized all 1681 sequences, whereas reader evaluation was limited to the 1580 sequences available in PACS. The most commonly acquired sequences during the evaluated period were axial and sagittal T1-weighted and axial T2-weighted spin echo, axial diffusion weighted (DWI), and axial fluid attenuated inversion recovery (FLAIR), respectively.

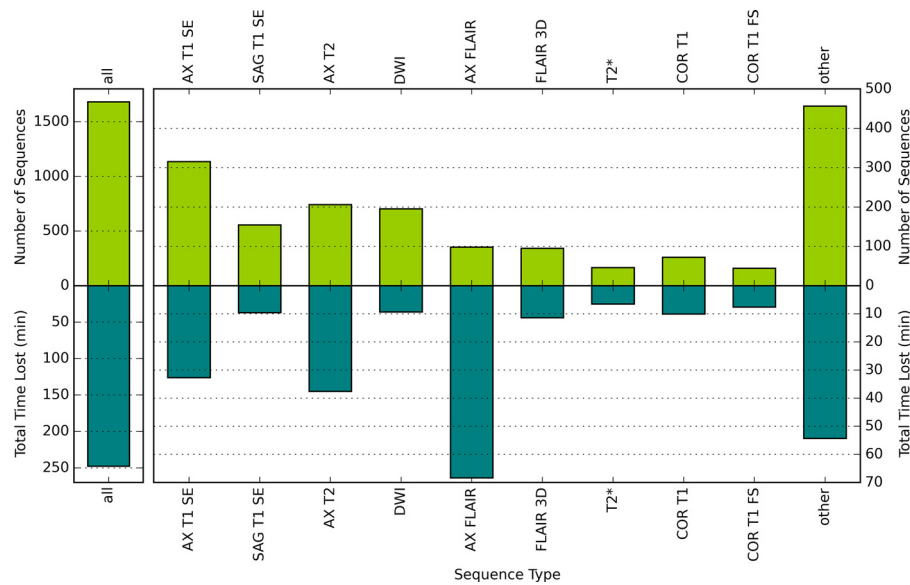
In [Figure 1](#), the total number of acquired sequences during the study period and the “Total Time Lost” due to the acquisition of “non-diagnostic” quality imaging data are depicted for the nine most commonly acquired sequences. A separate column “all” denotes the sum of all sequence weightings, while “other” includes all remaining sequences otherwise not individually specified.

The most frequently acquired sequence during the study period was the axial (pre- and post-GBCA) T1-weighted sequence (n = 315), followed by the axial T2-weighted sequence (n = 206), which was the most frequently repeated sequence, repeated 18 times during the study period. The DWI sequence was the third most frequently acquired sequence (n = 195), yet was responsible for only 3.8% of the Total Time Lost (9.38 min), while the T2-weighted sequence accounted for 15.2% of Total Time Lost (37.62 min.). Axial (2D) FLAIR was the fifth most frequently acquired sequence (n = 98), yet was responsible for a greater loss of time due to sequence repetition (68.37 min) than was the axial T2-weighted sequence (the second most commonly acquired sequence). The FLAIR 3D (3-dimensional readout) was acquired nearly as frequently (n = 95) as the axial 2D FLAIR (n = 98) yet was responsible for a notably lower loss of time from repeated sequence acquisition (11.4 min).

The per-sequence repetition ratio for the nine most commonly acquired sequences is depicted in [Figure 2](#). The repetition ratio represents the estimated probability that a sequence will be repeated within the same examination, derived from the documented repeats in the modality log files. The 2D axial FLAIR sequence had the highest repetition ratio (13.3%), while the axial 3D FLAIR sequence had the lowest (2.1%) of those listed. The repetition ratio across all sequences was 5.95%. Each bar in the plot is subcategorized into “exact” and “non-exact” repeats, as above defined. Examples of “non-exact” repeat sequences are provided in [Table 1](#).

[Figure 3](#) depicts expert reader-derived motion scores of all brain and head examinations (1580 sequences available in PACS) correlated with the corresponding repetition ratios including both “exact” and “non-exact” repetitions. The most notable change in this relationship is observed between reader-derived average motion scores classified as “mild” (score of “2”; repetition ratio = 4.09%) and those classified as “moderate” (score of “3”; repetition ratio = 20.1%). The highest repetition ratio was found for sequences classified as “severe” (score of “4”; repetition ratio = 21.4%), although the small sample size of 14 leads to relatively large error bars. For motion scores 0 and 1, only very small repetition ratios of 0.25% (motion score 0) and 0.59% (motion score 1) were observed.

Sequences can be subsequently grouped in terms of the observed sequence repetition state (“will be repeated” versus “is a repeat” versus “not repeated”). [Figure 4](#) depicts the expert-reader-derived



**FIG 1.** Total number of acquired sequences (green color bars, above) and total time lost, associated with re-acquiring imaging data to achieve diagnostic quality (teal color bars, below), derived from modality log files. The sum over all sequences acquired during the study period is shown on the left using a unique scale. The most commonly acquired sequences are displayed as individual bars, where “other” comprises all sequences not assigned to any of these sequence types. AX, axial; COR, coronal; DWI, diffusion weighted imaging; FLAIR, fluid attenuated inversion recovery; FS, fat saturation; SE, spin echo; SAG, sagittal; T2\*, gradient recalled echo. Color version of figure is available online.

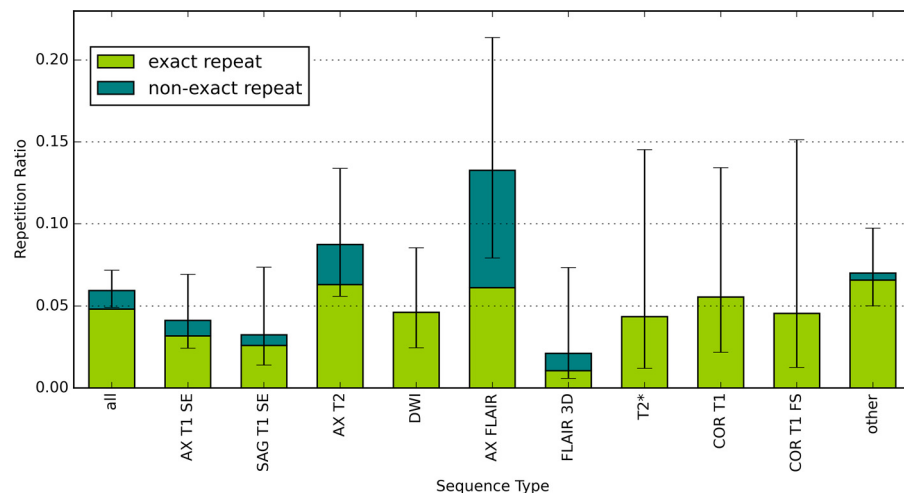
average motion score for such sequence grouping of the five most frequently acquired sequences. When evaluated across all sequences, the following trend was revealed: the highest motion scores were observed for the “will be repeated” sequences, with significantly lower scores assigned to the “is a repeat” category ( $2.51$  vs  $1.87$ , hypothesis of equal means rejected with  $P = 5.9 \times 10^{-5}$ ). “No repetition” sequences received the lowest motion scores, which achieved statistical significance compared to the “will be repeated” ( $1.08$  vs  $2.51$ ,  $P = 9.39 \times 10^{-16}$ ) and the “is a repeat” ( $1.08$  vs  $1.87$ ,  $P = 1.55 \times 10^{-12}$ ) categories, respectively.

## Discussion

The problem of patient motion and motion-associated image artifacts is ubiquitous, but also surprisingly under-documented; only a handful of studies have attempted to evaluate the prevalence of

motion artifacts and the impact of MR sequence repeats. Because estimation of motion artifact within an examination is neither reliably nor consistently reported by the reading radiologist, there exists no standardized way to evaluate the effect of motion within the acquisition protocols. As a result, we evaluated repeated sequences as a surrogate, correlated marker of motion. The current study attempts to further contribute to this body of knowledge by comparing average reader-derived per-sequence motion score with the incidence of MLF-documented sequence repeats within a given MR examination.

The results of this study suggest a monotonic relationship between average motion assessment scores, evaluated on a per-sequence basis, and the incidence of repeated sequences, identified from MLF data. This relationship suggests that log file data may help predict patterns of scanner and exam performance and may be useful in identifying pitfalls to diagnostic imaging in a clinical environment, particularly with respect to patient motion.



**FIG 2.** The sequence specific repetition ratio for “exact” and “non-exact” repeated sequences, plotted as a function of sequence type. The repetition ratio, derived from the MLF data, represents an estimated probability that a sequence will be repeated within the same examination, defined as the number of “will be repeated” sequences divided by the total number of sequences of the given type. Note: “all” comprises all sequences acquired during the study period; “other” comprises all sequences that are not assigned to any of the given sequence types. AX, axial; COR, coronal; DWI, diffusion weighted imaging; FLAIR, fluid attenuated inversion recovery; FS, fat saturation; SE, spin echo; SAG, sagittal; T2\*, gradient recalled echo. Error bars represent 95% confidence levels (CL) of the total repetition ratio, suggesting that there is a 95% chance that the “real” probability for a repetition lies within the interval.

**TABLE 1**  
Examples of “non-exact” repeat sequences

| Original “Will be repeated” Sequence | “Non-exact” Repeat Sequence (examples)                              |
|--------------------------------------|---------------------------------------------------------------------|
| AX FLAIR                             | Ssh_FLAIR, T2W_FLAIR, Ssh_FLAIR FAST                                |
| AX SWI                               | AX T2* GRE                                                          |
| AX T1 SE                             | AX T1 IR FS MV (motion-control), Ssh_T1W_TFE, Ssh_T1W_TFE FAST      |
| AX T2                                | AX T2W_TSE FAST, T2W_FFE, AX T2 PH AP, AX T2 FS MV (motion-control) |
| SAG FLAIR 3D GAD                     | AX Ssh_FLAIR, COR Ssh_FLAIR                                         |
| SAG T1 SE                            | T1W_FFE                                                             |

AX, axial; COR, coronal; FAST, technologist notation to denote a shorter acquisition; FLAIR, fluid attenuated inversion recovery; FFE, fast field echo (similar to GRE); FS, fat-saturated; GRE, gradient recalled echo; IR, inversion recovery; MV, MultiVane (proprietary Periodically Rotated Overlapping Parallel Lines with Enhanced Reconstruction (PROPELLER) technique); Ssh, single-shot; SWI, susceptibility-weighted imaging; SE, spin echo; TFE, turbo field echo; TSE, turbo spin echo.

\*Sequence names in boldface represent those that were the most commonly utilized.

<sup>1</sup>AX, axial.

When a motion-degraded sequence is going to be repeated within an examination, the current clinical paradigm often includes a technologist’s direct request for increased patient cooperation, subjective technologist-based assessment that the patient may move less upon re-imaging, and possibly the acquisition of similarly-weighted sequence that is more robust to motion (often at the cost of longer acquisition times, poorer signal-to-noise ratio, or reduced image quality). However, there is no guarantee that a patient will be better able to lie motionless during a subsequently repeated sequence, and the additional time requirements can be costly and without any guarantee that a diagnostic quality sequence will be successfully obtained. This point is perhaps best illustrated by the data presented in Figure 4; there is minimal change in the repetition ratio for sequences given a motion score of “4” (“severe” motion) compared to “3”, suggesting that technologists were less convinced that a repeated sequence acquisition would guarantee greater diagnostic value (only 3 of 14 sequences were repeated in this category).

It is important to note that different sequence readouts are variably affected by patient motion,<sup>17</sup> and subsequently may result in a protean degree of detectable motion artifacts. Along these lines, the AX DWI sequence was the third most commonly acquired sequence in this study ( $n = 195$ ), and was associated with a repetition rate of 4.6% (Fig 1). The AX FLAIR sequence, on the other hand, was acquired less than half as frequently ( $n = 98$ ), yet was associated with a three-

fold greater repetition rate of 13.3% (Fig 1). The echo planar imaging (EPI) readout employed in traditional AX DWI sequence, as in this study, is known to be relatively motion robust (due to its reduced acquisition time), whereas the AX FLAIR sequence usually employs a fast spin-echo readout that is more sensitive to motion artifacts, as supported by the results of this study. This substantiates the observation that sequence-specific readouts are associated with variable vulnerability to patient motion, as previously described<sup>17</sup>.

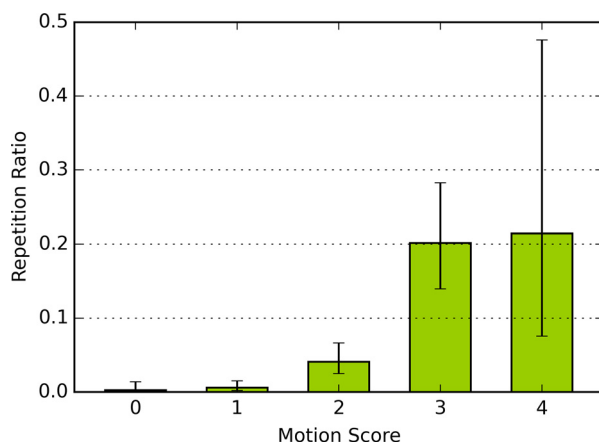
It is interesting that the 2D axial FLAIR sequence had the highest repetition ratio (13.3%), and was associated with the greatest loss of time due to sequence repetition (68.37 min), while the similar 3D version of the same sequence weighting, the axial 3D FLAIR sequence, had the lowest repetition ratio (2.1%) and a Total Time Lost of only 11.4 min. Furthermore, the differing repetition rates and associated Total Time Lost for axial versus sagittal versus coronal T1-weighted sequences (depicted in Figs 1, 2, and 5, respectively) suggest that it is not only the readout method that plays a significant role in sequence motion sensitivity, but perhaps also the acquisition orientation, which may be due to the primary axis of head motion versus the order of acquisition planes. This indicates that the association between sequence repeat frequency and corresponding time lost due to repetition may not always be linear in nature.

This study demonstrates the value of MLFs as a tool to measure the rate of repeat MR sequences. With increasing demands for the use of advanced imaging technology such as MR, and reduced reimbursement rates, radiology practices need to become ‘hyper-efficient’ to remain competitive and need a means to measure the clinical, resource and financial impacts of interventions.<sup>18</sup>

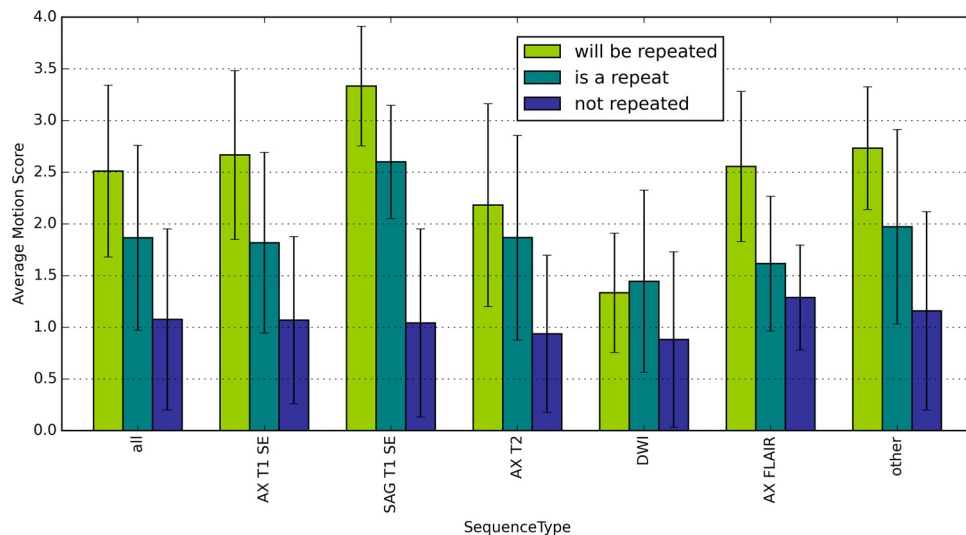
Several MR motion correction techniques have been proposed,<sup>19–32</sup> but were not readily available for clinical use during this study. In recognition of the temporal and financial opportunity costs associated with motion artifacts, estimated to incur a financial penalty that approaches \$115,000 (USD) per scanner per year,<sup>2</sup> we hope that future studies may evaluate the performance of such techniques. The MLF data may be employed as a performance indicator to monitor the incidence of repeated sequences, which in our current study, appear to be correlated strongly with motion artifacts. The ability to automatically measure repeated sequences, as detected by the MLFs, is viewed as a strong enabler for expeditiously measuring the efficacy of a proposed intervention in reducing the prevalence of motion artifacts, whether that intervention be an alternate sequence, patient education, patient calming, or a system to restrict and/or track patient motion.

This study has several limitations, including a relatively short evaluation timeframe and the use of a single expert reader; however, the extensive time required to manually score and quantify motion within 1580 sequences was prohibitive in successfully recruiting additional readers. Despite direct instruction that all acquired images be sent to PACS, the current study is also compromised by the observation that 6% of acquired diagnostic sequences were not available for image evaluation, as these were not successfully archived to the PACS. These limitations underscore the need for a more robust method of interrogating and quantifying the rate of MR sequence repetition that reliably captures all image acquisition data, and is independent of human factors as to which sequences are reliably sent to, or omitted from, PACS. While the current study did include the time loss associated with the acquisition of prematurely terminated, incompletely acquired sequences (halted at the discretion of technologists), none of these sequences were sent to PACS, and thus a motion score could not be assigned. The reported results thus likely underestimate the true impact of patient motion on the efficiency of MR systems, particularly those resulting from highly motion-degraded sequences, which were under-evaluated in this study.

The current study emphasized only neurological MR exams for the month of data acquisition. Typical MR systems (including the 2 used in this study) are employed for a variety of imaging protocols. The



**FIG 3.** Repetition ratio depicted as a function of the expert reader-derived motion score, on a per-sequence basis. The repetition ratio can be interpreted as an estimate of the probability that a sequence will be repeated within the same examination, derived from the documented repeats in the modality log files. Error bars represent 95% confidence levels (CL), suggesting that there is a 95% chance that the “real” probability for a repetition lies within the interval.



**FIG 4.** Expert-reader-derived average motion score for the most frequently acquired sequences, where “all” comprises all sequences and “other” includes all sequences that are not assigned to any of the given sequence types. Green color bars represent those sequences that will be repeated in the same examination. Teal color bars represent those sequences that are a repeat of a previously acquired sequence within the same examination, while blue color bars represent those sequences for which no repeat acquisition was performed. AX, axial; DWI, diffusion weighted imaging; FLAIR, fluid attenuated inversion recovery; SE, spin echo; SAG, sagittal. Error bars represent standard deviation. Color version of figure is available online.

current study found, for head examinations only, that over four hours (247 minutes) of scanner time was spent due to the mere acquisition of repeated sequences (not including associated time lost due to requests for the patient to hold still, scanner down-time, and other potential confounders). In future studies, it would be interesting to examine the total effect of motion on a typical scanner for other body parts to measure the full impact on lost time.

In this study, we compared the radiological assessment of motion artifacts to the rate of repeated sequences measured by corresponding MLFs. Despite the limitations of our study, we believe that MLF data may be a useful tool to predict patterns of scanner and sequence performance that may help identify pitfalls of diagnostic imaging in a clinical environment, particularly with respect to patient motion. Such tools would further expedite the evaluation and potential implementation of several proposed motion artifact correction techniques, reduce dependency upon the radiological identification of motion, and optimize scanner efficiency.

### Minimizing commercial interest

All data was collected and analyzed in-house, taken from routine clinical imaging, thus minimizing any potential for the introduction of commercial conflicts of interest.

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