

INTRODUCTION

MRI protocol management is a challenging and resource-intensive task in large enterprise imaging departments. Key challenges include:

1. **Scale** - The number of MRI protocols on each scanner can reach several hundred, spanning neuro, body, cardiac, breast, musculoskeletal, and other applications.
2. **Vendor heterogeneity** - Sequence implementation vary substantially across vendors, making cross-platform standardization non-trivial.
3. **Protocol volatility** - MRI protocols are inherently dynamic. Revisions driven by clinical needs and scanner software upgrades occur frequently, making change tracking labor-intensive and error-prone.

In this work, we present a Python-based platform that automates MRI protocol management and monitoring/inspection. The platform comprises two primary modules:

1. **Protocol Database Module** - Builds and maintains a structured MRI protocol repository, supporting protocol querying, version comparison, update tracking, and archiving.
2. **Protocol Monitoring Module** – Performs real-time protocol consistency monitoring, detecting protocol deviations across scanners and over time within the enterprise.

METHODS AND MATERIALS

Protocol Database Module

The protocol database module is designed to minimize scanner console time and manual input. Protocol information is extracted automatically from DICOM metadata retrieved via the hospital PACS server using the DICOMweb standard, requiring no direct interaction with the scanner console.

Each protocol is stored as a structured YAML file. YAML was selected for its lightweight footprint, human readability, and ease of programmatic parsing and manual editing when required. An example protocol in YAML structure is shown in Figure 1.

All protocol files are indexed in a SQLite database, enabling efficient querying and version control across the protocol library. The user interface of this module is presented in Figure 2.

```
brain_Dementia w NEUROQUANT
```

```
id : premier_024002_brain_dementia_w_neuroquant  
status : draft  
category : brain
```

```
[scanner]  
vendor : GE  
model : SIGNA Premier  
field_strength_t : 3.0  
station : GE [REDACTED]  
serial_number : 0031 [REDACTED] PREMIER2  
software_version : 30/LX/SIGNA_LX1.MR30_1_R01B_2430.c
```

```
[ownership]  
protocol_record_date : 20260504  
reference_study_acc : 26MR [REDACTED]
```

```
[exam]  
study_description : MRI BRAIN W/ CONTRAST  
exam_card : Dementia W/ NEUROQUANT  
receive_coil : 48HAP  
patient_position : HFS
```

```
#- #2 3D SAG T1 NeuroQuant  
seq_mode : 3D  
seq_class : GR/IR  
seq_name : BRAVO  
plane_orientation : sagittal  
nex : 1.0  
scan_time : 3:37  
sar : 0.1  
outputs : REFORMATTED  
[contrast]  
TR_ms : 7  
TE_ms : 3.0  
TL_ms : 600  
flip_angle : 8  
echo_train_length : 1  
bandwidth_hz_per_px : 122  
[geometry]  
fov_mm : 240 | 240  
phase_encoding_direction : AP  
base_resolution : 256  
phase_resolution_percent : 10.0  
kx : 256  
slice_thickness_mm : 1.2  
number_of_slices : 174  
number_of_3d_slabs : 1  
slices_per_slab : 174  
slice_resolution_percent : 100.0  
[acceleration]  
method : ARC  
acceleration_factor_phase : 2.0  
acceleration_factor_slice : 1.2  
acceleration_factor_kx : 1.0
```

Figure 1. An example protocol of YAML structure. It contains a section of protocol information (left panel) and a list of sequence sections (a 3D GRE sequence is shown on the right panel). The acquisition parameters of each sequence are grouped into contrast, geometry, acceleration, cardiac/resp, etc.

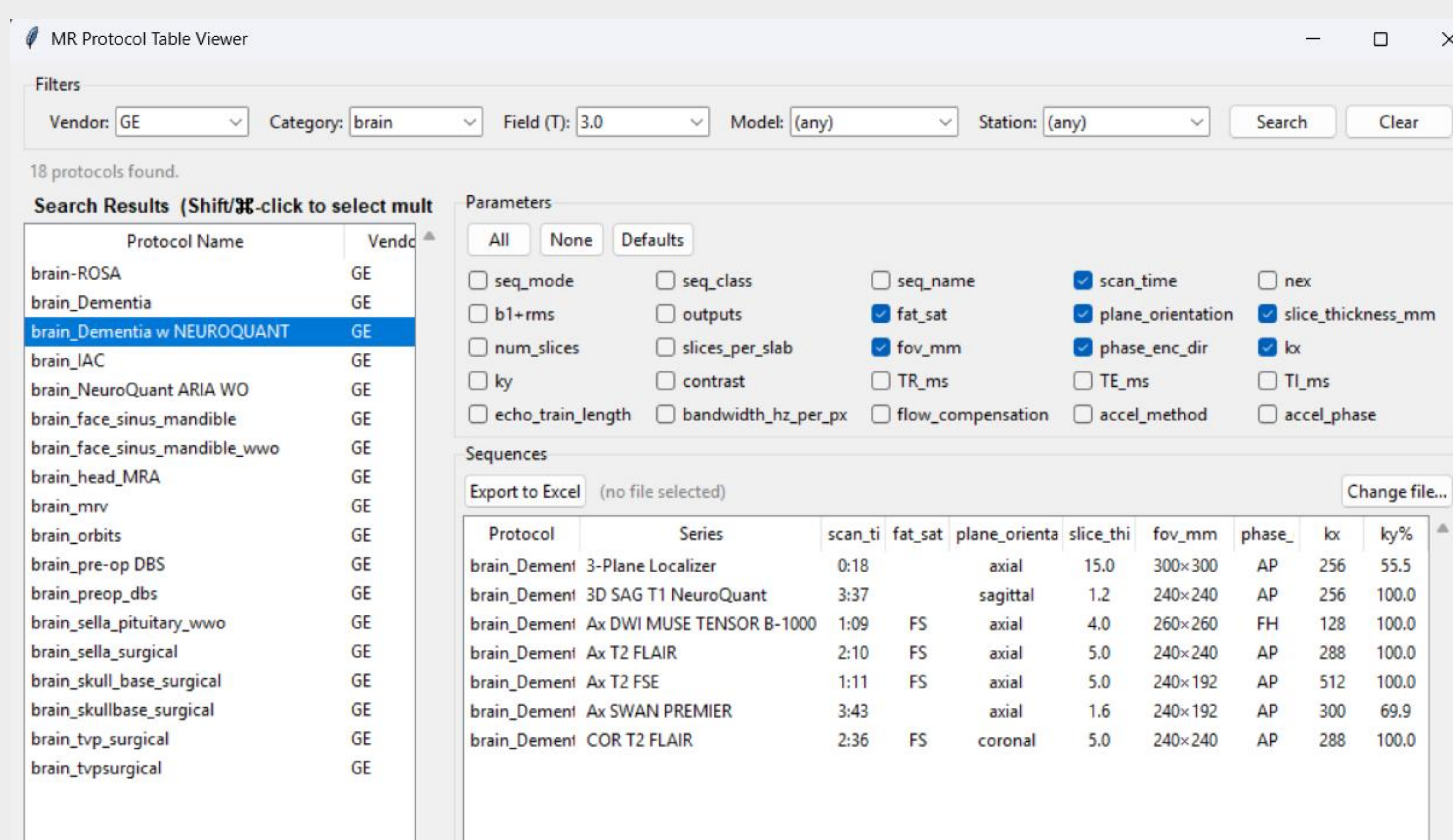


Figure 2. The user interface of Protocol Database Module. The top part is for filters including vendor, anatomy, field strength, magnet model and station name. The bottom left panel lists filtered protocols. Selected protocol is displayed in table format with user-selected parameters. The protocol(s) can also be exported into excel workbook.

Protocol Monitoring Module

The protocol monitoring module is designed to assist MRI physicists in identifying inconsistent protocols across a scanner fleet. The user interface is shown in Figure 3. The module operates through a 4-step workflow:

- **Step 1 — Study Retrieval.** The user specifies a date and body region (e.g., 2026-07-01, Brain). The program automatically retrieves DICOM metadata of all MRI studies matching those criteria via DICOMweb.
- **Step 2 — Sequence Classification.** Each series within a study is classified into a discrete sequence type (e.g., T1_FSE, T2_FLAIR, 3D_T1_GRE, DWI) using a pre-trained Random Forest classifier. Input features include repetition time (TR), echo time (TE), inversion time (TI), echo train length (ETL), flip angle, diffusion directions, and dynamic phases.

To train the sequence classifier, brain MRI studies acquired between June 1–20, 2026 were retrieved from the PACS server. A total of 988 series were allocated to the training set and 638 series to the test set. All series were manually labeled into 17 discrete sequence types. Hyperparameter tuning was performed and the model performance was evaluated on the test set.

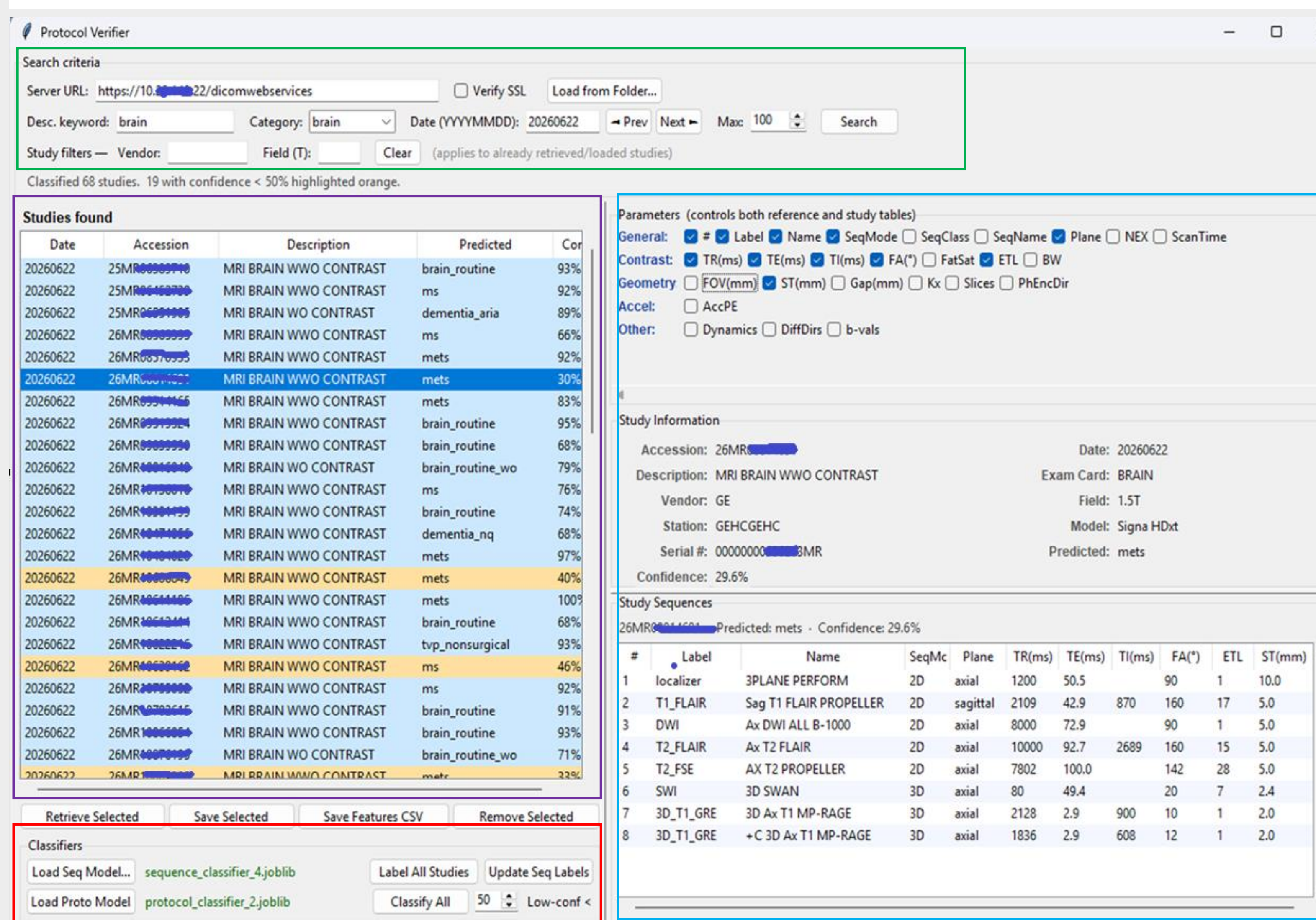


Figure 3. The user interface of Protocol Monitoring module. The top part (green box) is for study search criteria. Retrieved studies can be further filtered by vendor and field strength. Retrieved studies (purple box) first go through sequence classification then protocol classification with pretrained models (red box). Studies with protocol classification confidence lower than 50% are flagged with orange color. Protocol parameters of selected study are shown on the right panel for inspection (blue box).

- **Step 3 — Protocol Classification** A second Random Forest classifier identifies the clinical protocol. Each study is transformed into a fixed-length feature vector. For each predefined sequence type, the feature vector encodes: series count per sequence type, series count stratified by imaging plane, slice thickness, DTI directions, and dynamic phases. To train the protocol classifier, the same cohort of brain MRI studies for the sequence classifier was used. The training set comprised 96 studies spanning 16 protocol types, and the test set comprised 70 studies.
- **Step 4 — Protocol QA** Studies with a classifier confidence below 50% are flagged for manual review. The detailed acquisition parameters of a flagged study is displayed and inspected for follow-up action. (Figure 3)

RESULTS AND DISCUSSIONS

The test set accuracy of sequence classifier was 100%. The test set accuracy of protocol classifier was 92.9%.

68 brain MRI studies from June 22, 2026 were retrieved across 18 scanners enterprise-wide. Of these, 19 studies (27.9%) returned a classifier confidence below 50% and were flagged for manual review (Table 1).

Inspection of flagged studies revealed several protocol inconsistencies from reference protocols:

- Station **F** and **M** used 3D T1 GRE sequence in place of 2D FSE for pre and post contrast imaging;
- Station **P** used GRE-EPI sequence in place of SWI for hemorrhage evaluation;
- Station **G** contained an additional SWI sequence in the Dementia protocol.

Classification errors were attributable to two main factors.

1. *Limited training data coverage*: certain protocols or sequences were not represented in the training corpus.
2. *Inherent protocol complexity*: some protocols differ only subtly in their sequence composition, making discrimination challenging. Additionally, sequences repeated within an examination introduced variability in the per-study feature vectors that was not accounted for during training.

Scanning Protocol	Predicted protocol	Confidence	Protocol issue	Station
routine w and wo	met	30%	3D T1 pre/post replaced 2D T1	F
IAC	met	40%	not a brain protocol	M
ms	ms	46%	Extra cor t1	H
routine w and wo	met	33%	3D T1 pre/post replaced 2D T1	M
dementia wo	dementia_wo	37%	Extra SWI	G
dementia wo	dementia_wo	37%	Extra SWI	G
tumor	routine_wo	44%	missing Cor T1	P
TIA	tv _p _nonsurgical	32%	TIA is not in training set	G
routine_wo	routine_wo	41%	Missing SWI	E
routine_fast	routine_wo	25%	EPI GRE used for hemorrhage	P
routine w and wo	met	22%	extra Cor T2 sequence	M
routine_wo	routine_wo	18%	correct	M
routine_fast	met	32%	3D T1 pre/post replaced 2D T1	F
skull base	brain_routine	32%	not a brain protocol	F
routine w and wo	met	33%	3D T1 pre/post replaced 2D T1	M
IAC	met	41%	not a brain protocol	M
routine_wo	routine_wo	41%	correct, w several repeats	R
routine w and wo	dementia_wo	48%	correct	C
meg	meg	35%	correct	H

Table 1. Inspection results of flagged studies from Protocol Monitoring module.

CONCLUSIONS

The proposed platform transforms MRI protocol management by automating protocol retrieval, archiving, querying and version control, thereby reducing manual workload and minimizing the risk of human error. The protocol monitoring module has demonstrated its clinical utility in brain protocol consistency checking across a multi-vendor, multi-site scanner fleet. Further development could extend the platform's capabilities to encompass image quality control functions, supporting a comprehensive and integrated approach to MRI quality assurance.

REFERENCES

1. Fei Gao, et al. "MR efficiency using automated MRI-desktop eProtocol", Proc. SPIE 10138, Medical Imaging 2017, vol 10138