

Thank you very much for the opportunity to update our manuscript type to Datasets and Software and re-submit, comments and our responses are below

Editor's comments will be in italics

Author's comments will be in green

Manuscript text will be indented

...it occurred to me that the Journal has been considering development of a new manuscript type related to "Medical Physics Data Sets and Software." I think this manuscript could be well suited to that manuscript type, rather than a Technical Note.

However, the process for the Journal to create this manuscript type is just getting underway. I believe the Editors in Chief are in agreement that such a type will be created.

Therefore, I recommend the following for this manuscript to be considered further:

1. Remove "Technical Note" from the title.

We have removed 'Technical Note' from the title

"DICOM Attribute Manipulation Tool: Easily Change Frame of Reference, Series Instance, and Study Instance UID"

2. Rewrite the structured abstract as follows:

- Purpose: brief summary description of the software, including purpose, scope, target audience, and potential applications.

- Validation Methods: Briefly describe procedures for development and validation of the software, including sample datasets.

- Data or Software Format and Usage Notes: Describe software format / language, development and run environment, and link to repository

- Potential Applications: Brief description of proposed scientific and/or clinical applications of the dataset and important limitations.

We have rewritten the abstract to this new structure, as well as added a publicly available MRI dataset which we used to validate the software

Purpose: In radiation oncology, the integration and registration of multiple imaging modalities is a crucial aspect of the diagnosis and treatment planning process. Often, these images are inherently registered, a useful feature in most cases, but possibly a hindrance when manual adjustments and registration modifications are required. To break this registration requires expert knowledge of file structure or specialized software, posing challenges and potential errors in accidentally or unnecessarily changing other attributes. Barring these changes, the clinic would have to make do with imprecise registrations which add to overall treatment uncertainty.

To address these issues, we present a novel tool designed to simplify the task of changing three often edited attributes: the frame of reference, the series instance unique identifier, and the study instance unique identifier. The tool features an intuitive user interface that empowers practitioners, regardless of their expertise, to effortlessly modify these three commonly edited values.

Validation Methods: Publicly available brain MRI images (https://figshare.com/articles/dataset/Data_from_An_Investigation_of_Machine_Learning_Methods_in_Delta-radiomics_Feature_Analysis/9943334) were used as testing images. The ability to change the frame of reference, series instance identifier, and study instance identifier using the program was evaluated with both the RayStation treatment planning system and MIM.

Software format and usage notes: The program is written in C#, easily distributed via GitHub or Google drive and compatible with any Windows computer with .NET 4.8 (the standard as of 2023).

Potential applications: This innovation holds promise for improving the overall workflow efficiency and safety within radiation oncology and radiology, where breaking the frame of reference or changing the series/study unique identifiers is a common occurrence.

3. Revise the body text appropriately throughout according to the "Datasets and Software" manuscript type.

Unfortunately, at this time there is not explicit instructions on the Author Guidelines page for this manuscript type. We thought it would be a fair guess to make similar changes as to those requested in the abstract.

We have restructured our manuscript to the following format: Purpose, Validation Methods, Software format and usage notes, and Potential applications.

Similarly, we have reformatted the manuscript itself to follow similar headings.

Line 70-75: We have included a link to publicly available MRI data that we used to validate our model.

The program was tested with publicly available brain MRI scans available here: https://figshare.com/articles/dataset/Data_from_An_Investigation_of_Machine_Learning_Methods_in_Delta-radiomics_Feature_Analysis/9943334. This dataset contains several T1

and T2-FLAIR images. Our program was then used to change the series instance UID, frame of reference UID, and study instance UID.

Verification of the edited DICOM was evaluated within the RayStation treatment planning system. Further evaluation was performed with MIM to ensure that only the desired attributes were changed in the process.

Line 79: We added a new header 'Software Format and Usage Notes'

Within this header we also made a few small changes that we felt better explained the functionality of the program.

Line 128: Discussion -> Discussion and Limitations

We expanded the discussion to include the limitations of not running on a MAC/Linux system.

The program is designed to run on the Windows operating system and not MAC/Linux. There is concern that institutional internet security division (ISD) may prevent the installation of this program onto a computer. Within our institution we were able to circumnavigate this issue by placing the compiled program on a network drive location which was accessible to the team, which runs without the requirement of installation.

Line 133: We added a section on 'Potential applications'

The program presented here represents an easy, user-friendly method of changing three commonly changed DICOM attributes with a vendor agnostic solution. Because we have hosted the tool on GitHub, any user can provide feedback and new attributes can easily be added to the program in the future.

We have implemented this solution within two clinics: University of California, San Diego and University of North Carolina, Chapel Hill with positive feedback from the physics and dosimetry teams. The program is freely available and open for input from the community via GitHub, allowing future updates and improvements as requested.