# Abstract

**Background:** Consistency of nomenclature within radiation oncology is increasingly important as big data efforts and data sharing become more feasible. Automation of radiation oncology workflows depends on standardized contour nomenclature which enables toxicity and outcomes research, while also reducing medical errors and facilitating quality improvement activities. Recommendations for standardized nomenclature have been published in the American Association of Physicists in Medicine (AAPM) report from Task Group 263. Transitioning to TG-263 requires creation and management of structure template libraries and retraining of staff, which can be a considerable burden on clinical resources. Our aim is to develop a program that allows users to create TG-263 compliant structure templates in English, Spanish, or French to facilitate data sharing.

**Methods**: 53 pre-made structure templates were arranged by treated organ based on an American Society for Radiation Oncology (ASTRO) consensus paper. Templates were further customized with common target structures, relevant OARs (e.g., Spleen for anatomically relevant sites such as gastroesophageal junction or stomach), sub-site specific templates (e.g. partial breast, whole breast, intact prostate, postoperative prostate, etc.) and brachytherapy templates. An informal consensus on OAR and target coloration was also achieved, though color selections are fully customizable within the program.

**Results:** The resulting program is usable on any Windows system and generates template files in practice-specific DICOM or XML formats, extracting standardized structure nomenclature from an online database **maintained by members of the TG-263U1 Task Group which ensures continuous access to up-to-date templates**.

**Conclusions:** We have developed a tool to easily create and name DICOM-RT structures sets that are TG-263-compliant for all planning systems utilizing the DICOM standard. The program and source code are publicly available via GitHub, encouraging feedback from community users for improvement and guide further development.

# Introduction

The creation of treatment plans in radiation oncology requires the delineation of regions of interest (ROIs), which primarily represent structures such as treatment volumes (TVs) and organs at risk (OARs). Proper labeling is important in the evaluation of generated treatment plans, both for comparing plans from other individuals/institutions, and for curating large data sets from multiple institutions. With large datasets, incorrectly labels are extremely difficult to identify, and so proper and consistent labeling is exceedingly important. Standardized nomenclature also enables automated structure segmentation and treatment planning workflows.

While Digital Imaging and Communications in Medicine radiation therapy (DICOM-RT) standards specify data formats required to electronically communicate information about the structures, users are individually responsible for creating and naming these in the treatment planning systems (TPS). Labeling structures manually is tedious, error-prone (e.g., ‘Brian’ instead of ‘Brain’), and variable (e.g., ‘Lung\_R’ vs ‘Right Lung’)1.

While many TPS provide the option to maintain templates (groupings of specific treatment volumes and OARs), these templates are often manually created and maintained and not universally shared between institutions. Therefor, the creation process can be relatively time-intensive, and updates remain vulnerable to the issues listed above.

The American Association of Physicists in Medicine (AAPM) has published ‘Standardizing Nomenclatures in Radiation Oncology’1, a report from Task Group 263 (TG-263) in order to create a standard nomenclature for both treatment volumes and OARs. While adoption of the standard nomenclature has popular support, in a recent survey2 conducted by the TG-263U1 Task Group, the majority of respondents had not yet adopted the standardized nomenclature. From this survey, the largest difficulties were lack of time/resources to create new templates, and/or difficulty with retraining staff if templates were not available.

Our aim in this work is to lower the barrier to adopt standardized TG-263 nomenclature to facilitate data sharing and consistency. This includes tools to create patient-specific structure sets, import RT structure sets on an included anonymized patient to create templates, or update Varian eXtensible Markup Language (.xml) internal templates in English, Spanish, or French. The program presented (written using C#7) runs on any Windows system and ensures compatibility with all TPS by utilizing the DICOM-RT standard.

# Methods

To standardize the recommended targets and OARs, a subsection of the TG-263 group created 53 pre-made structure templates for external beam and brachytherapy sites. These templates are based on an American Society for Radiation Oncology (ASTRO) consensus paper3. Templates were further customized with common targets and relevant OARs. Additional subsite-specific templates (e.g., partial breast, whole breast, intact prostate, postoperative prostate, etc.) and brachytherapy templates were created. Brachytherapy templates were created with the guidance of the TG-263 brachytherapy members who share membership on the AAPM Brachytherapy Subcommittee and Working Group on Brachytherapy Clinical Applications. Common prefixes of template names include “Targets” (including 1 dose level, 2 dose levels, and 3 dose levels, and 4 dose level templates), “AbdPelv” (i.e., Abdomen and Pelvis primary disease sites), “Brachy” (i.e., Brachytherapy), “CNS” (Central Nervous System), “Extremities”, “H&N” (Head and Neck), and “Thorax”. Table S1 provides examples of all 53 provided site-specific templates at the time of publication.

An online spreadsheet, Airtable6, was utilized to house all templates in an evergreen fashion, which will be continually updated by members of TG-263 as recommendations continue to develop over time. by While the Airtable can be downloaded by anyone, only specific members of the working group with administrative privileges can make changes to the spreadsheet. The online spreadsheet containing the raw data for all templates may be found at the following link: [bit.ly/StructureNaming](https://airtable.com/shrojSoXyfnHHKzJV). Congruent with the ASTRO consensus paper3, there are two categories of structures: Recommend, which should be contoured in all adult definitive cases and may assist with organ selection for palliative cases; and Consider, for structures considered on a case-by-case basis.

An informal consensus on OAR and target coloration was achieved. Twenty-four colors were utilized in total (Supplementary Figure 1), loosely based on the 24 default colors available within Pinnacle. Target color selection (Supplementary Figure 2) was based on discussions with physicists and physicians at UCSF, MDACC, and Michigan, and reflects the available literature5. Due to the informal nature of color selection and difficulty achieving consensus, colors remain fully customizable within the program.

The program workflow is broken down into three major steps, as illustrated in Figure 1: (1) the population of templates (templates hereafter refers to a collection of structures: being ROIs or target volumes), (2) manipulation of ROIs within those templates, and (3) running a DICOM patient-specific server, and/or creating loadable DICOM/XML files. Resulting output is compatible with all treatment planning systems which utilize the DICOM-RT standard.

, see below

The language of the structures within each template can be selected as English, Spanish, or French, with English as default if Spanish or French translations are not available. Per TG-263, structures can be referred to as ‘primary’ (e.g., ‘Canal\_Anal’) or ‘reverse’ order (e.g., ‘Anal\_Canal’). After discussion with the piloting physicians and physicists, the program orders the structures using a combination of primary and reverse orders to best reflect natural language for certain structures (e.g., Anal\_Canal, Bowel\_Bag) along with organ-first naming, so that laterality did not dictate sorting order withing TPS (e.g., "Lung\_R” favored over “R\_Lung”). However, users can choose to import individual structures in either primary or reverse order according to their institutional preference.

# Results / Program Workflow

Ultimately, there are two main routes to use this program in practice. Some clinics may wish to utilize the program to create patient-specific structure sets that appears in a monitored folder. Other clinics may prefer to utilize the TPS to assign structure sets to patients, as the program may be used to automatically build over 50 site-specific structure sets which can be directly imported (and saved) to their TPS in a few clicks. An excel file of the site-specific structures as of the time of publications is available in Supplementary Table 1, although it is recommended that the user refer to the online AirTable in case of updates.

## Program Piloting

The program was successfully piloted at five institutions and enabled template creation using the Eclipse, Raystation, and Pinnacle systems. Users reported installation and setup times of less than ten minutes after watching the provided video tutorials, with no additional assistance required. To avoid institutional IT restrictions, most users downloaded the program onto non-hospital devices then transferred the created template files. Minor discrepancies in structure settings and colors were identified and corrected during this testing phase, and suggested improvements were implemented.

A series of video tutorials explaining each step of the program, including installation, is available on YouTube. These videos can be accessed through the link at the bottom of the program GitHub page: (**anon for review)** and are continually updated to demonstrate current features and performance of the program. A graphical abstract of the entire workflow is shown in Supplementary Figure 3.

## *Step 1: Creation of Template*

The program comes with a library of 53 premade structure set templates designed for specific anatomical sites and clinical indications which can be loaded from our online spreadsheet as described above.

A user can create their own template in several ways; 1) Copying a pre-made structure templates from the online Airtables, 2) creating a new template from a previous RT structure file or Varian xml file or 3) manual creation.

All default templates load in ABC order, arranged by the name of the template (Table S1). This plugin was coded to alleviate tedious manual work in exporting Varian templates to the program or can be used to populate the program from these Varian templates.

## *Step 2: Manipulation of ROIs*

After template(s) has been built, ROIs are listed alphabetically grouped within their Interpreted Type11 (PTV, CTV, Organ, etc.). This means any ROI with a type of PTV will be listed above CTV, then GTV, and then all other types, as shown in Figure 2. The list of ROI Interpreter Types can be found in the DICOM Standard Browser.11 If utilizing the premade structure sets, Recommend structures will populate first in alphabetical order as default-checked, while all Consider structures will populate below in alphabetical order as default-unchecked, per the ASTRO consensus paper.3

Additional ROIs can be added via the program interface or selection of an existing RT Structure file. This allows the user to easily combine structures from several RT Structure files into a single template.

## *Step 3a: Running as a server: Setting DICOM paths and requirements*

Some TPS do not enable the internal creation of site-specific templates. For these cases, the program can function as a server with which to create a structure set for any patient image that appears in a monitored folder location.

In server setup, the program will loop through each of the monitored paths defined within each template. A file system watcher monitors for file changes at each path, monitoring file changes to ensure all files are uploaded before processing begins. This file system watcher ensures the entire DICOM dataset is present before an RT structure is generated, regardless of network latency or scan size.

If DICOM images are consistently placed within a single folder location, the users can define values within the Series Description or Study Description to indicate which template should be created. For example, including the tag ‘Breast\_CW’ in the Series Description during acquisition would indicate the program to create the ‘Breast\_CW’ template.

DICOM files are internally separated based on the series instance UID. This ensures that a unique RT structure file will be made, even if multiple scans are placed within the same folder. For each unique series instance UID, a new RT-Structure file is created with the form ‘{Structure template name}\_{UID}.dcm’.

## *Step 3b: Creating loadable DICOM-RT*

If the user’s TPS enables the creation of templates, they can utilize the anonymous CT creator to generate a DICOM-RT file for each template using the ‘Create folder with loadable RTs’. This will create a folder with a previously anonymized four-slice CT and generate the available structure templates as described above.

## *Step 3c: Creating/Editing Varian XML templates*

The user may also create a series of loadable XML files by selecting the ‘Create folder with loadable Varian Xmls’. Generated .xml files follow the 2001 xmlscheme instance version 1.2. The default .xml file is present within our GitHub page named ‘Structure Template.xml’. By default the program will attempt to find the current Varian directory of .xml files, allowing for easy uploading and editing.

Detailed descriptions of what is occurring ‘behind the scenes’ can be found within the supplementary documentation.

## Creation of DICOM-RT files

DICOM-RT files are created via the publicly available FellowOakDicom package8, and a C# wrapper for the ITK coding package, SimpleITK9. The framework for creating RT Structure files in Python has been previously reported10, and a similar process is used here.

# Discussion

In this paper, we describe the first reported effort to create open-source software to create and maintain libraries of patient-specific treatment planning structure templates to lower the barrier to adoption of TG-263 standardized nomenclature and facilitate data sharing for toxicity and outcomes research. All outputs are consistent with TG-263 and TG-263U1 guidelines for nomenclature of structures, which is endorsed by multiple professional societies (AAPM, AAMD, ASTRO, ESTRO). This software was tested at multiple sites and ensured to be compatible with Pinnacle v16.2.1, Raystation v12.1, and Eclipse v15.6, although output should be compatible with all TPS utilizing the DICOM-RT standard. Early rollout required hands-on-training with video conferences to demonstrate how to use the software. Therefore, we had to create videos for other physicists to watch to learn how to use the software and hope this paper serves as a narrative review of its capabilities.

There have been previous reports of software tools used to homologate sets of previously treated structures to support retrospective data analysis12. There have also been tools created within the TPS to verify that structures names comply with TG-26313. With Open RT Structures, clinics can ensure that clinical standards are met, enable automated workflows, and facilitate data pooling and outcomes research. Furthermore, we hope that this tool can help reduce medical errors and facilitating quality improvement activities.

The Open RT Structures program reduces the burden of manual creation of structure templates by providing TG-263 designed templates and allowing users multiple pathways to ease the creation of user-defined templates. Templates can be easily edited in case of future changes, and a reasonable set of default TG-263 templates can be refreshed using the ‘Load Online Templates’ feature.

The largest risk that we could foresee is that the program continually updates its own previously generated RT Structure files. To ensure this does not happen, the program internally tracks which images have been previously viewed (via Series Instance UID) and creates each RT Structure file with that same Series Instance UID. The program is coded to check if each template RT Structure file already exists, and so prevents a continuous recreation of the same set. As an additional safety measure, the software is coded to only create new RT structure files and will not open or edit an already existing RT Structure file, and so presents no risk to existing work flows present by the user.

To support large-scale, multi-institutional, and international data sharing, the Open RT Structures enables users to create templates in English, French, or Spanish. French and Spanish language versions also follow TG-263 guidelines to enable easy mapping of structures between languages. The framework of Open RT Structure using AirTable enables the quick integration of TG-263 updates and new languages. The inclusion of other languages will be an ongoing effort within both TG-263 and Open RT Structures, along with field testing at several clinical sites.

# Conclusion

We have created open-source software that may reduce the burden of creating and maintaining TPS structure templates and facilitates the adoption of TG-263 standardized nomenclature. This program allows clinics to quickly create templates in English, Spanish, or French and allows for customization of laterality and color schemes. Both patient-specific DICOM RT Structure files and Varian XML template files can be easily created.

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