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rtdsm: An open-source software for dose-surface map generation and analysis

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INTRODUCTION

- Dose surface maps (DSMs) are valuable tools to visualize dose to hollow organs.
- DSMs have been used to identify spatial dose metrics predictive of radiation toxicities in the rectum, bladder, and vagina [1,2,3].
- ***However,*** calculation workflows remain largely in-house with notable methodological differences between research groups.

AIM

To develop an open-source DSM calculation code base capable of reproducing commonly-published DSM calculation and analysis methods.

METHOD

Design Process

A literature review was conducted to identify:

1) Dominant DSM calculation methodologies,
2) Common calculation frameworks and existing open-source packages,
3) Additional functionalities to include to improve user experience.

DSM Calculation Workflow

A modular branching workflow was designed to support the two dominant DSM slicing methods: planar and non-planar (**Fig 1**). Individual functions were designed with high customizability to allow users to tailor DSM resolution to their research needs.

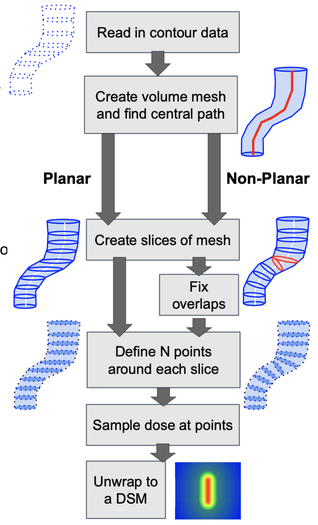

Figure 1: *Calculation workflow used to create DSMs (both planar and non-planar)*

Analysis Functionalities

The following functions were developed to support common DSM processing and analysis tasks:

- Equivalent dose conversions,
- DSM addition & subtraction,
- DSM feature extraction,
- Permutation testing.

RESULTS

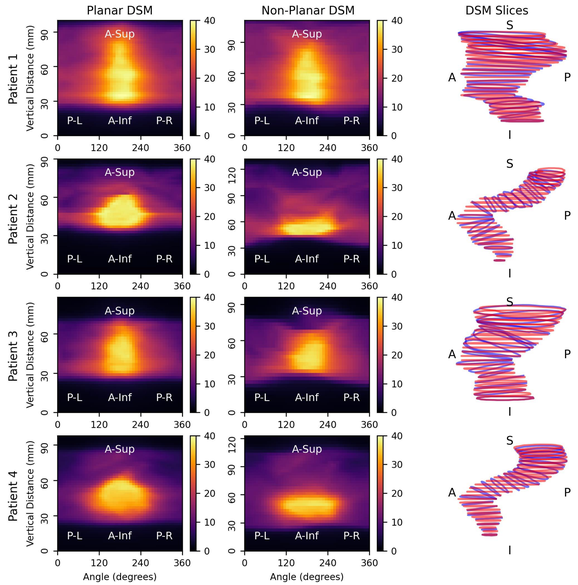

Figure 2: *Planar (left) and non-planar (centre) DSMs created from the rectums of four patients who underwent 36.25 Gy/5 fr SBRT. Every second slice used to construct the DSMs are shown in red for the planar style and blue for the non-planar (right)*

Dose Surface Maps (DSMs)

Examples of planar and non-planar DSMs of a rectum created by *rtdsm* are shown in **Figure 2**. Calculation time per DSM is under 8 seconds, making DSM calculation for large datasets feasible.

DSM Conversion and Combinations

rtdsm allows for visualization of inter-cohort dose variations through built-in functions to compute cohort averages and differences. DSMs can also be easily converted to EQD_{2Gy} in order to visualize differences between different fractionation schemes (**Fig 3**).

Analysis Functionalities

rtdsm supports the two most common DSM analysis approaches used in DSM literature: feature and pixel based. For feature-based analysis, *rtdsm* calculates the nine most common DSM features based on the definitions of Buettner *et al* [1], including cluster area and span (**Fig 4**). For pixel based analysis, *rtdsm* comes with a built-in implementation of multiple comparison permutation testing (MCP), which allows for direct pixel-to-pixel comparisons between datasets to identify statistically different subregions of dose.

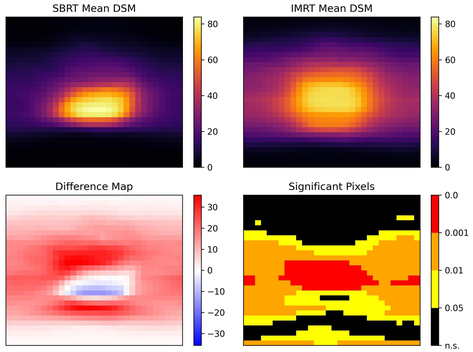

Figure 3*: Comparison of rectal dose between a 10 patient prostate SBRT cohort (36.25 Gy/5 fr) and a 10 patient prostate IMRT cohort (60 Gy/20 fr). The mean DSM of each cohort and their mean difference map are shown in EQD* $_{2Gy}$*. A map of the DSM pixels found to differ significantly between the two cohorts by MCP analysis are also shown.*

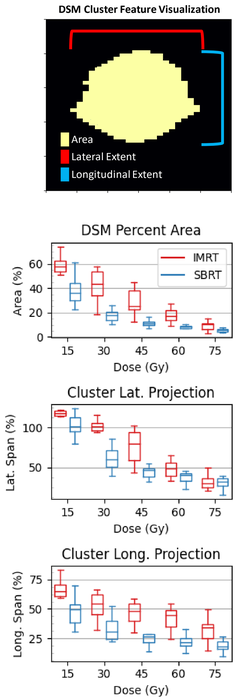

Figure 4: (a) *Visualization of the dose cluster based features derived from DSMs.* ***(b-d)*** *Boxplot distributions of the DSM cluster features for the SBRT and IMRT cohorts across multiple dose levels.*

CONCLUSIONS

- *rtdsm* is a standalone python software package that provides the essential functionalities required to perform a DSM study
- The code is available open-source at https://github.com/McGillMedPhys/rtdsm and comes with full documentation and a library of tutorials to make for easy implementation
- *rtdsm* has the potential to improve the reproducibility of and the access to DSM-based research in medical physics and radiation oncology

REFERENCES

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2) Palorini F, Cozzarini C, Gianolini S, et al. *First application of a pixel-wise analysis on bladder dose-surface maps in prostate cancer radiotherapy.* Radiother Oncol. 2016;119(1):123-128.
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CONTACT INFORMATION

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