

Python software for analysis of radiation treatment using radiobiological model

Sougoumarane Dashnamoorthy¹, Karthick Rajamanickam¹, Raghavendra D Sagar²,
Durga Prasad sahuo³, Ebenezar Jeyasingh⁴, Venkatraman Pitchaikannu⁵

¹Thangam Cancer Hospital, Namakkal, Tamil Nadu, India

²JN Medical College, KLE Academy of Higher Education and Research, Belagavi, Karnataka, India

³Department of Radiation Oncology, Acharya Harihar PG Institute, Mangalabag, India

⁴PG & Research Department of Physics, Jamal Mohamed College (Autonomous), Tamil Nadu, India

⁵Department of Medical Physics, Bharathidasan University, Trichy, India

ABSTRACT

Introduction: It was a century ago, whether used separately or in combination with other medicines, that radiotherapy evolved into a successful cancer treatment. In traditional radiation therapy, a Dose Volume Histogram (DVH) is utilized for quantitative analysis of the treatment plan after the adoption of the treatment planning system. An isodose distribution is also used for qualitative analysis and evaluation of the treatment plan during this phase. The right treatment plan is assessed using physical and radiobiological models by in-house software developed for radiation oncologists.

Materials and Methods: The first process was the OSCAR (Object Scoring with Coloured Area of Regret) treatment planning system, developed by Theratronics International, Kanata, Canada in 1991, which was one of the numerous plan evaluation software programs that were established in the field of radiation medicine to analyse and regularize the dose distribution. Many plan evaluation programs have been created over the developing years, with the commercial software used primarily and the primary inclusion MATLAB, and very few have been created using Microsoft Visual Basic, C++, and Java. As a substitute for MATLAB, Python is utilized because it is freely available and has no commercial value.

Results: This study's primary objective is to personalize the radiobiological effects to predict each patient by using the DVH data, which are now accessible, to improve the overall performance of the prior model. Several programming languages were initially investigated to check the portability and quick program execution to illustrate the novel ideas. It was discovered that Python was adequate for this research even if it has no economic value compared to other languages. The software receives the DVH data in text format as an input, and for convenience, it displays the output using a variety of Python widgets.

Discussion: The major radiobiological parameter values, TD50/5, slope parameter (m), and volume parameter (n), are used to calculate the Tumour Control Probability (TCP) and NTCP values of numerous targets and organs from their respective DVH statistics using Python software. The evaluation of the physical indices of the treatment plans, the AAPM, RTOG, and QUANTEC protocols were used in a clinical analysis for the execution of treatment plans.

Conclusion: The problem in the previous plan evaluation tool was fixed by the custom-made PYTHON program used for this research investigation, which also added clinical and radiobiological understanding of the treatment plan. The software produces a report using Microsoft Excel for the comprehensive radiobiological and dosimetric plan evaluation study for cancer patients.

Keywords: DVH, python, eclipse, tkinter, oracle, IMRT, rapid arc

Address for correspondence:

Ebenezar Jeyasingh, Assistant Professor

PG & Research Department of Physics Jamal Mohamed College (Autonomous), Affiliated to Bharathidasan University, Tiruchirappalli 620020, Tamil Nadu, India, E-mail: ebey_ebenezar@yahoo.com, Contact No: +91-9865007640

Word count: 3404 **Tables:** 03 **Figures:** 11 **References:** 13

Received: 08 February, 2024, Manuscript No. OAR-24-127269

Editor Assigned: 13 February, 2024, Pre-QC No. OAR-24-127269 (PQ)

Reviewed: 18 February, 2024, QC No. OAR-24-127269 (Q)

Revised: 26 February, 2024, Manuscript No. OAR-24-127269 (R)

Published: 05 March, 2024, Invoice No. J-127269

INTRODUCTION

Internationally, there is a propensity to incorporate daily radiotherapy with predictions from radiobiological models. In-depth use of cell cycle forecasts can increase the likelihood that a tumor can be controlled, leading to more successful therapies and fewer patient delays due to side effects. This is demonstrated experimentally and theoretically using radiobiology research. The method of image processing (using MAT Lab) of structures and radiation dose calculation during the treatment period is a very crucial phase in radiotherapy. Additionally, many commercial software solutions and methods have been created for these procedures [1-4].

Radiation oncologists and medical physicists can use radiobiological models, such as Tumor Control Probability (TCP) and Normal Tissue Complication Probability (NTCP), and biological variables for their clinical applications in conventional or hypofractionated radiotherapy to predict specific treatment schedules with a high TCP and a low (NTCP) [5, 6]. The use of radiobiological models has been demonstrated as a significant factor in deciding whether to accept or to reject a treatment plan for radiotherapy. Importing data from the DVH, which was created through the planning of the Clinical Target Volume (CTV), Planning Target Volume (PTV), and all of the organs that are at risk, enables the production of generalized predictions about future therapy. This work aims to provide thorough, user-friendly internal software for DVH analysis and clinical application of the radiobiological model for treatment plan quality analysis [7].

One needs accessories to assess the potential clinical outcome of any radiation treatment to take full advantage of the available technology and optimize and individualize radiation treatment. Increasing the effectiveness of radiation therapy depends on improving our understanding of dose-volume factors affecting tolerance and local control and tools that quantify the probability of an endpoint of interest, e.g., Tumor Control Probability (TCP) and Normal Tissue Complication Probability (NTCP).

The effects of dosage on inhomogeneity can also be explained by phenomenological models, such as dose-volume histogram reduction methods based on the power law. It is anticipated to claim that it is nearly hard to construct a thorough biological model of tissue reaction to radiation; hence, these phenomenological approaches may present a better or at least less model dependency

[8].

In-house Python-based software was created to record persistent features identified in earlier treatment plan assessments. This application is based on the input value for the Dose-Volume Histogram (DVH), which was exported as a text file from the radiation Treatment Planning System (TPS). However, radiobiology plan evaluation is not included in the majority of commercial treatment planning systems [9]. A radiobiological plan evaluation tool is fairly costly to buy compared to the cost of a treatment planning system. The lack of a built-in radiobiological model for usage in clinical applications and for research purposes is largely addressed by this Python program.

MATERIAL AND METHOD

In-house Python-based software was created to record persistent features identified in earlier treatment plan assessments. The application is based on the input value for the Dose-Volume Histogram (DVH), which was exported as a text file from the radiation Treatment Planning System (TPS). However,

radiobiology plan evaluation is not included in the majority of commercial treatment planning systems. A radiobiological plan evaluation tool is fairly costly to buy in addition to the treatment planning system. The lack of a built-in radiobiological model for usage in clinical applications and for research purposes is largely addressed by this Python program [9].

The tables in the Oracle database include the radiobiological parameters for healthy and cancerous tissue at various treatment sites, which are enabled to run the program. The Python program is structured using object-oriented programming, also known as Class Object (an extensible program-code-template for creating objects), as shown in Table 1, which provides initial values for state (member variables) and implementations of actions (member functions or methods) to integrate with various modules of execution from Python libraries, as shown in Table 2. [10-12].

The Python application for this study is run on Windows, Mac, and Linux using the Integrated Development Environment (IDE) software PyCharm 2020.1.5 (COMMUNITY EDITION), which is also freely available as shown in Table 2 and Table 3.

Tab. 1. Major user-defined class objects defined in the Python application	Class Object	Description
	dvh_statistic	This class is used to create graphs, calculate formulas from various radiobiological models and save data in arrays along with Oracle tables
	GUI_app	This class serves as a building block for creating tools with graphical user interfaces that display output from program execution, i.e., interfacing both the front and back ends.
	dose_constrain	This class object is used to deliver data to a GUI interface for the evaluation of physical dose from the standard radiation oncology dose tolerance protocol, i.e., physical plan evaluation.
	GUI_label	This class object is programmed with GUI-driven interactions like a button press, mouse movements, checkboxes, dropdown boxes, and out-of-focus and in-focus text and label functions.

Tab. 2. Python libraries applicable for Python Application	Library function	Description
	Numpy array	Numpy array library is used to create graphs, calculate formulas from various radiobiological models and save data in arrays along with Oracle tables
	Tkinter	Tkinter library serves as a building block for creating tools with graphical user interfaces that display output from program execution, i.e., interfacing both the front and back ends.
	Oracle	Oracle library object is used to load the data from oracle to GUI interface for the evaluation of physical dose from the standard radiation oncology dose tolerance protocol, i.e., physical plan evaluation.
	Matplotlib	Matplotlib library object is programmed with GUI-driven interactions displaying 2-dimensional graph in Tkinter frame.
	Openpyxl	Openpyxl is a Python library that is used to read from an Excel file or write to an Excel file for report generation

Tab. 3. Python libraries applicable for Python Application	Sl.No	Description
	1	From a single DVH text file, the Python application reads many normal and tumor structures.
	2	The probability functions for the dose volume histogram of the normal and tumor structures are shown on the graph.
	3	A toggle button allows users to display differential and cumulative DVH in a single graphical frame.
	4	The Niemierko and Poisson models' tumor control probabilities (TCP) are estimated.
	5	The Normal Tissue Complication Probability (NTCP) for the LKB and Niemierko models is computed.
	6	The therapeutic ratio and effective volume of the LKB are computed and shown.

7	The graph depicts the calculated and determined uncomplicated tumor control probability (UTCP).
8	All structures' dose statistics are calculated and shown in a single window.
9	Equivalent Uniform Dose (EUD) from homogeneous and heterogeneous dose distribution.
10	The Conformity and Homogeneity Index (physical index) is computed and shown.
11	For convenience, the tolerance doses for TD50/5 and TD5/5 are provided.
12	Normal Tissue Integral Dose (NTID) is calculated and displayed.
13	Physical treatment plan evaluation based on (QUANTTEC/EMAMI/RTOG) protocol.
14	The provided radio-biological input parameters can be modified and saved in an Oracle table for the normal and tumor structures.
15	The Hotness and Cold Index of the treatment plan is displayed.
16	Physical dose statistics display of treatment plan with BED and EQD2
17	The toolbox provides input from the user to determine the absolute doses (cGy) and absolute volumes (Cubic Centimeters) for the normal and tumor structures.
18	The "clear" option eliminates all of the widgets from the window frame for upcoming studies without reopening the program (saving time for re-execution)

Radiobiological Dose Evaluation Software (RDS) is an open-source software system designed for clinical and research applications in radiation therapy 20016-2023. This work is dedicated to the cancer care community to improve the quality of radiation-guided treatments in cancer. The program is primarily useful for the efficient and accurate analysis of multidimensional dose-volume histograms, evaluation of advanced radiotherapy treatment plans, appraisal of radiobiological modelling outcomes, dose-response modelling, and physical parameterization of normal organs using radiotherapy treatment plans in the Radiation Therapy Oncology Group (RTOG) [11]. Although the program has been successfully designed for research applications, it is also useful for direct clinical analysis of advanced radiation therapy treatment plans following extensive validation of the dosimetric parameters.

The Oracle Database 19c Standard edition 2 Release 19.0.0.0.0 versions 19.3.0.0.0 was used to interface with Python for executing the SQL query, as shown in Table 4. The program accepts as input a kilobyte-sized Notepad file (txt file) in the relative mode of a dose volume histogram exported from the treatment planning system. In the beginning, the software was tested to see if the dose-volume histogram could be reproduced from a text file. This was later verified by taking actual dosage and volume measurements of the target and normal structures using the original DVH from the treatment planning system, which confirmed that the error percentage was within the accepted limits.

The values of radiobiological models were manually produced, and then values were reviewed step-by-step using values calculated with Python.

The Tkinter library toolbox's label, text, combo box, check, and

radio button controls are used to display the proper output with the initial input for developing the radiobiological model, which was obtained from an Oracle table. The application is very soothing and provides all the estimated values for the development of physical and radiobiological parameters in a single window frame for comparison and quick reference, along with an associated graph.

RESULTS

Python application extensive features and modules are displayed in Figure 1.

Basic system requirements

Recommended settings for system and file configuration are Platform: Windows-XP, 2000-2008, Vista, Linux, and MATLAB software. The IMRT, 3DCRT, IGRT and Rapid arc plans were exported in DVH text formats. Oracle Database 19c Standard edition 2 Release 19.0 and IDE PyCharm Community edition 2020.1 are interfaced with this application. The Python application is executed from the Python Integrated Development Environment (IDE), PyCharm 2020.1.5, with all standard libraries as shown in Figure 2.

The Python programming code (RDS_V15_11_Mar_2023.py) is opened from PyCharm IDE using file  open and browse the folder for the executable Python code. After the selection of Python code, execute the program using the RUN command in the IDE application. After execution, the RDS application front page will be loaded for DVH analysis, as shown in Figure 3.

<p style="color: red; font-weight: bold;">RDS Software application Version 3.0 RDS Program (2016-2023)</p>		Cumulative DVH Statistical Analysis (cDVH Analysis)	
	Dose- Volume Histogram Analysis (Module 1)	Dose Statistics (Minimum, Mean and Max) Volume	Normalized cDVH Statistics Absolute and Relative cDVH Statistics Absolute and Relative cDVH Statistics
	Plan-Indices Evaluation (Module 2)	Biological Equivalent Dose (BED) Equivalent Dose (EQD2) Conformity Index (CI) Homogeneity Index (HI)	
	Radiobiological Probability Analysis (Module 3)	Tumor Control Probability (TCP)/Normal Tissue Complication Probability (NTCP) Parameters. Uncomplicated Tumor Control Probability (UTCP)	Poisson's Model Lyman, Kutcher, and Burman Model
			Niemierko Model
	Physical Plan Evaluation (Module 4)	RTOG/AAPM/EMAMI	Physical plan evaluation Index
	Radiobiological Parameter of the OAR/PTV (Module 5)	Equivalent Uniform Dose (EUD) Effective Volume (Eff) TD50/TCD 50 for OAR/Target tolerance dose.	Emami TD50/5 LKB effective volume gEUD Therapeutic Index effective volume (Veff) Normal tissue integral dose

Fig. 1. Flow chart of radiobiological methods and calculation methods in Python application

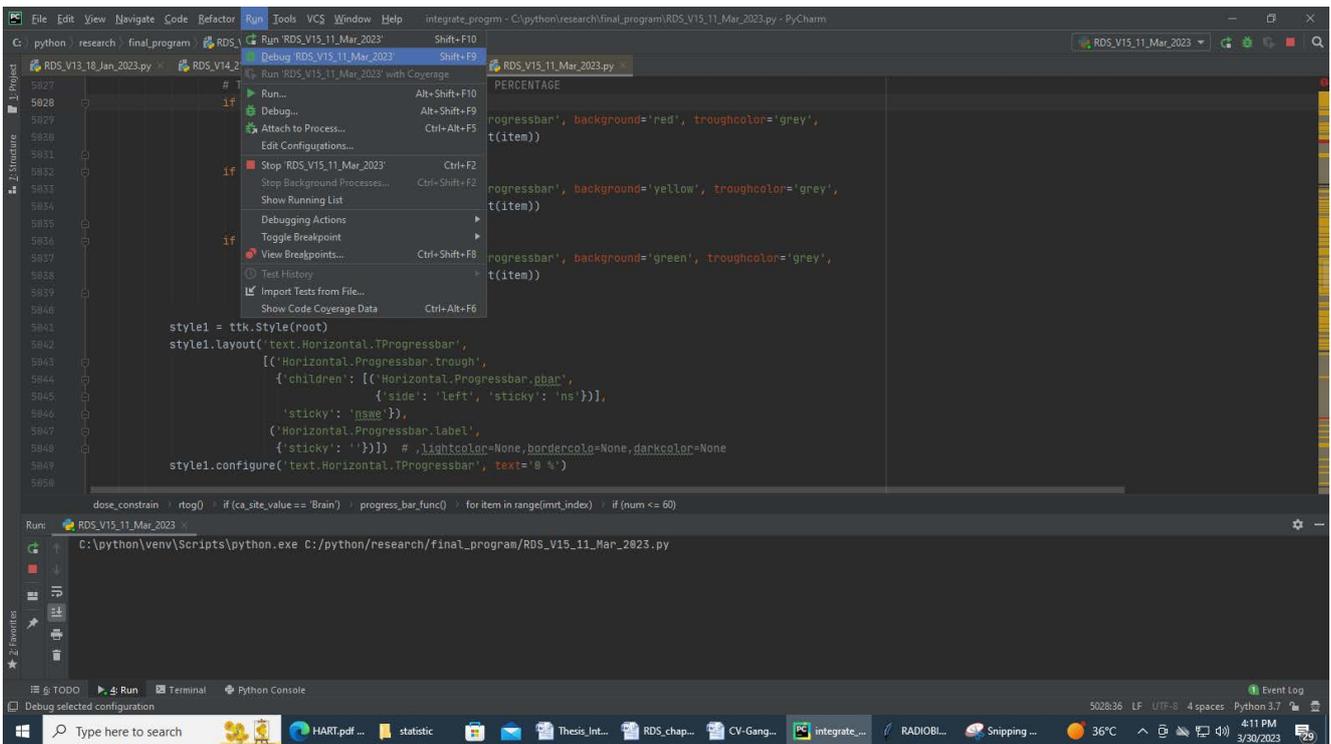


Fig. 2. Integrated development environment (IDE) from PyCharm for execution of the python program to run the software code

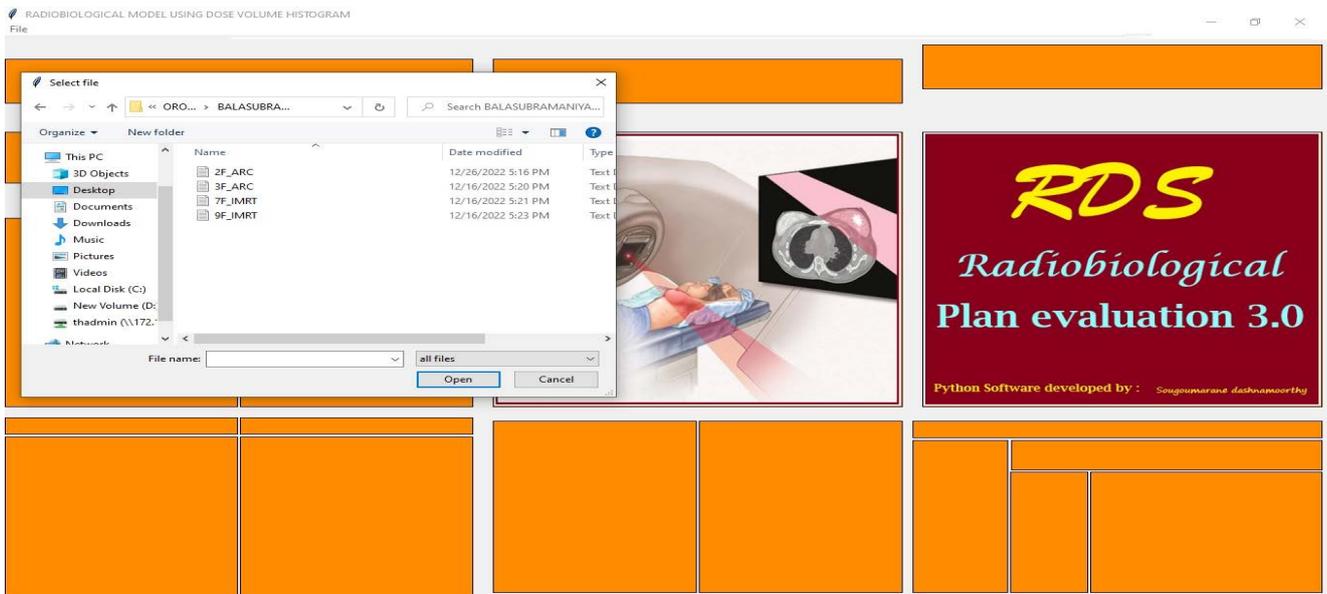


Fig. 3. Python application main window for the patient dvh file import option

The RDS graphical user interface application prompts users to select the appropriate patient dvh file for analysis and subsequently to select the treatment site from the dropdown combo box, cancer site, and click OK. The system will execute and analyse the DVH in the background. After execution, the load parameter button will be enabled to continue the application further. To Launch RDS software, install Python and Oracle; Select the Set Path tab from the edit configuration of the PyCharm IDE for Python interpreter as Python 3.7 and Click Ok → Save → Close as shown below step by step.

RDS offers the following functionalities by processing Dose Volume Histogram (DVH) data-text files: in radiation therapy treatments. The application functionality is shown in Figure 4.

- Multistucture histogram (MSH) analyses:
- DVH and NTCP/TCP probability graph:
- Plan-Indices (UPI) evaluation:
- Physical plan evaluation module:
- NTID and dose statistic:
- Radiobiological parameter edition (option):
- Radiobiological modelling for the outcome analysis (ROA):
- Therapeutic ratio and uncomplicated tumor control probability
- LKB model effective volume analysis
- Report generation

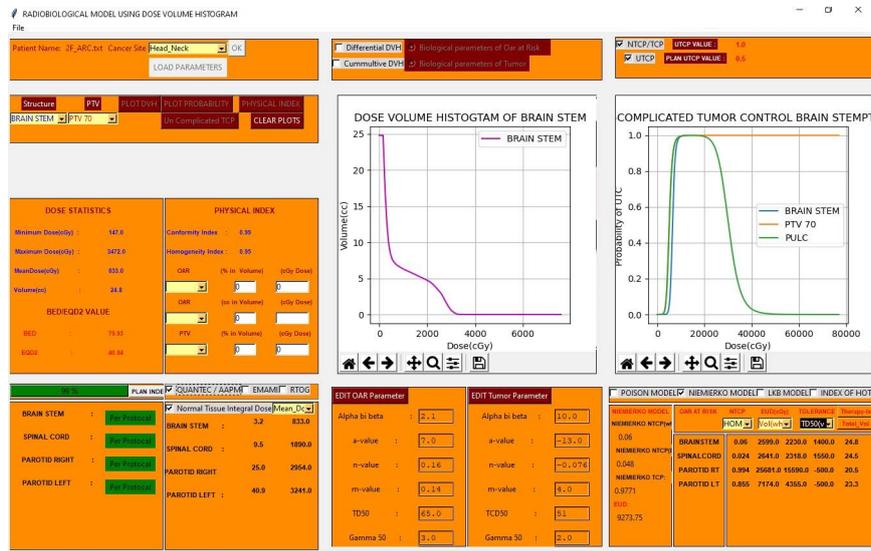


Fig. 4. Complete functionality of the python application with a user-friendly single window page

DISCUSSION

Multi Structure Histogram (MSH) analyses
 Conventional Dose-Volume Histogram (cDVH) analysis provides the foundation for MSH analysis. The programs uses specific arrays known as a Numpy array to swift and precisely transform the cDVH data to a curve in milliseconds for effective cDVH analysis

DVH and NTCP/TCP probability graph

The separate combo box is filled with the normal and target structures from the treatment plan. The dosage volume histogram, probability graph, and uncomplicated Tumor Control Probability (UTCP) can all be seen in the same probability window after the selection of the structure (normal/target) from the user, as shown in Figure 5.

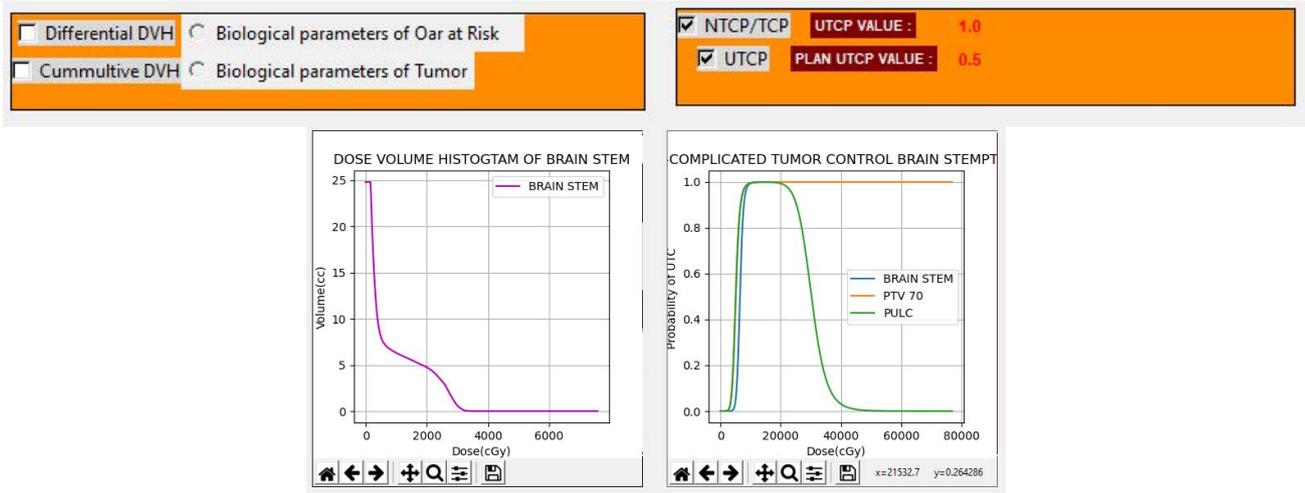


Fig. 5. The dose-volume histogram and probability graph window with the navigation bar

The RDS's Graphical User Interface (GUI) provides a brief graphical toolbar with the rest of the options, back, forward, pan, zoom, configure, and save, to allow users to quickly traverse the plot. Two-dimensional histogram analysis is far more user-friendly than other applications due to these specific qualities. When a button is clicked, a specific class object from the radiological index, such as Normal Tissue Complication Probability (NTCP), Tumor Control Probability (TCP), and Uncomplicated Tumor Control Probability (UTCP), is executed in the background, and a corresponding probability curve is generated in the

graphical window, as shown above.

Plan Indices (PI) evaluation

The Conformity Index (CI), Homogeneity Index (HI), Biologically Effective Dose (BED), Equivalent Dose (EQD2), and dose statistics are displayed from a selected list of the combo box. The absolute and relative values of the dose-volume histogram from normal and target structures can be calculated from a user-friendly window, as shown in Figure 6.



Fig. 6. Physical and dose statistic window with input to relative and absolute values

Physical plan evaluation and NTID and dose statistic

When the mouse is clicked on the plan index button, a separate Python class object is executed to generate the physical plan index based on the (a) QUANTEC, (b) EMAMI, and (c) RTOG protocol, as shown in Figure 7. The planning index is calculated based on criterion ranking and used to show the index value with acceptance status in (green/yellow/red) for the suitability of the treatment plan. The mean and maximum doses of the normal tissue integral dose and dose statistics (mean and max doses) are shown next to the plan index window for quick reference and comparison with the physical dose statistics to determine whether the treatment plan needs to be implemented.

Radiobiological parameter edition (option)

The Normal Tissue Integral Dose (NTCP) and Tumor Control Probability (TCP) calculations recommended by the poison model, Lyman Kutcher and Burman (LKB) model, and Niemierko model are inextricably linked to the radiobiological parameters. Incorrect numbers may underestimate or overstate the radiobiological effects. These factors determine the degree of tumor control and complications in normal tissue.

The user-level editable parameters for each normal and tumor structure include the tolerance dosage (TD50/5 Gy), slope parameter (γ_{50}), alpha/beta ratio (α/β), and volume parameter (n). These parameters are saved in an Oracle database and are available for review and analysis, as shown in Figure 8.

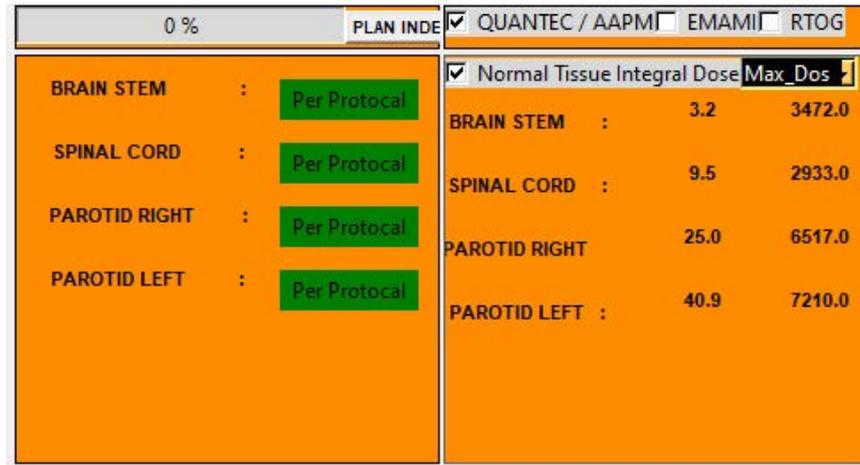


Fig. 7. Physical plan evaluation window with reference to NTID and dose statistic

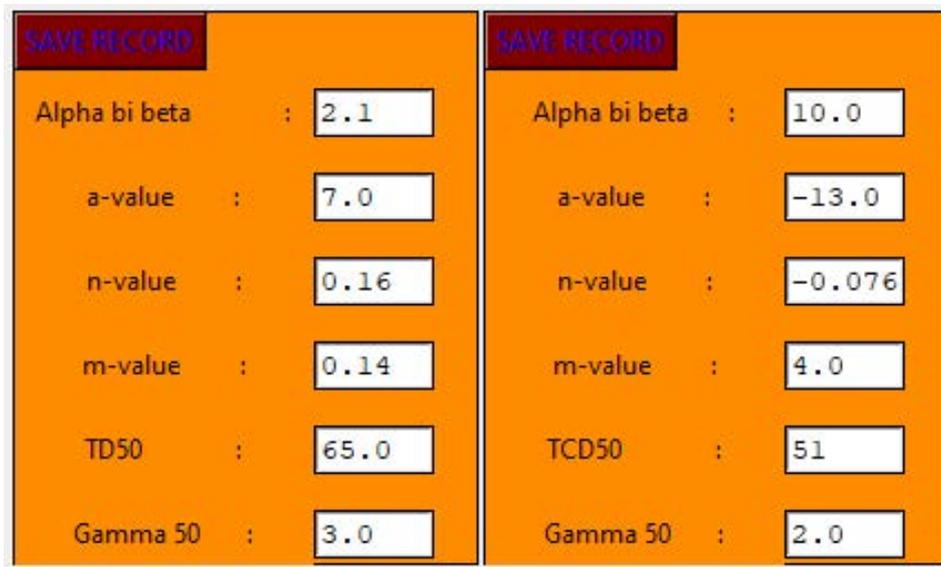


Fig. 8. Radiobiological parameters used in the models for different cancer sites

Radiobiological modelling for the outcome analysis (ROA)

The radiobiological parameters are first loaded into the Python GUI from the Oracle database, and then an event-open dialogue box appears, prompting the selection of the patient's DVH file and the cancer site from a dropdown menu. The radiobiological parameters for OARs and tumors can be edited according to user convenience and stored in the database for reanalysis. The successive steps of the radiobiological parameters and radiobiological model results are shown below based on figure 9 as a snapshot.

The toggle button to switch from the desired results displays the UTCP and Lyman Kutcher Burman model effective volume (veff), as shown in Figure 10.

Report generation

The Openpyxl library is used to export all the data displayed in the widgets objects to Microsoft excel for report generation. The new excel sheets are created and data from tkinter are inserted for every row and column of the cell. The sample report is shown in Figure 11.

Therapeutic ratio and LKB model effective volume analysis

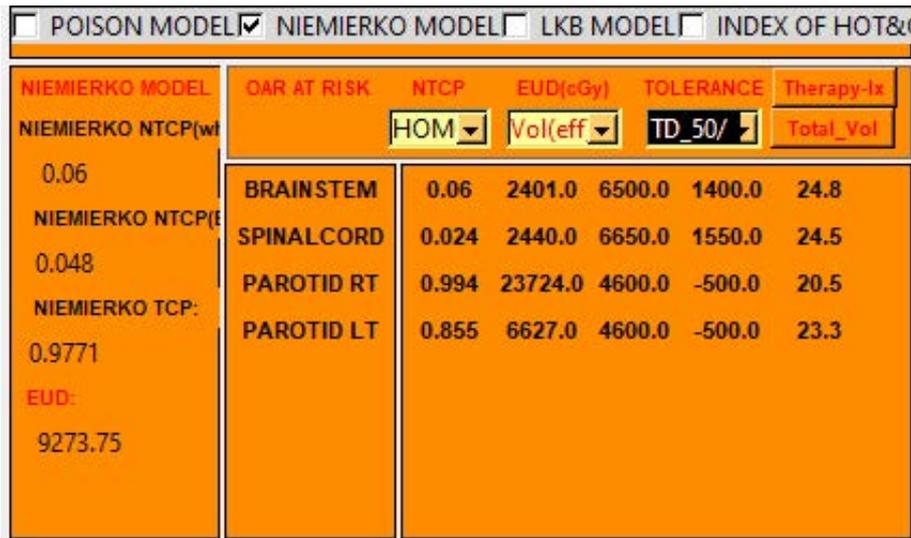


Fig. 9. The radiobiological model results window with therapeutic index values



Fig. 10. Toggle button for display of UTCP and LKB's effective volume

THANGAM HOSPITAL-NAMAKKAL						
DEPARTMENT OF RADIOTHERAPY						
RADIOBIOLOGICAL TREATMENT PLAN EVALAUTION REPORT						

PATIENT NAME:	SAWITHRI,	BED VALUE:	52			
CANCER SITE:	Cervix	EQD2 VALUE:	43.3333			
PLAN NAME:	Plan1_25#					
TOTAL FRACTION:	25	COMFORMITY INDEX:	1			
TOTAL DOSE:	5000	HOMOGENEITY INDEX:	0.93			

RADIOBIOLOGICAL PARAMETER OF NORMAL TISSUE						
	NTCP	EUD	Eff(vol)	Mean dos	Max Dose	Total Vol
BLADDER	0.998	3168	69	4755	5490	445.7
FEMUR_LEFT	0.422	3671	1.2	1915	5220	99.4
FEMUR_RIGHT	0.477	3671	1.7	1995	5245	101.7
RECTUM	0.309	4198	1.9	3710	5130	30.6
BOWEL	0.859	3969	15.2	1640	5380	1699.4
RADIOBIOLOGICAL PARAMETER OF TUMOUR TISSUE						
	TCP	EUD	Eff(vol)	Mean dos	Max Dose	Total Vol
PTV 50/25	0.1419	5958.12	0	5190	5490	5487.5
RADIOBIOLOGICAL PARAMETER VALUES OF NORMAL TISSUE						
	alpha/beta-value	n-value	TD 50	Gamma 50		
BLADDER	2.5	2	0.5	80	3.63	
FEMUR_LEFT	3	4	0.08	65	2.7	
FEMUR_RIGHT	6	4	0.08	65	2.7	
RECTUM	5.4	8.33	0.12	80	2.66	
BOWEL	3	6	0.15	55	4	
RADIOBIOLOGICAL PARAMETER VALUES OF TUMOUR TISSUE						
	alpha/beta-value	n-value	TCD 50	gamma 5m-value		
PTV 50/25	10	-13	-0.0769	68	3	0.1

RADIOLOGICAL PLAN EVALATION OF NORMAL STRUCTURE						
	QUANTITEC	EMAMI	RTOG			
BLADDER	0.75	0.75	0.5			
FEMUR_LEFT	0.5	0.5	0.5			
FEMUR_RIGHT	0.5	0.5	0.5			
RECTUM	0.5	0.5	0.5			
BOWEL	0.75	0.75	0.75			

MEDICAL PHYSICIST			RADIATION ONCOLOGIST			

Fig. 11. Report generated from python software for complete dosimetric and radiobiological analysis of treatment plan

CONCLUSION

The entire application, which was developed over three years and involved the use of numerous models and physical plan analysis, centered on building a radiobiological plan evaluation. We created a single platform for radiotherapy calculation using the Python front-end tool Tkinter and an Oracle database. Students have the chance to put all of the radiobiological models and parameters

used in radiotherapy effectively into practice with this application. They can also import treatment plans from the Eclipse treatment planning system using text files and change the radiobiological parameters of the treatment plan in a robust data analysis and programming environment. This study will be expanded upon in the future for the use of additional treatment planning systems, including Elekta, Philips, and Ray research.

REFERENCES

1. Baxter BS, Hitchner LE, Maguire Jr GQ. A standard format for digital image exchange. *Publ Am Assoc Phys Me Am Inst Phys.* 1982.
2. Goitein M. Calculation of the uncertainty in the dose delivered during radiation therapy. *Med Phys.* 1985;12:608-612.
3. Gomez A, (2013), "Medical Image Processing Toolbox", W, (1997); "Specifications for Tape/Network Format for Exchange of Treatment Planning Information, version 3.22," Image Guided Therapy Center at Washington University.
4. Deasy JO, Blanco AI, Clark VH. CERR: a computational environment for radiotherapy research. *Med phys.* 2003;30:979-985.
5. Sanchez-Nieto B, Nahum AE. The delta-TCP concept: a clinically useful measure of tumor control probability. *Int J Radiat Oncol Biol Phys.* 1999;44:369-380.
6. Niemierko A, Goitein M. Modeling of normal tissue response to radiation: the critical volume model. *Int J Radiat Oncol Biol Phys.* 1993;25:135-145.
7. Nahum AE, Uzan J. (Radio) biological optimization of external-beam radiotherapy. *Comput Math Methods Med.* 2012;2012.
8. Petrova D, Smickovska S, Lazarevska E. Conformity index and homogeneity index of the postoperative whole breast radiotherapy. *Open access Maced J Med Sci.* 2017;5:736.
9. Zhao B, Joiner MC, Orton CG, Burmeister J. "SABER": a new software tool for radiotherapy treatment plan evaluation. *Med Phys.* 2010;37:5586-5592.
10. Dashnamoorthy S, Rajamanickam K, Jeyasingh E, Pandey VP, Nachimuthu K, et al. Comparison of Dose Statistics of Intensity-Modulated Radiation Therapy Plan from Varian Eclipse Treatment Planning System with Novel Python-Based Indigenously Developed Software. *Prog Med Physic.* 2022;33:25-35.
11. Dashnamoorthy S, Jeyasingh E, Rajamanickam K. Validation of esophageal cancer treatment methods from 3D-CRT, IMRT, and Rapid Arc plans using custom Python software to compare radiobiological plans to normal tissue integral dosage. *Rep Pract Oncol Radiother.* 2023;28:54-65.
12. Dashnamoorthy S, Jeyasingh E, Pandey VP, Rajamanickam K, Kotur SS, et al. Dosimetric Validation of Physical and Biological Indexes from the Dose-Volume Histogram for Evaluation of 3D-CRT and IMRT Techniques with VMAT Treatment Plan Techniques in Cervical Tumors from In-House Developed Software. *Iran J Med Phys.* 2024;21.
13. Patel G, Mandal A, Choudhary S, Mishra R, Shende R. Plan evaluation indices: a journey of evolution. *Reports of Practical Oncology and Radiotherapy.* 2020;25:336-344.