PyTRiP - a toolbox and GUI for the proton/ion therapy planning system TRiP

J Toftegaard¹, J B Petersen², N Bassler¹,³
¹ Department of Physics and Astronomy, Aarhus University, Aarhus, DENMARK
² Department of Medical Physics, Aarhus University Hospital, Aarhus, DENMARK
³ Department of Experimental Clinical Oncology, Aarhus University Hospital, Aarhus, DENMARK
E-mail: bassler@phys.au.dk

Abstract.
Purpose: Only very few treatment planning systems (TPS) are capable of handling heavy ions. Commercial heavy ion TPS are costly and normally restrict the possibility to implement new functionalities. PyTRiP provides Python bindings and a platform-independent graphical user interface (GUI) for the heavy ion treatment program TRiP, and adds seamless support of DICOM files. We aim to provide a front-end for TRiP which does not require any special computer skills.

Methods: PyTRiP is written in Python combined with C for fast computing. Routines for DICOM file import/export to TRiP’s native file format are implemented. The GUI comes as an executable with all its dependencies including PyTRiP making it easy to install on Windows, Mac and Linux.

Results: PyTRiP is a comprehensive toolbox for handling TRiP. Treatment plans are handled using an object oriented structure. Bindings to TRiP (which only runs on Linux, either locally or on a remote server) are performed through a single function call. GUI users can intuitively create treatment plans without much knowledge about the TRiP user interface. Advanced users still have full access to all TRiP functionality. The user interface comes with a comprehensive plotting tool, which can visualize 2D contours, volume histograms, as well as dose- and linear energy transfer (LET) distributions.

Conclusion: We developed a powerful toolbox for ion therapy research using TRiP as backend. The corresponding GUI allows to easily and intuitively create, calculate and visualize treatment plans. TRiP is thereby more accessible and simpler to use.

1. Introduction
TRiP98 [1,2] is a well known heavy ion treatment planning system for heavy ions, which was developed at GSI Helmholtzzentrum für Schwerionenforschung, Darmstadt, Germany. PyTRiP [3] started as a package for handling VOXELPLAN [4] formatted files, which are used by TRiP. Since then it has been extended with a series of functions for pre and post processing of TRiP generated-data [5]. In its current version it is possible to execute TRiP from simple python scripts. A graphical user interface (GUI) is developed as well, from which most features of TRiP can be accessed.
2. Methods

2.1. DICOM support

As TRiP98 only is capable of reading files in VOXELPLAN format, PyTRiP features a full converter of DICOM files to TRiP format. DICOM 2D CT images are recombined to a single 3D cube containing the Hounsfield units in floating point notation. A header file describes the format. Dose cubes are prepared in a similar way, however here the dose is represented as integer ranging from 0 to 1000, specifying the relative dose in steps of tenths of a percent. All voxels can be shifted with the DICOM offset tag, which is retained in the VOXELPLAN format. The conversion of structures (or volumes of interest (VOIs)) is less trivial, though. A structure can consist of one or more separated contours, where the contours themselves are handled equally in DICOM and VOXELPLAN format. In both cases, the structure is divided into slices which match the placement of the respective CT slice. The problem however arises from a limitation in TRiP that in a given slice, there can only be a single contour per structure. In practice, this is handled by manually connecting contours with an area with the width of 0. The two contours can then in topological sense be regarded as a single contour. To automate this process and to avoid user interaction for this tedious and time consuming step, a function is written which fulfills the following criteria:

- If one contour is located inside another contour, then the inner contour is regarded as a hole in the outer contour.
- If two contours have no overlap, these must be connected with an infinitely thin area, i.e. two overlapping connecting lines, which combines the two contours to a single contour with a single surface.
- A connecting line between two contours may not pass a third contour.

To fulfill these requirements, an algorithm is conceived where first all contours are organized in a tree. The contours are organized within a top-level contour (K0), and all subsequent contours (Ki) are various generations of child nodes of the parent contour. This is illustrated for a case with 4 contours (K1-K4) in figure 1 and 2. Here, K3 and K4 are holes in K1, and K2 is an independent contour.

![Figure 1. Example of a structure in a CT slice containing several contours.](image1.png)

![Figure 2. Contour tree defining the structure from figure 1.](image2.png)

To test whether a contour is located within another one, a point is taken from the list of points which defines the contour, and then it is investigated whether this point is inside the other contour using a ray casting algorithm [6]. This algorithm calculates a parameter representation of a line which crosses the investigated area. The points of interception with the contours are calculated. If there is an odd number of solutions in the positive directions, then the point
is within the structure, and vice versa. Once the tree is constructed, contours are coalesced recursively. In the example shown in figure 1 this means that K3 and K4 are connected first, and the resulting contour is connected with K1, which then again is connected to K2. Finally, K0 is representing the entire contour. If a contour has more than 2 child contours attached, a child contour and its closest neighbour are joined first. This way it is ensured that no line will cross a third contour.

The inverse process, converting VOXELPLAN structures to DICOM is straightforward, since there are no additional requirements how contours in a structure are organized.

2.2. DVH and LVH calculation

Once the structures are established, dose-volume histograms and also LET-volume histograms can be calculated in PyTRiP, thereby reducing the need to interact directly with TRiP. LET-volume histograms are a new feature which illustrate the LET-coverage within a tumour in a similar way as dose coverage is shown in a regular dose-volume histogram. This gives a feeling for e.g. the presence of LET hot-spots or cold spots within the volume of interest, which is of relevance for the recent focus on LET-optimized particle therapy methods [7–11].

2.3. TRiP execution and platform considerations

One aim with PyTRiP is to simplify parametric studies, where many treatment plans are calculated while varying one or more parameters. PyTRiP supplies classes for TRiP execution, following an object oriented design paradigm. The treatment plan is thus an object which can be executed and contains the results after execution. A client-server model is applied, since TRiP itself only is compiled for a limited number of platforms. PyTRiP in turn, is functional on Linux, Mac and Windows based operating systems. The client-server model enables users to use PyTRiP on client PCs, even where TRiP is not installed, as long as an encrypted connection is possible to the server where TRiP is installed. Multiple users can use TRiP simultaneously from several different computers.

2.4. Graphical user interface

A graphical user interface to PyTRiP is provided using the platform independent wxWidgets set [12]. The GUI purports to minimize (and ideally obsolete) direct user interaction with TRiP. A demonstration of an early version of the graphical user interface can be seen on youtube [13] - See more at: http://youtu.be/6ZqcJ6OZ598.

3. Discussion and Conclusion

PyTRiP has already demonstrated to be a versatile package for generating ion treatment plans and perform parametric studies. As an example, PyTRiP was recently used for calculating maps of robust angles for treating patients with protons and heavier ions [5]. Here, a robustness factor is defined which expresses the sensitivity of a given irradiation field towards setup errors. The field is then applied iteratively for a fine meshed grid of couch and gantry angles, generating a robustness map. These maps show islands of robustness, which suggest preferred treatment angles.

PyTRiP is also used for demonstrating the potential of LET-painting [7]. Here, high-LET components of heavy ion beams are targeted to hypoxic tumour compartments in order to achieve a better therapeutic outcome. Extensive studies to quantify the alleged benefit was recently carried out, where radiobiologic models are included in order to determine the tumour control probability [5]. PyTRiP along with TRiP and the Monte Carlo particle transport code SHIELD-HIT12A [14–16] was used to also investigate whether tumour hypoxia could be overcome using ions heavier than carbon ions, such as oxygen-16 ions, which are available at Heidelberg Ionentherapiezentrum (HIT), Universitätsklinikum Heidelberg, Germany [17].
Using the connectivity between PyTRiP, TRiP and SHIELD-HIT12A it is possible to prepare and calculate depth-dose data sets for any primary ion and facility specific beam lines [18], and apply these for treatment plan studies. The same tool set was also used recently to investigate the impact of secondary ions in clinical settings [19,20].

Next, we foresee to use this combination of tools to generate antiproton treatment planning studies [21,22], carefully benchmarked against the radiobiologic data acquired at CERN [21,23]. We also anticipate PyTRiP will be useful to compare radiobiology models as these evolve, and more data from existing and future radiation laboratories become available [24].

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