1 About dta1d

Program can be used in radiotherapy departments by physicists to perform some QA procedures. It is published under GPL licence so everyone can make some modifications if needed.

Program compares two dose profiles. Calculaded in treatment planning system Monaco and measured in water phantom.

The measurement data is exported from IBA OmniPro Accept application. Tested version of this application was 7.2.

The other profile is taken from dose plane. Dose plane is exported from Monaco treatment planning system by choosing: Tools-Dose Export (tested version of Monaco was 3.2). That dose plane is two dimentional table of values. Program extracts one dimentional "line" of dose values from it.

The OmniPro files (unfortunately) must be exported as .csv. Values should be separated by comma, and decimal sign should be dot. You may export .opab file as excel's .xls first, then using i.e. OpenOffice export it to csv.

For now, both, profile and dose matrix must be exported with $0.1cm$ resolution.

2 How does it work

After loading, both profiles are normalized to 100% in central axis. Values are set in percents. The wider profile is truncated, so both are the same size.

You can extract dose line, you want, from monaco dose plane. You also can save it in file. Then comparition parameters must be defined by checking options menu. There are some defaults. Then you can compare profiles.

2.1 Dose difference - distance to agreement - comparision method

Each point is checked, beginning from left to right. We have to determine if the doses in point x are aqual (against assumed criteria) or not.

We will have to calculate dose distance - dd, and distance to agreement - dta. And compare these values to defined criteria $dd_{defined}$ and $dta_{defined}$. These values are set in options menu.

First, dose values are compared. For example 51.5% and 51.3%. If the difference is less than defined dose difference $dd_{defined}$, we assume that points are equal. Otherwise we check dta (distance to agreement).

In that method it is needed to define if we compare first profile against second (1vs2) or vice versa (2vs1). Let us say, one of them is "checked profile" and the other is that we want to check against.

To explain the algorithm, let us define:

- checked profile - T_1,
- the profile we compare with - T_2,
- checked point from T_1 profile - x,
- corresponding dose values - $T_1(x)$,$T_2(x)$

Let's say $T_1(x) = D_x$ - dose in checked point.

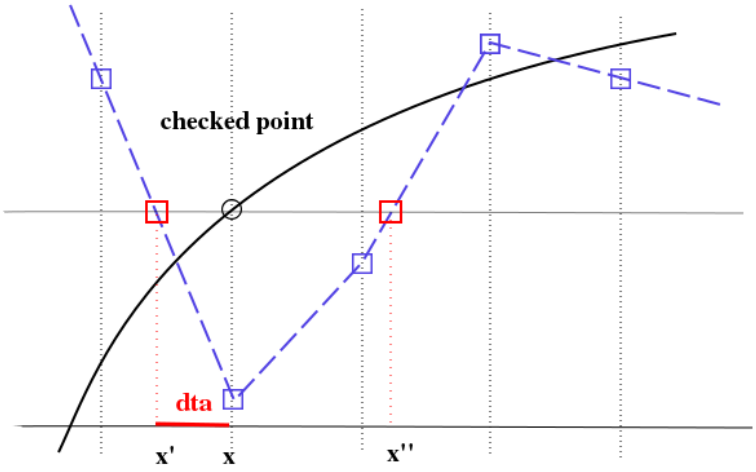

Figure 1: The explanation of dta algorithm used. There are two sets of data. The blue, are the points we compare to. There are two places where the dose is the same as in point x. The smallest difference is searched dta value

Point x hasn't meet the dose difference criteria (in other words):

$$|T_1(x) - T_2(x)| > dd_{defined}$$

We find points from T_2, that have exact same dose value. To find them we look for two adjacent points in T_2: x_n and x_{n+1} which meet the following rule

$$T_2(x_n) < D_x < T_2(x_{n+1})$$

or

$$T_2(x_n) > D_x > T_2(x_{n+1})$$

From those points we can estimate place where dose is the same as for point located in x. Than we find the closest point to the point we are checking. This distance is dta we were looking for.

If $dta < dta_{defined}$ the points at x are treated as the same.

The figure (1) tries to explain it.