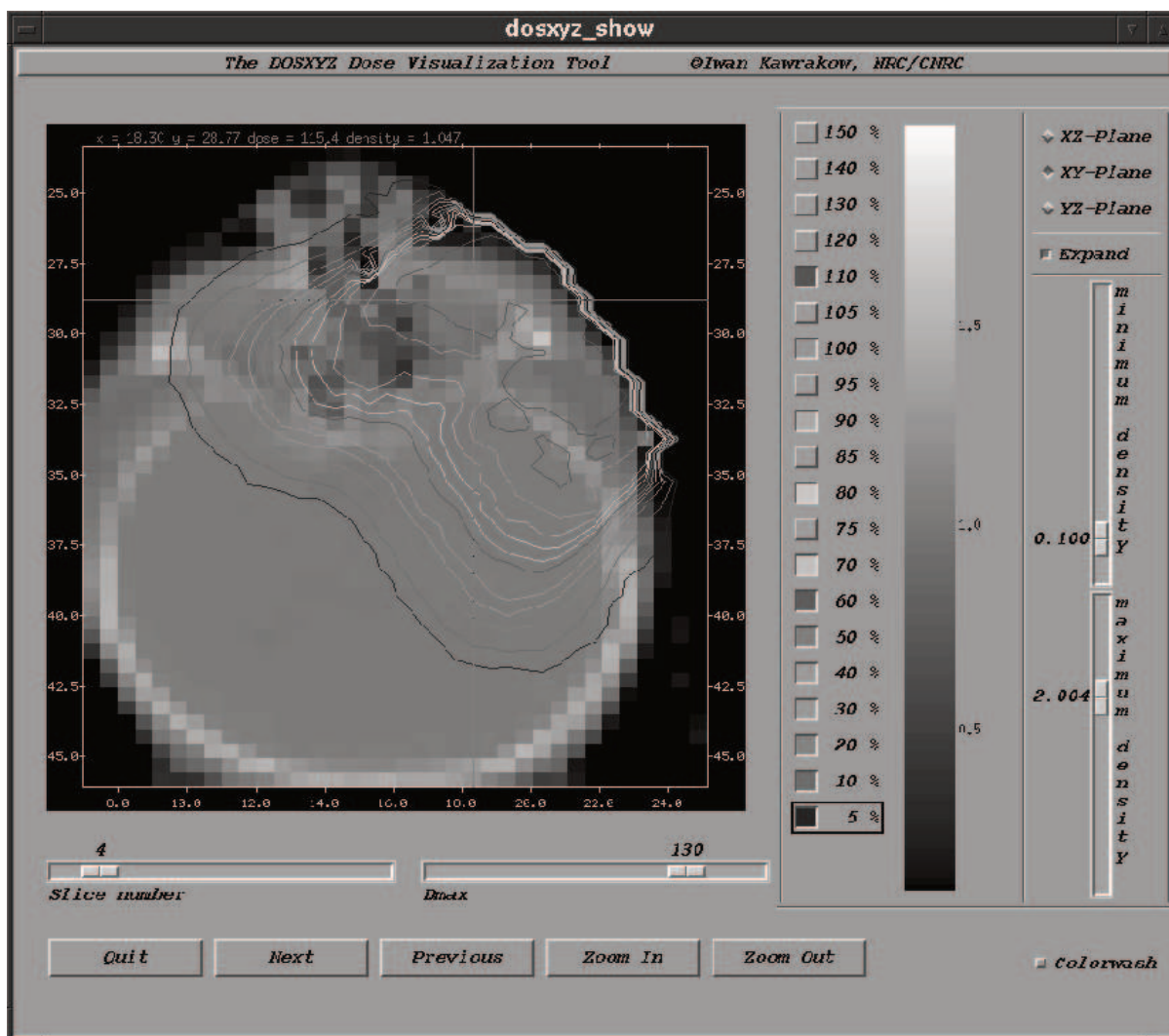# The dose visualization tool `dosxyz_show`

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1   Short description

dosxyz_show is a slightly modified version of vmc_show, a small utility program from the VMC distribution, adapted to work with the DOSXYZ CT data and dose formats. It displays dose isolines on top of the corresponding CT data. dosxyz_show is a public domain software distributed under the terms of the GNU Affero General Public Licence 3.0. It was included as part of the BEAM distribution starting in 1998.

Note that dosxyz_show does not run on Windows.

2   Compiling and running

The program is written in C using the OSF Motif widget set and consists of a single file, dosxyz_show.c. If you don't have Motif installed on your system, you can use LessTif, a public domain implementation of Motif which is relatively easy to install. To compile the code, type

```
cc -o dosxyz_show [preprocessor options] dosxyz_show.c -lXm -lXt -lX11 -lm
```

Note that the order of the libraries is important. The preprocessor options available will be described below. If you use LessTif and have not installed the Xm library on the system area, you must specify the path where the library is installed with the -L option, e.g.

```
cc -o dosxyz_show ...   -L$HOME/lesstif/lib
```

On the NRC system, the X toolkit and X11 libraries are in /usr/X11R6/lib and therefore -L/usr/X11R6/lib must be added to the compiler options.

To run the code, type

```
dosxyz_show CT_file [dose_file]
```

Here, CT_file and dose_file are the names of the CT data file and 3D dose distribution file, both in DOSXYZ format. If no file extensions are specified (.egs4phant and .3ddose), they will be automatically appended to the names. Note that dosxyz_show expects at least one argument (the CT data file), otherwise it will stop. The dose file argument is optional. As there is no default directory for the CT data files, CT_file must contain the absolute path if not in the working directory. If not found in the working directory, the dose file is assumed to be in $HOME/egs4/dosxyz.

By default, the colors for the isolines are uniformly distributed along the hue co-ordinate in the TekHVC color space (see *e.g.* Adrian Nye, Xlib Programming Manual, O'Reilly & Associates, Inc., for a short description of various color representations) and should be device independent. However, it seems that there is a bug in the Linux implementation of TekHVC and so the resulting isoline colors differ from those on other systems. Therefore, a RGB representation of isoline colors was implemented which can be put into effect by using -DMY_COLOR preprocessor option. If you don't like the isoline colors, you can change them by modifying some of the components of the red, green and blue arrays defined at the

beginning of `dosxyz_show.c`.

Another preprocessor option can be used to change the density to gray shade conversion function. By default (no preprocessor option specified), a linear mapping is employed. With `-DDG_SQRT` you can turn on square root mapping, *i.e.*

$$i_{\mathrm{gray}} = \frac{\sqrt{\rho} - \sqrt{\rho_{min}}}{\sqrt{\rho_{max}} - \sqrt{\rho_{min}}} N_{\mathrm{gray}}$$

where ρ is the the actual voxel density, ρ_{min} and ρ_{max} the minimum and maximum density of the specified displayable density window (see below) and N_{gray} the number of gray shades allocated. Note that the requirement $N_{\mathrm{gray}} \geq 64$ is coded so that the program will stop if not able to allocate at least 64 gray shades (it seemed to me that it does not make sense to try to visualize CT images with less than 64 gray shades). You can implement your own density to gray conversion function by introducing additional `DensityToGray` functions and preprocessor options.

3   Functionality

`dosxyz_show` shows the density distribution in a given xy-, xz- or yz-plane as a gray scale representation together with the corresponding isoline or color wash representation of the dose distribution (if a `.3ddose` file was specified). The isolines are calculated using linear interpolation between the dose grid points. Note that isolines are approximated as straight line segments in every voxel (for efficiency). This approximation produces good result, except in regions with sharp dose gradients where a difference between the isoline and color was representations might br observed.

Note that the visualization of an arbitrary xyz-geometry is not implemented yet but it is assumed that the planes are distributed equidistantly (the voxel size in a given direction is assumed to be the distance between the second and first plane read in from the `.egs4phant` file).

Changing the slice The user can change the slice by clicking on the `Next` or `Previous` buttons or by using the `Slice number` scale below the viewing area.

Selecting the view plane To select the plane (xy, xz or yz) to be shown in the viewing area, click on the corresponding radio button in the upper-right part of the `dosxyz_show` window.

Zoom in To use the zoom in function, click on the `ZoomIn`-button, position the mouse pointer on the upper left corner of the image portion that you want to zoom in and click the left mouse button, then move the mouse until the rectangle that appears encloses the desired image portion and click again the left button.

Zoom out To return to the original image size simply press the `ZoomOut` button.

Dose normalization When the dose array is read in, the data is normalized to 100% for the global dose maximum. This normalization can be changed with the `Dmax` scale below the viewing area.

<u>Isoline levels</u> The display of a given contour level can be switched on and off by clicking on the corresponding toggle button right of the viewing area. If you wish to change the set of switched on isolines at start time, search for the boolean array `set_isolines` in `dosxyz_show.c` and edit it according to your needs.

<u>Density range</u> The `minimum density` and `maximum density` scales can be used to define the displayable density range.

<u>Image expansion</u> When the `Expand`-button is on, the image is expanded to fill the entire viewing area which may lead to a different length scale (cm per pixel) in x- and y-direction. If you wish to have the same length scale in x- and y-direction, simply switch off the `Expand`-button (when `Expand` is deactivated, only square image portions can be selected with the zoom in function).

<u>Point dose values</u> There are two ways to obtain point dose values: (i) Go to the point of interest with the mouse and click the left button. The dose value at this point will appear on the screen; (ii) Place the mouse pointer in the viewing area and click the right button activating in this way the `GetDose` function. `GetDose` shows a cross hair which follows the mouse motions and prints the corresponding co-ordinates, dose and density values in the upper portion of the viewing area. `GetDose` is deactivated by clicking the middle mouse button or leaving the viewing area.

<u>Color wash representation</u> A color wash representation of the dose distribution can be switched on with the `Colorwash` button (note, however, that method (i) for point dose does not produce very good results with color wash on).

4   Resources

Contrary to the recommendations of all Motif manuals to specify widget resources (font, colors, geometry etc.) in a resources file (`.Xdefaults` or the application-defaults file), I have hard coded most of the resources to avoid dealing with various, possibly difficult to handle, user settings.