





Joint ICTP-IAEA Workshop on Monte Carlo Radiation Transport and Associated Data Needs for Medical Applications

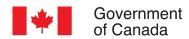
28 October – 8 November 2024 ICTP, Trieste, Italy

Lecture 18

Dose analysis and visualization tools

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The *.3ddose format

- Plain text file
- Dose and uncertainty are slice-by-slice (X Y planes)
- **1.** Number of voxels in X , Y , Z directions (e.g., n_x , n_y , n_z)
- **2.** Voxel boundaries (cm) in X direction ($n_x + 1$ values)
- **3.** Voxel boundaries (cm) in Y direction (n_y+1 values)
- **4.** Voxel boundaries (cm) in Z direction (n_z+1 values)
- **5.** Dose values array ($n_x n_y n_z$ values)
- **6.** Statistical uncertainty values array (relative errors, $n_x n_y n_z$ values)

Reading *.3ddose is easy

- Read one by one (across columns) to get dose readings in $\,X\,$ direction
- Read every (n_x) -th value to get readings in Y direction
- Read every $(n_x n_y)$ -th value to get readings in Z direction

Row (block)	Column Number				
Number	1	2	3	4	5
1	4	3	2		
2 3 4	-2.0000 -2.0000 0.0000	-1.0000 -1.0000 1.0000	0.0000 1.0000 2.0000	1.0000 2.0000	2.0000
5	1.0e-12 0.9e-12 0.9e-12	2.1e-12 0.9e-12 0.9e-12	2.0e-12 0.9e-12 0.9e-12	1.1e-12 0.8e-12 0.8e-12	
6	1.0e-12 0.9e-12 0.9e-12	2.1e-12 0.9e-12 0.9e-12	2.0e-12 0.9e-12 0.9e-12	1.1e-12 0.8e-12 0.8e-12	
7	1.0000E-01 1.0000E-01 1.0000E-01	1.0000E-01 1.0000E-01 1.0000E-01	1.0000E-01 1.0000E-01 1.0000E-01	1.0000E-01 1.0000E-01 1.0000E-01	
8	1.0000E-01 1.0000E-01 1.0000E-01	1.0000E-01 1.0000E-01 1.0000E-01	1.0000E-01 1.0000E-01 1.0000E-01	1.0000E-01 1.0000E-01 1.0000E-01	

Reading *.3ddose in c++

```
// Read in number of voxels
fscanf(f, "%d_%d_%d\n", &x_num, &y_num, &z_num);

// Read in boundaries
for(i = 0; i < x_num+1; i++) {
    fscanf(f, "%f", &x_bound[i]);
}

for(i = 0; i < y_num+1; i++) {
    fscanf(f, "%f", &y_bound[i]);
}

for(i = 0; i < z_num+1; i++) {
    fscanf(f, "%f", &z_bound[i]);
}</pre>
```

Reading *.3ddose in c++ (cont.)

```
// Read in the dose data
for (k = 0; k < z_num; k++) {
    for(j = 0; j < y_num; j++) {
        for (i = 0; i < x_num; i++) {
            fscanf(f, "%f", &data[i][j][k]);
        }
    }
// Read in the dose error
for (k = 0; k < z_num; k++) {
    for(j = 0; j < y_num; j++) {
        for (i = 0; i < x_num; i++) {
            fscanf(f, "%f", &error[i][j][k]);
        }
```

The *.egsphant format

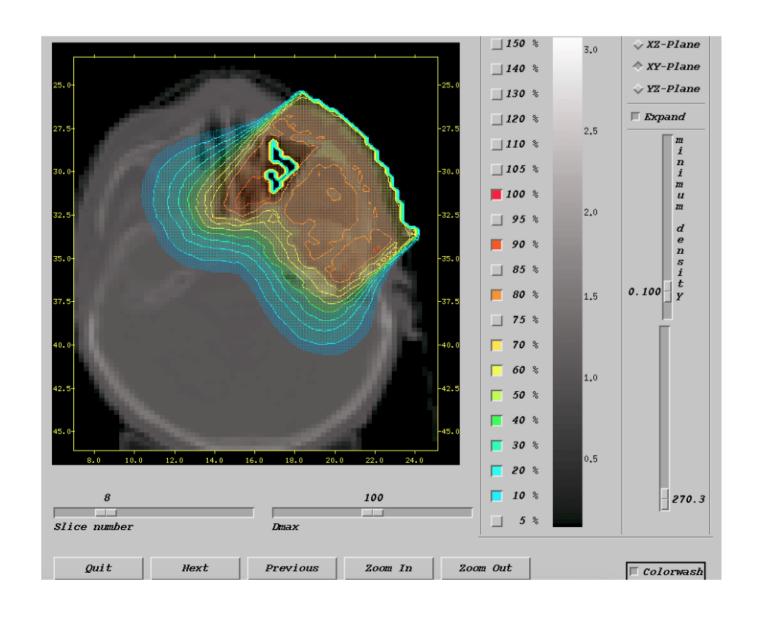
- The number of media in the phantom
- **2.** The names of the media
- **3.** The ESTEPE value for each medium (now a dummy input)
- **4.** The number of voxels in the X, Y and Z directions
- **5.** A list of the voxel boundaries in the X direction
- **6.** A list of the voxel boundaries in the Y direction
- **7.** A list of the voxel boundaries in the Z direction
- **8.** For each Z slice, an X-Y array containing the medium number in each voxel
- **9.** For each slice in the Z direction, an X Y array containing the densities in each voxel

Visualizing dose with dosxyz_show

```
dosxyz_show density_file [dose_file]
```

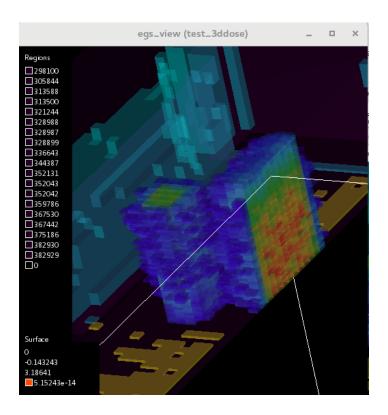
- Displays slices of a phantom (.egsphant)
- Overlays dose on each slice (.3ddose)
- The dose and density files must be on the same grid
- Open Motif is required to compile (e.g. libmotif-dev)

Visualizing dose with dosxyz_show

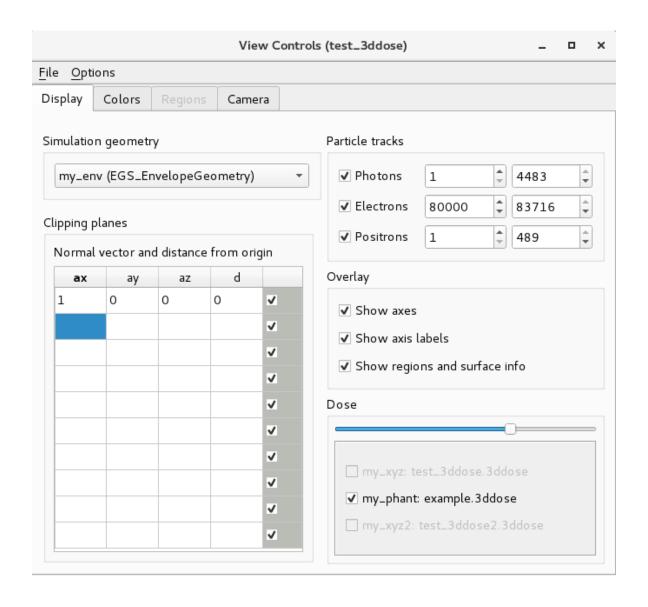


Dose display in egs_view

- Recent developments have added dose display to egs_view
- Only 3ddose files supported for XYZ geometries
- Currently no isodose lines or dose smoothing



Dose display in egs_view

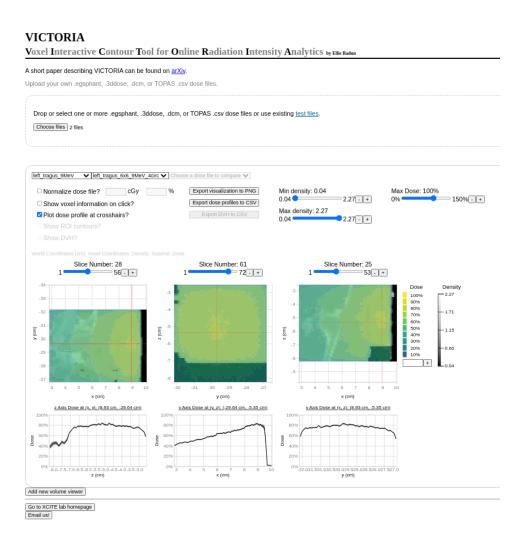


egsphant and 3ddose in egs_view

```
:stop geometry definition:
  :start geometry:
        name = my_phant
        library = egs_ndgeometry
        type = EGS_XYZGeometry
        egsphant file = slice_files.egsphant
        ct ramp = 5MeV.ramp # this requirement will be removed in future PR
  :stop geometry:
  simulation geometry = my_phant
:stop geometry definition:
:start ausgab object definition:
  :start ausgab object:
        library = egs_dose_scoring
        name = example
        medium dose = no
        region dose = no
        :start output dose file:
            geometry name = my_phant
            file type = 3ddose
        :stop output dose file:
  :stop ausgab object:
:stop ausgab object definition:
```

VICTORIA: 3ddose, egsphant and DICOM viewer

http://web.uvic.ca/ bazalova/VICTORIA/



Importing *.3ddose to a TPS

- Import into a TPS by overwriting DICOM RD dose values
- Requires a DICOM library (e.g. pydicom, CERR) and some coding!
- Update DICOM image parameters:
 - Image Position (0x00200032)
 - Image Orientation (0x00200037)
 - Number of Frames (0x00280008)
 - Rows (0x00280010)
 - Columns (0x00280011)
 - Pixel Spacing (0x00280030)
 - Dose Units item (0x30040002)
 - Grid Offset Vector (0x3004000C)
 - Dose Grid Scaling (0x3004000E)
 - Pixel Data (0x7FE00010)

STATDOSE for Analyzing . 3ddose **files**

- Compiled automatically with BEAMnrc installation
- Generates dose profiles as xmgrace plots
- Dose distributions can be normalized, rebinned
- Statistical comparisons can be performed if only two or more dose distributions have been read in, and the voxel geometries are identical

STATDOSE voxel grid dimensions

For larger voxel grids, adjust the dimensions in \$HEN_HOUSE/omega/progs/statdose/statdose.mortran and recompile.

```
REPLACE {$MAXVOXX} WITH {128};
REPLACE {$MAXVOXY} WITH {128};
REPLACE {$MAXVOXZ} WITH {128};
```

STATDOSE Example

Begin by reading in one or more . 3ddose files.

```
*************
      STATDOSE.MORTRAN(Rev 1.3)
      Max array dimensions: 128 128 128
      Max # data sets: 15
***********
MAIN MENU
0 - Exit
1 - Read dose distributions
2 - Statistical analysis
3 - Normalization
4 - Rebinning
5 - Plot
6 - Save
Selection: 1 # Begin by reading dose files
```

STATDOSE: Assign each file a reference

```
READ DOSE DISTRIBUTIONS
 1 16MVp_h2o_phantom_phsp_example
 2 5MeV-2
 3 5MeV
Input file number to Read in: (1- 7 or 0-Main Menu): 3
File number for temporary storage: (1-* or 0-Main Menu): 1
Number of voxels in X,Y,Z directions:
                                                      50
                                                               51
                                            51
Voxel-boundary values in X-direction: -5.10 - 5.10
Voxel-boundary values in Y-direction:
                                         0.00 - 10.00
Voxel-boundary values in Z-direction: -5.10 - 5.10
Reading dose distribution...
Reading in the uncertainties on DOSE Distribution...
Have read dose distributions
```

STATDOSE: Statistical analysis

STATS MENU ----0 - Return to main menu 1 - Plot frequency vs. D1-D2 2 - Plot frequency vs. (D1-D2)/[(D1+D2)/2] * 100% 3 - Plot frequency vs. (D1-D2)/max central axis dose * 100% 4 - Plot frequency vs. (D1-D2)/sqrt(err1**2+err2**2)

STATDOSE: Normalization

NORM MENU

- 0 Main menu
- 1 Apply scaling factor
- 2 Normalize to average dose
- 3 Normalize to maximum dose along central axis
- 4 Normalize to dose in specific voxel
- 5 Denormalize

STATDOSE: Rebinning

```
REBINNING
Files currently loaded:
1 - 5MeV
2 - 5MeV - 2
Number of file to Rebin (0-MainMenu): 1
Number of Rebinned File (1-5,0-MainMenu): 3
Name of rebinned file (default=5MeV.rb):
Axis for rebinning (1-X,2-Y,3-Z): 1
Rebinning factor: 2
REBINNING....
                                             26
NUMBER OF VOXELS IN X,Y,Z DIRECTIONS:
                                                       50
                                                                 51
Voxel-boundary values in X-direction:
                                          -5.10 - 5.10
Voxel-boundary values in Y-direction:
                                         0.00 - 10.00
Voxel-boundary values in Z-direction:
                                          -5.10 - 5.10
```

STATDOSE: Plotting

If plot axis falls on voxel boundaries, then the plotted dose is the voxel with the lower index (lower X and/or Y value)

PLOT MENU

- 0 Main menu
- 1 Plot profiles
- 2 Comparison plot

STATDOSE: Plotting

```
COMPARE-PLOT
Axis for Compare-plot (0-PlotMenu, 1-X, 2-Y, 3-Z): 1
Coordinates of Axis (y,z): 0,0
Graph Title (default=Compareplot at (0.0,0.0)):
Output Filename (default=Compareplot.agr): # Remember what you put here!
Generate Automatic Offset? (y/n) [n]:
Files currently loaded:
1 - 5MeV
2 - 5MeV - 2
Input curve # to be plotted in this graph (0=>View Graph): 1
3D-dose distribution 1: 5MeV
Files currently loaded:
1 - 5MeV
2 - 5MeV - 2
Input curve # to be plotted in this graph (0=>View Graph): 2
3D-dose distribution 2: 5MeV
```

STATDOSE: Plotting

5MeV depth dose curves

