# GATE-RTion DoseActor validation procedure II: Voxelized geometry

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## **Test specifications**

Test name: Dose Actor, Voxelized geometry

Type of test: Functional testing

Configuration: GATEv8.1, Geant4.10.3.patch3, Rootv6.12/06

## **Background**

Dose actor can be used on a digital phantom or patient data as a voxelized geometry. Voxelized geometry is given as a HU distribution map and it is associated to material composition and material density. For details, please refer to the <u>GATE manual</u>.

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## 1- Disclaimer

This validation test aims at providing confidence that the Dose Actor works on a voxelized geometry as specified and the installation is correct.

This validation test does not cover all possibilities offered for voxelized geometries. It is recommended that the user adapt the test macros as closely as possible to its intended use, if different from the one proposed here.

## 2- Purpose of the test

This test validates that the Dose Actor applied to a voxelized geometry works as specified:

- The Hounsfield Material Generator and the density tolerance parameter works as expected.
- The energy deposited in a voxel defined by a HU value can be converted into dose to the material using the material density provided by the density/material/HU conversion tables.
- The dose deposited in a voxel defined by a certain HU value,  $HU_0$ , is the same as the dose deposited in a voxel defined by a material with the same density and composition properties that are related to  $HU_0$ .
- Complex voxelized geometry is placed in space as the users desires.

## 3- Overview of the test

The test is divided in four main parts. The first and second (A and B) parts use an image consisting of a single voxel (defined by a HU value). The third part (C) uses a box created in GATE. A, B and C parts require the use of the macro 'mac/mac1voxel.mac' and the last part (D), the 'mac/maincomplex.mac' file. Part D uses an image consisting of 8 voxels and 3 different materials.

# 4- Material provided

For this test you will need the following material:

- Validation procedure [this file]: overview of voxelized geometry in Gate, explanation of the test exercises and results.
- Results.xlsl. It's an excel template where the user must copy and check the results of the test.
- Images:
  - o data/1-voxels.mhd 1 voxel containing HU value of 0
  - data/1-voxel-bone.mhd 1 voxel containing HU value of 950
  - o data/phantom.mhd 8 voxels containing HU value of 0, -1000 and 950
- Macro files for the simulation:
  - PART A,B and C: mac/main1voxel.mac, data/actor-1voxel.mac, data/voxelized\_phantom.mac, data/simple\_phantom.mac
  - PART D: mac/maincomplex.mac, data/actor-complex.mac, data/complex\_phantom.mac
- Other text files necessaries for the simulation:
  - data/Scheneider2000DensitiesTable.txt and
     data/Schneider2000MaterialsTable.txt (it is described in section 5)
  - data/PlanDescriptionFile\_singlespot.txt,
     data/PlanDescriptionFile\_4spots.txt,
     data/PlanDescriptionFile\_1spot\_offcenter.txt and
     data/SourceDescriptionFile.txt required for the TPS source.

# 5- Available options

A digital phantom or patient data as a voxelized geometry can be used as input in Gate. The user must include several options in GATE macros to handle a voxelized geometry. A brief summary of some of the most important steps is given below:

#### 1. Conversion into material definitions.

Two input files are required in order to convert voxel values (expressed in HU) into materials:

/gate/HounsfieldMaterialGenerator/SetMaterialTable data/Schneider2000MaterialsTable.txt /gate/HounsfieldMaterialGenerator/SetDensityTable data/Schneider2000DensitiesTable.txt

The first file ('data/Scheneider2000MaterialsTable.txt') is a calibration text that splits the HU range into several materials.

The second file ('data/Scheneider2000DensitiesTable.txt') is the CT calibration of your scanner and indicates the relation in between HU values and mass density (g/cm³). Instead of defining a new Geant4 material (atomic composition and density) for each different HU, a single material is defined for a range of HU values belonging to the same material range in the first file ('data/Scheneider2000MaterialsTable.txt'). The densities of those single materials differ less than the density tolerance value. The smaller the density tolerance value, the larger the number of materials generated by Gate. This parameter can be defined by the user as follows:

/gate/HounsfieldMaterialGenerator/SetDensityTolerance 0.1 g/cm<sup>3</sup>

## Two output files are generated by the HounsfieldMaterialGenerator in Gate:

/gate/HounsfieldMaterialGenerator/SetOutputHUMaterialFilename data/HU2mat.txt
/gate/HounsfieldMaterialGenerator/SetOutputMaterialDatabaseFilename data/HUmaterials.db
/gate/HounsfieldMaterialGenerator/Generate

These output files are required by Geant4 and they had to be imported using the following commands:

/gate/geometry/setMaterialDatabase data/HUmaterials.db /gate/patient/geometry/setHUToMaterialFile data/HU2mat.txt

If the simulation needs to be repeated (and the same density tolerance is desired), the HounsfieldMaterialGenerator can be deactivated. However, the user must not forget to import HUmaterials.db and HU2mat.txt files. In this way, one can spare the initialization time used by the HounsfieldMaterialGenerator.

## 2. Patient virtual container

A patient virtual container needs to be created. It consists on a rectangular box called in this example patient\_box (set to Air) where a daughter, called patient, is created. The voxelized image is attached to patient.

/gate/patient/geometry/setImage

images/{image\_name}.mhd

## 3. Navigation algorithm

Gate has available three different "navigator" algorithms that allow to track particles from voxel to voxel. However, only one of them is recommended for its use in dosimetry: the *Nested Parametrised method* (available since Gate 6.1).

/gate/patient\_box/daughters/insert

Image Nested Parametrised Volume

Based on parameterized volume, this method allows Gate storing single voxel representation in memory and dynamically changing its location and composition at runtime during the navigation. The main advantaged is the high efficiency in memory space. Images are split into sub-volumes of homogeneous composition, which are parallelepipeds, either of the voxel size or larger. The main drawback is that all the particles are forced to stop at the boundaries of all parallelepipeds, generating a supplementary step and additional time cost, even if the two neighbouring parallelepipeds share the same content.

## 6- Validation test

## A. HU generator

For Part A, we are going to use the macro file 'mac/main1voxel.mac'.

- 1. Density tolerance selection works as expected:
  - a. Open 'mac/main1voxel.mac' and activate the command:

```
/control/alias type "voxelized"
```

iii /control/alias type "simple" must be deactivated (commented) !!!

b. Select a density tolerance of 0.1 g/cm3

/control/alias dt "0.1"

c. Run the simulation with a small number of primaries (e.g. 1)

**Result:** 2 files have been generated: 'data/HU2mat-0.1.txt' and 'data/HUmaterials-0.1.db'. To verify the results, open 'HUmaterials-0.1.db' and look for arbitrary materials. Observe the contiguous materials and verify that the density grid is not greater than 0.1 g/cm<sup>3</sup>.

When the density difference in between 2 materials (see Schneider table file) is higher than the density tolerance, new sub-materials are created. This case is illustrated in the Example 1 (see below). AmalgamTooth\_32, AmalgamTooth\_33 and AmalgamTooth\_34 have the same material composition but different densities. The density difference is 0.1 g/cm³, the same as the density tolerance.

#### Example 1:

```
# Material corresponding to H=[
                                    # Material corresponding to H=[
                                                                         # Material corresponding to H=[
                                                                         1975.01;2142.51
1640;1807.5]
                                    1807.5;1975.01
AmalgamTooth_32: d=2.03808
                                    AmalgamTooth_33: d=2.13808
                                                                         AmalgamTooth_34: d=2.23808
                                    g/cm3; n=4;
                                                                         g/cm3; n=4;
g/cm3; n=4;
+el: name=Copper; f=0.04
                                    +el: name=Copper; f=0.04
                                                                         +el: name=Copper; f=0.04
+el: name=Zinc: f=0.02
                                    +el: name=Zinc: f=0.02
                                                                         +el: name=Zinc; f=0.02
+el: name=Silver; f=0.65
                                    +el: name=Silver; f=0.65
                                                                         +el: name=Silver; f=0.65
+el: name=Tin: f=0.29
                                    +el: name=Tin; f=0.29
                                                                         +el: name=Tin; f=0.29
```

```
\begin{split} |d({\rm AmalgamTooth\_33}) - d({\rm AmalgamTooth\_32})| &= |2.13808 - 2.03808 | = 0.1 \\ |d({\rm AmalgamTooth\_33}) - d({\rm AmalgamTooth\_34})| &= |2.13808 - 2.23808 | = 0.1 \\ \end{split}
```

When the density different in between 2 materials (see Schneider table file) is smaller than the density tolerance, new sub-materials are not needed. This case is illustrated in the Example 2 (see below). AT\_AG\_SI3\_12, AT\_AG\_SI4\_13 and AT\_AG\_SI5\_14 are 3 materials with different material compositions.

## Example 2:

```
# Material corresponding to H=[
                                  # Material corresponding to H=[
                                                                    # Material corresponding to H=[
-52;-22]
                                  -22;8]
                                                                    8;19]
AT_AG_SI3_12: d=984.277
                                  AT_AG_SI4_13: d=1.01117
                                                                    AT_AG_SI5_14: d=1.02955
mg/cm3; n=8;
                                  g/cm3; n=7;
                                                                    g/cm3; n=8;
+el: name=Hydrogen; f=0.11
                                  +el: name=Hydrogen; f=0.108
                                                                    +el: name=Hydrogen; f=0.106
+el: name=Carbon; f=0.458
                                  +el: name=Carbon; f=0.356
                                                                    +el: name=Carbon; f=0.284
+el: name=Nitrogen; f=0.015
                                  +el: name=Nitrogen; f=0.022
                                                                    +el: name=Nitrogen; f=0.026
+el: name=Oxygen; f=0.411
                                  +el: name=Oxygen; f=0.509
                                                                    +el: name=Oxygen; f=0.578
+el: name=Sodium; f=0.001
                                  +el: name=Phosphor; f=0.001
                                                                    +el: name=Phosphor; f=0.001
                                  +el: name=Sulfur; f=0.002
+el: name=Phosphor; f=0.001
                                                                    +el: name=Sulfur; f=0.002
+el: name=Sulfur; f=0.002
                                  +el: name=Chlorine; f=0.002
                                                                    +el: name=Chlorine; f=0.002
+el: name=Chlorine; f=0.002
                                                                    +el: name=Potassium; f=0.001
```

```
|d(AT_AG_SI4_13) - d(AT_AG_SI3_12)| = |1.01117 - 0.984277| = 0.0269
|d(AT_AG_SI4_13) - d(AT_AG_SI5_14)| = |1.01117 - 1.02955| = 0.0184
```

d. Select a density tolerance of 0.01 g/cm³: /control/alias dt "0.01"

e. Run the simulation with a small number of primaries (e.g. 1)

**Result:** 2 new files have been generated: HU2mat-0.01.txt and HUmaterials-0.01.db. To verify the results, open 'HUmaterials-0.01.db' and look for an arbitrary material (for example, now HU=0 corresponds to a different material (AT\_AG\_SI4\_98) than in the previous Example 2). Observe the contiguous materials and verify that the density grid is not greater than 0.01 g/cm<sup>3</sup>.

```
# Material corresponding to H=[ -22;-10.8458 ]

AT_AG_SI4_97: d=1.00273 g/cm3; n=7;

[..]

# Material corresponding to H=[ -10.8458;0.308419 ]

AT_AG_SI4_98: d=1.01273 g/cm3; n=7;

[..]

# Material corresponding to H=[ 0.308419;8 ]
```

AT\_AG\_SI4\_99: d=1.02117 g/cm3; n=7;

$$|d(AT_AG_SI4_98) - d(AT_AG_SI4_97)| = |1.00273 - 1.01273| = 0.01$$
  
 $|d(AT_AG_SI4_98) - d(AT_AG_SI4_99)| = |1.01273 - 1.02117| = 0.00844$ 

 f. As explained before, one can spare time during initialization by deactivating the Hounsfield Material Generator ('data/voxelized\_phantom.mac').

#/gate/HounsfieldMaterialGenerator/Generate

g. Do not forget to give as input the conversion tables generated in the previous exercises.

/gate/geometry/setMaterialDatabase data/HUmaterials-{dt}.db /gate/patient/geometry/setHUToMaterialFile data/HU2mat-{dt}.txt

## **B.** Dose calculation from energy deposited

For Part B, we are going to still use the macro file 'mac/main1voxel.mac' and a density tolerance of 0.01 g/cm<sup>3</sup>. If you have generated the files 'HUmaterials-0.01.db' and 'HU2mat-0.01.txt' in section A, you don't need to generate them again.

- a. Run the simulation two times: first time, using image `1-voxels.mhd' and then `1-voxel-bone.mhd' (`mac/main1voxel.mac'). We recommend 10.000 primaries the computation time is less than 2 min.
- b. Fill the following empty fields in the provided excel file 'Sheet 1':
  - i. HU: It must be 0 when using image `1-voxels.mhd' and 950 when using `1-voxel-bone.mhd'
  - ii. Density tolerance: 0.01 g/cm<sup>3</sup>
  - iii. HU min, HU max, Materials: Look for these data on files HU2mat-0.01.txt or HUmaterials-0.01.db
  - iv. Write down the total dose and deposited energy
  - v. The voxel size of the provided images is 10<sup>9</sup> cm<sup>3</sup>.
  - vi. You can find the density of both materials (HU=0 and 950) in HUmaterials-0.01.db

- c. The excel file will compute automatically the dose from the deposited energy (see Dose Actor validation procedure for more details). A small difference, about 0.01% is expected due to, for example, rounding errors. If the difference is less than 0.1% the field will change to green (accepted).
- C. Dose deposited in a voxel expressed by HU or defined by material.

In Part B, we have calculated the dose deposited in a voxel expressed by HU. In Part C, we will calculated in a simple geometry created in Gate ('data/simple\_phantom.mac'). It consists on a box of the same dimensions as the images in Part B.

- a. Open 'mac/main1voxel.mac' and activate the command: /control/alias type "simple"
- a. Run the simulation two times (we recommend 10.000 primaries or at least the same number of primaries that you have chosen in B.a.). First, in setMaterial command choose the material corresponding to HU=0 (which is AT\_AG\_SI4\_98 when using a density tolerance of 0.01 g/cm³) and the second time, set the material corresponding to HU=950 (which is Marrow\_Bone09\_162 when using a density tolerance of 0.01 g/cm³). iii If you use a different density tolerance you may need to use other materials!!!

Note: Gate can find the definition (density and composition) of these materials in the file 'Humaterials-0.01.db'. Make sure this file is still in your data folder.

- b. Copy the total dose and deposited energy in the excel template and check if the dose calculated from the deposited energy is below 0.1% as well as if these values are the same as the one obtained with the voxelized images in Part B.
- c. Additionally, one can verify if the I-value and/or stopping power values calculated in Geant4 for these two materials when using the simple geometry are the same that the ones calculated when using the voxelized image. To do this, they user needs to look into the electromagnetic (em) actor output files. Since HU refers to a certain material and we use the definition of this material for building our box in the simple geometry, I-value and stopping power values must be the same.

## **D.** Complex voxelized geometry

For the last part, an 8-voxel image ('phantom.mhd') (Figure 1) will be used. It contains 8 pixels of 10x10x10 cm<sup>3</sup> and 3 different materials. Each voxel contains the HU of the corresponding material: water (HU=0), bone (HU=900) and air (HU=-1000).

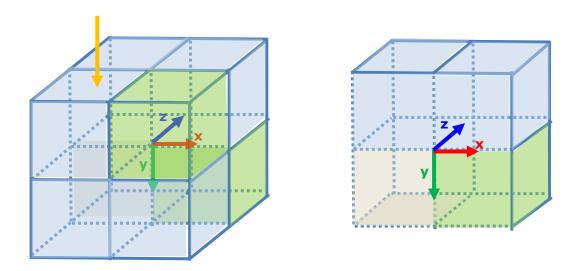


Figure 1. On the right, the complete 8-voxel image and on the left, the pixels that are located in the negative xy plane of the image. Blue, green and white correspond to HU=0, -1000 and 950, respectively. The yellow arrow indicates the direction and sense of the pencil beam ('data/PlanDescriptionFile\_1spot\_offcenter.txt').

The user must now use the macro 'mac/maincomplex.mac' and the irradiation plan 'data/PlanDescriptionFile\_1spot\_offcenter.txt'.

Before you start this test, you must know that, by default, HounsfieldMaterialGenerator is deactivated ('data/complex\_phantom.mac'). If you didn't perform part A to C, you need to activate this command to create the conversion tables.

The purpose of this test is to visualize the phantom in the space. The voxelized image (called 'patient') is a daughter geometry of a box called 'patient\_box'. We can change the position of the patient in space with different commands. By default, this test has zero translation and zero rotation.

a. In 'mac/maincomplex.mac', activate the visualization and run the simulation with a low number of primaries (e.g. 1).

**Result:** the pencil beam starts at the surface of the voxelized geometry and travels in the direction +y.

b. In 'data/complex\_phantom.mac', change the configuration as follows:

#### i. setTranslate

```
/gate/patient_box/placement/setTranslation 0.0 -10.0 0.0 cm
/gate/patient_box/placement/setRotationAxis 1 0 0
/gate/patient_box/placement/setRotationAngle 0 deg
/gate/patient/geometry/TranslateTheImageAtThisIsoCenter 0.0 0.0 0.0 mm
```

**Result:** patient geometry was translated 10 cm in -y direction. 'setTranslate' vector place the centre of the image at the indicated position (in this example, x=0.0 cm, y=-10.0cm and z=0.0cm).

## ii. TranslateTheImageAtThisIsoCenter

```
/gate/patient_box/placement/setTranslation 0.0 0.0 0.0 cm
/gate/patient_box/placement/setRotationAxis 1 0 0
/gate/patient_box/placement/setRotationAngle 0 deg
/gate/patient/geometry/TranslateTheImageAtThisIsoCenter 0.0 -100.0 0.0 mm
```

**Result:** Since the isocenter in Geant4 world is placed at (0,0,0), this option allows us to move our CT image so that the isocenter in patient coordinates is placed according to the treatment plan prescription. For example, if isocenter in treatment plan is (0,-100,0) mm, this corresponds to a translation in the opposite direction in Geant4 world coordinates ((0,+100.0,0)) mm).

Before continuing, you must de-activate the visualization.

- c. Re-run the simulation with the default values (zero translation, zero rotation) with a higher number of primaries (e.g. 10.000).
- d. In 'data/complex\_phantom.mac', change the configuration as follows:

#### iii. setRotation

```
/control/alias/ dg "-90"
/gate/patient_box/placement/setTranslation 0.0 0.0 0.0 cm
/gate/patient_box/placement/setRotationAxis 0 1 0
/gate/patient_box/placement/setRotationAngle {dg} deg
/gate/patient/geometry/TranslateTheImageAtThisIsoCenter 0.0 0.0 0.0 mm
```

#### e. Re-run the simulation

f. Paste `complex\_0\_Profile\_justWater-Edep.txt' and `complex\_-90\_Profile\_WaterBone-Edep.txt' in the corresponding space of the excel file Sheet 2.

**Result:** In the excel file we must observe a plot which is similar to Figure 2. The blue line corresponds to a rotation angle of 0 degree. It represents a smooth Bragg peak curve since the beam has traversed 2 voxels of the same material (water, HU=0). The red line corresponds to a rotation angle of -90 degree. In this case, the beam impinged at a different location of the image. The red Bragg peak curve contains a step at 10 cm which corresponds to the boundary in between the two voxels: water (HU=0) and bone (HU=950).

Note: The coordinates of the dose actor are the same as the one of the geometry to which it is attached. When no rotation is applied (angle=0), the dose actor profile must be centred (setPosition command) at (-50, 0, -50) mm in order to record the proton beam (see Figure 1). When we rotate the geometry, the beam impinges in a new location of the image and a new position of the profile ((-50, 0, 50) mm) is required in order to keep recording the energy deposited by our single beam.

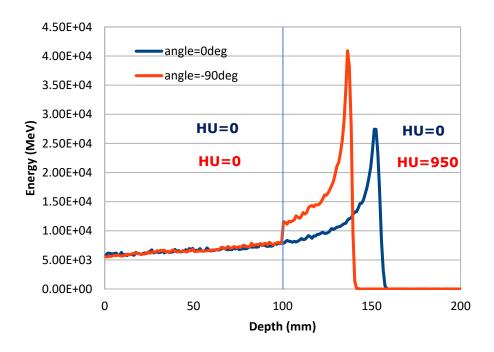


Figure 2. Deposited energy profile of a pencil beam traversing 2 voxels with HU of 0 (blue) and 2 voxels with HU of 0 and 950 (red).

#### **Annex**

This annex does not consist in a quantitative evaluation. It allows the user to get familiar with the use of voxelized images.

- a. Use 'mac/maincomplex.mac' but now, load the irradiation plan called 'data/PlanDescriptionFile\_4spots.txt'.
- b. Re-run the simulation (number of primaries recommended: > 10.000)
- c. An output consisting in a 3D image (1 mm spacing) is generated.
- d. Open the 'output/\*-Dose.mhd' with VV (or an analogous software).
- e. Your result must be similar to the one presented in Figure 3 (zero rotation and zero translation).

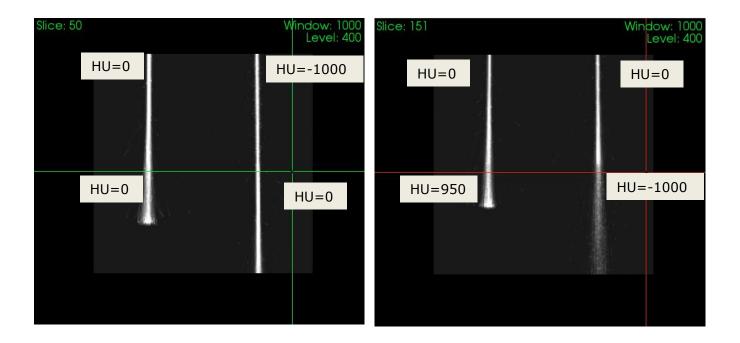


Figure 3. Dose distribution of 4 pencil beams (zero rotation). Image visualized with VV.