MEDLINAC2 & DICOM

ANDENNA C, CACCIA B, CHAUVIE S

- Istituto Superiore di Sanità Roma, Italy
- Ospedale Santa Croce e Carle, Cuneo
- INFN Italy
MC Dose calculation in Radiotherapy

How accurate is the dose calculation?

- Description of patients
- Energy deposition
- Geometry
- Physics
- DICOM
- Validation studies

[Image of dose distribution]
Why a new MedLinac

Necessity to have a general purpose program to

- Select accelerator/phantom
- Type of particles source (use of the phase space)
- Check results against experimental data
- Output in ‘small’ size files
- Convergence criteria
- Error estimation
Medical Linac advanced example

Advanced example released since 2009

Typical linac with fake data (avoiding top secret!)
The example is based on a typical structure of a medical linear accelerator for Intensity Modulated Radiation Therapy (IMRT), such as Varian Clinac 2100 accelerator.

Documentation about the Geant4 medical linac advanced example:

http://geant4advancedexampleswg.wikispaces.com/ExamplesDocumentation
Different configuration
  Phase space data
Two type of particle sources may be chosen, a random generator of electrons gun shooting the target or particles loaded from a phase space. The program allows the generation of a plane phase space.

Documentation about the Geant4 medical linac advanced example:

http://geant4advancedexampleswg.wikispaces.com/ExamplesDocumentation
All in one simulation

/primaryParticleData/idParticleSource 1

```cpp
switch (this->idCurrentParticleSource)
{
    case idParticleSource_Random:
        this->GenerateFromRandom();
        break;
    case idParticleSource_CalculatedPhaseSpace:
        this->GenerateFromCalculatedPhaseSpace();
        break;
}
```
Phase Space data

switch (this->idCurrentParticleSource)
{
    case idParticleSource_Random:
        this->GenerateFromRandom();
        break;
    case idParticleSource_CalculatedPhaseSpace:
        this->GenerateFromCalculatedPhaseSpace();
        break;
}
Phase space data

• Type of data saved

<table>
<thead>
<tr>
<th>n</th>
<th>X [mm]</th>
<th>Y [mm]</th>
<th>Z [mm]</th>
<th>dx</th>
<th>dy</th>
<th>dz</th>
<th>kinEnergy [MeV]</th>
<th>Part Type</th>
<th>Prim part type</th>
<th>Prim part</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>18.57</td>
<td>45.06</td>
<td>-831</td>
<td>0.03934</td>
<td>0.095413</td>
<td>0.99455</td>
<td>1.41684</td>
<td>22</td>
<td>11</td>
<td>33</td>
</tr>
<tr>
<td>1</td>
<td>57.61</td>
<td>27.74</td>
<td>-831</td>
<td>0.12265</td>
<td>0.058820</td>
<td>0.99004</td>
<td>1.35906</td>
<td>22</td>
<td>11</td>
<td>71</td>
</tr>
</tbody>
</table>
Phantoms calculation

- Dose calculation in 2 phantoms:
  - 1 homogeneous and 1 with cubic etereogeneity

- The user may choose a cubic phantom filled with water or a phantom filled with an equivalent lung-tissue with a inhomogeneity (a 6 cm sided PMMA cube) located in the centre of the phantom.
Energy deposition calculation

\[
\bar{d} = \frac{\sum_{i}^{N} d_i}{N}
\]

\[
\sigma^2_{\bar{d}} = \sum_{i}^{N} \frac{(d_i - \bar{d})^2}{N(N-1)} = \frac{\sum_{i}^{N} d_i^2 - N\bar{d}^2}{N(N-1)} = \frac{\sum_{i}^{N} d_i^2 - \left(\sum_{i}^{N} d_i\right)^2}{N(N-1)}
\]

- G4double depEnergy= aStep->GetTotalEnergyDeposit();
- voxelMass=density*voxels.halfSize.X*voxels.halfSize.Y*voxels.halfSize.Z;
- dose=depEnergy/voxelMass;
- Voxels.nEvents++;
- voxels.depEnergy+=dose;
- voxels.depEnergy2+=dose*dose;
# Phantom voxelization

- Type of data saved

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>fullWaterPhantomPV</td>
<td>-297</td>
<td>-297</td>
<td>-177</td>
<td>0</td>
<td>0</td>
<td>27</td>
<td>1.78e-09</td>
<td>1.36e-18</td>
<td>9</td>
</tr>
<tr>
<td>...</td>
<td></td>
<td></td>
<td>...</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Experimental vs Calculated data

• Type of data saved

% 6 MeV Tutte le misure gaf 10 luglio 2009 campo 3x3
n208=2;
fh208=[
  0 10 3.10291e+07
  10 758 2.73489e+07
];

%d208=[
  0 0 -300 0.6644 5.93877e-09 1.01606e-18 49 0.184275 0.0170647
  0 0 -290 4.3128 1.44254e-07 1.05554e-15 274 4.47607 0.972941
  0 0 -258 2.7057 7.59039e-08 2.80751e-16 65 2.35523 0.433426
  ....
];

% x [mm], y [mm], z [mm], expDose [Gy], Calculated dose [Gy], Calculated dose2 [Gy^2], nEvents, normDose [Gy], normDoseError [Gy]
Convergence

- Simulation is stopped when simulation accuracy is comparable to experimental data
Analysis

- Lefto to the user (matlab)
Medical Linac - DICOM

Patient

Linac

Quads: 7272
Triangles: 4272
DICOM

- Phantom is good for Moving towards real patient
- DICOM CT interface
What’s a patient?
This file is used by NIM image to dump DICOM file headers during import of DICOM images. It must be located in the same folder as NIM image or in the System folder.

The elements were cut, unmodified from "datadict.txt" used by the unix program "dicojump.c". That header was derived from the AN/AFI Data Dictionary.

The data elements listed in this file must be defined with the following format:

```
  { Group, Element, 'VR', 'Name' }
```

Each line must be preceded by the left curly bracket ("{").

The group and element number MUST be defined as hexadecimal numbers and must be preceded by the small letter '0'.

The 'VR' code must be in single quotes and is defined by the DICOM Part 6 document.

Duplicate and improperly formatted lines will be ignored.
well defined physical quantity. For the case of polychromatic x-rays, one could assume that the reconstructed attenuation values are mean values according to the spectral function \( f(E) \). Unfortunately, the attenuation value of one and the same tissue depends on the location within the patient. This effect is caused by beam hardening: the energy spectrum of a polychromatic x-ray is shifted towards higher energies while penetrating a medium, because the physical cross sections are bigger for low-energy photons. On state-of-the-art CT scanners, this disturbing effect can be eliminated to a high degree by correcting the projection value \( \lambda \) of each line integral. In the following, we will assume that the reconstructed attenuation values of the
We must determine: mass density $\rho$ and elemental composition $w_i$.

\[ \tilde{\mu}(s) = \frac{\int \hat{f}(E) \mu(E, s) \, dE}{\int \hat{f}(E) \, dE} \]

\[ H = \left( \frac{\tilde{\mu}}{\tilde{\mu}_{H_2O}} - 1 \right) 1000 \]

\[ \frac{1}{\tilde{\mu}_{H_2O}} N_A \sum_{i=1}^{n} \left[ \frac{w_i}{A_i} \tilde{\sigma}_i \right] \quad (\text{cm}^3/\text{g}) \]
From phantom to MC

Rows,columns(#): 512 512
PixelSpacing_X,Y(mm): 0.875 0.875
SliceThickness(mm): 5.0
SliceLocation(mm): 20.0

Header + DATA SETS
...cont...

<table>
<thead>
<tr>
<th>Density Range</th>
<th>Materials</th>
</tr>
</thead>
<tbody>
<tr>
<td>[ 0.100 , 0.351 ]</td>
<td>Lungs (inhale)</td>
</tr>
<tr>
<td>[ 0.351 , 0.800 ]</td>
<td>Lungs (exhale)</td>
</tr>
<tr>
<td>[ 0.919 , 0.979 ]</td>
<td>Adipose</td>
</tr>
<tr>
<td>[ 0.979 , 1.004 ]</td>
<td>Breast</td>
</tr>
<tr>
<td>[ 1.004 , 1.043 ]</td>
<td>Phantom</td>
</tr>
<tr>
<td>[ 1.043 , 1.109 ]</td>
<td>Liver</td>
</tr>
<tr>
<td>[ 1.109 , 1.113 ]</td>
<td>Muscle</td>
</tr>
<tr>
<td>[ 1.113 , 1.400 ]</td>
<td>Trabecular Bone</td>
</tr>
<tr>
<td>[ 1.496 , 1.654 ]</td>
<td>Dense Bone</td>
</tr>
</tbody>
</table>

ICRU 46

y = 995.06x - 1000.1
R² = 0.9981

Density step

3-D view

Density step

Geant 4
... and ends.
ML2-DICOM

35 million particles in 1 hour (512x512x3 voxel, 40x40 field)
Patient modelling is not sophisticated.

**Soft tissue:**
- HU tissue as given by ICRU are position dependent

**Bone:**
- Linearity HU-$\rho_{el}$
- Bone to bone marrow dilution

**Lung:** HU-$\rho$

linearity
**Medical_linac folder structure:**

<table>
<thead>
<tr>
<th>File</th>
<th>Size</th>
<th>Date/Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>acc1.mac</td>
<td>4 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>GNUmakefile</td>
<td>4 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>History</td>
<td>8 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>include</td>
<td>188 KB</td>
<td>17/dic/2010 11.00</td>
</tr>
<tr>
<td>Launches</td>
<td>17 MB</td>
<td>17/dic/2010 11.00</td>
</tr>
<tr>
<td>ml2</td>
<td>45 KB</td>
<td>Today, 07.55</td>
</tr>
<tr>
<td>ml2.cc</td>
<td>8 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>ml2.mac</td>
<td>8 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>phan1.mac</td>
<td>4 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>README_MedLinac2.txt</td>
<td>12 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
<tr>
<td>src</td>
<td>352 KB</td>
<td>17/dic/2010 11.00</td>
</tr>
<tr>
<td>vis.mac</td>
<td>4 KB</td>
<td>17/dic/2010 10.24</td>
</tr>
</tbody>
</table>
Launches folder structure:

- **Launches**
  - **dicom**
    - Input data (dicom format images and experimental measurements on a dosimetric phantom)
  - **experimental**
  - **macro_files**
    - Macro file containing user accelerator specifications
  - **results**
    - Results (matlab format)
Macro_files folder structure:

- **accelerator**: Defines Energy and field size for the accelerator (*acc1.mac*).
- **phantom**: Contains different phantoms (dicom images set included).
- **main**: file.mac, an ascii file with geant4 command user may customize the macro file.
In this file a field 200x200mm is defined for an energy value of 6MeV.
In this file is specified where is the set of the DICOM images that define the phantom, the dimensions, the conversion table.
### Launch parameters

#### Visualization

/OnlyVisio true  # switch the visualization mode

#### Experimental comparison and convergence

#### Phase space

#### Simulation output

#### Number of primary events

#### NUMBER STORED

#### Primary generator

#### PHANTOM

#### ACCELERATOR

#### INFO

# All possible choices

# Particle sources
# randomTarget // random from target
# phaseSpace // from phase space

# Accelerators
# acc1 // non real accelerator but working

# Phantoms
# fullWater // water box
# boxInBox // box in a box phantom
# Dicom1 // phantom dicom
Ready to run the example

$G4WORKDIR/medical_linac/ml2 ml2.mac 22

executable

macro file

seed
Navigation

- The 1D optimisation. It will be very slow because each time a track exits a voxel it has to loop to all other voxels to know which one it may enter.
- The 3D optimisation with G4SmartVoxel: a 3D grid is built, so that the location of voxels is fast, but it requires a lot of memory.
- Using G4NestedParameterisation. The search is done hierarchically in X, Y and Z. It is fast and does not require big memory.
- Using G4PhantomParameterisation/G4RegularNavigation: an special algorithm to navigate in regular voxelised geometries (see GEANT4 doc). This is the fastest way without any extra memory requirement (and it is the default in this example). It includes an option (default) to skip frontiers between voxels when they have the same material. When using this option at each step the energy is all deposited in the last voxel; for proper distribution of the dose (=energy/volume) the G4PSDoseDeposit_RegNav scorer can be used (see below).
Conclusions

- Developing MC application is not a core activity of my research group (no more)

- We provide scientific community with a tool that could be the base of their own application

- Complete simple trade off

- ML2-DICOM will be released on December
  (http://geant4.web.cern.ch/geant4/)
Thanks for the attention