



蘭州大學
LANZHOU UNIVERSITY

# Medical applications (part I)

23rd FLUKA Beginner's Course
Lanzhou University
Lanzhou, China

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# Medical Physics and related disciplines applications



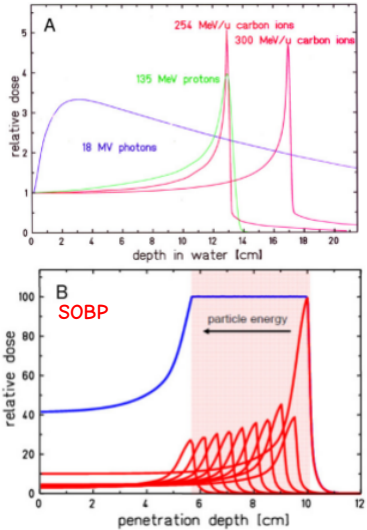
- Nuclear Medicine
  - Dosimetry
- Radiotherapy
  - Simulation of therapy devices
  - Simulations of treatments / treatment assessment
- Particle Therapy
  - Shielding
  - Facility commissioning
  - Treatment planning and forward checks
  - Predictions and data processing for monitoring applications (imaging for hadrontherapy)
  - Design of instruments, dosimetry
  - Calculation for shielding and rad. protection in facilities

# Medical applications: Particle Therapy



One of the powerful applications of FLUKA & FLAIR is related to Particle Therapy.

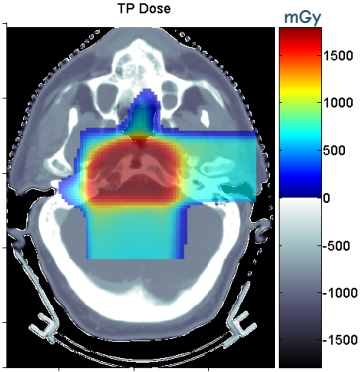
- Particle Therapy is a radiation therapy to treat tumors (deep seated, resistant to conventional RT with photons…)
- Exploits "heavy" charged particle beams (p, 12C,..); typical energy loss in matter characterized by the Bragg Peak (BP)
- With higher beam kinetic energy, particles will travel further and the BP will be situated deeper inside the target (the patient)
- Several Bragg Peaks with different energies can be summed up to cover the full tumor volume ("Spread-Out-Bragg-Peak (SPOB)"

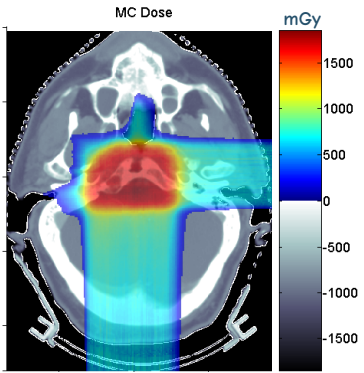


# The issue of complex geometries: patient cases



In clinics, treatment plans are needed. The medical physicists have to decide in advance how to target the tumor based on patient CT. CT scans of a human body are important also for dosimetric calculations of the planned treatment in radiotherapy.

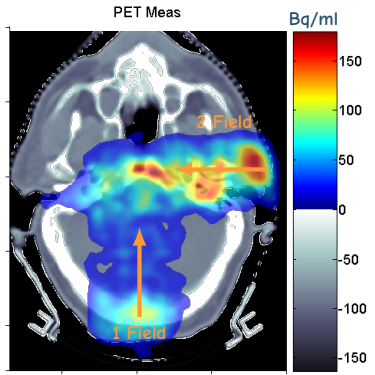


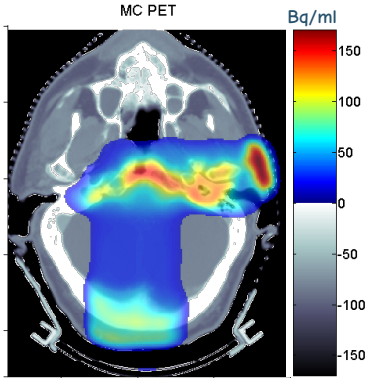




Example: Patient with clival chordoma receiving a posterior–anterior followed by a lateral field (0.96 GyE each), K. Parodi et al., Int J Radiat Oncol Biol Phys. 2007 July 1; 68(3): 920–934

# Post irradiation PET/CT@MGH

Patient with clival chordoma receiving a posterior–anterior followed by a lateral field (0.96 GyE each). PET imaging 26 min and 16 min after field applications, respectively:



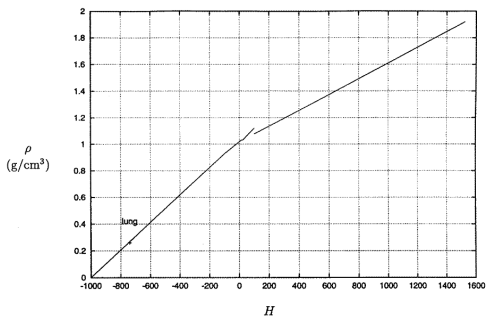




K. Parodi et al., Int J Radiat Oncol Biol Phys. 2007 July 1; 68(3): 920–934

# CT stoichiometric calibration



- The CT scan contains integer values in units of "Hounsfield" reflecting the x-ray attenuation coefficient $\mu_X$:
  $HU_X = 1000\ (\mu_X - \mu_{H_2O}) / \mu_{H_2O}$, typically $-1000 \leq HU \leq 3500$
- Assign to each material a "nominal mean density", e.g. using the density at the center of each HU interval **(Jiang et al, MP 2004)**




But "real density" (and related physical quantities) varies continuously with HU value!!

W. Schneider *et al* 2000 Phys. Med. Biol. 45 459

# Practical issues: Assigning materials to organs



- How to assign realistic human tissue parameters (=materials) for MC calculations?
- How to find a good compromise between the number of different HU values ($\sim 3000 - 5000$) and the materials to be considered in the MC? (issues on memory and computation speed when attemtping to treat each HU number as a different material)
- How to preserve continuos, HU-dependent information when segmenting the HU numbers into intervals sharing the same "tissue" material? critical for ion range calculation in PT!)

# CT stoichiometric calibration

CT segmentation into 24 materials of defined elemental composition (from analysis of 71 human CT scans)

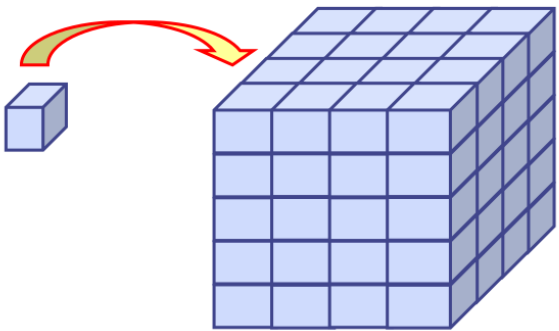
| | | $w_i$ (pp) | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $H$ | H | C | N | O | Na | Mg | P | S | Cl | Ar | K | Ca |
| Air, Lung | −1000—−950 | | | 75.5 | 23.2 | | | | | | 1.3 | | |
| adipose tissue | −950—−120 | 10.3 | 10.5 | 3.1 | 74.9 | 0.2 | | 0.2 | 0.3 | 0.3 | | 0.2 | |
| | −120—−83 | 11.6 | 68.1 | 0.2 | 19.8 | 0.1 | | | 0.1 | 0.1 | | | |
| | −82—−53 | 11.3 | 56.7 | 0.9 | 30.8 | 0.1 | | | 0.1 | 0.1 | | | |
| Soft tissue | −52—−23 | 11.0 | 45.8 | 1.5 | 41.1 | 0.1 | | 0.1 | 0.2 | 0.2 | | | |
| | −22–7 | 10.8 | 35.6 | 2.2 | 50.9 | | | 0.1 | 0.2 | 0.2 | | | |
| | 8–18 | 10.6 | 28.4 | 2.6 | 57.8 | | | 0.1 | 0.2 | 0.2 | | 0.1 | |
| | 19–80 | 10.3 | 13.4 | 3.0 | 72.3 | 0.2 | | 0.2 | 0.2 | 0.2 | | 0.2 | |
| | 80–120 | 9.4 | 20.7 | 6.2 | 62.2 | 0.6 | | | 0.6 | 0.3 | | | |
| | 120–200 | 9.5 | 45.5 | 2.5 | 35.5 | 0.1 | | 2.1 | 0.1 | 0.1 | | 0.1 | 4.5 |
| | 200–300 | 8.9 | 42.3 | 2.7 | 36.3 | 0.1 | | 3.0 | 0.1 | 0.1 | | 0.1 | 6.4 |
| Skeletal tissue | 300–400 | 8.2 | 39.1 | 2.9 | 37.2 | 0.1 | | 3.9 | 0.1 | 0.1 | | 0.1 | 8.3 |
| | 400–500 | 7.6 | 36.1 | 3.0 | 38.0 | 0.1 | 0.1 | 4.7 | 0.2 | 0.1 | | | 10.1 |
| | 500–600 | 7.1 | 33.5 | 3.2 | 38.7 | 0.1 | 0.1 | 5.4 | 0.2 | | | | 11.7 |
| | 600–700 | 6.6 | 31.0 | 3.3 | 39.4 | 0.1 | 0.1 | 6.1 | 0.2 | | | | 13.2 |
| | 700–800 | 6.1 | 28.7 | 3.5 | 40.0 | 0.1 | 0.1 | 6.7 | 0.2 | | | | 14.6 |
| | 800–900 | 5.6 | 26.5 | 3.6 | 40.5 | 0.1 | 0.2 | 7.3 | 0.3 | | | | 15.9 |
| | 900–1000 | 5.2 | 24.6 | 3.7 | 41.1 | 0.1 | 0.2 | 7.8 | 0.3 | | | | 17.0 |
| | 1000–1100 | 4.9 | 22.7 | 3.8 | 41.6 | 0.1 | 0.2 | 8.3 | 0.3 | | | | 18.1 |
| | 1100–1200 | 4.5 | 21.0 | 3.9 | 42.0 | 0.1 | 0.2 | 8.8 | 0.3 | | | | 19.2 |
| | 1200–1300 | 4.2 | 19.4 | 4.0 | 42.5 | 0.1 | 0.2 | 9.2 | 0.3 | | | | 20.1 |
| | 1300–1400 | 3.9 | 17.9 | 4.1 | 42.9 | 0.1 | 0.2 | 9.6 | 0.3 | | | | 21.0 |
| | 1400–1500 | 3.6 | 16.5 | 4.2 | 43.2 | 0.1 | 0.2 | 10.0 | 0.3 | | | | 21.9 |
| | 1500–1600 | 3.4 | 15.5 | 4.2 | 43.5 | 0.1 | 0.2 | 10.3 | 0.3 | | | | 22.5 |

W. Schneider *et al* 2000 Phys. Med. Biol. 45 459

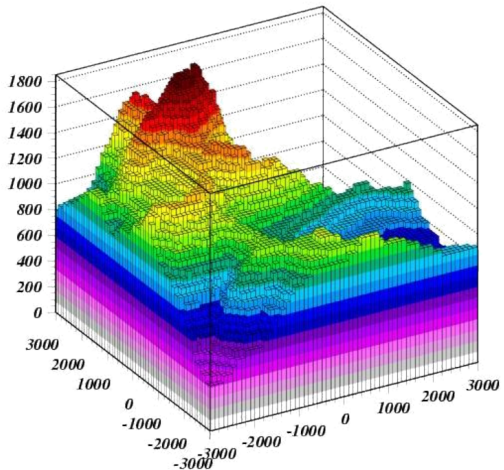
# From CT to FLUKA voxel geometry



- The user must convert his CT scan or equivalent data to a format understood by FLUKA: VOXEL geometry. (When starting from DICOM images, this is performed directly by FLAIR).
- It is possible to describe a geometry in terms of "voxels", i.e., tiny parallelepipeds (all of equal size) forming a 3-dimensional grid

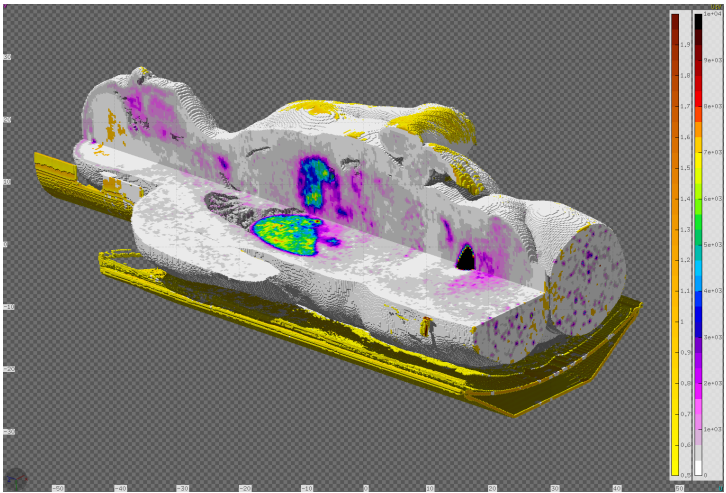


## The Gran Sasso mountain (Italy) in FLUKA:



# Voxel geometries: Examples

## Voxel geometry with PET-CT:



# From CT to FLUKA voxel geometry



- We will use loosely the word "organ" to indicate a group of voxels (or even more than one group) made of the same "tissue" material (same HU value or in a given HU interval)
- Assign an organ index to each voxel. In many practical cases, the user will have a continuum of CT values (HU), and may have to group these values in intervals
- Each organ is identified by a unique integer $\leq$ 32 767. The organ numbering does not need to be contiguous, i.e. "holes" in the numbering sequence are allowed.
- One of the organs must have the number **0** and plays the role of the medium surrounding the voxels (usually vacuum or air).
- Assign to each non-zero organ a voxel-region number. The voxel-region numbering has to be contiguous and starts from 1.

# The FLUKA voxel geometry



- All CT information can be given as input to FLUKA through a special file "*vxl" containing:
  - The number of voxels in each coordinate
  - The number of voxel-regions, and the maximum organ number
  - The voxel dimension in each coordinate
  - A list of the organ corresponding to each voxel
  - A list of the voxel-region number corresponding to each organ
  - Definition of Regions of Interests (ROI)
    - A list of the ROIs for each voxel
- The code handles each organ as a "Comb Geo" region, possibly in addition to other conventional "non-voxel" regions defined by the user
- The voxel structure can be complemented by parts written in the standard combinatorial geometry
- The code assumes that the voxel structure is contained in a parallelepiped. This RPP is automatically generated from the voxel information.

# How to convert a patient's CT to a VOXEL geometry



## What is needed:

- ☐ Patient's CT: Directory with DICOM files (.dcm)
- ☐ FLUKA input file (example.inp) with VOXEL card (and CORRFACT card)
- ☐ Process DICOM files to transform the patient's CT in a VOXEL geometry:
  - material.inp: file with conversion of HU to materials nominal density and composition
  - calib_curve.mat: file with density correction factors to be applied to the lower/upper limit of the HU range

(examples for the files material.inp and calib_curve.mat can be found in the `Medical_exercise/`-folder, see the following lecture).

# The material.inp-file



```
*
* Schneider parametrisation of HU to materials
* This file should be used together with the dicom/material.inp
*
* Based on the work of Andrea Mairani
*
MATERIAL         16.    32.066       2.0                              SULFUR
MATERIAL         15. 30.973761       2.2                              PHOSPHO
MATERIAL         17.   35.4527 0.0029947                              CHLORINE
MATERIAL         19.   39.0983     0.862                              POTASSIU
* MIXTURE : HU<-1020
MATERIAL                        .00315972                          0.HU<-1020
COMPOUND      -0.755  NITROGEN    -0.232    OXYGEN    -0.013     ARGONHU<-1020
STERNHEI     10.5961    1.7418    4.2759   0.10914    3.3994          HU<-1020
MAT-PROP                            85.7  HU<-1020
* MIXTURE : HU<-1015
MATERIAL                        .00717201                          0.HU<-1015
COMPOUND      -0.755  NITROGEN    -0.232    OXYGEN    -0.013     ARGONHU<-1015
* MIXTURE : HU<-1010
MATERIAL                         .0121874                          0.HU<-1010
COMPOUND      -0.755  NITROGEN    -0.232    OXYGEN    -0.013     ARGONHU<-1010
* MIXTURE : HU<-1000
MATERIAL                         .0207135                          0.HU<-1000
COMPOUND      -0.755  NITROGEN    -0.232    OXYGEN    -0.013     ARGONHU<-1000
* MIXTURE : HU<-995
MATERIAL                          .027735                          0.HU<-995
COMPOUND      -0.755  NITROGEN    -0.232    OXYGEN    -0.013     ARGONHU<-995
* MIXTURE : HU<-988
MATERIAL                         .0333252                          0.HU<-988
COMPOUND      -0.755  NITROGEN    -0.232    OXYGEN    -0.013     ARGONHU<-988
```

# The calib_curve.mat-file



```
#
# Schneider parametrisation of HU to materials
# This file should be used together with the dicom/material.inp
#
# Based on the work of Andrea Mairani
#
-1020 AIR 0.6825432 1.3174568
-1015 HU<-1015 0.720281108 1.27971895
-1010 HU<-1010 0.835391418 1.16460858
-1000 HU<-1000 0.733656625 1.16949124
-995 HU<-995 0.909584201 1.05424948
-988 HU<-988 0.909502356 1.09049764
-974 HU<-974 0.85108832 1.14891168
-962 HU<-962 0.902912681 1.09708732
-950 HU<-950 0.919883508 1.08011649
-925 HU<-925 0.862306423 1.13769358
-900 HU<-900 0.893000468 1.10699951
-830 HU<-830 0.783902333 1.21609767
-700 HU<-700 0.75158871 1.24841129
-500 HU<-500 0.765689411 1.23431059
-120 HU<-120 0.734835247 1.26516475
-83 HU<-83 0.980501545 1.01835909
-53 HU<-53 0.98600717 1.01305997
-23 HU<-23 0.986384099 1.01270032
7 HU<7 0.98674495 1.01236373
15 HU<18 0.995655766 1.00173225
80 HU<80 0.972407965 1.03421835
101 HU<120 0.980146255 1.00104493
120 HU<120 0.962511989 0.973311932245
200 HU<200 0.973911929092 1.02131168
```

# The input file



Prepare the usual input file.

The geometry is written like a normal Combinatorial Geometry input, but in addition a VOXELS card must be inserted right after the GEOBEGIN card and before the Geometry title card:

- WHAT(1), WHAT(2), WHAT(3) = x, y, z coordinates chosen as the origin of the "voxel volume", (i.e. of a region made of a single RPP body extending from WHAT(1) to WHAT(1) + NX*DX, …) which contains all the voxels
- WHAT(4) ROT-DEFI transformation applied to whole voxel RPP
- WHAT(5), WHAT(6): not used
- SDUM = name of the voxel file (extension will be assumed to be .vxl)

```
VOXELS      -35.068359-35.068359   -88.6855                          bodyCT
```

# The region-dependent CORRFACT card



- Materials are defined from groups of HU, but "real densities" varies continuously with HU
- The "CORRFACT" card allows to alter material density for dE/dx and nuclear processes
- The first two inputs specify a density scaling factor (restricted to the interval [2/3,3/2]) for charged particle ionization processes (WHAT(1)) and for all other processes (WHAT(2)) to the region(s) specified by the inputs WHAT(4-6) *[cf. manual]*
- This is especially important in ion beam therapy to force the MC to follow the same semi-empirical HU-range calibration curve as the Treatment Planning System (TPS) for dosimetric comparisons
- FLAIR automatically appends the CORRFACT cards calculated taking into account the calibration curves provided by the user at the end of the .vxl file.

# How to account for HU-dependent dEdx



- In the input
  - Let several regions share the same material composition and mean density according to CT segmentation (reduced number of materials to save memory / initialization time)

```
ASSIGNMA    BONE    VOXEL005 (region number 25)
ASSIGNMA    BONE    VOXEL016 (region number 31)
```

  - Use CORRFACT to impose the desired correction for stopping power ($\Rightarrow$ ion range!) in the regions corresponding to different organs IO (i.e., different HU values) sharing the same MATERIAL assignment

```
CORRFACT   0.85   0.0   0.0   VOXEL005
CORRFACT   1.30   0.0   0.0   VOXEL016
```

(region 25 corresponds to "softer" bone than region 31)

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