

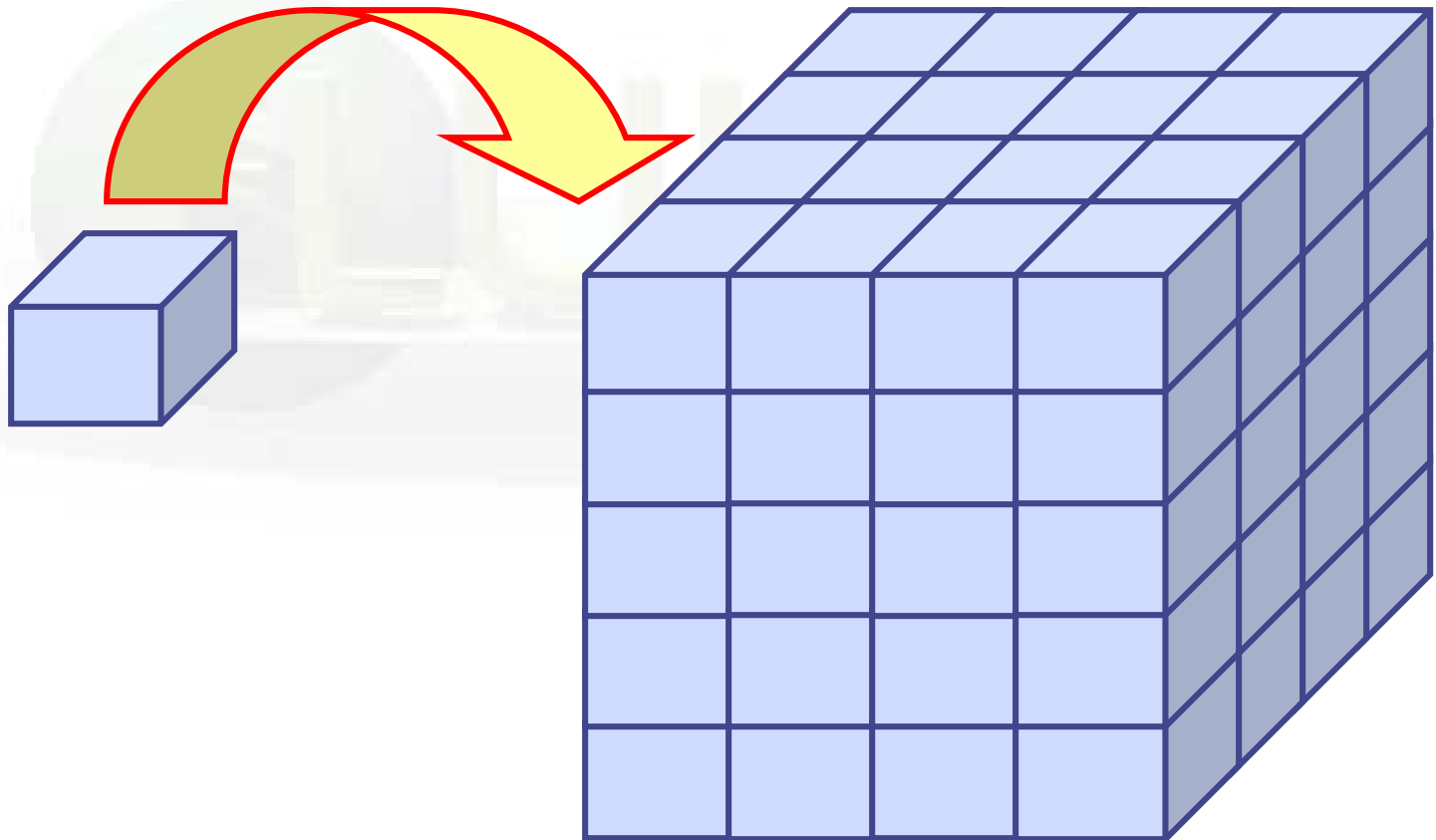


Voxels and Medical Applications

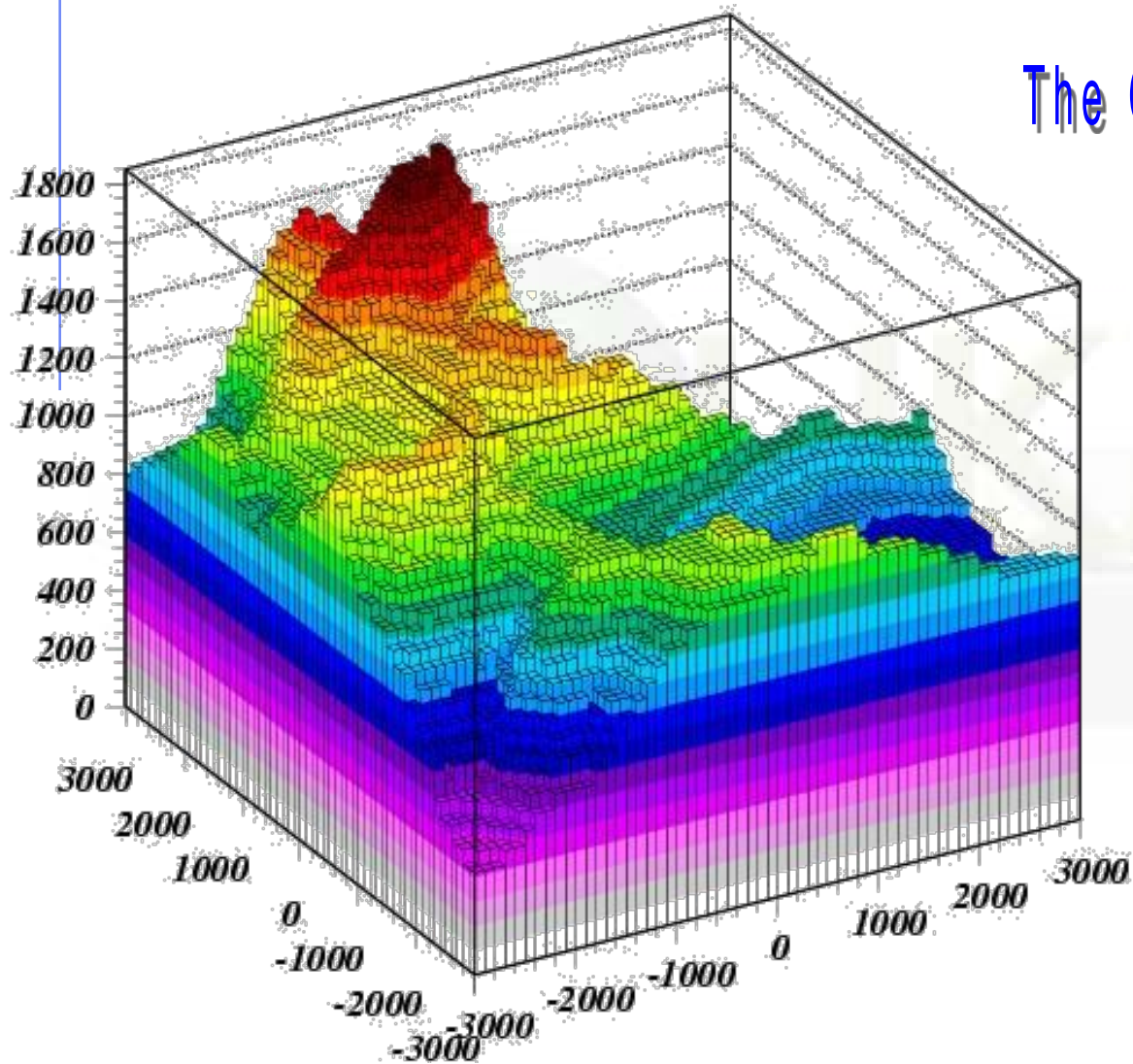
FLUKA Advanced course

The FLUKA voxel geometry

- It is possible to describe a geometry in terms of “**voxels**”, i.e., tiny parallelepipeds (all of equal size) forming a 3-dimensional grid



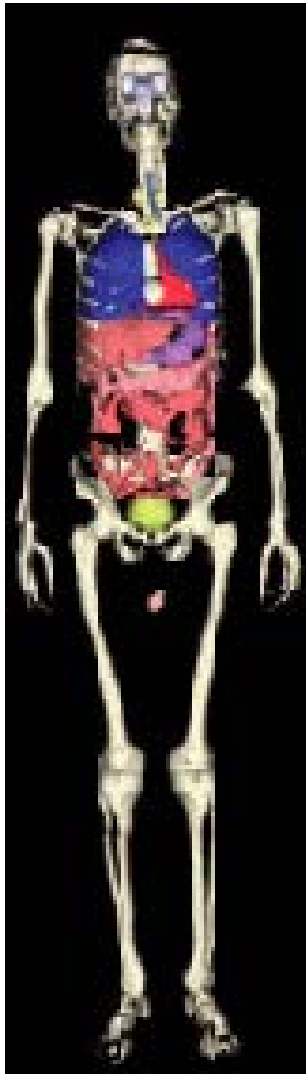
Voxel geometries: examples



The Gran Sasso in FLUKA

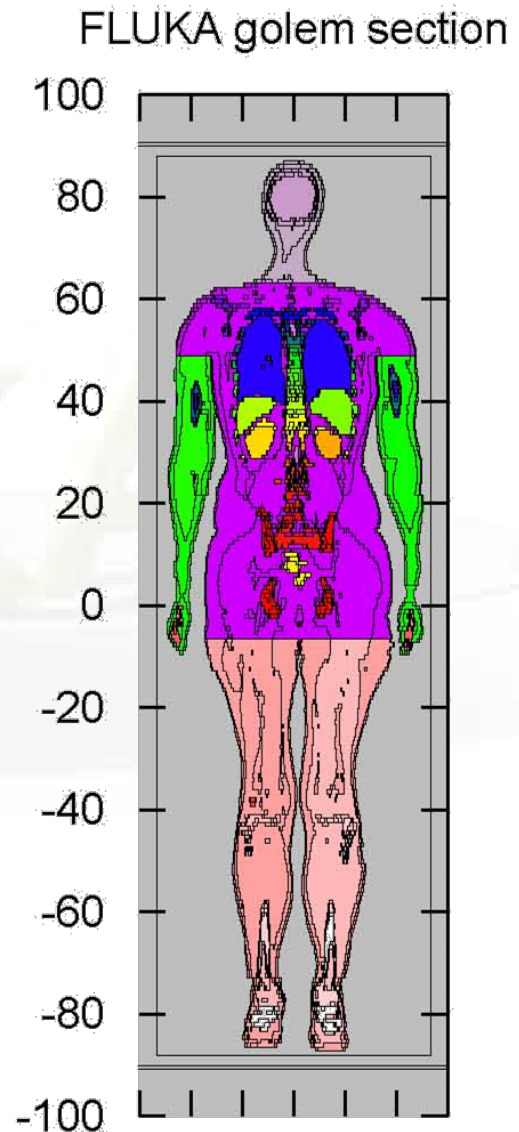
Voxel geometries: examples

The anthropomorphic **GOLEM** phantom



Implementation
in FLUKA
(radioprotection
applications)

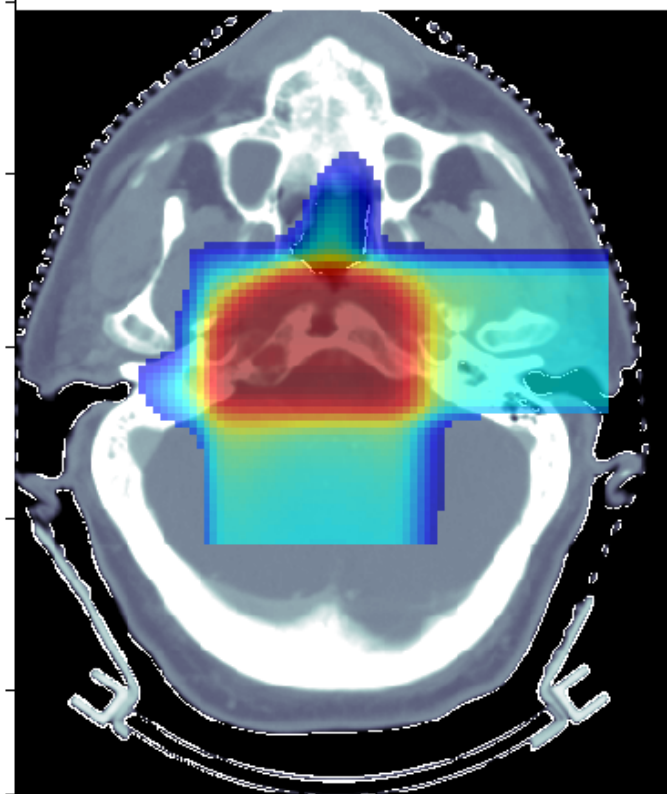
Petoussi-Henss
et al, 2002



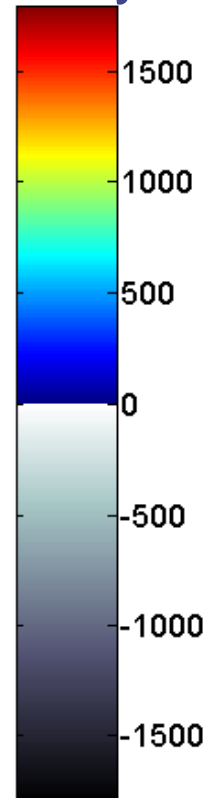
Voxel geometries in medical applications

- Voxel geometries are especially useful to import CT scan of a human body, e.g., for dosimetric calculations of the planned treatment in radiotherapy

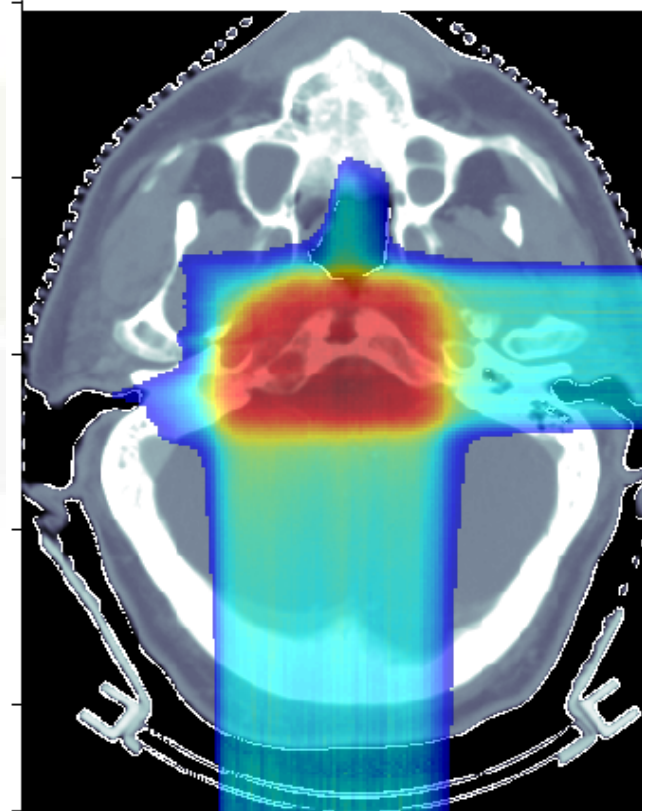
Commercial TPS



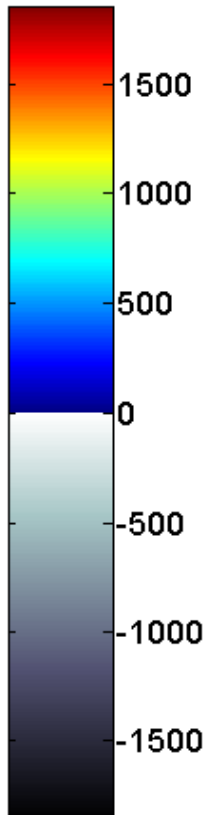
mGy



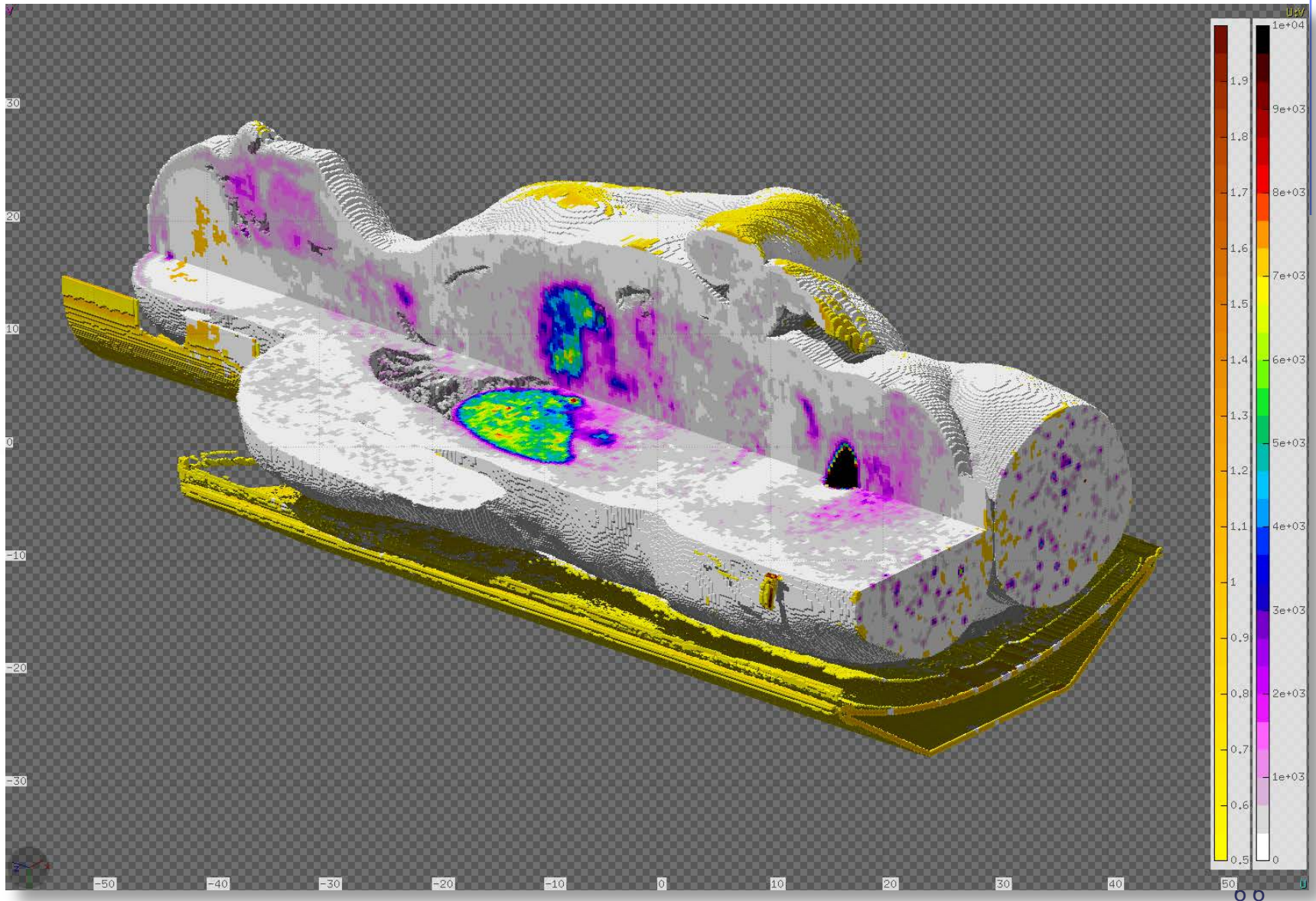
FLUKA



mGy



Voxel geometry with PET-CT



The FLUKA voxel geometry

- The CT scan contains integer values “Hounsfield Unit” reflecting the X-ray attenuation coefficient μ_x
$$HU_x = 1000 (\mu_x - \mu_{H20}) / \mu_{H20} , \quad \text{typically } -1000 \leq HU \leq 3500$$
- 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)
- The code handles each **organ** as a **CG 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.
- In the past conversion programs customized by the user were needed, **recently** for medical applications **FLAIR** takes care of the conversion.

The FLUKA voxel geometry

- To describe a voxel geometry, the user must **convert** his **CT** scan or equivalent data to a format understood by FLUKA. Starting from DICOM images, this is performed directly by FLAIR.
- This stage should :
 - Assign an **organ index** to **each voxel**. In many practical cases, the user will have a **continuum of HU (CT values)**, and may have to **group these values in intervals**.
 - Each **organ** is identified by a unique integer ≤ 32767 . The organ numbering **does not need to be contiguous** i.e. “holes” in the numbering sequence are allowed.
 - **One of the organs** must have number **0** and plays the role of the **medium surrounding the voxels** (usually vacuum or air).
 - The user assigns to **each NONZERO organ** a **voxel-region number**. The voxel-region numbering has to be **contiguous** and starts **from 1**.

The FLUKA voxel geometry

- The information is input to FLUKA through a special file *.vxl containing:
 - The number of voxels in each coordinate axis
 - The voxel dimension in each coordinate axis
 - The number of voxel-regions, and the maximum organ number
 - A list of the organ corresponding to each voxel
 - A list of the voxel-region number corresponding to each organ

Input file

Prepare the usual FLUKA input file.

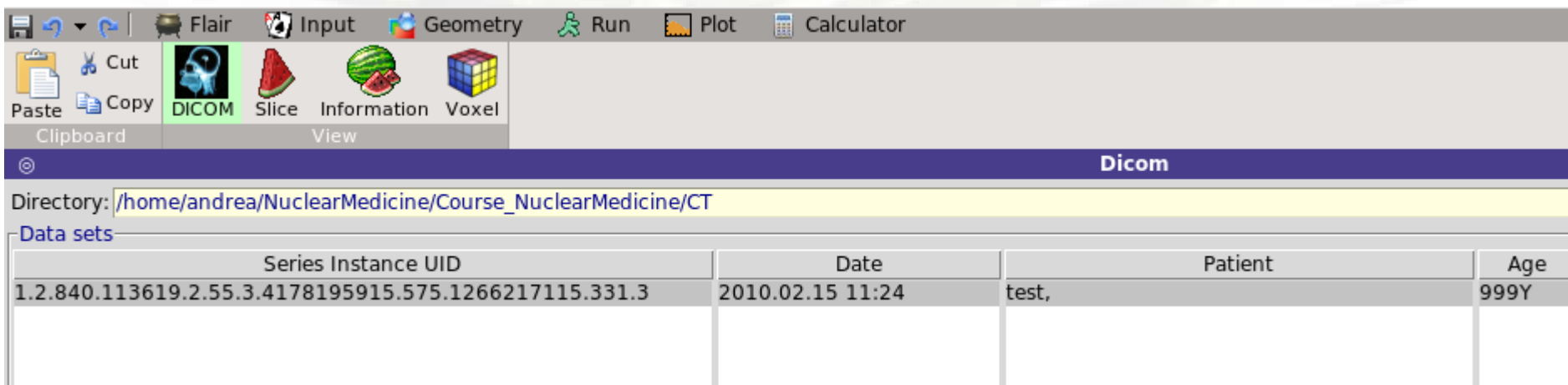
The geometry is written like a normal Combinatorial Geometry input, but in addition a **VOXELS** card must be inserted right after the GEOBEGIN card and before the Geometry title card

- **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	x: -35.068359	y: -35.068359	z: -88.6855
	Trans: ▼	Filename: VOXEL1 ▼	

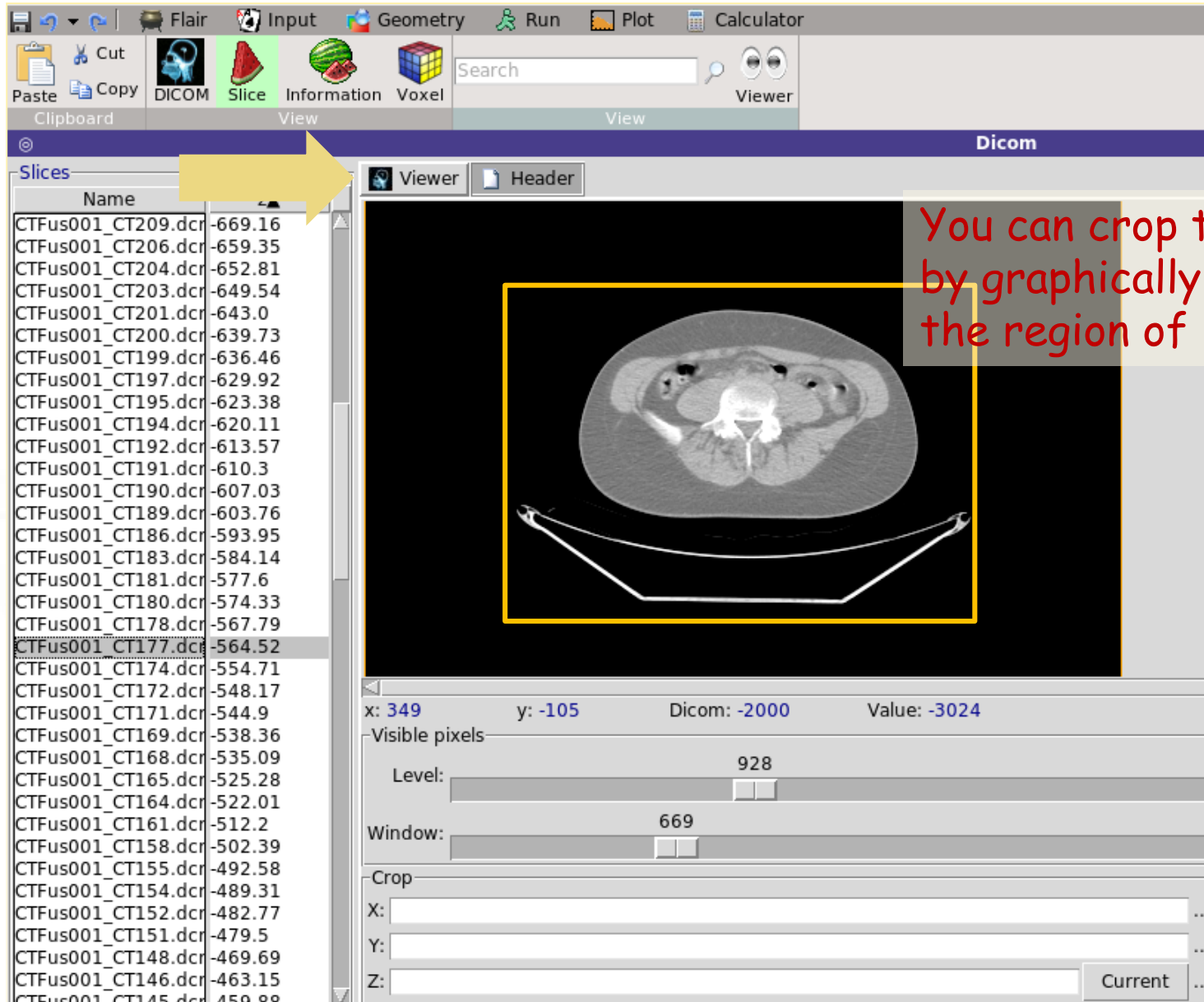
Processing the DICOM files with FLAIR I

- DICOM = Digital Imaging and Communications in Medicine is a medical standard for distributing any kind of medical image.
- FLAIR has a capability to process the DICOM files using the **pydicom** module and convert them to FLUKA VOXELS or USRBIN compatible files.
- First select the “Directory” where the DICOM data sets are located (if you have doubts press F1 and the flair manual will help you).

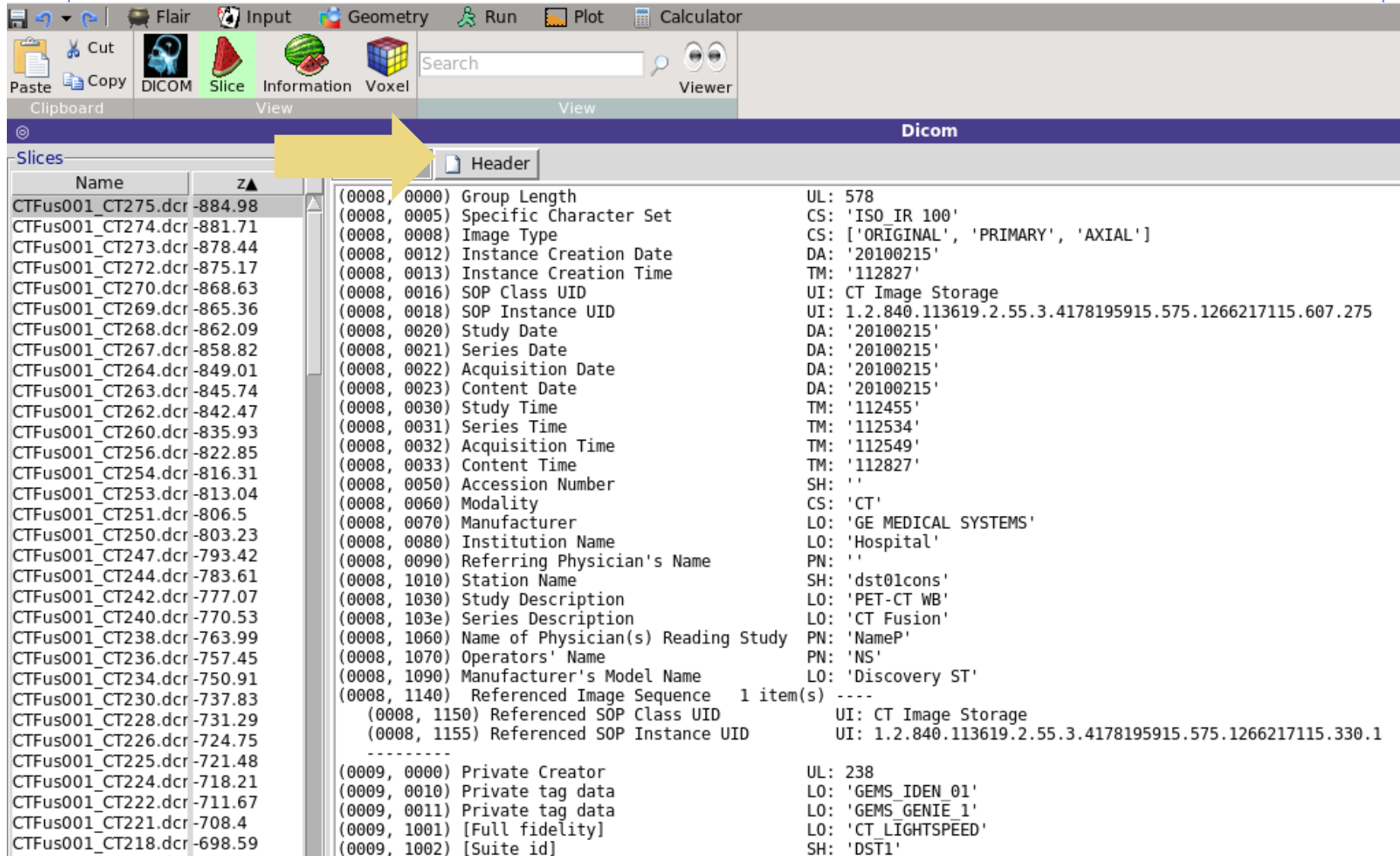


- Select one “Data sets” and inspect the images.

Processing the DICOM files with FLAIR II



Processing the DICOM files with FLAIR III



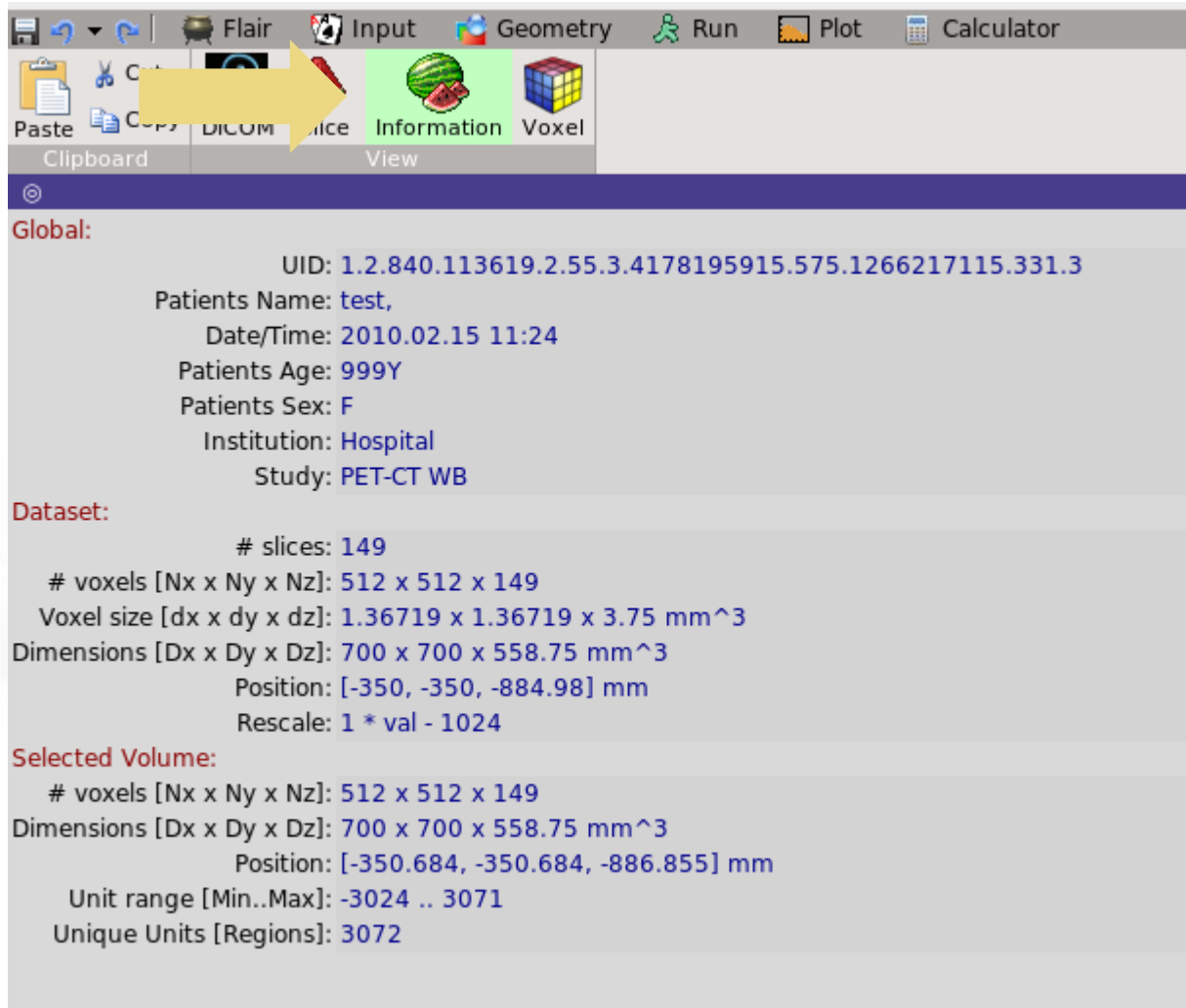
The screenshot displays the FLAIR III software interface. The top menu bar includes options like Flair, Input, Geometry, Run, Plot, and Calculator. Below the menu is a toolbar with icons for Cut, Paste, Copy, DICOM, Slice, Information, Voxel, and a Search field. The main window is divided into several panels. The 'Dicom' panel is active, showing a list of DICOM files in the 'Slices' tab. A yellow arrow points to the 'Header' tab, which is currently selected. The 'Header' tab displays the DICOM metadata for the selected file, including fields like Group Length, Specific Character Set, Image Type, Instance Creation Date, Instance Creation Time, SOP Class UID, SOP Instance UID, Study Date, Series Date, Acquisition Date, Content Date, Study Time, Series Time, Acquisition Time, Content Time, Accession Number, Modality, Manufacturer, Institution Name, Referring Physician's Name, Station Name, Study Description, Series Description, Name of Physician(s) Reading Study, Operators' Name, Manufacturer's Model Name, and Referenced Image Sequence. The 'Referenced Image Sequence' section shows a list of referenced SOP Class UIDs and Instance UIDs.

Name	zA
CTFus001_CT275.dcm	-884.98
CTFus001_CT274.dcm	-881.71
CTFus001_CT273.dcm	-878.44
CTFus001_CT272.dcm	-875.17
CTFus001_CT270.dcm	-868.63
CTFus001_CT269.dcm	-865.36
CTFus001_CT268.dcm	-862.09
CTFus001_CT267.dcm	-858.82
CTFus001_CT264.dcm	-849.01
CTFus001_CT263.dcm	-845.74
CTFus001_CT262.dcm	-842.47
CTFus001_CT260.dcm	-835.93
CTFus001_CT256.dcm	-822.85
CTFus001_CT254.dcm	-816.31
CTFus001_CT253.dcm	-813.04
CTFus001_CT251.dcm	-806.5
CTFus001_CT250.dcm	-803.23
CTFus001_CT247.dcm	-793.42
CTFus001_CT244.dcm	-783.61
CTFus001_CT242.dcm	-777.07
CTFus001_CT240.dcm	-770.53
CTFus001_CT238.dcm	-763.99
CTFus001_CT236.dcm	-757.45
CTFus001_CT234.dcm	-750.91
CTFus001_CT230.dcm	-737.83
CTFus001_CT228.dcm	-731.29
CTFus001_CT226.dcm	-724.75
CTFus001_CT225.dcm	-721.48
CTFus001_CT224.dcm	-718.21
CTFus001_CT222.dcm	-711.67
CTFus001_CT221.dcm	-708.4
CTFus001_CT218.dcm	-698.59

```

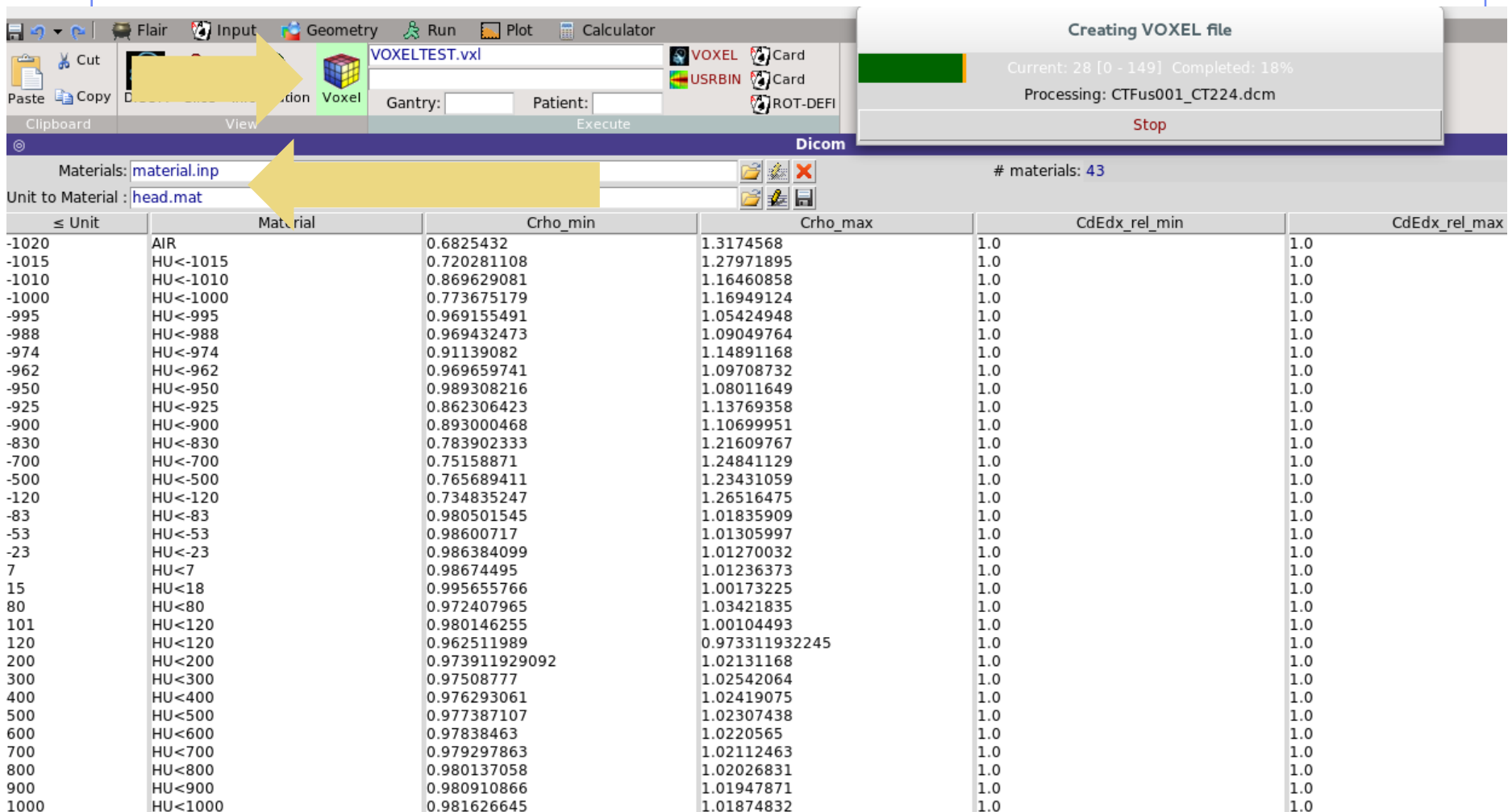
(0008, 0000) Group Length          UL: 578
(0008, 0005) Specific Character Set CS: 'ISO_IR 100'
(0008, 0008) Image Type             CS: ['ORIGINAL', 'PRIMARY', 'AXIAL']
(0008, 0012) Instance Creation Date DA: '20100215'
(0008, 0013) Instance Creation Time TM: '112827'
(0008, 0016) SOP Class UID          UI: CT Image Storage
(0008, 0018) SOP Instance UID       UI: 1.2.840.113619.2.55.3.4178195915.575.1266217115.607.275
(0008, 0020) Study Date             DA: '20100215'
(0008, 0021) Series Date            DA: '20100215'
(0008, 0022) Acquisition Date       DA: '20100215'
(0008, 0023) Content Date           DA: '20100215'
(0008, 0030) Study Time             TM: '112455'
(0008, 0031) Series Time            TM: '112534'
(0008, 0032) Acquisition Time       TM: '112549'
(0008, 0033) Content Time           TM: '112827'
(0008, 0050) Accession Number       SH: ''
(0008, 0060) Modality               CS: 'CT'
(0008, 0070) Manufacturer           LO: 'GE MEDICAL SYSTEMS'
(0008, 0080) Institution Name        LO: 'Hospital'
(0008, 0090) Referring Physician's Name PN: ''
(0008, 1010) Station Name           SH: 'dst01cons'
(0008, 1030) Study Description       LO: 'PET-CT WB'
(0008, 103e) Series Description      LO: 'CT Fusion'
(0008, 1060) Name of Physician(s) Reading Study PN: 'NameP'
(0008, 1070) Operators' Name        PN: 'NS'
(0008, 1090) Manufacturer's Model Name LO: 'Discovery ST'
(0008, 1140) Referenced Image Sequence 1 item(s) ----
    (0008, 1150) Referenced SOP Class UID UI: CT Image Storage
    (0008, 1155) Referenced SOP Instance UID UI: 1.2.840.113619.2.55.3.4178195915.575.1266217115.330.1
-----
(0009, 0000) Private Creator        UL: 238
(0009, 0010) Private tag data       LO: 'GEMS_IDEN_01'
(0009, 0011) Private tag data       LO: 'GEMS_GENIE_1'
(0009, 1001) [Full fidelity]        LO: 'CT_LIGHTSPEED'
(0009, 1002) [Suite id]            SH: 'DST1'
  
```

Processing the DICOM files with FLAIR IV



Processing the DICOM files with FLAIR V

- The “Voxel” tab is used in order to convert the dataset to VOXELS or USRBIN format. For the VOXEL geometry two additional files are needed (example: material.inp and head.mat in the flair/dicom dir).



The screenshot shows the FLAIR V software interface. The 'Voxel' tab is selected, and a 'Creating VOXEL file' dialog box is open. The dialog box shows the current progress: 'Current: 28 [0 - 149] Completed: 18%' and 'Processing: CTFus001_CT224.dcm'. The 'Stop' button is visible. In the background, the 'Dicom' tab is active, showing a table of materials and their properties. The table has columns for '≤ Unit', 'Material', 'Crho_min', 'Crho_max', 'CdEdx_rel_min', and 'CdEdx_rel_max'. The table lists materials from -1020 to 1000, including AIR, HU<-1015, HU<-1010, HU<-1000, HU<-995, HU<-988, HU<-974, HU<-962, HU<-950, HU<-925, HU<-900, HU<-830, HU<-700, HU<-500, HU<-120, HU<-83, HU<-53, HU<-23, HU<7, HU<18, HU<80, HU<120, HU<200, HU<300, HU<400, HU<500, HU<600, HU<700, HU<800, HU<900, and HU<1000. The 'Crho_min' and 'Crho_max' columns show values ranging from 0.6825432 to 1.01874832. The 'CdEdx_rel_min' and 'CdEdx_rel_max' columns show values ranging from 1.0 to 1.0.

≤ Unit	Material	Crho_min	Crho_max	CdEdx_rel_min	CdEdx_rel_max
-1020	AIR	0.6825432	1.3174568	1.0	1.0
-1015	HU<-1015	0.720281108	1.27971895	1.0	1.0
-1010	HU<-1010	0.869629081	1.16460858	1.0	1.0
-1000	HU<-1000	0.773675179	1.16949124	1.0	1.0
-995	HU<-995	0.969155491	1.05424948	1.0	1.0
-988	HU<-988	0.969432473	1.09049764	1.0	1.0
-974	HU<-974	0.91139082	1.14891168	1.0	1.0
-962	HU<-962	0.969659741	1.09708732	1.0	1.0
-950	HU<-950	0.989308216	1.08011649	1.0	1.0
-925	HU<-925	0.862306423	1.13769358	1.0	1.0
-900	HU<-900	0.893000468	1.10699951	1.0	1.0
-830	HU<-830	0.783902333	1.21609767	1.0	1.0
-700	HU<-700	0.75158871	1.24841129	1.0	1.0
-500	HU<-500	0.765689411	1.23431059	1.0	1.0
-120	HU<-120	0.734835247	1.26516475	1.0	1.0
-83	HU<-83	0.980501545	1.01835909	1.0	1.0
-53	HU<-53	0.98600717	1.01305997	1.0	1.0
-23	HU<-23	0.986384099	1.01270032	1.0	1.0
7	HU<7	0.98674495	1.01236373	1.0	1.0
15	HU<18	0.995655766	1.00173225	1.0	1.0
80	HU<80	0.972407965	1.03421835	1.0	1.0
101	HU<120	0.980146255	1.00104493	1.0	1.0
120	HU<120	0.962511989	0.973311932245	1.0	1.0
200	HU<200	0.973911929092	1.02131168	1.0	1.0
300	HU<300	0.97508777	1.02542064	1.0	1.0
400	HU<400	0.976293061	1.02419075	1.0	1.0
500	HU<500	0.977387107	1.02307438	1.0	1.0
600	HU<600	0.97838463	1.0220565	1.0	1.0
700	HU<700	0.979297863	1.02112463	1.0	1.0
800	HU<800	0.980137058	1.02026831	1.0	1.0
900	HU<900	0.980910866	1.01947871	1.0	1.0
1000	HU<1000	0.981626645	1.01874832	1.0	1.0

Processing the DICOM files with FLAIR VI

- **≤ Unit:** specify the upper limit of the range. Every entry will correspond to a range from the previous upper limit+1 until the current upper limit.
- **Material:** select any of the predefined FLUKA materials defined previously.


Optionally you can specify correction factors for the density and dE/dx

- **Crho_min/Chro_max:** density correction factors to be applied on the lower/upper limit of the unit range (see next slides).
- **CdEdx_rel_min/CdEdx_rel_max:** relative correction factors on dE/dx for minimum/maximum unit in the range (see next slides).

≤ Unit	Material	Crho_min	Crho_max	CdEdx_rel_min	CdEdx_rel_max
-1020	AIR	0.6825432	1.3174568	1.0	1.0
-1015	HU<-1015	0.720281108	1.27971895	1.0	1.0
-1010	HU<-1010	0.869629081	1.16460858	1.0	1.0
-1000	HU<-1000	0.773675179	1.16949124	1.0	1.0
-995	HU<-995	0.969155491	1.05424948	1.0	1.0
-988	HU<-988	0.969432473	1.09049764	1.0	1.0
-974	HU<-974	0.91139082	1.14891168	1.0	1.0
-962	HU<-962	0.969659741	1.09708732	1.0	1.0
-950	HU<-950	0.989308216	1.08011649	1.0	1.0
-925	HU<-925	0.862306423	1.13769358	1.0	1.0
-900	HU<-900	0.893000468	1.10699951	1.0	1.0
-830	HU<-830	0.783902333	1.21609767	1.0	1.0
-700	HU<-700	0.75158871	1.24841129	1.0	1.0
-500	HU<-500	0.765689411	1.23431059	1.0	1.0
-120	HU<-120	0.734835247	1.26516475	1.0	1.0
-83	HU<-83	0.980501545	1.01835909	1.0	1.0
-53	HU<-53	0.98600717	1.01305997	1.0	1.0

Voxel Body

- The usual list of **NB bodies**, not including the **RPP** corresponding to the “**voxel volume**” (see **VOXELS** card above). This **RPP** will be generated and added automatically by the code as the **(NB+1)th** body, with one corner in the point indicated in the **VOXELS** card, and dimensions **NX*DX, NY*DY** and **NZ*DZ** as read from the voxel file.
- The usual region list of **NR regions**, with the space occupied by body named **VOXEL** or numbered **NB+1** (the “**voxel volume**”) subtracted. In other words, the **NR** regions listed must cover the whole available space, excepted the space corresponding to the “**voxel volume**”. This is easily obtained by subtracting body **VOXEL** or **NB+1** in the relevant region definitions, even though this body is not explicitly input at the end of the body list.

 VOXELS		x: -35.068359	y: -35.068359	z: -88.6855
		Trans: ▼	Filename: VOXEL1 ▼	
 SPH	BODY1	x: 0.	y: 0.	z: 0.
		R: 10000.		
 SPH	BODY2	x: 0.	y: 0.	z: 0.
		R: 1000.		
 END				
 REGION	REG1	Neigh: 5		Volume:
expr: BODY1-BODY2				
 REGION	REG2	Neigh: 5		Volume:
expr: BODY2-VOXEL				
 END				
 GEOEND				

Voxel Regions

The code will automatically generate and add several regions:

- **NO** additional regions, where **NO** = number of non-zero organs:

Name	Number	Description
VOXEL	NR+1	sort of a “cage” for all voxels. Nothing should ever be deposited in it. The user shall assign vacuum to it.
VOXEL001	NR+2	containing all voxels belonging to organ number 0. There must be at least 2 of such voxels, but in general they should be many more. Typical material assignment to this region is air
VOXEL002	NR+3	corresponding to organ 1
VOXEL003	NR+4	corresponding to organ 2
VOXEL###	NR+2+NO	corresponding to organ NO

Few remarks

- The assignment of materials is made directly by FLAIR. The user has to assign the materials to the regions defined by combinatorial geometry.
- The “**head.mat**” and “**material.inp**” files are examples, the user should update these files taking into account his calibration curves.

Practical issues for Medical Applications

General problems for MC calculations on CT scans

- How to assign realistic human tissue parameters (= materials) for MC Calculation?
- How to find a good compromise between the number of different HU values (~ 3000-5000) and the materials to be considered in the MC?

(issues on memory and computation speed when attempting to treat each HU number as a different material !!!)

- How to preserve continuous, HU-dependent information when segmenting the HU numbers into intervals sharing the same “tissue” material ?

(critical for ion range calculation in hadron therapy !!!)

CT stoichiometric calibration (I)

CT segmentation into 27 materials of defined elemental composition (from analysis of 71 human CT scans)

Air, Lung,
Adipose tissue

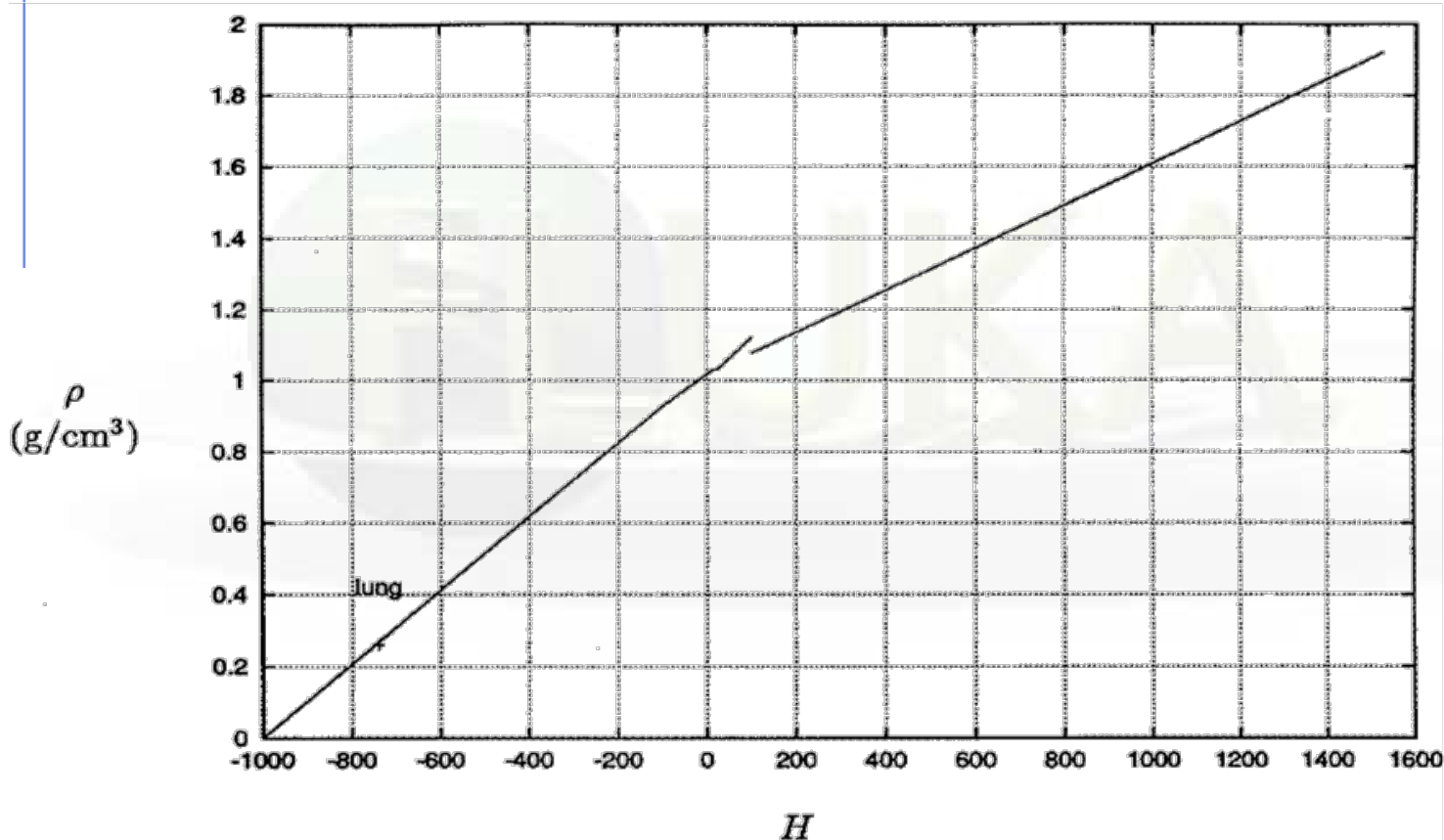
Soft tissue

Skeletal tissue

	$w_i(\text{pp})$											
<i>H</i>	H	C	N	O	Na	Mg	P	S	Cl	Ar	K	Ca
-1000--950			75.5	23.2						1.3		
-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			
-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
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

CT stoichiometric calibration (II)

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)



Schneider et al
PMB 45, 2000

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

The region-dependent CORRFAC card

- “CORRFAC” card allows to alter material density for dE/dx and nuclear processes
- 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 CORRFAC 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)

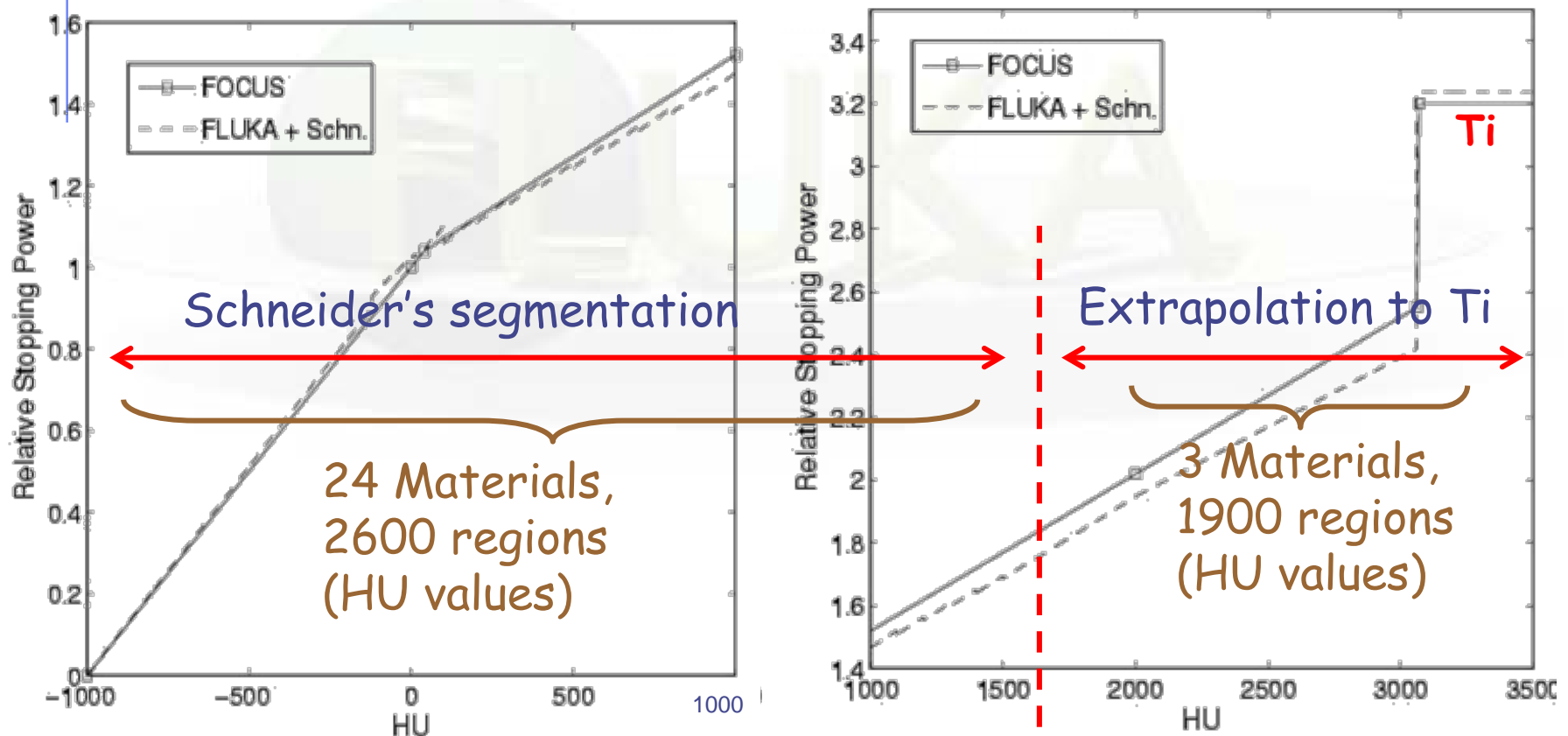
ASSIGNMA BONE VOXEL016 (region number 31)

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

CORRFACT 0.85 0.0 0.0 VOXEL005 Region #25 corresponds
CORRFACT 1.3 0.0 0.0 VOXEL016 to "softer" bone than #31

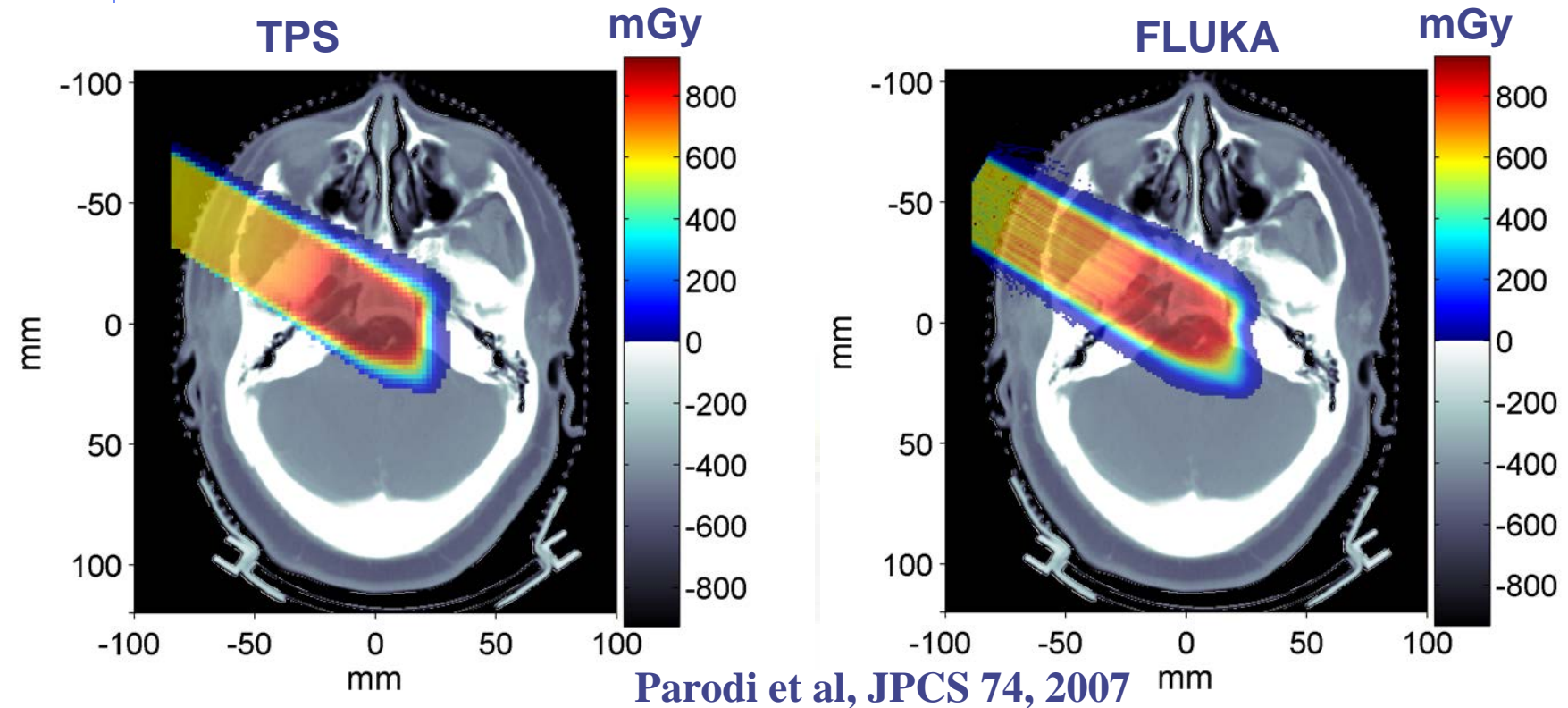
Forcing FLUKA to follow the same range calibration curve as TPS for p @ MGH Boston

The CORRFAC ionization scaling factors were obtained from the dEdx ratio between TPS and FLUKA (+ Schneider "mass density") -> The user should update the "head.mat" file with his own calibration for CdEdX_rel taking into account his TPS.



Applications of FLUKA to p therapy @ MGH

Input phase-space provided by H. Paganetti, MGH Boston



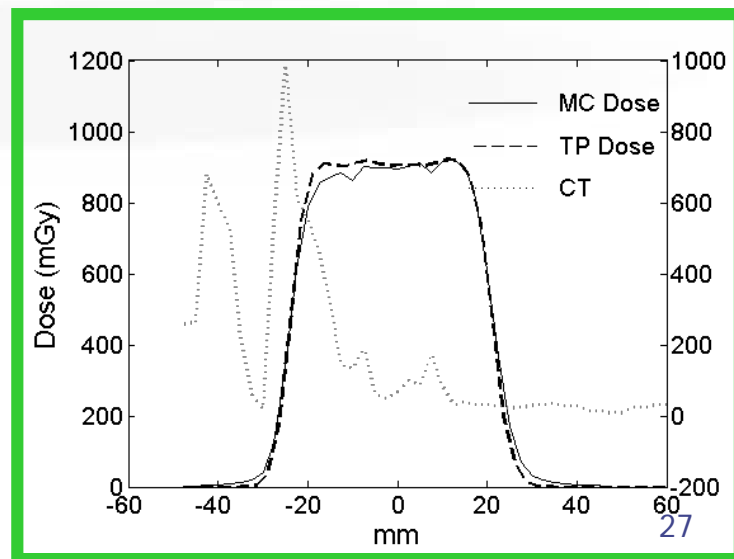
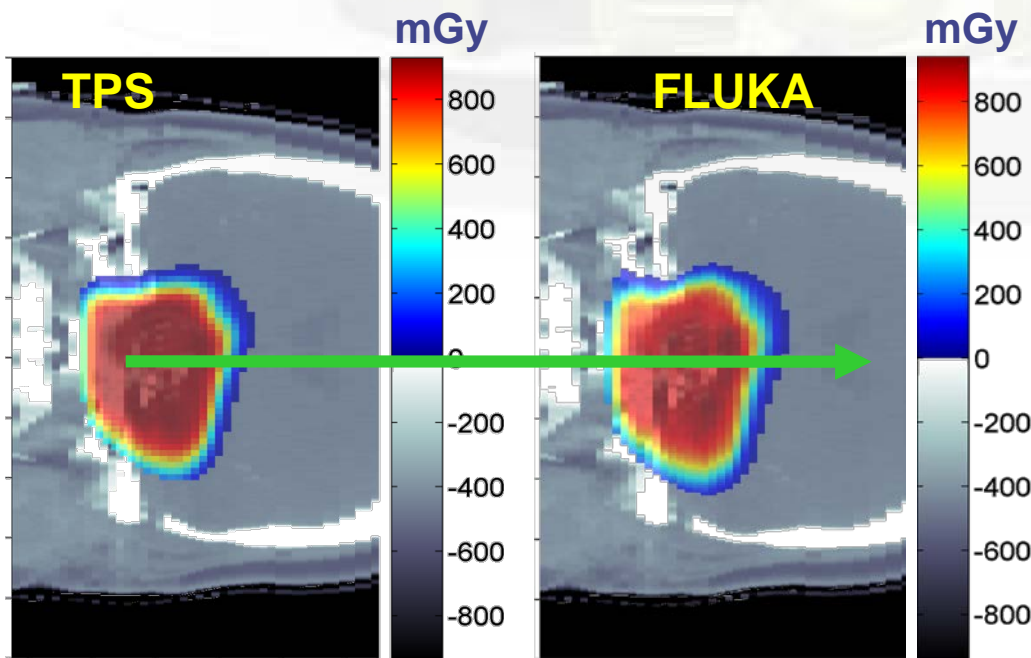
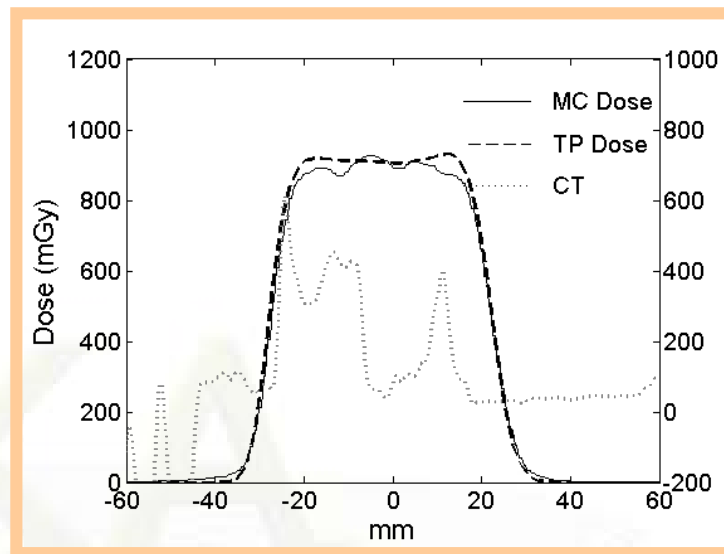
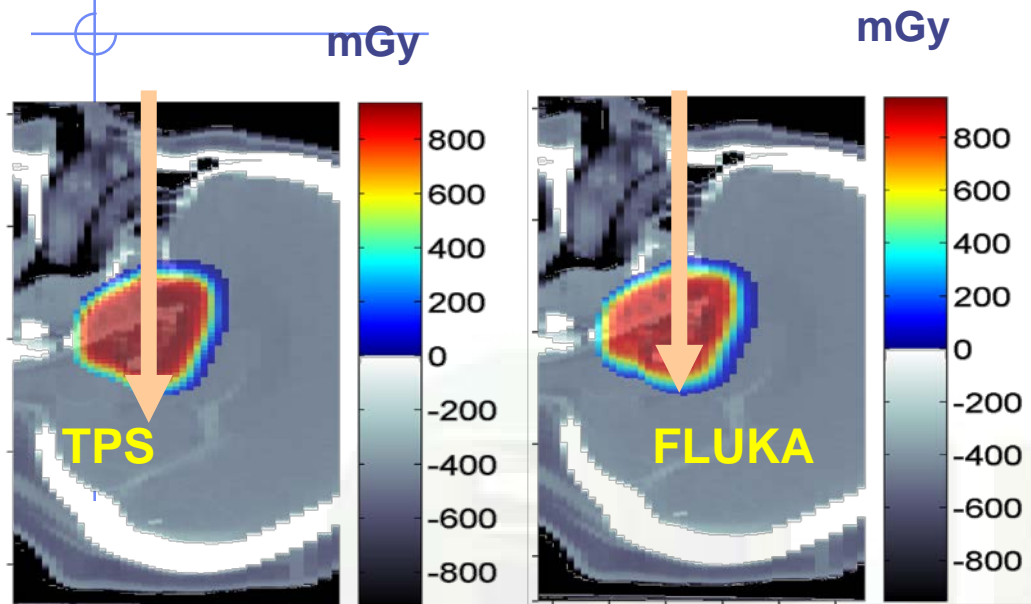
Prescribed dose: 1 GyE

MC : $\sim 5.5 \cdot 10^6$ protons in 10 independent runs

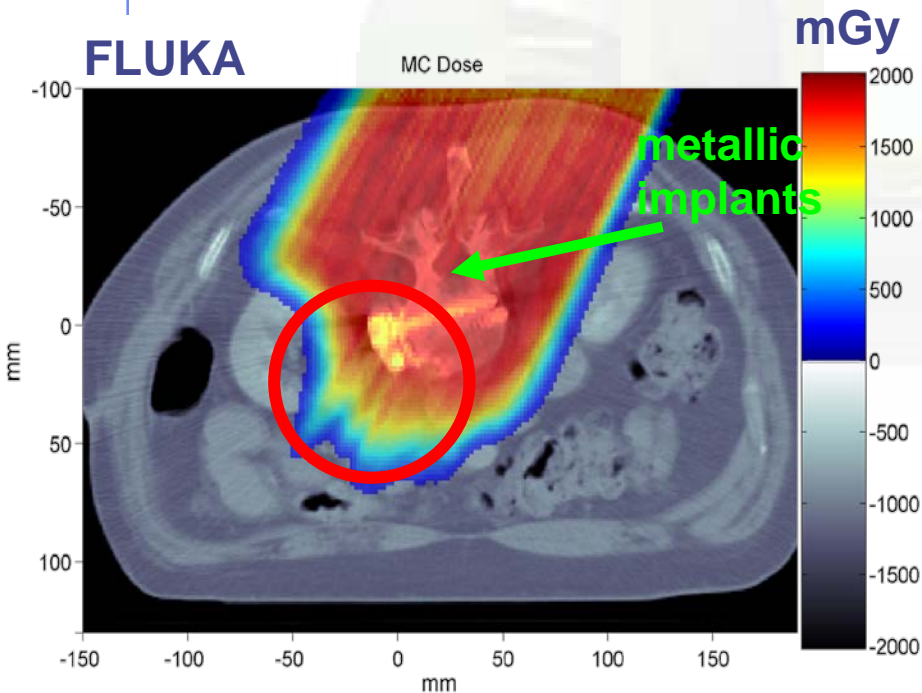
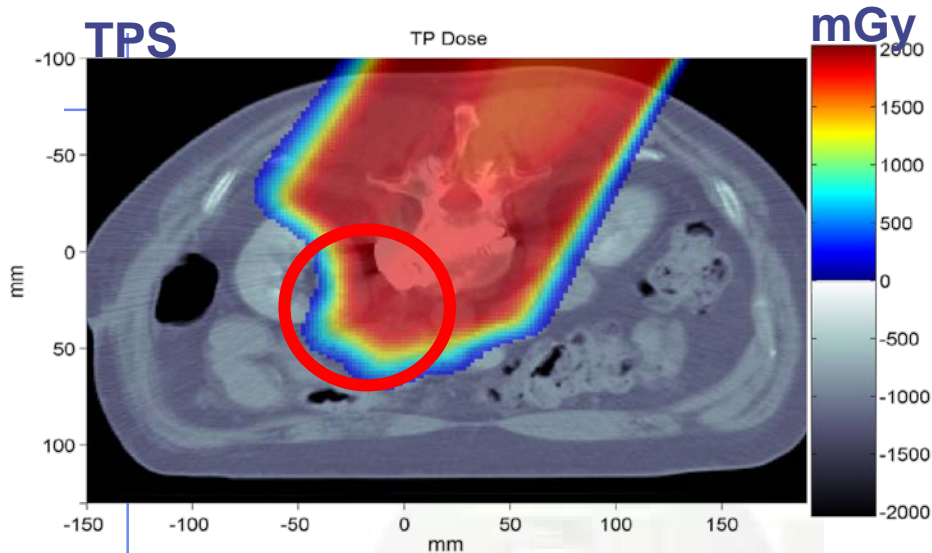
(11h each on Linux Cluster mostly using 2.2GHz Athlon processors)

Applications of FLUKA to p therapy @ MGH

Parodi et PMB 52, 2007



Applications of FLUKA to p therapy @ MGH



Prescribed dose: 2 GyE
MC : $\sim 7.4 \cdot 10^7$ p in 12 independent runs (~ 130 h each on 2.2 GHz Linux cluster)

Biological predictions with mixed field

Estimation of the biological effect is important in many applications (hadron therapy, space radiation, etc...)

The linear-quadratic model for the biological response predictions is often used :

$$S = \exp (-\alpha * D - \beta * D * D)$$

where S is the (cell, tissue) survival and α and β are the linear and quadratic term for the dose response.

α and β values depends from many factors:

- Particle type (Z, A)
- Particle energy
- Cell / Tissue type
- Biological endpoint
- ...

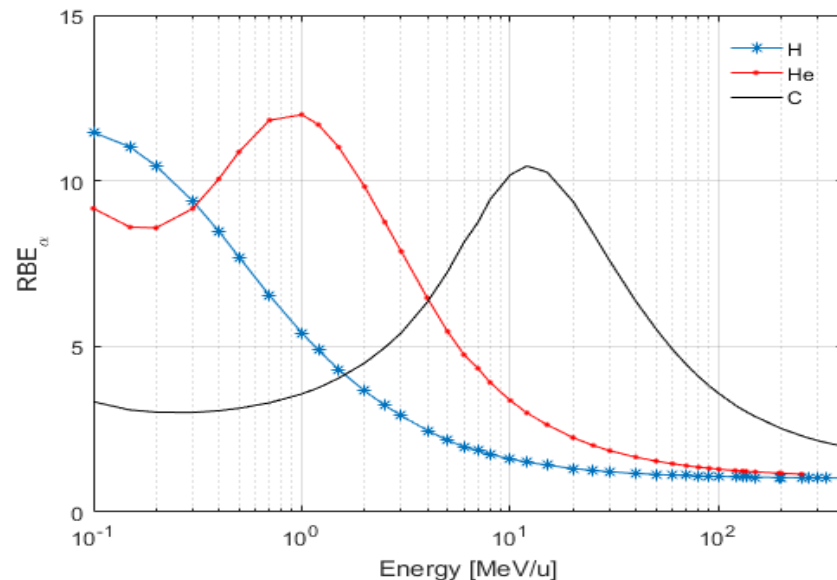
α and β values are passed to FLUKA with **RAD-BIOL** card

RAD-BIOL

RAD-BIOL: reading biological parameter cards

- **WHAT(1)** = 0 always
- **WHAT(2-6)**: not used
- **SDUM** = biological data file name (10 character long) the file must be named <sdum>.dat

Example of an input biological table for H, He and C ions expressed as $RBE_{\alpha} = \alpha_{\text{ion}} / \alpha_{\text{photons}}$ as function of MeV /u



TPSSCORE

This card controls some scoring parameters relevant for TPS-like calculations.

For **SDUM = BIOTOBIN**

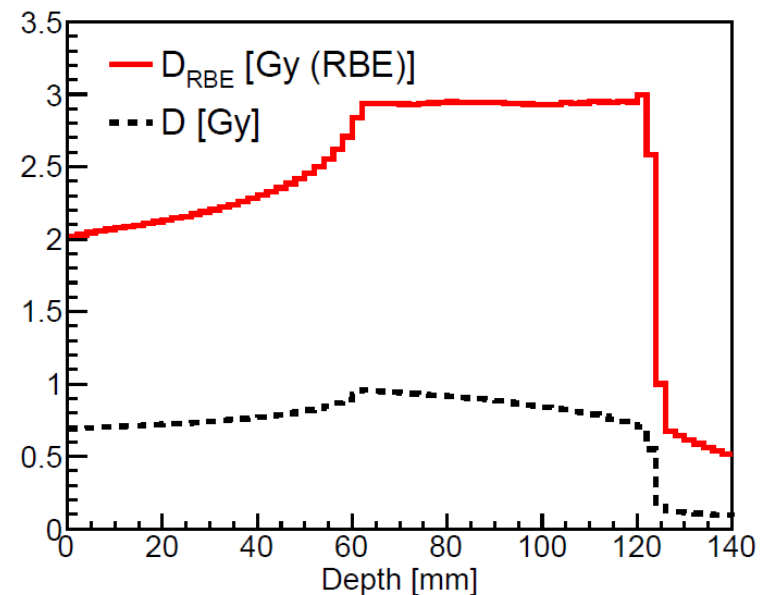
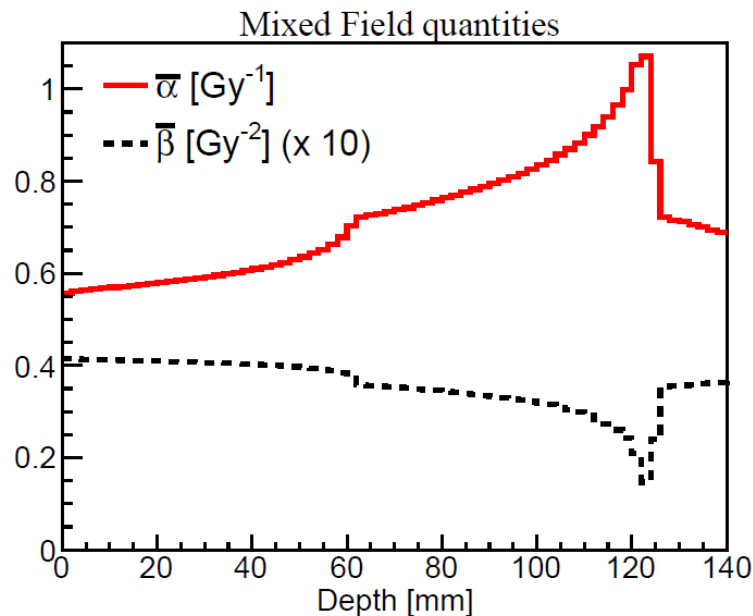
- **WHAT(1)** = > 0, alpha-beta cellular line index to be associated to the USRBIN defined by **WHAT(4)**-**WHAT(6)** (see **RAD-BIOL**)
- **WHAT(2)**, **WHAT(3)** = not used
- **WHAT(4)** = from binning **WHAT(4)**
- **WHAT(5)** = to binning **WHAT(5)**
- **WHAT(6)** = in step of **WHAT(6)**

RAD-BIOL

USRBIN	11.	ALPHA-D	-42.	10.	0.	30.0ALPHADa
USRBIN	0.	0.	0.0	100.	600.0 &	
USRBIN	11.	SQBETA-D	-42.	10.	0.	30.0BETADa
USRBIN	0.	0.	0.0	100.	600.0 &	
TPSSCORE	1.		ALPHADa	BETADa		BIOTOBIN

TPSSCORE

- Use TPSSCORE to calculate the mixed radiation field liner and quadratic term (left panel)
- Use USRBIN dose (D) and TPSSCORE to calculate biological dose (D_{RBE} , right panel in red) in the post-processing

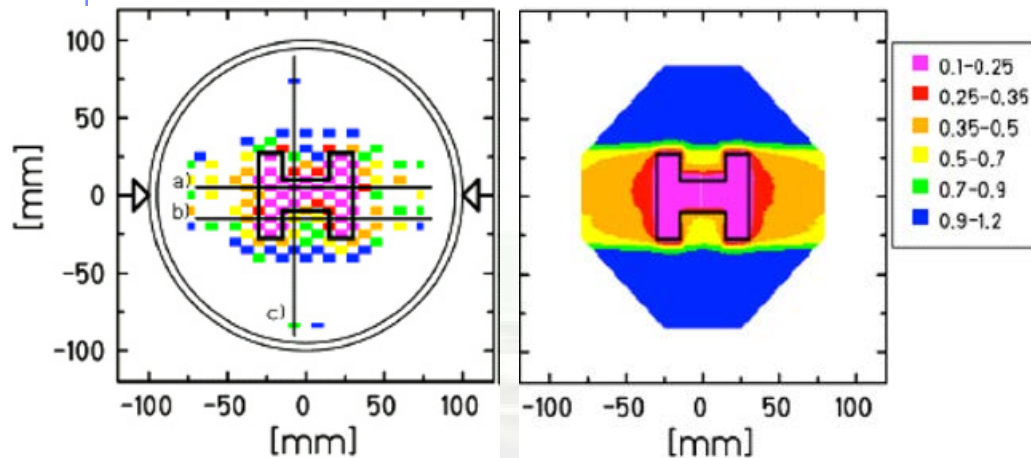


FLUKA biological application for ^{12}C ion therapy

A. Mairani, et al. PMB 2010

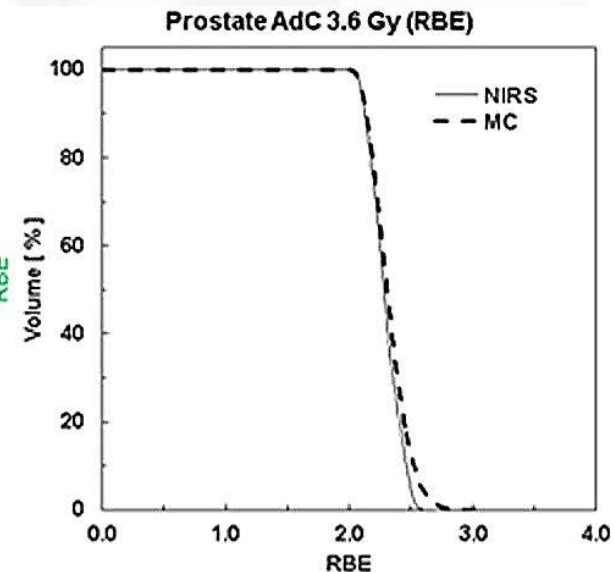
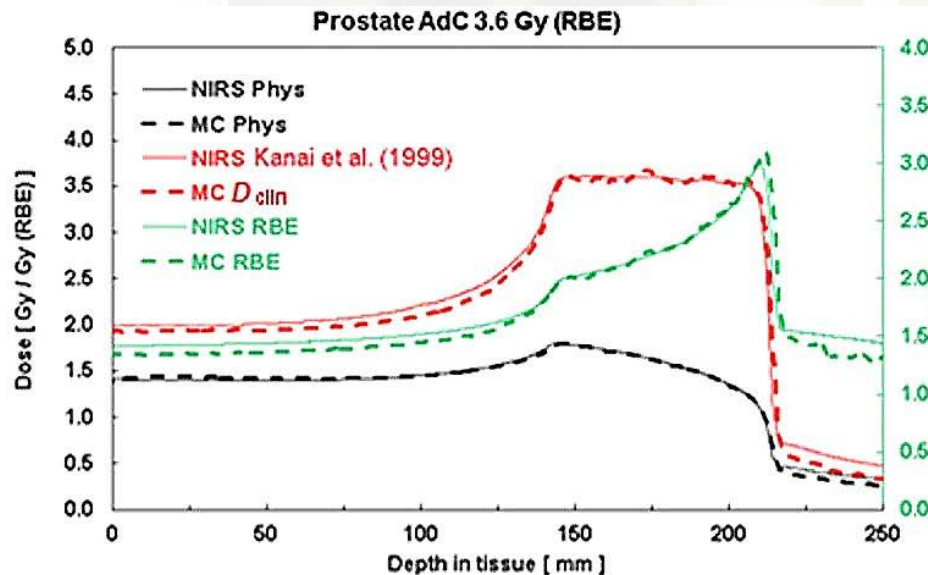
in vitro data

predictions



FLUKA + LEM model

FLUKA + NIRS approach



G. Magro, et al. PMB 2017

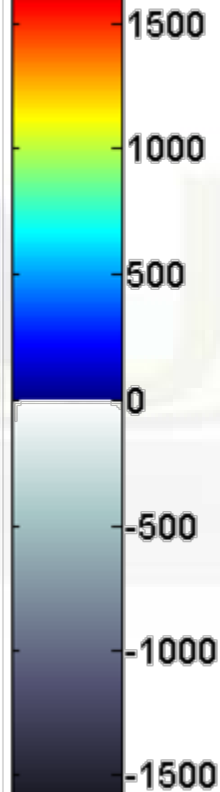
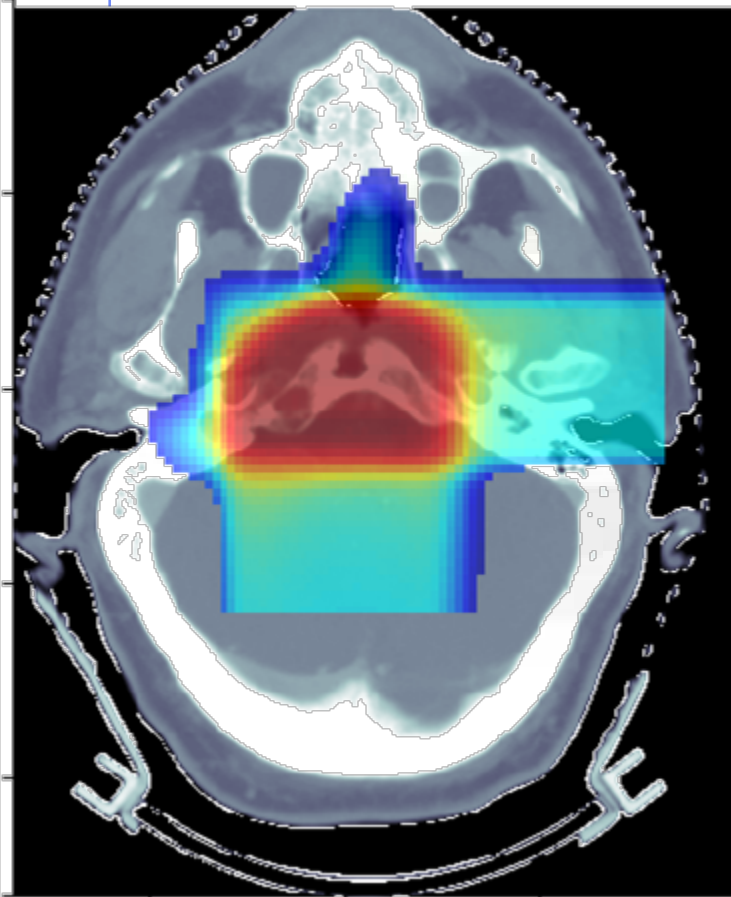
Applications of FLUKA to p therapy @ MGH

Clival Chordoma, 0.96 GyE / field

Planned dose

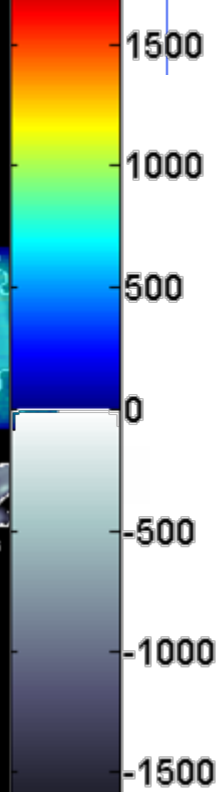
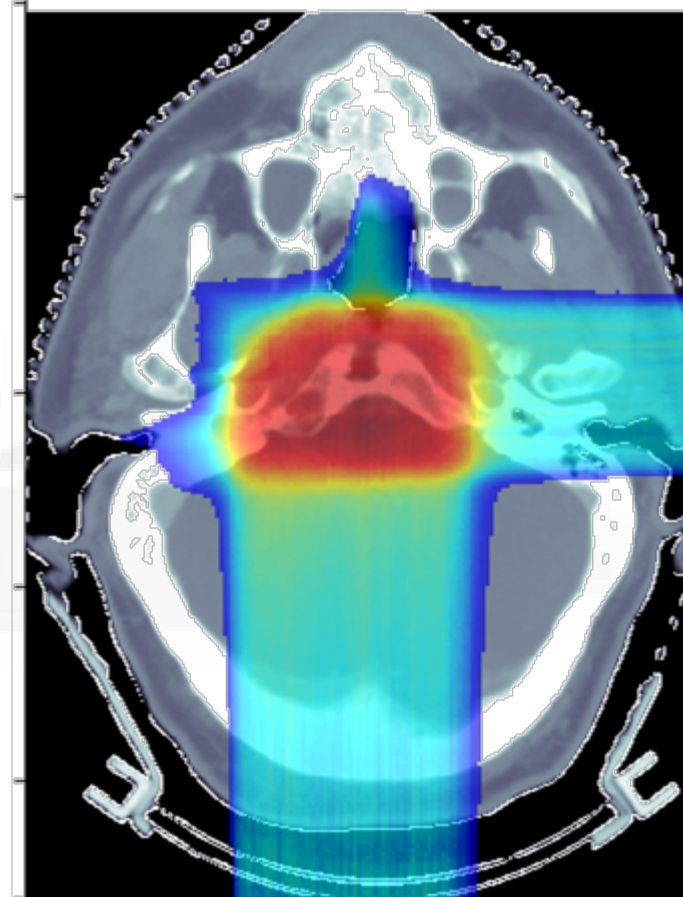
TP Dose

mGy



MC Dose

mGy



Post-radiation PET/CT @ MGH

Average Activity

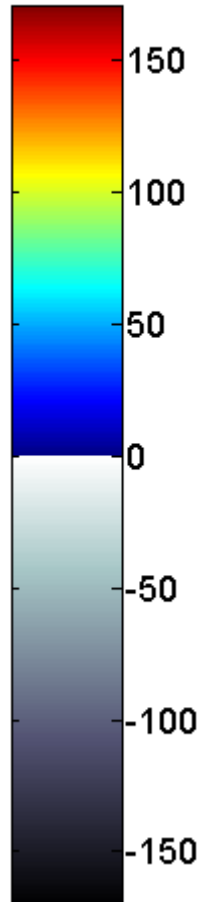
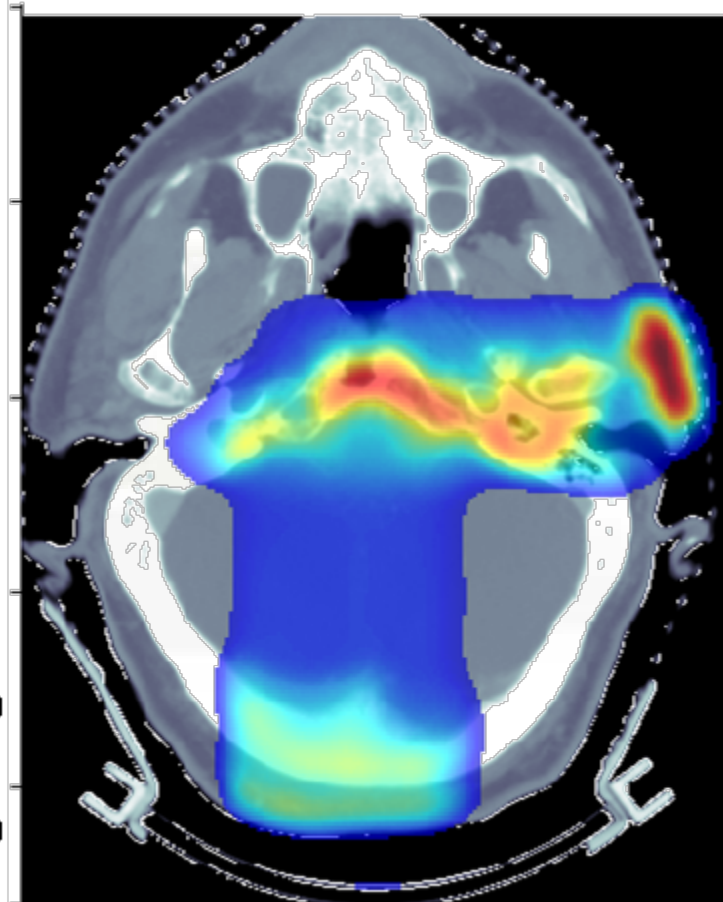
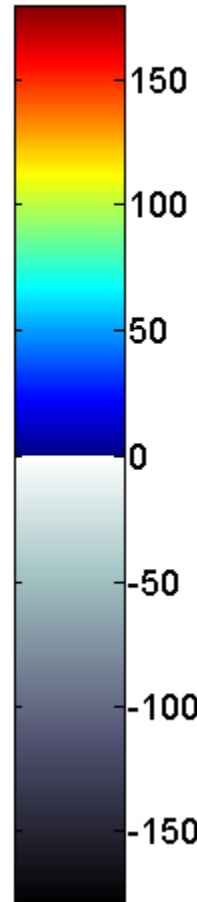
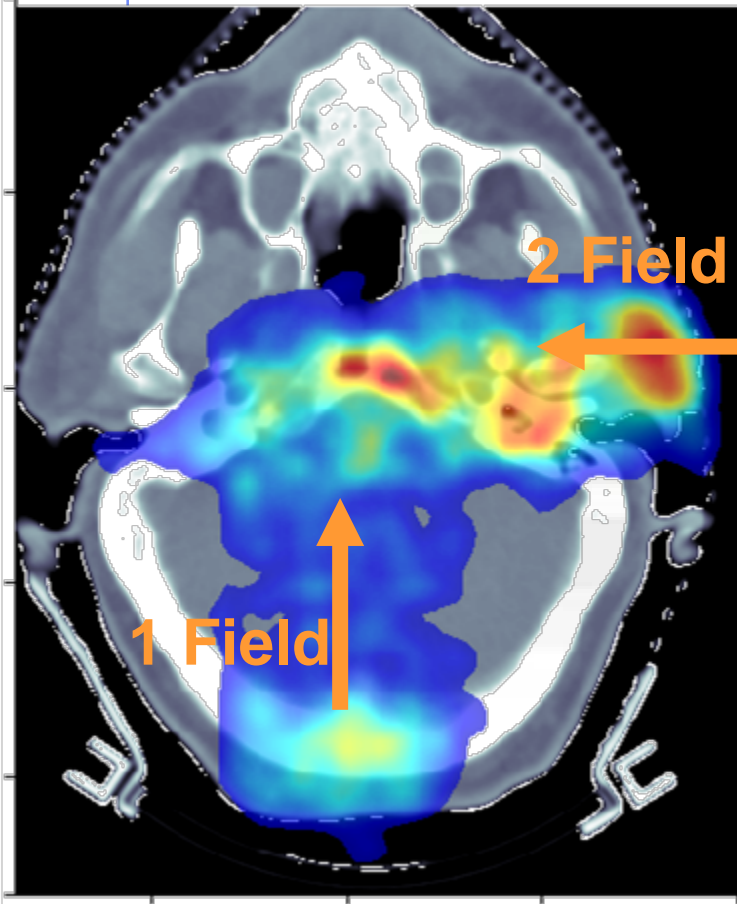
Clival Chordoma, 0.96 GyE / field, $\Delta T1 \sim 26$ min, $\Delta T2 \sim 16$ min

PET Meas

Bq / ml

MC PET

Bq / ml



K. Parodi et al, IJROBP 2007

... and FLUKA-voxel functionalities
being also used at HIT and CNAO ...