

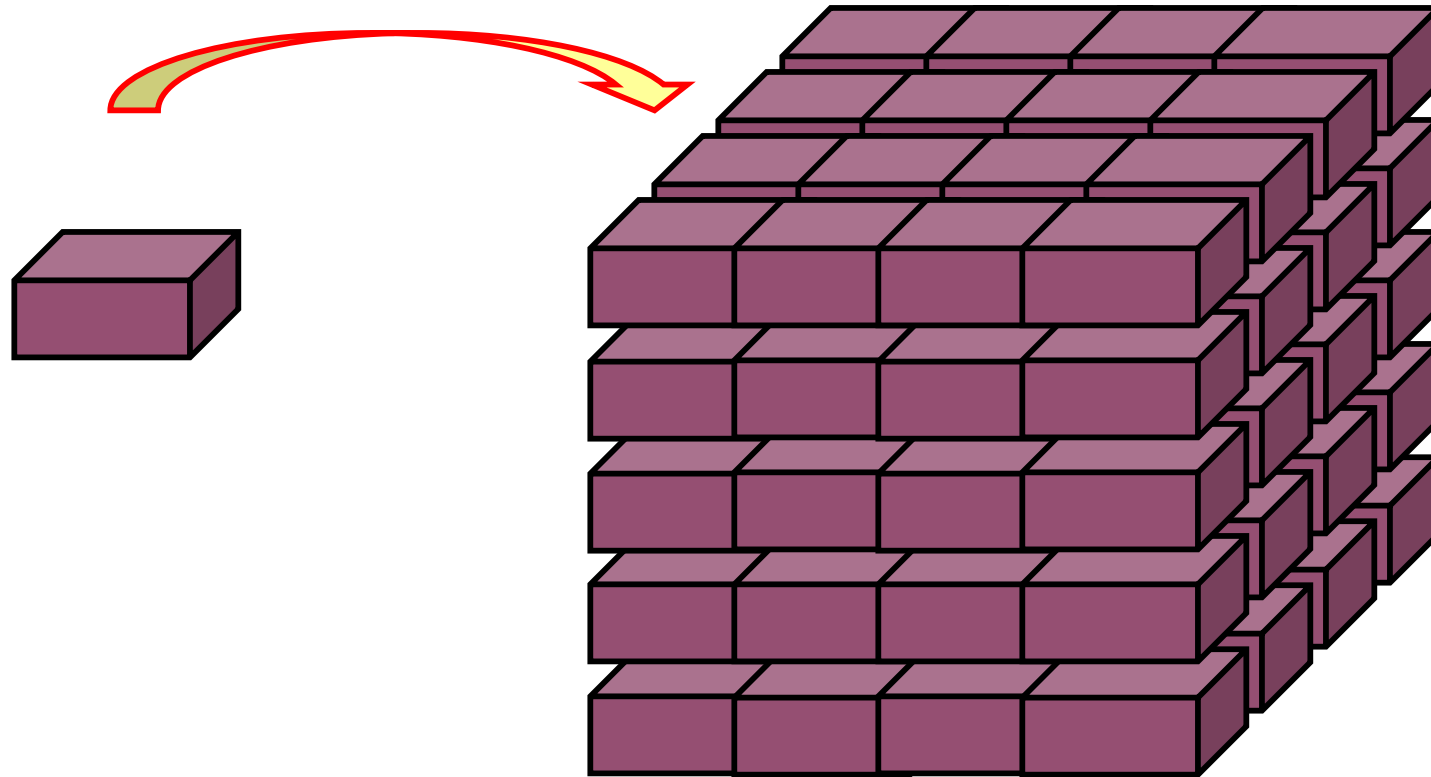


# Medical Applications

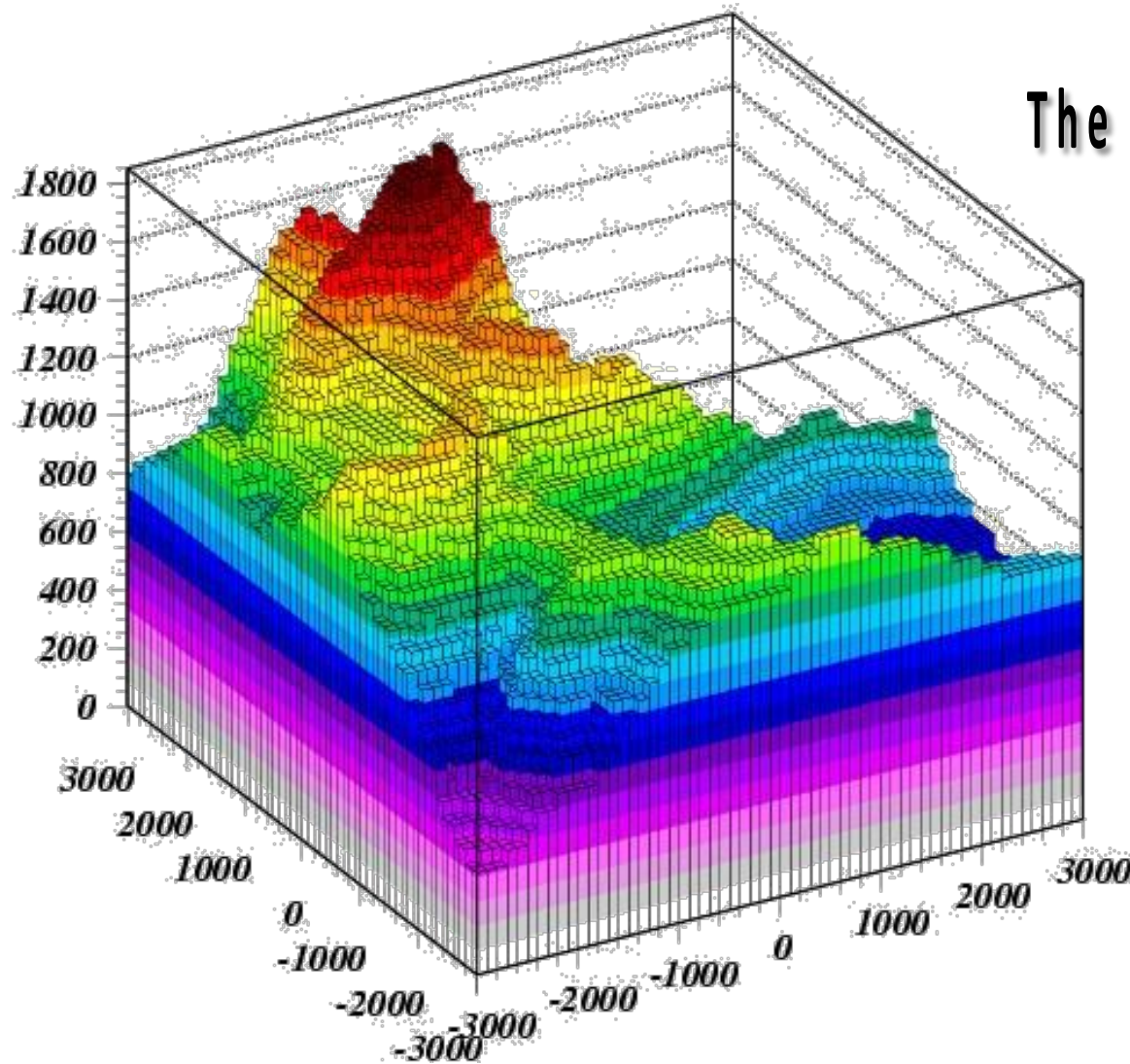
Tutorial on flair & FLUKA capabilities for medical applications

# 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

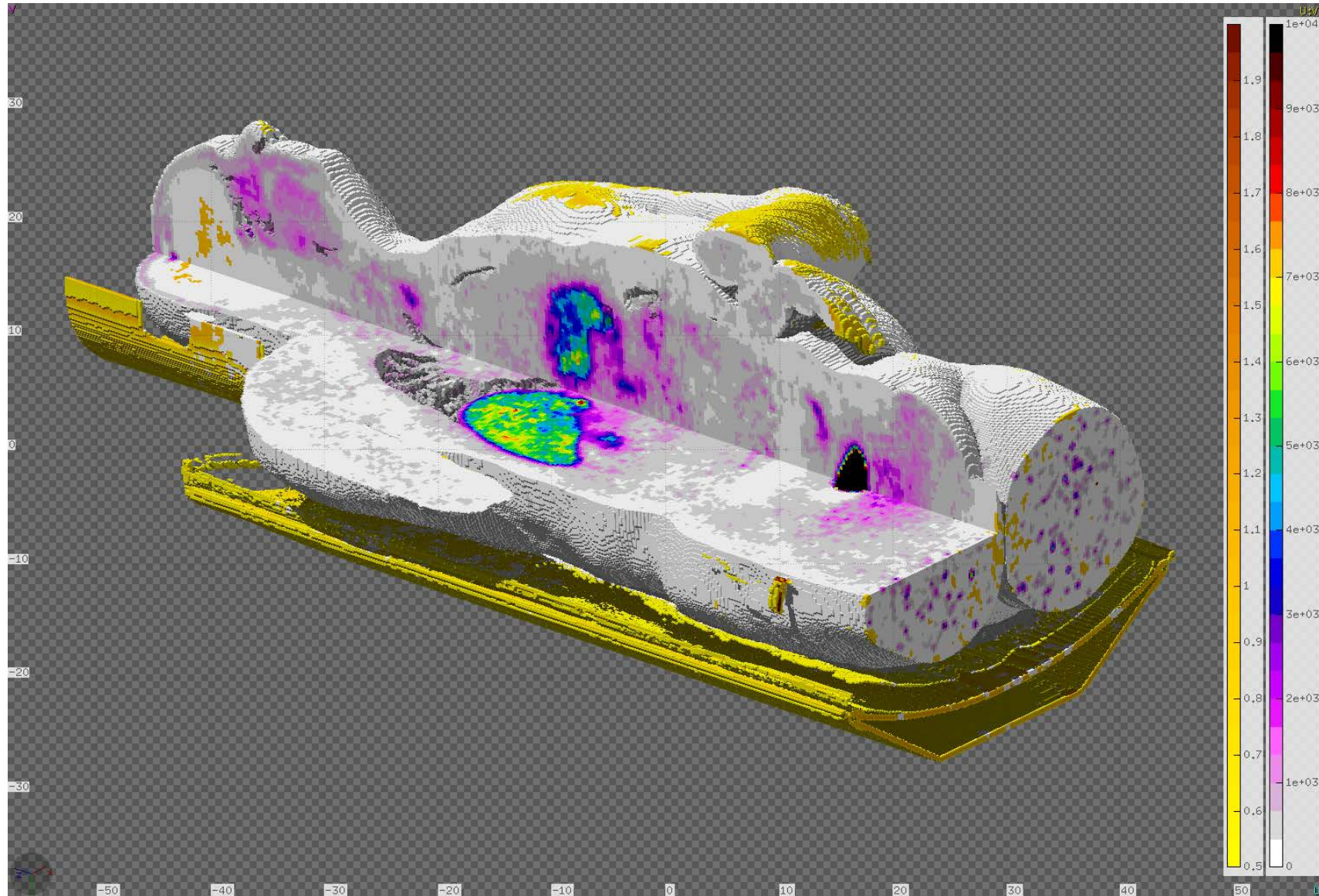


# Voxel geometries: examples

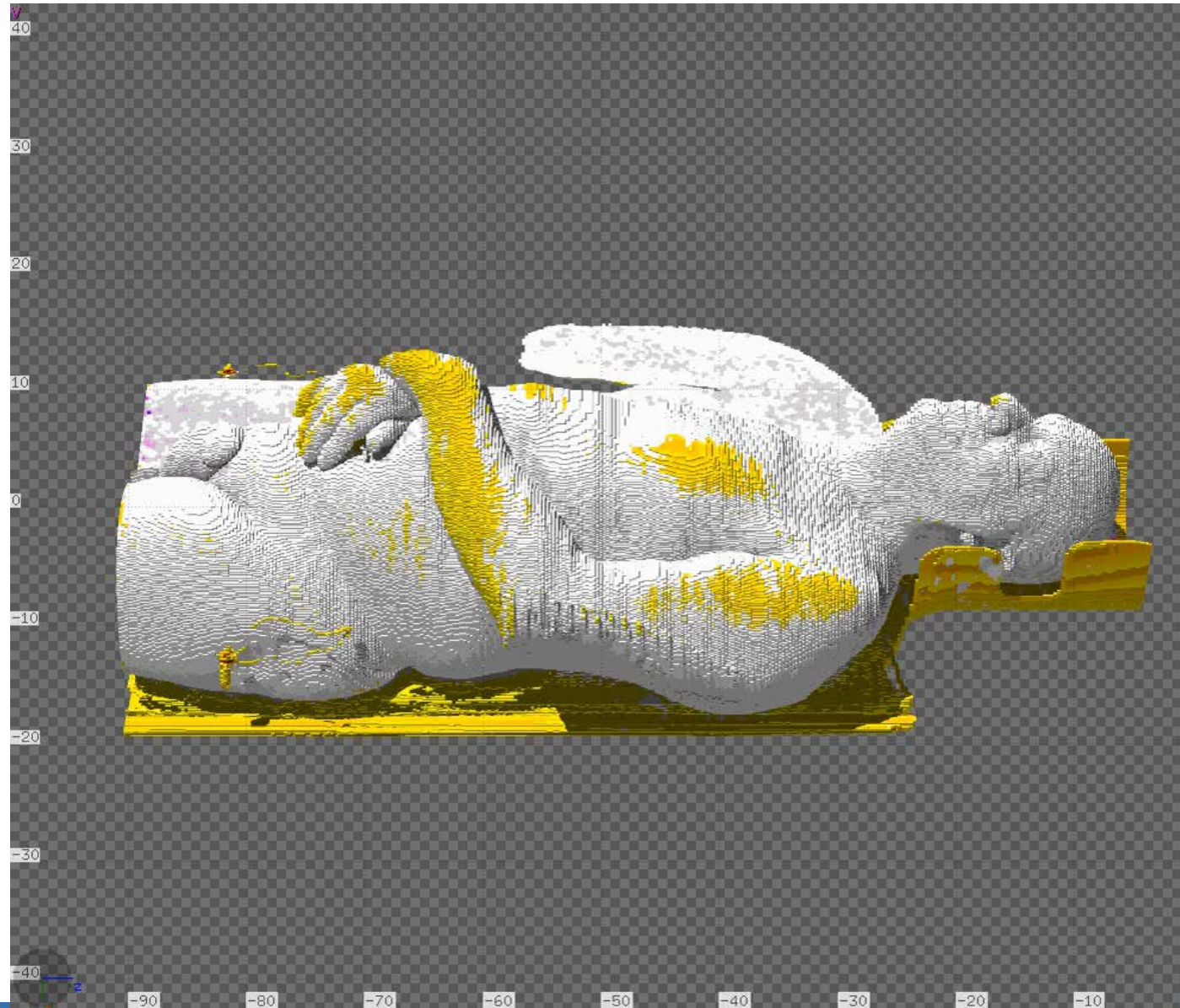


The Gran Sasso in FLUKA

# Voxel geometry with PET-CT

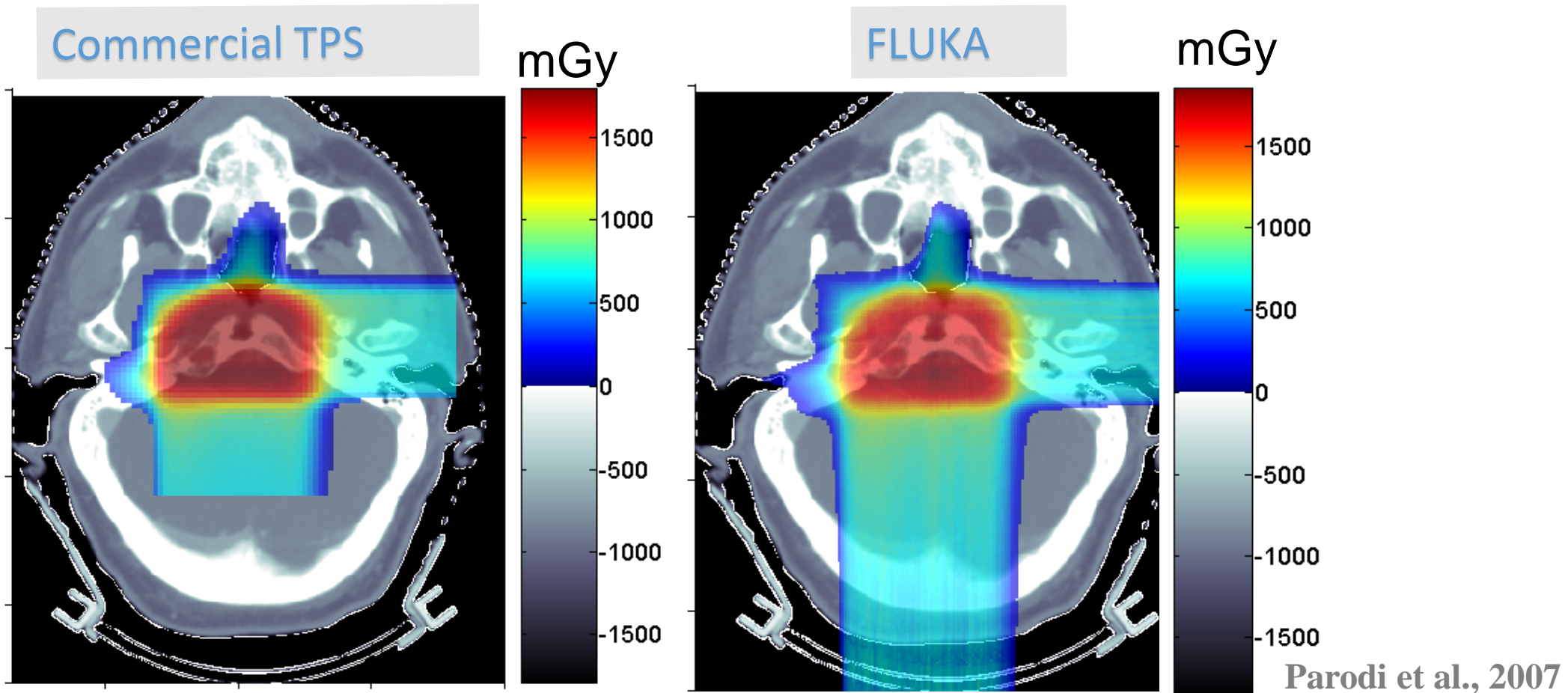


# Voxel geometry with PET-CT



# 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



# The FLUKA voxel geometry

- The CT scan contains integer values “Hounsfield Unit” reflecting the X-ray attenuation coefficient  $\mu_x$   
$$HU_x = 1000 (\mu_x - \mu_{H20}) / \mu_{H20}$$
, 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  $\leq 32767$** .  
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
- Optionally
  - ROI structures (Regions Of Interest).
    - A list of the ROIs, id, name, color and volume
    - A dictionary of the unique ROIs combinations per voxel
    - a 3D ROIs voxel array with ROIs combinations
  - A list of FLUKA cards with materials, assignments, correction coefficients etc..  
Each card is an 80 character long string in FLUKA fixed format

# 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  
Trans: ▼

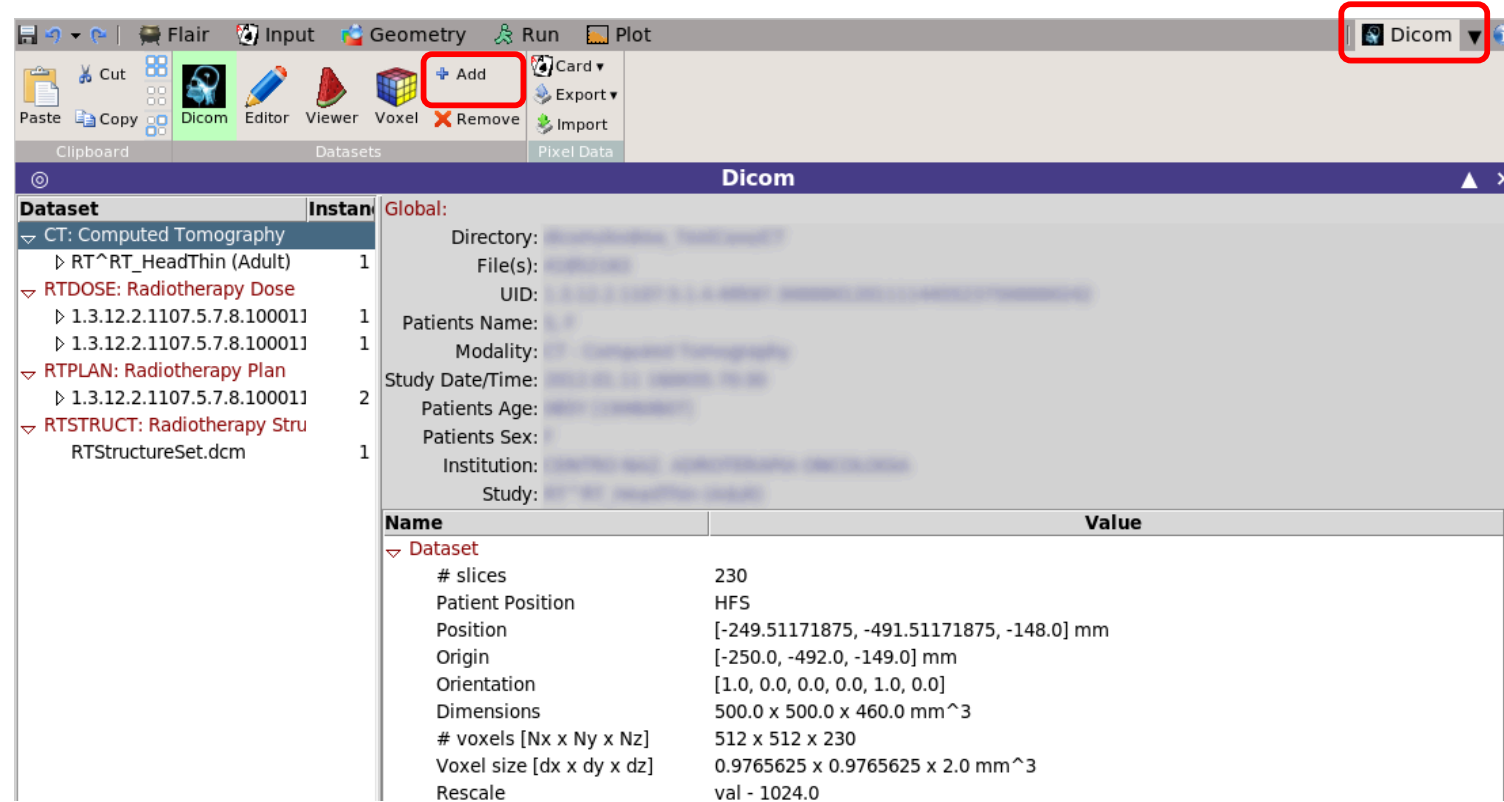
y: -35.068359  
Filename: VOXEL1 ▼

z: -88.6855

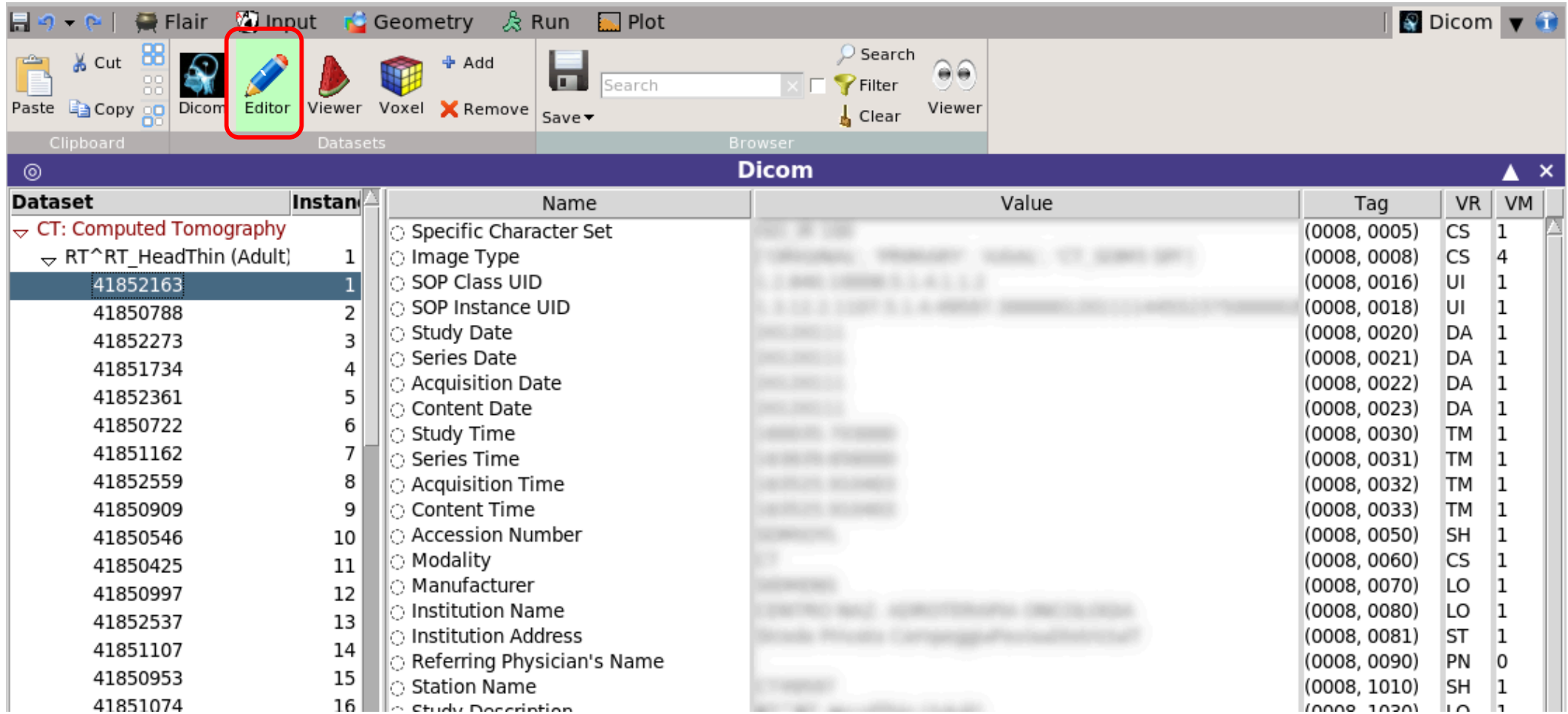
---

# Processing the DICOM files with FLAIR [1]

- 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 [2]



The screenshot shows the FLAIR software interface. The top toolbar includes icons for Flair, Input, Geometry, Run, and Plot. Below the toolbar, there are icons for Cut, Paste, Copy, Dicom, Editor (highlighted with a red box), Viewer, Voxel, Add, Remove, Save, Search, Filter, and Clear. The main window is titled 'Dicom' and contains a table with the following columns: Dataset, Instance, Name, Value, Tag, VR, and VM.

Dataset	Instance	Name	Value	Tag	VR	VM
CT: Computed Tomography		○ Specific Character Set		(0008, 0005)	CS	1
RT^RT_HeadThin (Adult)	1	○ Image Type		(0008, 0008)	CS	4
	1	○ SOP Class UID		(0008, 0016)	UI	1
41850788	2	○ SOP Instance UID		(0008, 0018)	UI	1
41852273	3	○ Study Date		(0008, 0020)	DA	1
41851734	4	○ Series Date		(0008, 0021)	DA	1
41852361	5	○ Acquisition Date		(0008, 0022)	DA	1
41850722	6	○ Content Date		(0008, 0023)	DA	1
41851162	7	○ Study Time		(0008, 0030)	TM	1
41852559	8	○ Series Time		(0008, 0031)	TM	1
41850909	9	○ Acquisition Time		(0008, 0032)	TM	1
41850546	10	○ Content Time		(0008, 0033)	TM	1
41850425	11	○ Accession Number		(0008, 0050)	SH	1
41850997	12	○ Modality		(0008, 0060)	CS	1
41852537	13	○ Manufacturer		(0008, 0070)	LO	1
41851107	14	○ Institution Name		(0008, 0080)	LO	1
41850953	15	○ Institution Address		(0008, 0081)	ST	1
41851074	16	○ Referring Physician's Name		(0008, 0090)	PN	0
		○ Station Name		(0008, 1010)	SH	1
		○ Study Description		(0008, 1020)	LO	1

Browse & edit (e.g. anonymize) the dicom files

# Processing the DICOM files with FLAIR [3]

The screenshot displays the FLUKA software interface. The top toolbar includes icons for 'Flair', 'Input', 'Geometry', 'Run', and 'Plot'. A red box highlights the 'Viewer' icon, which is a green square with a white triangle. Below the toolbar, there are input fields for 'Xmin:', 'Xmax:', 'Ymin:', 'Ymax:', 'Zmin:', and 'Zmax:', along with 'Reset' and 'Slice → Zmin' buttons. The main window is titled 'Dicom' and contains a table of datasets and a corresponding image.

Dataset	Instan	ROI	Id
CT: Computed Tomography		check	1
▶ RT^RT_HeadThin (Adult)	1	nonusareGTVold	2
RTDOSE: Radiotherapy Dose		Optic Chiasm	3
▶ 1.3.12.2.1107.5.7.8.100011	1	Brain Stem	4
▶ 1.3.12.2.1107.5.7.8.100011	1	Optic Nerve(R)	5
RTPLAN: Radiotherapy Plan		Temp lobe dx	6
▶ 1.3.12.2.1107.5.7.8.100011	2	Temp lobe sn	7
RTSTRUCT: Radiotherapy Stru		Optic Nerve(L)	8
RTStructureSet.dcm	1	Eye(R)	9
		Eye(L)	10
		Lens(R)	11
		Lens(L)	12
		Ear(R)	13
		Ear(L)	14
		brain	15
		orch med dx	16
		orch med sx	17
		ATMsx	18
		ATMdx	19
		GTVpreop	20
		GTVpf	21
		CTV74	26
		ipofisi	23
		CTV54	24
		PTV54	29

The image on the right shows an axial CT scan of a head with various colored contours overlaid, representing different anatomical structures and regions of interest. A coordinate system is visible in the top left corner of the image, with axes labeled A (Anterior), P (Posterior), R (Right), and L (Left).

Visualize the dicom if possible

# Processing the DICOM files with FLAIR [4]

- 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: head.mat in the flair/dicom dir).

Creating VOXEL file

Current: 28 [0 - 149] Completed: 18%

Processing: CTFus001\_CT224.dcm

Stop

Materials: material.inp # materials: 43

Unit to Material : head.mat

≤ 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 [5]

- **≤ 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.

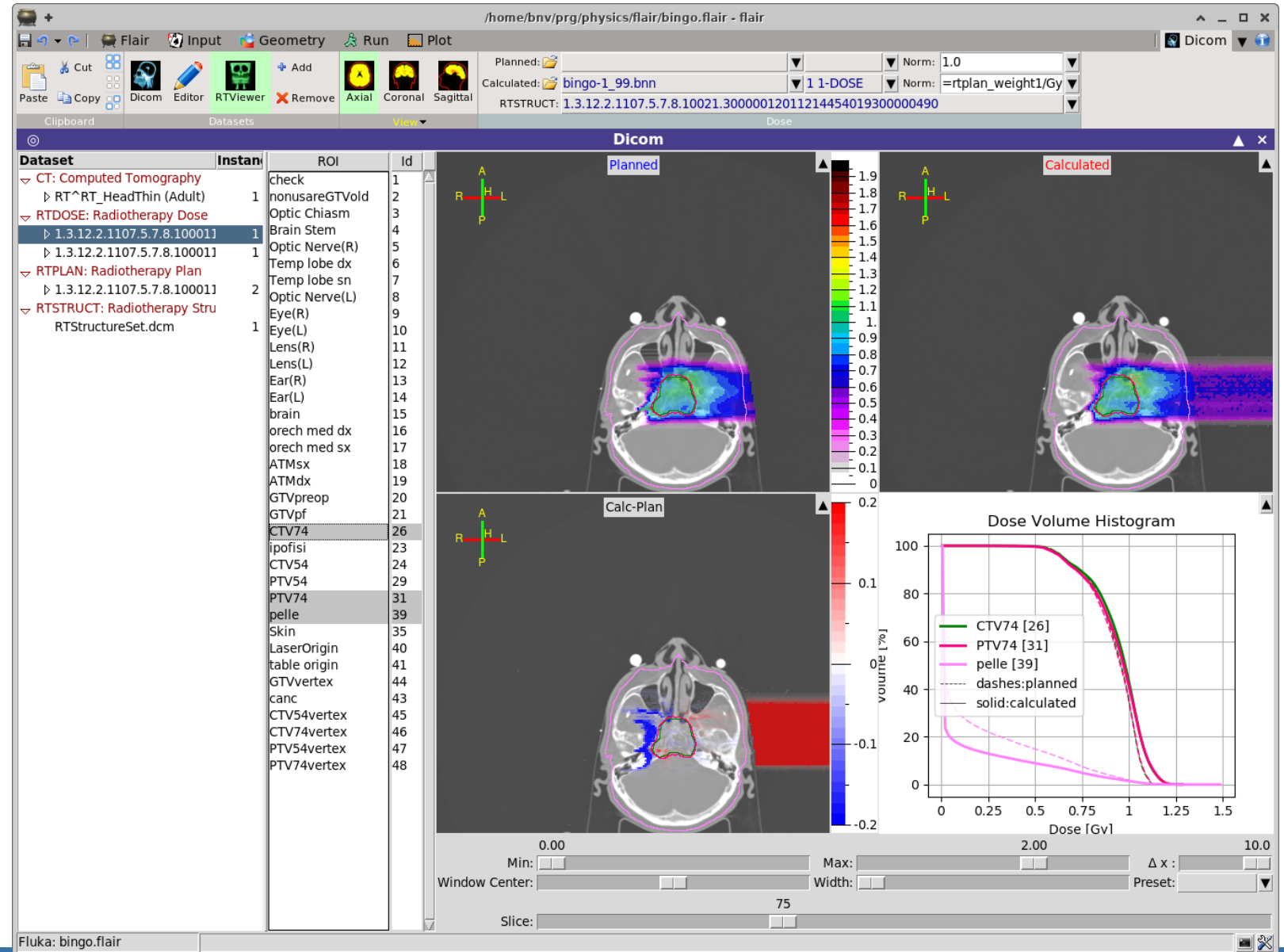
Optionally you can specify correction factors for the density and dE/dx

- **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

# Processing the DICOM files with FLAIR [6]








- Convert the RTPLAN to FLUKA input
- RTDOSE Compare the planned vs calculated data
- Automatically generate DVH
- Coordinate system: everything will be relative to the patient system as described in the DICOM files





# 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.

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

# 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 “**body.mat**” files are examples, the user should update these files taking into account his calibration curves.

# Practical issues for Medical Applications

- 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 [1]

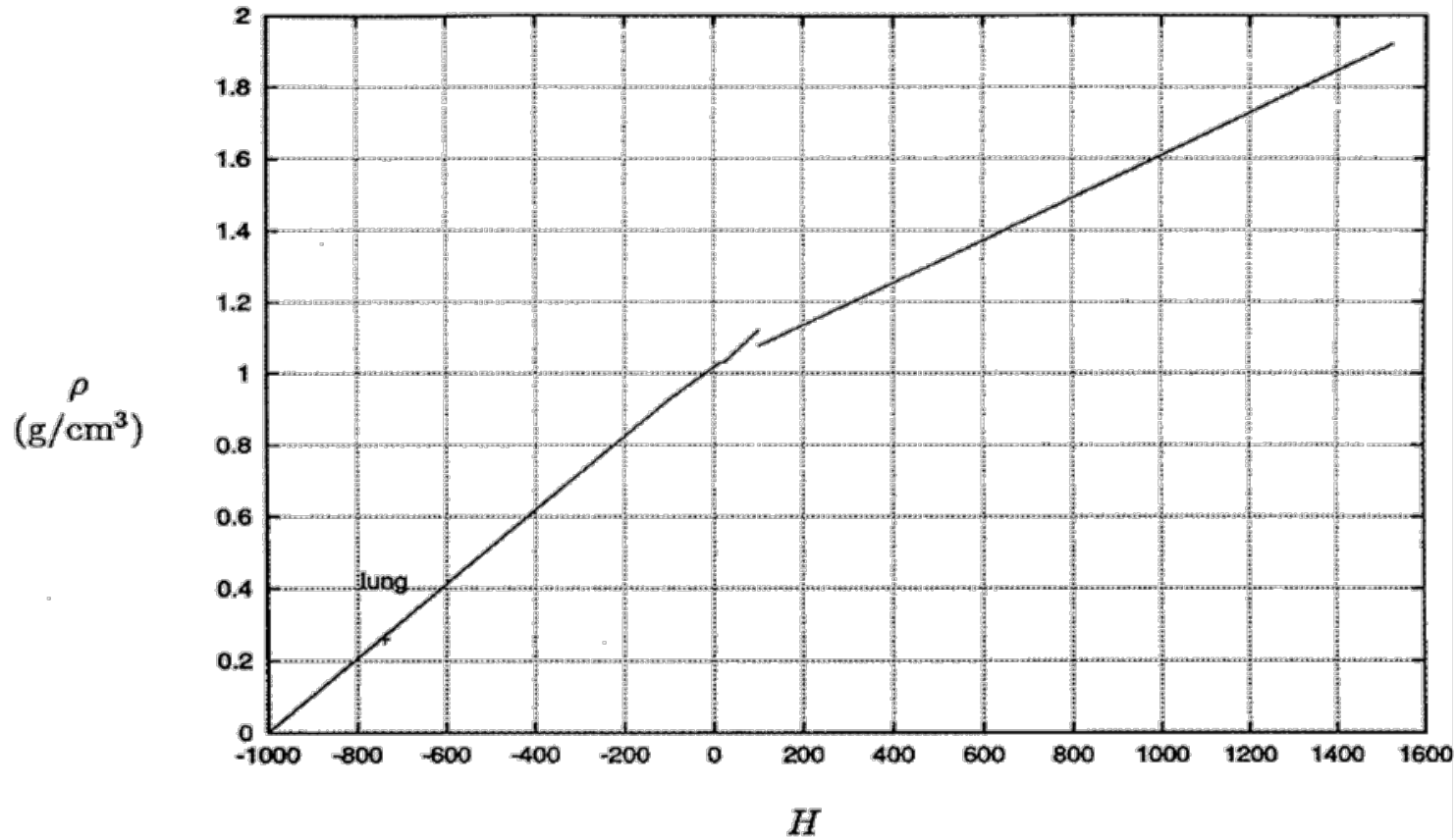
CT segmentation into 27 materials of defined elemental composition (from analysis of 71 human CT scans)

<i>H</i>	$w_j(\text{pp})$											
	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

Schneider et al PMB 45, 2000

# CT stoichiometric calibration [2]

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 CORRFACt card

- **CORRFACt** 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 **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 dE/dx

- 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 CORRFAC 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

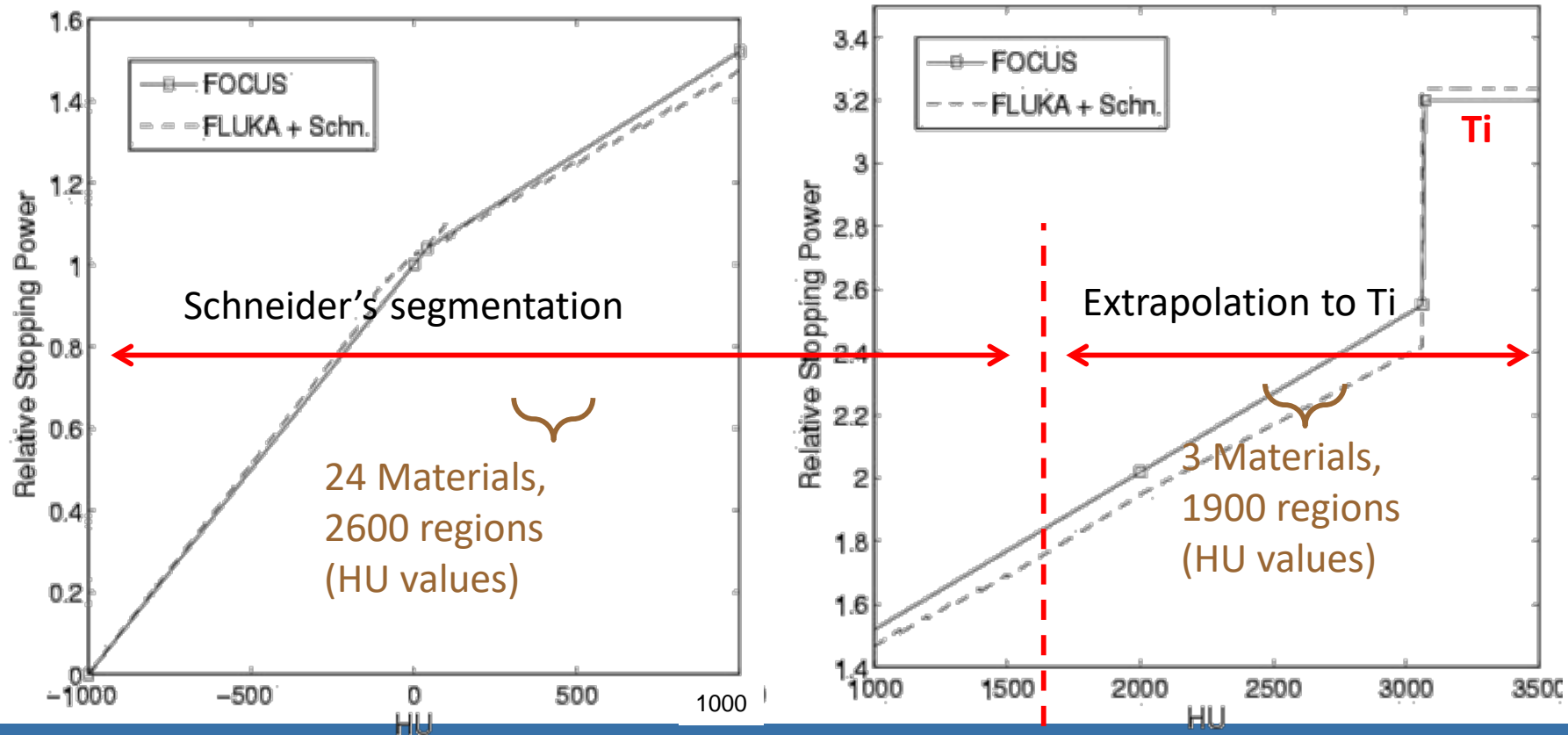
**CORRFAC** 0.85 0.0 0.0 VOXEL005 Region #25 corresponds

**CORRFAC** 1.3 0.0 0.0 VOXEL016 to “softer” bone than #31



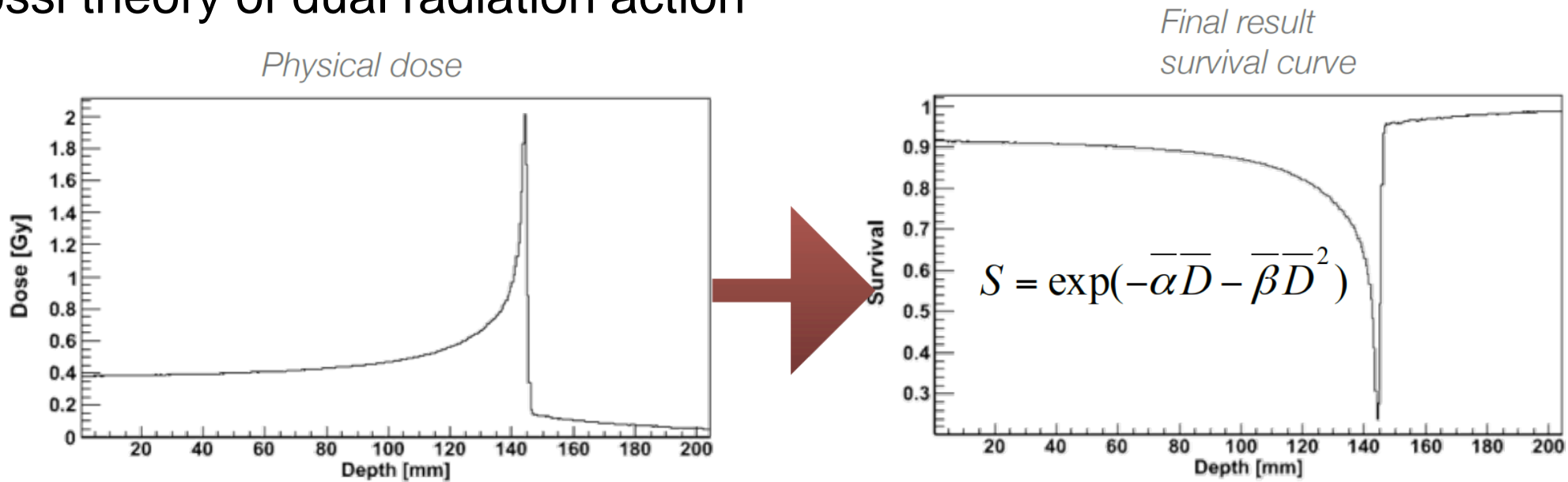
# Tune FLUKA calibration curve

- The **CORRFAC** ionization scaling factors were obtained from the  $dE/dx$  ratio between TPS and FLUKA (+ Schneider “mass density”)  
→ The user should update the “**head.mat**” or “**body.mat**” file with his own calibration for CdEdX\_rel taking into account his TPS.



# RBE: Relative Biological Effective dose scoring

- Under the standard assumption of a linear-quadratic dose-effect relationship, for each energy deposition  $i$ , FLUKA interpolates from a radiobiological database the  $\alpha_{D,i}$  and  $\beta_{D,i}$  parameters for the specific ion with a certain charge at a certain energy.
- Then FLUKA sums up properly the mixed radiation effect applying the Kellerer and Rossi theory of dual radiation action



270 MeV/u 12C ions on V79 cell line

# Cards: TPS-SCORE, RAD-BIOL

 **RAD-BIOL**  
 **TPSSCORE**

File: V79\_MCTPS  
Type: BIOTOBIN ▼  
Bin: AlphaD ▼

Bio set: V79\_MCTPS ▼  
to Bin: SqBetaD ▼  
Unit: 21 BIN ▼

Step:  
Name: AlphaD

 **USRBIN**

Type: X-Y-Z ▼  
Part: ALPHA-D ▼

Xmin: -10  
Ymin: -10  
Zmin: -10

Xmax: 10  
Ymax: 10  
Zmax: 10

NX: 100  
NY: 100  
NZ: 100

 **USRBIN**

Type: X-Y-Z ▼  
Part: SQBETA-D ▼

Xmin: -10  
Ymin: -10  
Zmin: -10

Unit: 21 BIN ▼  
Xmax: 10  
Ymax: 10  
Zmax: 10

Name: SqBetaD  
NX: 100  
NY: 100  
NZ: 100

**RAD-BIOL** loads an ASCII file containing the Alpha, Beta parameters for a linear quadratic cell survival curve for various particles

**TPSSCORE** associates a cellular line file with USRBIN scorings

**USRBIN** specialized particles **ALPHA-D**, **SQBETA-D** score the dose weighted of the alpha (linear) and square root of beta, cell killing coefficients

# RAD-BIOL Cell lines

The file must contain the Alpha and Beta parameters for a linear-quadratic cell survival curve for the various particles involved in the simulation.

Line:

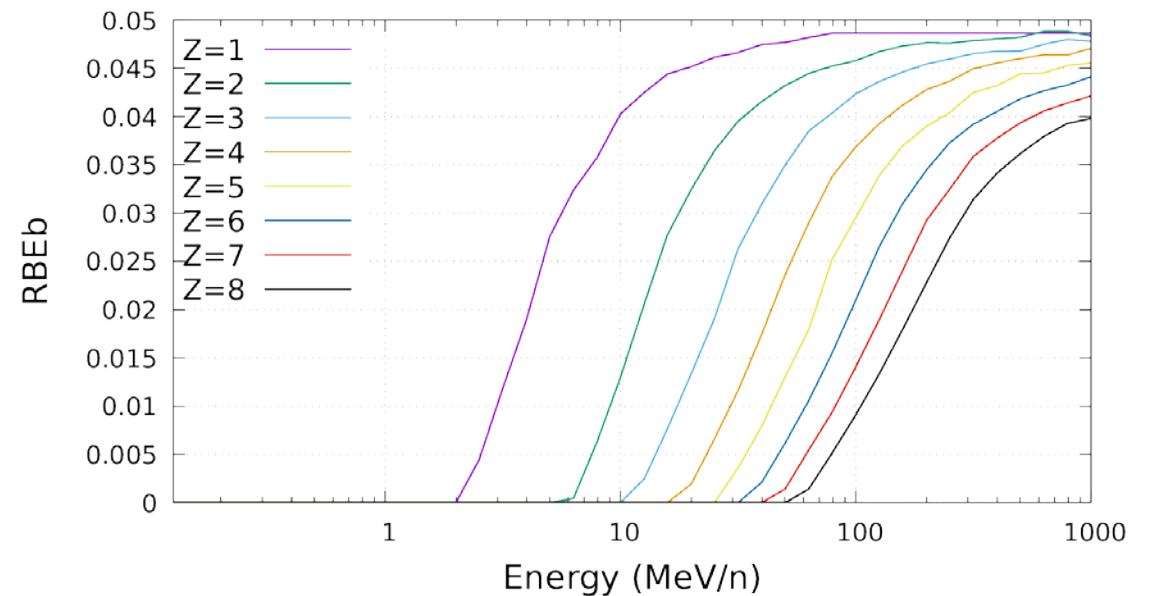
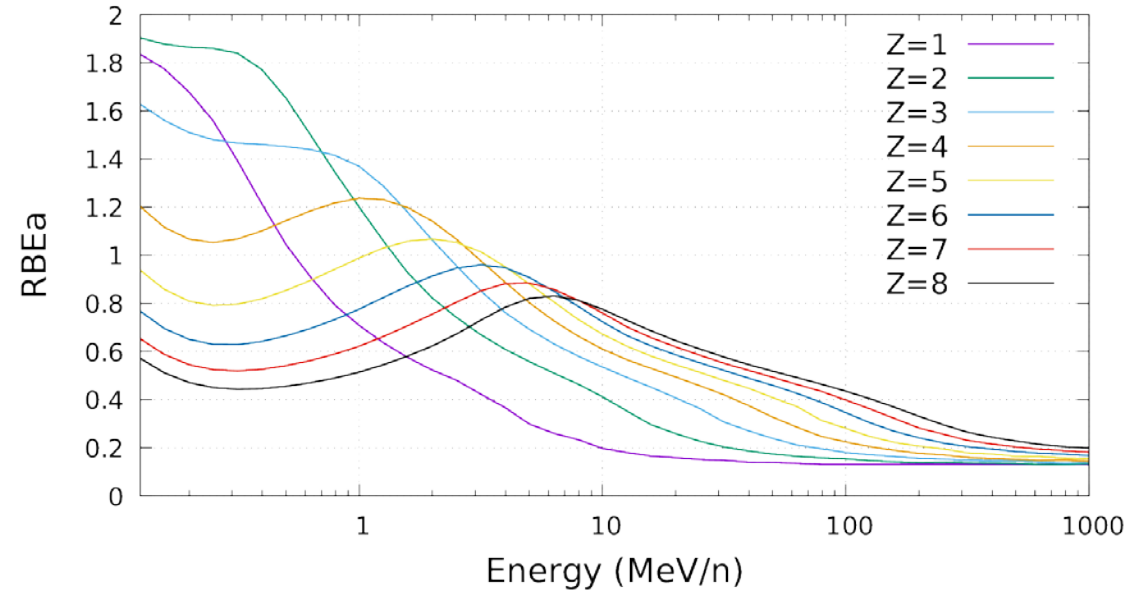
1. Alpha ( $\text{Gy}^{-1}$ ) and Beta ( $\text{Gy}^{-2}$ ) for X-rays
2. number of ions species  $N_{\text{ion}}$  (charges) starting from  $Z=1$

Repeated:

- # number of entries for this  $Z$
- tabulation:
  - i. kinetic energy (MeV/n) or LET (keV/um)
  - ii. Alpha value
  - iii. Beta value for this ion  $A=Z$

last line (optional) with ENERGY or LET (default kinetic energy per nucleon)

V79 cell lines for  $Z=1..8$





# Applications of FLUKA to p therapy @ MGH

Parodi et PMB 52, 2007

