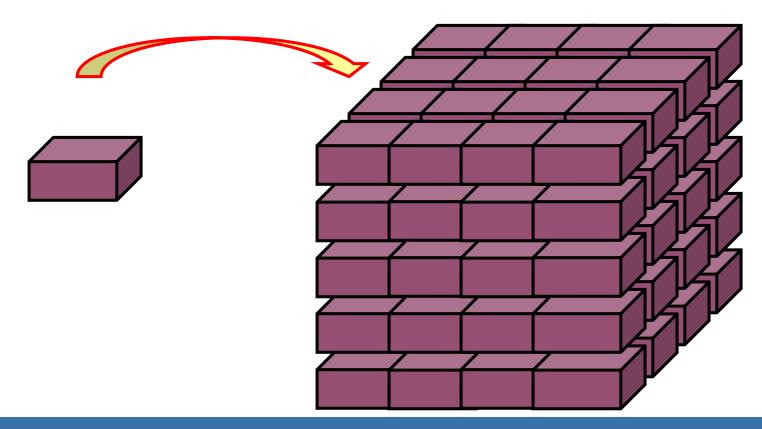


Medical Applications

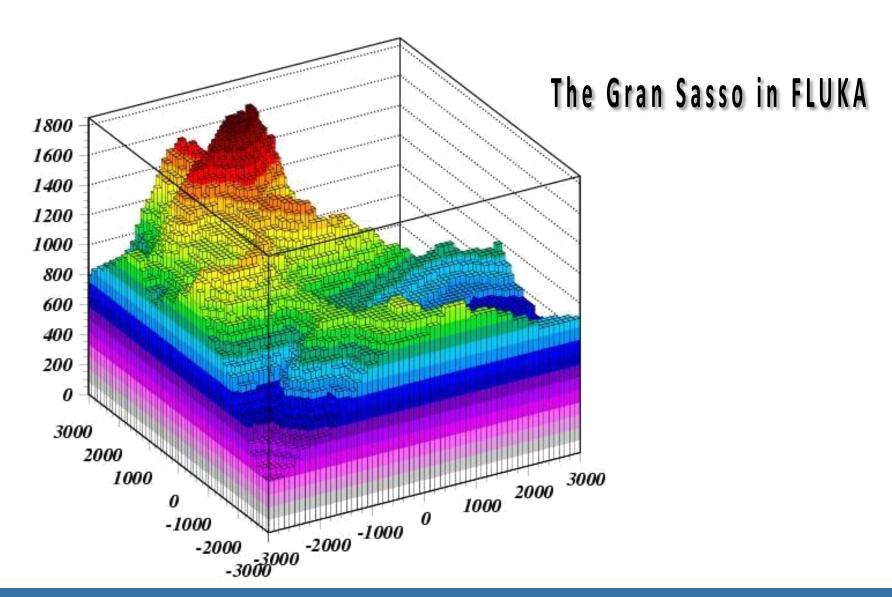
Tutorial on flair & FLUKA capabilities for medical applications

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



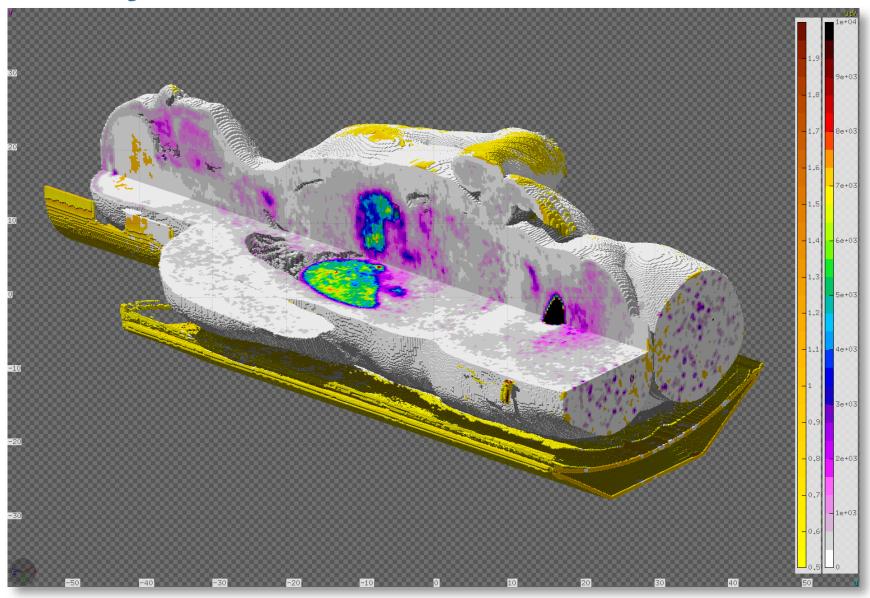


Voxel geometries: examples



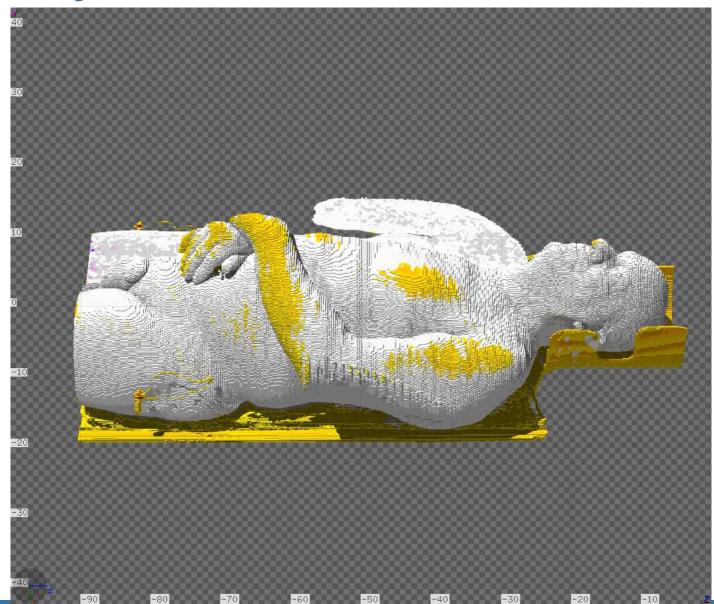


Voxel geometry with PET-CT





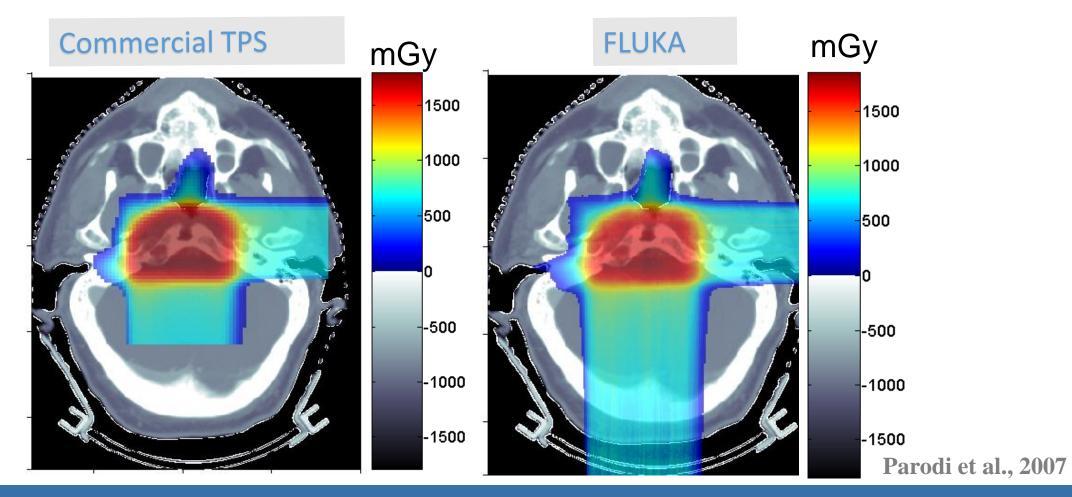
Voxel geometry with PET-CT





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 CT scan contains integer values "Hounsfield Unit" reflecting the X-ray attenuation coefficient μ_x HU_x = 1000 (μ_x - μ_{H20}) / μ_{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.



- 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 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



x: -35.068359

y:-35.068359

z: -88.6855

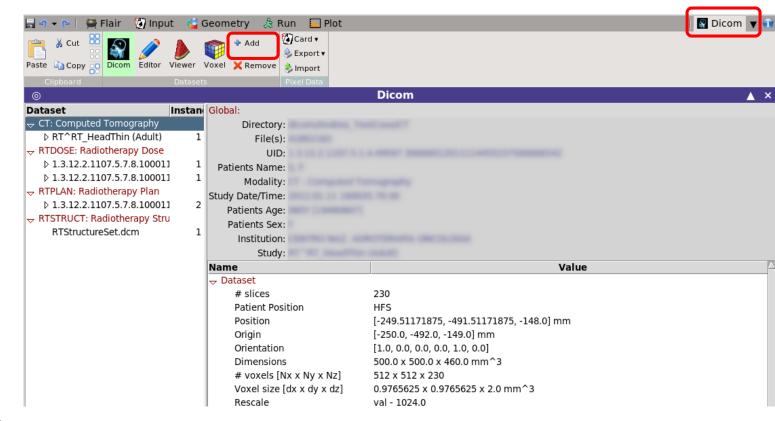
Trans: 🔻

F

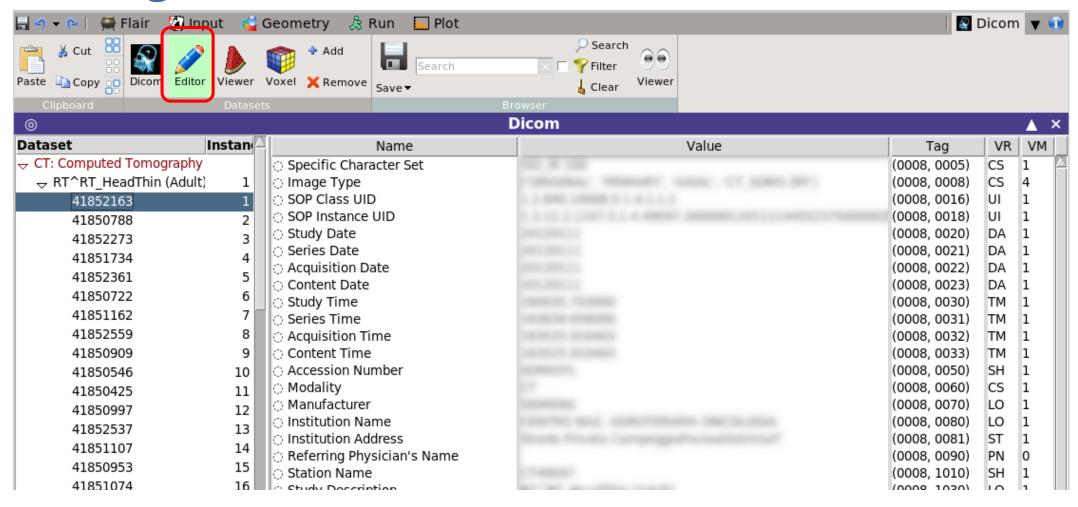
Filename: VOXEL1 ▼

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.



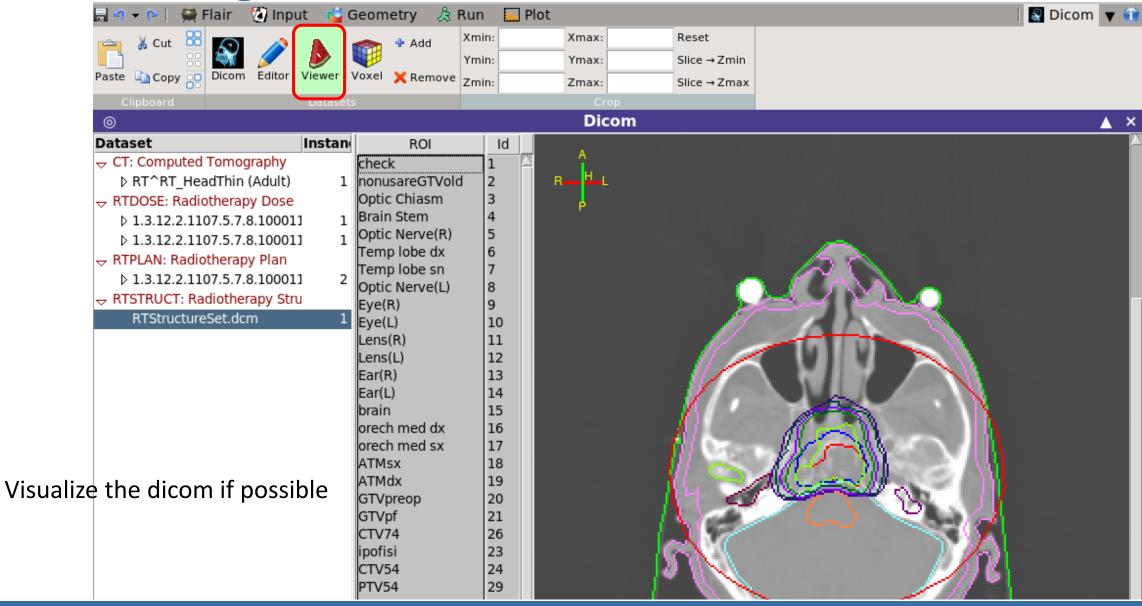
Processing the DICOM files with FLAIR [2]



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



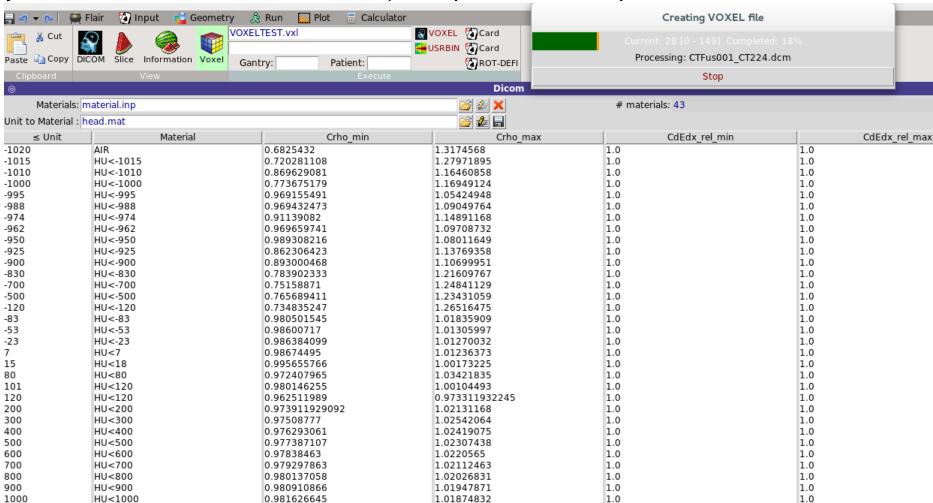
Processing the DICOM files with FLAIR [3]





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: material.inp and head.mat in the flair/dicom dir).





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

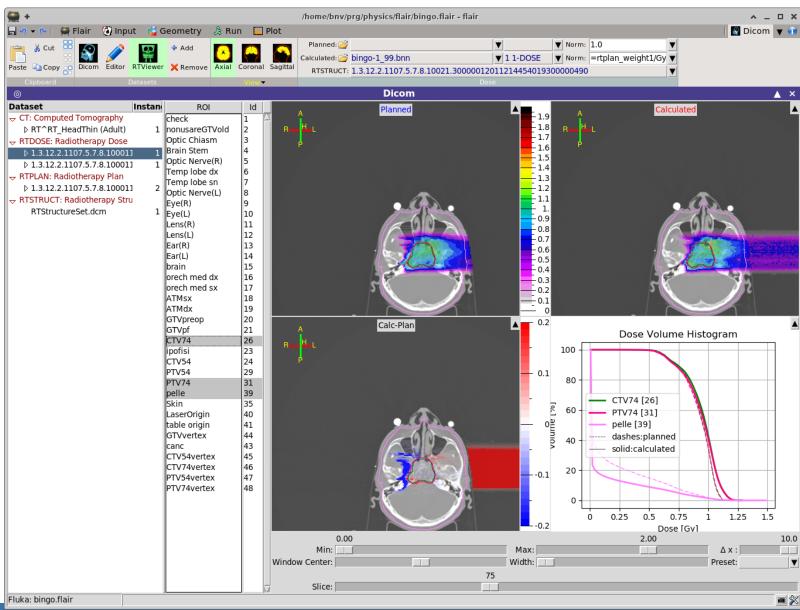
- Crho_min/Chro_max: density correction factors to be applied on the lower/upper limit of the unit range (see next slides).
- CdEdx_rel_min/CdEdx_rel_max: relative correction factors on dE/dx for minimum/maximum unit in the range (see next slides).

≤ Unit	Material	Crho_min	Crho_max	CdEdx_rel_min	CdEdx_rel_max	4
-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
- Compare the planned vs calculated data
- Automatically generate
 DVH





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 Trans: ▼	y: -35.068359 Filename: VOXEL1 ▼	z: -88.6855
SPH	BODY1	x: 0. R: 10000.	у: 0.	Z: 0.
SPH	BODY2	x: 0. R: 1000.	у: 0.	z: 0.
♠ END				
REGION e	REG1 xpr: BODY1-BODY2		Neigh: 5	Volume:
REGION e	REG2 xpr: BODY2-VOXEL		Neigh: 5	Volume:
♦ 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 "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)

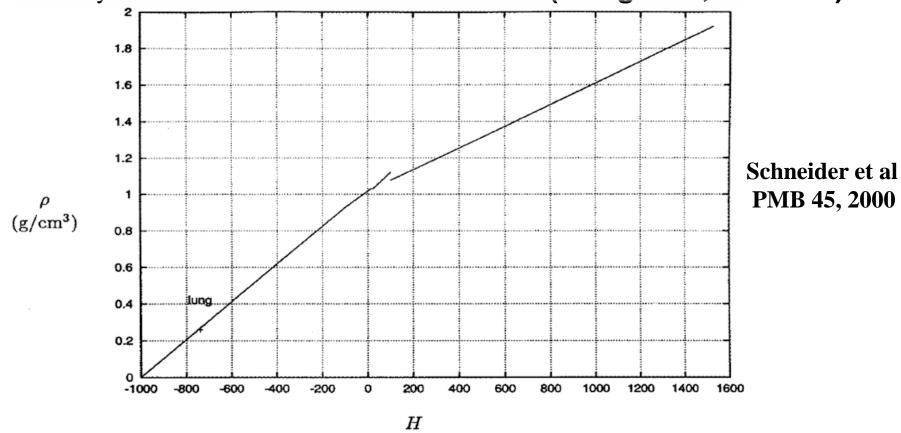
								$w_i(p$	p)					
		H	Н	С	N	0	Na	Mg	P	S	C1	Ar	K	Ca
Air, Lung,		-1000950			75.5	23.2						1.3		
	7	-950120	10.3	10.5	3.1	74.9	0.2		0.2	0.3	0.3		0.2	
Adipose tissue		-12083	11.6	68.1	0.2	19.8	0.1			0.1	0.1			
Adipose tissue		-8253	11.3	56.7	0.9	30.8	0.1			0.1	0.1			
		-5223	11.0	45.8	1.5	41.1	0.1		0.1	0.2	0.2			
		-22-7	10.8	35.6	2.2	50.9			0.1	0.2	0.2			
0 - (((!	J	8-18	10.6	28.4	2.6	57.8			0.1	0.2	0.2		0.1	
Soft tissue	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
Skeletal tissue	~	900-1000	5.2	24.6	3.7	41.1	0.1	0.2	7.8	0.3				17.0
Skeletal tissue)	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)



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)
```

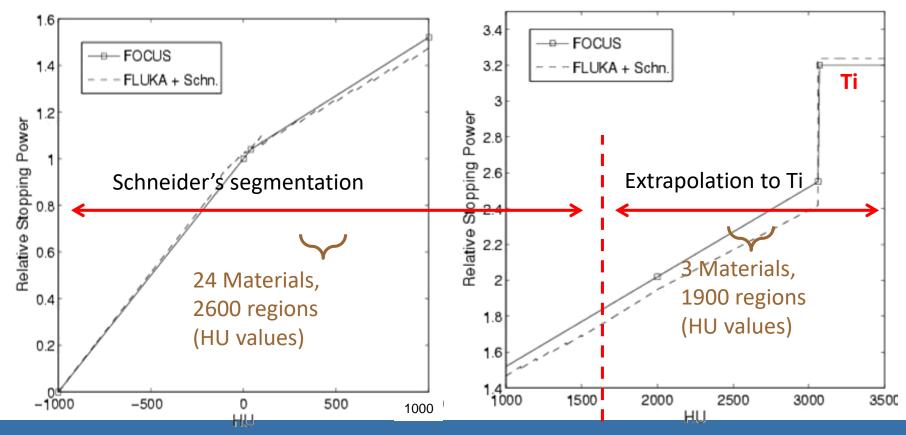
■ Use CORRFACT to impose the desired correction for stopping power (⇒ ion range!) in the regions KREG corresponding to different organs IO (i.e., different HU values) sharing the same MATERIAL assignment

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



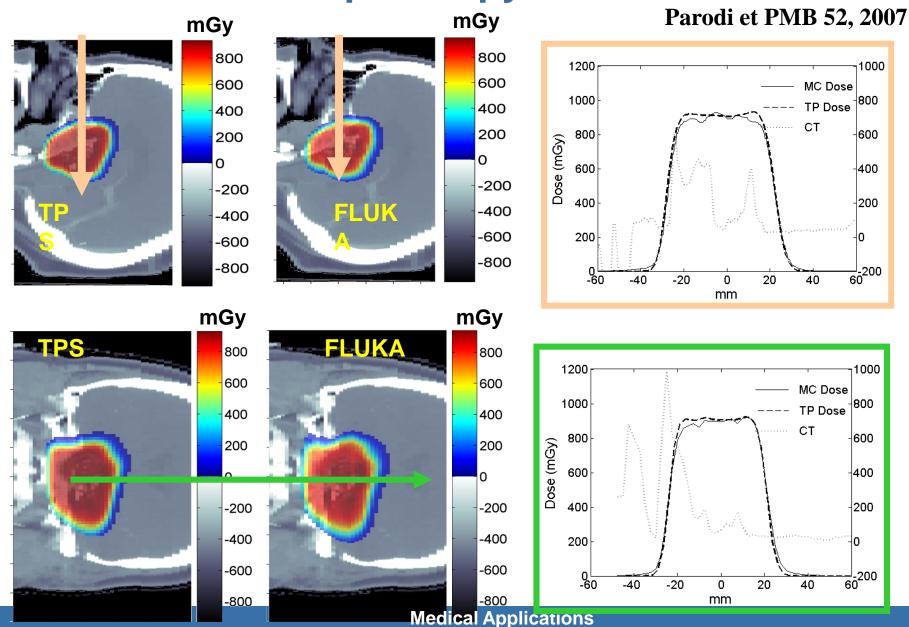
Tune FLUKA calibration curve

- The CORRFACT 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.

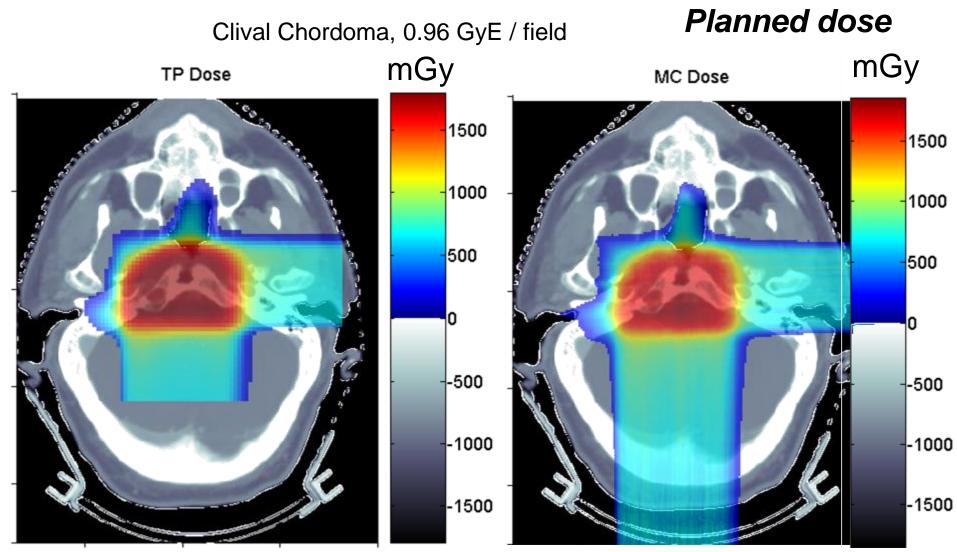




Applications of FLUKA to p therapy @ MGH



Applications of FLUKA to p therapy @ MGH







Post-radiation PET/CT @ MGH

Average Activity

Clival Chordoma, 0.96 GyE / field, DT1 ~ 26 min, DT2 ~ 16 min Bq/ml Bq / ml **PET Meas** MC PET 150 150 100 100 50 50 -50 -50 -100 -100 -150 -150





