

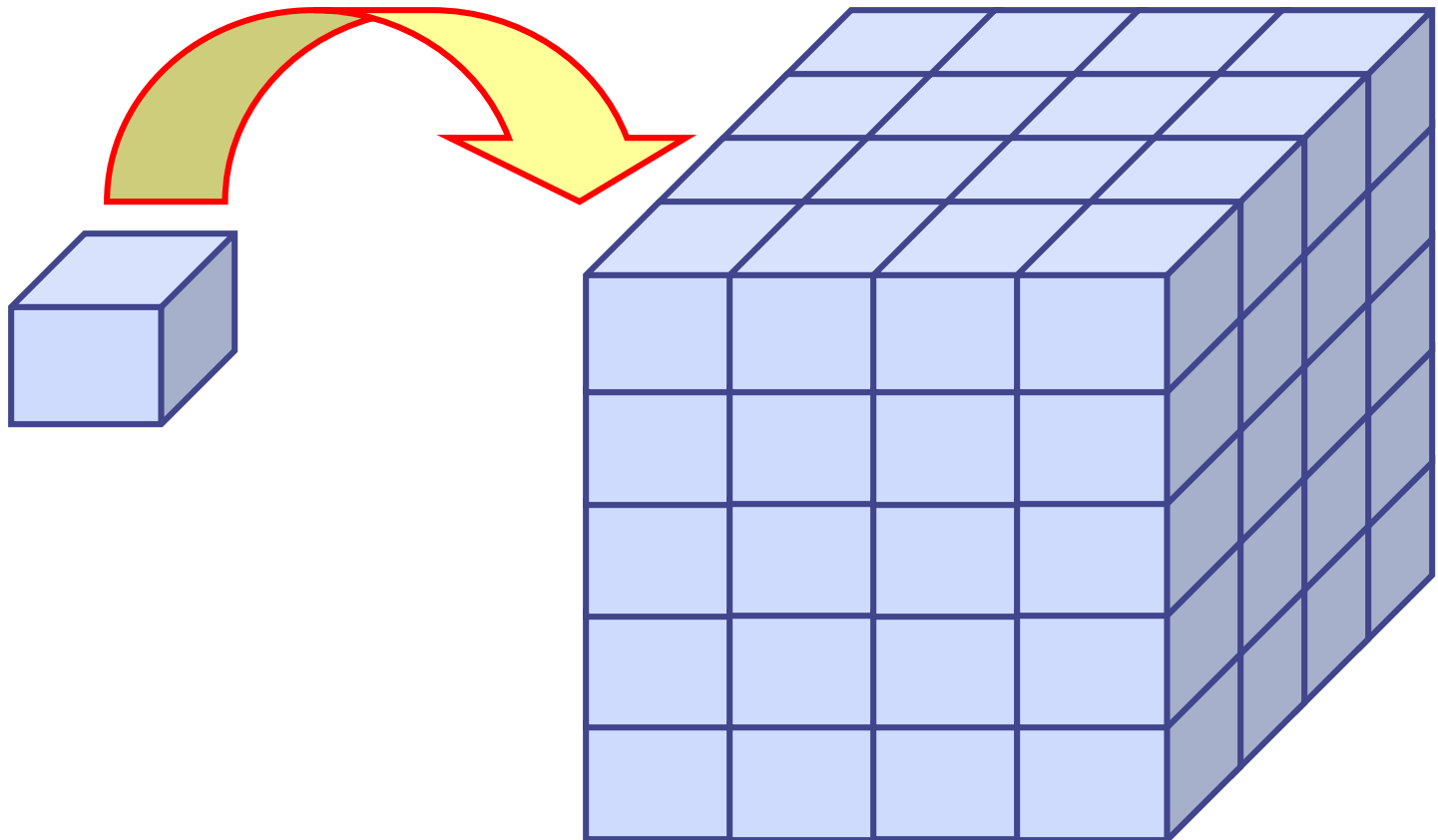


Voxels and Medical Applications

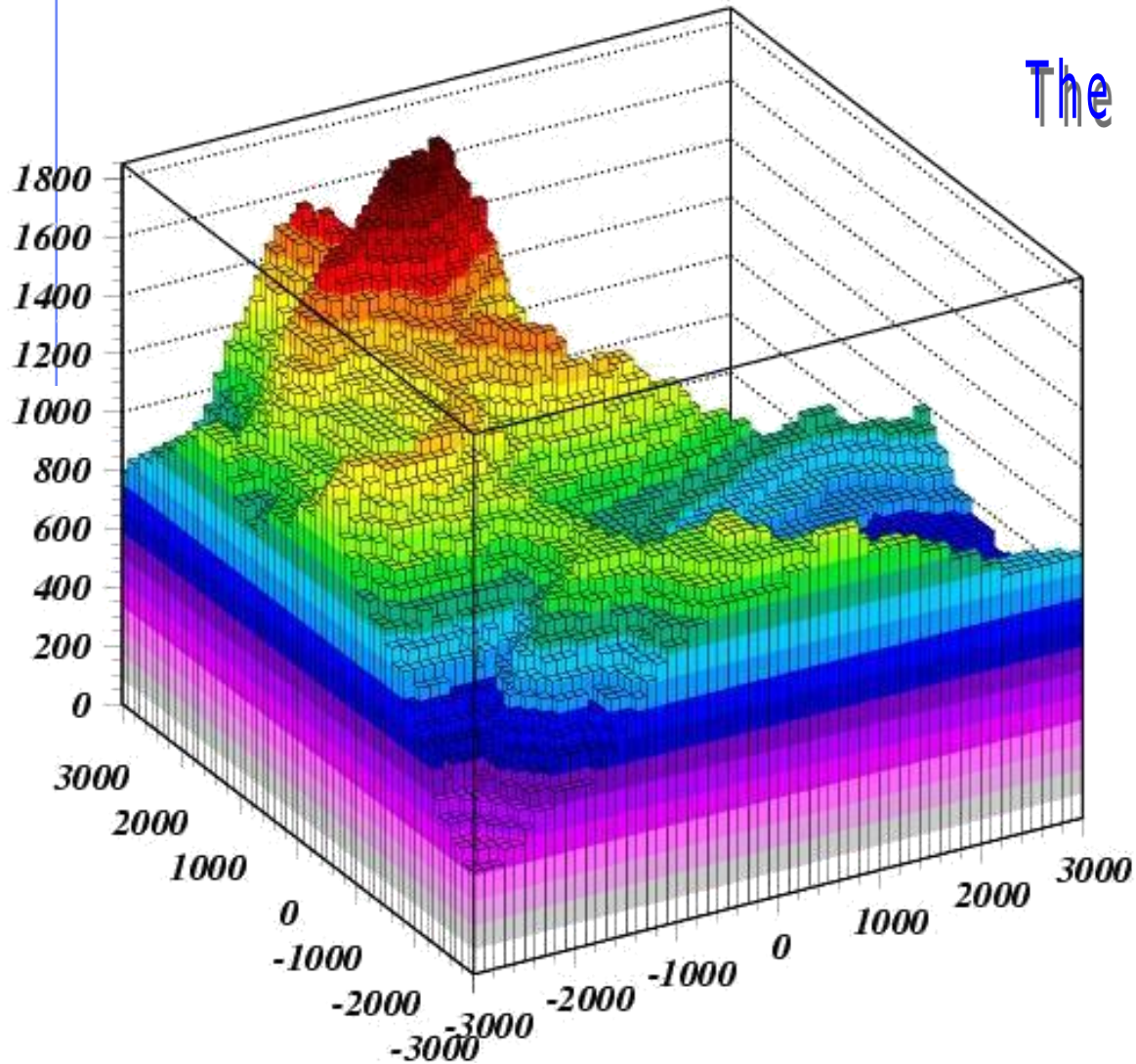
FLUKA Beginners course

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**



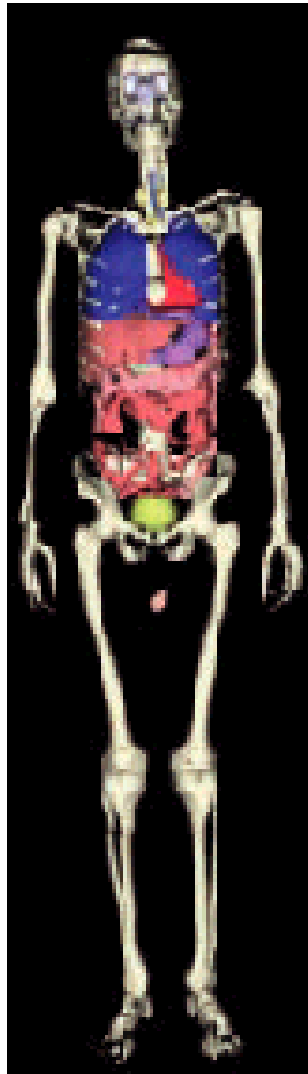
Voxel geometries: examples



The Gran Sasso in FLUKA

Voxel geometries: examples

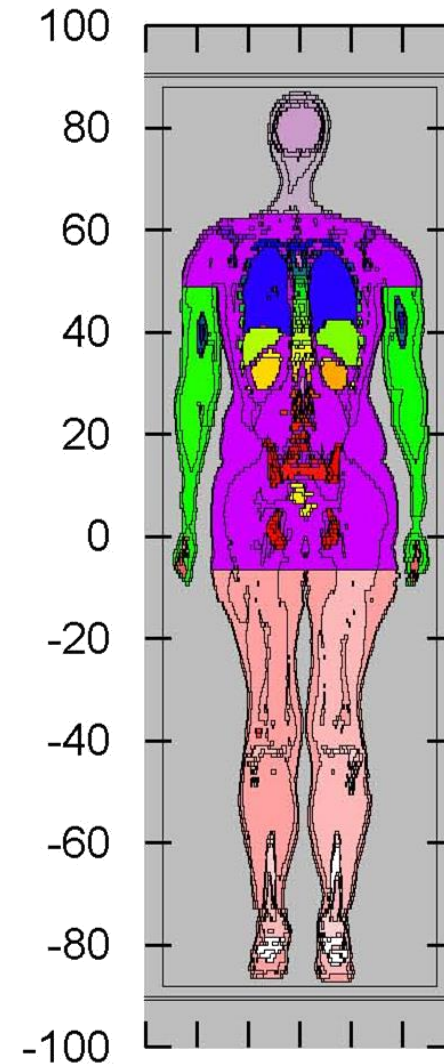
The anthropomorphic **GOLEM** phantom



Implementation in
FLUKA
(radioprotection
applications)

**Petoussi-Henss
et al, 2002**

FLUKA golem section

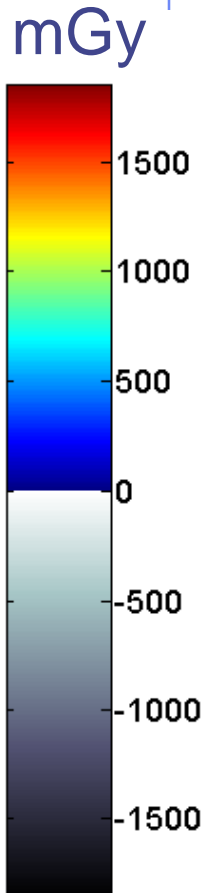
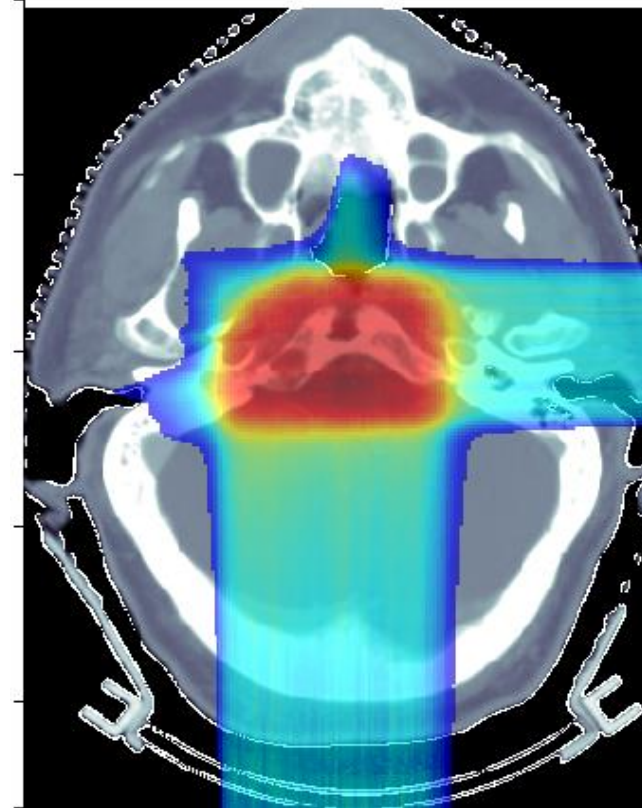
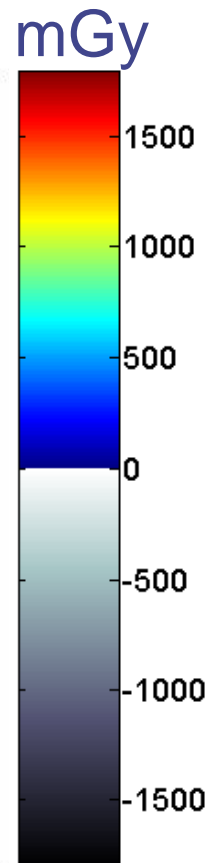
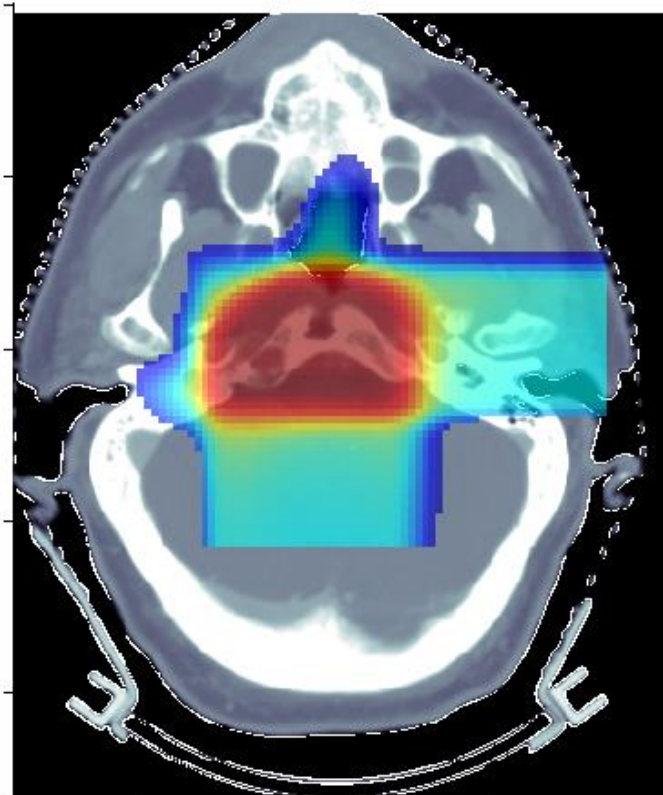


Voxel geometries in medical applications

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

FLUKA



The FLUKA voxel geometry

- The CT scan contains integer values “Hounsfield Unit” reflecting the X-ray attenuation coefficient μ_x
$$HU_x = 1000 (\mu_x - \mu_{H2O}) / \mu_{H2O} , \quad \text{typically } -1000 \leq HU \leq 3500$$
- 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.

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 (see next slides).
- This stage should :
 - 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 ≤ 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).
 - Assign 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
 - 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
 - (In the new release) definition of Regions of Interests (ROI)
 - ◆ A list of the ROIs for each voxel

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 the whole voxel
- **WHAT(5), WHAT(6)**: not used
- **SDUM** = name of the voxel file
extension will be assumed to be **.vxl**)

 **VOXELS**

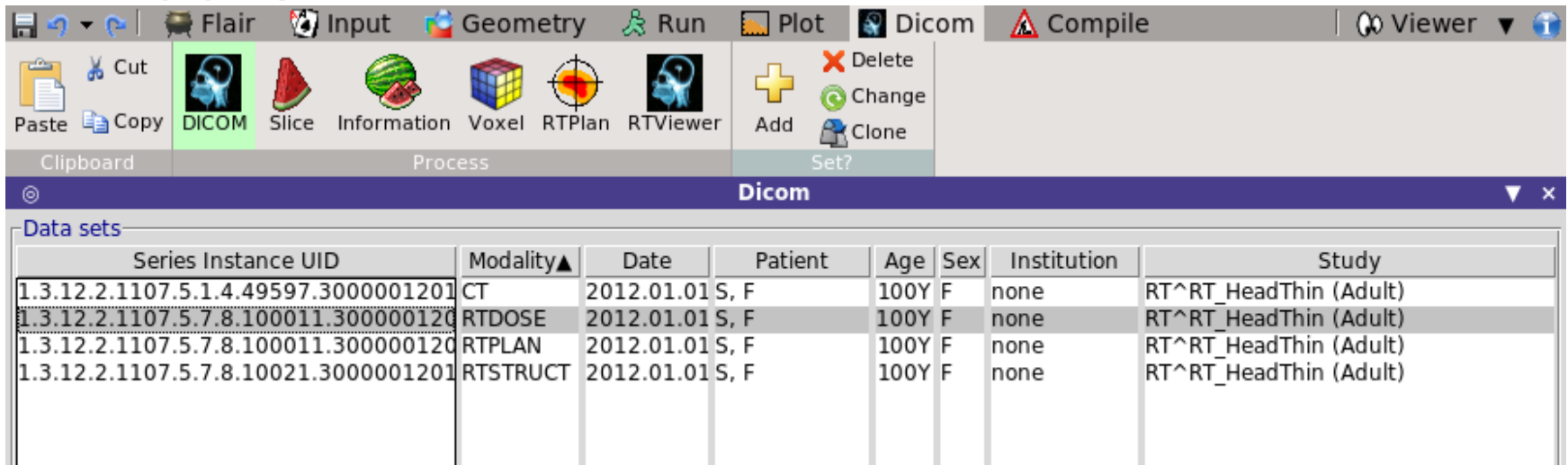
x: -35.068359
Trans: ▼

y: -35.068359
Filename: VOXEL1 ▼

z: -88.6855

Processing the **DICOM** files with FLAIR 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, USBIN compatible files as well as providing input for Treatment Plan simulations
- First select the "Directory" where the DICOM data sets are located (if you have doubts press F1 and the flair manual will help you).



The screenshot shows the FLAIR I software interface. The top menu bar includes Flair, Input, Geometry, Run, Plot, Dicom, Compile, and Viewer. The toolbar contains icons for Cut, Copy, Paste, DICOM, Slice, Information, Voxel, RTPlan, RTViewer, Add, Delete, Change, and Clone. The main window is titled "Dicom" and displays a table of data sets.

Series Instance UID	Modality▲	Date	Patient	Age	Sex	Institution	Study
1.3.12.2.1107.5.1.4.49597.3000001201	CT	2012.01.01	S, F	100Y	F	none	RT^RT_HeadThin (Adult)
1.3.12.2.1107.5.7.8.100011.3000001201	RTDOSE	2012.01.01	S, F	100Y	F	none	RT^RT_HeadThin (Adult)
1.3.12.2.1107.5.7.8.100011.3000001201	RTPLAN	2012.01.01	S, F	100Y	F	none	RT^RT_HeadThin (Adult)
1.3.12.2.1107.5.7.8.10021.3000001201	RTSTRUCT	2012.01.01	S, F	100Y	F	none	RT^RT_HeadThin (Adult)

Processing the **DICOM** files with FLAIR II

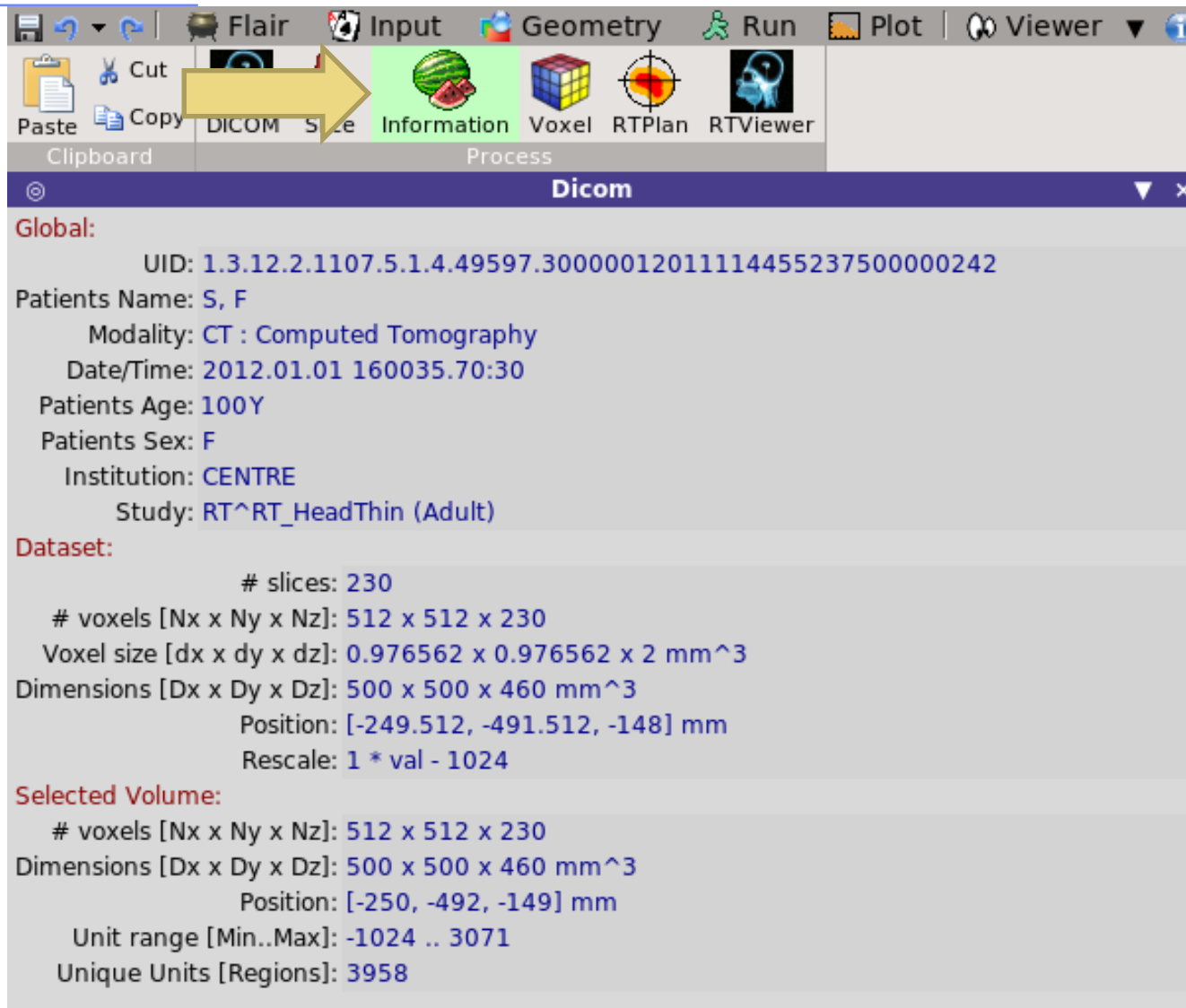
Select one "Data sets" and inspect the images.

The screenshot displays the FLAIR II software interface. The top menu bar includes options: Flair, Input, Geometry, Run, Plot, Dicom, and Compile. Below the menu is a toolbar with icons for Cut, Paste, Copy, DICOM, Slice, Information, Voxel, RTPlan, and RTViewer. To the right of the toolbar are input fields for Xmin, Xmax, Ymin, Ymax, Zmin, and Zmax, along with buttons for Reset, Slice → Zmin, and Slice → Zmax. A yellow arrow points to the 'DICOM' icon in the toolbar.

The main window is titled 'Dicom' and contains a list of files on the left and a viewer on the right. The file list has the following columns: Name and a numerical value. The file '41851932' is selected, and its corresponding value is 14.0. The viewer displays an axial CT scan of a head, showing the brain and surrounding structures. Below the viewer, there are controls for windowing and zooming, including fields for x, y, z coordinates, Dicom number, and Value, as well as sliders for Window Center, Width, and Slice.

Name	Value
41850678	-36.0
41850436	-34.0
41851085	-32.0
41852581	-30.0
41852900	-28.0
41852207	-26.0
41852119	-24.0
41852570	-22.0
41851239	-20.0
41852735	-18.0
41851635	-16.0
41852603	-14.0
41850667	-12.0
41851294	-10.0
41851646	-8.0
41852339	-6.0
41852438	-4.0
41851921	-2.0
41852449	0.0
41851965	2.0
41851800	4.0
41851173	6.0
41851569	8.0
41851008	10.0
41852196	12.0
41851723	14.0
41851932	16.0
41851811	18.0
41851954	20.0
41851404	22.0
41850711	24.0
41852130	26.0
41851822	28.0
41852592	30.0
41851338	32.0
41851668	34.0
41850766	36.0
41850733	38.0
41850810	40.0
41852306	42.0
41852834	...

Processing the **DICOM** files with FLAIR IV



The screenshot shows the FLAIR IV software interface. The top menu bar includes File, Edit, Flair, Input, Geometry, Run, Plot, and Viewer. Below the menu bar is a toolbar with icons for Cut, Copy, Paste, DICOM, Size, Information, Voxel, RTPlan, and RTViewer. A yellow arrow points to the 'DICOM' icon. The main window is titled 'Dicom' and displays the following information:

Global:
UID: 1.3.12.2.1107.5.1.4.49597.30000012011114455237500000242
Patients Name: S, F
Modality: CT : Computed Tomography
Date/Time: 2012.01.01 160035.70:30
Patients Age: 100Y
Patients Sex: F
Institution: CENTRE
Study: RT^RT_HeadThin (Adult)

Dataset:
slices: 230
voxels [Nx x Ny x Nz]: 512 x 512 x 230
Voxel size [dx x dy x dz]: 0.976562 x 0.976562 x 2 mm³
Dimensions [Dx x Dy x Dz]: 500 x 500 x 460 mm³
Position: [-249.512, -491.512, -148] mm
Rescale: 1 * val - 1024

Selected Volume:
voxels [Nx x Ny x Nz]: 512 x 512 x 230
Dimensions [Dx x Dy x Dz]: 500 x 500 x 460 mm³
Position: [-250, -492, -149] mm
Unit range [Min..Max]: -1024 .. 3071
Unique Units [Regions]: 3958

Processing the **DICOM** files with FLAIR V

The "Voxel" tab is used in order to convert the CT dataset to VOXELS. For the VOXEL geometry two additional files are needed (example: material.inp and head.mat).

The screenshot displays the FLAIR V software interface. The main window is titled 'Dicom' and shows the following fields:

- Materials: `../flair/dicom/material.inp`
- Unit to Material: `../flair/dicom/head.mat`
- Field: `7.8.10021.30000012011214454019300000490`

The 'Dicom' window contains a table with the following columns: < Unit, Material, Crho_min, Crho_max, CdEdx_rel_min, and CdEdx_rel_max. The table lists material properties for various units (HU values).

< 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			1.0	1.0
-700	HU<-700			1.0	1.0
-500	HU<-500			1.0	1.0
-120	HU<-120			1.0	1.0
-83	HU<-83			1.0	1.0
-53	HU<-53			1.0	1.0
-23	HU<-23			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

A dialog box titled 'Creating VOXEL file' is overlaid on the table, showing progress: 'Current: 78 [230] Completed: 33% [0:00:00 | 0:00:00]' and 'Processing: 41851008'. A 'Stop' button is visible at the bottom of the dialog.

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	expr: BODY1-BODY2	Neigh: 5	Volume:
 REGION REG2	expr: 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 “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 charged 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

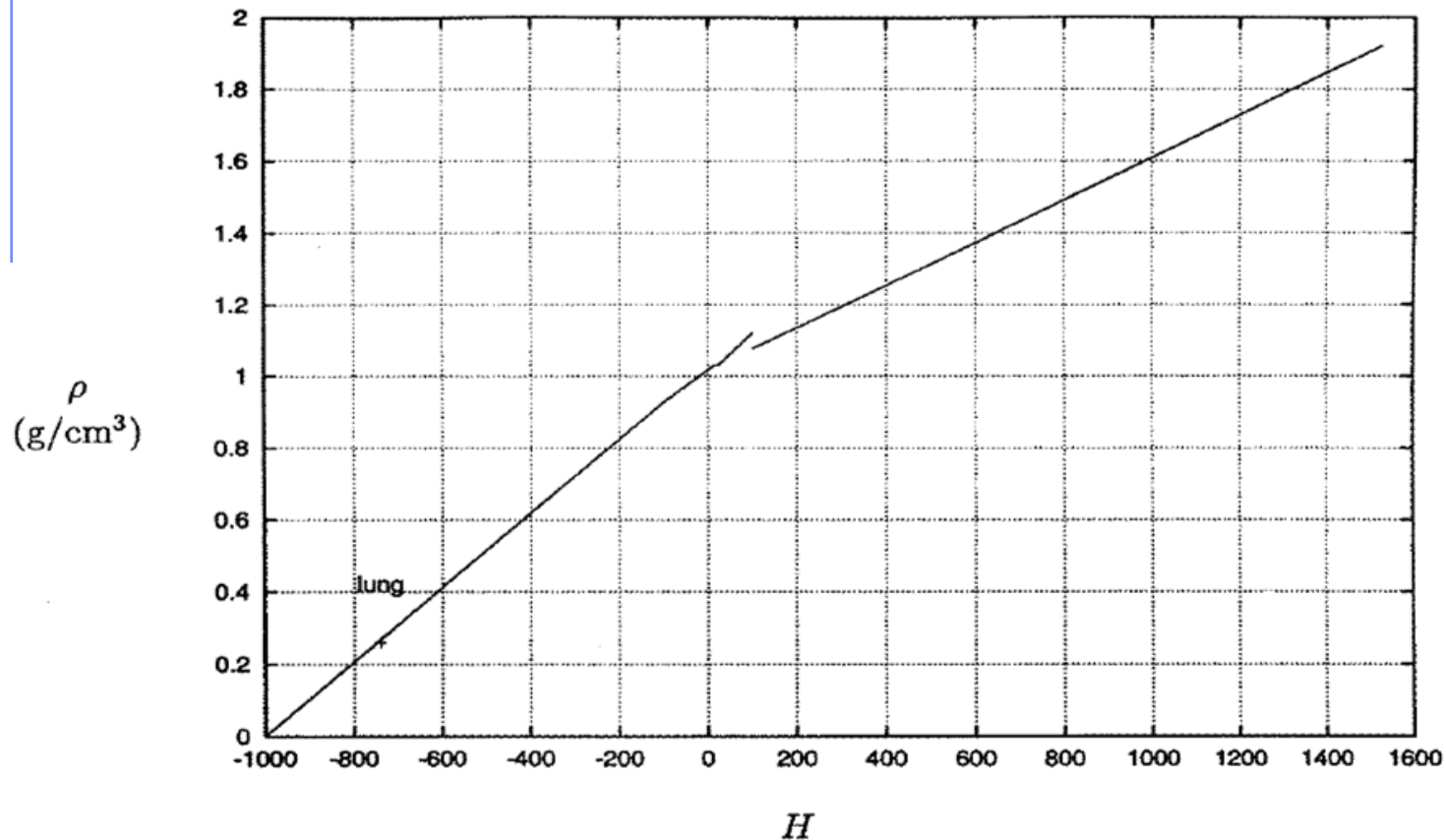
Soft tissue

Skeletal tissue

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

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

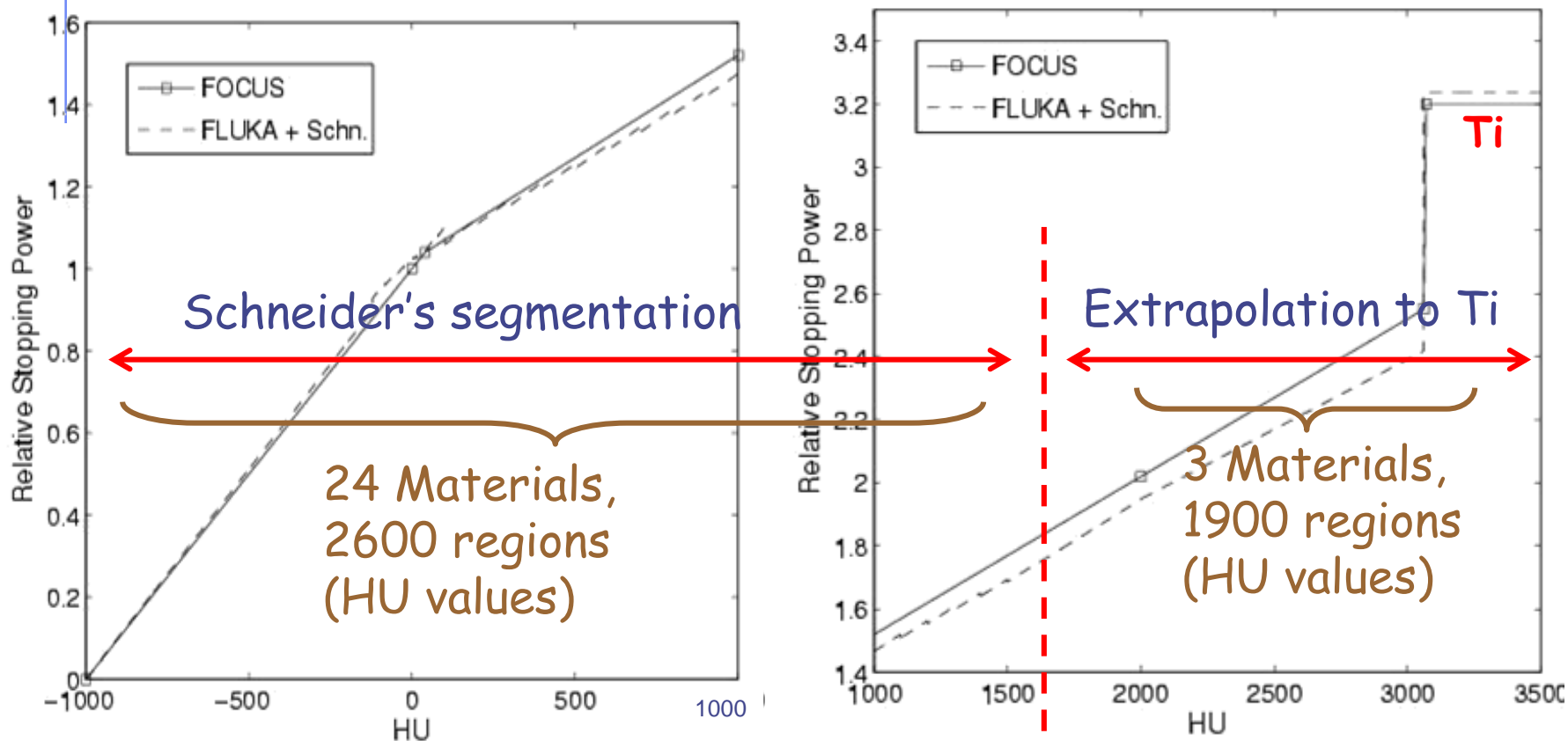
CORRFACT 0.85 0.0 0.0 25

CORRFACT 1.3 0.0 0.0 31

Region #25 corresponds to "softer" bone than #31

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

The CORRFAC_T 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.



The FLUKA voxel with ROI (new release)

- The information for regions of interest (ROIs) and points of interests (eg. dose reference points) are included in RTSTRUCT file
- ROIs are represented as the points belonging to a **closed polygon using 2D coordinates** (not rounded to the pixel size of the corresponding CT image).
- User can **embedded RTSTRUCT file into the VOXEL**
 - For each voxel Flair identifies list of ROIs and creates ROI to voxel correspondence matrix
 - Voxel **with RT STRUCT** information can be currently used as an input for DVH calculations, however **simulations will be available with the next FLUKA release**
 - Flair provides some checks on the structures, like calculating volumes using the true polygonal information or the discretization to voxels. Differences up to few percent can be visible due to quantification process

Processing the **DICOM** files with FLAIR VII

Select RTSTRUCT "Data sets" and inspect the ROI's

The screenshot displays the FLAIR VII software interface. The top menu bar includes options like Flair, Input, Geometry, Run, Plot, Dicom, and Compile. Below the menu bar is a toolbar with icons for Cut, Paste, Copy, DICOM, Slice, Information, Voxel, RTPlan, and RTViewer. The main window is titled "Dicom" and contains a "Viewer" tab. On the left side of the viewer, there is a list of ROIs with their names and IDs. The central viewer area shows a CT scan of a head and neck, with several colored ROIs overlaid: a green outline for the head and neck, a purple outline for the oral cavity, an orange outline for the pharynx, and blue and pink circles for the eyes. At the bottom of the viewer, there are input fields for "x:", "y:", "z: 0", "Dicom:", and "Value:", along with "Window Center:" and "Width:" sliders. The "Slice:" field is set to 86.

Name	Id
check	1
nonusareGTVold	2
Optic Chiasm	3
Brain Stem	4
Optic Nerve(R)	5
Temp lobe dx	6
Temp lobe sn	7
Optic Nerve(L)	8
Eye(R)	9
Eye(L)	10
Lens(R)	11
Lens(L)	12
Ear(R)	13
Ear(L)	14
brain	15
orech med dx	16
orech med sx	17
ATMsx	18
ATMdx	19
GTVpreop	20
GTVpf	21
CTV74	26
ipofisi	23
CTV54	24
PTV54	29
PTV74	31
pelle	39
Skin	35
LaserOrigin	40
table origin	41
GTVertex	44
canc	43
CTV54vertex	45
CTV74vertex	46
PTV54vertex	47
PTV74vertex	48

Processing the DICOM files with FLAIR VIII

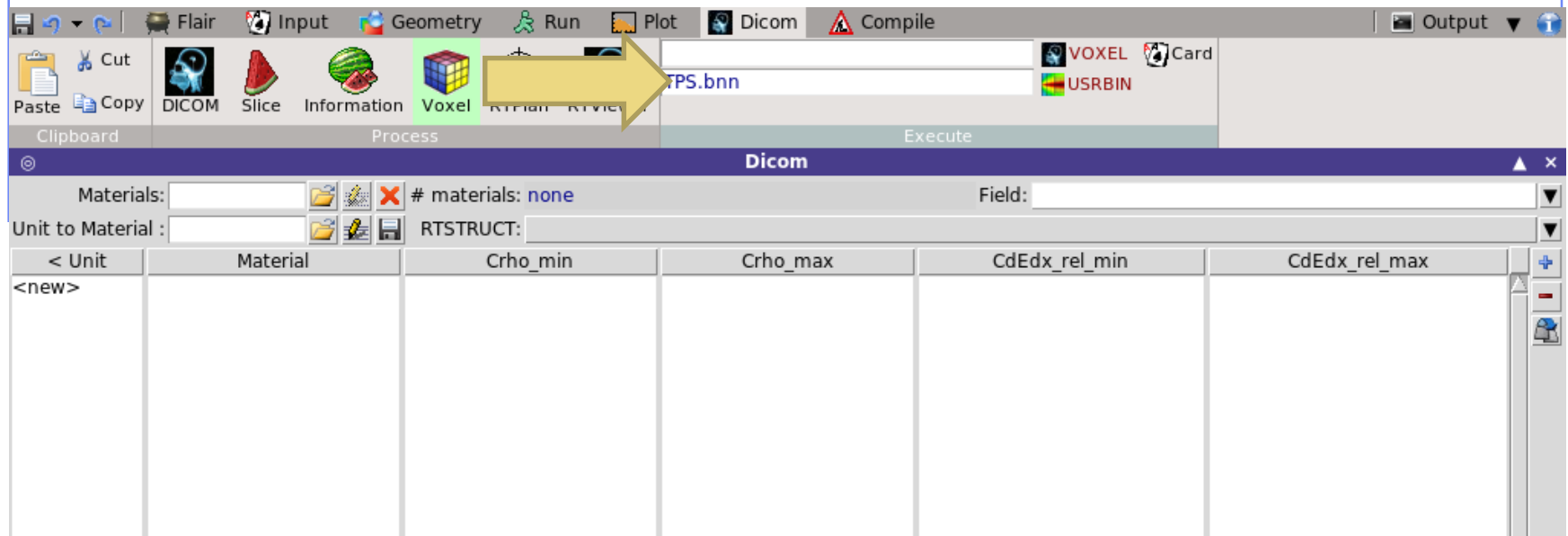
User can include ROIs imported from RTSTRUCT. Selection of corresponding file is done in VoxelTab.

The screenshot displays the FLAIR VIII software interface. The main window is titled 'Dicom' and shows a table of materials. A yellow arrow points to the 'Unit to Material' field, which is set to '..../flair/dicom/head.mat'. A dialog box titled 'Processing RTSTRUCTS' is overlaid on the table, showing a progress bar and the text 'Current: 38 [230] Completed: 16% [0:00:10 | 0:01:00]'. The dialog box also displays the RTSTRUCT ID '1.3.12.2.1107.5.1.4.49597.30000012011114455237500000281' and a 'Stop' button.

< 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				1.0
-700	HU<-700				1.0
-500	HU<-500				1.0
-120	HU<-120				1.0
-83	HU<-83				1.0
-53	HU<-53				1.0
-23	HU<-23				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

Processing the **DICOM** files with FLAIR IX

The "VoxelTab" is also for converting the RTDOSE dataset to FLUKA understandable format — USRBIN. This can be further used for postprocessing and plotting purposes.



Processing the **DICOM** files with FLAIR X

The "RTPlan" tab is used to modify input file for Treatment Plan Simulations using data from RTPLAN and RTDOSE

The screenshot displays the FLAIR X software interface. The top menu bar includes options like Flair, Input, Geometry, Run, Plot, Dicom, Compile, and Output. Below the menu is a toolbar with icons for Cut, Copy, Paste, DICOM, Slice, Information, Voxel, RTPlan (highlighted in green), and RTViewer. The main window is divided into several panes:

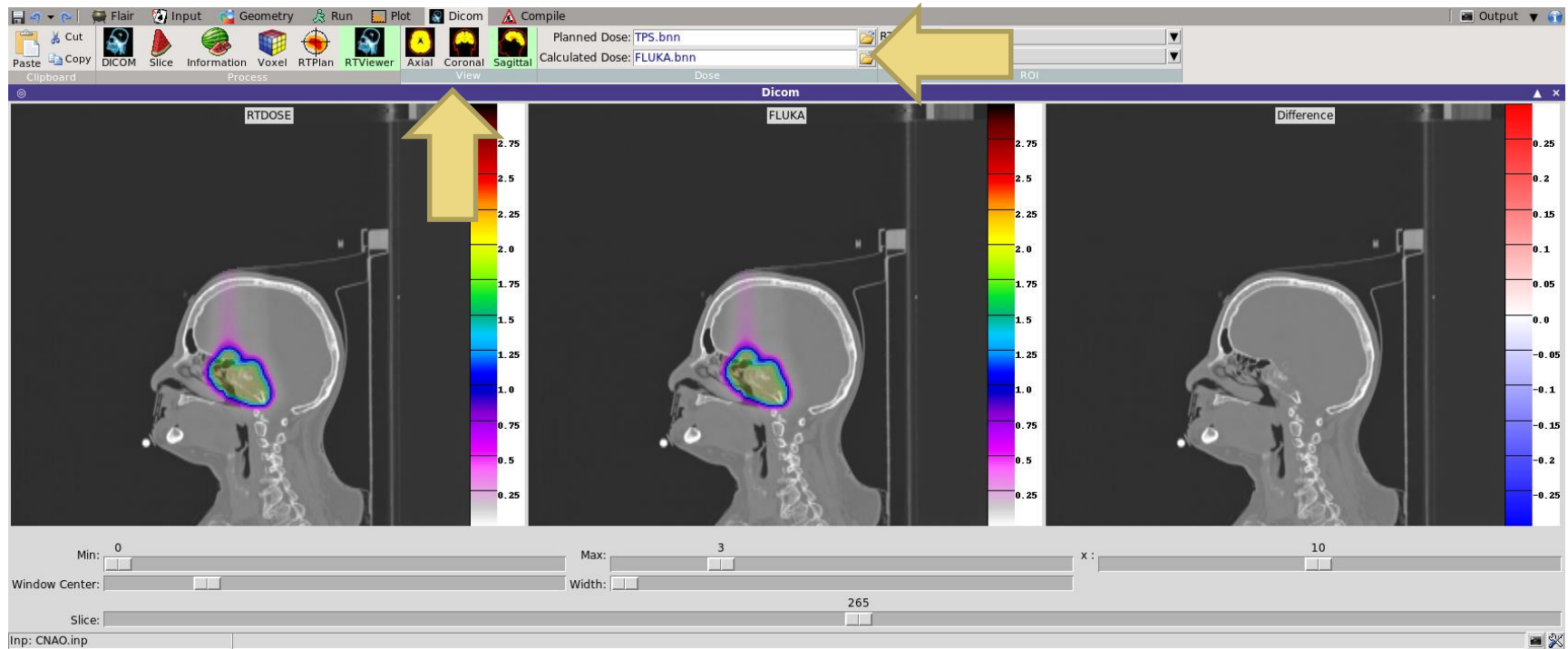
- Additional info:** Contains fields for Beam FWHM [cm], Beam ang div [rad], and Momentum spread. The RTDOSE field is set to 1.3.12.2.1107.5.7.8.100011.30000012.
- Process RTPlan:** Includes a 'Create' button with a gear icon, highlighted by a yellow arrow.
- Dicom:** A central pane with two tables:
 - Choose RT file:**

RTPlan	Date
RTPlan74GyE.dcm	2012.01.20
 - Choose Beam Number:**

Beam	# points	Gantry Ang	Patient Ang
1	98	90.0	0
2	92	90.0	180.0
3	48	90.0	270.0
- Information:** A right-hand pane displaying patient and plan details:
 - Patient Info:** Patient's Name: S, F; Patient's Age: 100Y; Patient's Sex: F.
 - RT Plan Info:** RT Plan Name: 2Beam54; Dose Type: EFFECTIVE; Plan Intent: CURATIVE; Approval Status: APPROVED; Review Date: 2012.01.20 130922.64:89; Reviewer Name.
 - General Beam Info:** Beam Name: B1; Beam Weight: 15331795521.4688; Beam Type: STATIC; Radiation Type: PROTON; Scan Mode: MODULATED; # Control Points: 98.
 - Rotations Info:** Gantry Angle: 90.0; Gantry Pitch Angle: 0; Patient Support Angle: 0; Table Top Pitch Angle: 0; Table Roll Angle: 0.

Processing the **DICOM** files with FLAIR XI

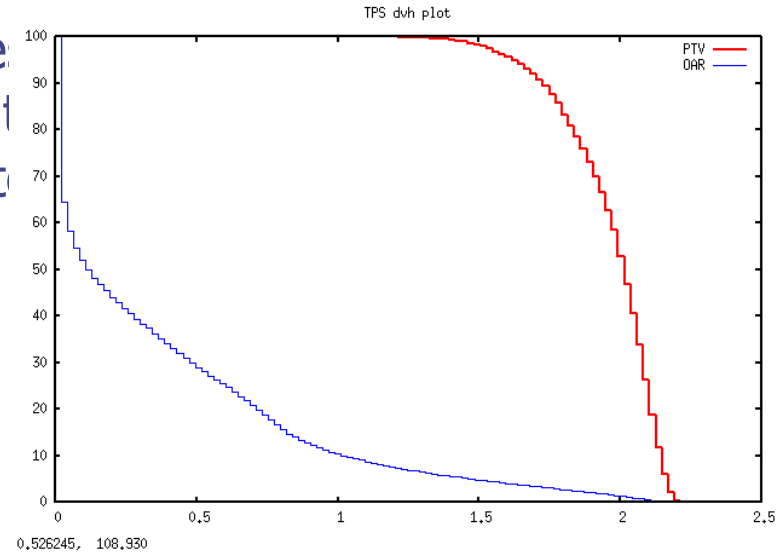
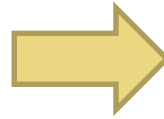
- The "RTViewer" tab provides graphical comparison of TPS and FLUKA calculations using USRBIN files
- Available views for Axial, Coronal and Sagittal planes



Processing the **DICOM** files with FLAIR XII

FLAIR allows Dose-Volume plots

to postprocess create Histogram



error

The screenshot shows the FLAIR software interface. The 'Run' window is active, displaying a table of runs and their associated commands and outputs. A yellow arrow points to the 'usrbin2dvh' command in the 'Run' table.

Run	Command	Output	Unit
TPS	usrbin	TPS_22.bnn	22
TPS	usrbin	TPS_23.bnn	23
TPS	usrbin	TPS_24.bnn	24
TPS	usrbin2dvh	TPS_dvh_tab.lis	0

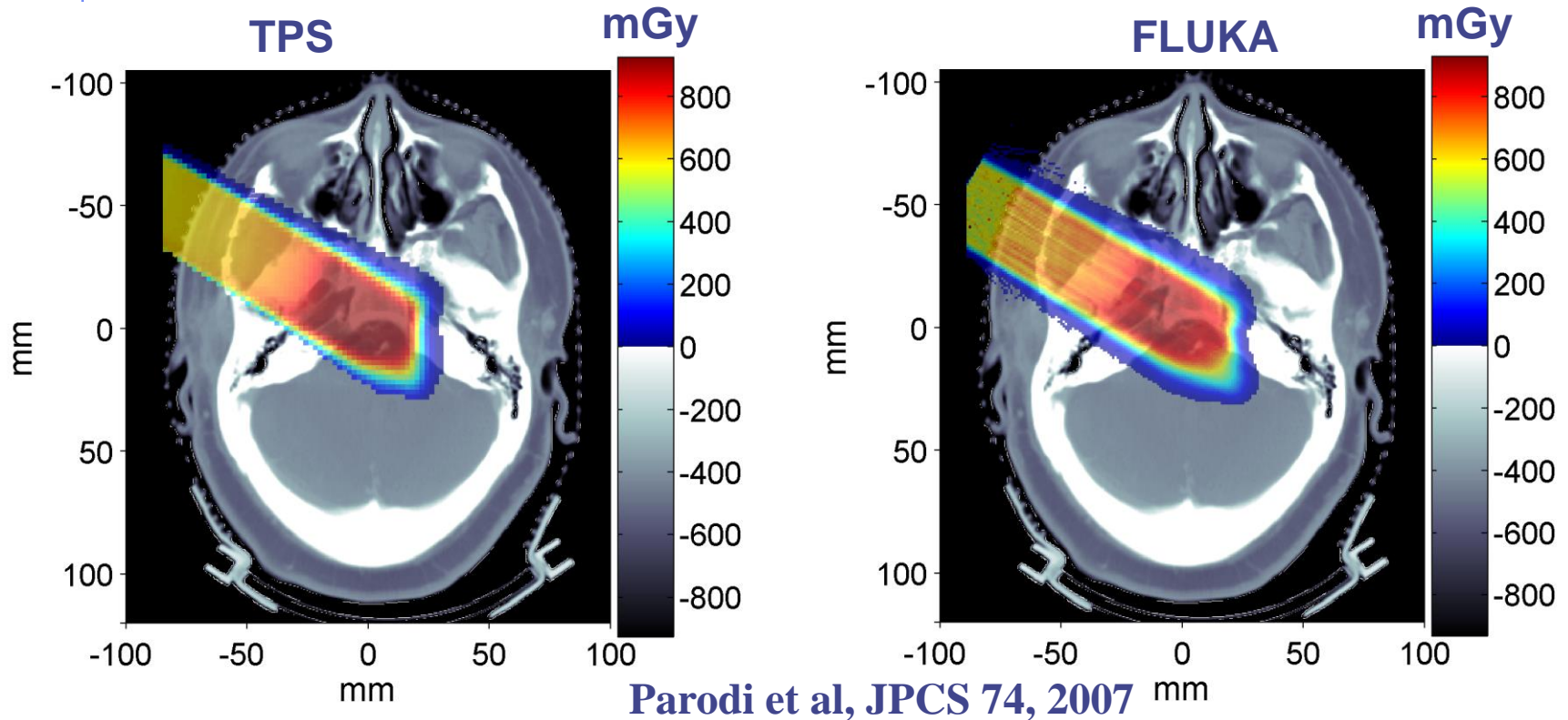
Name	Tag	Value	Type	Default
Output file	-o	TPS_dvh_tab.lis	output	V:\U_dvh_tab.lis
Usrbin file	-u	TPS.bnn	file	V:\U.bnn
Detector index	-d	1	int	1
Voxel file	-v	test_struct.vxl	file	=C(VOXELS,0,0)+".vxl"
Relative dose (Gray)	-r	0.0	float	0.0
Voxel x	-x	-25	float	=C(VOXELS,0,1)
Voxel y	-y	-49.2	float	=C(VOXELS,0,2)
Voxel z	-z	-14.9	float	=C(VOXELS,0,3)

Few remarks

- Updated input file from RTPlan Tab uses #include cards in order to import pencil beam parameters. Due to typical vast number of described beams user needs to **activate/deactivate** these cards.
- Simulated and processed FLUKA files have to be **weighted** according to the information from RTPlan – usrwei routine available in FLAIR.
- DVH plots requires *.vxl file **with RTSTRUCT** information.
- In RTViewer graphical comparison is available only for the *.bnn files with the **same binnings and positions**. Editing input file by RTPlan Tab allows to provide correct parameters – user chooses corresponding RTDOSE file.

Applications of FLUKA to p therapy @ MGH

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



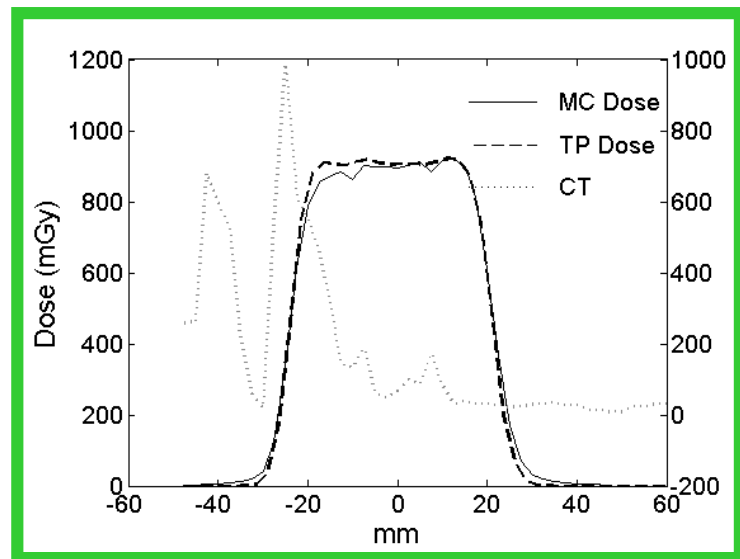
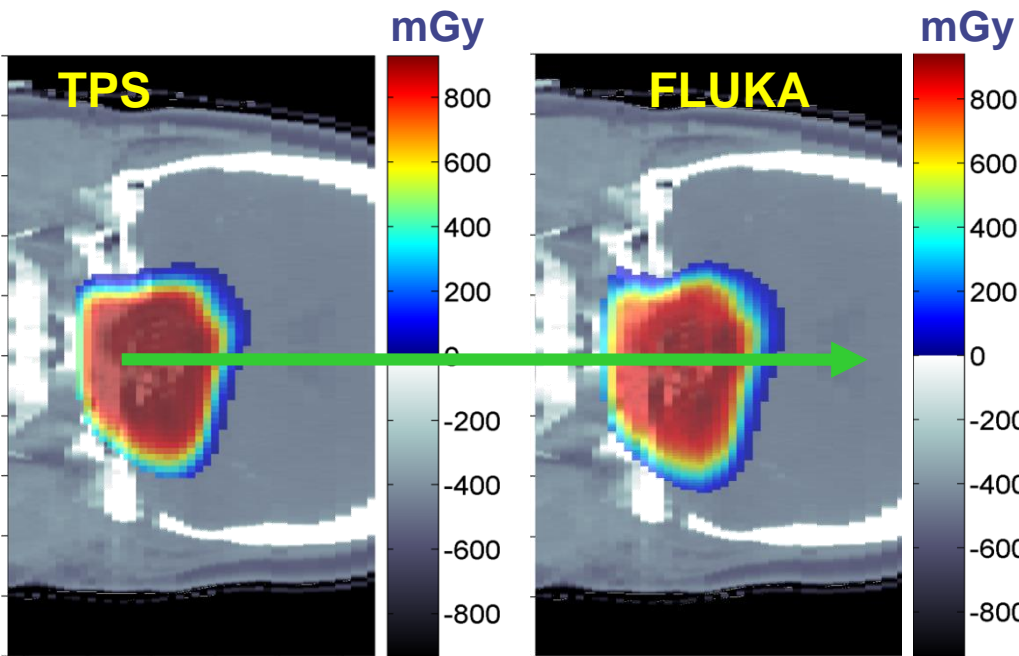
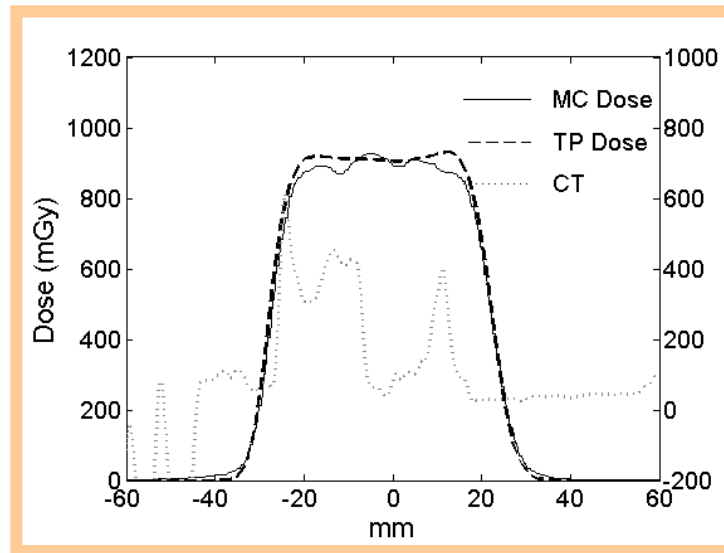
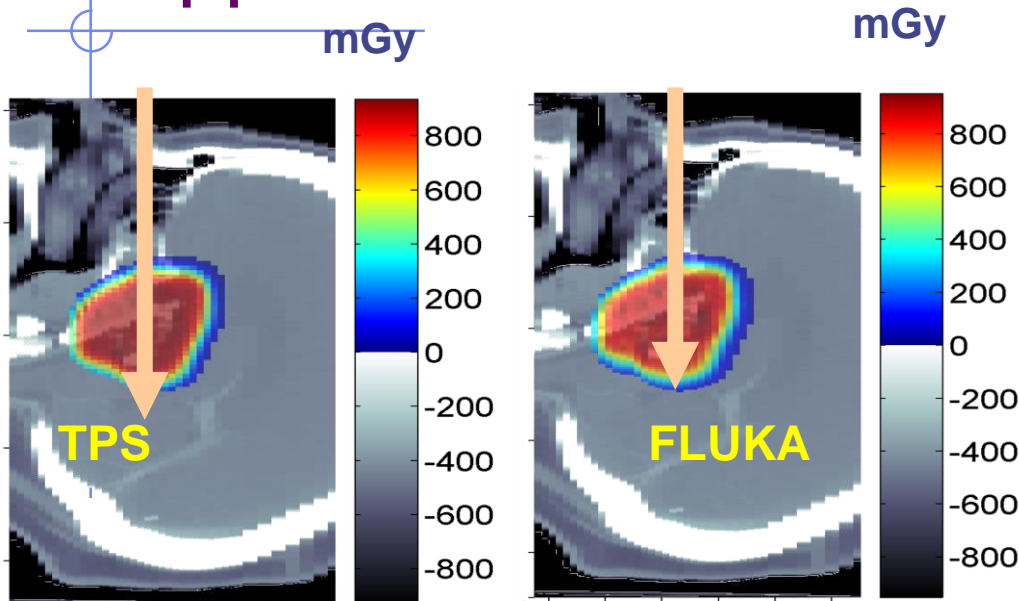
Prescribed dose: 1 GyE

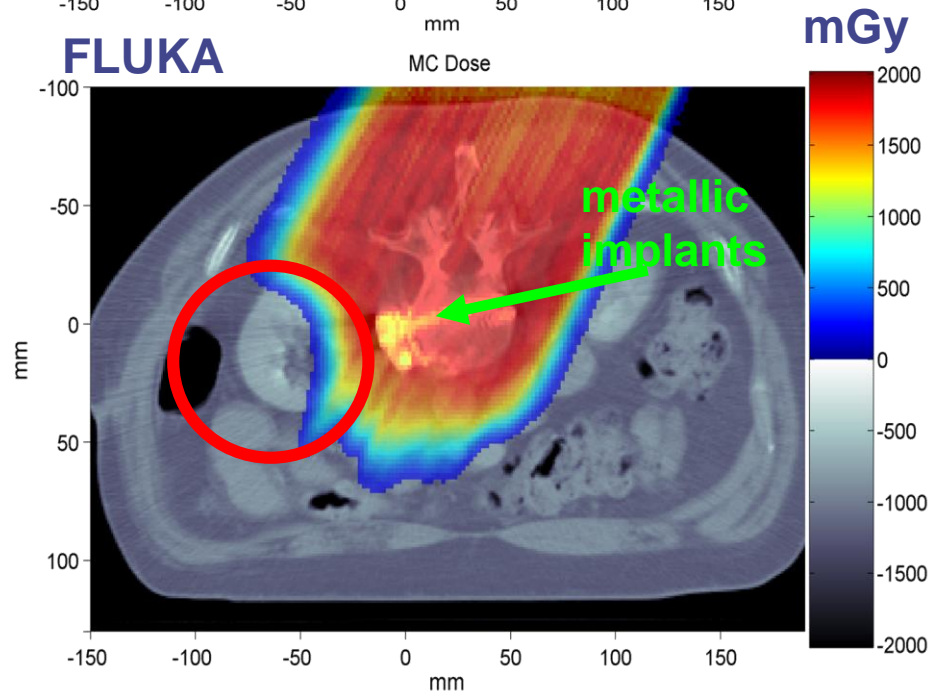
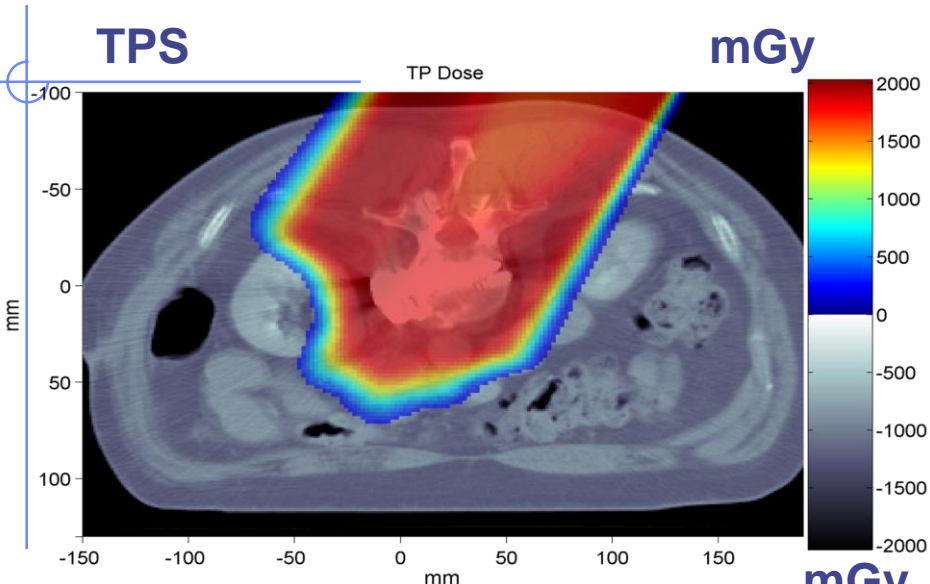
MC : $\sim 5.5 \cdot 10^6$ protons in 10 independent runs

(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)

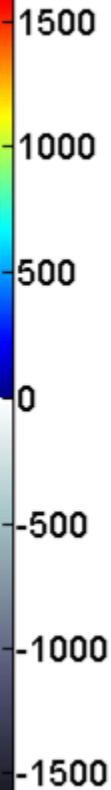
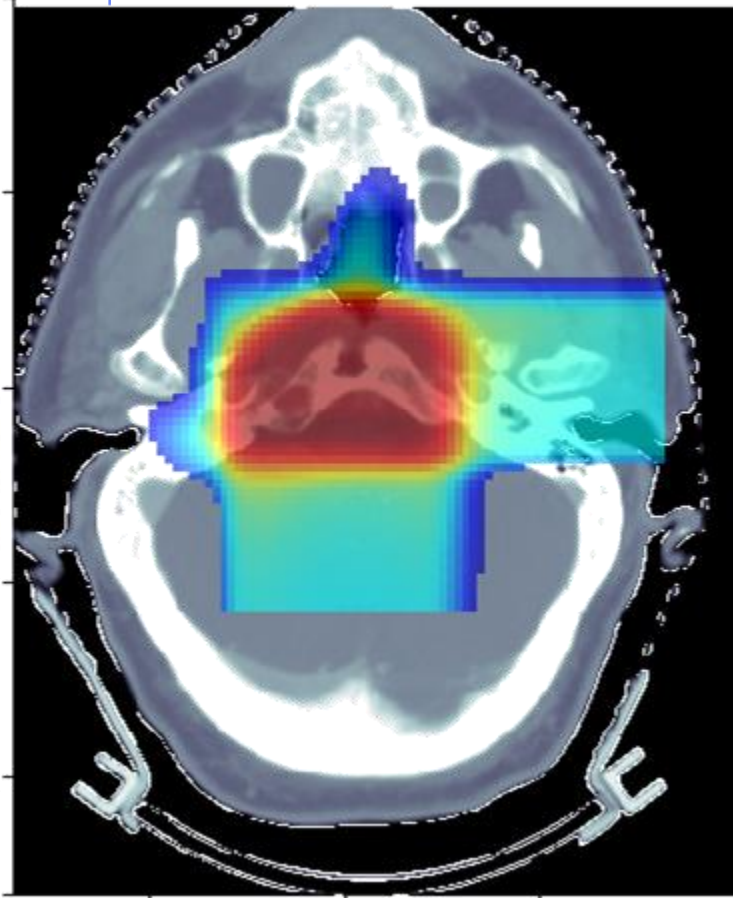
Applications of FLUKA to p therapy @ MGH

Clival Chordoma, 0.96 GyE / field

Planned dose

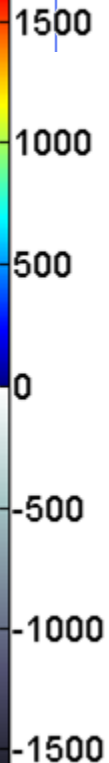
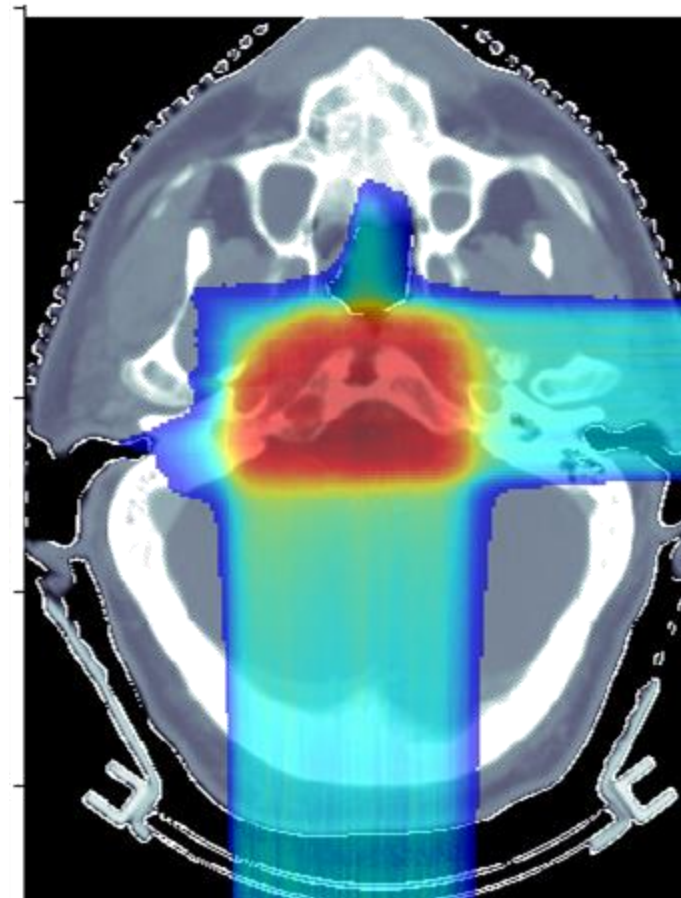
TP Dose

mGy



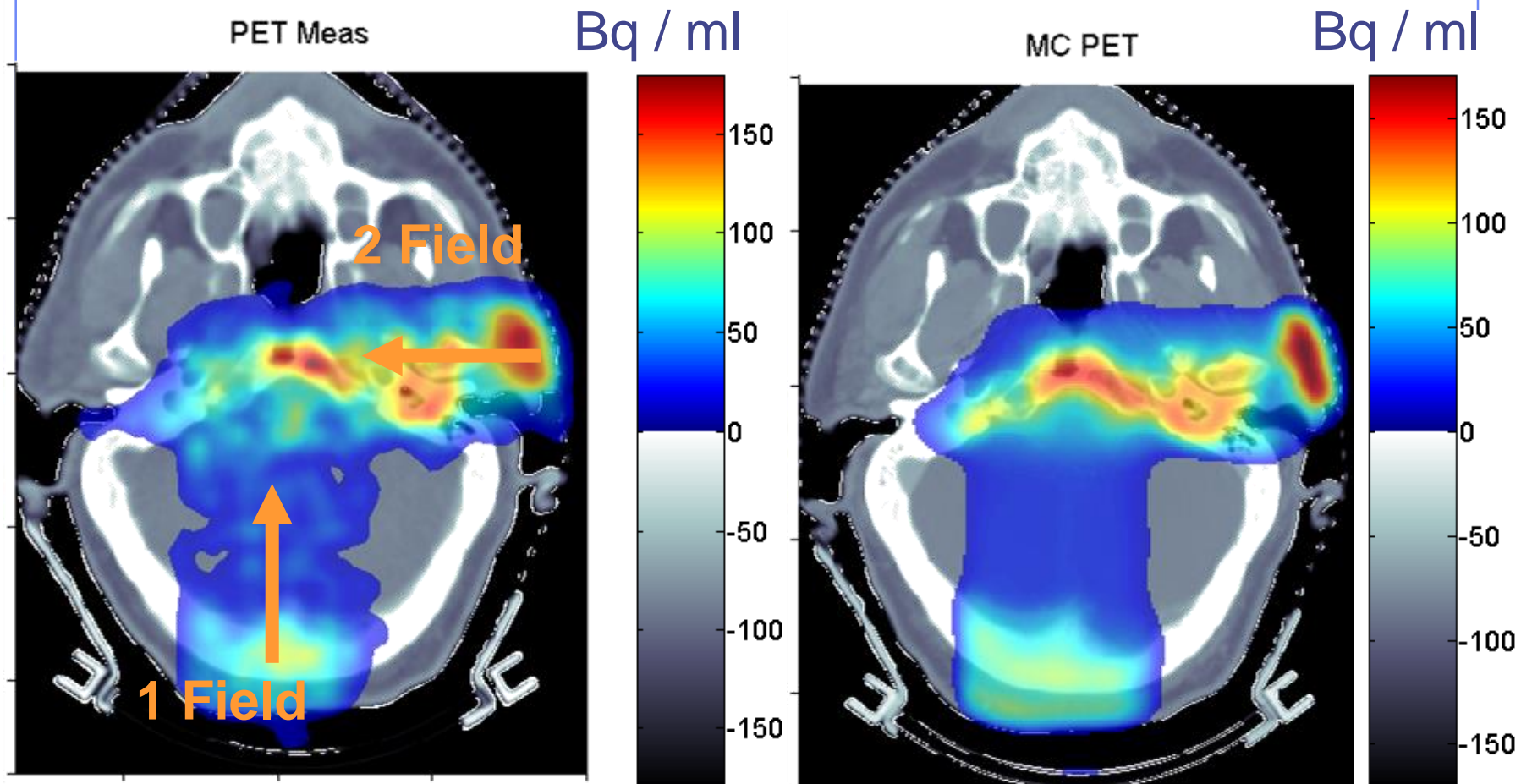
MC Dose

mGy



Post-radiation PET/CT @ MGH *Average Activity*

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



K. Parodi et al, IJROBP 2007

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

Additional material – user routine

- In current version user needs to compile special routine for defining pencil beam source parameters.
- In the next FLUKA release new cards will allow user to simulate RTPLAN without external routines.

