



Voxels and Medical Applications

FLUKA Beginners course

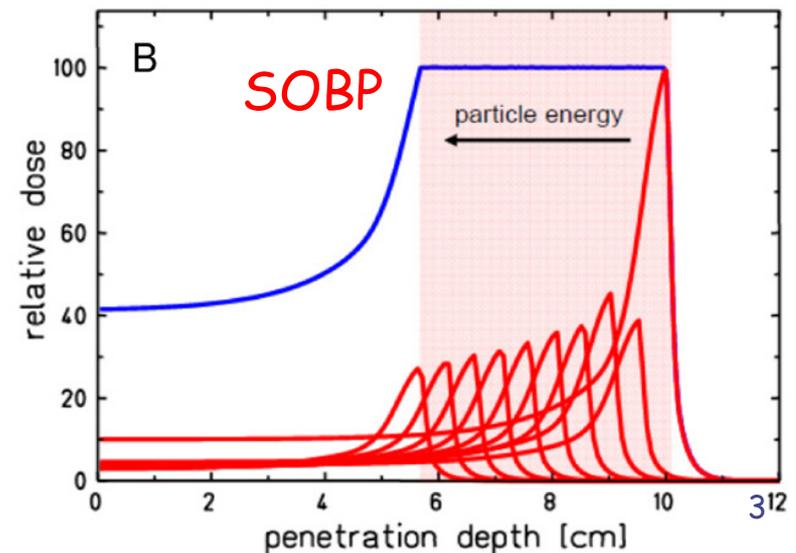
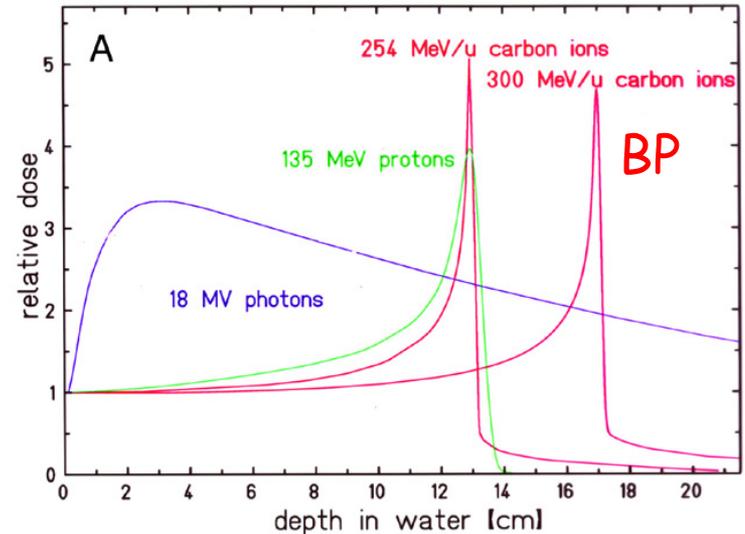
Medical Physics and related disciplines applications

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

Medical applications: Particle Therapy

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

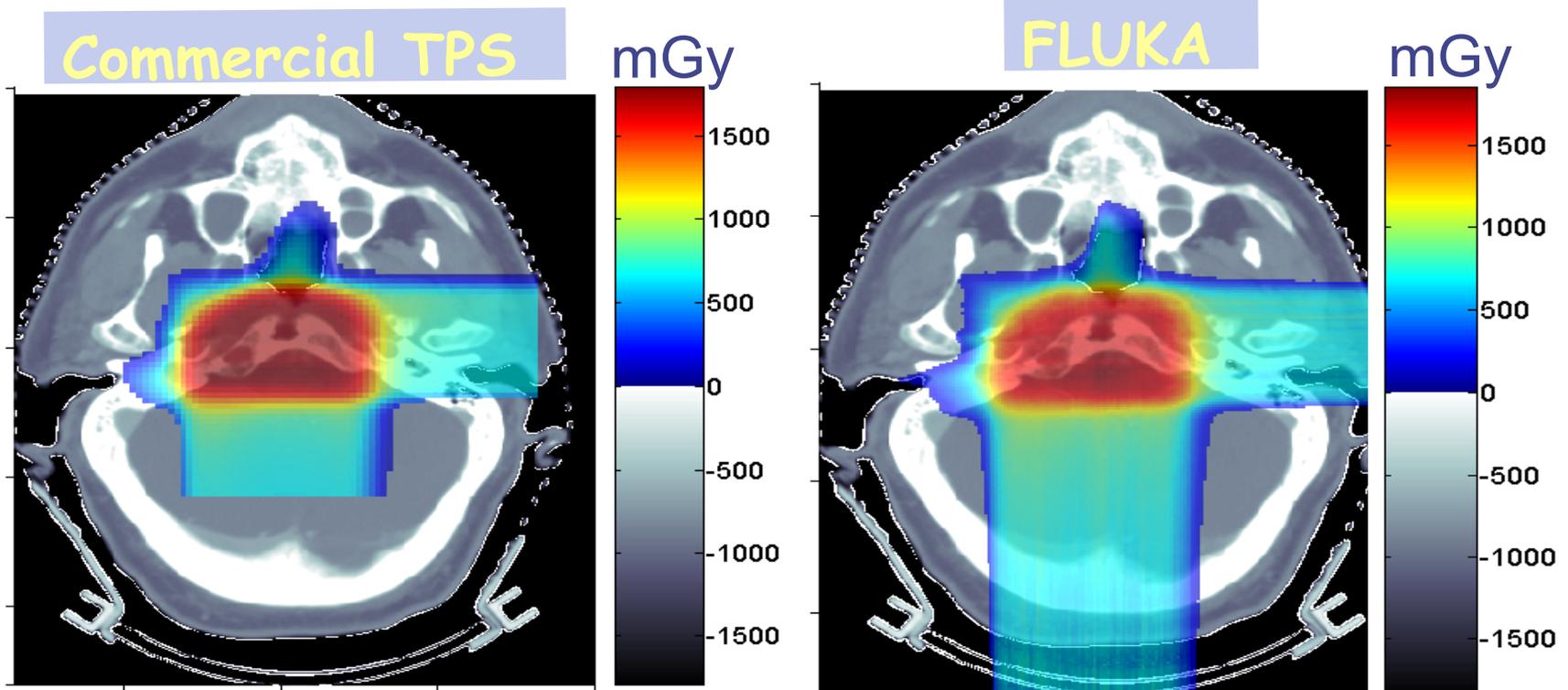
- **Particle Therapy** is a radiation therapy to treat tumors (deep seated, resistant to conventional RT with photons...)
- Exploits “heavy” **charged particle beams** (p, ^{12}C ...) typical energy loss in matter, characterized by the **Bragg peak** (BP)
- The more the beam kinetic energy the deeper the BP position
- Several BPs are summed up to cover the tumor volume (**SOBP**)



The issue of complex geometries: patient cases

In clinics, treatment plans are needed. The medical physicist have to decide in advance how to "shoot" the tumor based on patient CT.

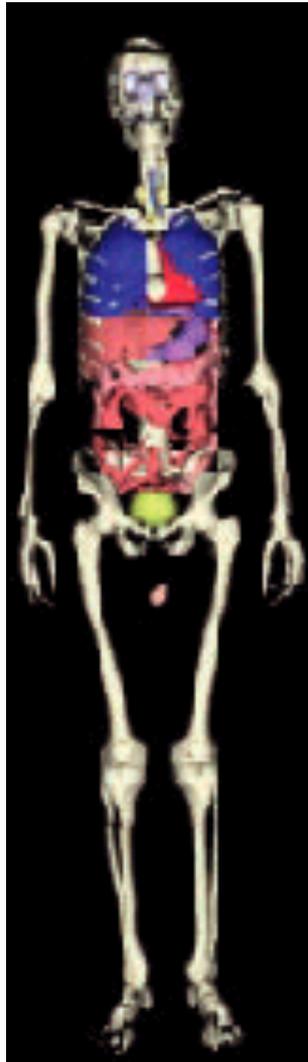
CT scans of a human body are important also for dosimetric calculations of the planned treatment in radiotherapy.



Voxel geometries

The anthropomorphic

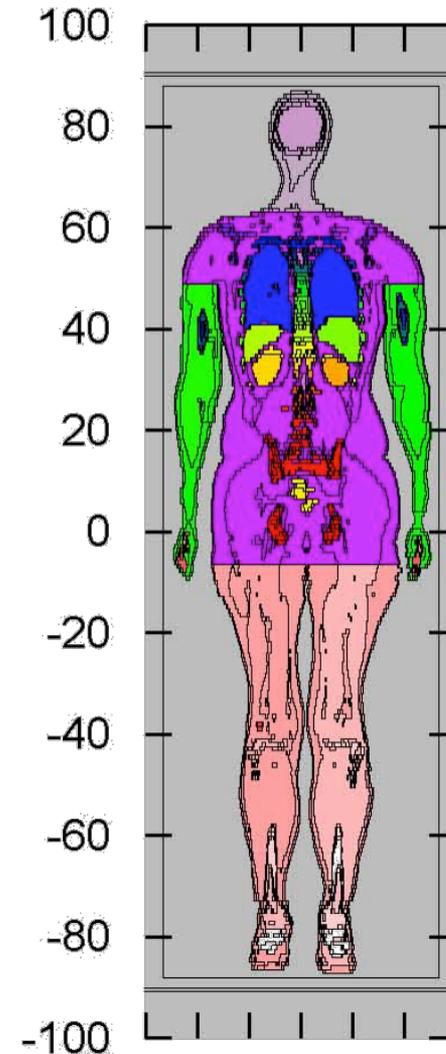
GOLEM phantom



Implementation in
FLUKA
(radioprotection
applications)

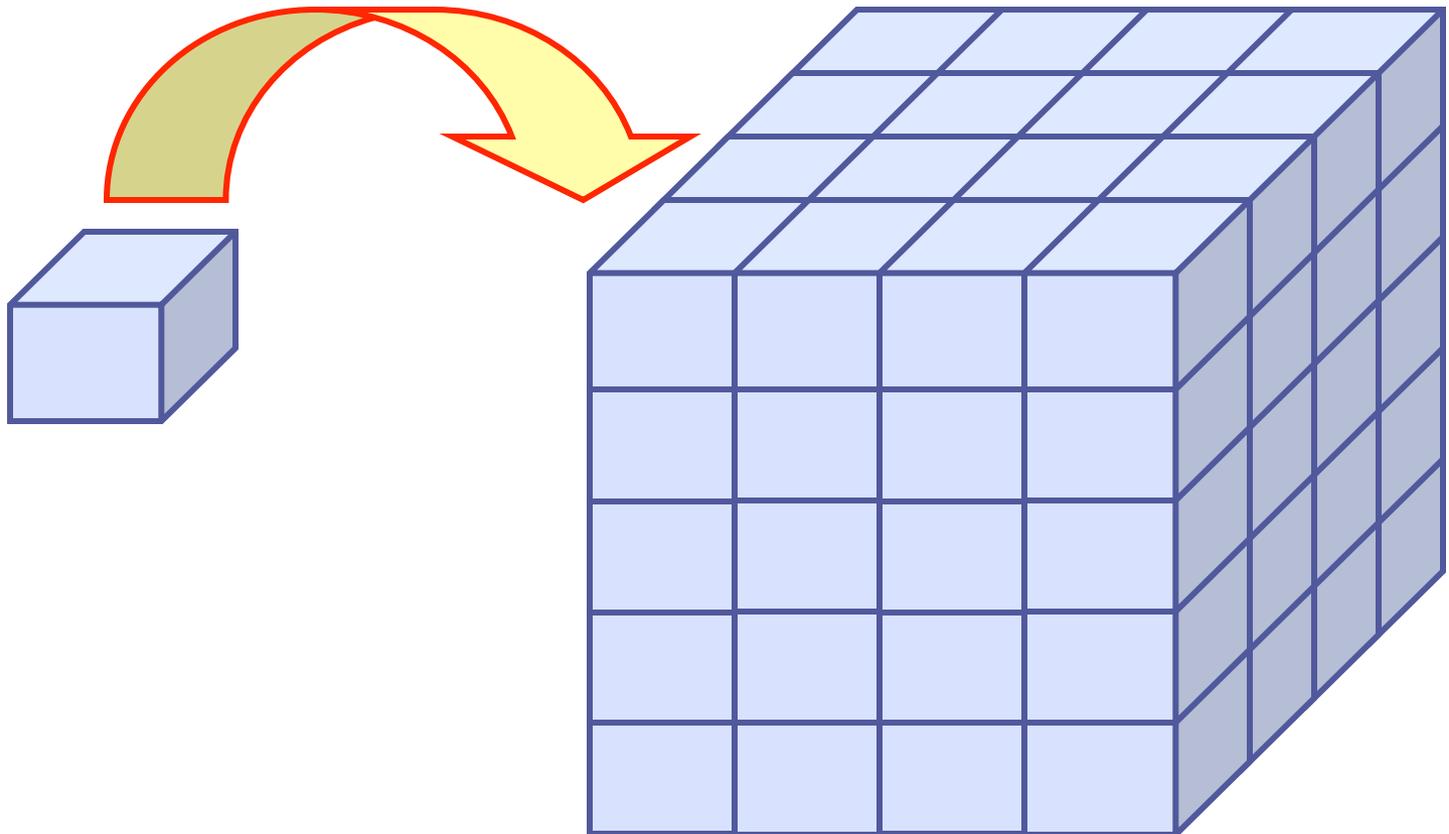
**Petoussi-Henss
et al, 2002**

FLUKA golem section



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**



From CT to FLUKA voxel geometry

- The CT scan contains integer values “Hounsfield Unit” reflecting the X-ray attenuation coefficient μ_x

$$HU_x = 1000 (\mu_x - \mu_{H20}) / \mu_{H20}, \text{ typically } -1000 \leq HU \leq 3500$$

- The user must convert his CT scan or equivalent data to a format understood by FLUKA: **VOXEL geometry**. (Starting from DICOM images, this is performed directly by FLAIR - see next slides).
- 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)

From CT to FLUKA voxel geometry

- 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.

Practical issues for Medical Applications: assigning a material to an *organ*

- 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 PT!!!)

CT stoichiometric calibration (I)

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

<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

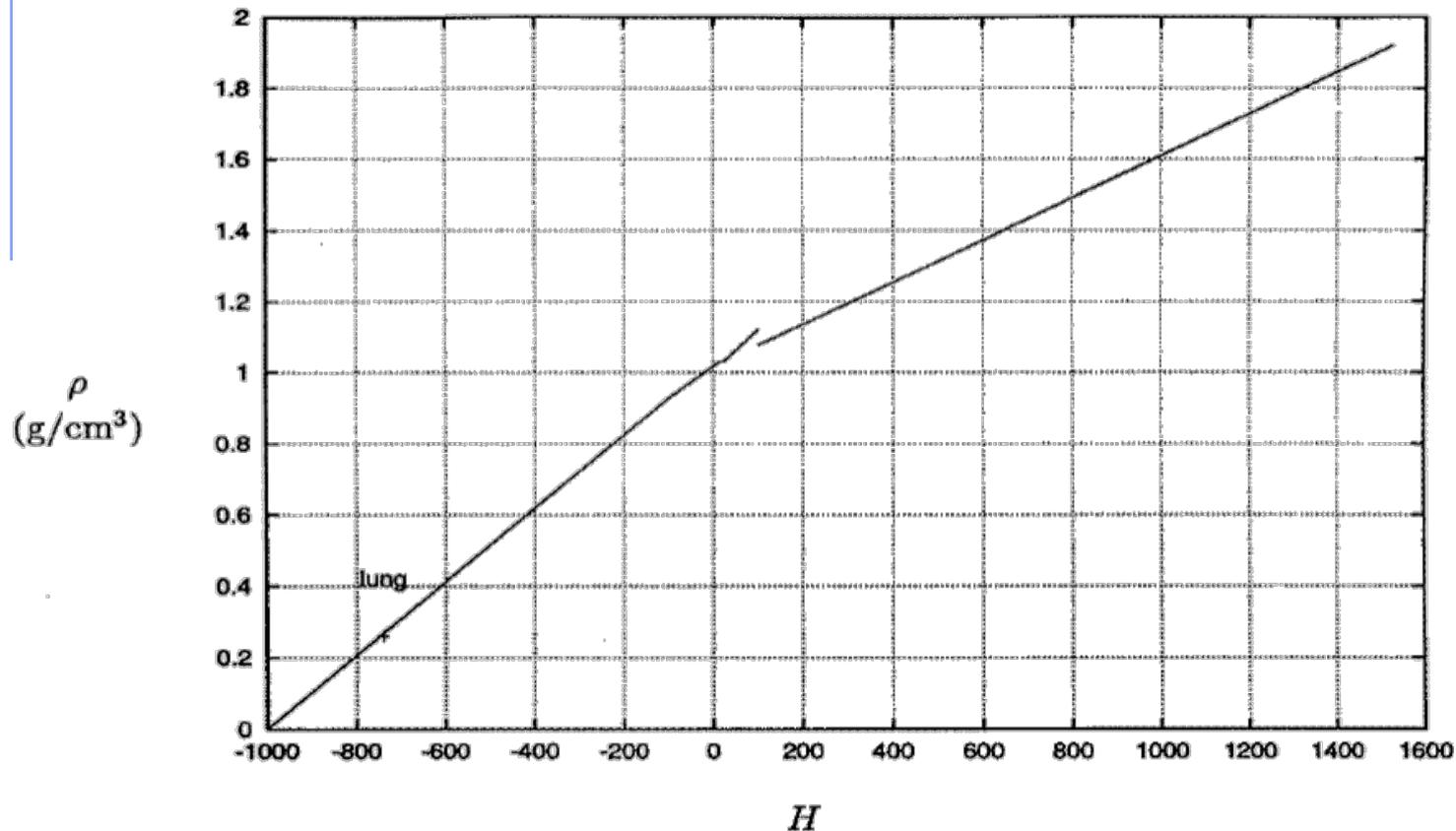
Air, Lung,
Adipose tissue

Soft tissue

Skeletal tissue

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)

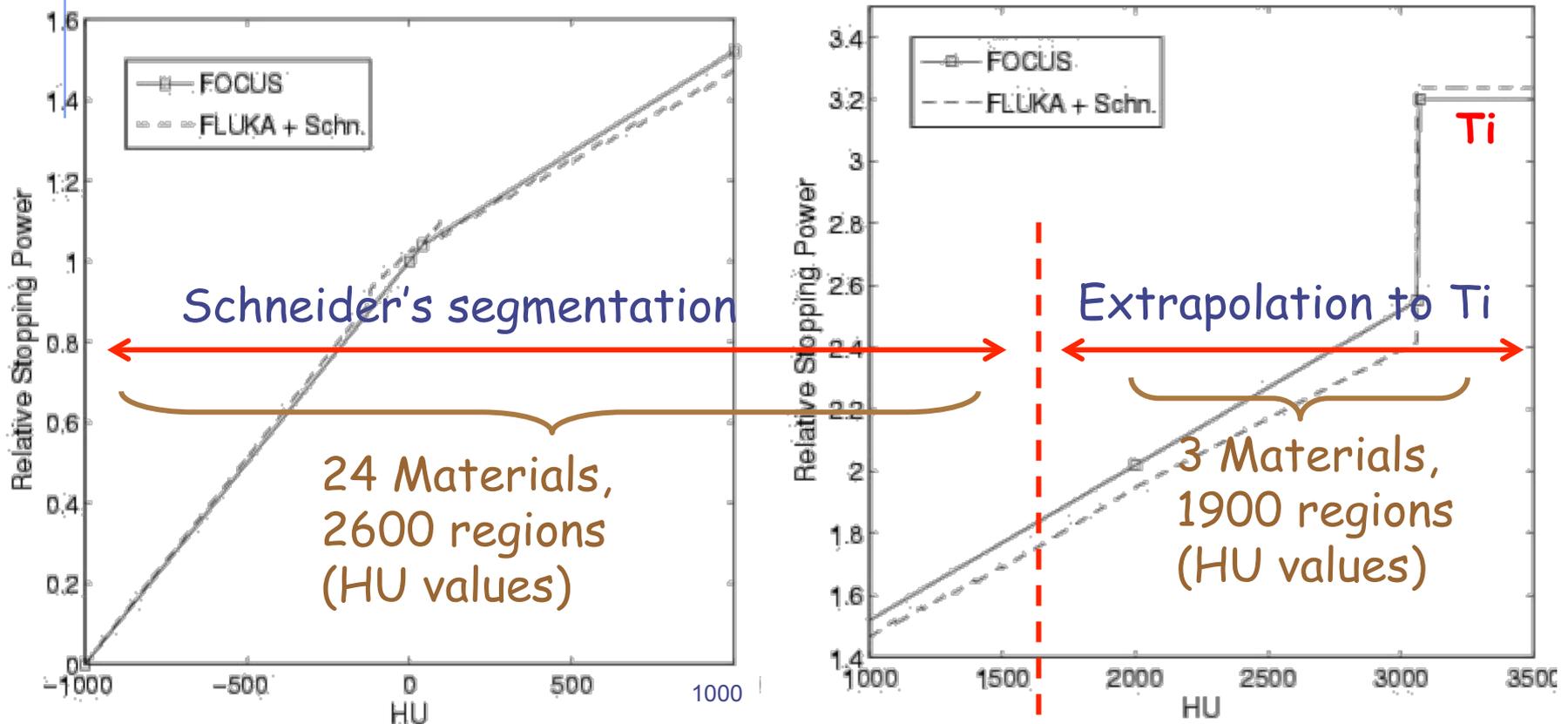


Schneider et al
PMB 45, 2000

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

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 a file with his own calibration for CdEdX_{rel} taking into account his TPS.



The FLUKA voxel geometry

- All the CT 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
- The code handles each organ as a Comb Geo region, possibly in addition to other conventional “non-voxel” regions defined by the user
- The voxel structure can be complemented by parts written in the standard Combinatorial geometry
- The code assumes that the voxel structure is contained in a parallelepiped. This RPP is automatically generated from the voxel information.

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

What is needed:

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

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: bodyCT ▾

z: -88.6855

The region-dependent CORRFAC card

- Materials are defined from groups of HU (see slide 9), but “real densities” varies continuously with HU
- “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*]
- Especially important in PT 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

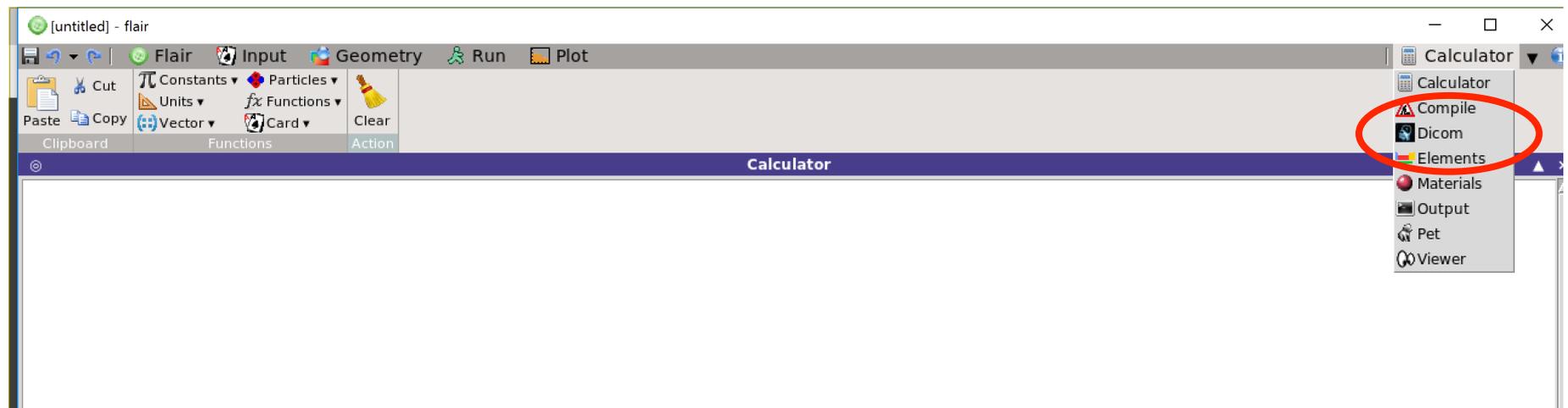
CORRFACT 0.85 0.0 0.0 25

CORRFACT 1.3 0.0 0.0 31

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

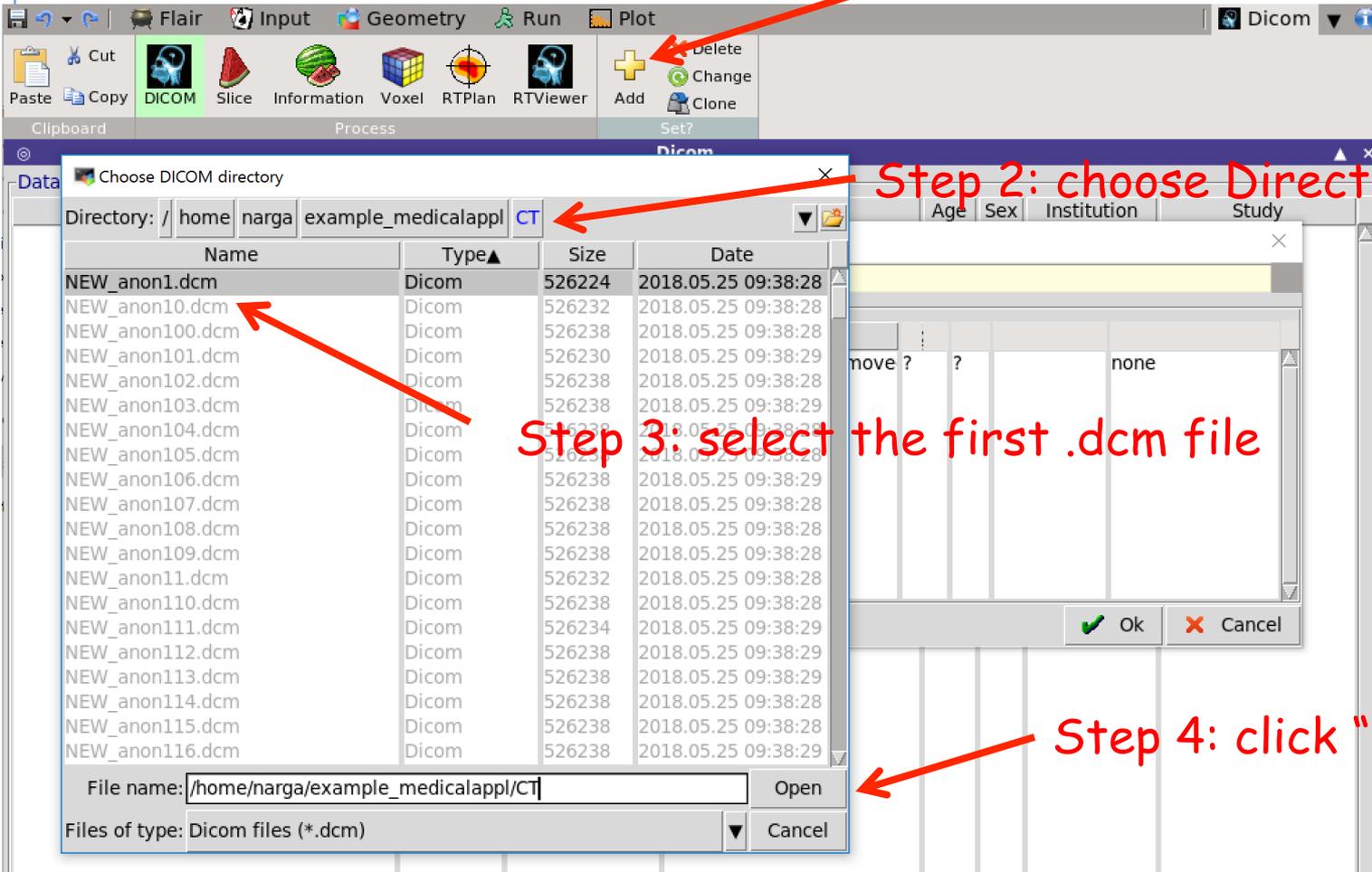
Processing the **DICOM** files with FLAIR

- 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, USRBIN 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).



Choose DICOM

Step 1: click "Add"



Step 2: choose Directory path

Step 3: select the first .dcm file

Step 4: click "Open"

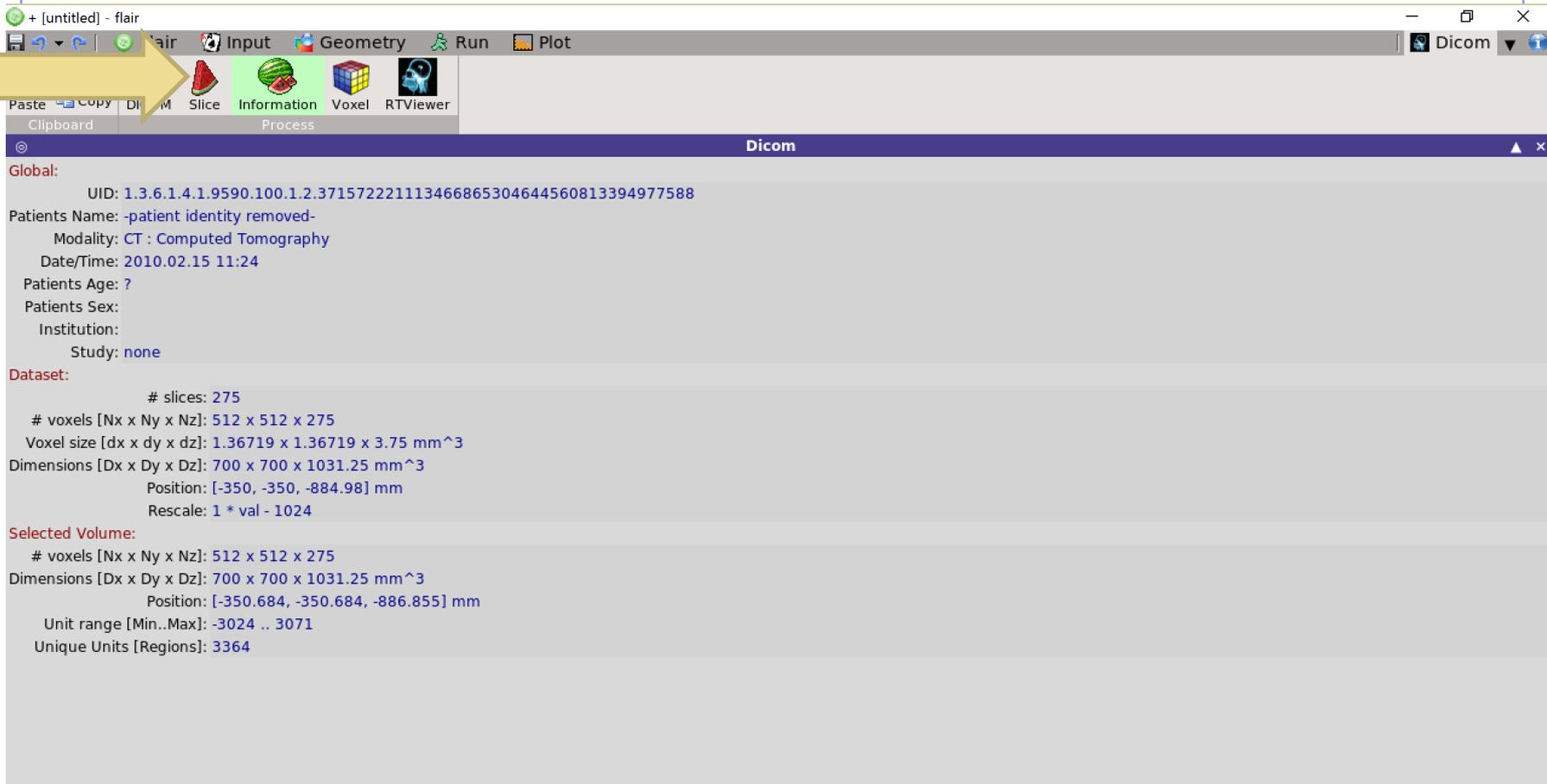
Open DICOM

The screenshot shows the 'flair' software interface. The 'Dicom' window is active, displaying a table of data sets. A dialog box titled 'Select DICOM data set' is open, showing a directory path of './CT' and a table with the following data:

Series Instance UID	Modality	Date	Patient	Age	Sex	Institution	Study
1.3.6.1.4.1.9590.100.1.2.3715722211	CT	2010.02.15 11:	-patient identity removed-	?			none

A red arrow points to the selected row in the table. A red text box on the right says: "Step 5: Select the Data Set and click "Ok"".

Infos about CT just loaded



The screenshot shows a software interface with a toolbar at the top containing icons for 'Fair', 'Input', 'Geometry', 'Run', and 'Plot'. Below the toolbar are icons for 'Slice', 'Information', 'Voxel', and 'RTViewer'. A yellow arrow points to the 'Information' icon. The main window, titled 'Dicom', displays the following metadata:

Global:
UID: 1.3.6.1.4.1.9590.100.1.2.371572221113466865304644560813394977588
Patients Name: -patient identity removed-
Modality: CT : Computed Tomography
Date/Time: 2010.02.15 11:24
Patients Age: ?
Patients Sex:
Institution:
Study: none

Dataset:
slices: 275
voxels [Nx x Ny x Nz]: 512 x 512 x 275
Voxel size [dx x dy x dz]: 1.36719 x 1.36719 x 3.75 mm³
Dimensions [Dx x Dy x Dz]: 700 x 700 x 1031.25 mm³
Position: [-350, -350, -884.98] mm
Rescale: 1 * val - 1024

Selected Volume:
voxels [Nx x Ny x Nz]: 512 x 512 x 275
Dimensions [Dx x Dy x Dz]: 700 x 700 x 1031.25 mm³
Position: [-350.684, -350.684, -886.855] mm
Unit range [Min..Max]: -3024 .. 3071
Unique Units [Regions]: 3364

Inspecting the Images: Slices I

Each .dcm file represents a CT slice.

The screenshot shows a software interface with a menu bar (Flair, Input, Geometry, Run, Plot) and a toolbar. The toolbar includes buttons for Cut, Paste, Copy, DICOM, Slice, Information, Voxel, and RTViewer. A red arrow points to the 'Slice' button, with the text "Step 6: Go to 'Slice'" written in red next to it. Below the toolbar is a table of DICOM files with columns for Name and z. The 'Dicom' viewer window shows a CT slice of a human torso with anatomical markers (A, H, L, R, P) and a coordinate system. The viewer also displays a list of files and a 'Dicom' panel with fields for x, y, z, Dicom, Value, Window Center, Width, and Slice.

Name	z
NEW_anon145.dcm	-459.88
NEW_anon144.dcm	-456.61
NEW_anon143.dcm	-453.34
NEW_anon142.dcm	-450.07
NEW_anon141.dcm	-446.8
NEW_anon140.dcm	-443.53
NEW_anon139.dcm	-440.26
NEW_anon138.dcm	-436.99
NEW_anon137.dcm	-433.72
NEW_anon136.dcm	-430.45
NEW_anon135.dcm	-427.18
NEW_anon134.dcm	-423.91
NEW_anon133.dcm	-420.64
NEW_anon132.dcm	-417.37
NEW_anon131.dcm	-414.1
NEW_anon130.dcm	-410.83
NEW_anon129.dcm	-407.56
NEW_anon128.dcm	-404.29
NEW_anon127.dcm	-401.02
NEW_anon126.dcm	-397.75
NEW_anon125.dcm	-394.48
NEW_anon124.dcm	-391.21
NEW_anon123.dcm	-387.94
NEW_anon122.dcm	-384.67
NEW_anon121.dcm	-381.4
NEW_anon120.dcm	-378.13
NEW_anon119.dcm	-374.86
NEW_anon118.dcm	-371.59
NEW_anon117.dcm	-368.32
NEW_anon116.dcm	-365.05
NEW_anon115.dcm	-361.78

Inspecting the Images: Slices II

The screenshot shows the Flair DICOM browser interface. The top menu bar includes 'Flair', 'Input', 'Geometry', 'Run', and 'Plot'. Below the menu is a toolbar with icons for 'Paste', 'Copy', 'DICOM', 'Slice', 'Information', 'Voxel', and 'RTViewer'. A search bar is located to the right of the toolbar. The main window is titled 'Dicom' and contains a list of DICOM files on the left and a detailed view of the selected file's metadata on the right. A yellow arrow points from the 'NEW_anon127.dcm' entry in the list to the 'Referenced Image Sequence' field in the metadata view.

Name	Value	Tag	VM	VR
NEW_anon145.dcm	-459.88			
NEW_anon144.dcm	-456.61			
NEW_anon143.dcm	-453.34			
NEW_anon142.dcm	-450.07			
NEW_anon141.dcm	-446.8			
NEW_anon140.dcm	-443.53			
NEW_anon139.dcm	-440.26			
NEW_anon138.dcm	-436.99			
NEW_anon137.dcm	-433.72			
NEW_anon136.dcm	-430.45			
NEW_anon135.dcm	-427.18			
NEW_anon134.dcm	-423.91			
NEW_anon133.dcm	-420.64			
NEW_anon132.dcm	-417.37			
NEW_anon131.dcm	-414.1			
NEW_anon130.dcm	-410.83			
NEW_anon129.dcm	-407.56			
NEW_anon128.dcm	-404.29			
NEW_anon127.dcm	-401.02			
NEW_anon126.dcm	-397.75			
NEW_anon125.dcm	-394.48			
NEW_anon124.dcm	-391.21			
NEW_anon123.dcm	-387.94			
NEW_anon122.dcm	-384.67			
NEW_anon121.dcm	-381.4			
NEW_anon120.dcm	-378.13			
NEW_anon119.dcm	-374.86			
NEW_anon118.dcm	-371.59			
NEW_anon117.dcm	-368.32			
NEW_anon116.dcm	-365.05			
NEW_anon115.dcm	-361.78			

Name	Value	Tag	VM	VR
Specific Character Set	ISO_IR 100	(0008, 0005)	1	CS
Image Type	['ORIGINAL', 'PRIMARY', 'AXIAL']	(0008, 0008)	3	CS
Instance Creation Date	20100215	(0008, 0012)	1	DA
Instance Creation Time	112745	(0008, 0013)	1	TM
SOP Class UID	CT Image Storage	(0008, 0016)	1	UI
SOP Instance UID	1.3.6.1.4.1.9590.100.1.2.203210842112899385017924509543781971078	(0008, 0018)	1	UI
Study Date	20100215	(0008, 0020)	1	DA
Series Date	20100215	(0008, 0021)	1	DA
Acquisition Date	20100215	(0008, 0022)	1	DA
Content Date	20100215	(0008, 0023)	1	DA
Study Time	112455	(0008, 0030)	1	TM
Series Time	112534	(0008, 0031)	1	TM
Acquisition Time	112549	(0008, 0032)	1	TM
Content Time	112745	(0008, 0033)	1	TM
Accession Number		(0008, 0050)	1	SH
Modality	CT	(0008, 0060)	1	CS
Manufacturer	GE MEDICAL SYSTEMS	(0008, 0070)	1	LO
Institution Name		(0008, 0080)	1	LO
Referring Physician's Name		(0008, 0090)	1	PN
Manufacturer's Model Name	Discovery ST	(0008, 1090)	1	LO
Referenced Image Sequence		(0008, 1140)	1	SQ
Patient's Name		(0010, 0010)	1	PN
Patient ID		(0010, 0020)	1	LO
Patient's Birth Date		(0010, 0030)	1	DA
Patient's Sex		(0010, 0040)	1	CS
Patient Identity Removed	YES	(0012, 0062)	1	CS
De-identification Method	DICOMANON (rev R2010a) - PS 3.15-2008 Table E.1-1 - nondefault	(0012, 0063)	1	LO
Scan Options	HELICAL MODE	(0018, 0022)	1	CS
Slice Thickness	3.75	(0018, 0050)	1	DS

Creating the VOXEL file

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

Step 8: Create the .vxl file

The screenshot shows the software interface with the 'Dicom' window. The 'Materials' field is set to './material.inp' and the 'Unit to Material' field is set to './calib_curve.mat'. A table of material properties is displayed, with columns for HUmin, HUmax, Material, Crho_min, Crho_max, CdEdx_rel_min, and CdEdx_rel_max. A dialog box titled 'Creating VOXEL file' is open, showing progress: 'Current: 225 [275] Completed: 81% [1s Tot: 1s Rem: 0s]' and 'Processing: NEW_anon50.dcm'. A 'Stop' button is visible in the dialog box. A yellow arrow points to the 'Voxel' tab, and a red arrow points to the 'VOXEL' button.

HUmin	HUmax	Material	Crho_min	Crho_max	CdEdx_rel_min	CdEdx_rel_max
-3072	-1021	AIR	0.6825432	1.3174568	1.0	1.0
-1020	-1016	HU<-1015	0.720281108	1.27971895	1.0	1.0
-1015	-1011	HU<-1010	0.835391418	1.16460858	1.0	1.0
-1010	-1001	HU<-1000	0.733656625	1.16949124	1.0	1.0
-1000	-996	HU<-995	0.909584201	1.05424948	1.0	1.0
-995	-989	HU<-988	0.909502356	1.09049764	1.0	1.0
-988	-975	HU<-974	0.85108832	1.14891168	1.0	1.0
-974	-963	HU<-962	0.902912681	1.09708732	1.0	1.0
-962	-951	HU<-950			1.0	1.0
-950	-926	HU<-925			1.0	1.0
-925	-901	HU<-900			1.0	1.0
-900	-831	HU<-830			1.0	1.0
-830	-701	HU<-700			1.0	1.0
-700	-501	HU<-500			1.0	1.0
-500	-121	HU<-120			1.0	1.0
-120	-84	HU<-83	0.980501545	1.01835909	1.0	1.0
-83	-54	HU<-53	0.98600717	1.01305997	1.0	1.0
-53	-24	HU<-23	0.986384099	1.01270032	1.0	1.0
-23	6	HU<7	0.98674495	1.01236373	1.0	1.0
7	14	HU<18	0.995655766	1.00173225	1.0	1.0
15	79	HU<80	0.972407965	1.03421835	1.0	1.0
80	100	HU<120	0.980146255	1.00104493	1.0	1.0
101	119	HU<120	0.962511989	0.973311932245	1.0	1.0
120	199	HU<200	0.973911929092	1.02131168	1.0	1.0
200	299	HU<300	0.97508777	1.02542064	1.0	1.0
300	399	HU<400	0.976293061	1.02419075	1.0	1.0
400	499	HU<500	0.977387107	1.02307438	1.0	1.0
500	599	HU<600	0.97838463	1.0220565	1.0	1.0
600	699	HU<700	0.979297863	1.02112463	1.0	1.0

Step 7: Add materials and calibration files

Creating the VOXEL file: the .mat file

- **<= 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.
- **CdEdx_rel_min/CdEdx_rel_max:** relative correction factors on dE/dx for minimum/maximum unit in the range.

HUmin	HUmax	Material	Crho_min	Crho_max	CdEdx_rel_min	CdEdx_rel_max
-3072	-1021	AIR	0.6825432	1.3174568	1.0	1.0
-1020	-1016	HU<-1015	0.720281108	1.27971895	1.0	1.0
-1015	-1011	HU<-1010	0.835391418	1.16460858	1.0	1.0
-1010	-1001	HU<-1000	0.733656625	1.16949124	1.0	1.0
-1000	-996	HU<-995	0.909584201	1.05424948	1.0	1.0
-995	-989	HU<-988	0.909502356	1.09049764	1.0	1.0
-988	-975	HU<-974	0.85108832	1.14891168	1.0	1.0
-974	-963	HU<-962	0.902912681	1.09708732	1.0	1.0
-962	-951	HU<-950	0.919883508	1.08011649	1.0	1.0
-950	-926	HU<-925	0.862306423	1.13769358	1.0	1.0
-925	-901	HU<-900	0.893000468	1.10699951	1.0	1.0
-900	-831	HU<-830	0.783902333	1.21609767	1.0	1.0
-830	-701	HU<-700	0.75158871	1.24841129	1.0	1.0
-700	-501	HU<-500	0.765689411	1.23431059	1.0	1.0
-500	-121	HU<-120	0.734835247	1.26516475	1.0	1.0
-120	-84	HU<-83	0.980501545	1.01835909	1.0	1.0
-83	-54	HU<-53	0.98600717	1.01305997	1.0	1.0
-53	-24	HU<-23	0.986384099	1.01270032	1.0	1.0
-23	6	HU<7	0.98674495	1.01236373	1.0	1.0
7	14	HU<18	0.995655766	1.00173225	1.0	1.0
15	79	HU<80	0.972407965	1.03421835	1.0	1.0
80	100	HU<120	0.980146255	1.00104493	1.0	1.0
101	119	HU<120	0.962511989	0.973311932245	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: bodyCT ▾	
 SPH blk	x: 0.0	y: 0.0	z: 0.0
	R: 1000.		
 SPH void	x: 0.0	y: 0.0	z: 0.0
	R: 100.		
 END			
 REGION BLKBODY		Neigh: 5	Volume:
expr: +blk -void			
 REGION VOID		Neigh: 5	Volume:
expr: +void -VOXEL			
 END			
 GEOEND			

Voxel Regions

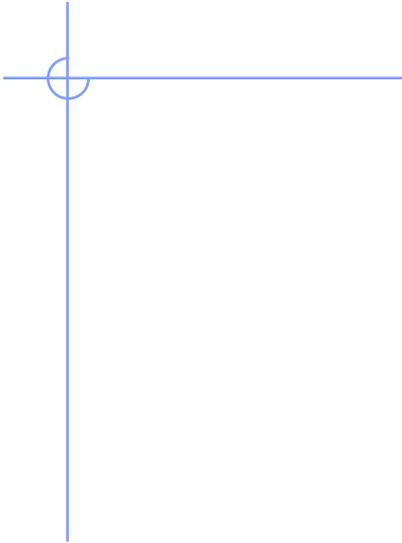
The code will **automatically generate** and add several regions:

- **NM** additional regions, where **NM = 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+NM	corresponding to organ NM

Few remarks

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



Additional Infos

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 window shows a CT scan of a head and neck, with several colored ROIs overlaid: a green outline for the head, a purple outline for the oral cavity, a blue circle for the right eye, a pink circle for the left eye, and an orange outline for the tongue. 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
GTVvertex	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.

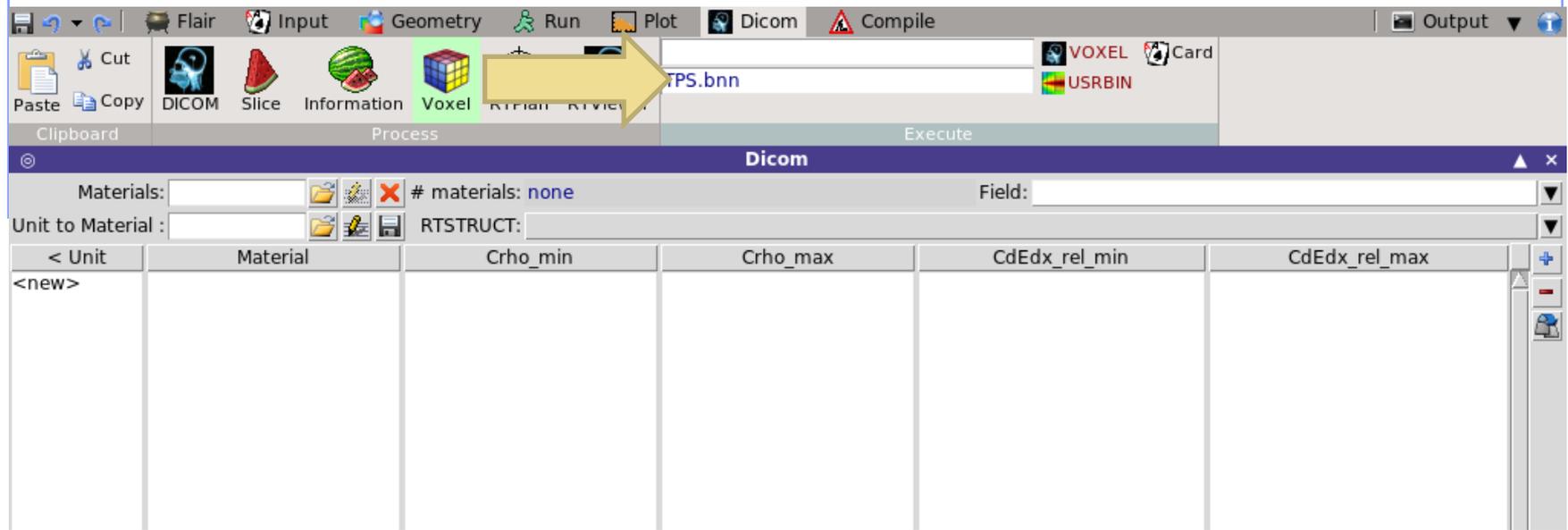
The screenshot displays the FLAIR VIII software interface. The main window is titled 'Dicom' and shows a table of materials. A yellow arrow points to the 'Unit to Material' field, which is set to '..../flair/dicom/head.mat'. A dialog box titled 'Processing RTSTRUCTS' is overlaid on the table, showing a progress bar and the current RTSTRUCT file being processed: '1.3.12.2.1107.5.1.4.49597.30000012011114455237500000281'. The table lists materials with their corresponding density and relative electron density 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
-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

Beam FWHM [cm]:
Beam ang div [rad]: 1.3.12.2.1107.5.7.8.100011.30000012
Momentum spread:

RTDOSE: [dropdown menu]
Create

Choose RT file		Choose Beam Number			
RTPlan	Date	Beam	# points	Gantry Ang	Patient Ang
RTPlan74GyE.dcm	2012.01.20	1	98	90.0	0
		2	92	90.0	180.0
		3	48	90.0	270.0

Information

Patient Info:
Patient's Name: S, F
Patient's Age: 100Y
Patient's Sex: F

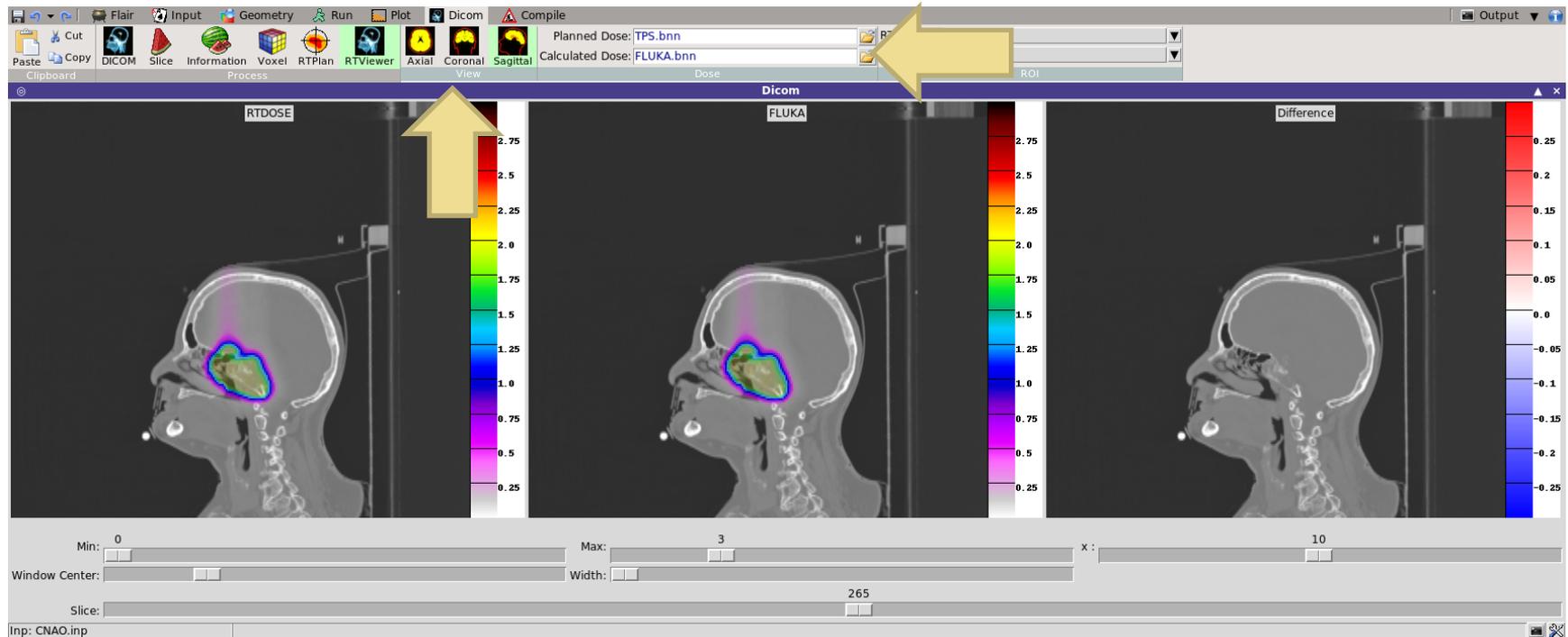
RT Plan Info:
RT Plan Name: 2Beam54
Dose Type: EFFECTIVE
Plan Intent: CURATIVE
Approval Status: APPROVED
Review Date: 2012.01.20 130922.64:89
Reviewer Name

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

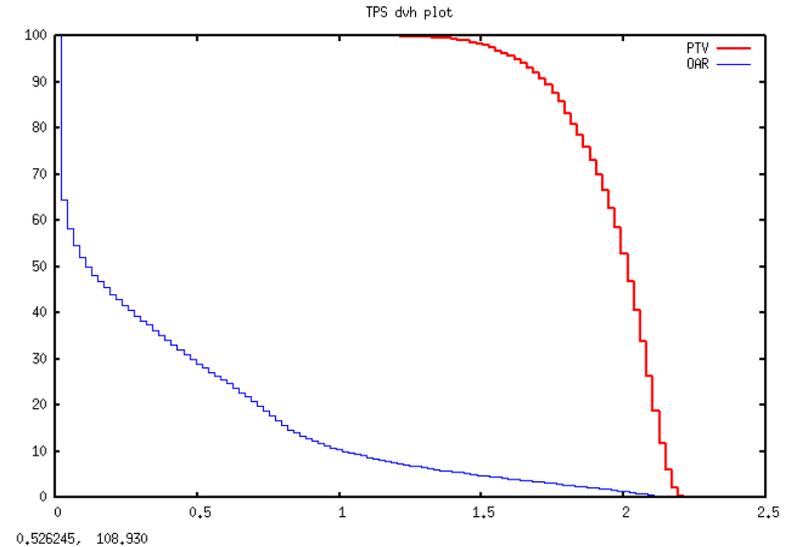
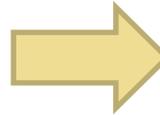
Processing the **DICOM** files with FLAIR XI

- 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 postprocessing routine allows to create data for Dose-Volume Histograms (DVH) plots



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

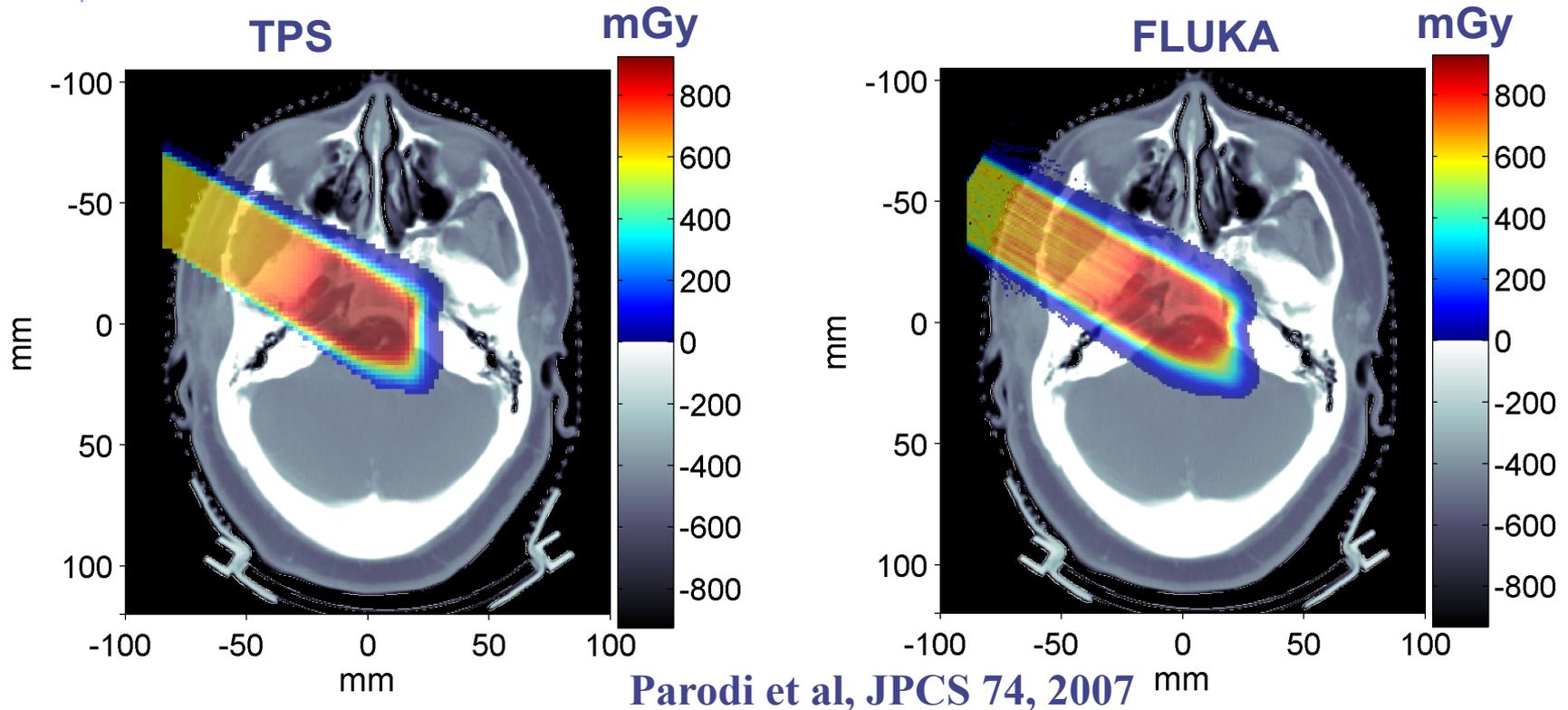
Name	Tag	Value	Type	Default
Output file	-o	TPS_dvh_tab.lis	output	V_\U_dvh_tab.lis
Usrbin file	-u	TPS.bnn	file	V_\U.bnn
Detector index	-d	1	int	1
Voxel file	-v	test_struct.vxl	file	=C(VOXELS,0,0)+".vxl"
Relative dose (Gray)	-r	0,0	float	0,0
Voxel x	-x	-25	float	=C(VOXELS,0,1)
Voxel y	-y	-49,2	float	=C(VOXELS,0,2)
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



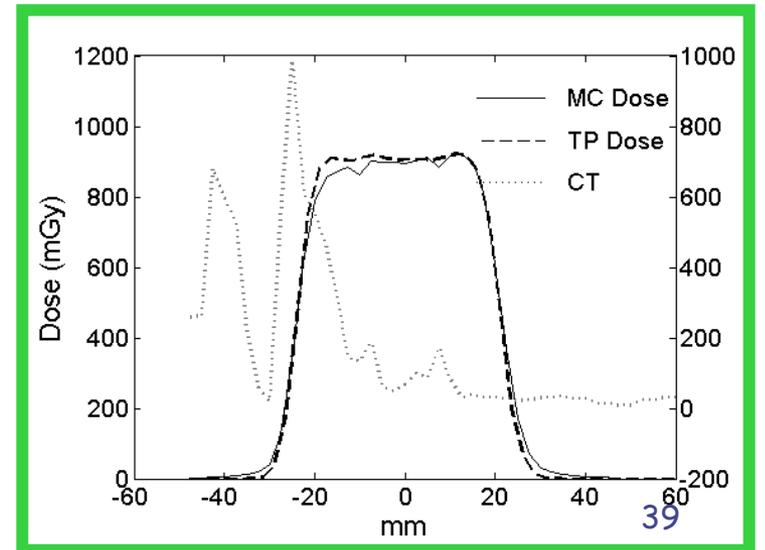
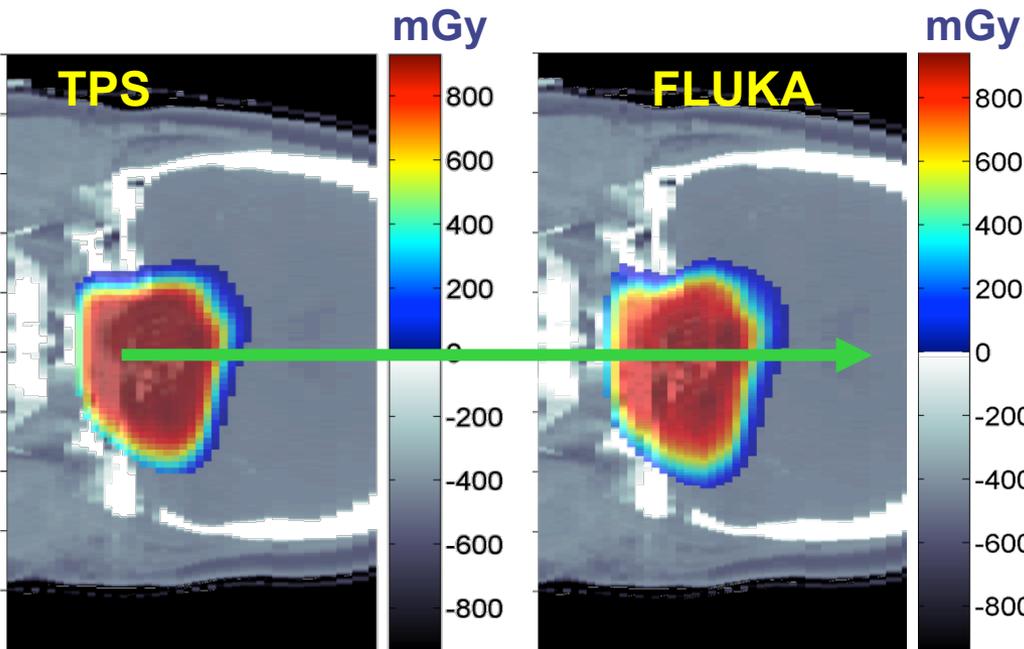
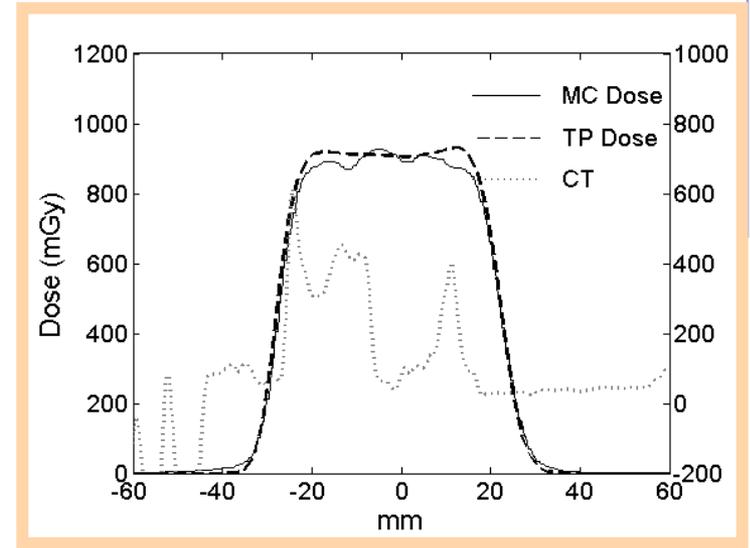
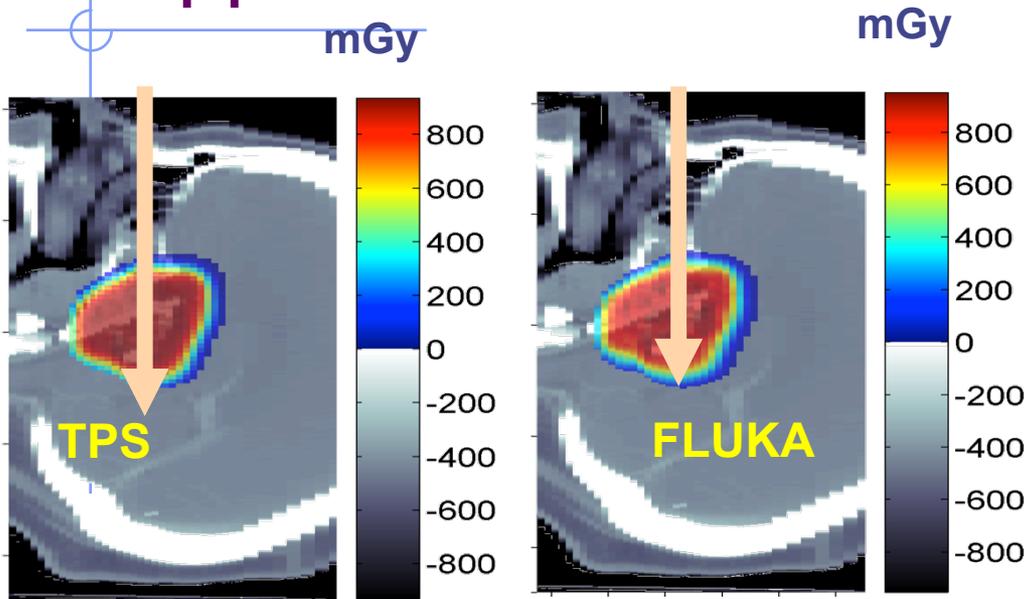
Prescribed dose: 1 GyE

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

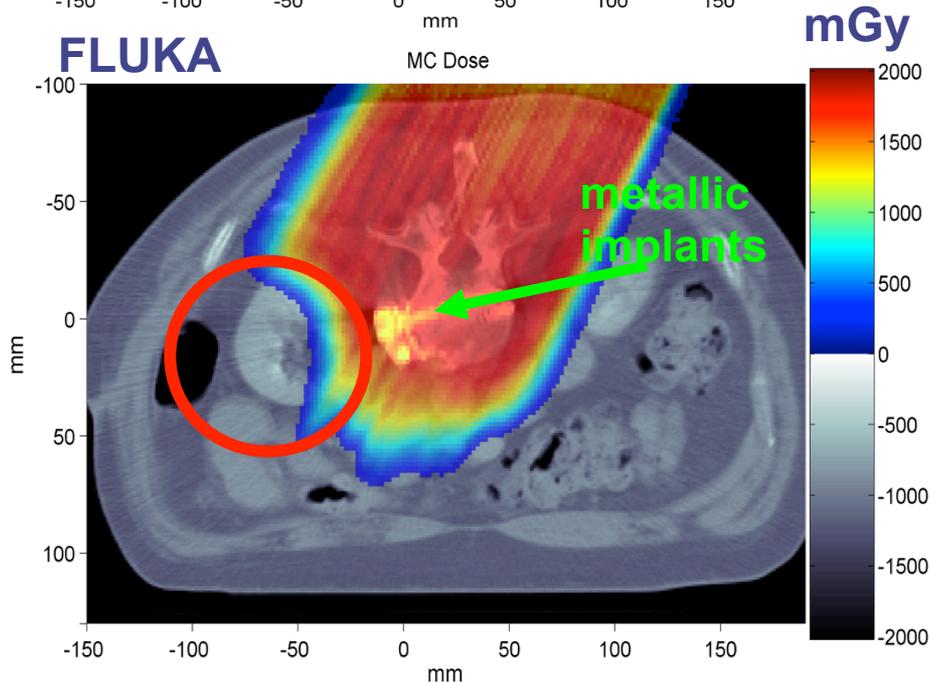
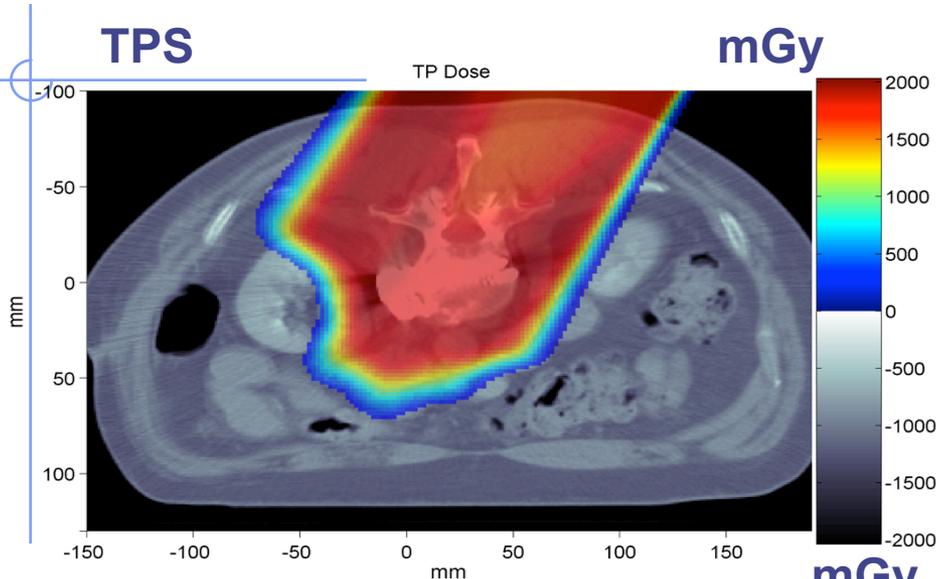
(11h each on Linux Cluster mostly using 2.2GHz Athlon processors)

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)

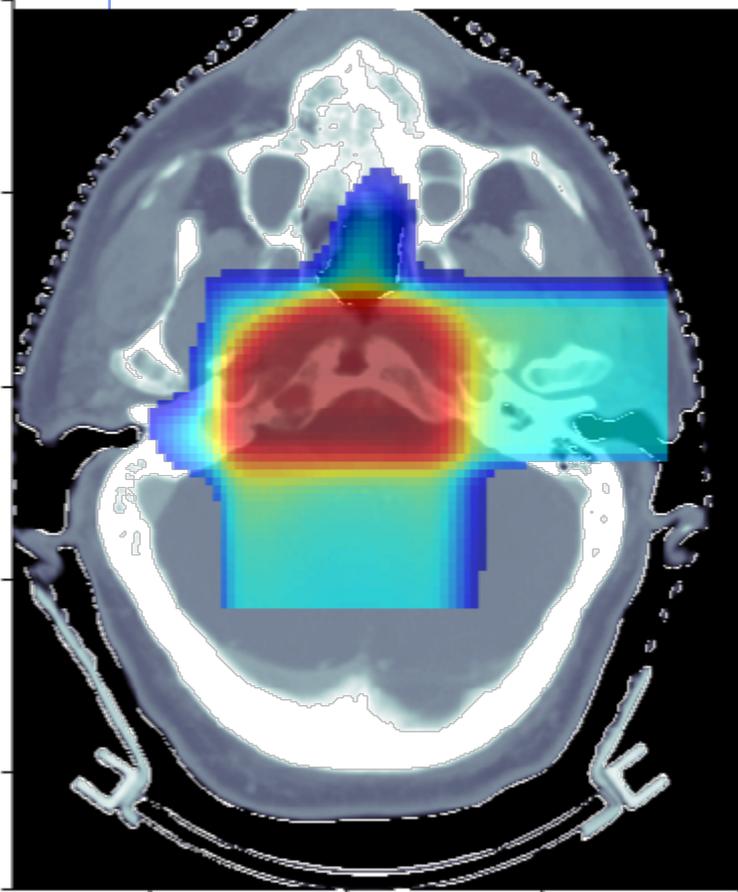
Applications of FLUKA to p therapy @ MGH

Clival Chordoma, 0.96 GyE / field

Planned dose

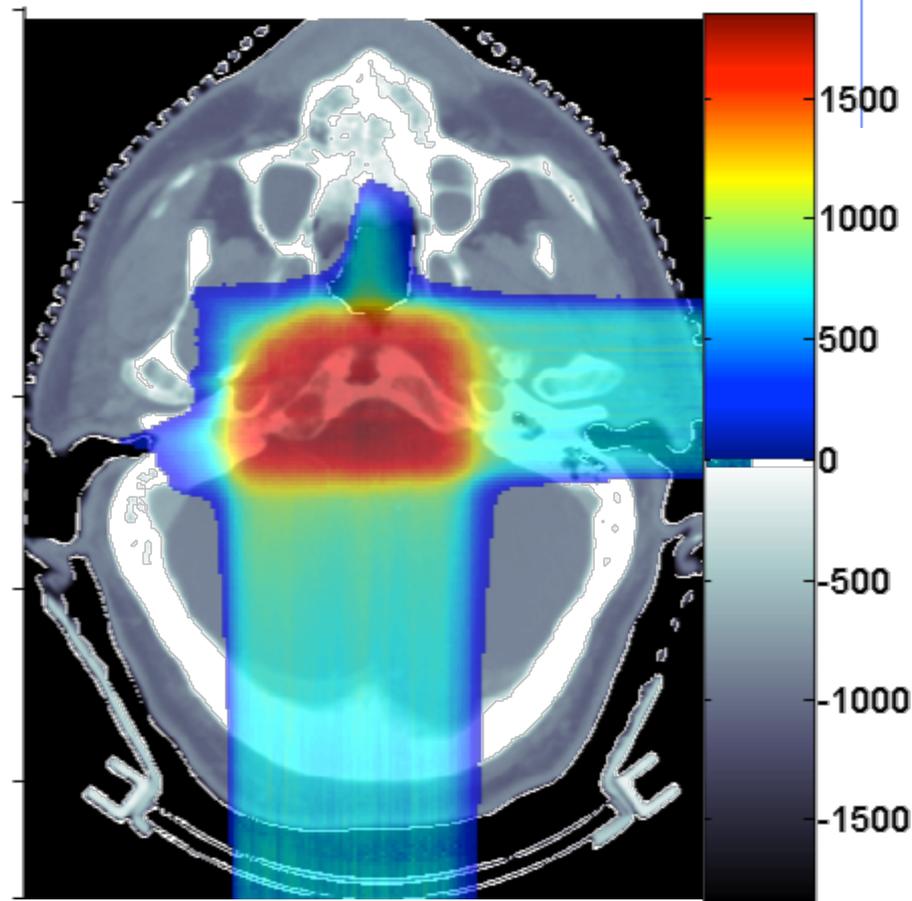
TP Dose

mGy



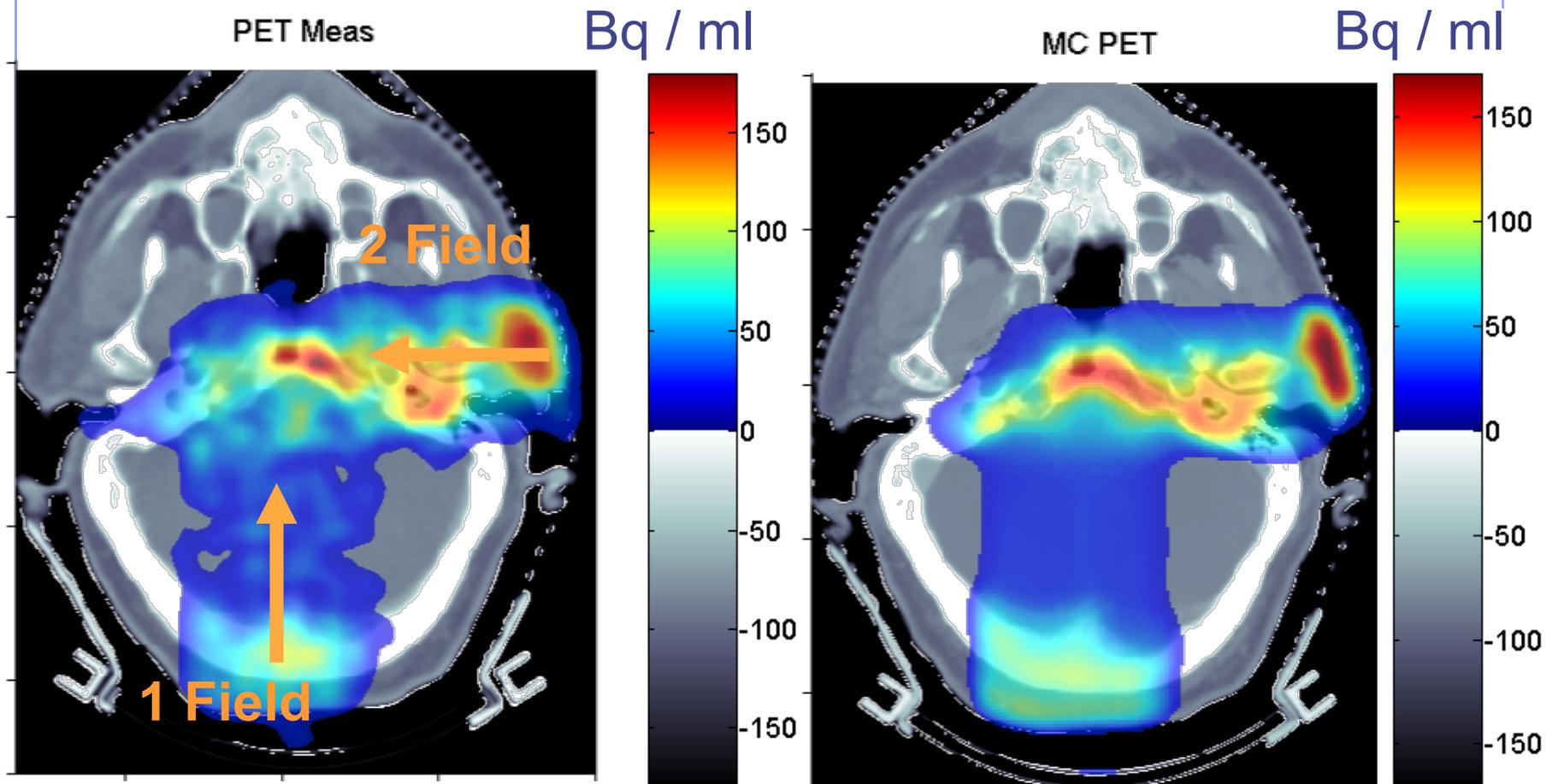
MC Dose

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 CNAO⁴²...

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.

