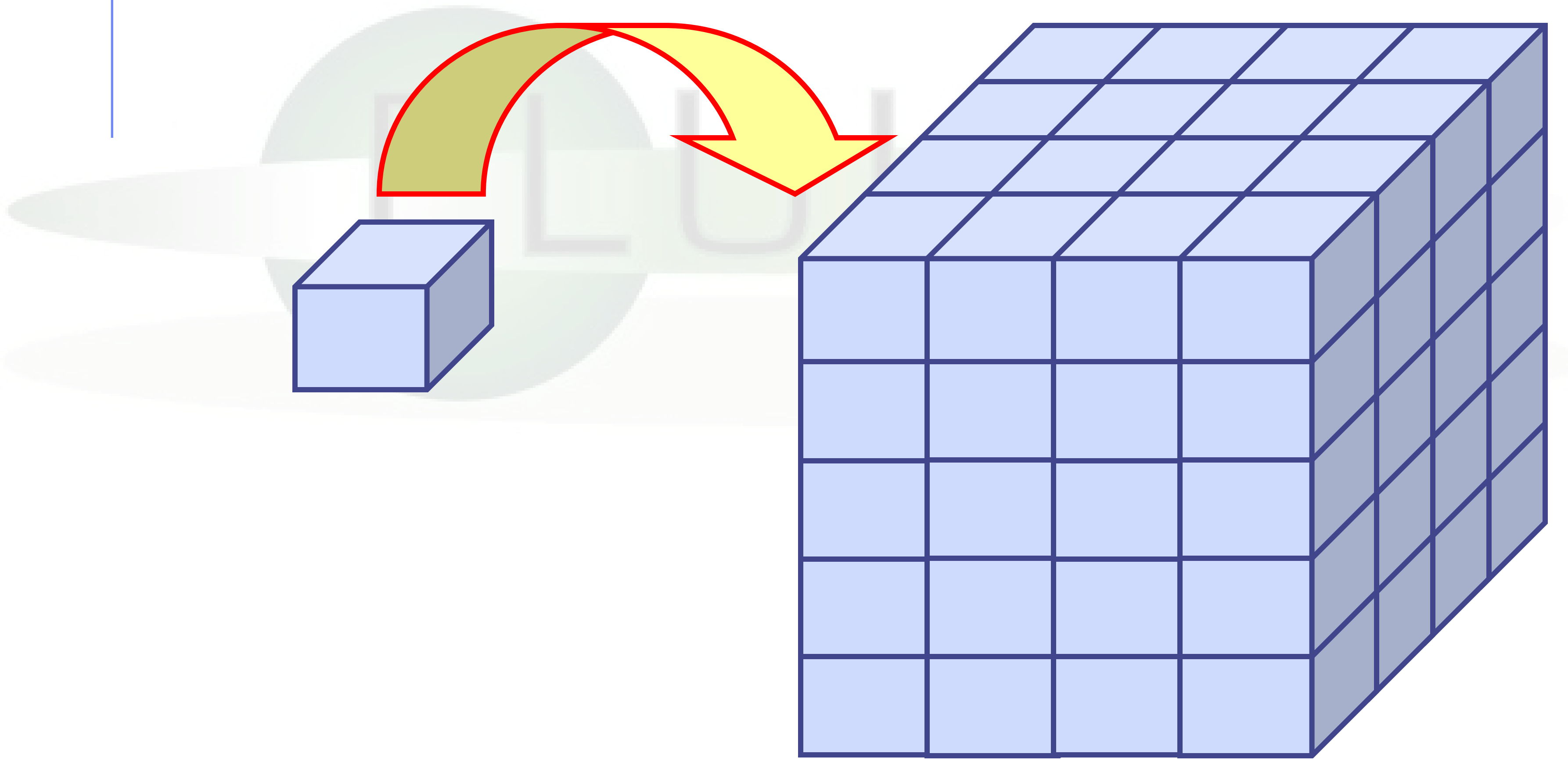
Voxels and Medical Applications

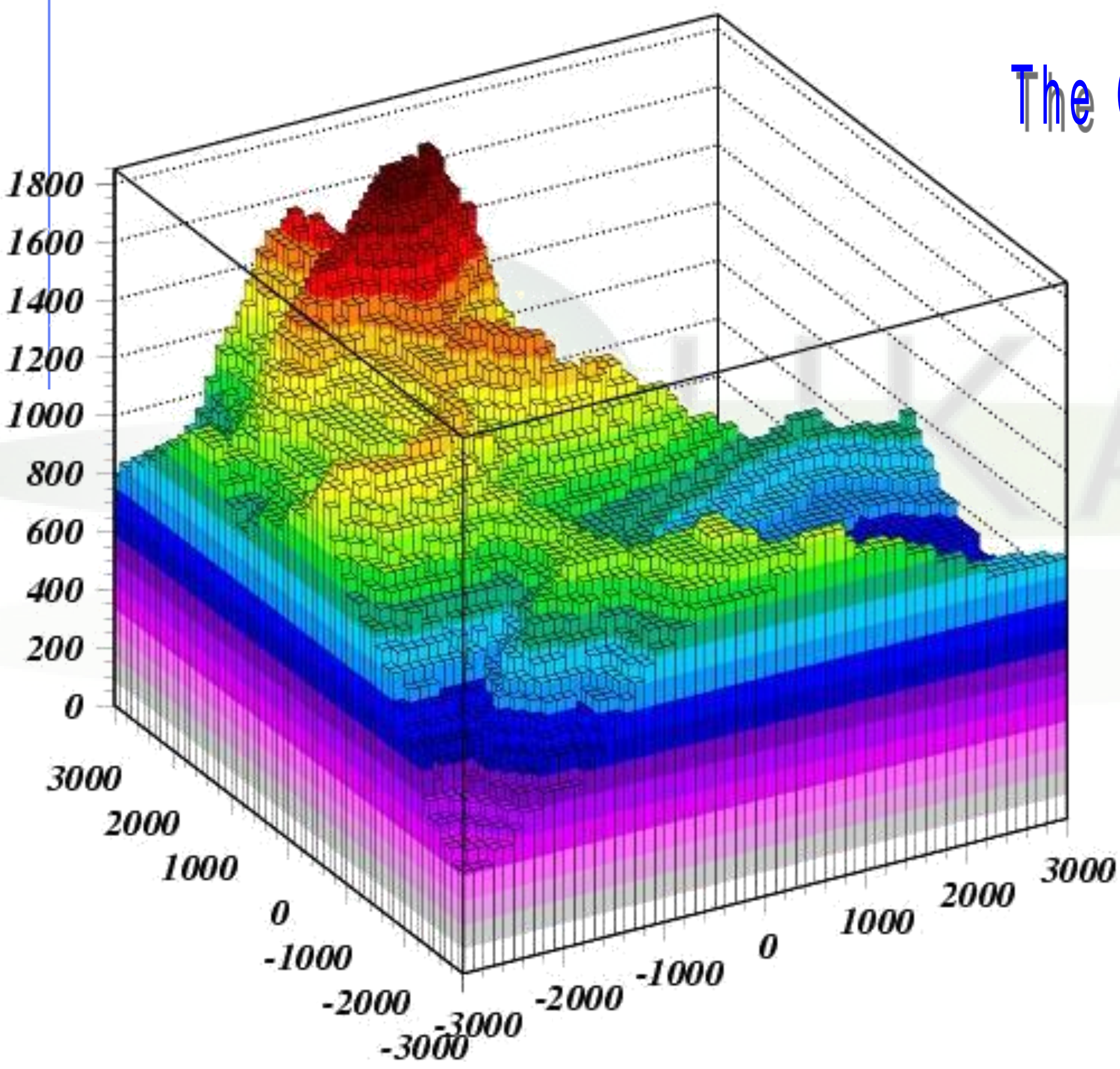
FLUKA Beginners course

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



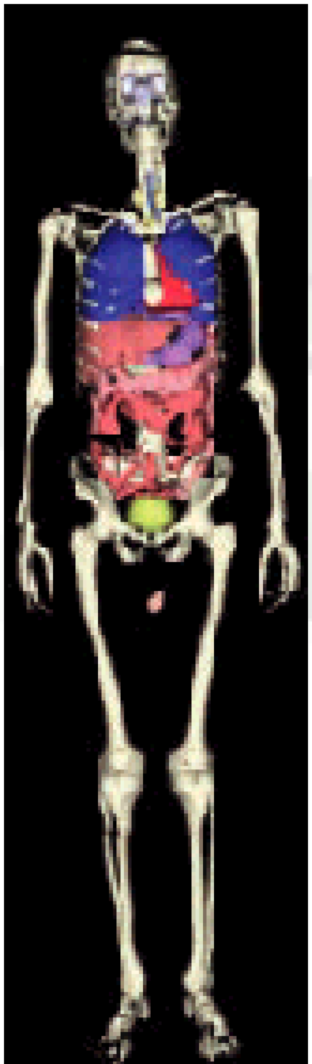
Voxel geometries: examples



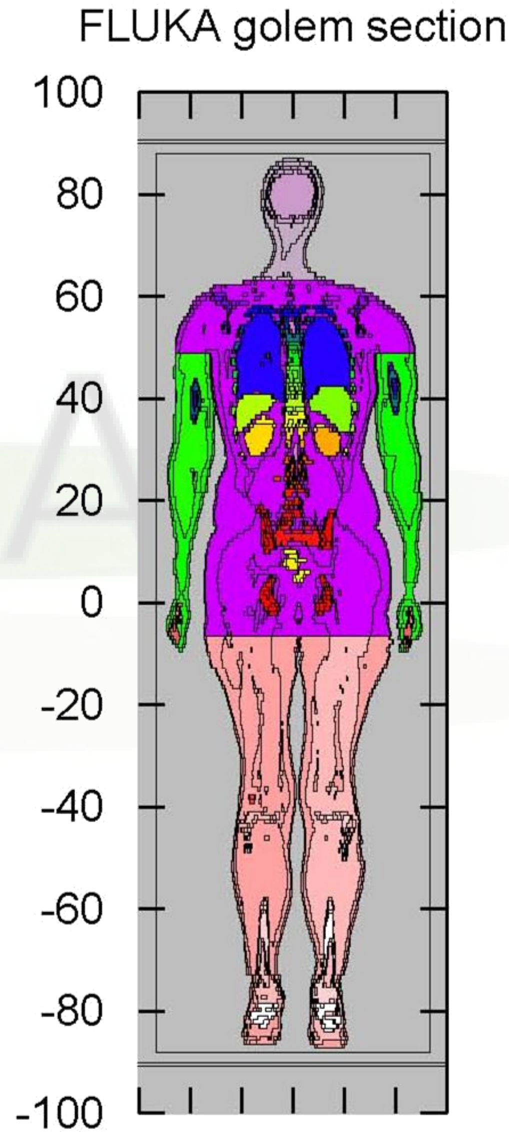
The Gran Sasso in FLUKA

Voxel geometries: examples

The anthropomorphic
GOLEM phantom



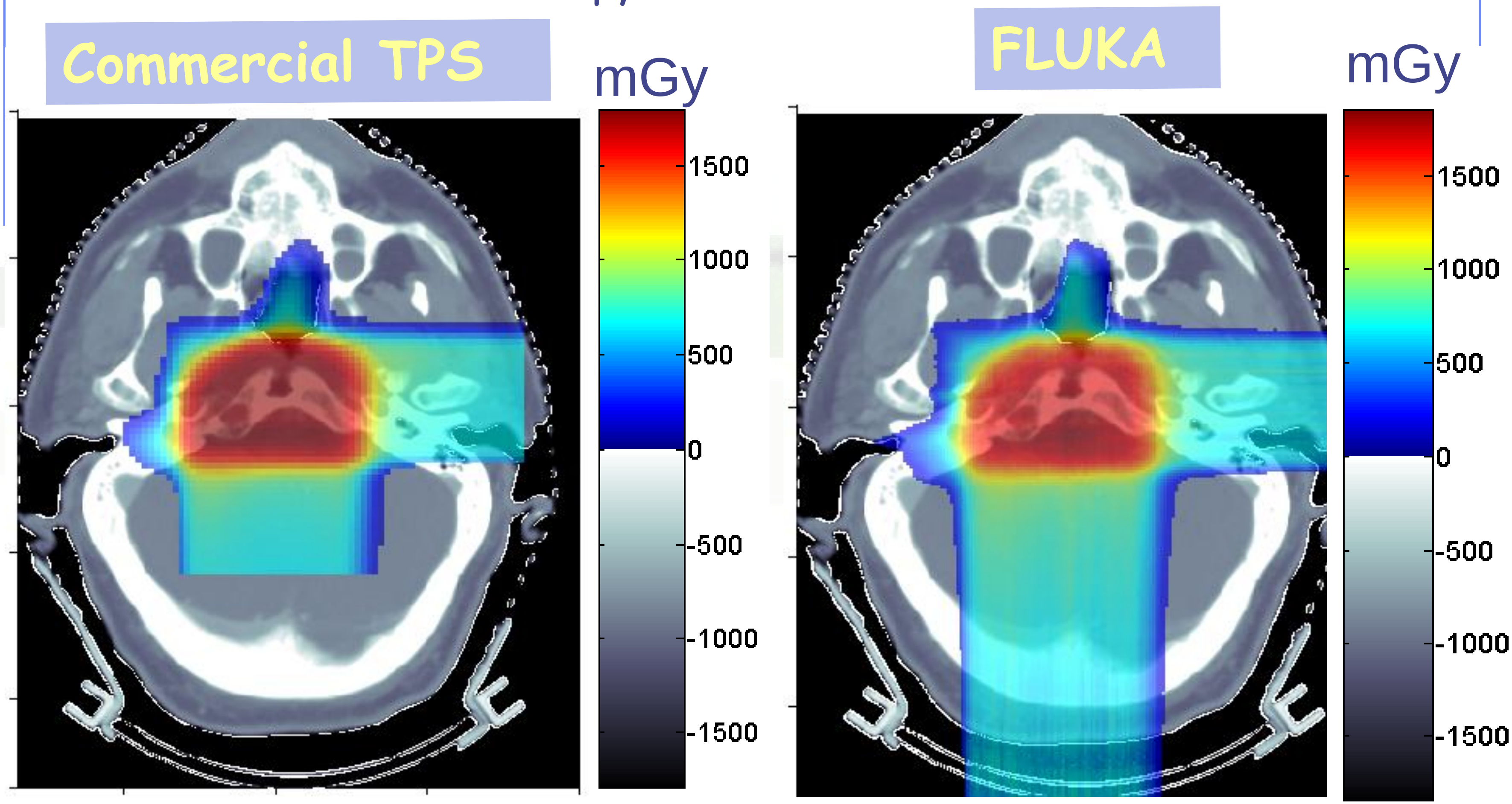
Implementation in FLUKA (radioprotection applications)



Petoussi-Henss et al, 2002

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



Parodi et al., 2007

The FLUKA voxel geometry

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

  $HU_x = 1000\ (\mu_x - \mu_{H20})\ /\ \mu_{H20}$, 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
- A prototype of conversion program is in writect.f
- 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).
  - 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
  - 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

    in Fortran list-oriented format, with the x coordinate running faster than y, and y running faster than z.

val(1)	corresponds to 1,1,1 == organ n. of first voxel
…	…
val(Nx)	corresponds to Nx,1,1
val(Nx+1)	corresponds to **1**,**2**,1
val(2*Nx)	corresponds to Nx,2,1
…	
val(Nx*Ny)	corresponds to Nx,Ny,**1**
…	…
val(Nx*Ny*Nz)	corresponds to Nx,Ny,Nz == organ n. of last voxel

  - A list of the voxel-region number corresponding to each organ

Voxel Example

in the directory ex12_Voxel you find

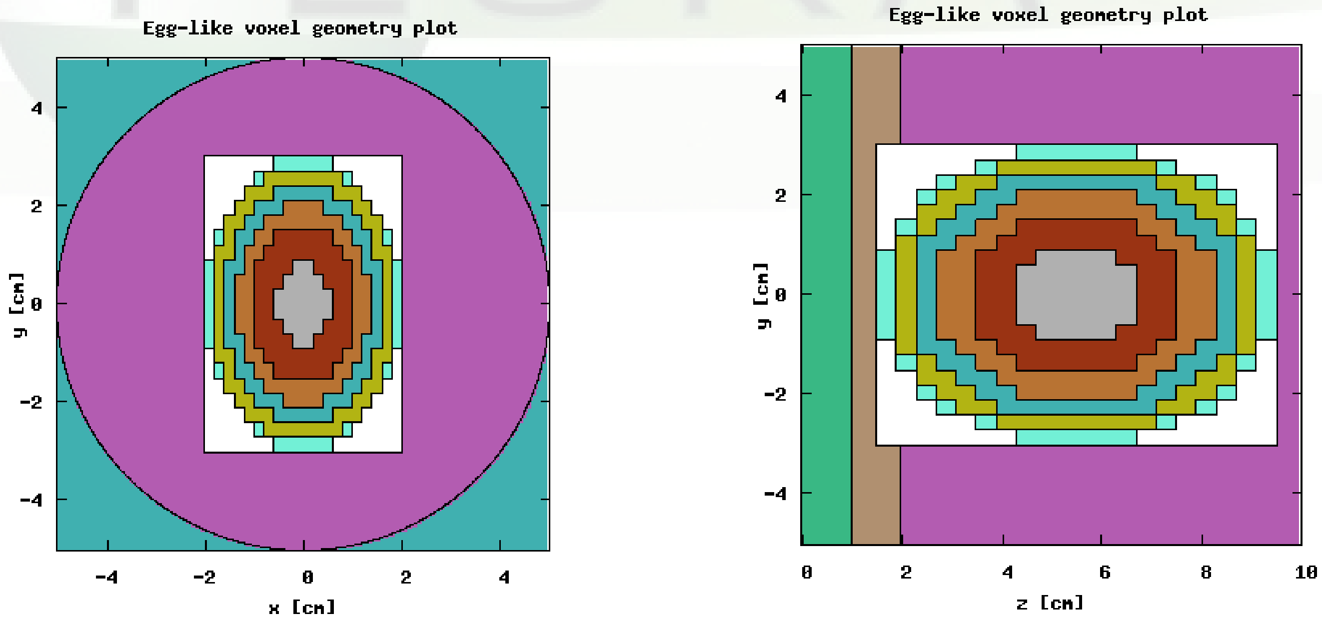
ex12.flair: flair project file

ex12.inp: input file

ascii_ct.txt: txt file representing a dummy scan of an egg-shaped body with 6 different material zones (HU: 0,1,2,3,8,10,12)

writect.f: program to generate the .vxl file

ct.vxl: file generated by writect



Modifying writect

- The writect.f program has to be adapted to the user's need: The user will have to adapt the reading of the scan, and if needed to group continuous values
- The user will need to modify the values of the parameters DX, DY DZ, NX, NY, NZ (respectively voxel size and number of voxels for each coordinate).
- writect.f takes also care of re-compacting the original organ numbers by eliminating all gaps in the sequence, and writes a translation table to the screen:

```
WRITE(*,'(A,2I10)') 'New number, old number: ', NO, IC
```

writect.f

```
      PROGRAM WRITECT
      IMPLICIT DOUBLE PRECISION ( A-H, O-Z )
*  COLUMNS: FROM LEFT TO RIGHT
*  ROWS: FROM BACK TO FRONT
*  SLICES: FROM TOP TO BOTTOM
      PARAMETER ( DX = 2.0D+00 )
      PARAMETER ( DY = 3.0D+00 )
      PARAMETER ( DZ = 4.0D+00 )
      PARAMETER ( NX = 20 )
      PARAMETER ( NY = 20 )
      PARAMETER ( NZ = 20 )
      DIMENSION CT(NX,NY,NZ)
      INTEGER*2 CT
      DIMENSION VXL(NX,NY,NZ)
      INTEGER*2 VXL
      CHARACTER TITLE*80
      DIMENSION IREG(1000), KREG(1000)
      INTEGER*2 IREG, KREG
*
      CALL CMSPPR
      DO IC = 1, 1000
         KREG(IC) = 0
      END DO
      OPEN(UNIT=30,FILE='ascii_ct.txt',STATUS='OLD')
      READ(30,*) CT
*
*
      NO=0
      MO=0
```

Number and Dimensions of voxels

read the original CT scan

In this example, the organ number is simply set equal to the CT number for each voxel

For each voxel

```
      DO IZ=1,NZ
        DO IY=1,NY
          DO IX=1,NX
                IF (CT(IX,IY,IZ) .GT. 0) THEN
                  IO= CT(IX,IY,IZ)
                  VXL(IX,IY,IZ) = IO
                  MO = MAX (MO,IO)
                  DO IR=1,NO
                    IF (IREG(IR) .EQ. IO) GO TO 1000
                  END DO
                  NO=NO+1
                  IREG(NO)=IO
                  KREG(IO)=NO
                  WRITE(*,'(A,2I10)')' New number, old number: ', NO, IO
 1000             CONTINUE
                END IF
          END DO
        END DO
      END DO
*    NO = number of different organs
*    MO = max. organ number before compacting
*
      WRITE(*,*) ' NO,MO ',NO,MO
      OPEN(UNIT=31,FILE='ct.vxl',STATUS='UNKNOWN',FORM='UNFO
     RMATTED')
      TITLE = 'Egg-like CT scan'
      WRITE(31) TITLE
      WRITE(31) NX,NY,NZ,NO,MO
      WRITE(31) DX,DY,DZ
      WRITE(31) VXL
      WRITE(31) (KREG(IC),IC=1,MO)
      STOP
      END
```

Assign organ IO to this voxel

If new organ: assign new region NO to organ IO

Write the file for FLUKA

Modifying writect

- In the considered example the CT numbers 0,1,2,3,8,10,12 have been converted to
  - organs "IO" 0 1 2 3 8 10 12 (Max. MO=12)
  - regions "NO" 0 6 5 4 3 2 1 (...because of the order of appearance)

- After having modified the program (assumed to be in a file writect.f), compile it and link with the FLUKA library, and then execute:

```
ct > $FLUPRO/flutil/lfluka -o writect.x writect.f
ct > ./writect.x
```

- The result will be a file ct.vxl (or equivalent name chosen by the user) which will be referred to by a special command line in the geometry input

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     -20.0     -30.0     -40.0   transf                    ct
```

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.

Example: `TARGS2 5 +TARG -T1seg +T2seg -VOXEL`

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

Voxel Material Assignment

- The assignment of materials shall be made by command ASSIGNMAt (and in a similar way other region-dependent options) referring to the first NR regions in the usual way, and to the additional regions using the correspondence to organs as explained before.

```
ASSIGNMA   BLCKHOLE    BLKH
ASSIGNMA     VACUUM    VACO
ASSIGNMA   ALUMINUM      AL
ASSIGNMA     VACUUM    VACI
```

cage

```
ASSIGNMA     VACUUM   VOXEL
```

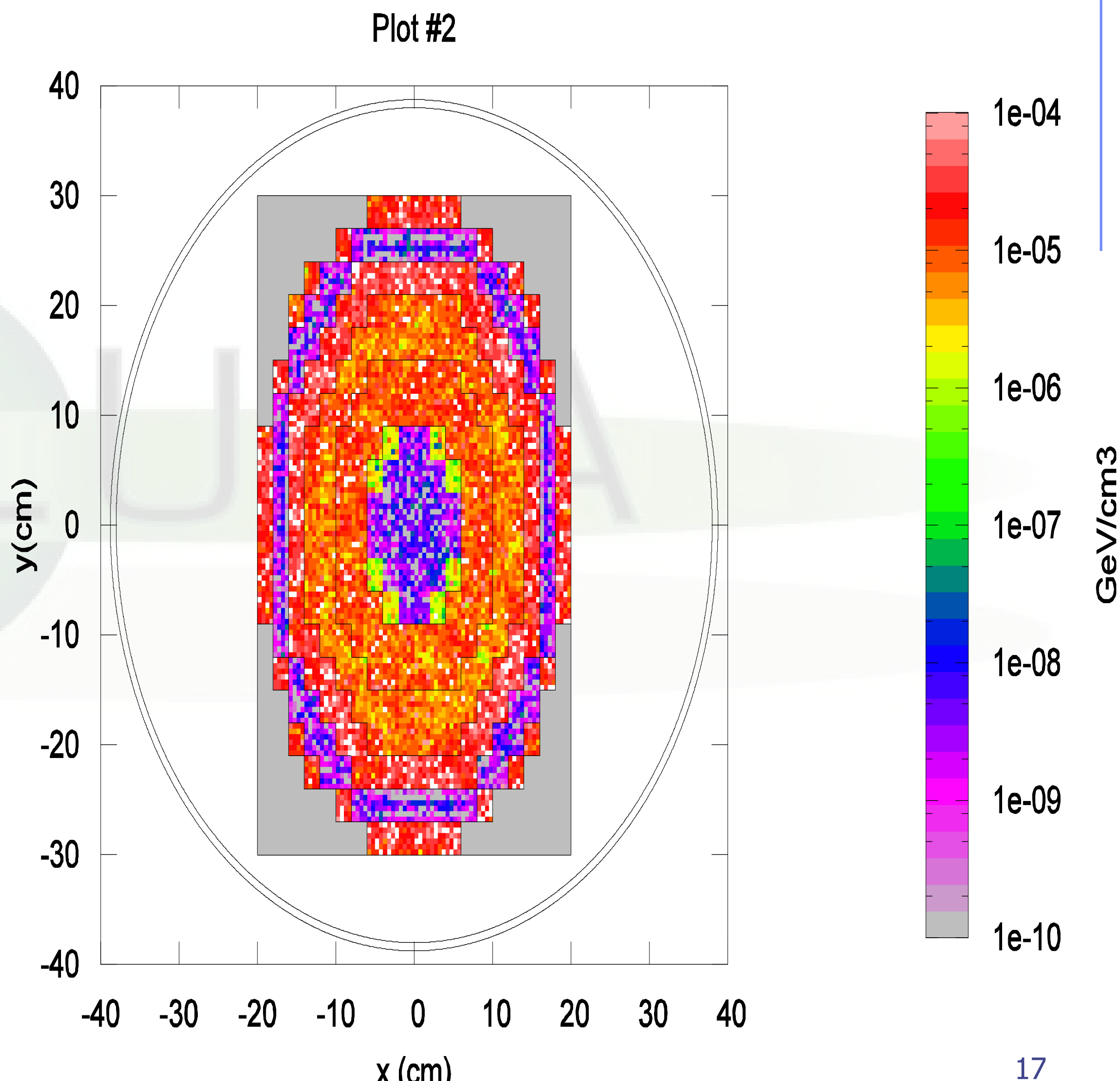
0 Organ

```
ASSIGNMA     VACUUM  VOXEL001
```

6 "Non-zero" organs

```
ASSIGNMA   TITANIUM  VOXEL002
ASSIGNMA        AIR  VOXEL003
ASSIGNMA     COPPER  VOXEL004
ASSIGNMA    CALCIUM  VOXEL005
ASSIGNMA     CARBON  VOXEL006
ASSIGNMA        AIR  VOXEL007
```

Energy deposition
in the voxel structure,
cut at z=0,
10 GeV protons,
through
cartesian USRBIN



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

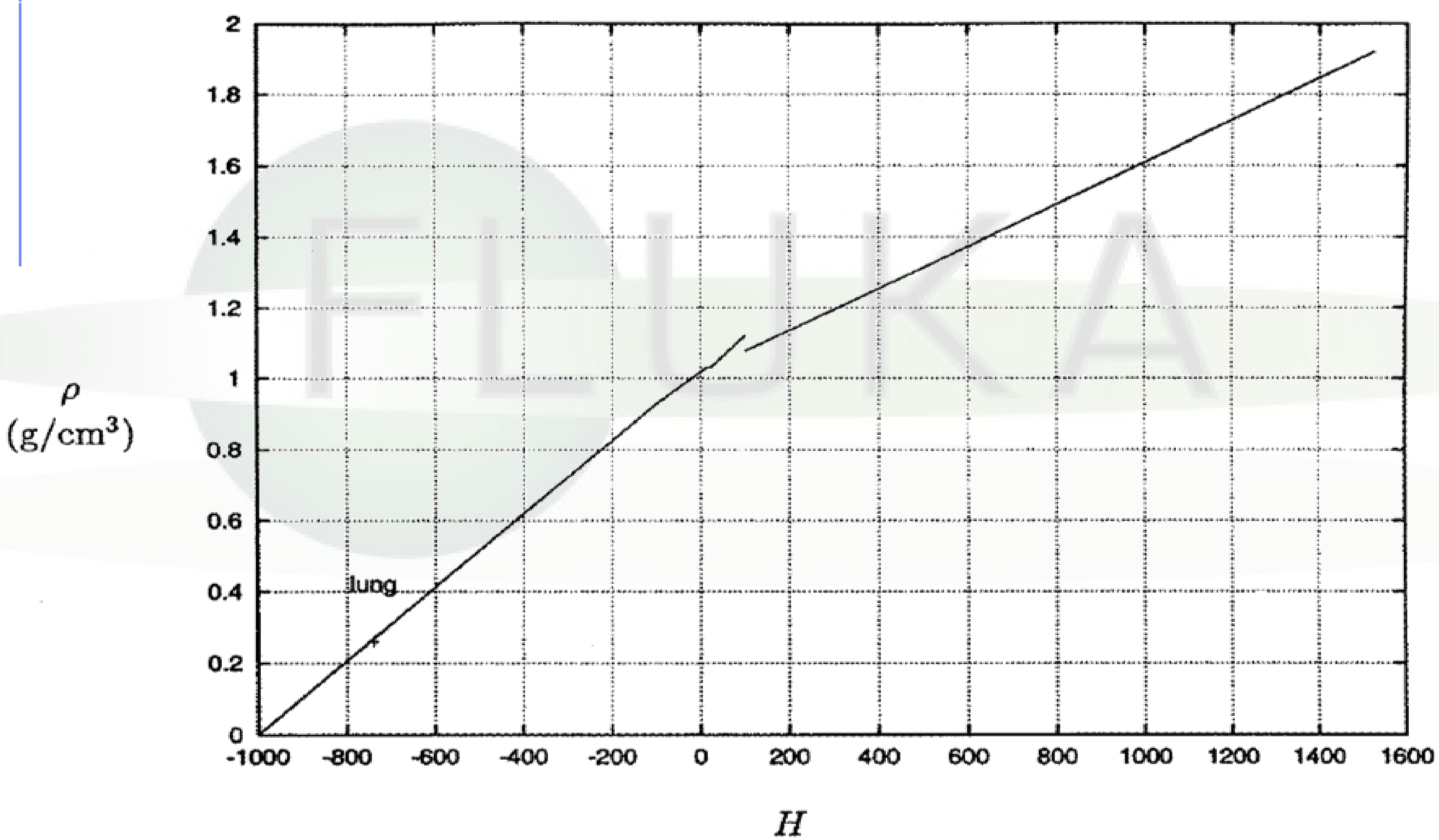
Skeletal tissue

H	w_i (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 (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 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

How to account for HU-dependent dEdx

- In writect.f identify each HU value of CT as an organ IO to which the region number KREG(IO) is assigned

CT scan dependent

```
      READ(30,*) HU
       MINHU=-1000
     NO=0
     MO=0
       DO IZ=1,NZ
         DO IY=1,NY
            DO IX=1,NX
      IF (HU(IX,IY,IZ)-MINHU .GT. 0) THEN
                IO= HU(IX,IY,IZ)-MINHU
                VXL(IX,IY,IZ) = IO
                MO = MAX (MO,IO)
                DO IR=1,NO
                   IF (IREG(IR) .EQ. IO) GO TO
     1000
                END DO
                NO=NO+1
                IREG(NO)=IO
                KREG(IO)=NO
                WRITE(*,'(A,2I10)')' New number,
     old number: ', NO, IC
1000                    CONTINUE
              END IF
            END DO
         END DO
     END
```

MINHU (e.g., air HU ~ -1000) goes into 0 organ!

Correspondence HU ⇔ Region NR, where HU=IO+MINHU

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)

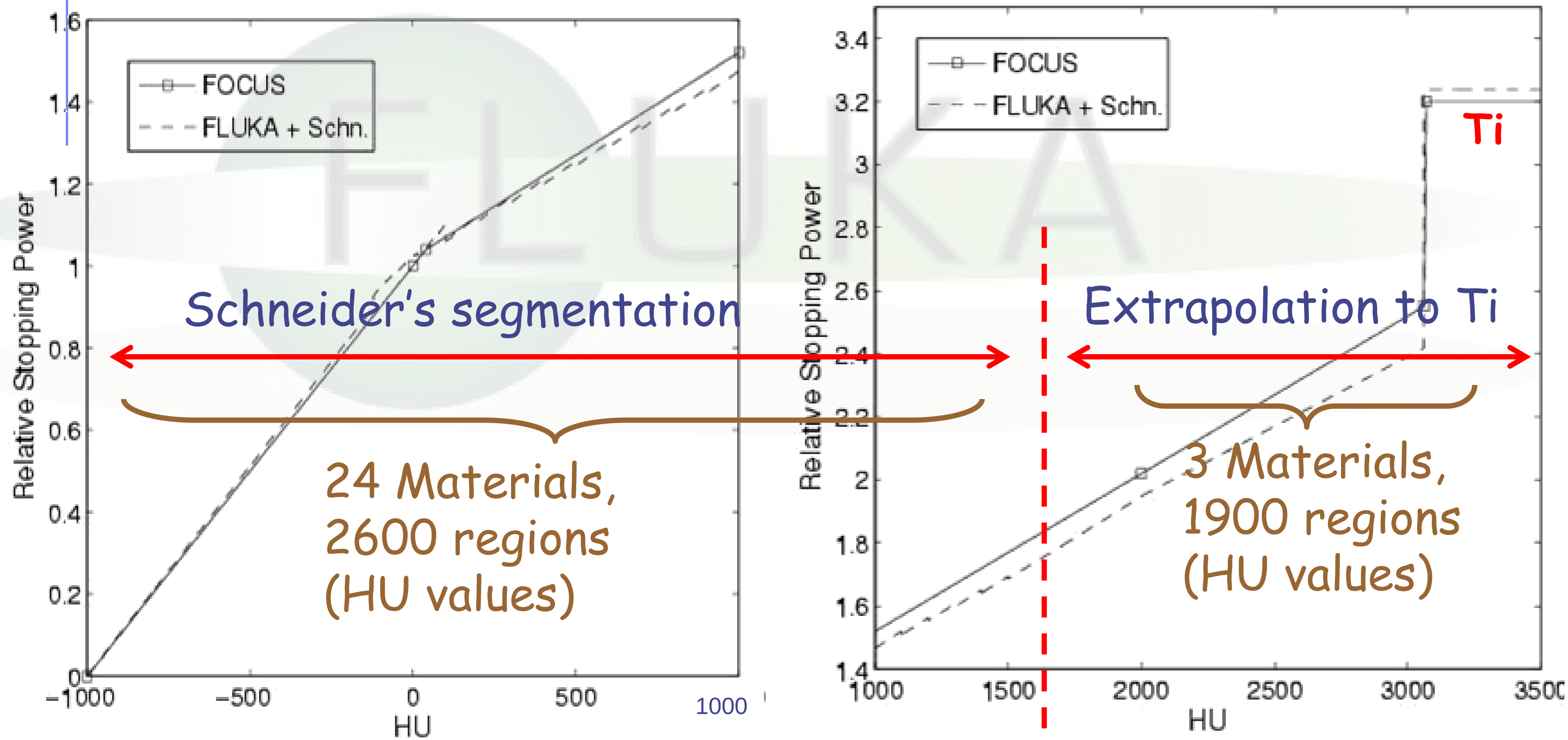
  - Use CORRFACT to impose the desired correction for stopping power (⇒ ion range!) in the regions KREG corresponding to different organs IO (i.e., different HU values) sharing the same MATERIAL assignment

```
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

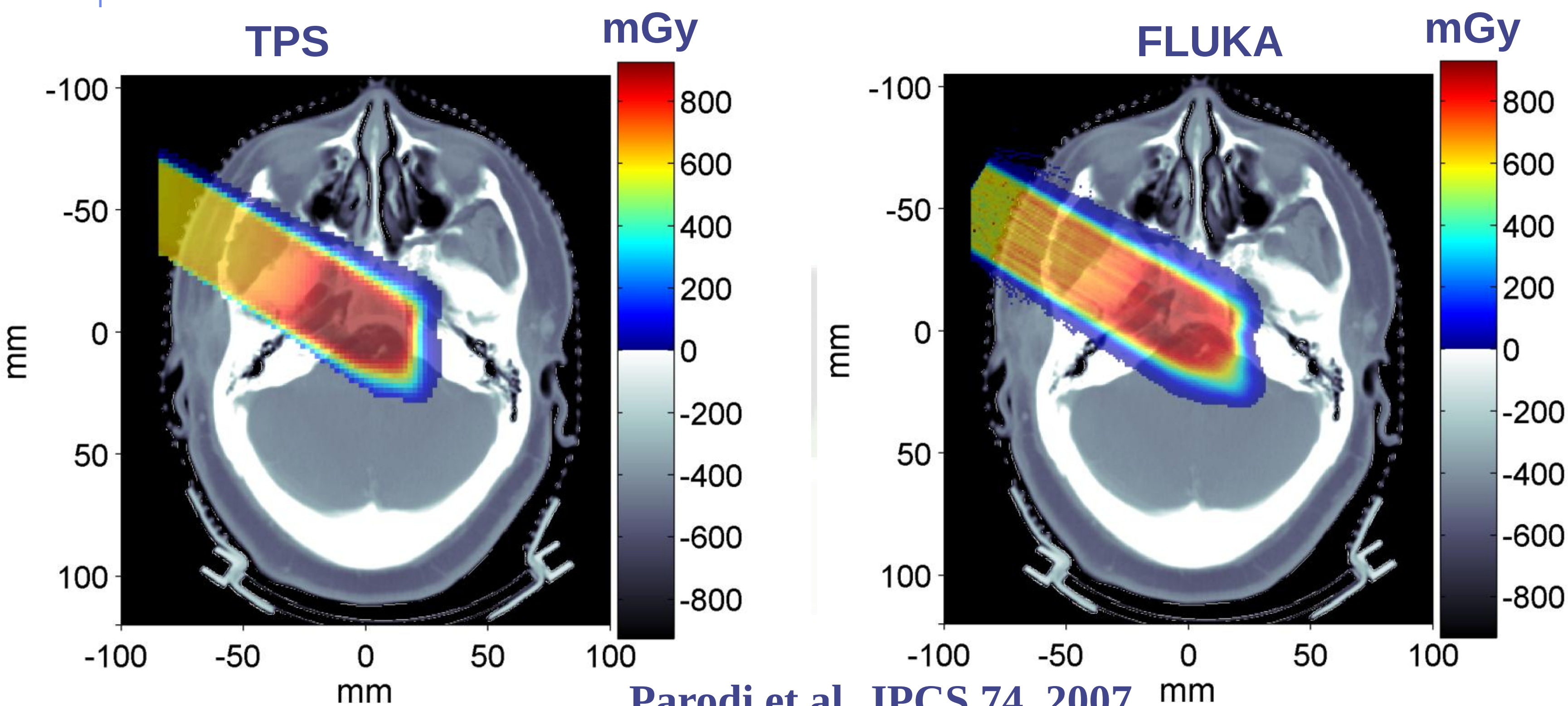
The CORRFACT ionization scaling factors were obtained from the dEdx ratio between TPS and FLUKA (+ Schneider "mass density")



Parodi et al MP 34, 2007, Parodi et PMB 52, 2007

Applications of FLUKA to p therapy @ MGH

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

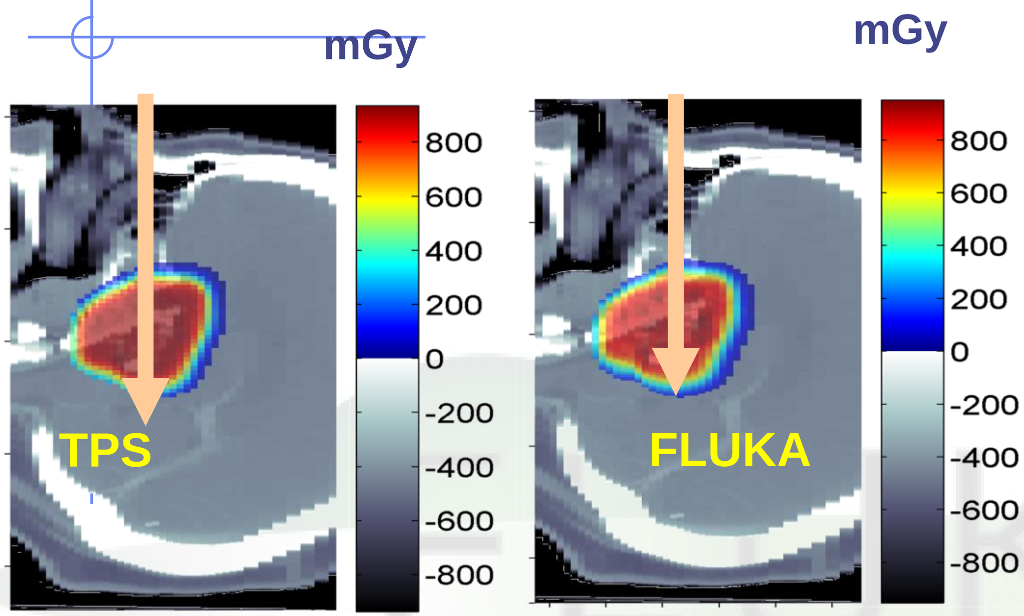


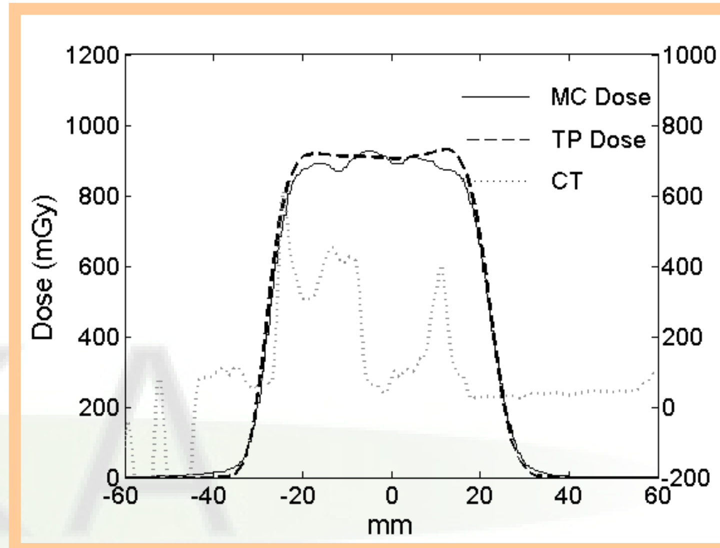
Parodi et al, JPCS 74, 2007

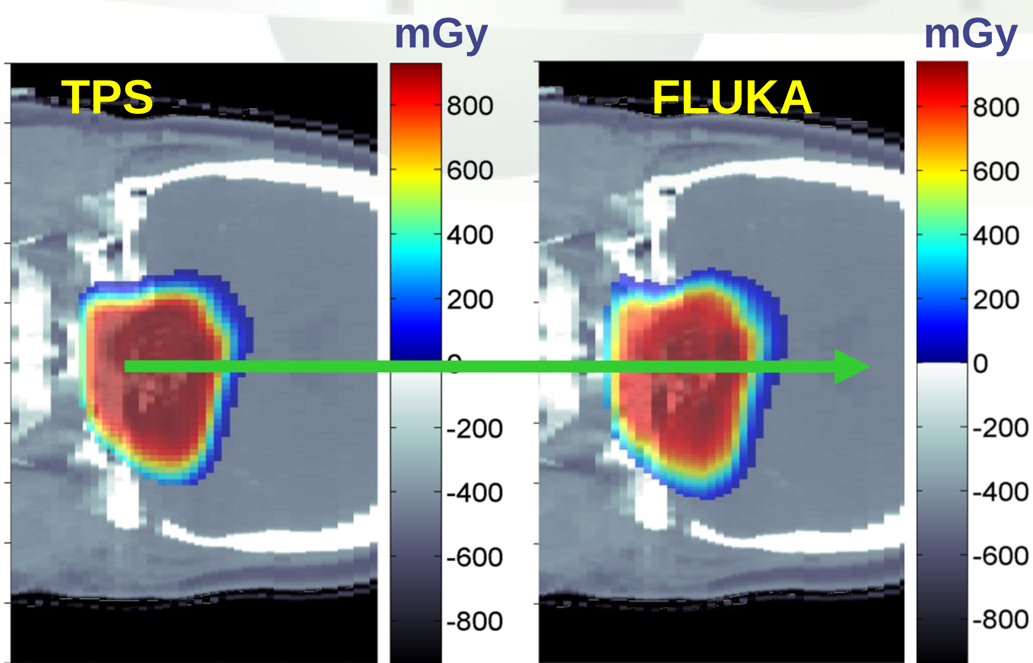
Prescribed dose: 1 GyE
MC : ~ 5.5 10^6 protons in 10 independent runs
(11h each on Linux Cluster mostly using 2.2GHz Athlon processors)

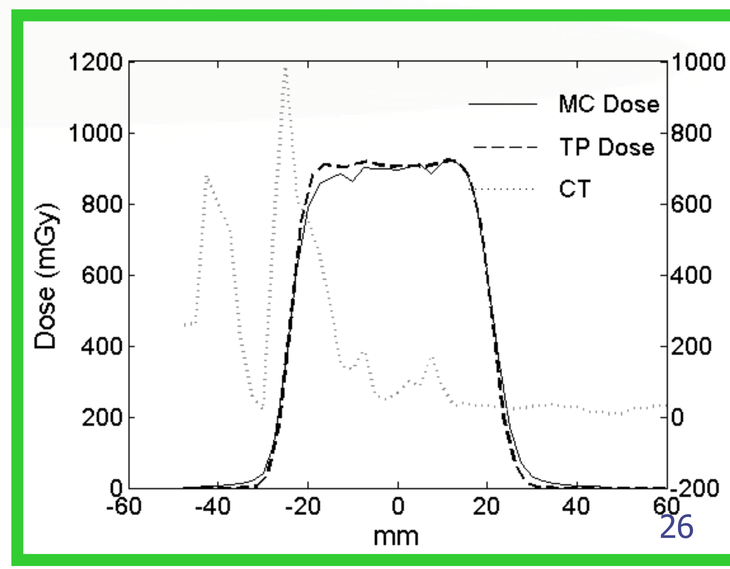
Applications of FLUKA to p therapy @ MGH

Parodi et PMB 52, 2007

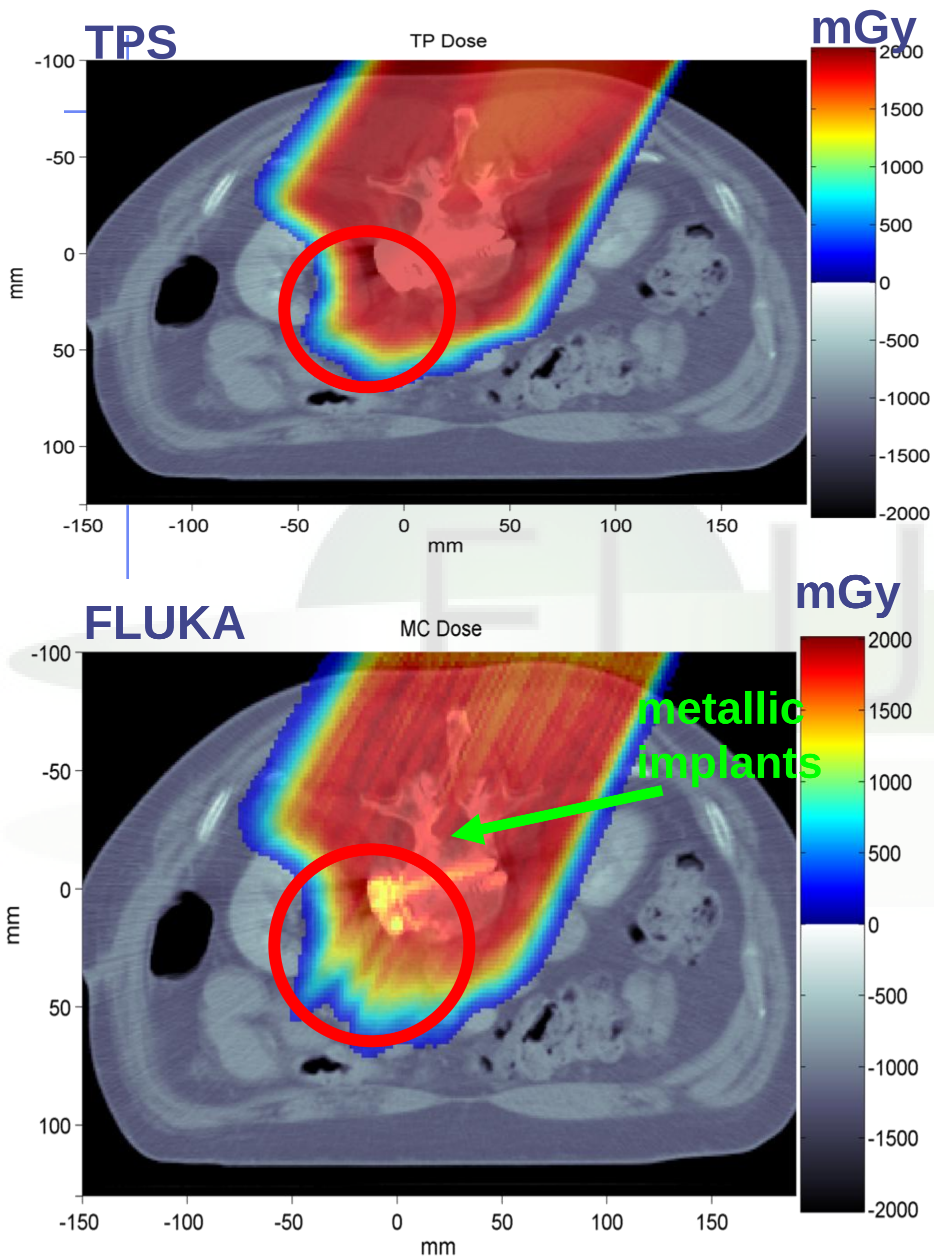








Applications of FLUKA to p therapy @ MGH



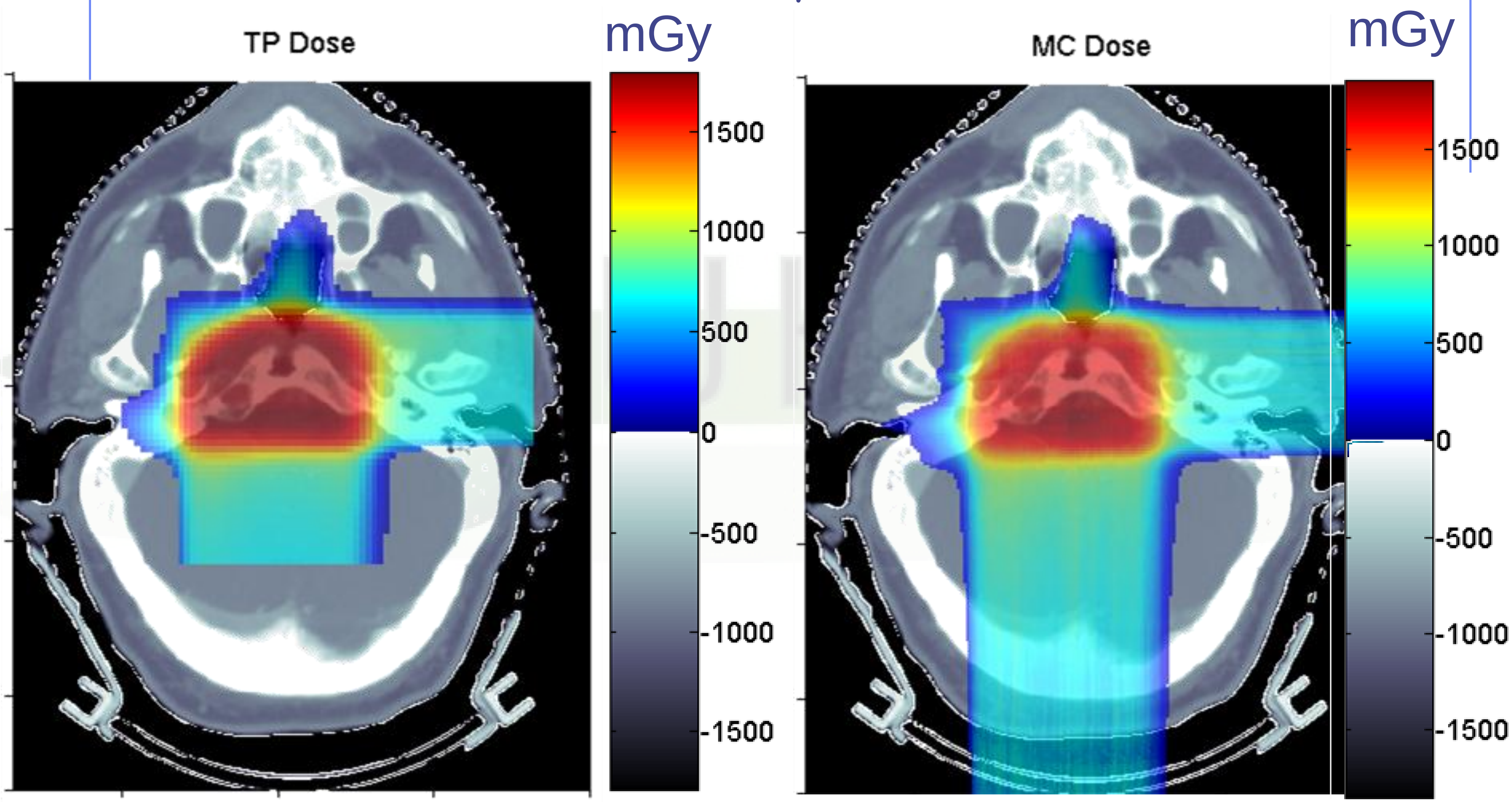
Prescribed dose: 2 GyE
MC : ~ 7.4 10^7p in 12 independent runs (~ 130h each on 2.2 GHz Linux cluster)

K. Parodi et al, IJROBP 2007

Applications of FLUKA to p therapy @ MGH

Clival Chordoma, 0.96 GyE / field

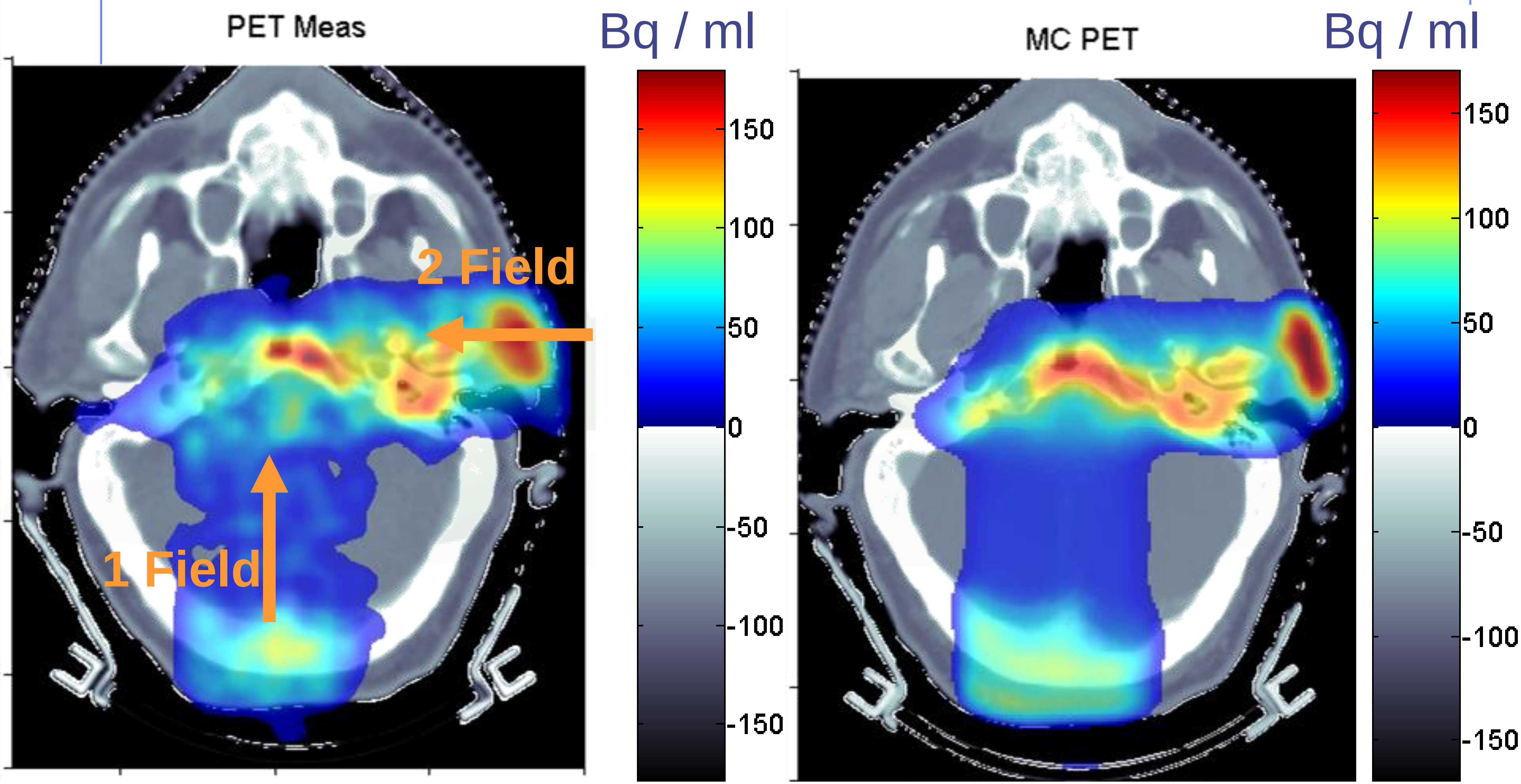
Planned dose



Post-radiation PET/CT @ MGH

Average Activity

Clival Chordoma, 0.96 GyE / field, ΔT1 ~ 26 min, ΔT2 ~ 16 min



K. Parodi et al, IJROBP 2007

… and FLUKA-voxel functionalities being also used at HIT …