

Parallelization of Monte Carlo simulations GATE for medical applications

The scenario of a typical radiotherapy treatment

WP10



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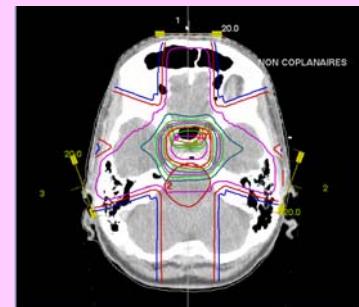
Radiotherapy is widely used to treat cancer

1°) Obtain scanner slices images



The head is imaged using a MRI and/or CT scanner

2°) Treatment planning



Calculation of deposit dose on the tumor (~1mn):
A treatment plan is developed using the images

3°) Radiotherapy treatment



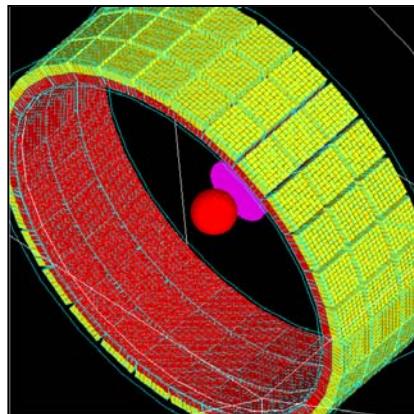
Irradiation of the brain tumor with a linear accelerator

Better treatment requires better planning

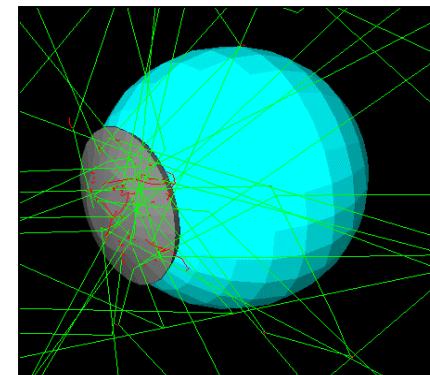


- ◆ Today: analytic calculation to compute dose distributions in the tumor
 - For new Intensity Modulated Radiotherapy treatments, analytic calculations off by **10 to 20% near heterogeneities**
- ◆ Alternative: Monte Carlo (MC) simulations in medical applications
- ◆ The GRID impact: reduce MC computing time to a few minutes

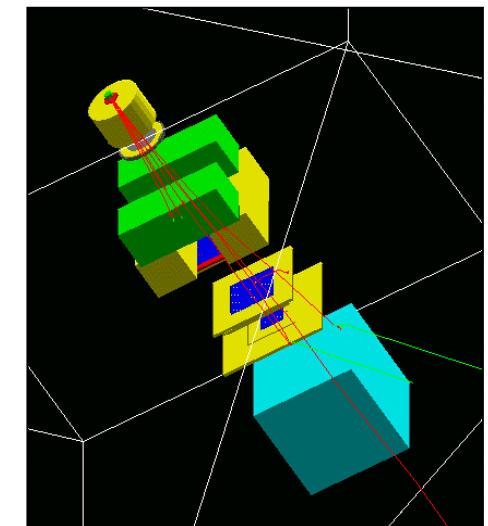
WP10 Demo: gridification of GATE MC simulation platform on the DataGrid testbed



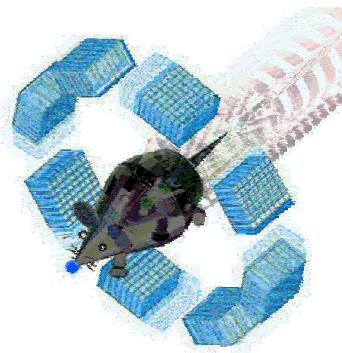
PET camera



Ocular brachytherapy treatment



Radiotherapy



Creatis



Computation of a radiotherapy treatment on the Datagrid: Let's go....

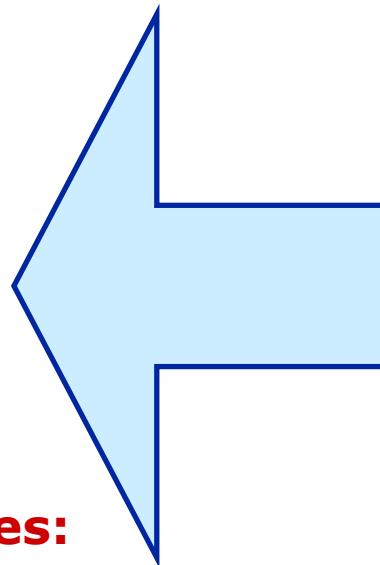
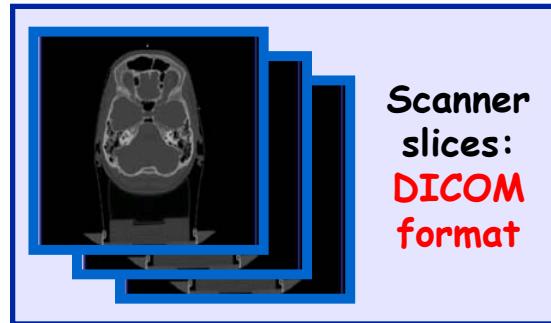


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Clermont-Ferrand - Auvergne

1°) Obtain the medical images of the tumor:

- ◆ 38 scanner slices of the brain of a patient are obtained



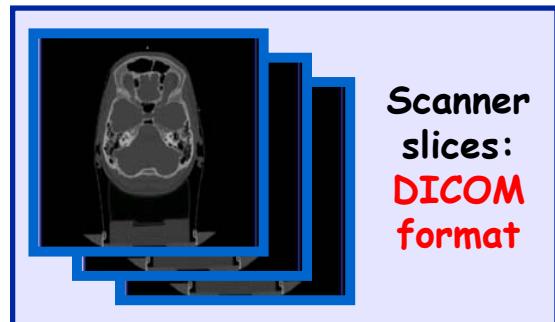
- **Format of the slices:**
512 X 512 X 1 pixels

- **Size of a voxel in the image:**
0,625 X 0,625 X 1,25 mm

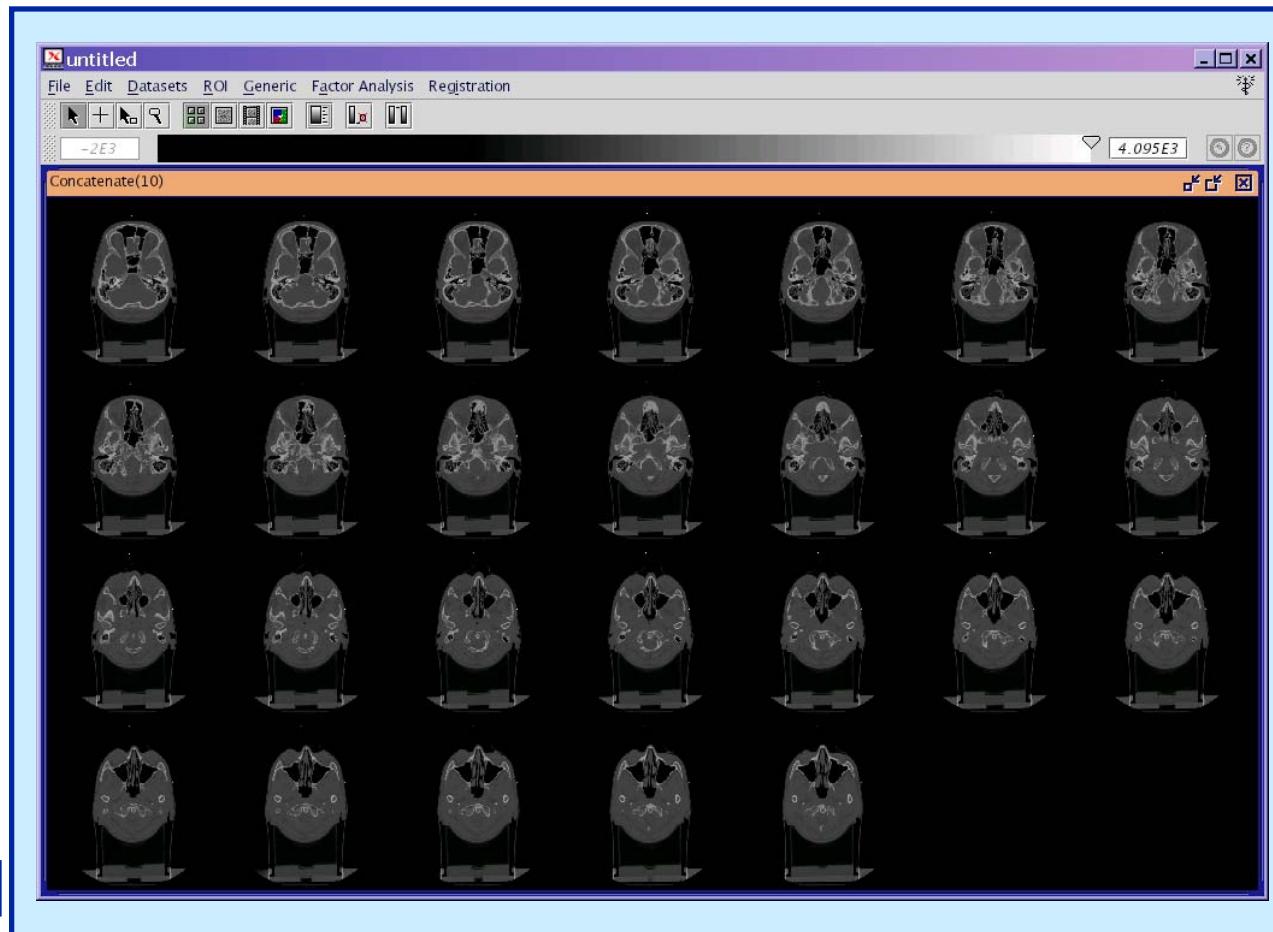
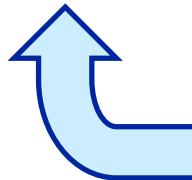


2°) Concatenate these slices in order to obtain a 3D matrix:

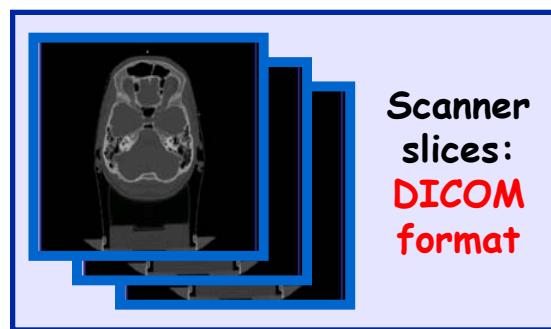
Pixies software



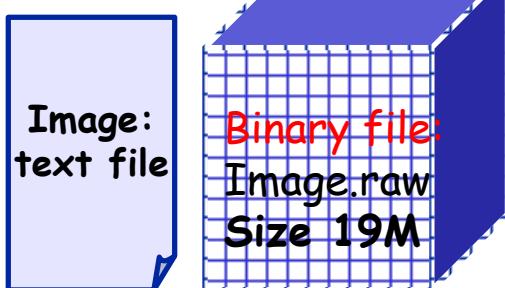
Concatenation



3°) Transform the DICOM format of the image into an Interfile format



Concatenation



Anonymisation

Pixies software

```
!INTERFILE :=
!imaging modality := nucmed
!originating system :=
!version of keys := 3.3
conversion program := Pixies developer
program author := Apteryx
program version := 1.09pre
!GENERAL DATA :=
!data starting block := 0
!name of data file := image.raw
!patient id :=
!study id :=
!GENERAL IMAGE DATA :=
!type of data := Dynamic
!total number of images := 38
!imagedata byte order := BIGENDIAN
number of energy windows := 1
!energy window [1] :=
!DYNAMIC STUDY (General) :=
!number of frame groups := 1
!Dynamic Study (each frame group) :=
!frame group number := 1
!matrix size [1] := 512
!matrix size [2] := 512
!number format := unsigned integer
!number of images := 38
!scaling factor (mm/pixel) [1]:= 0.625
!scaling factor (mm/pixel) [2]:= 0.625
!slice thickness (pixels):= 1.25
!number of bytes per pixel := 2
!number of images this frame group := 38
!image duration (sec) :=
!maximum pixel count in group := 4095.0
!END OF INTERFILE :=
```

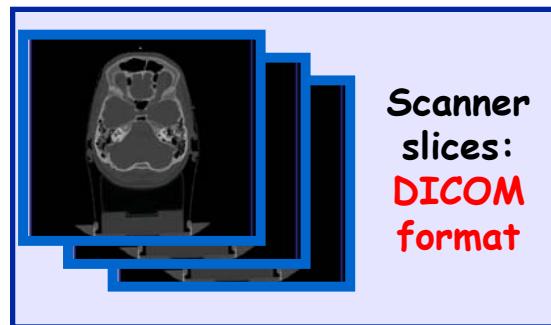
Binary image of
the scanner
slices

Size of the
matrix

Size of the
pixels

Number of slices

4°) Register and replicate the binary image on SEs:



Concatenation

Image:
text file

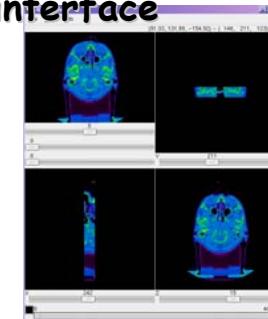
Binary file:
Image.raw
Size 19M



Replicate
Ifns on the
other SEs

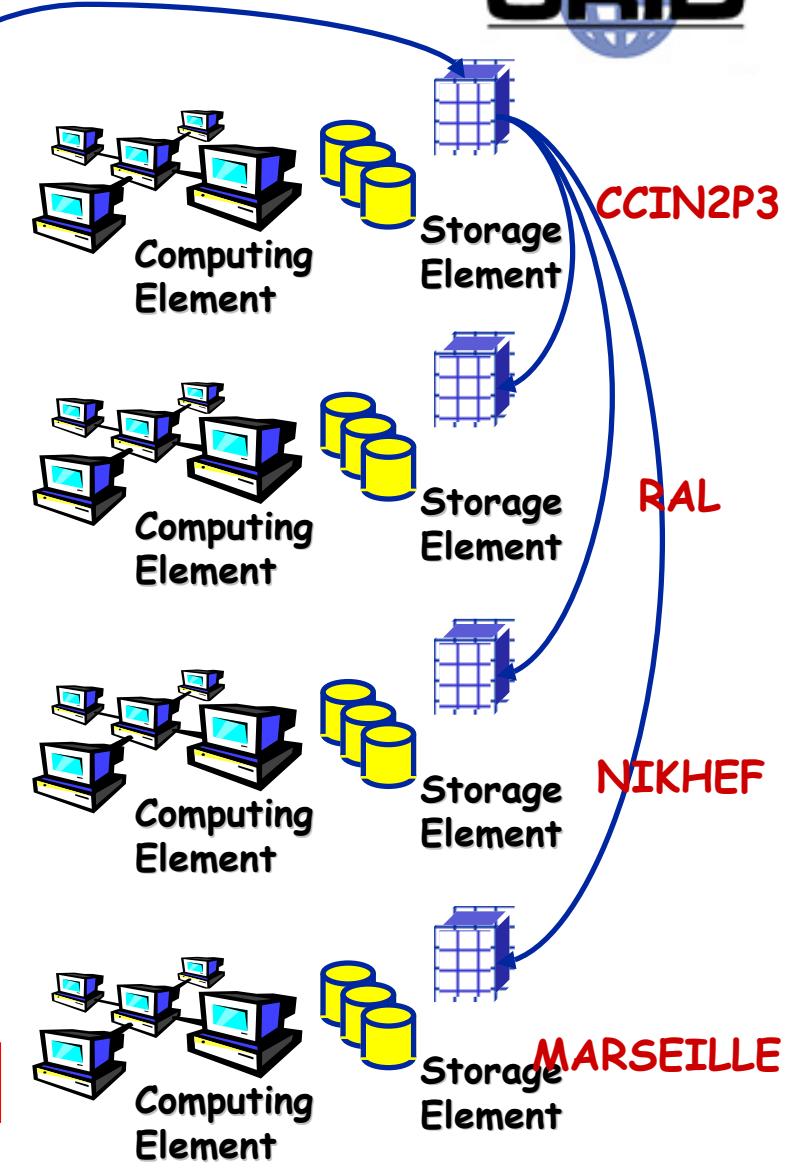


User interface



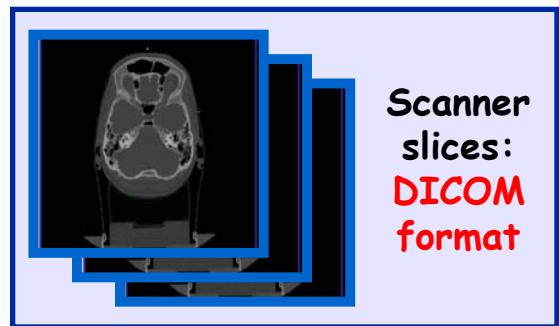
Visualization

Anonymisation



5°) Register the Ifn of an image:

- ◆ WP2 spitfire or local database



Concatenation

Image:
text file

Binary file:
Image.raw
Size 19M



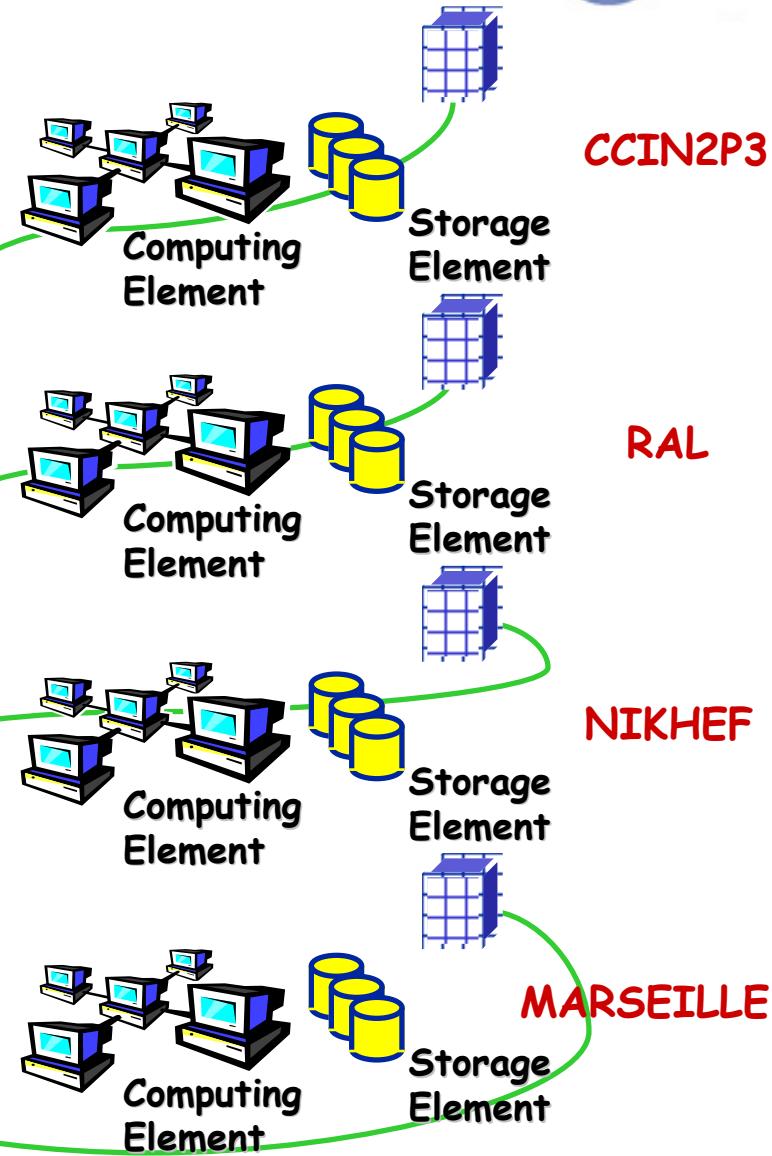
Query a Ifn
to the
database



User interface

Anonymisation

Database

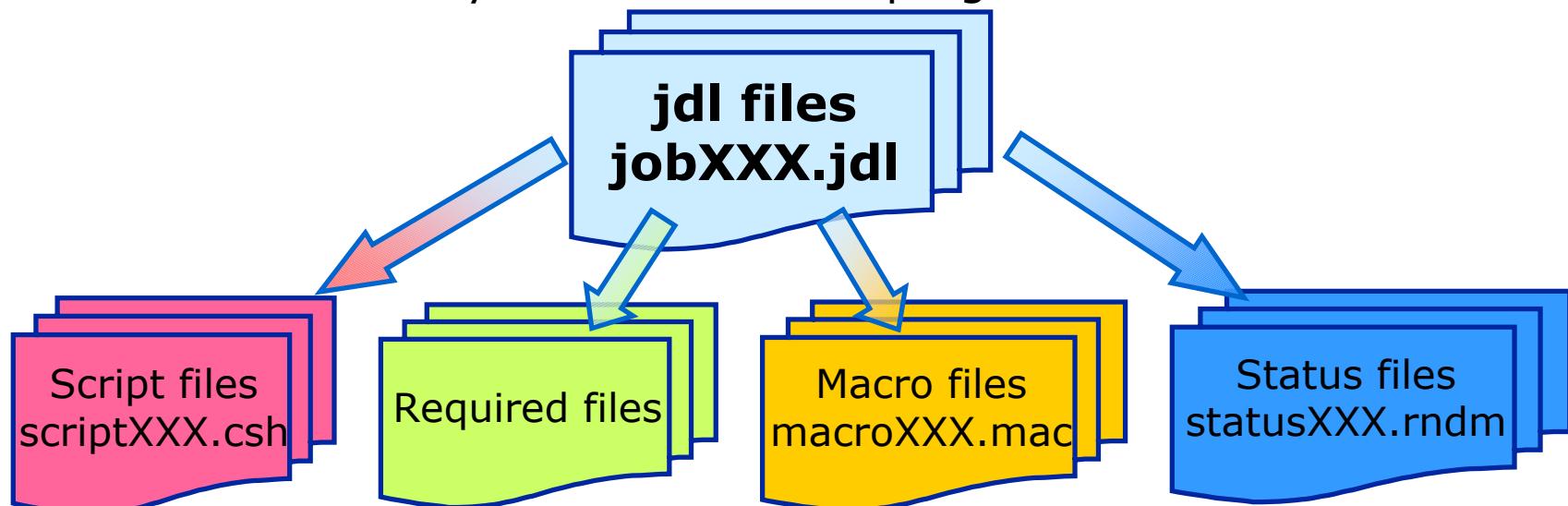


6°) Split the simulations:

JobConstructor C++ program



- ◆ A GATE simulation generating a lot of particles in matter could take a very long time to run on a single processor
 - So, the big simulation generating 10M of particles is divided into little ones, for example
 - ◆ 10 simulations generating 1M of particles
 - ◆ 20 simulations generating 500000 particles
 - ◆ 50 simulations generating 200000 particles
 - All the other files needed to launch Monte Carlo simulations are automatically created with the program.



A typical jdl file:

```

[VirtualOrganisation = "biome";
 Executable = "/bin/tcsh";
 Arguments = "./script000.csh";
 StdOutput = "std.out";
 StdError = "std.err";
 OutputSandbox = {
    "std.out",
    "std.err",
    "Brain_radioth000.root"
};
 RetryCount = 3;
 InputData = "lfn:lmaigne_BrainTOT_demo";
 DataAccessProtocol = {
    "file",
    "gridftp"
};
 JobType = "normal";
 Type = "Job";
 InputSandbox = {
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/script/script000.csh",
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/macro/macro000.mac",
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/status/status000.rndm",
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/required/prerunGate.mac",
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/required/rangeInterfile2.dat",
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/required/CJP_BrainTOT",
    "/afs/cern.ch/user/l/lmaigne/JOBS/jobGate_5/required/GateMaterials.db"
};
 rank = (-other.GlueCEStateEstimatedResponseTime);
 requirements = (Member("GATE-1.0.0-3",other.GlueHostApplicationSoftwareRunTimeEnvironment)&&(other.GlueCEStatus=="Production"))
]

```

A typical script file:

```
#!/bin/tcsh

#Script de lancement de simulation Gate sur DataGrid
#Auteur :Lydia Maigne
#Date:
#Version :

#####
###Mise en place de l'environnement pour l'exécution de Gate#
#####

#get the LFN passed in arguments

#flist="$@"
#for lfn in $flist; do

#echo "Get File"
#edg-rm --vo=biome copyFile $lfn file://$PWD/image.raw
edg-rm --vo=biome copyFile lfn:maigne_BrainTOT_demo file://$PWD/image.raw

#list content of PWD
ls -l $PWD

#####
#Lancement de la simulation#
#####

eval `\$EDG_LOCATION/bin/edg-vo-env --shell=csh biome'
source \$BIOME_ROOT_DIR/gate_env_main.csh
setenv LD_LIBRARY_PATH \$LD_LIBRARY_PATH:\$BIOME_ROOT_DIR/gate/lib/root
\$BIOME_ROOT_DIR/gate/bin/Linux-g++/Gate macro000.mac
```

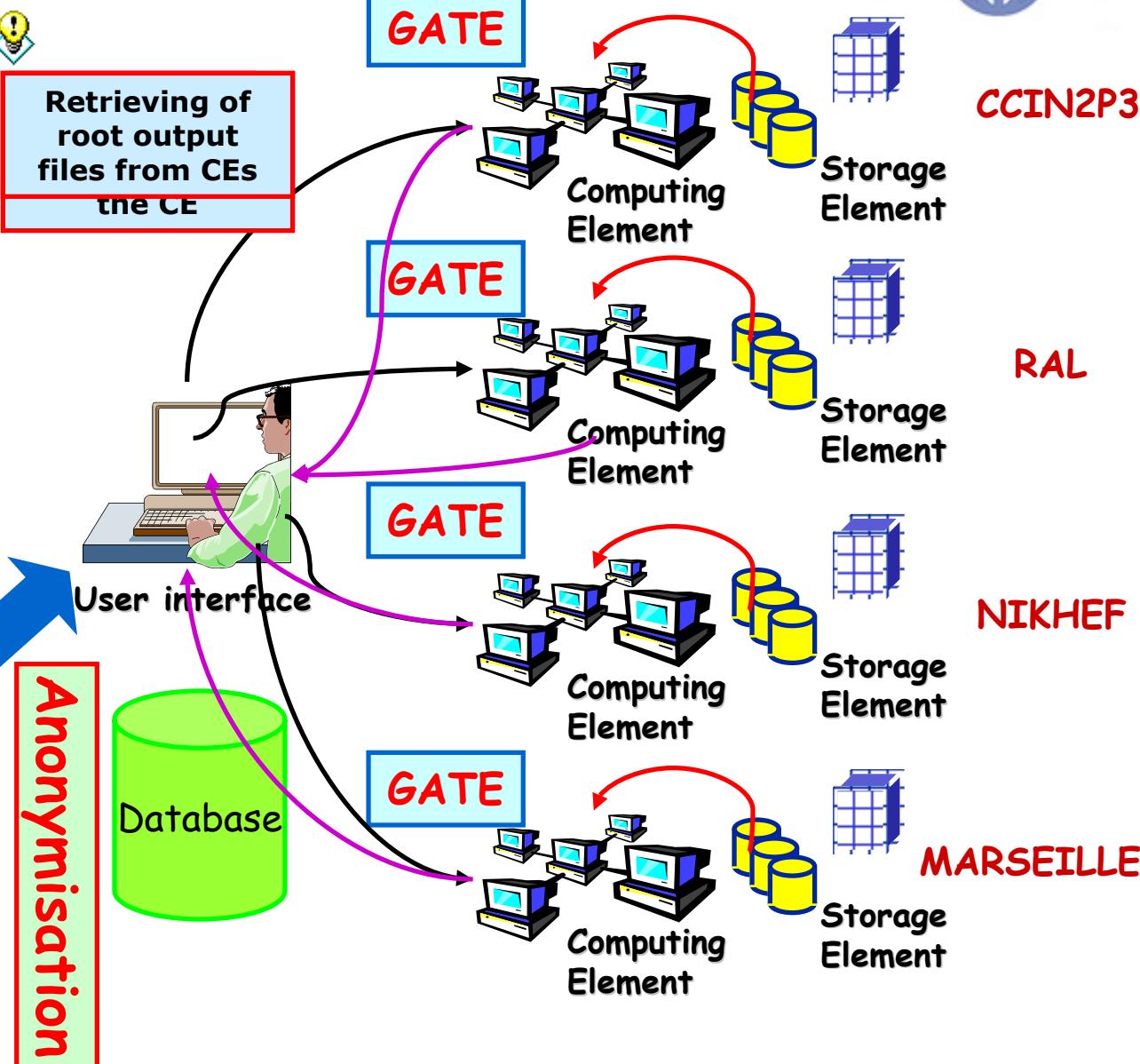
7°) Submission on the DataGrid:

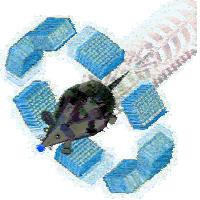
- ◆ GUI of WP1:



Concatenation

Image:
text file
Binary file:
Image.raw
Size 19M

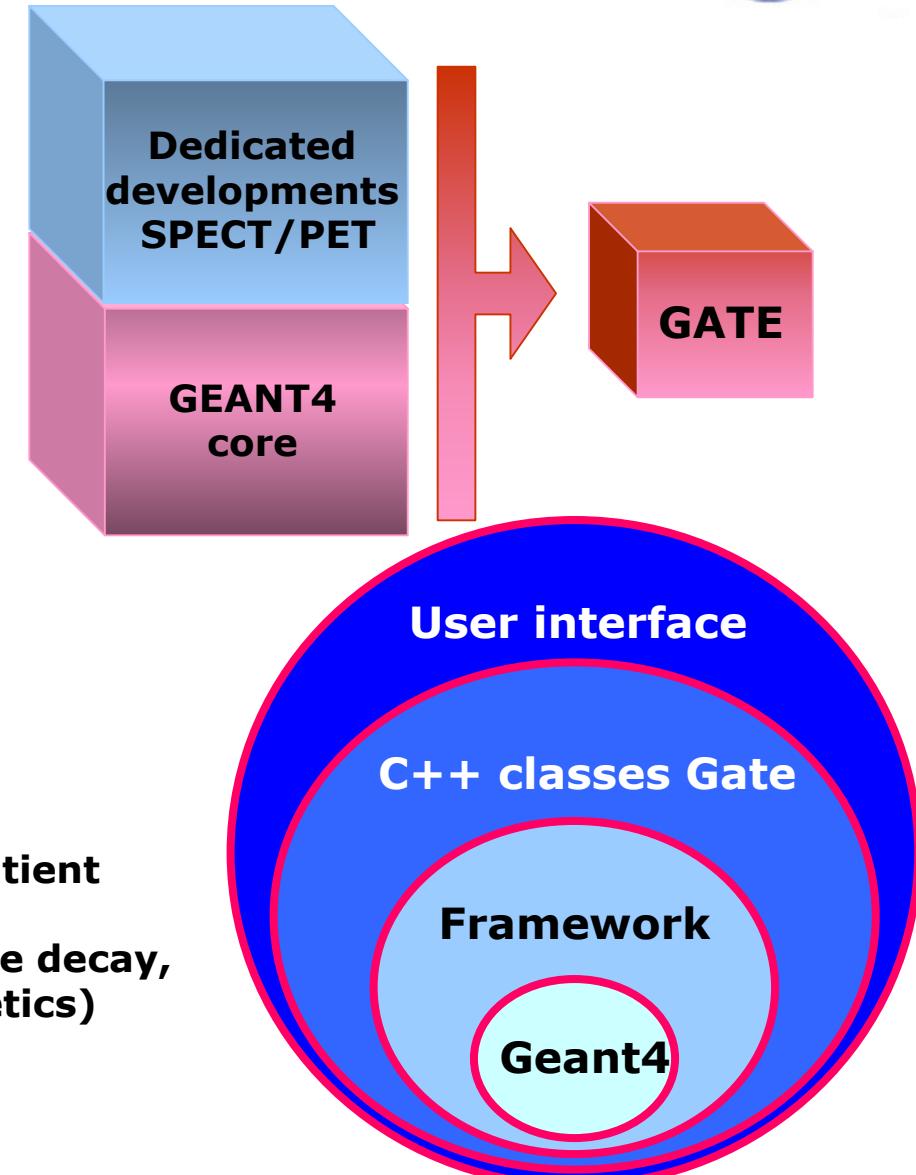




GATE: Geant4 Application for Tomographic Emission

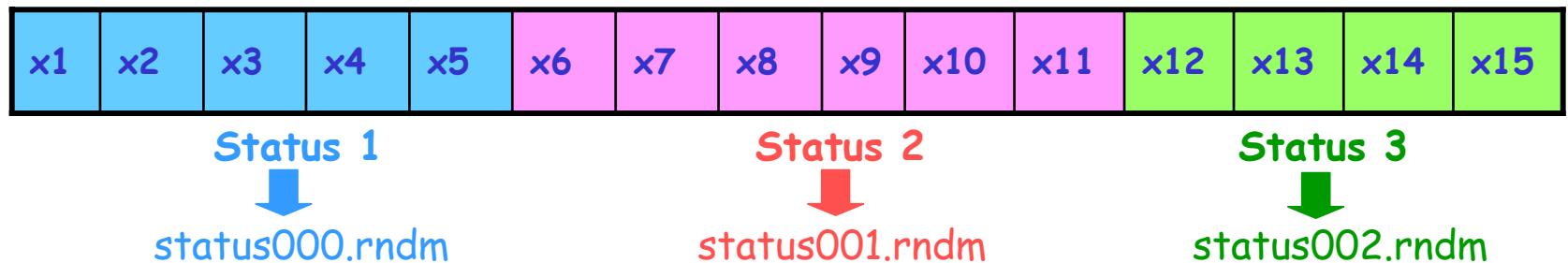


- Develop a simulation platform for SPECT/PET imaging
 - Based on Geant4
 - Enrich Geant4 with dedicated tools SPECT/PET
 - User friendly
- Ensure a long term development
 - Effort of shared development
 - Collaboration: OpenGATE
- ❖ Based on Geant4
 - C++ object oriented language
 - Reliable cross sections
- ❖ Framework: interface
- ❖ GATE development
 - modelisation of detectors, sources, patient
 - movement (detector, patient)
 - time-dependent processes (radioactive decay, movement management, biological kinetics)
- ❖ Ease of use
 - Command scripts to define all the parameters of the simulation



Parallelization technique of GATE

- ◆ The random numbers generator (RNG) in GATE
 - CLHEP libraries: HEPJamesRandom (deterministic algorithm of F.James)
 - ◆ Characteristics:
 - Very long period RNG: 2^{144}
 - Creation of 900 million sub-sequences non overlapping with a length of 10^{30}
 - Pregeneration of random numbers
 - ◆ The Sequence Splitting Method



- ◆ Until now, 200 status files generated with a length of 3.10^{10}

Each status file is sent on the grid with a GATE simulation

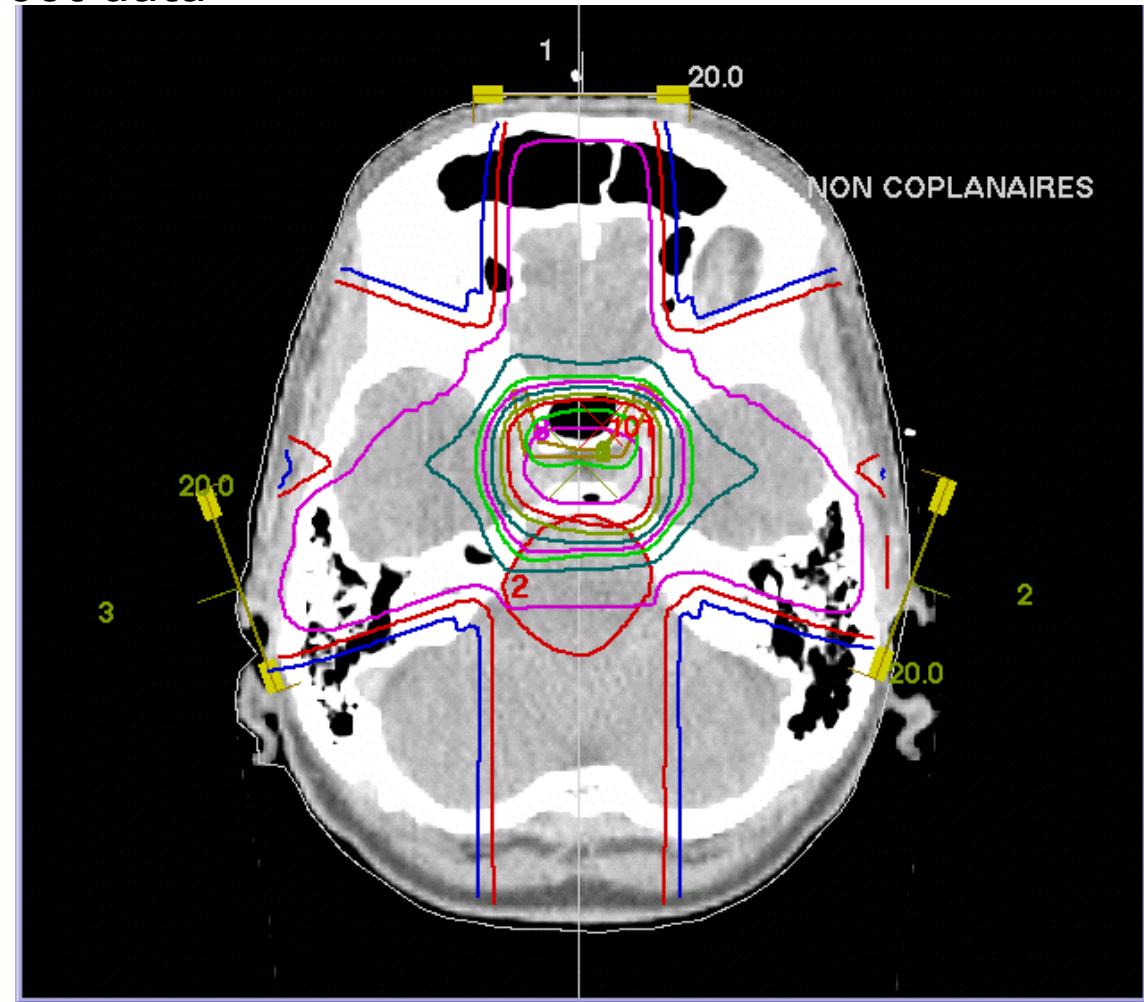
8°) Analysis of output root files

- ◆ Typical dosimetry:
 - Merging of all the root files
 - Computation of the root data

Brain_radioth000.root: **20 MB**
 Brain_radioth001.root: **20 MB**
 Brain_radioth002.root: **20 MB**
 Brain_radioth003.root: **20 MB**
 Brain_radioth004.root: **20 MB**
 Brain_radioth005.root: **20 MB**
 Brain_radioth006.root: **20 MB**
 Brain_radioth007.root: **20 MB**
 Brain_radioth008.root: **20 MB**
 Brain_radioth009.root: **20 MB**

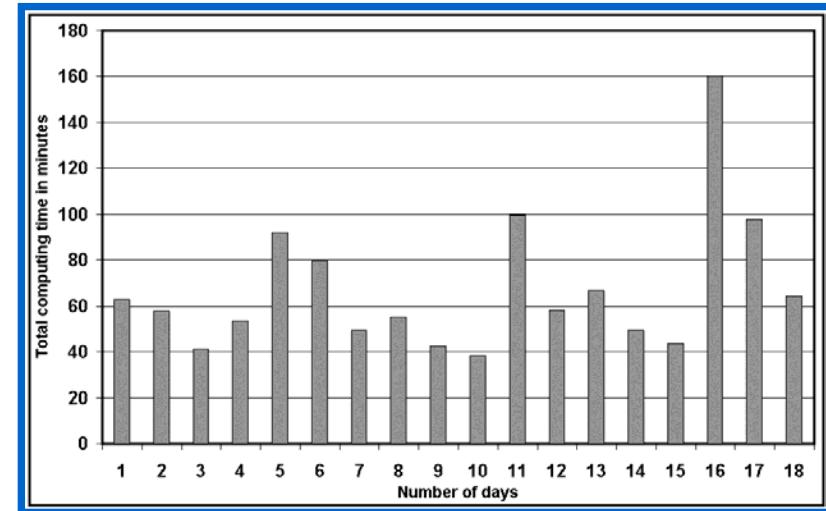
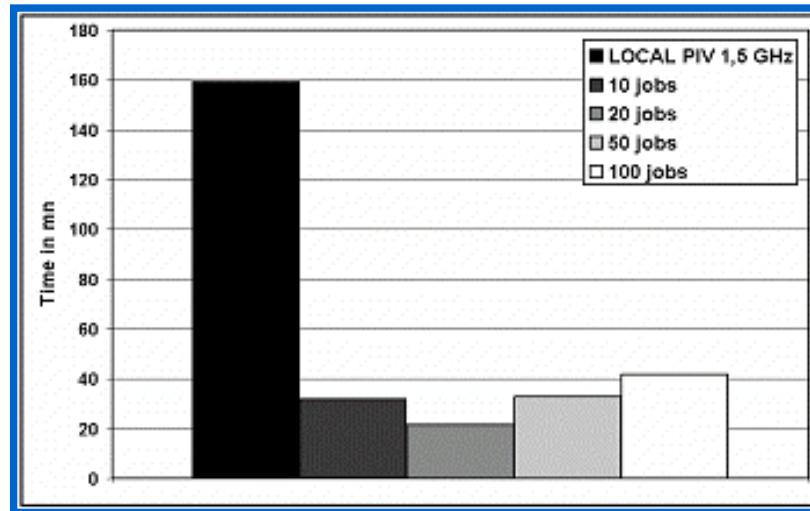
transversal view

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Conclusion and future prospects

- ◆ The parallelization of GATE on the DataGrid testbed has shown significant gain in computing time (factor 10)



- ◆ It is not sufficient for clinical routine
- ◆ Necessary improvements
 - Dedicated resources (job prioritization)
 - Graphical User interface

Acknowledgements

- ◆ WP1:
 - Graphical User Interface, JobSubmitter
- ◆ WP2:
 - Spitfire
- ◆ WP6:
 - RPMs of GATE
- ◆ WP8
- ◆ WP10:
 - 4D Viewer (Creatis)
 - Centre Jean Perrin
 - LIMOS
- ◆ System administrators
 - Installations on UIs