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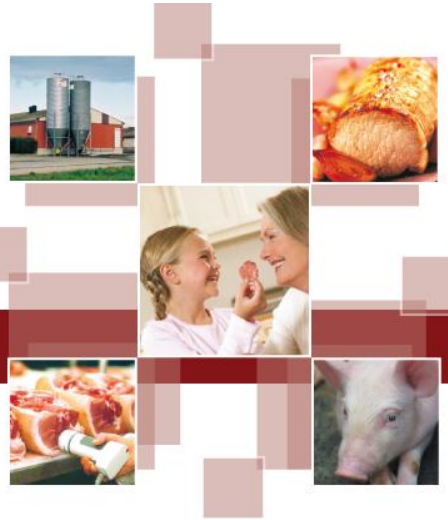

Software for automatic treatment of large biomedical Images Databases

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Context

- CT generates 512 Kb images
- Pig half-carcass with 3mm slice thickness => 450 images
- Pig half carcass data => 225 Mb
- Experiments with 200 or more half carcasses generate large amounts of images to analyze

Old way of analyzing (1)

- With Image J macros
  - Advantages :
    - Simple to use
    - On Windows (main OS in our institute)
  - Disadvantages :
    - Stack by stack ... (one “patient” at a time)
    - Lot of wasted time for large databases

Old way of analyzing (2)

- With C programs compiled with GCC on Linux
  - Advantages :
    - Can be fully automatic by designing loops
    - Calculation time reduced
  - Disadvantages :
    - Needs a relatively skilled code programmer
    - Generally needs renaming
    - Linux is not the main OS in the institute (double boot is needed)
    - Line of commands (terminal) interface...

Old way of analyzing (conclusion)

- None of these methods were really acceptable on a long term base
- Data management was also run in an old fashion way (Dicom images in folders created at each study)

Decision taken: to develop a specific software integrated in a Dicom images management platform

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Dicom images management (1)

- Our CT is mobile
  - In our experimental station in Romillé it is directly linked with our servers
  - Out of Romillé it is not
- Images are saved on a DCM4CHEE server via Dicom nodes
- Server queries are made with Kpacs from a computer
- Kpacs creates a virtual Dicom server

Dicom images data management (2)

- Based on Dicom nodes

CT scanner

Direct upload (Dicom node)

DCM4CHEE server in Le Rheu

Query and retrieve Kpacs

Upload with a virtual dicom node (kpacs)

Direct upload (Dicom node)

Laptop with KPACS

Desktop with KPACS for analysis in le RHEU

Initial objectives for the image analysis software

- User friendly
  - For non specialists
  - For advanced users too
- Dicom format compatible
- Evolutive (possibility to implement new analysis)
- On Windows (main OS in the institute)
- Relatively optimized

Initial objectives for the image analysis software (2)

- What we wanted
  - Open a Dicom image or a lot of Dicom images
  - Make a number of analysis operations on one or a lot of images
  - Give outputs as images or text files

- What we did not want
  - To be a viewer (the net is full of Dicom viewer)
  - To stop after the first image !!!
  - To ask the user for command lines

Development language

- Developed in C# with Visual Studio and Microsoft dot.net 2.0
  - Main development environment is used by our informatics team
  - More effective for looping (automatization) than Java
  - New image analysis module can be developed in C (Mathieu is not informatics engineer he only “knows” C)

Dicom manipulation

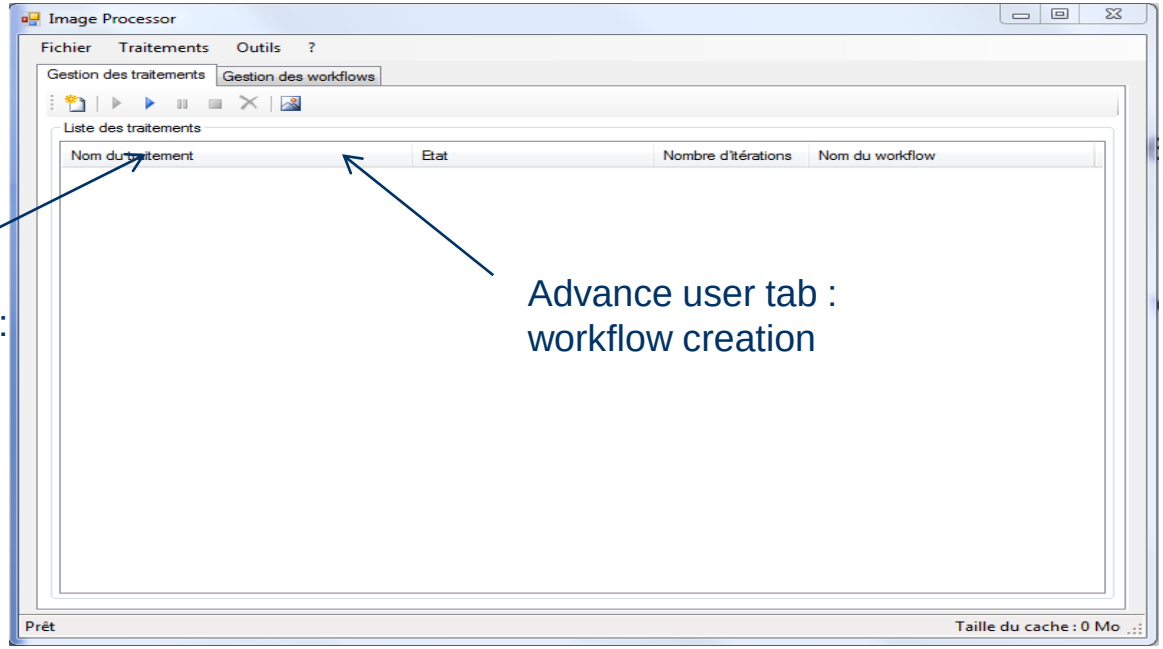
- Software needed to be able to directly work with Dicom format
- Clearcanvas framework was chosen for deal with Dicom format :
  - Maintained
  - Open source
  - C# compatible

Other development features

- After first steps of development we needed
  - More advanced mathematical possibilities than the one offered by C# language
  - 3D graphics for 3D reconstruction
- So the software is compatible with (and requires now)
  - Python xy library for the possibility to introduce python language for advance mathematical features
  - Slim DX library for 3D reconstruction

Software structure

- Around two main tabs:
  - The casual user tab : treatment
  - The image analysis advance user tab : workflow



Friendly user tab : treatments

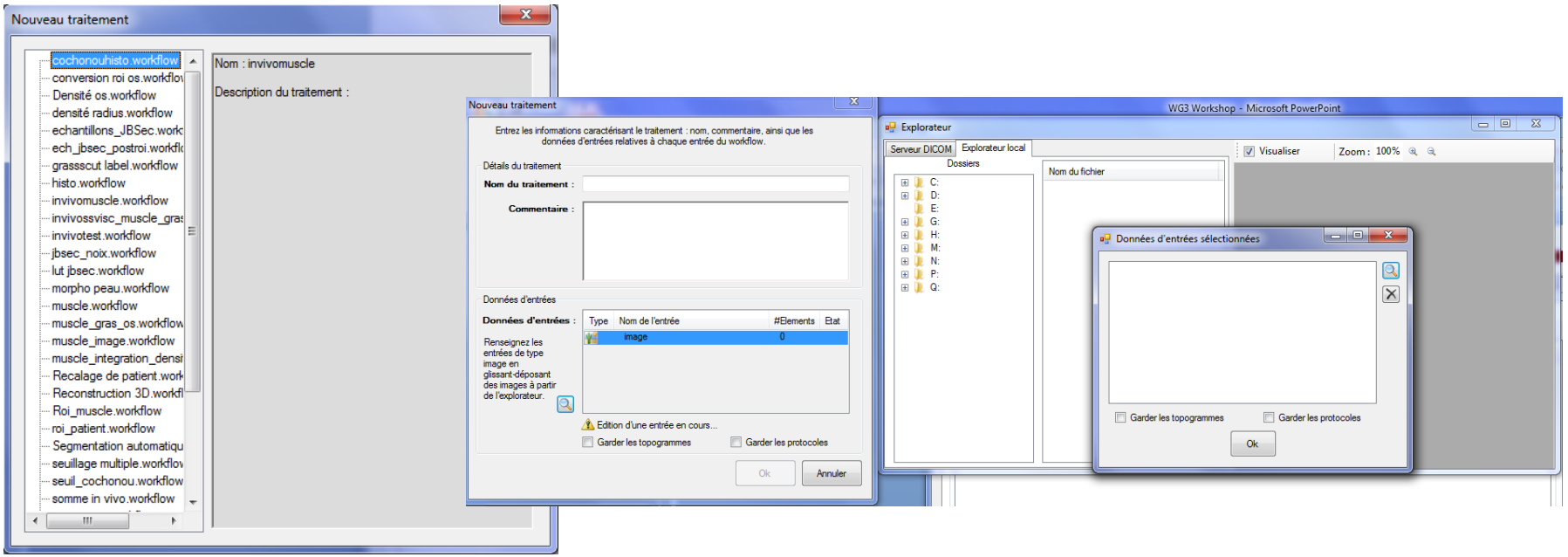
Advance user tab : workflow creation

Software structure

- The “treatment” tab
  - Allows to choose which analysis will be done (workflow)
  - Then choose the different inputs (image, value)
    - Images or “patients” (set of images) can be dragged and dropped from an explorer like window
    - The inputs can be iterated, indeed if a workflow takes an image as input and if n images are dragged and dropped in the image input zone then these n images will be analyzed successively
  - And launch the analysis

Software structure

- The “treatment” tab



Workflow choice

Inputs choice

Software structure

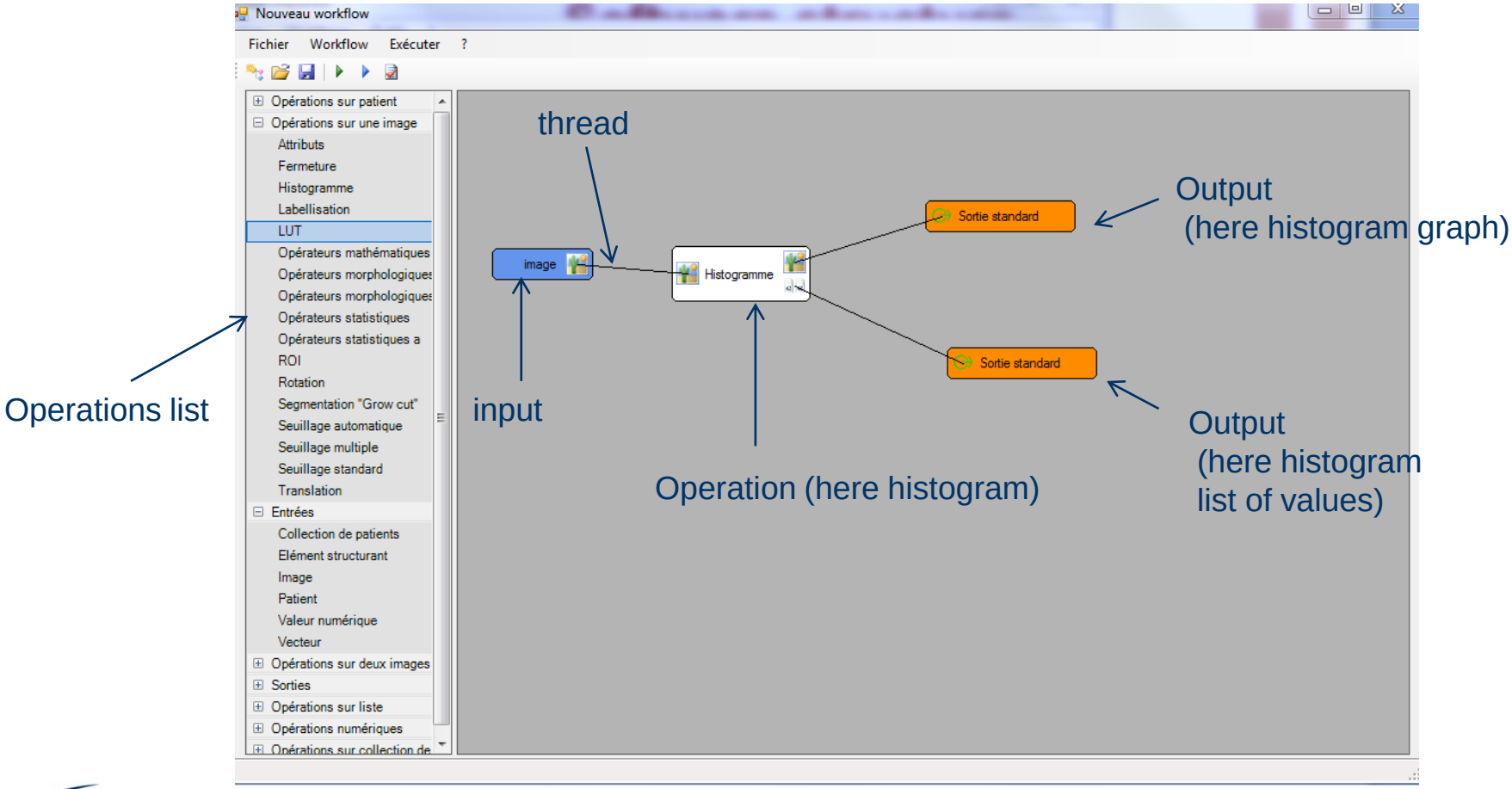
- The “workflow” tab
  - Allows to graphically design a new analysis scheme (“workflow”)
  - The creation consists in choosing inputs, operations and outputs
  - Inputs are generally images or group of images (patients) and other inputs that can be necessary to an operation (values, structural element, list)
  - Operations are data manipulation already developed in the program
  - Output(s) are generic and depends on the “last” operation(s), it can be images or values

Software structure

- The “workflow” tab
  - Graphic designed
    - Operation are represented as white “bricks” with outputs and inputs anchors
    - Workflow inputs are in blue brick with only outputs anchor
    - Workflow outputs in orange with only inputs anchor
    - The workflow is designed by linking with a thread the different outputs anchors with inputs anchors

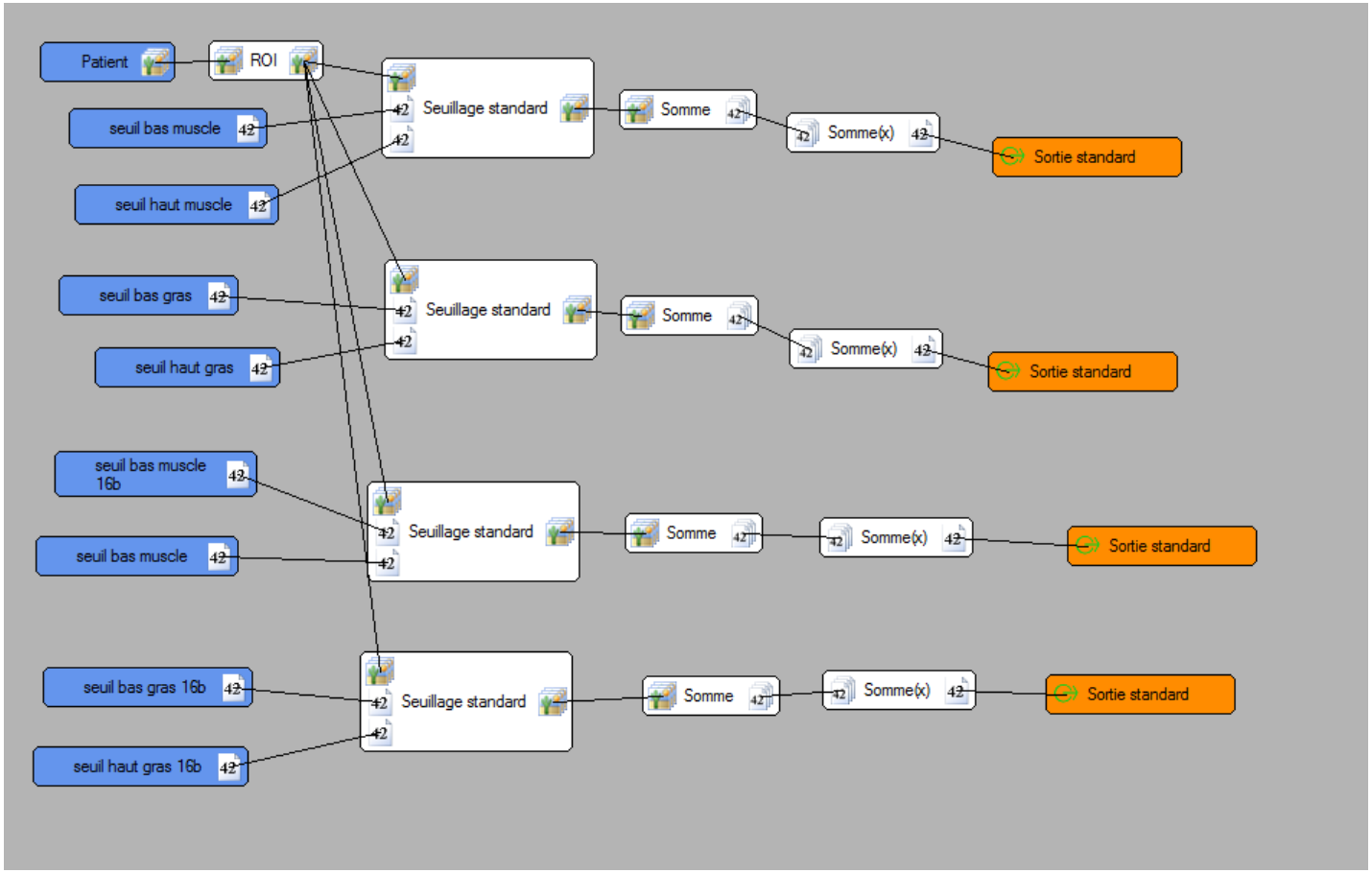
Software structure

- The “workflow” tab



Software structure

- It is possible to create complex workflows



Operations

- Operations are all stored in dynamic libraries (DLL)
- New operations can be developed and implemented in the program as plug-ins
- If it makes sense, operations can become iterative
  - Iterate = to pass from a single input-output to a multiple input-output
  - For example: the operation of giving the mean of an image signal can become the operation of giving the means of several images signal

Example of Operations implemented (1)

- Inputs
  - Image
  - Patient (several images)
  - Numerical values ...
- Single image operations
  - ROI selection
  - Threshold (fixed and automatic)
  - Grow cut (growing seed segmentation)
  - Apply LUT
  - Statistical measurements
  - Mathematic morphology

Example of Operations implemented (2)

- Single image operations
  - Labelization
  - Histogram...
- Two images operations
  - Mathematical operations
- Patients operations
  - ROI selection
  - 3D reconstruction....

Execution

- Two executions are implemented
  - The first one is the “step by step” execution
    - Only available from the workflow tab
    - It executes each operation one after the other
    - It can be paused for workflow tests
  - The second one is the normal execution
    - It is a multi-agent execution
    - It allows highly parallelized execution and a better memory management

Conclusions

- The software is operational
- It is used for all the large analysis we had to run
- It is complementary with Image J (for visualisation and image format management) and turtleseg (for 3D semi manual segmentation)

Still need to work

- The software
  - has no official name (Image Processor until now)
  - is still in a sort of beta state (some bugs remain)
  - Is in French ....
  - Difficult to continue the development of new operations (lack of time)
  - Needs to install the cache on a SSD, because a lot of cache access is done due to dot.net limitation to 2 GB ram usage for a unique application
  - Is compiled on Visual Studio 10 and Microsoft dot.net 4.0 but not tested

Demo

- In vivo pig abdomen image
  - Removal of the table
  - Removal of the viscera
  - Histogram of the other tissues (muscle, fat and bone)

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Thank you

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