Through the forest of open source segmentation tools

Frederic Cervenansky

PRIMES
UNIVERSITE DE LYON

Creatis

What is Open-Source

Open source doesn't just mean access to **source code**

1 - Free Redistribution (no restriction from selling or giving away the software as a component)

2 - Source Code (as well as compiled form)

3 - Derived Works (copyleft license)

4 - Integrity of The Author's Source Code (users have a right to know who is the original author)

5 – Distribution of License (no need of a third license)

6 and more

What criteria to discriminate software?

Usability
Code Langage
Segmentation methods
Plugins – Extensions
Organ/structure specificity

Software	Organs specific	Code Language	Segmentation Methods	Plugins	Citations*
ImageJ	no	Java	Automatic	Yes	**723**
Fiji	No (Cell)	Java	Automatic	Yes	**1254**
Freesurfer	Brain	C++, bash	Automatic	no	**470**
ITK	no	C++	Automatic	Yes-no	**512**
Slicer3D	No (Brain)	C++	Manual- Automatic	Yes	**75**
FSL	Brain	C++, bash	Automatic	No	**690**
SPM	Brain	matlab	Automatic	Yes	**7574**
…	---	---	---	---	---

*: pubmed

JAVA

Bio-imaging

IMAGEJ

Plugins system
User friendly
2D and 3D limitation
No hierarchy in plugins

ImgLib (n-dimensional, repackaging, sharing improvement)

Fiji

Marching
Learning
Squassh
Level Set
Graph Cut
Bad Indexation: **dithering** as segmenation tool

IMAGEJ2

KMeans Clustering
Maximum Entropy Threshold
Maximum Multi Entropy Threshold
Seeded Region Growing
Snake.

Icy

KMeans Color Quantization
Color Picker
Threshold
Active Contours
Texture
HK-Means
Active Cells
Toolbox

Organ specific

FreeSurfer
- **F**ully automatic
- **A**llow to restart at divergent steps.

FSL
- **F**ully automatic
- **C**atalog of tools
- **B**ET (Brain Extraction)
- **F**AST (GM and WM automated Segmentation).

Both available through VIP

SPM
- **M**odified gaussian mixture model
- **N**eed a matlab license.
- **S**everal extensions available

BrainVisa
- **P**ipeline of independant features

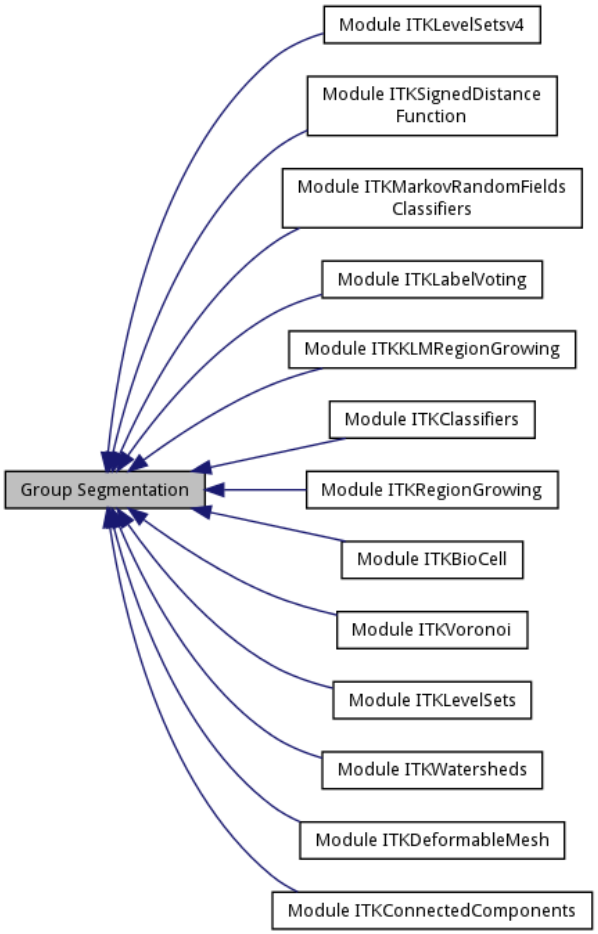
Nypipe
- **U**niform Python API for Freesurfer, FSL and SPM

Medical Imaging

C++

ITK

Features growing
Dashboard
Large community
Open Science => **200** papers concerning ITK, 10% moved to the toolkit.



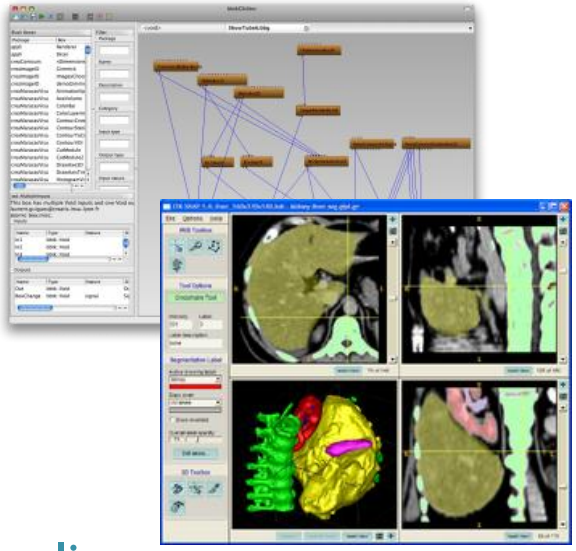
N-dimensional
Many data readers
13 segmentation subgroups
Nightly Dashboard

Medical Imaging

ITK

Slicer3D MITK Gimias CreaTools MedInria MevisLab ITK-SNAP NiftSeg

Common to all



- **M**anual Segmentation
- **H**idden Markov random field model and associated Expectation-Maximization algorithm.
- **A**ctive Contours
- **F**riendly (or not) interface. Interactive Pipeline
- **E**ach framework has its own specificity (VTK link, GPU based, …)
- **M**ore or less large community

Medical Imaging

ITK

Expectation Maximization with the use of atlases (**Brain**)

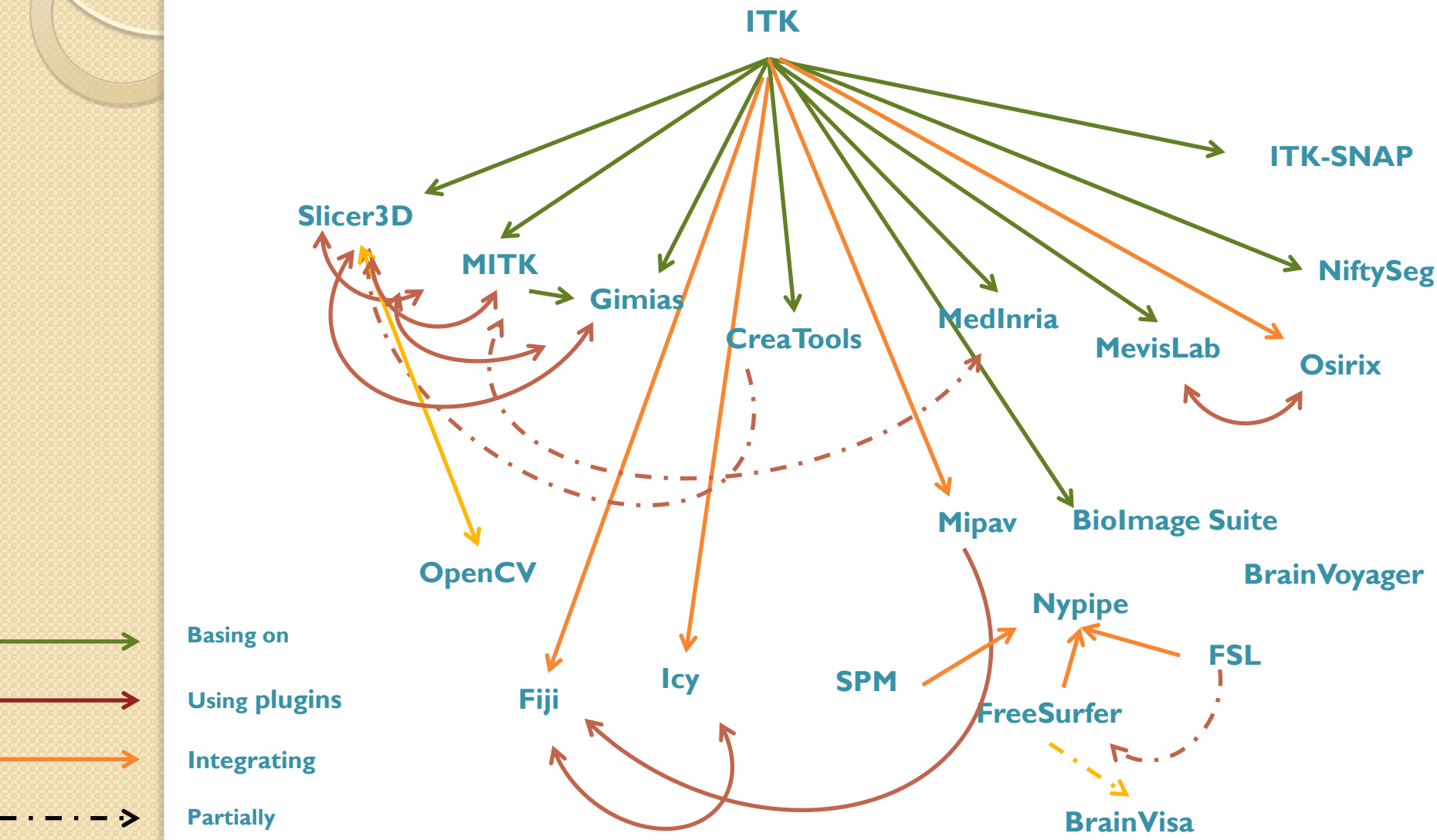
Level-set (**Vascular Tree**)

Cellular automata

Allow annotation and links with specific axonomy/ontology

AppStore for extensions

Interoperability issues

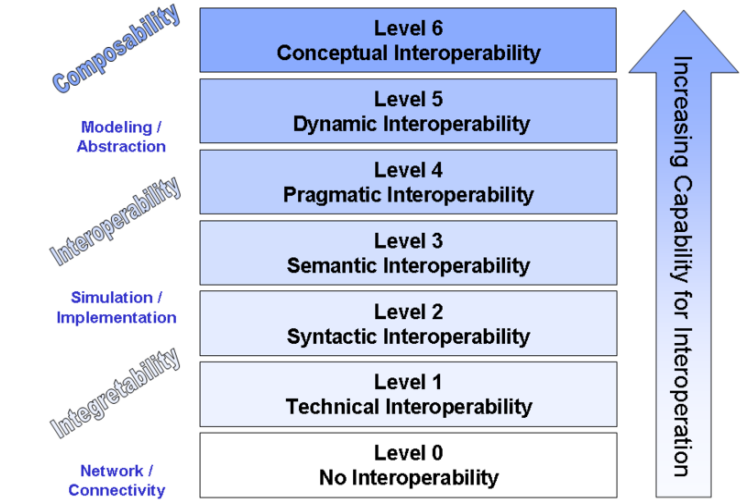


Interoperability : Workflows

Knime

Improving integration and sharing of segmentation methods.

Fostering interoperability issues



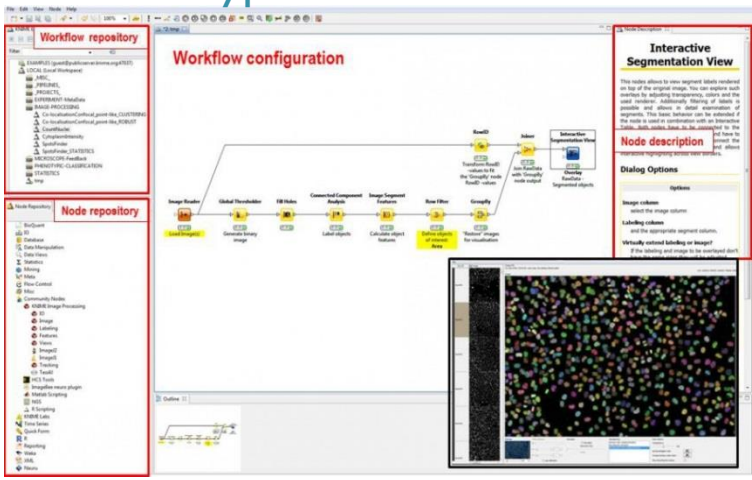
Levels of Conceptual Interoperability Model (LCIM)

Data analytics, reporting and integration platform.

Connections with OMERO, CellProfiler, Fiji, VTK

Own open API, based on Eclipse plugins mecanisms.

Data type – format.



Interoperability : Workflows

CommonTK – Command Line Plugins

Simple: xml description of parameters, C++ command line application using specific macro to parse input arguments

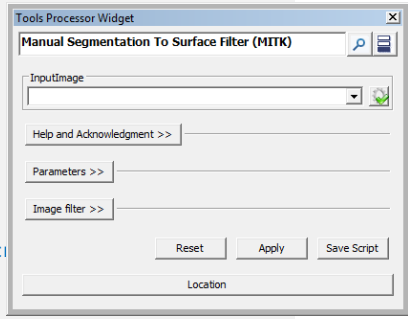
Specific data input/output, generic GUI (defined upon parameter type)

First tests (october 2012)

CLI	Gimias	Niftyview	Slicer	CTK cli	Creatools
niftyreg	2	2	2	2	-1
slicer cli (affine)	2	0	1	0	1
gimias cli (add)	2	0	1	0	1
ctk cli (blur)	0	0	2	2	-1

	Success	-1	Nothing
	Failure	0	Load
		1	Execute
OS: windows		2	Results

```
1.  <?xml version="1.0" encoding="utf-8"?>
2.  <executable>
3.    <category>Segmentation</category>
4.    <title>My Command Line Plugin</title>
5.    <description>A description of its
    functionality.</description>
6.    <version>0.1</version>
7.    <license>Open Source</license>
8.
9.    <parameters>
10.     <label>IO</label>
11.     <description>Input/output parameters</description>
12.     <image>
13.       <name>imageFileName</name>
14.     </image>
15.   </parameters>
16.
17.   <parameters>
18.     <label>Options</label>
19.     <description>Filter Options.</desc
20.     <integer>
21.       <name>paddingValue</name>
22.     </integer>
23.   </parameters>
24.
25. </executable>
```

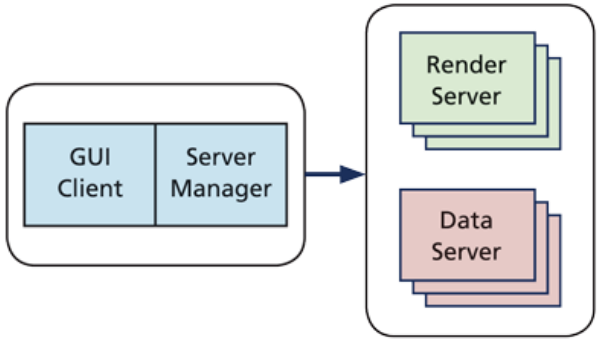


Emerging projects/ new soluces

To compute massive data (number, size) and massive amount of results, different startegies should be used:

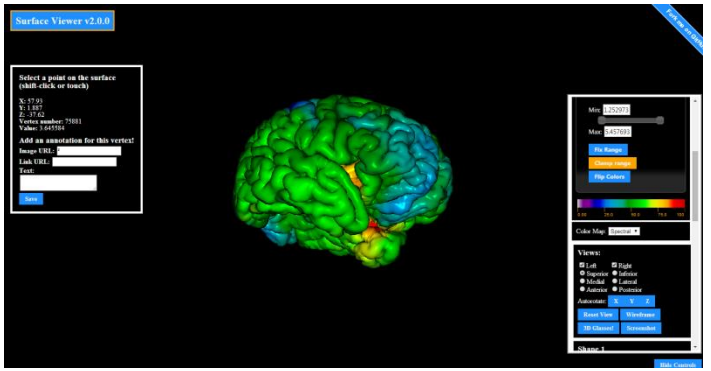
Parallelization

- Paraview (ITK, VTK) massive parallel computations (such as clusters or supercomputers)
- VIP, Cbrain, …



Web Client Server

- **W**ebDesk (graph cut, region growing)
- **B**rainBrowser
- **M**ni2tal
- **L**ONI Pipeline Web Start (PWS)



Conclusion

Large choice of tools

- **P**urpose
- **E**nd-user or developer
- **D**istribution
- **W**orkflow integration

Improvement of interoperability

Missing key points

- **L**icense
- **W**arehouse
- **D**ata reproductibility
- **T**axonomy- ontology

Links and references

ITK http://www.itk.org/

BrainSuite: http://neuroimage.usc.edu/neuro/BrainSuite

ITK-SNAP: http://www.itksnap.org/pmwiki/pmwiki.php

MeVisLab: http://www.mevislab.de/

NiftySeg http://cmic.cs.ucl.ac.uk/home/software/

Slicer: http://www.slicer.org/

TurtleSeg: http://www.turtleseg.org/

ImageJ http://imagej.net/docs/intro.html

ImageJ2 http://developer.imagej.net/about

Fiji http://fiji.sc/Fiji

Icy http://icy.bioimageanalysis.org/

ImgLib http://imglib2.net/

Creatools http://www.creatis.insa-lyon.fr/site/fr/creatools_accueil

Gimias http://sourceforge.net/projects/gimias/

MedInria http://med.inria.fr/

Knime http://www.knime.org

CommonTk http://www.commontk.org

SPM http://www.fil.ion.ucl.ac.uk/spm

FreeSurfer http://surfer.nmr.mgh.harvard.edu/

FSL http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/

BrainVisa http://brainvisa.info/index_f.html

BrainVoyager http://www.brainvoyager.com/

WebDesk http://www.creatis.insa-lyon.fr/site/fr/desk

Mipav: http://mipav.cit.nih.gov/

BrainBrowser https://brainbrowser.cbrain.mcgill.ca/

Mni2tal http://noodle.med.yale.edu/~papad/mni2tal/

LONI Pipeline Web Start http://loni.usc.edu/Software/webapps.php

Nypipe http://nipy.sourceforge.net/nipype/

Biological imaging software tools, K W Eliceiri, M R Berthold,I G Goldberg, L. Ibáñez, and al**, Nature Methods** 9, 697–710 (2012)