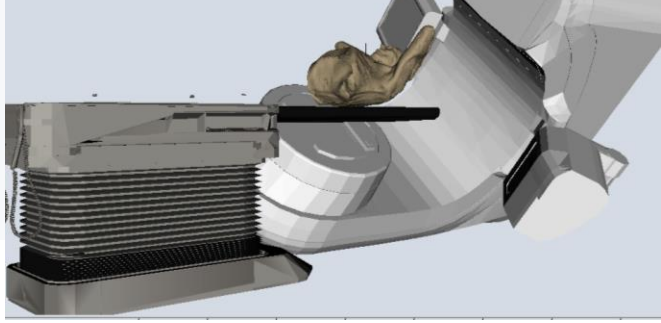
What Software Libraries Can You Use to Extract and Visualize Datasets ?

Eduard Schreibmann

Department of Radiation Oncology and Winship Cancer Institute, Atlanta, GA

Aims



Beyond Scripting: What's available out there ?

Familiarize yourself with software options to select the library that is best suited for your project.

- Data extraction versus algorithm development.
- Should I invest in getting familiarized with a tool ?

This presentation introduces a few software libraries that you may (or may not) use in your research projects.

Options at a Glance

- Vendor-provided scripts great for simple data-analytics type projects
  - RaySation, Varian ESAPI, Varian Velocity, Elekta IQScripts
    - **Provide direct access to your clinical system database, algorithms**
    - **Perfect for customized interfaces to your clinical system**
- Development Libraries
  - ITK, VTK, RTK, TubeTK
    - **Offered as code that has to be compiled for your computer configuration**
    - **Learning curve to understand the algorithms**
    - **Flexibility in creating your own algorithm**

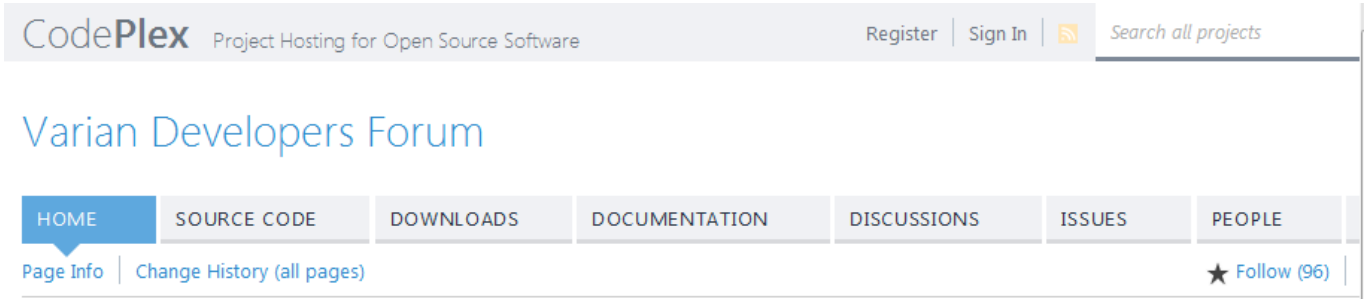
Existing functionality in your clinical system ?	**Use scripts.**
Want to build your own algorithm ?	**Look at other libraries.**

Scripts

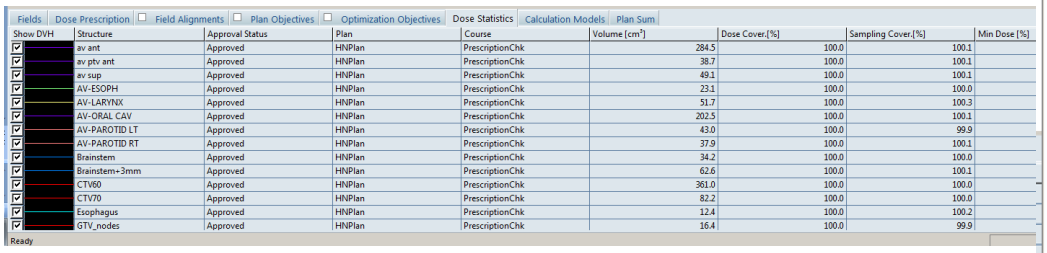
Or how to quickly customize your clinical system

Sample Scripting: ESAPI

C# code to access objects in Varian's database



Any value that you see in Eclipse can be accessed directly from code.

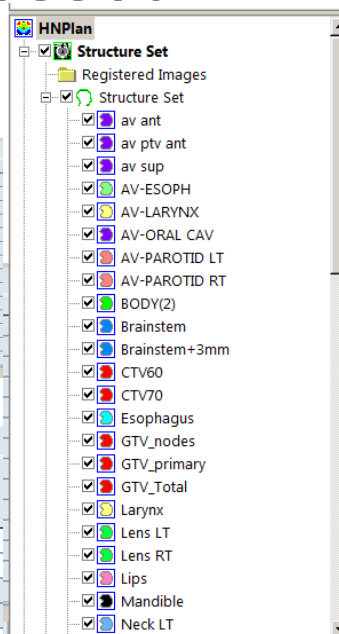


Show DVH	Structure	Approval Status	Plan	Course	Volume [cm³]	Dose Cover.[%]	Sampling Cover.[%]	Min Dose [%]
	av ant	Approved	HNPlan	PrescriptionChk	284.5	100.0	100.1	
	av ptv ant	Approved	HNPlan	PrescriptionChk	38.7	100.0	100.1	
	av sup	Approved	HNPlan	PrescriptionChk	49.1	100.0	100.1	
	AV-ESOPH	Approved	HNPlan	PrescriptionChk	23.1	100.0	100.0	
	AV-LARYNX	Approved	HNPlan	PrescriptionChk	51.7	100.0	100.3	
	AV-ORAL CAV	Approved	HNPlan	PrescriptionChk	202.5	100.0	100.1	
	AV-PAROTID LT	Approved	HNPlan	PrescriptionChk	43.0	100.0	99.9	
	AV-PAROTID RT	Approved	HNPlan	PrescriptionChk	37.9	100.0	100.1	
	Brainstem	Approved	HNPlan	PrescriptionChk	34.2	100.0	100.0	
	Brainstem+3mm	Approved	HNPlan	PrescriptionChk	62.6	100.0	100.1	
	CTV60	Approved	HNPlan	PrescriptionChk	361.0	100.0	100.0	
	CTV70	Approved	HNPlan	PrescriptionChk	82.2	100.0	100.0	
	Esophagus	Approved	HNPlan	PrescriptionChk	12.4	100.0	100.2	
	GTV_nodes	Approved	HNPlan	PrescriptionChk	16.4	100.0	99.9	

Ready

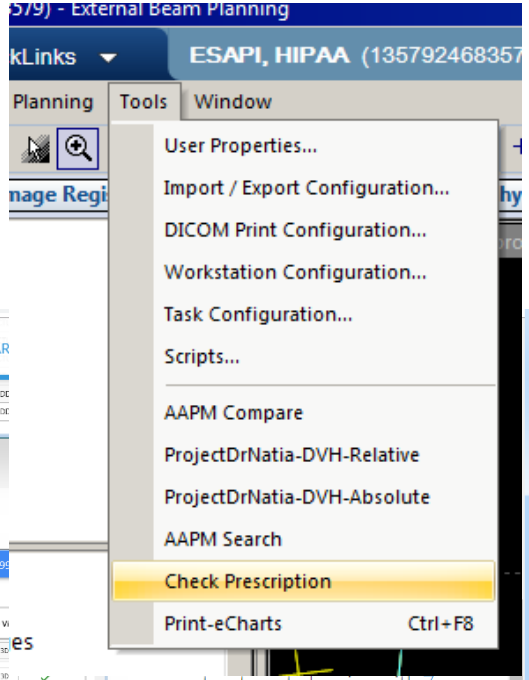
ose Prescription | Field Alignments | Plan Objectives | Optimization Objectives | Dose Statistics | Calculation Models | Plan Sum

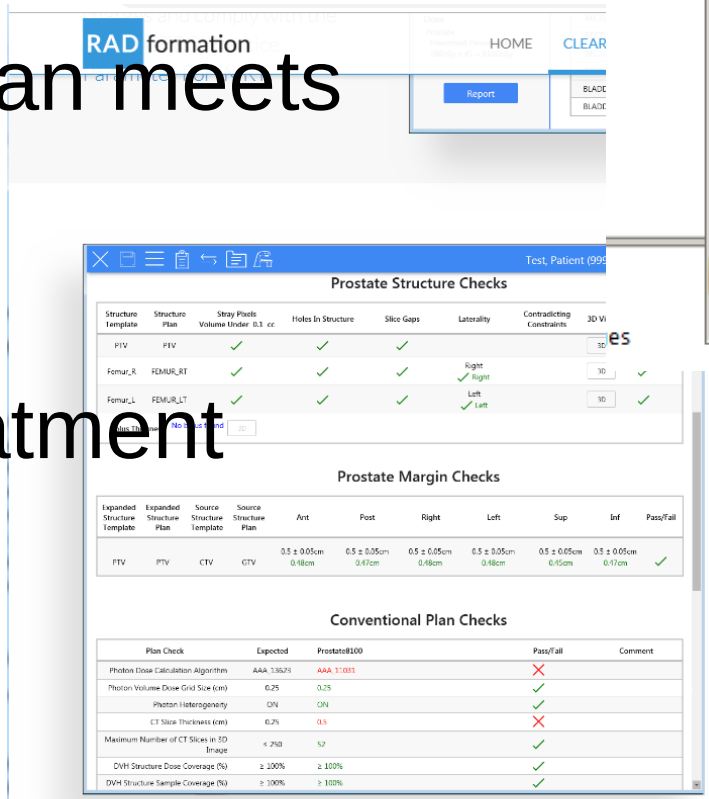
Field ID	Technique	Machine/Energy	MLC	Field Weight	Scale	Gantry Rtn [deg]	Coll Rtn [deg]	Couch Rtn [deg]	Wedge	Field X [cm]	X1 [cm]	X2 [cm]
RLAT kV	STATIC-I	TEC1 - 6X		0.000	Varian IEC	270.0	0.0	0.0	None	20.0	+10.0	+10.0
AP kV	STATIC-I	TEC1 - 6X		0.000	Varian IEC	0.0	0.0	0.0	None	20.0	+10.0	+10.0
01-CCW	ARC-I	TEC1 - 6X	VMAT	1.000	Varian IEC	179.9 CCW 180.1	10.0	0.0	None	15.0	+7.5	+7.5
02-CW	ARC-I	TEC1 - 6X	VMAT	1.000	Varian IEC	180.1 CW 179.9	350.0	0.0	None	15.0	+7.5	+7.5



Sample Scripts (ESAPI)

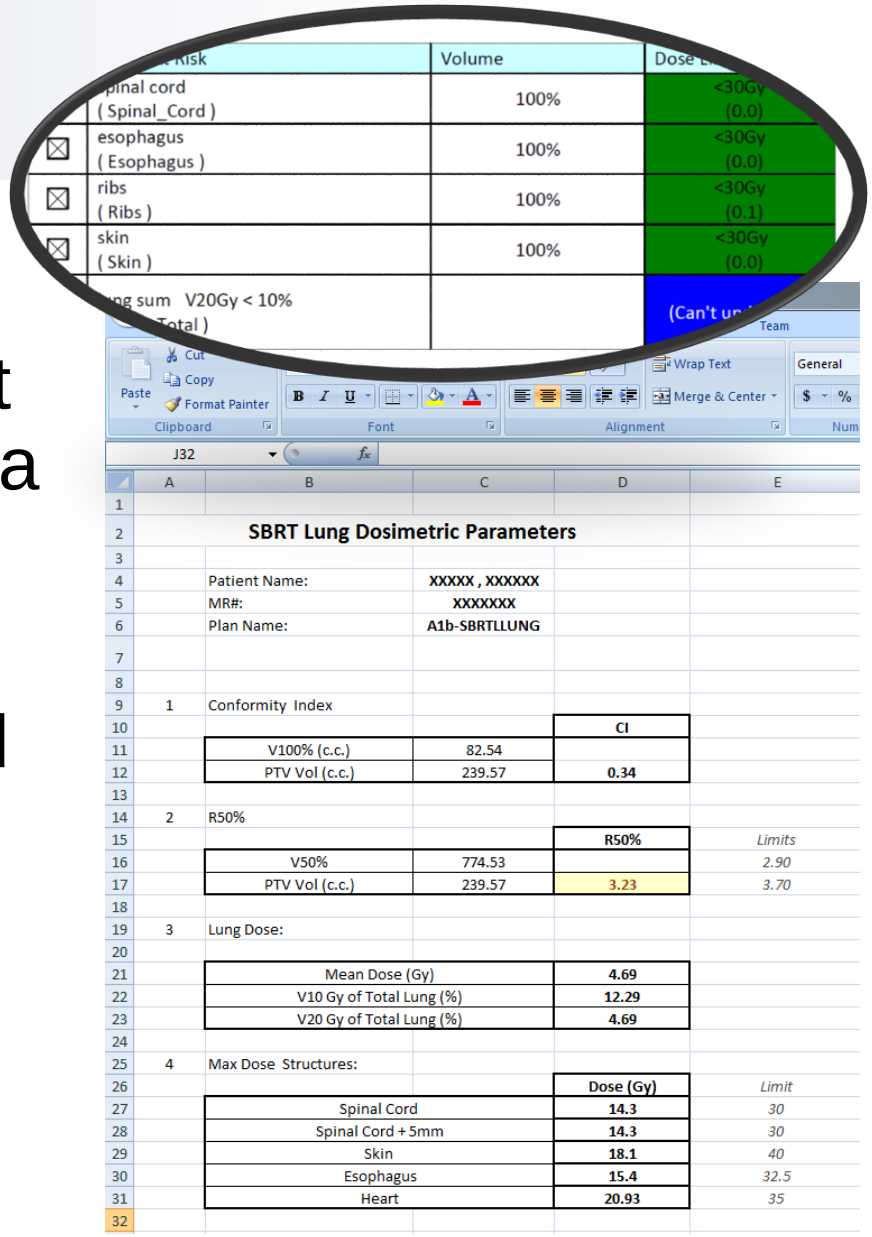
- Extracting patient statistics from database
- Checking if a plan meets constraints
- Automating treatment planning





Data Extraction

- Automated extraction of RTOG protocols, treatment logs, dose and contour data for research projects.
- Input : A list of patients and what to extract
- Output: An Excel file to interpret



Risk		Volume	Dose
	spinal cord (Spinal_Cord)	100%	<30Gy (0.0)
☒	esophagus (Esophagus)	100%	<30Gy (0.0)
☒	ribs (Ribs)	100%	<30Gy (0.1)
☒	skin (Skin)	100%	<30Gy (0.0)
	ng sum V20Gy < 10% Total)		(Can't up

Team

Cut
Copy
Format Painter
Paste
Clipboard
Font
Wrap Text
Merge & Center
Alignment
General
Num

J32

	A	B	C	D	E
1					
2		**SBRT Lung Dosimetric Parameters**			
3					
4		Patient Name:	**XXXXX , XXXXXX**		
5		MR#:	**XXXXXXX**		
6		Plan Name:	**A1b-SBRTLLUNG**		
7					
8					
9	1	Conformity Index			
10				**CI**	
11		V100% (c.c.)	82.54		
12		PTV Vol (c.c.)	239.57	**0.34**	
13					
14	2	R50%			
15				**R50%**	*Limits*
16		V50%	774.53		*2.90*
17		PTV Vol (c.c.)	239.57	3.23	*3.70*
18					
19	3	Lung Dose:			
20					
21		Mean Dose (Gy)		**4.69**	
22		V10 Gy of Total Lung (%)		**12.29**	
23		V20 Gy of Total Lung (%)		**4.69**	
24					
25	4	Max Dose Structures:			
26				**Dose (Gy)**	*Limit*
27		Spinal Cord		**14.3**	*30*
28		Spinal Cord + 5mm		**14.3**	*30*
29		Skin		**18.1**	*40*
30		Esophagus		**15.4**	*32.5*
31		Heart		**20.93**	*35*
32					

Scripts are perfect for batch extraction of patient statistics

EMORY | WINSHIP CANCER INSTITUTE

A Cancer Center Designated by the National Cancer Institute

Advantages\Disadvantages

- **Access:** Your code has direct access to the clinical data
- **Practical:** Easily integrates your with your clinical workflow.
- **Automation** of repetitive and tedious tasks best suited for scripting.

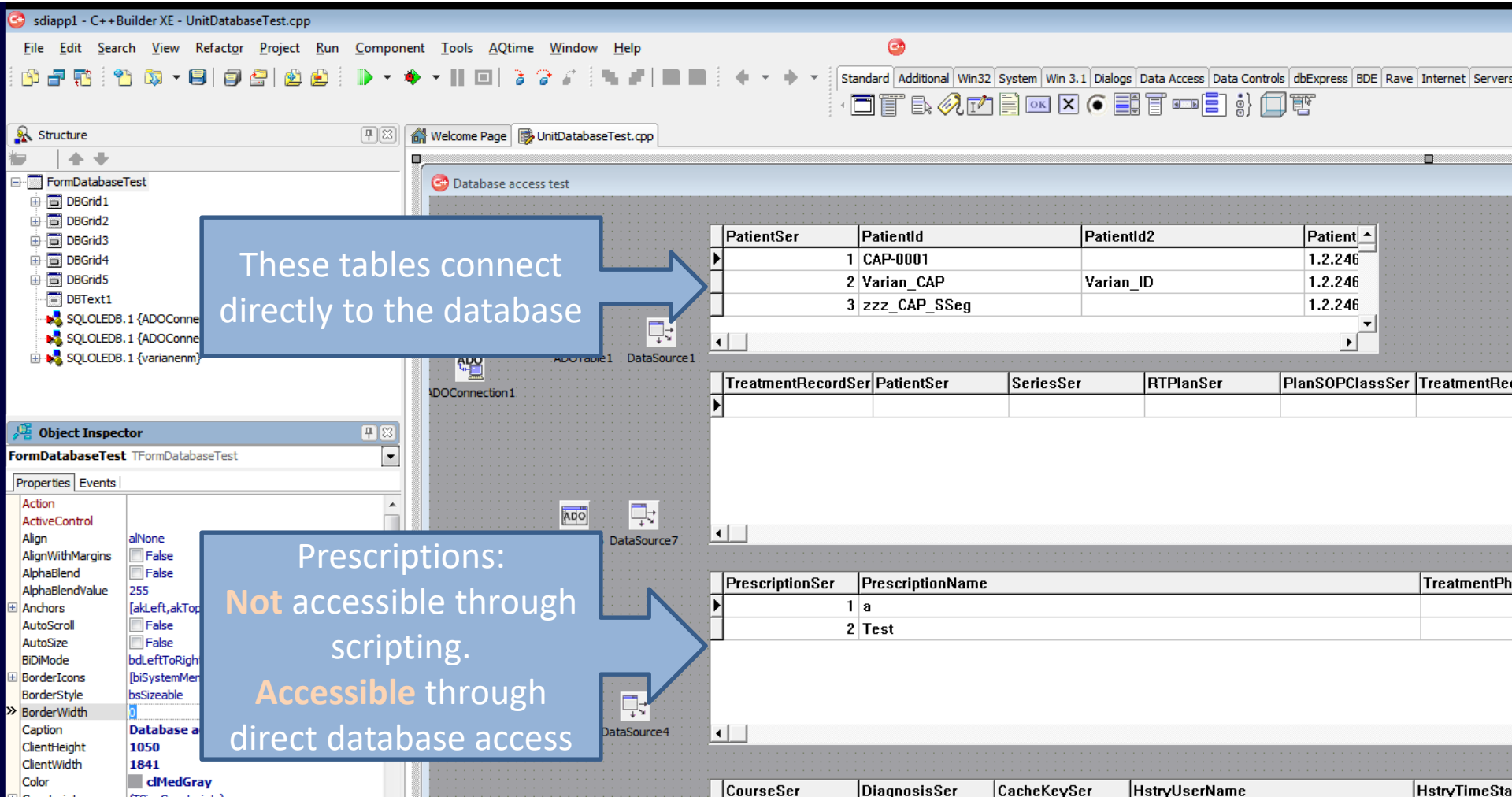
- **Limited functionality:** Only algorithms available in the clinical system can be used
- **Mostly Clinical:** Not a good tool for developing “your idea”.

Data Access

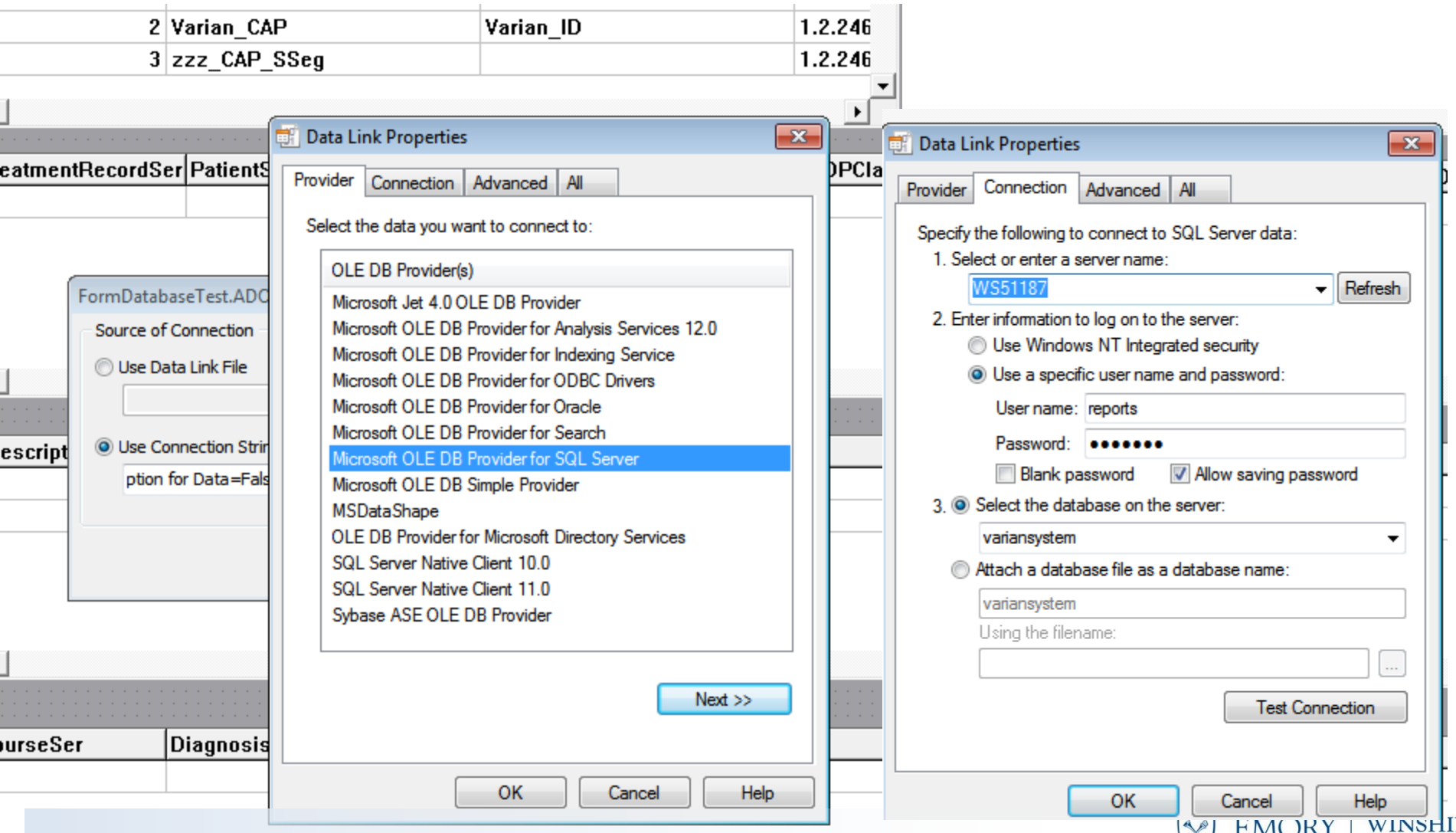
Or how to access any data in the database

Direct Database Access

Using C++ Builder to connect directly to the database. Other compilers can be used as well



Database Access Configuration

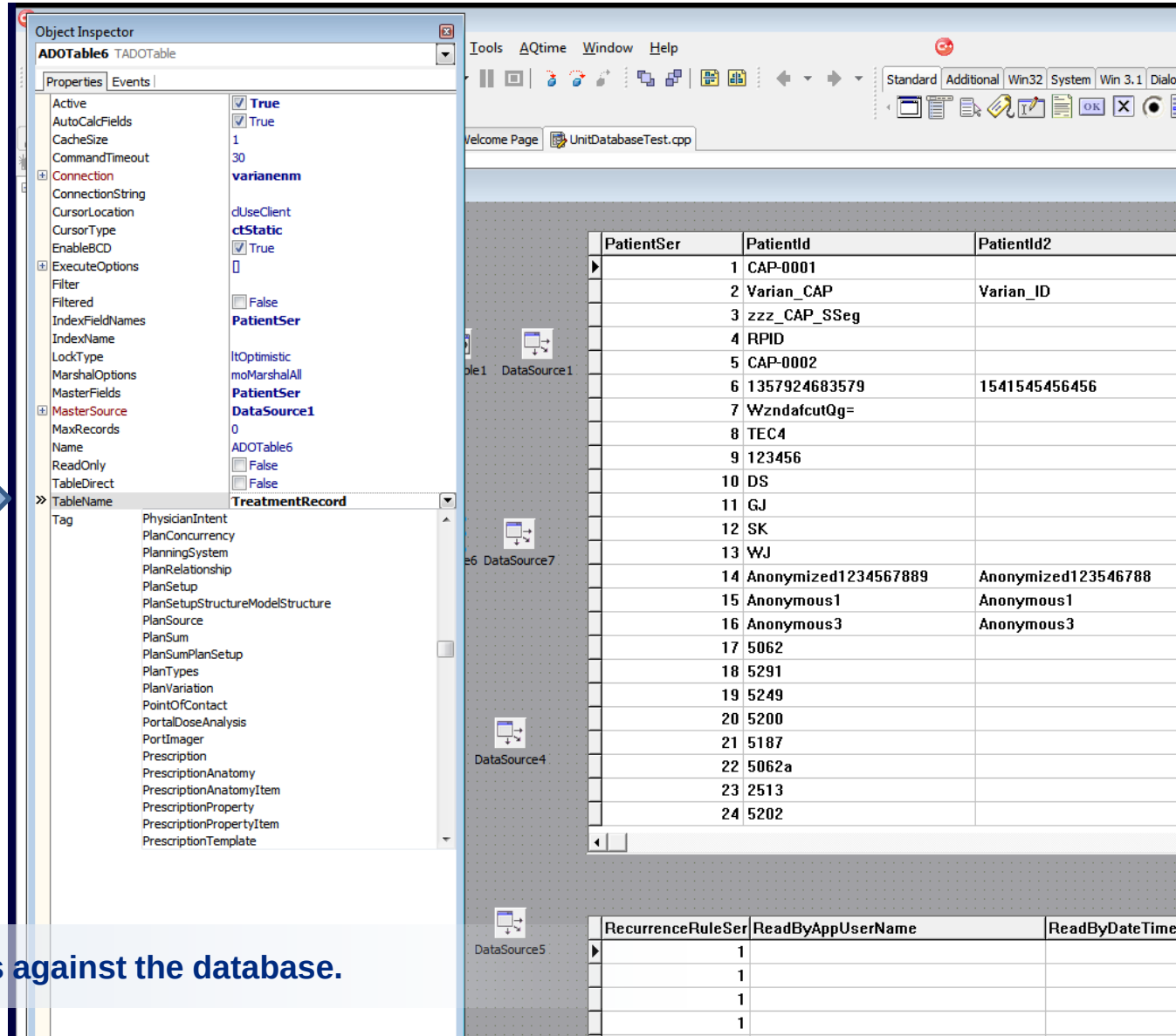


You may be able to get direct access to your vendor's database.

Database Access Without Code

Just select your data table from a list .

Zero lines of code.



You can also run SQL queries against the database.

What Can Be Accessed ?

Beyond Scripting

Or libraries to for developing your algorithm

Beyond Scripting

- **Open source:** Set of library offered as code. You can modify it in any way your like.
- **Don’t invent the wheel:** Set of standard building block performing common tasks that you can configure to your needs.
- **Feel free to modify:** You can change the code according to your project needs.

Here is the code. You have complete control.

Sample Library: ITK

Kitware

Search

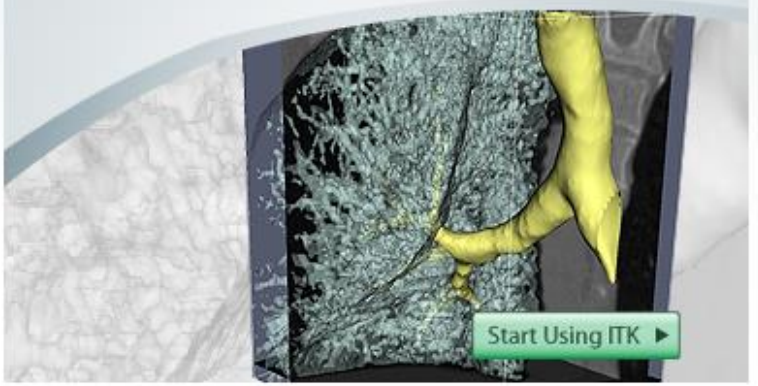
PROJECT RESOURCES HELP OPEN SOURCE

Welcome to the National Library of Medicine **Insight Segmentation and Registration Toolkit (ITK)**. ITK is an open-source, cross-platform system that provides developers with an extensive suite of software tools for image analysis. Developed through extreme programming methodologies, ITK employs leading-edge algorithms for registering and segmenting multidimensional data. The goals for ITK include:

- Supporting the Visible Human Project.
- Establishing a foundation for future research.
- Creating a repository of fundamental algorithms.
- Developing a platform for advanced product development.
- Support commercial application of the technology.
- Create conventions for future work.
- Grow a self-sustaining community of software users and developers.

ITK

ITK provides leading-edge segmentation and registration algorithms in two, three, and more dimensions; it is distributed as an open-source software package.



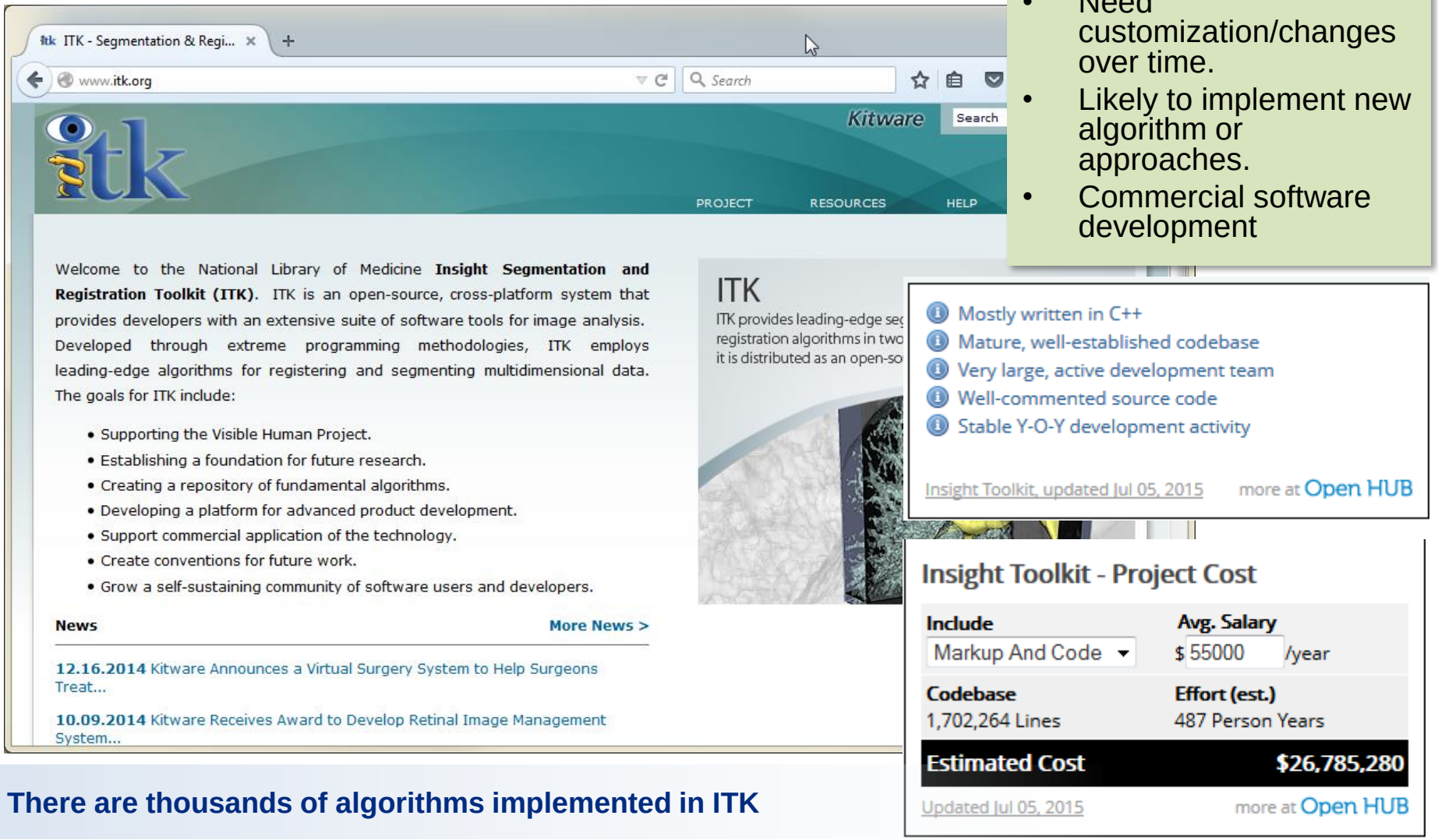
NSF NLM NIH NATIONAL CANCER INSTITUTE

NIMH NIDCD NIDCR

Many Algorithms Available

Best suited for :

- Larger research projects.
- Need customization/changes over time.
- Likely to implement new algorithm or approaches.
- Commercial software development



There are thousands of algorithms implemented in ITK

Scripting versus ITK

- **Scripts sample applications:**
  - I don’t like the buttons in the commercial application
  - My colleagues would need to print customized reports
  - Would like to do some analysis with the clinical data

- **ITK sample applications:**
  - I want to develop a new segmentation algorithm for my images.
  - Need a customized image registration for my images
  - Want to develop an image reconstruction algorithm.
  - Some insight into images

Scripting is easier to learn. ITK gives you more flexibility.

A family of libraries

VTK: Visualization Toolkit

ITK: Insight Toolkit

Visualize images

Visualize meshes

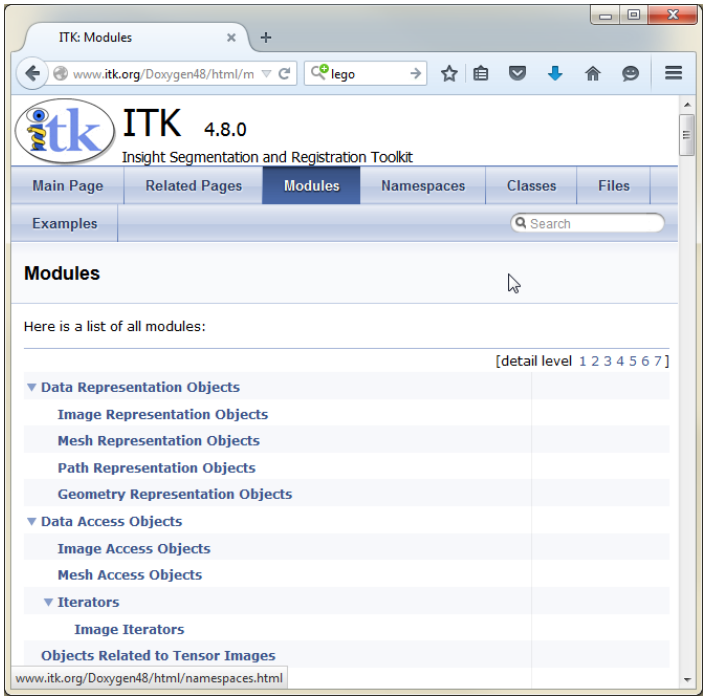
Rapid prototyping

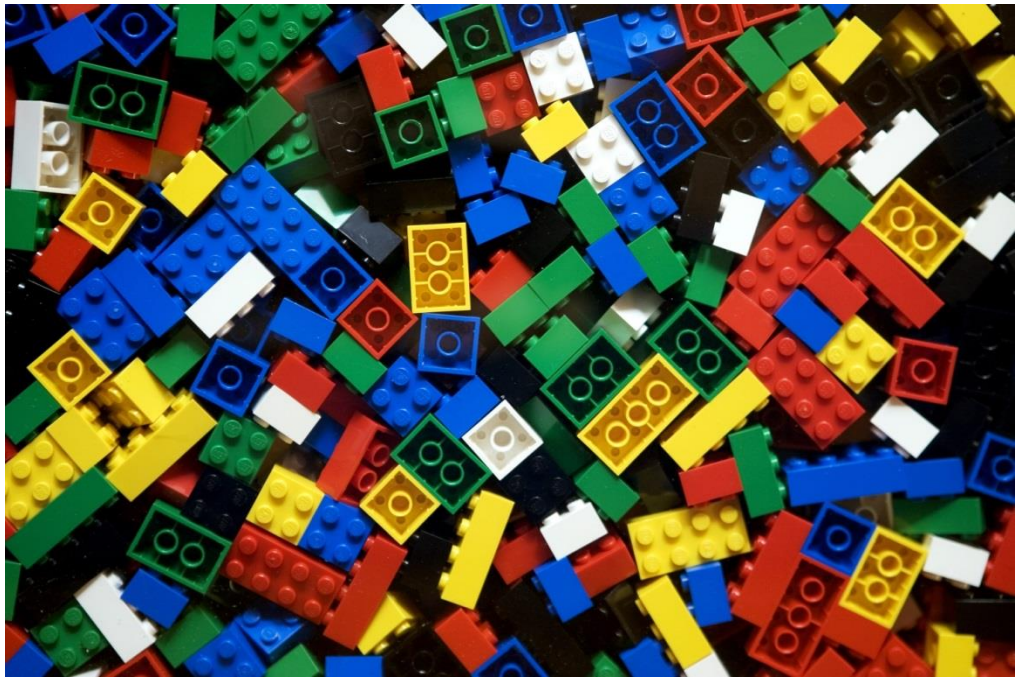
Multi-platform build system

All these libraries use same concepts and are connected.

Why I Like It ?

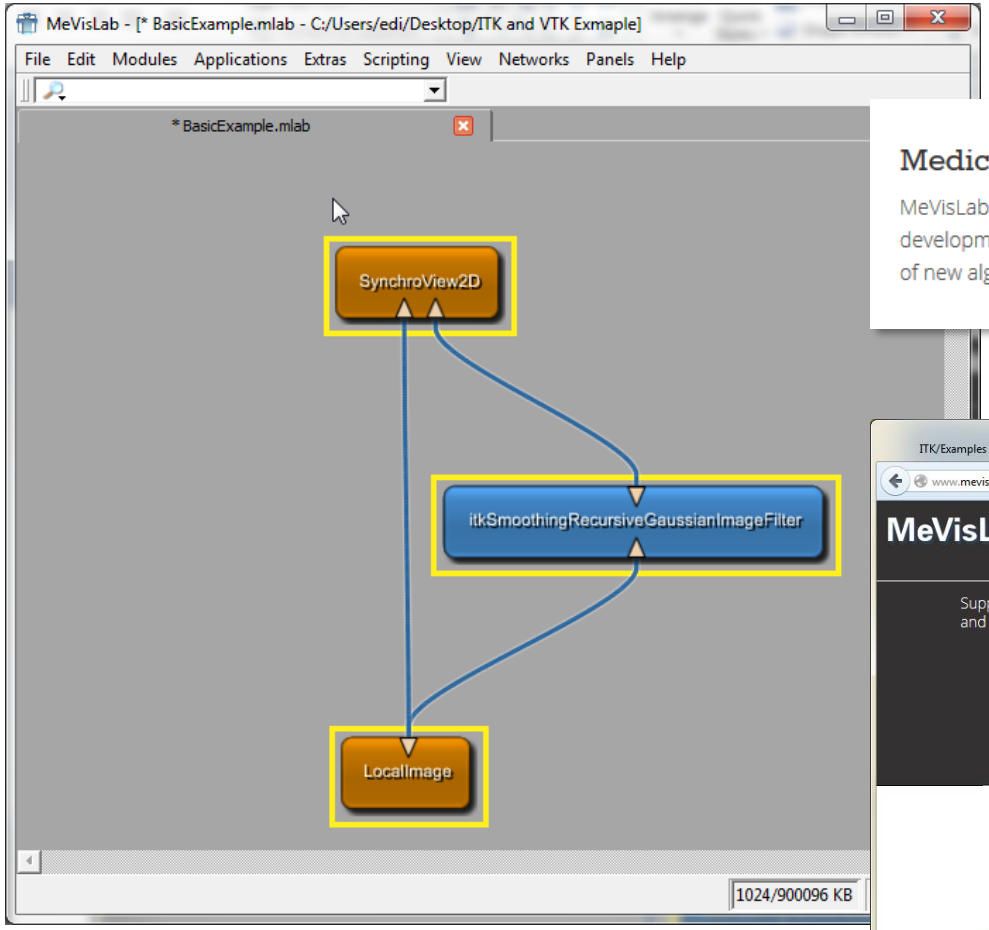
- ITK and VTK are like Legos
  - ITK designed as building blocks from which customized applications are created.





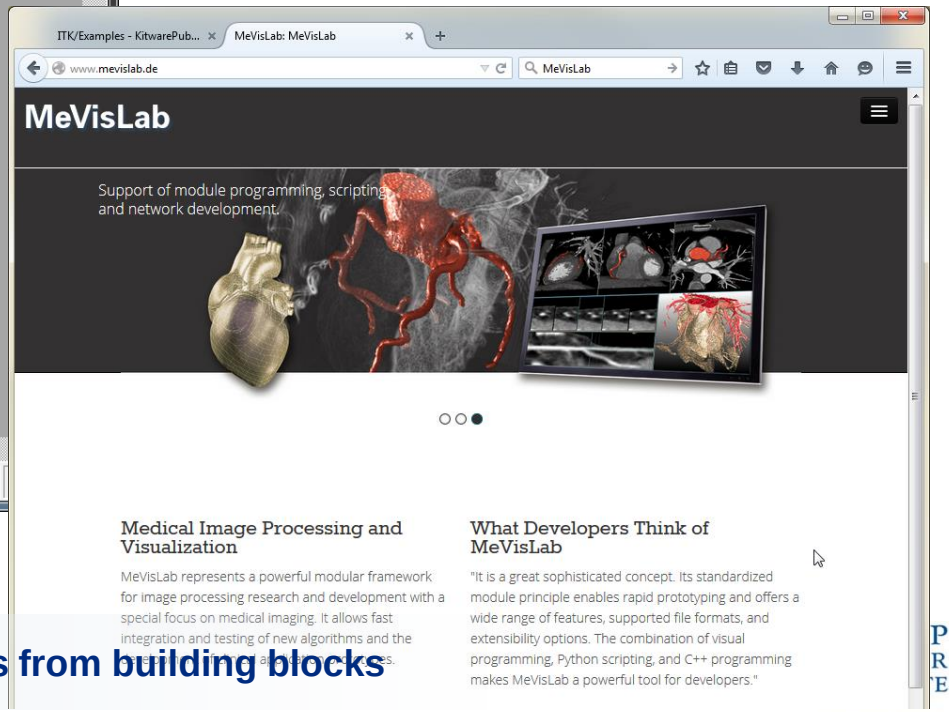
Build your own toy from code snippets

Prototyping



Medical Image Processing and Visualization

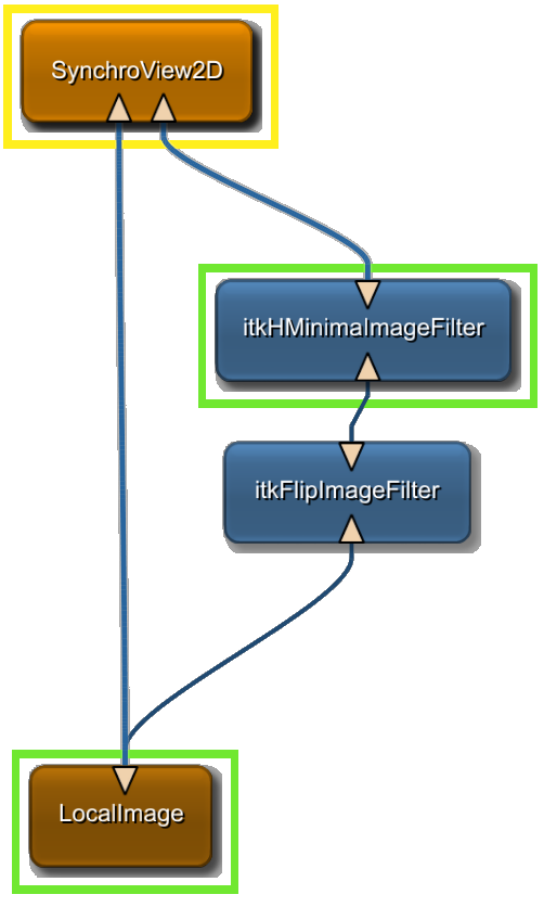
MeVisLab represents a powerful modular framework for image processing research and development with a special focus on medical imaging. It allows fast integration and testing of new algorithms and the development of clinical application prototypes.

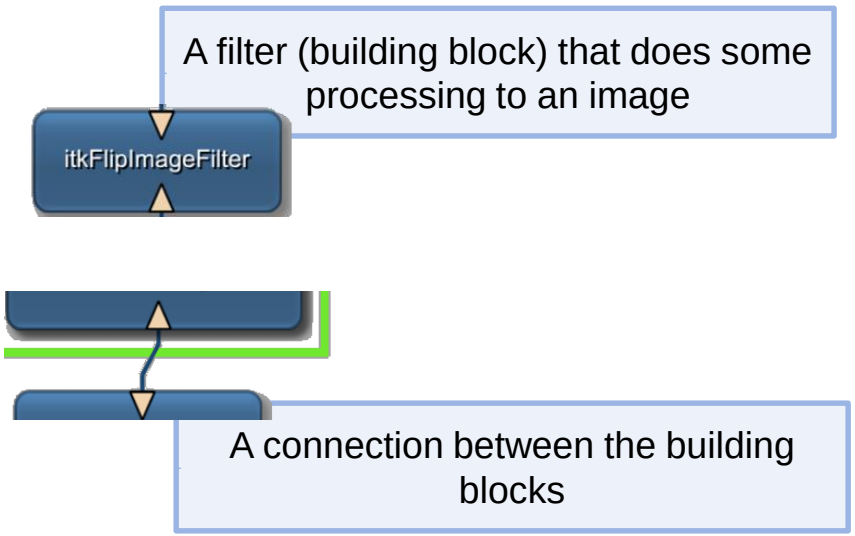


Drag-drop interface to create customized algorithms from building blocks

Why the Lego Analogy ?

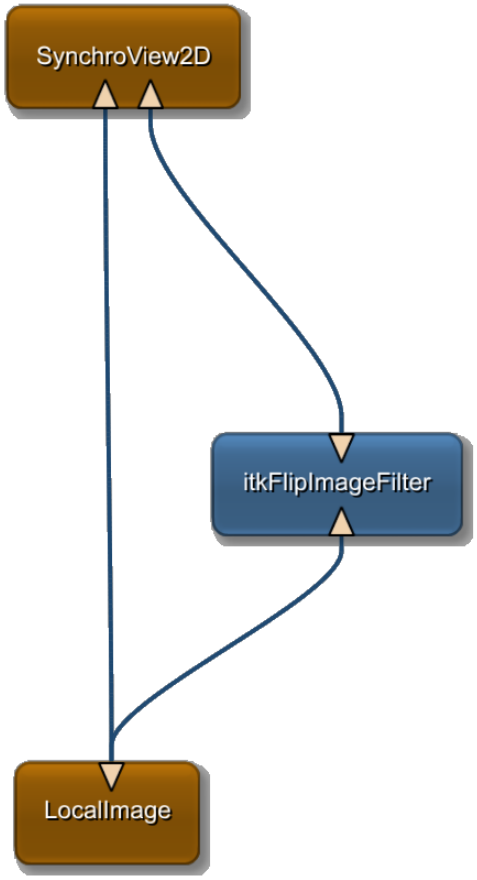
Libraries are a collection of “building blocks” that can be connected to **your** needs.

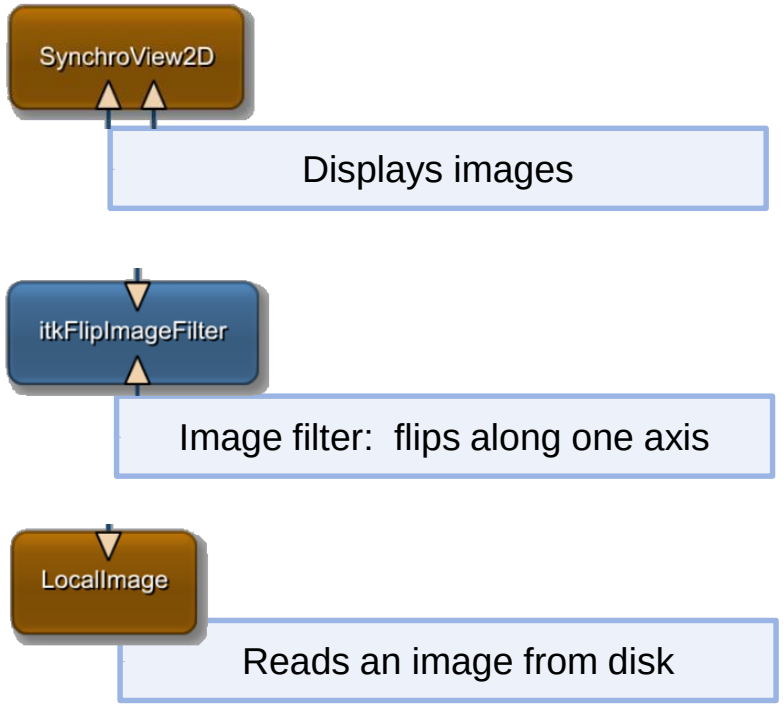




Example

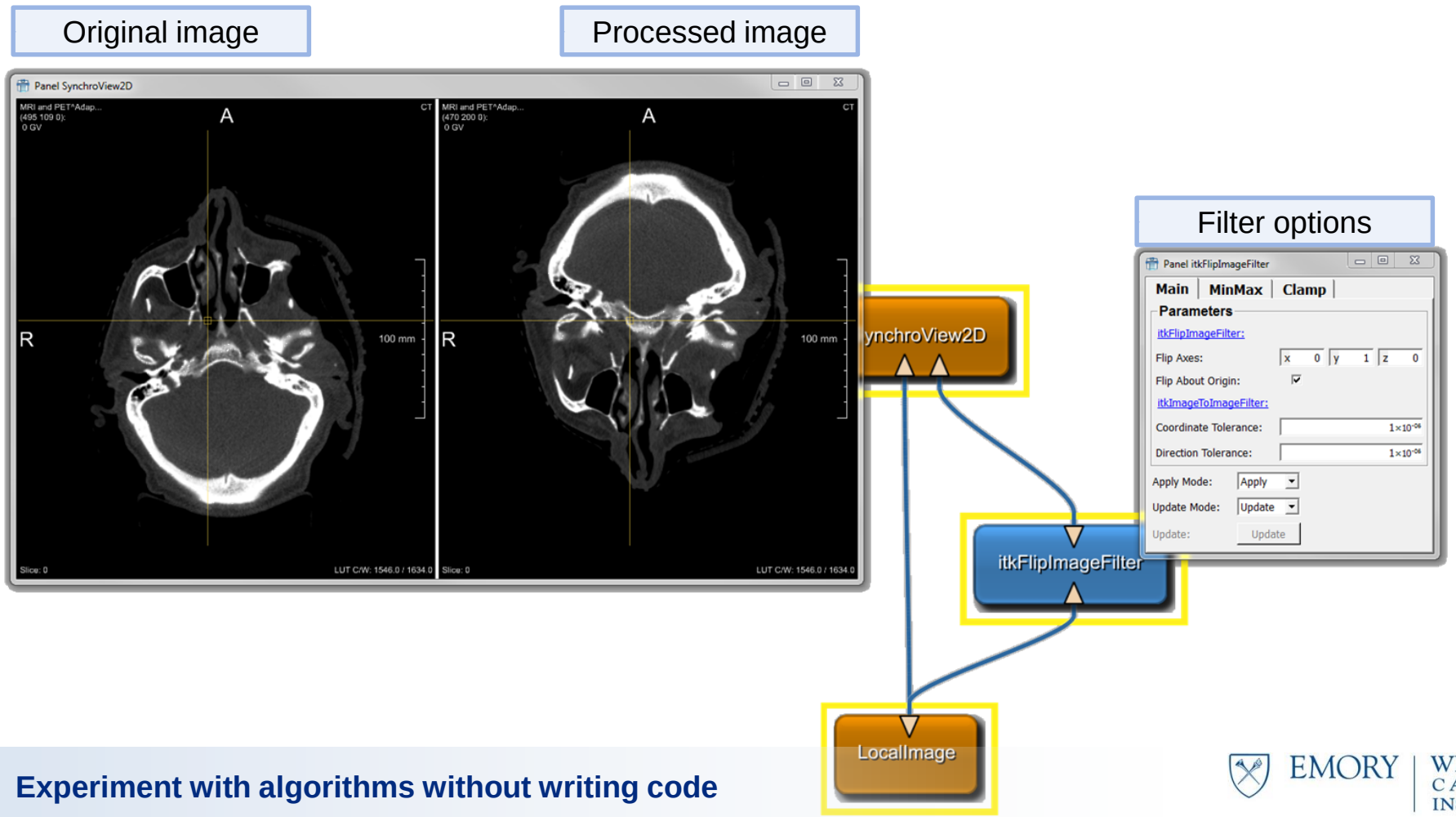
The itkFlipImageFilter image filter will flip an image along a user specified axis.





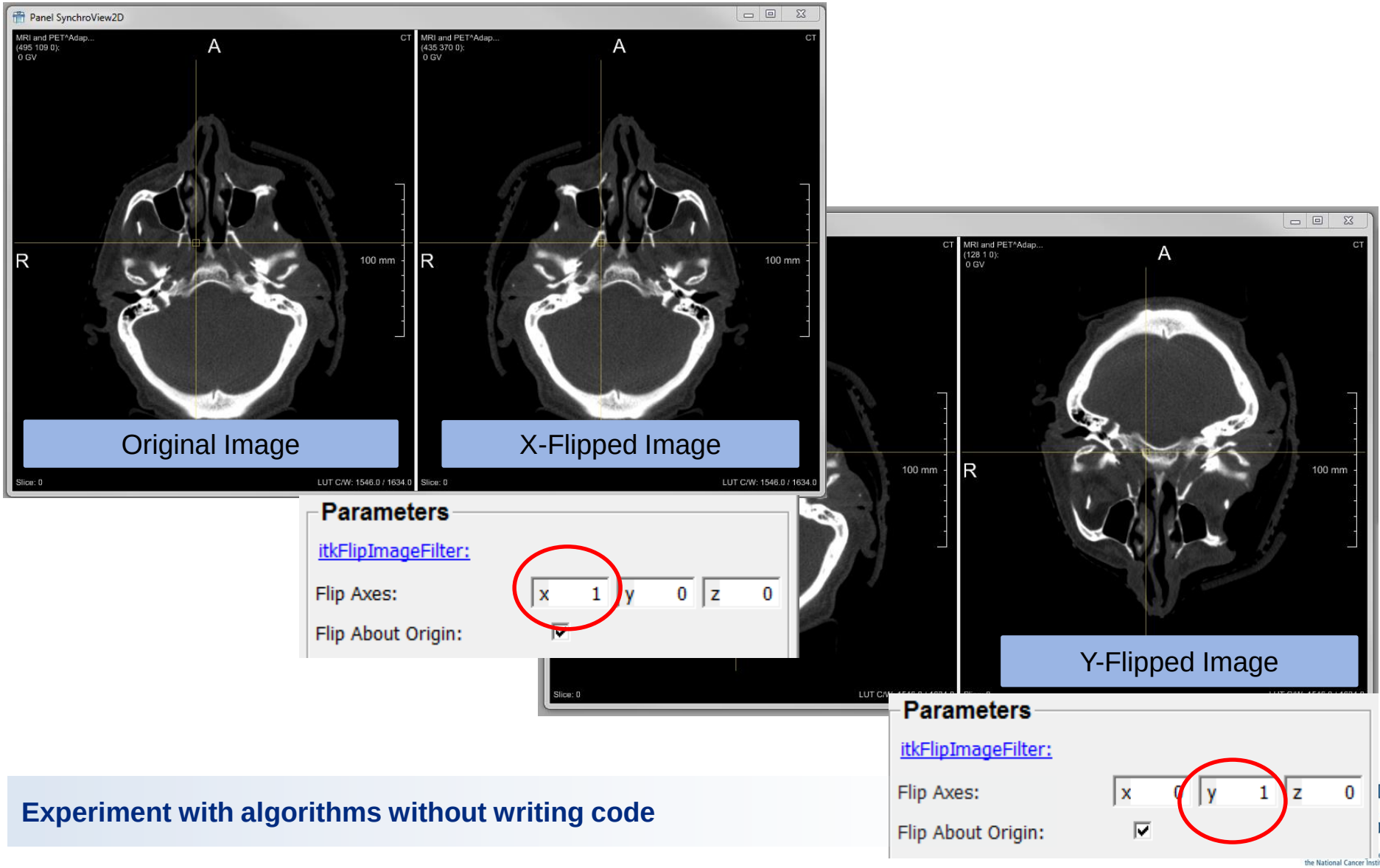
Example

Easy to change setting to experiment on your images



Experiment with algorithms without writing code

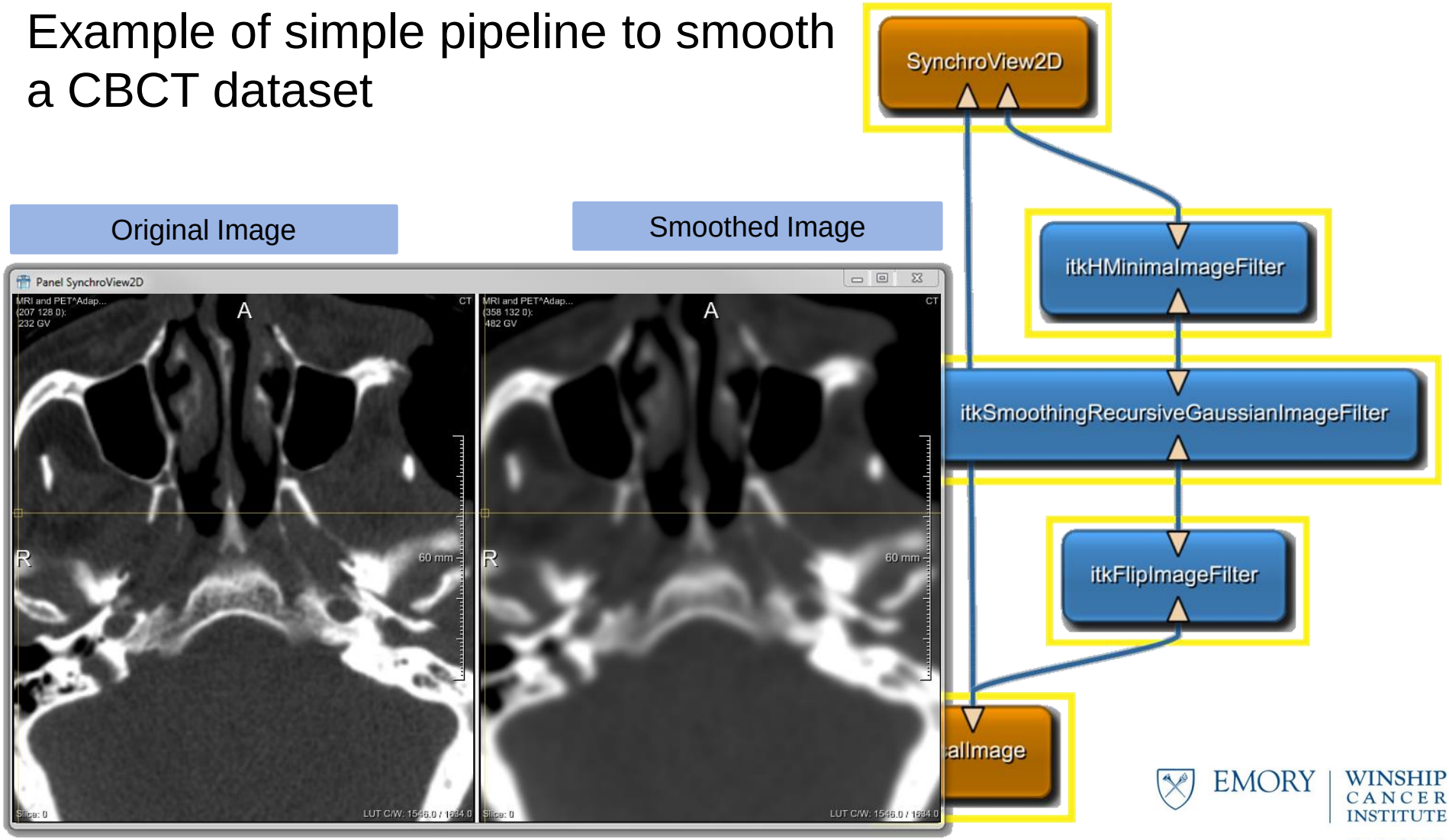
Experimenting With Options



Experiment with algorithms without writing code

Example

Example of simple pipeline to smooth a CBCT dataset



Example Coding

From prototype to coding

```
int  main (int argc, char *argv[])
{
    //define the image type
    typedef itk::Image< long, 3 >        ImageType;

    //read an image
    typedef itk::ImageFileReader< ImageType > ReaderType;
    ReaderType::Pointer imageReader=  ReaderType::New();
    imageReader->SetFileNames("c:\\myFile.dcm");

    //smoothing filter
    typedef itk::SmoothRecursiveGaussianFilter< ImageType, ImageType > SmoothFilter;
    SmoothFilter::Pointer smoothFilter = SmoothFilter::New();
    smoothFilter->SetInput( imageReader->GetOutput() );
    smoothFilter->Update();



}
```

Once you prototyped your pipeline and settings, you can write corresponding code to build an application

Template Code

It's easy to readapt to code to new situations

ITK Definition:

```
template< class TPixel, unsigned int VImageDimension >
Image< TPixel, VImageDimension >
::Image()
{
  m_Buffer = PixelContainer::New();
}
```

Your Code:

```
int  main (int argc, char *argv[])
{

    typedef itk::Image< long, 2 >      SliceType;          // a CT slice

    typedef itk::Image< long, 3 >      VolumeType;         // a CT volume

    typedef itk::Image< long, 4 >      Scan4DType;         // a 4D CT scan

    typedef itk::Image< float, 3 >     DoseType;           // a dose volume
```

Your Own Filter

Deriving a filter from the ITK objects is simple:

Deriving a new inherited filter

```
template< class TImage>
class MyOwnImageFilter:public ImageToImageFilter< TImage, TImage >
{
    public:
```

Implementing your own equation, $f(x) = x^{1.23456}$

```
inline TOutput operator()(const TInput & A) const
 {
   const double input  = ( static_cast< double >( A )) ;
   const double output = pow(input,1.23546);

   return static_cast< TOutput >( output );
 }
```

Catalog of ITK Features

- Image IO
- Image processing
  - Canny Edge
  - Hough Transform (lines/ellipsoids)
  - Variable Conductance Diffusion
- Geometry IO/representation/processing (Spatial Objects)
- Statistics
- Registration/Segmentation
- Numerics (VXL)
- Optimizers
- Finite Element Simulation

There are thousands of algorithms implemented in ITK

Sample Project: Radiomics

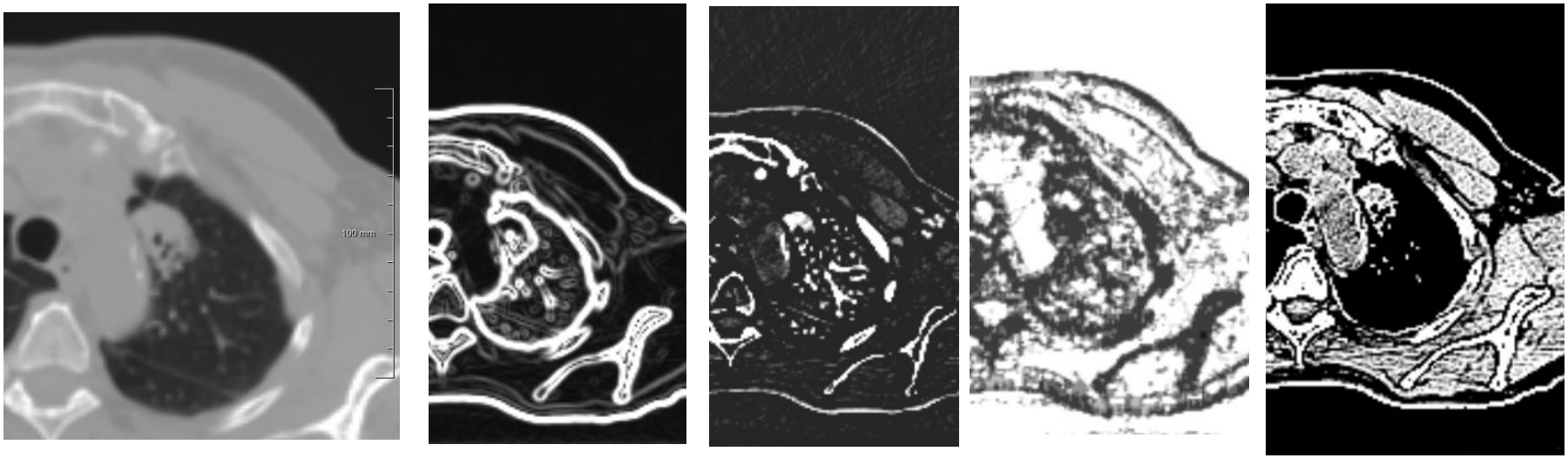
Simple voxel statistics: minimum, maximum, mean, standard deviation, variance.

Image filters: Canny, Laplacian, Sobel, derivative, Hessian, Sharpening, gradient magnitude, HMinima, HMaxima, HConvex, Hconcave.

Shape statistics: elongation, perimeter, radius, flatness, roundness, volume, etc.

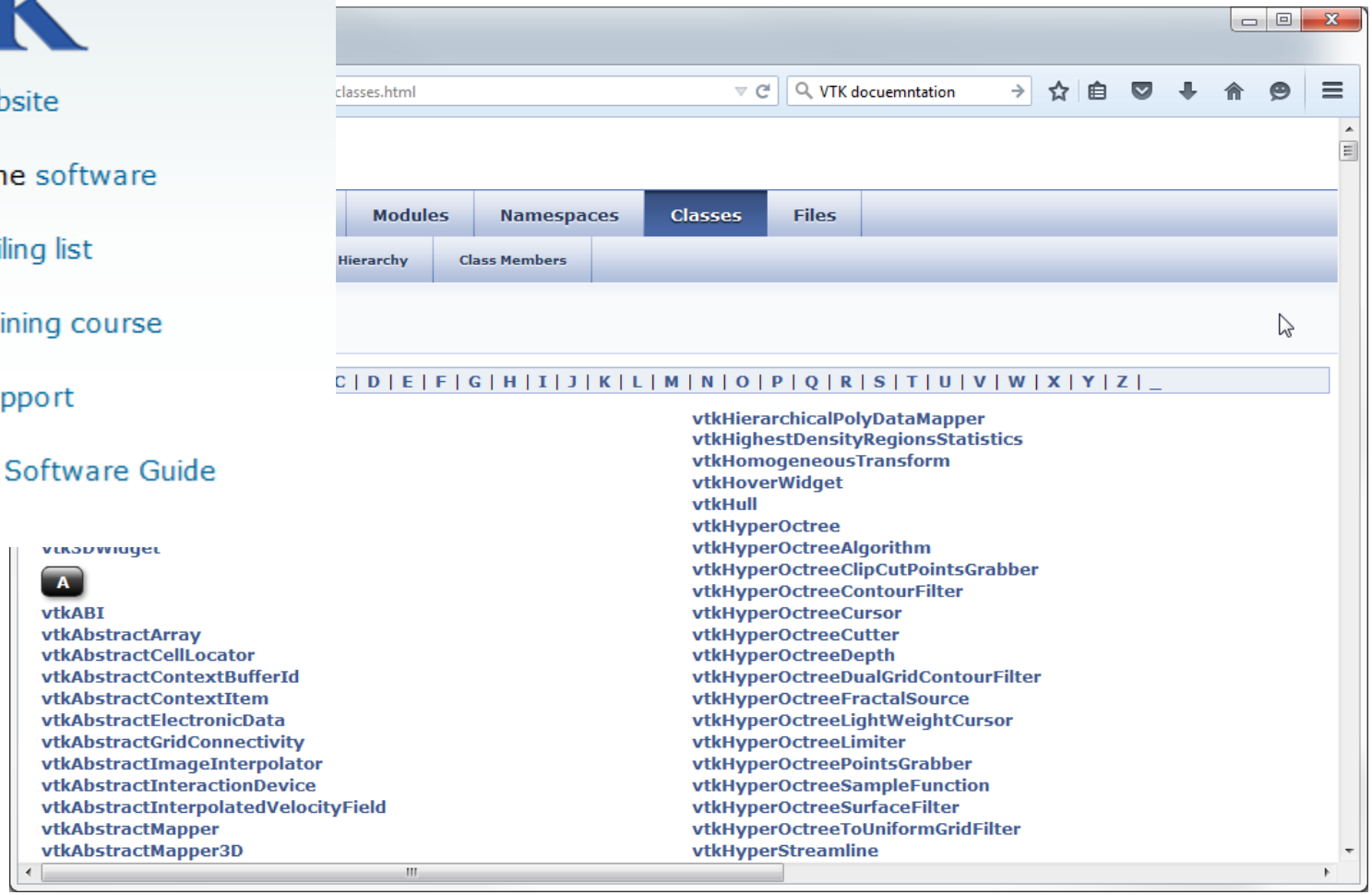
First order textures: energy, entropy, inverse difference moment, inertia, cluster prominence, cluster shade.

Second order textures: short run emphasis, long run emphasis, grey level non- uniformity, run length non-uniformity, low gray level run emphasis, high gray level run emphasis, short run low grey level emphasis, short run high grey level emphasis, long run low grey level emphasis, long run high grey level emphasis.

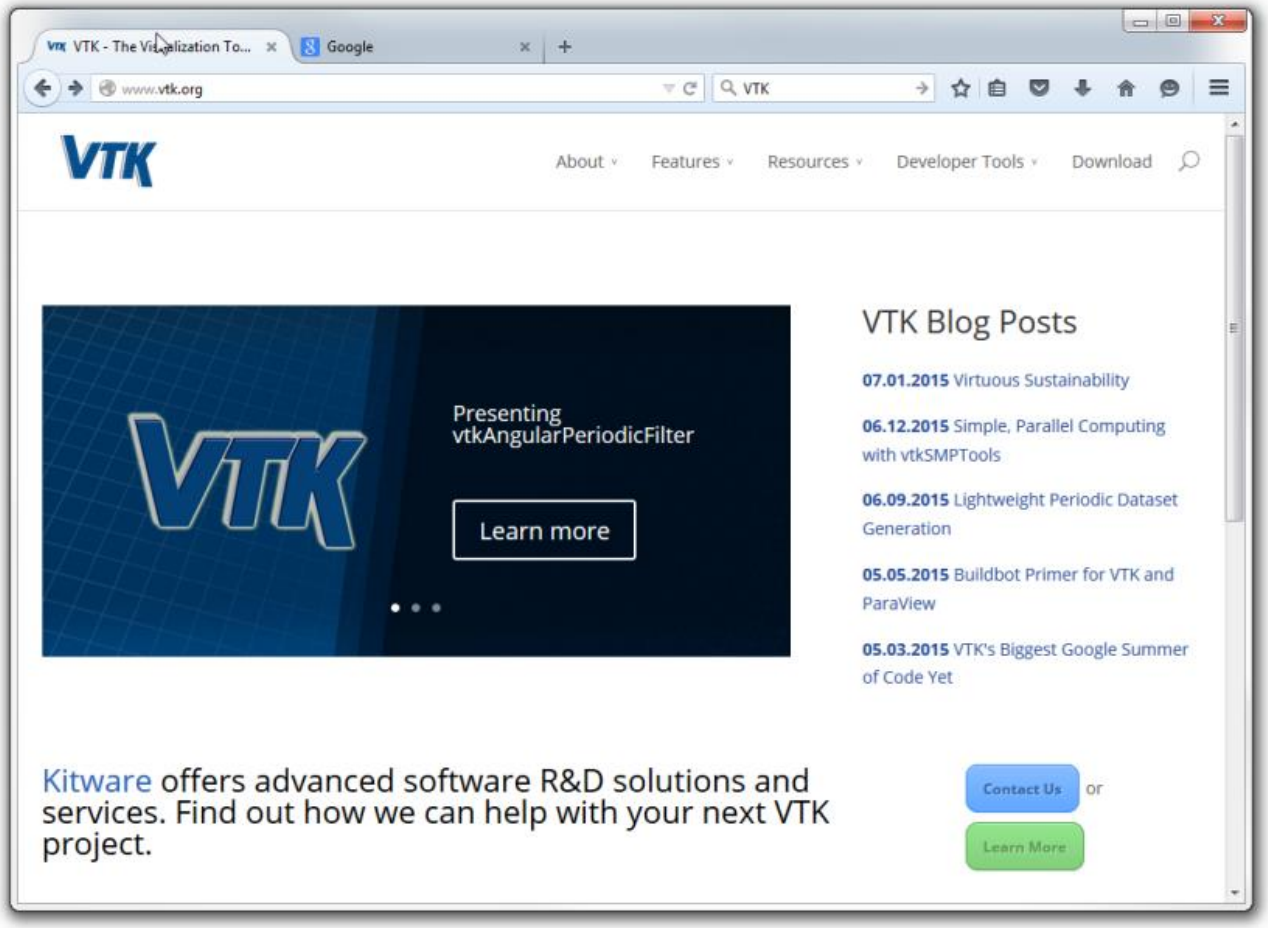


Sample features extracted with ITK: (a) Original CT (Figure 1). (b) Gradient magnitude. (c) HConvex with a threshold of 500 HU (d) Homogeneity texture (e) Laplacian sharpening.

Where To Find Help



Visualization Tool Kit

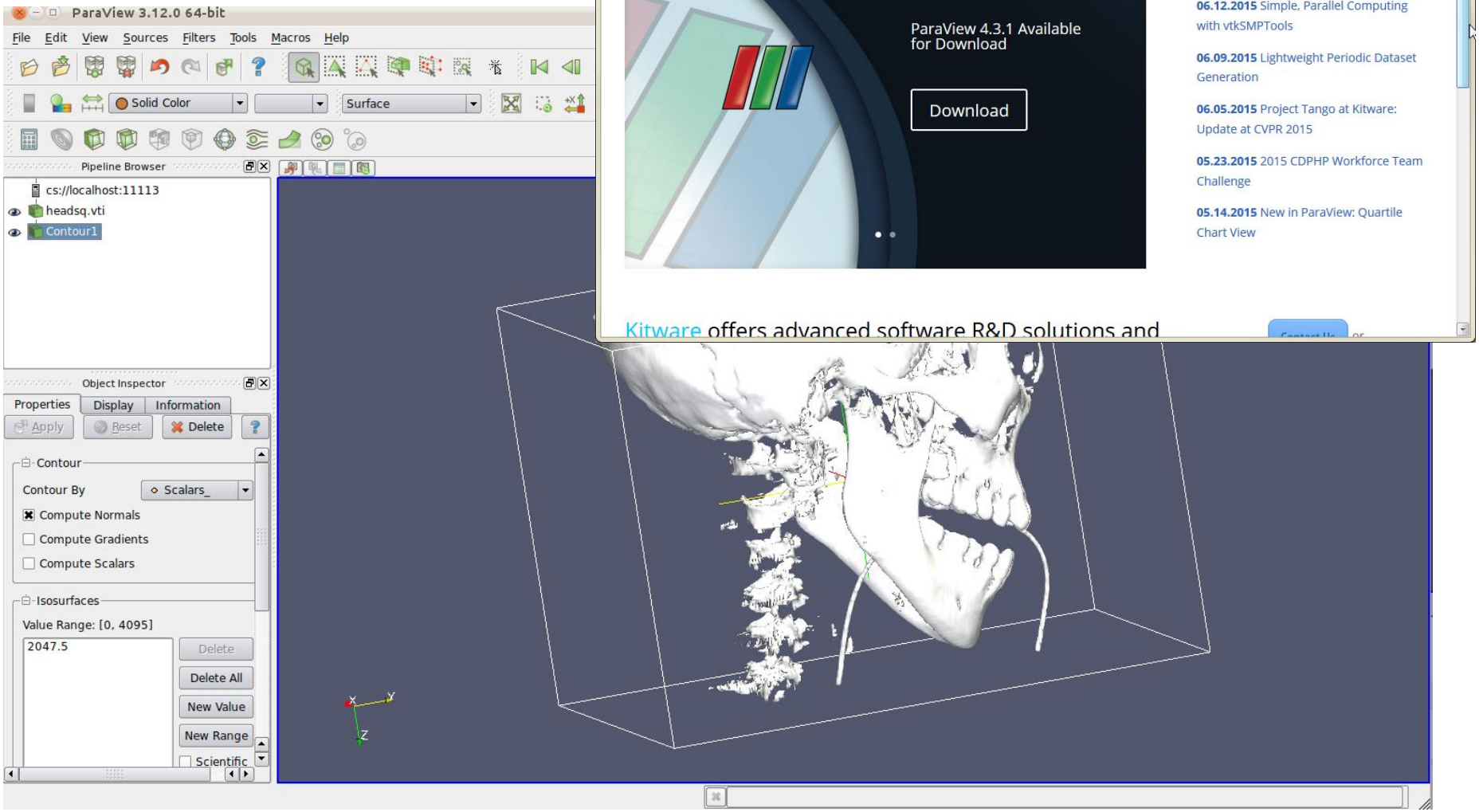


Features ▾ Resources ▾ D

- Open Source
- Platform Agnostic
- Language Agnostic
- Data Model
- Visualization
- Modelling
- Imaging
- 3D Graphics
- 2D Plots and Charts
- Interaction
- InfoVis
- Parallel Processing

VTK – Algorithms to visualize the data

Paraview

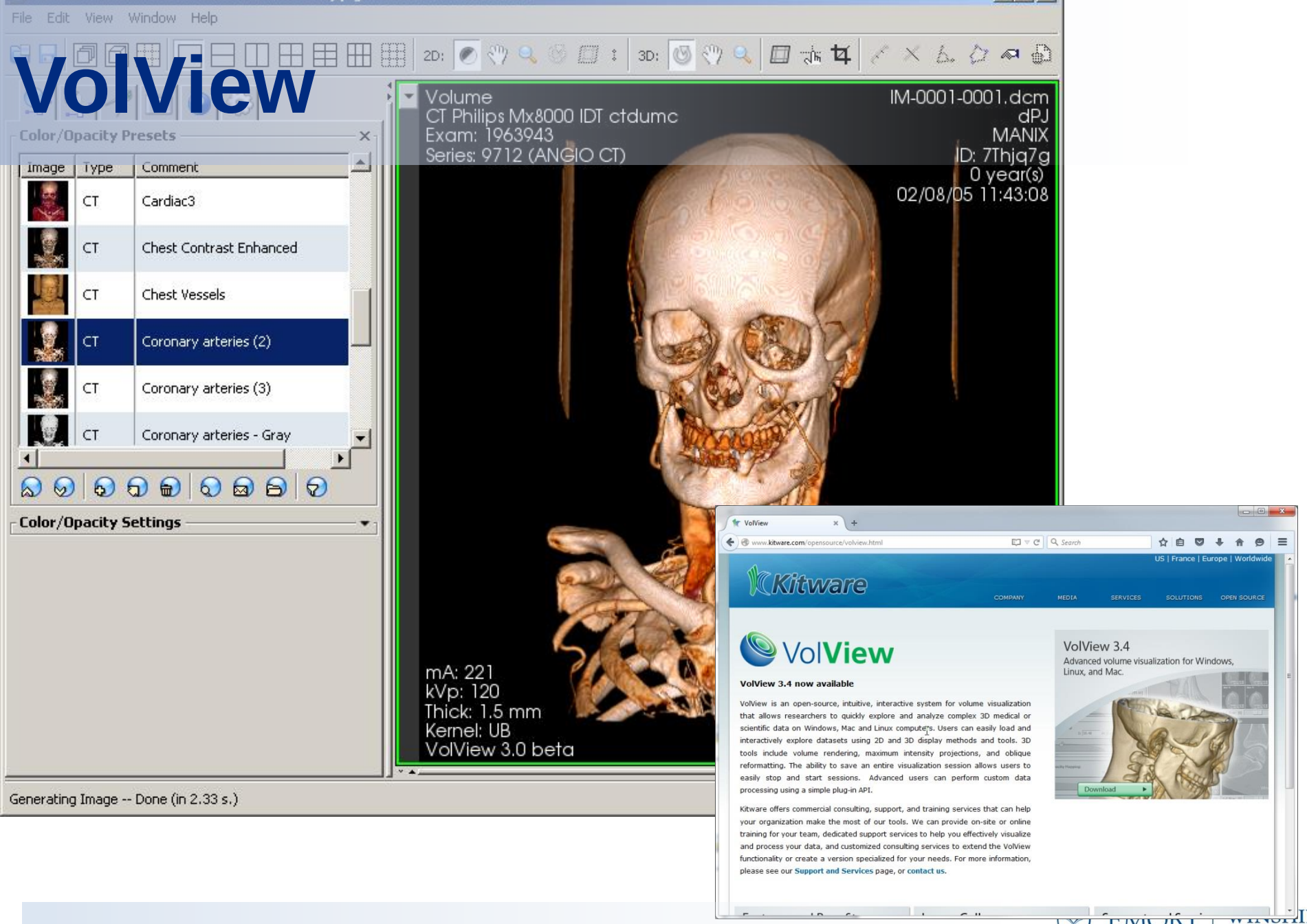


Open-source application to visualize meshes

EMORY | WINSHIP CANCER INSTITUTE

A Cancer Center Designated by the National Cancer Institute

VolView



Open-source application to visualize images

Thank you

www.mevislab.de

www.itk.org

www.volview.org

www.itk.org

www.paraview.org

www.cmake.org

EMORY | WINSHIP CANCER INSTITUTE

A Cancer Center Designated by the National Cancer Institute