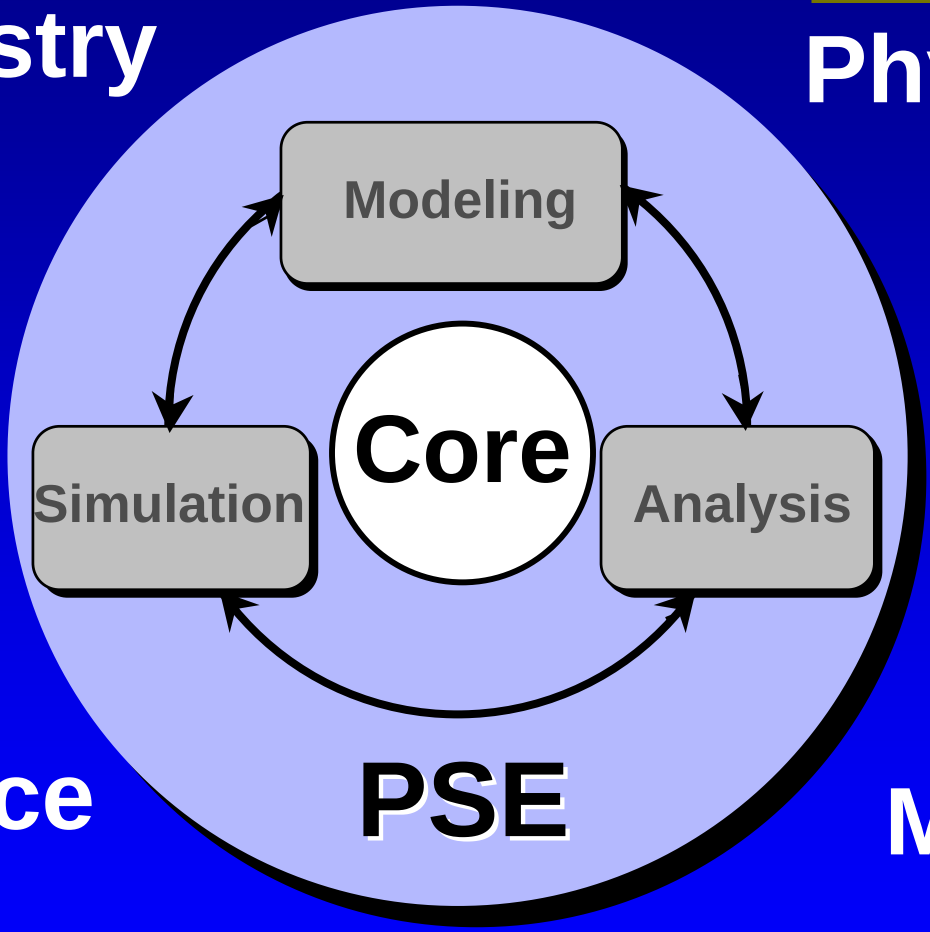
SCIRun / BioPSE System Overview

Problem Solving Environments (PSEs)

System Overview

Chemistry

Physics



Modeling

Simulation

Core

Analysis

PSE

Core

Memory Mgmt

Process Mgmt

Framework

Libraries

Biology

Geoscience

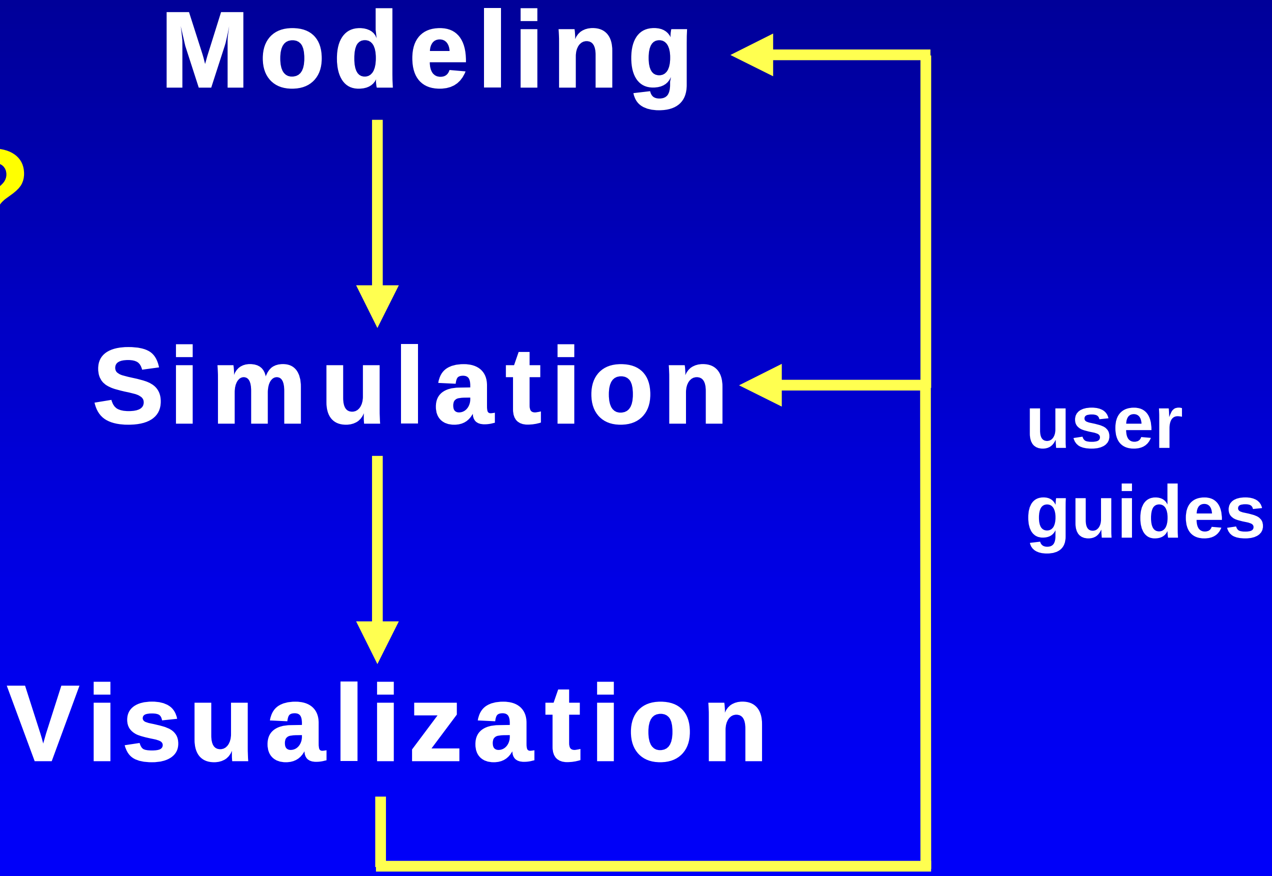
Medicine

Astronomy

Integration and Interaction

System Overview

What If?

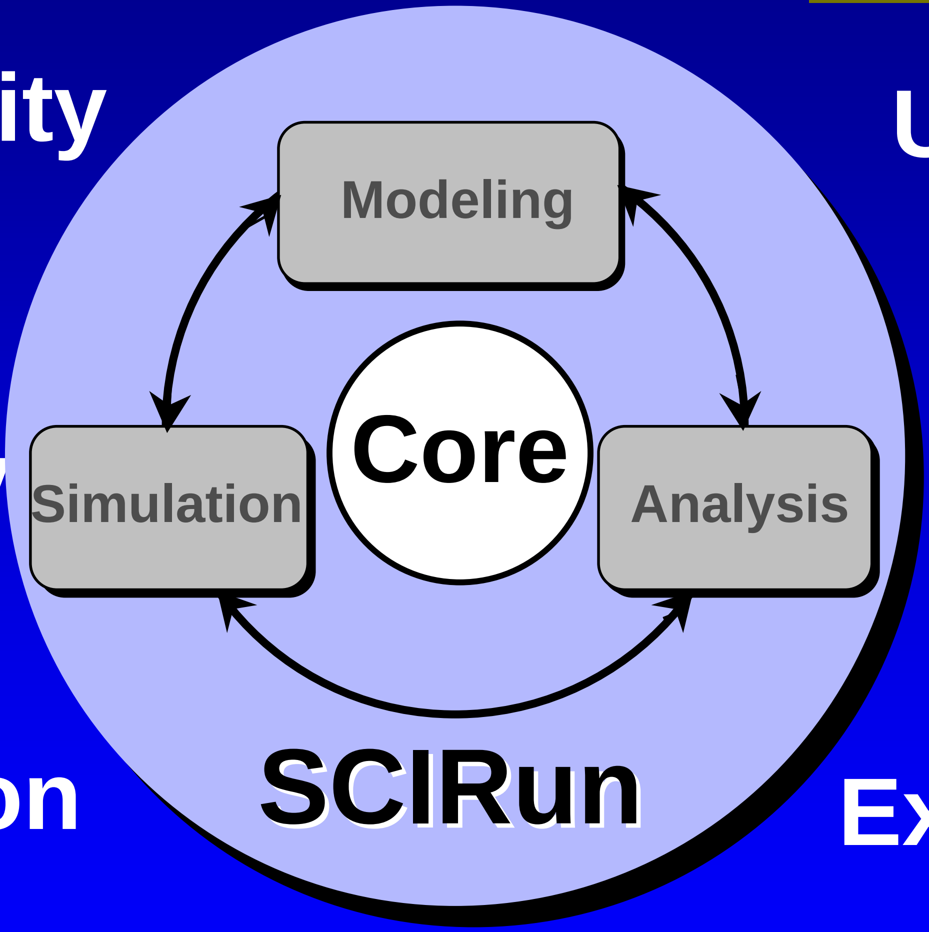


SCIRun Goals

System Overview

Interactivity

Usability



Portability

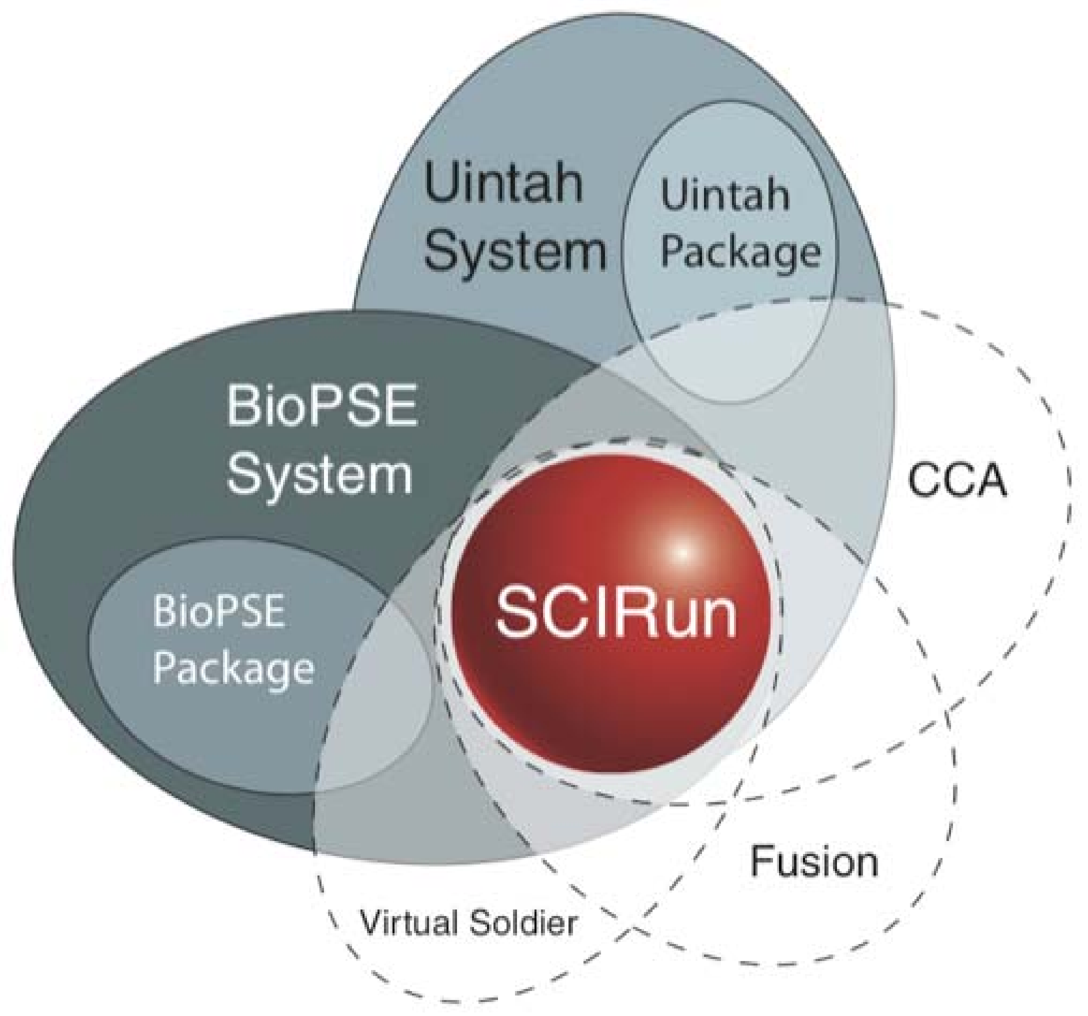
Utility

Integration

Extensibility

SCIRun and BioPSE

System Overview



Overview

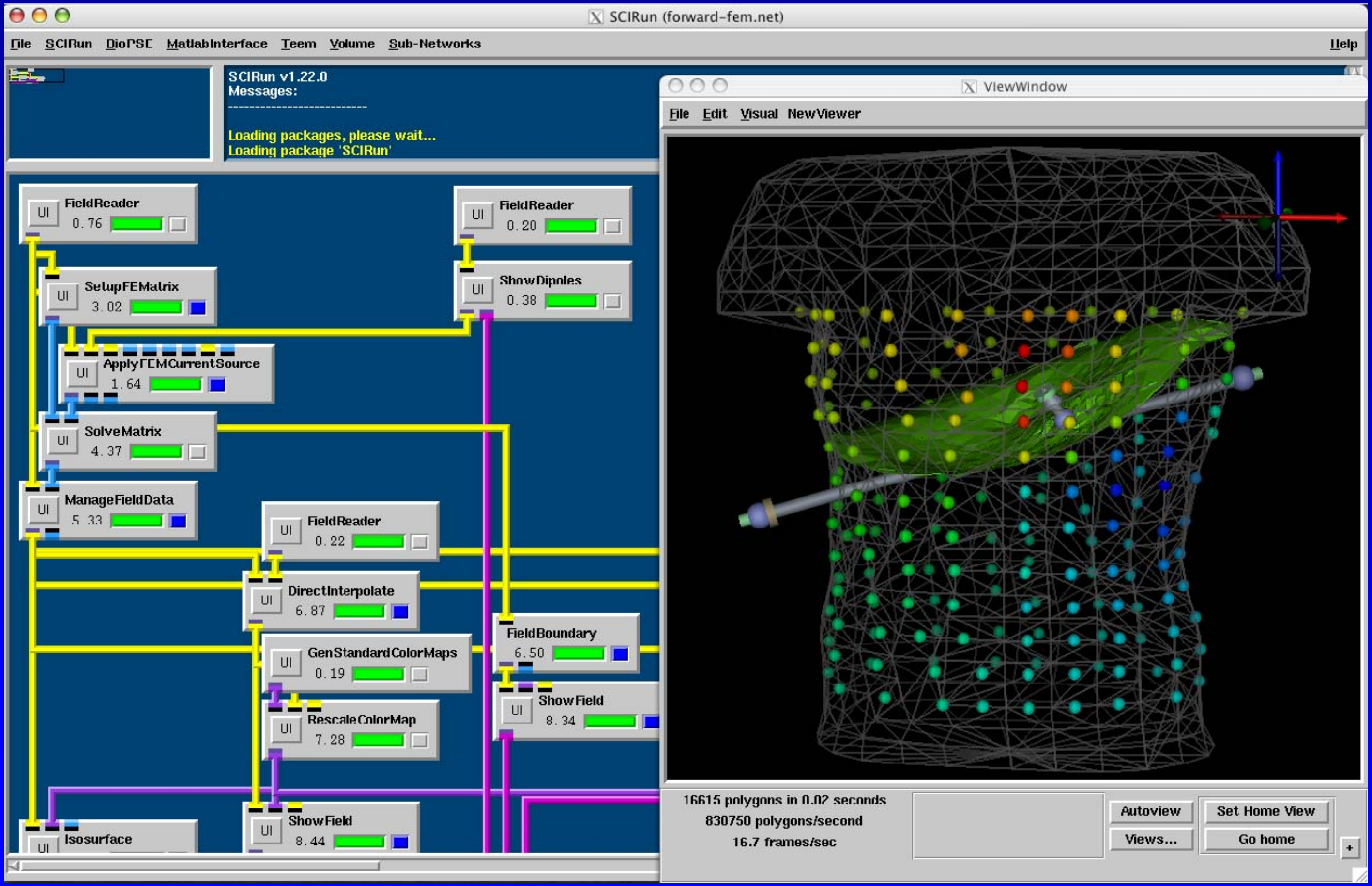
System Overview

- Computational Science
- Problem Solving Environments
- Dataflow
- Datatypes
- Software Organization
- Extensibility
- PowerApps

Elements of SCIRun

System Overview

Visual programming Environment



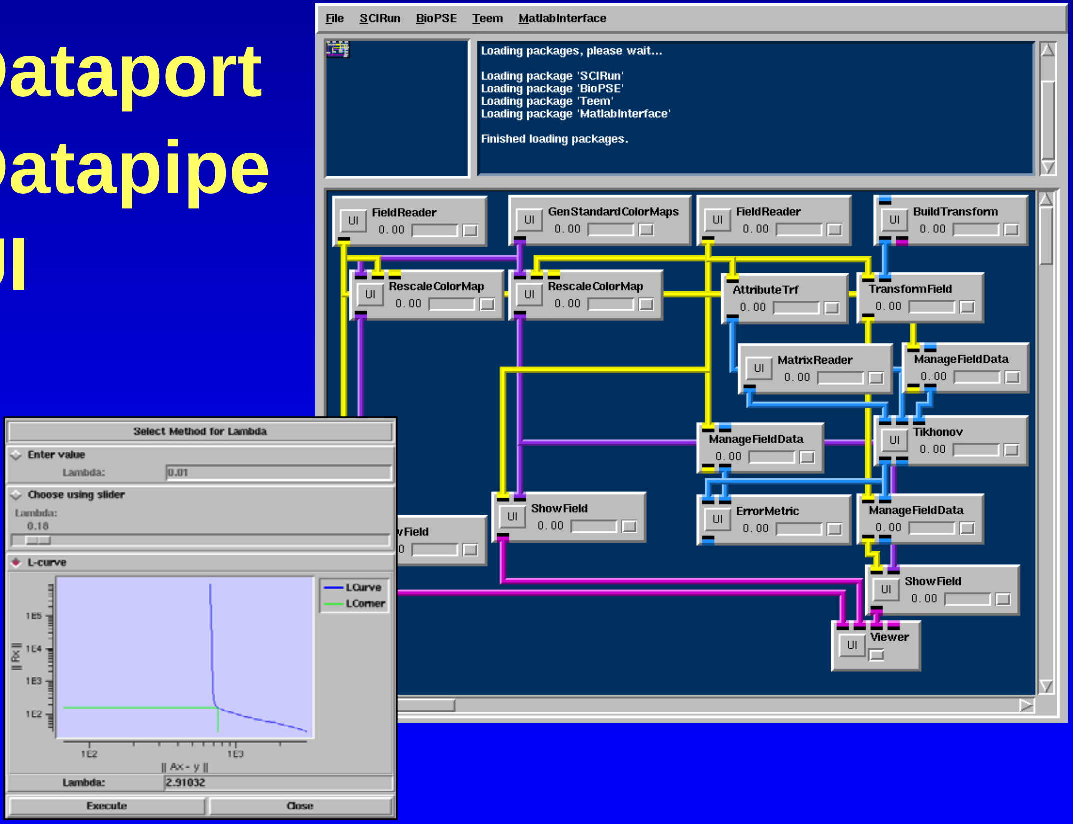
SCIRun v1.22.0
Messages:

Loading packages, please wait...
Loading package 'SCIRun'

16615 polygons in 0.02 seconds
830750 polygons/second
16.7 frames/sec

Network Elements

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Select Method for Lambda

◇ Enter value

Lambda: 0.01

◇ Choose using slider

Lambda: 0.18

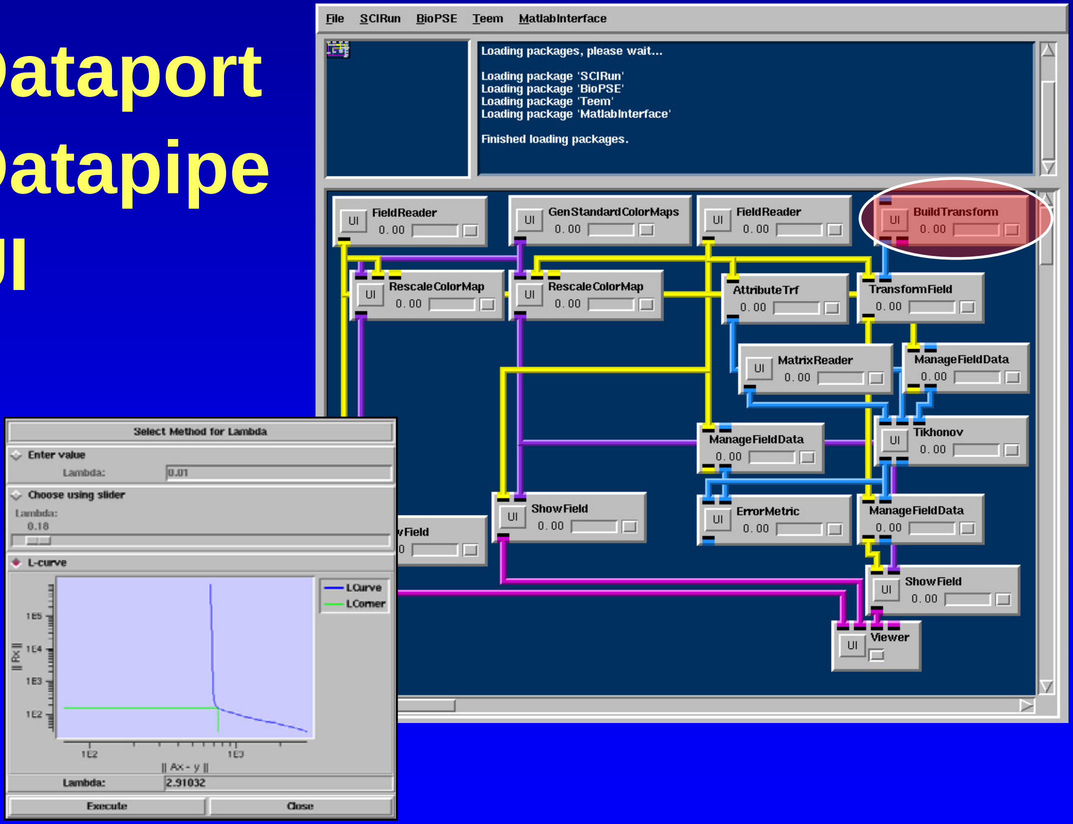
◆ L-curve

Lambda: 2.91032

Network Elements

System Overview

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Select Method for Lambda

○ Enter value
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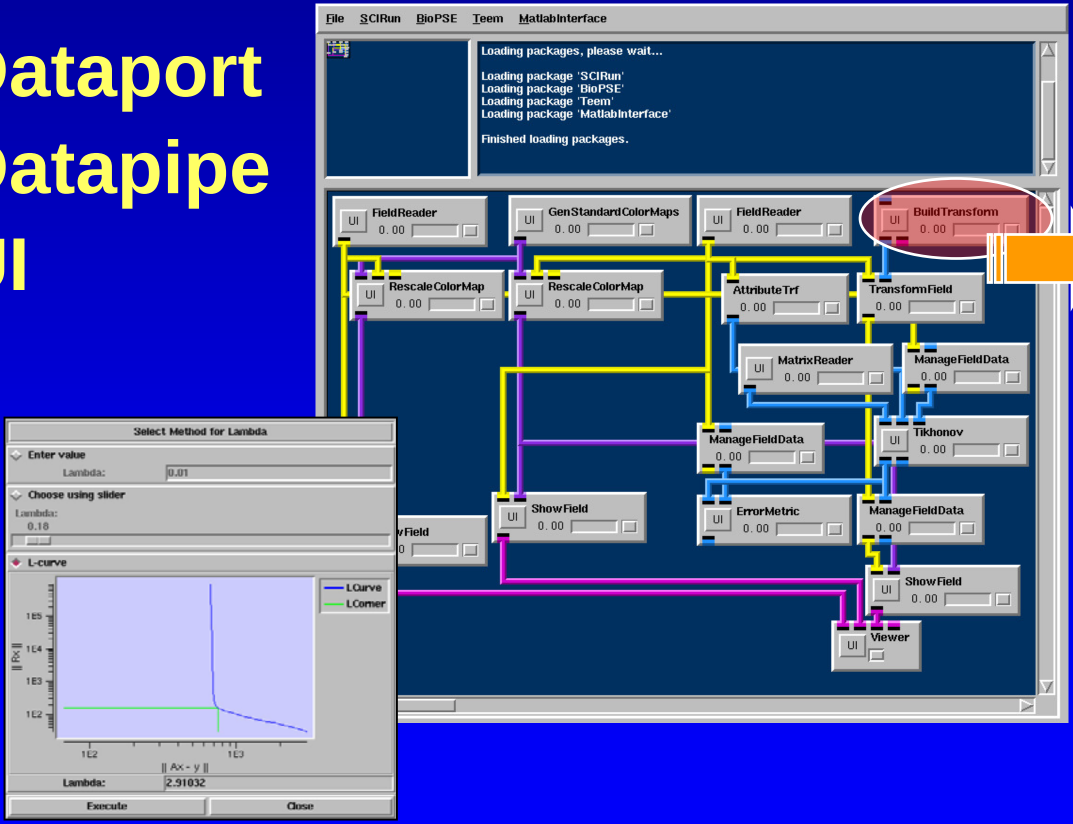
● L-curve

Lambda: 2.91032

Network Elements

System Overview

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Lambda: 0.01

Lambda: 0.18

Lambda: 2.91032

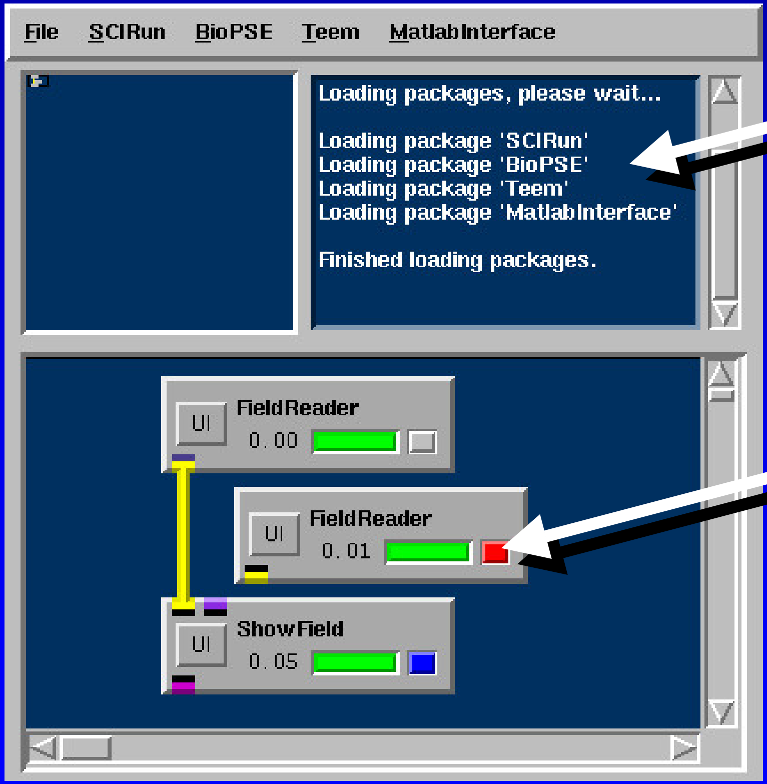
MODULE

```
void execute() {
  // get data from ports
  // get data from UI
  // … do work …
  // set data on UI
  // send data out ports
}
```

CIBC

Module Status

- Run-time messages are sent to the module's "log"



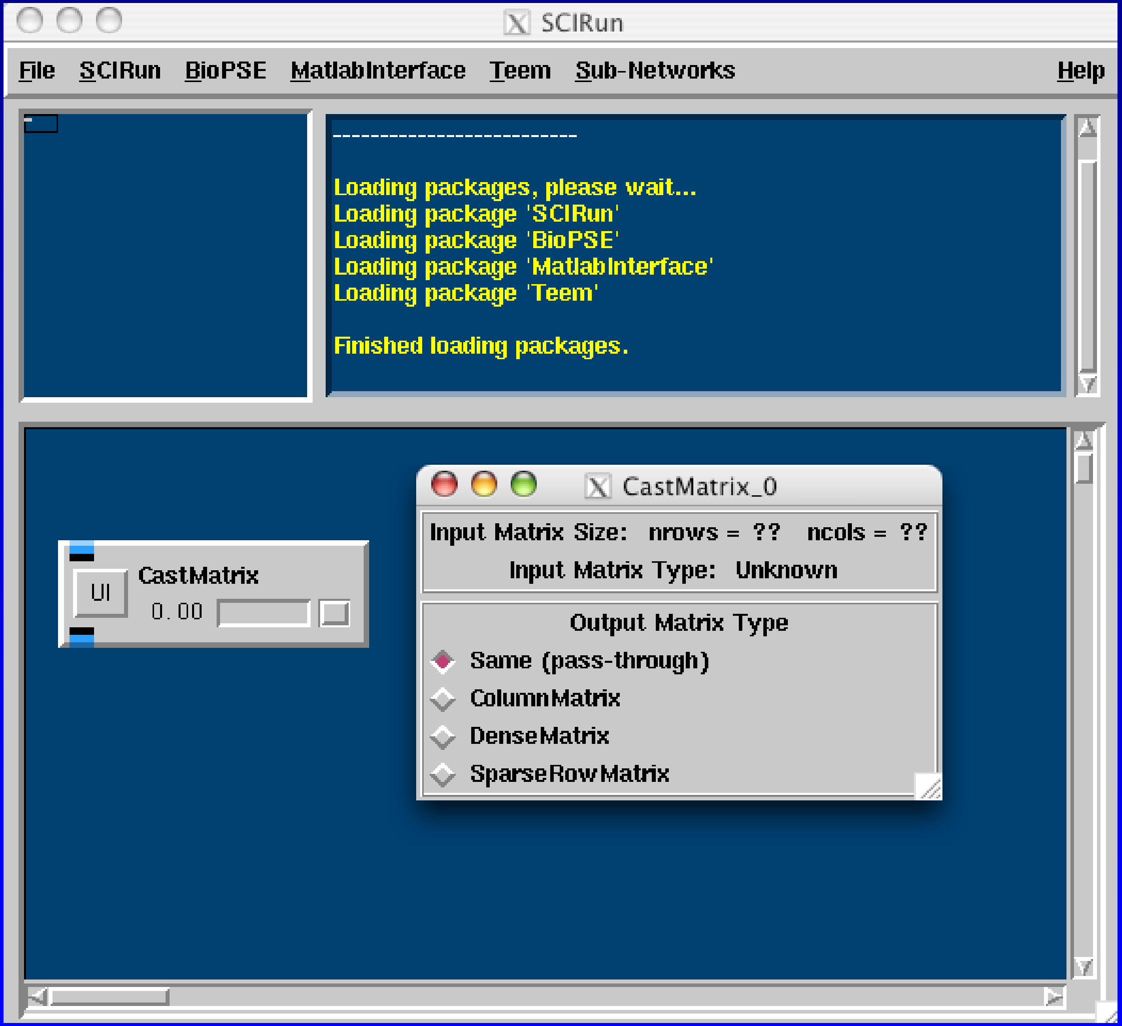
```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Startup messages

Log message indicator
Gray: no messages
Red: error
Blue: warning/remark

Example Module: CastMatrix

System Overview



```
--------------------------

Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'

Finished loading packages.
```

Input Matrix Size: nrows = ?? ncols = ??

Input Matrix Type: Unknown

Output Matrix Type

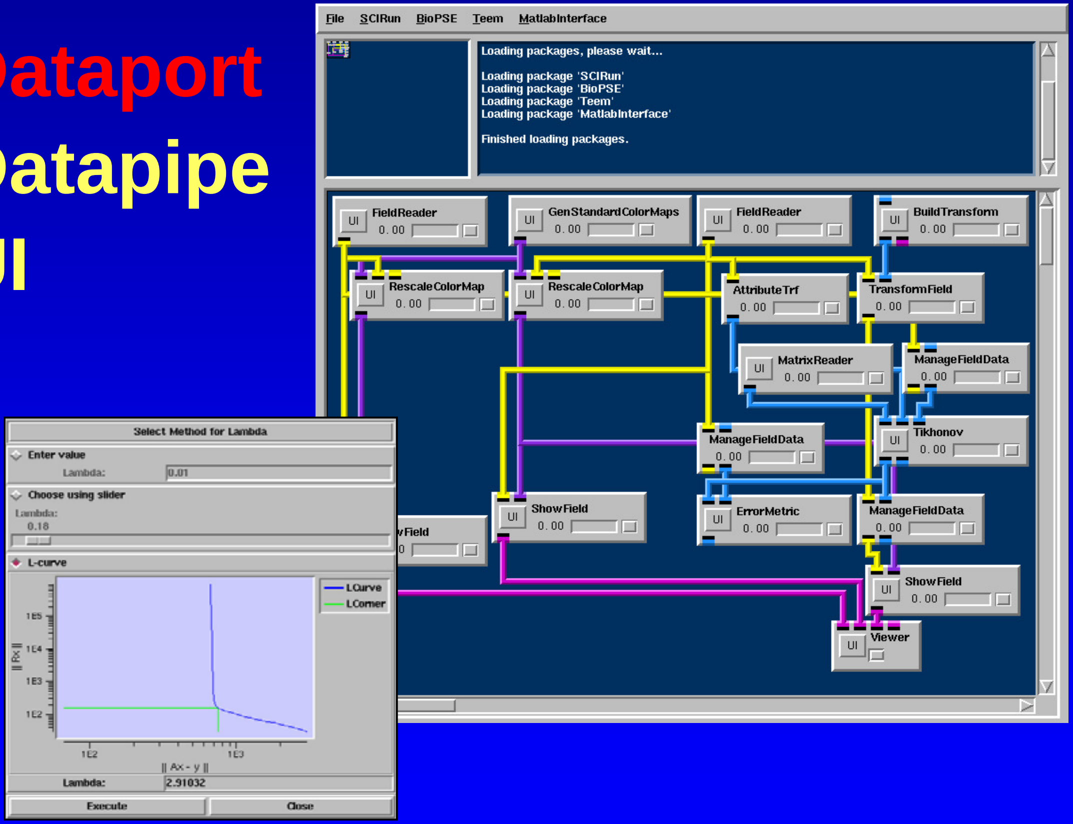
- ◆ Same (pass-through)
- ◇ ColumnMatrix
- ◇ DenseMatrix
- ◇ SparseRowMatrix

SCIRun/src/Dataflow/
Modules/Math/CastMatrix.cc
GUI/CastMatrix.xml
XML/CastMatrix.xml

Network Elements

System Overview

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Select Method for Lambda

◇ Enter value

Lambda: 0.01

◇ Choose using slider

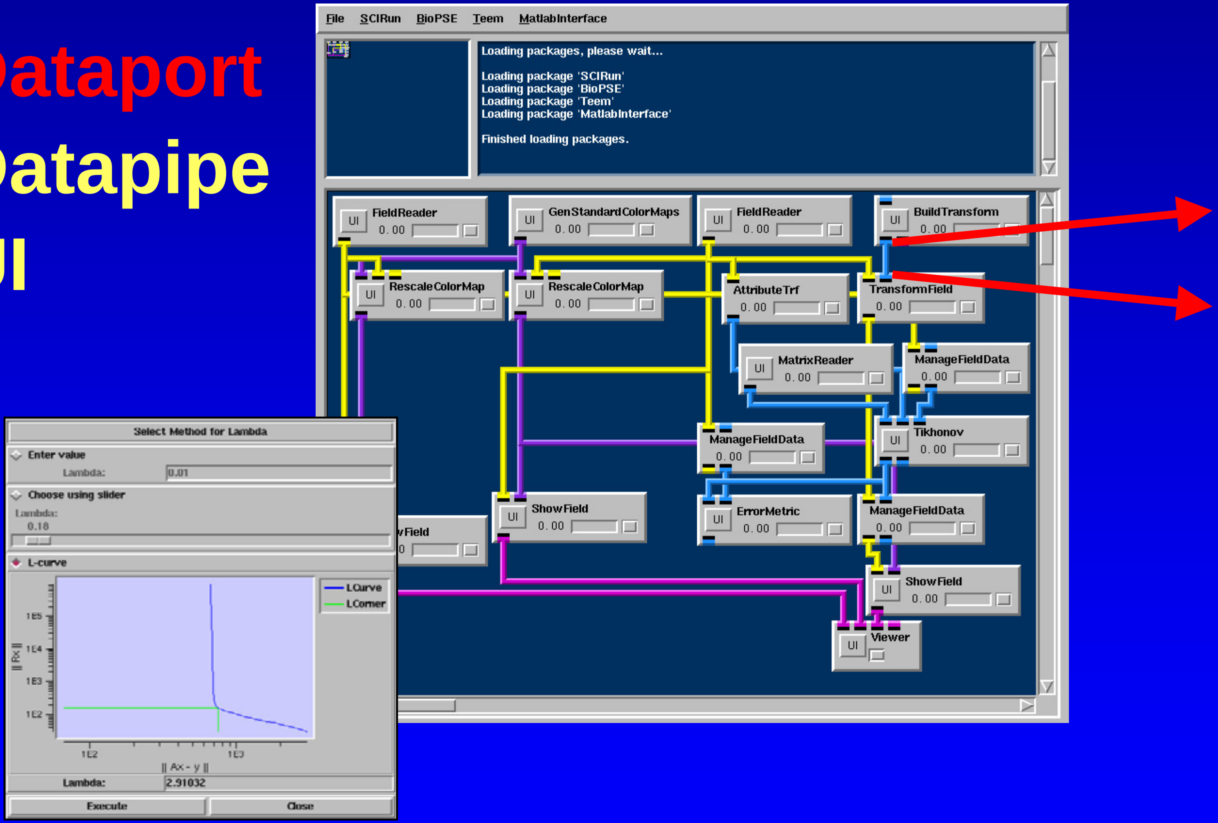
Lambda: 0.18

◆ L-curve

Lambda: 2.91032

Network Elements

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Select Method for Lambda

◇ Enter value

Lambda: 0.01

◇ Choose using slider

Lambda: 0.18

◆ L-curve

Lambda: 2.91032

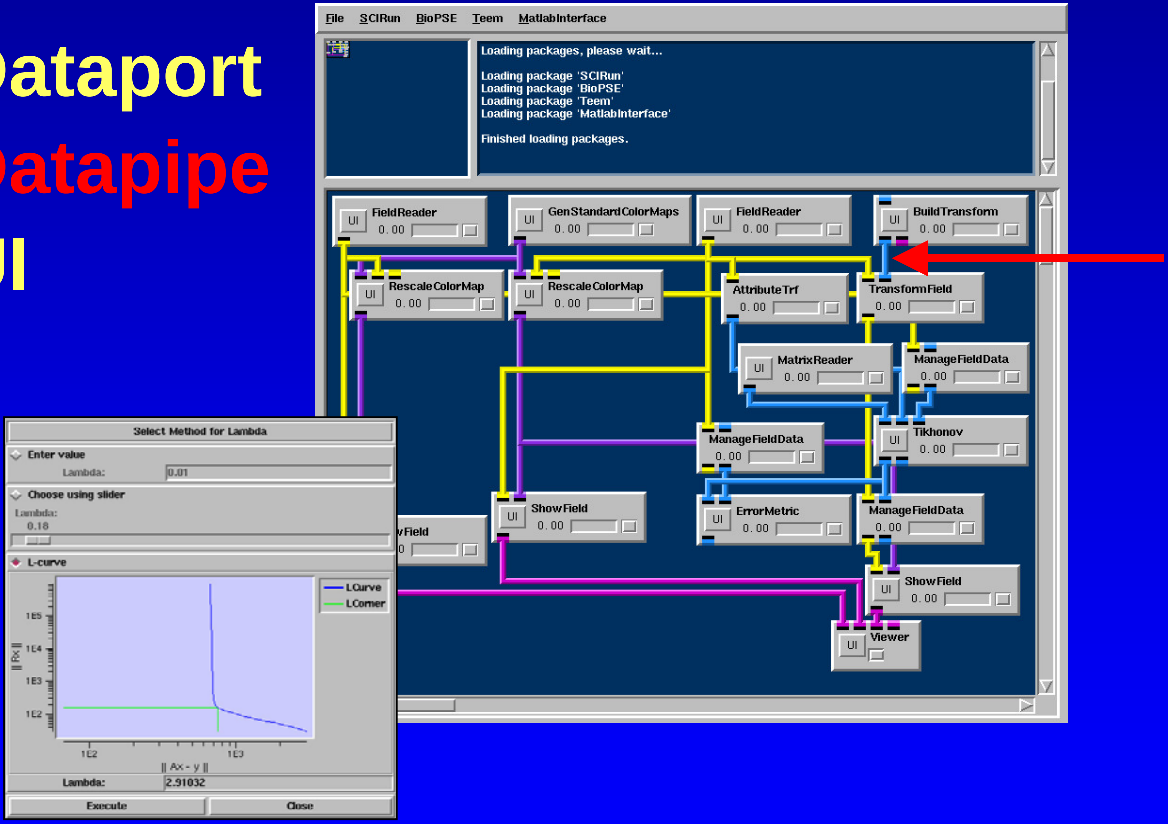
Execute | Close

….send

get……

Network Elements

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.

Lambda: 0.01

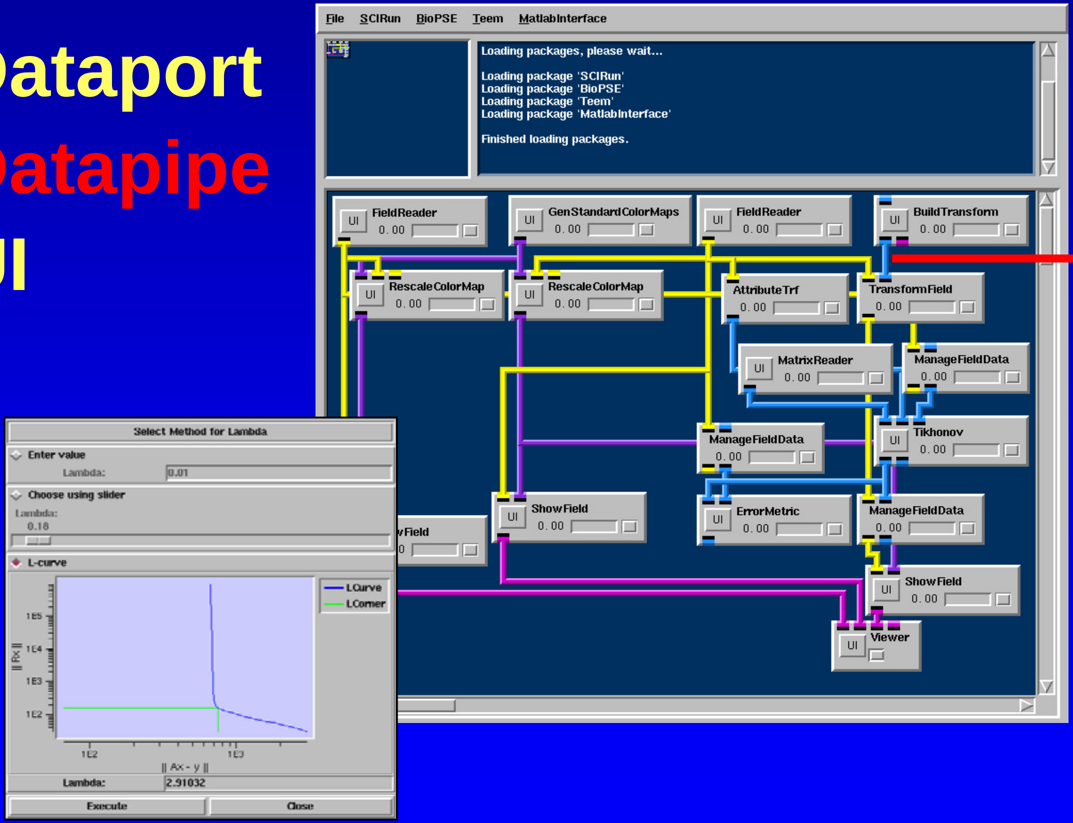
Lambda: 0.18

Lambda: 2.91032

Network Elements

System Overview

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Select Method for Lambda

○ Enter value

Lambda: 0.01

○ Choose using slider

Lambda: 0.18

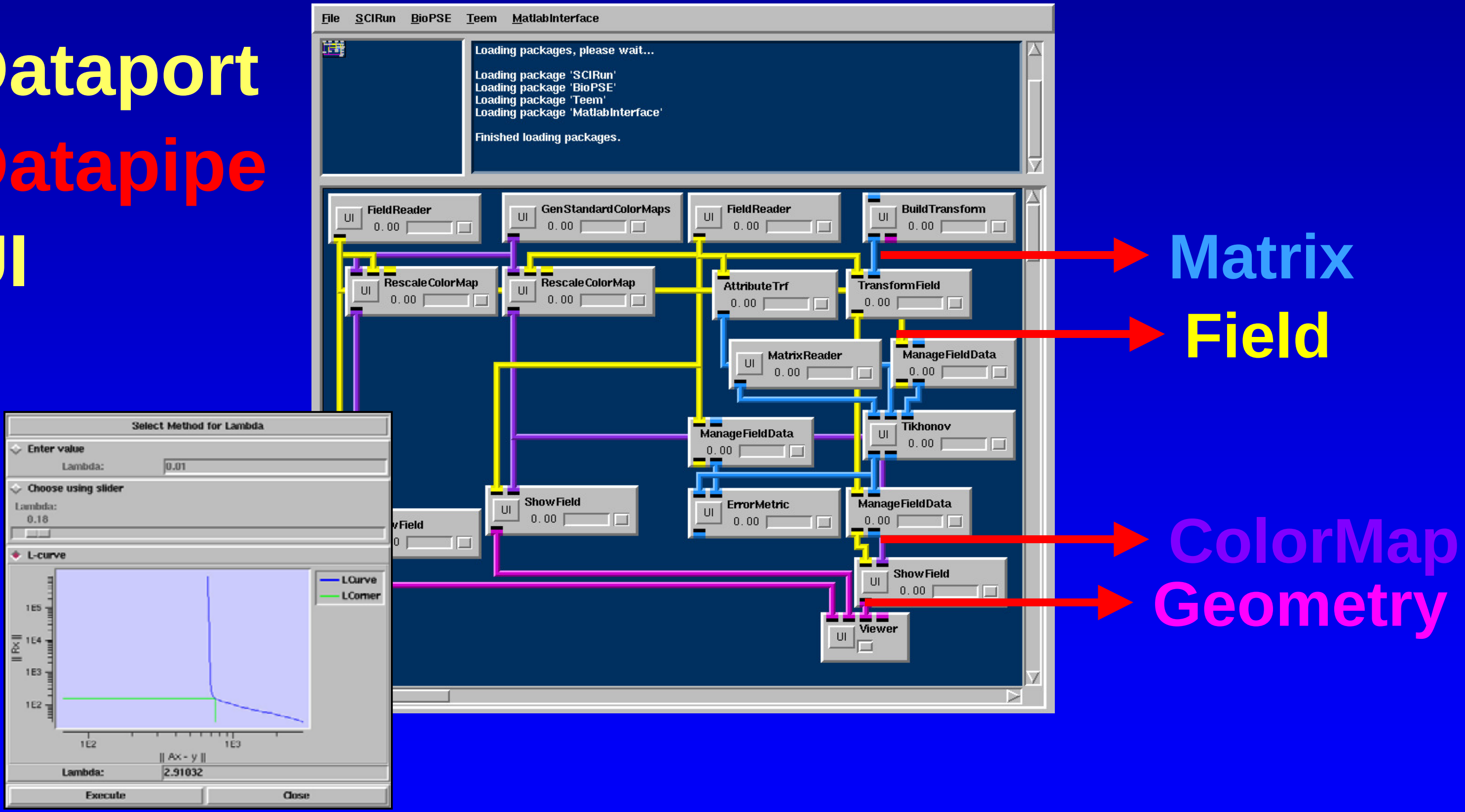
● L-curve

Lambda: 2.91032

Matrix

Network Elements

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI



Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.

Select Method for Lambda

Enter value

Lambda: 0.01

Choose using slider

Lambda: 0.18

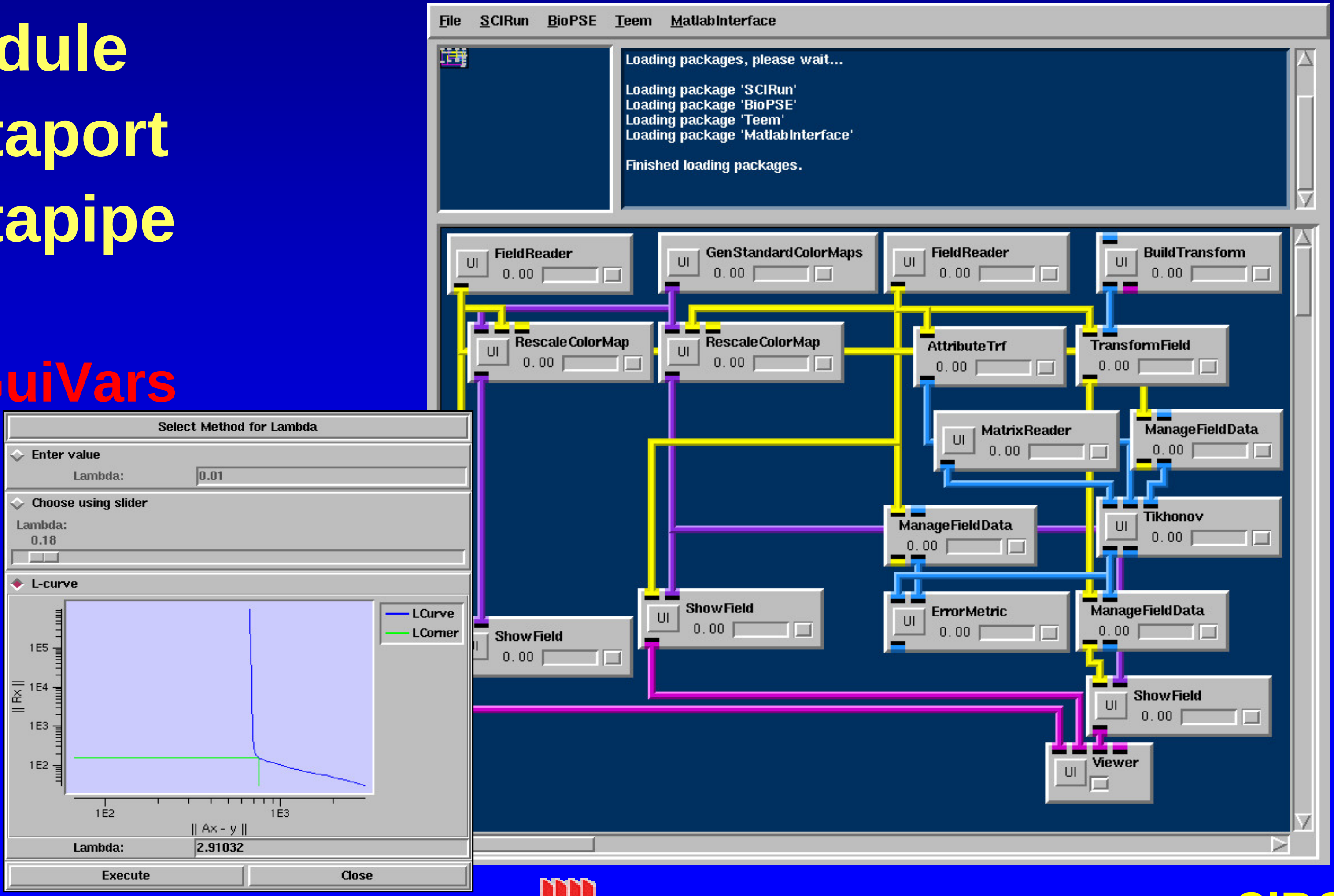
L-curve

Lambda: 2.91032

Network Elements

System Overview

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI
    - – GuiVars



Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.

Select Method for Lambda

◇ Enter value

Lambda: 0.01

◇ Choose using slider

Lambda: 0.18

◆ L-curve

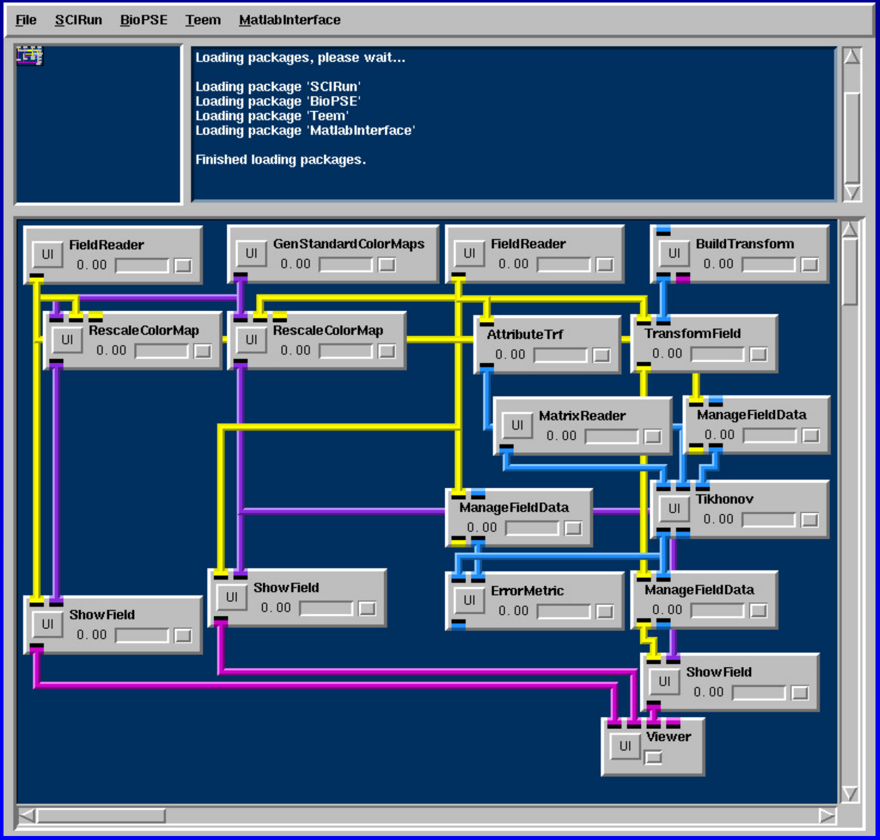
Lambda: 2.91032

CIBC

Network Design

- Dataflow Vocabulary
  - Module
  - Dataport
  - Datapipe
  - UI
- Send and Get
- GuiVars
- **Scheduler**
  - Dependencies
  - loops: send_intermediate

System Overview

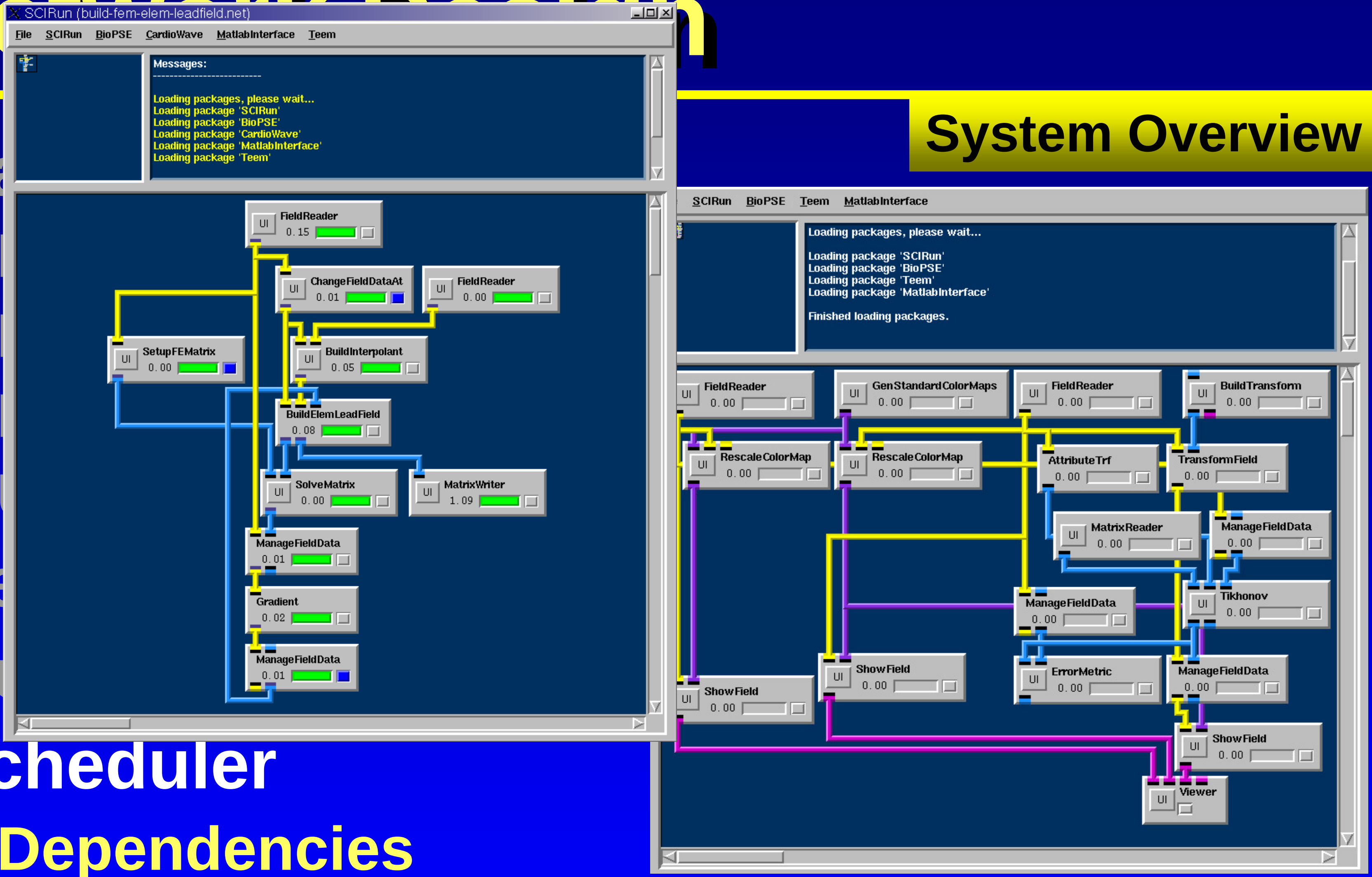


```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Network Design

- Da
- Se
- Gu
- Scheduler
  - Dependencies
  - loops: send_intermediate

System Overview

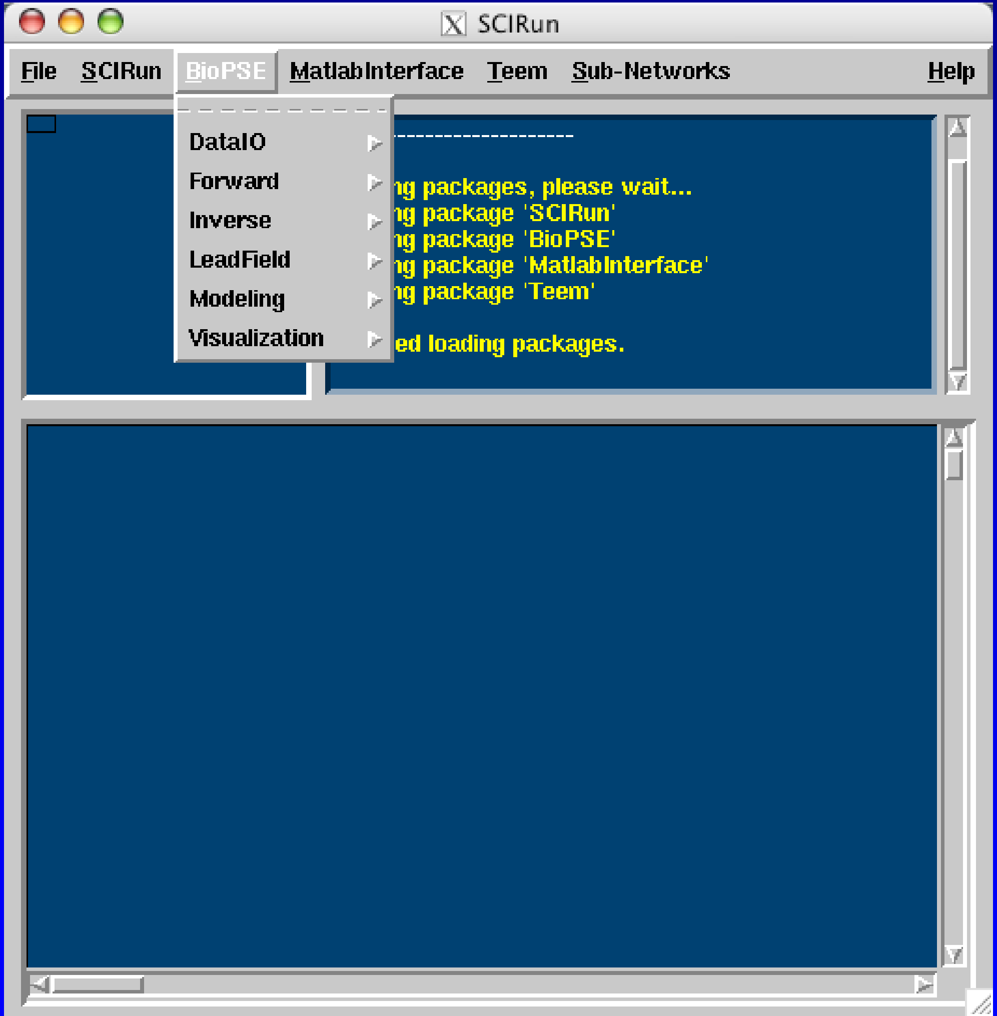


```
Messages:
---------------------------

Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'CardioWave'
Loading package 'MatlabInterface'
Loading package 'Teem'
```

```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Packages and Categories

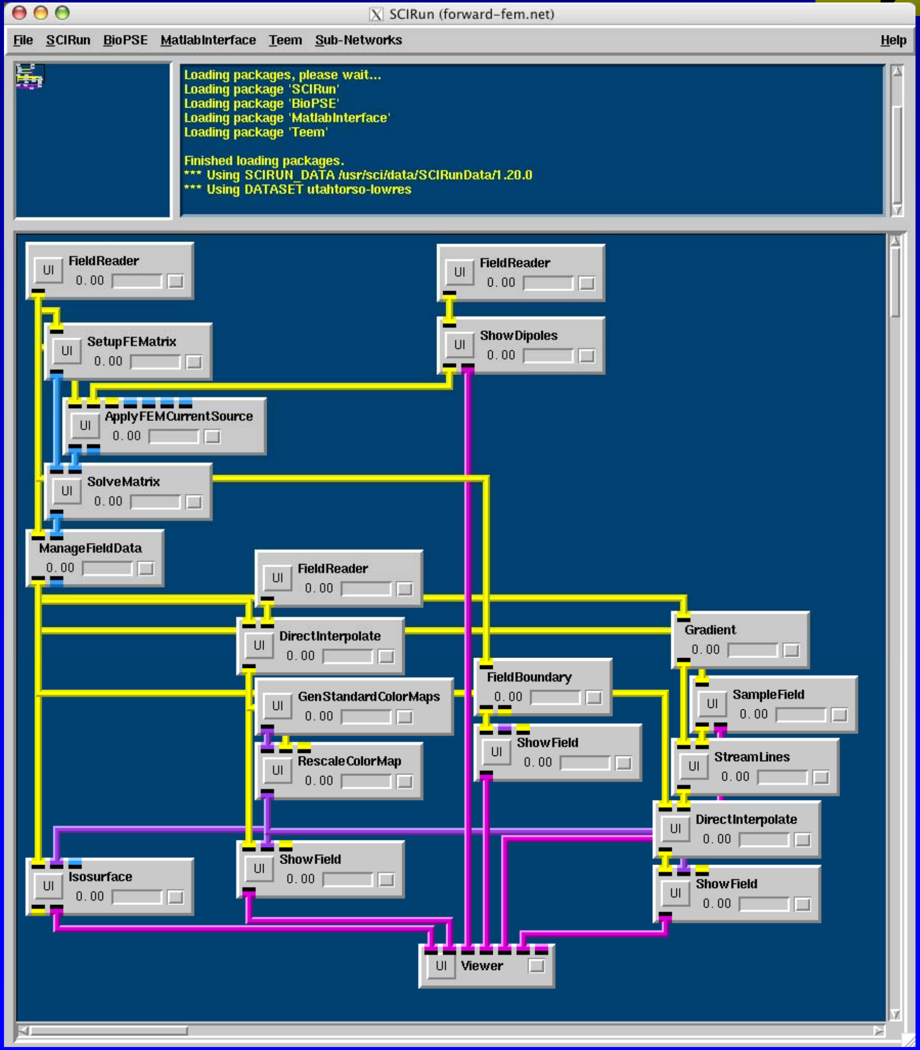
System Overview



```
--------------------

ng packages, please wait...
ng package 'SCIRun'
ng package 'BioPSE'
ng package 'MatlabInterface'
ng package 'Teem'

ed loading packages.
```

Managing Complexity: Subnets

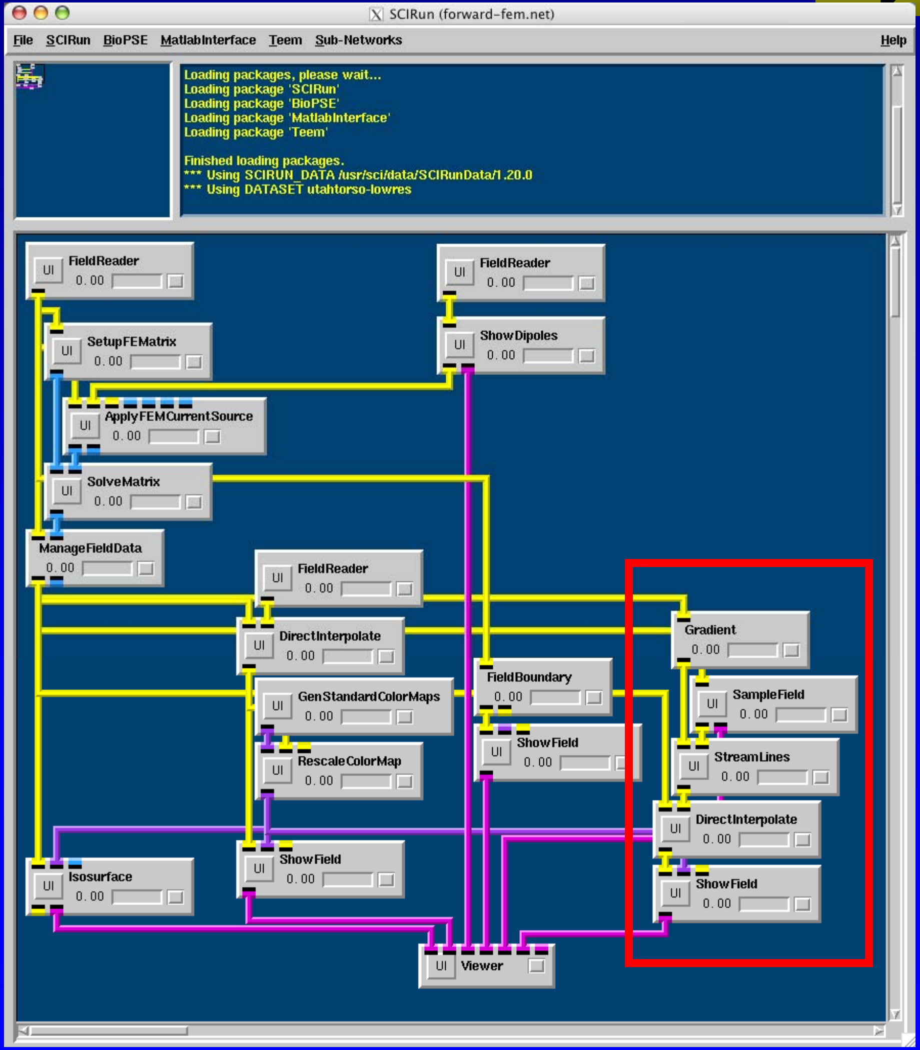
System Overview



```
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'

Finished loading packages.
*** Using SCIRUN_DATA /usr/sci/data/SCIRunData/1.20.0
*** Using DATASET utahtorso-lowres
```

Managing Complexity: Subnets

System Overview

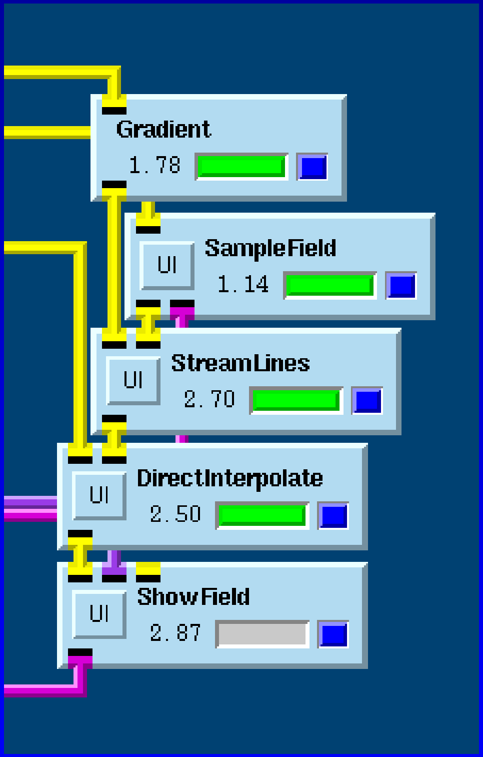


```
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'

Finished loading packages.
*** Using SCIRUN_DATA /usr/sci/data/SCIRunData/1.20.0
*** Using DATASET utahtorso-lowres
```

CIBC

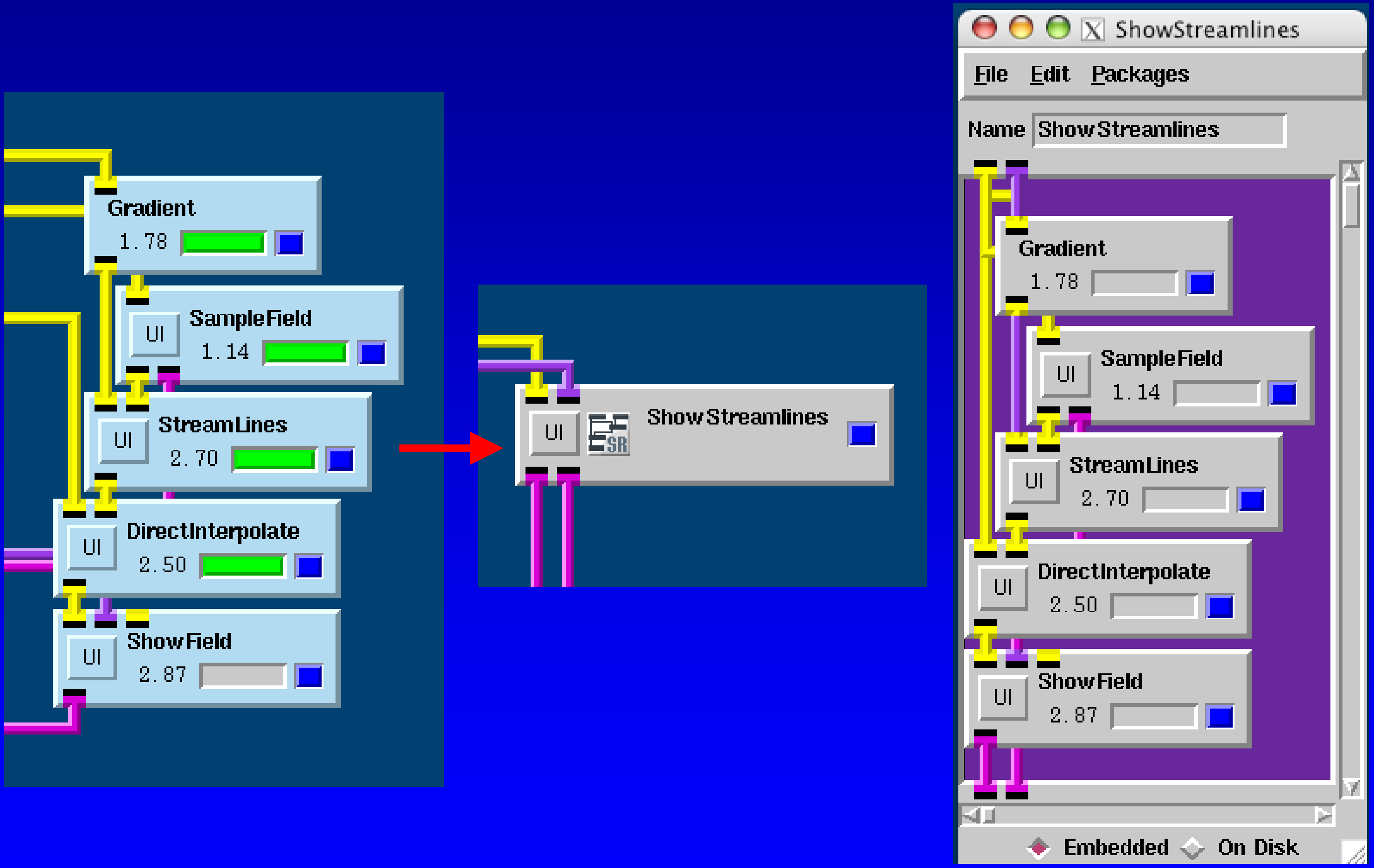
Managing Complexity: Subnets

System Overview



Managing Complexity: Subnets

System Overview

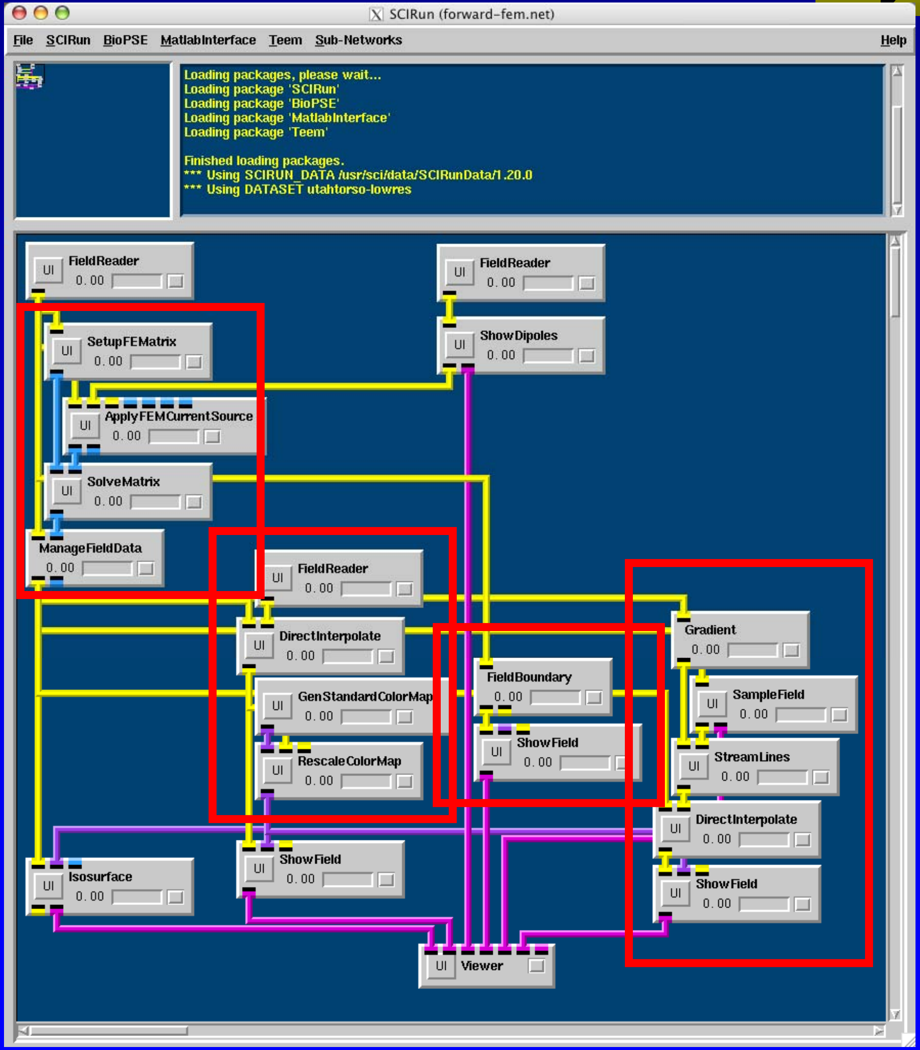


Name ShowStreamlines

◆ Embedded ◇ On Disk

Managing Complexity: Subnets

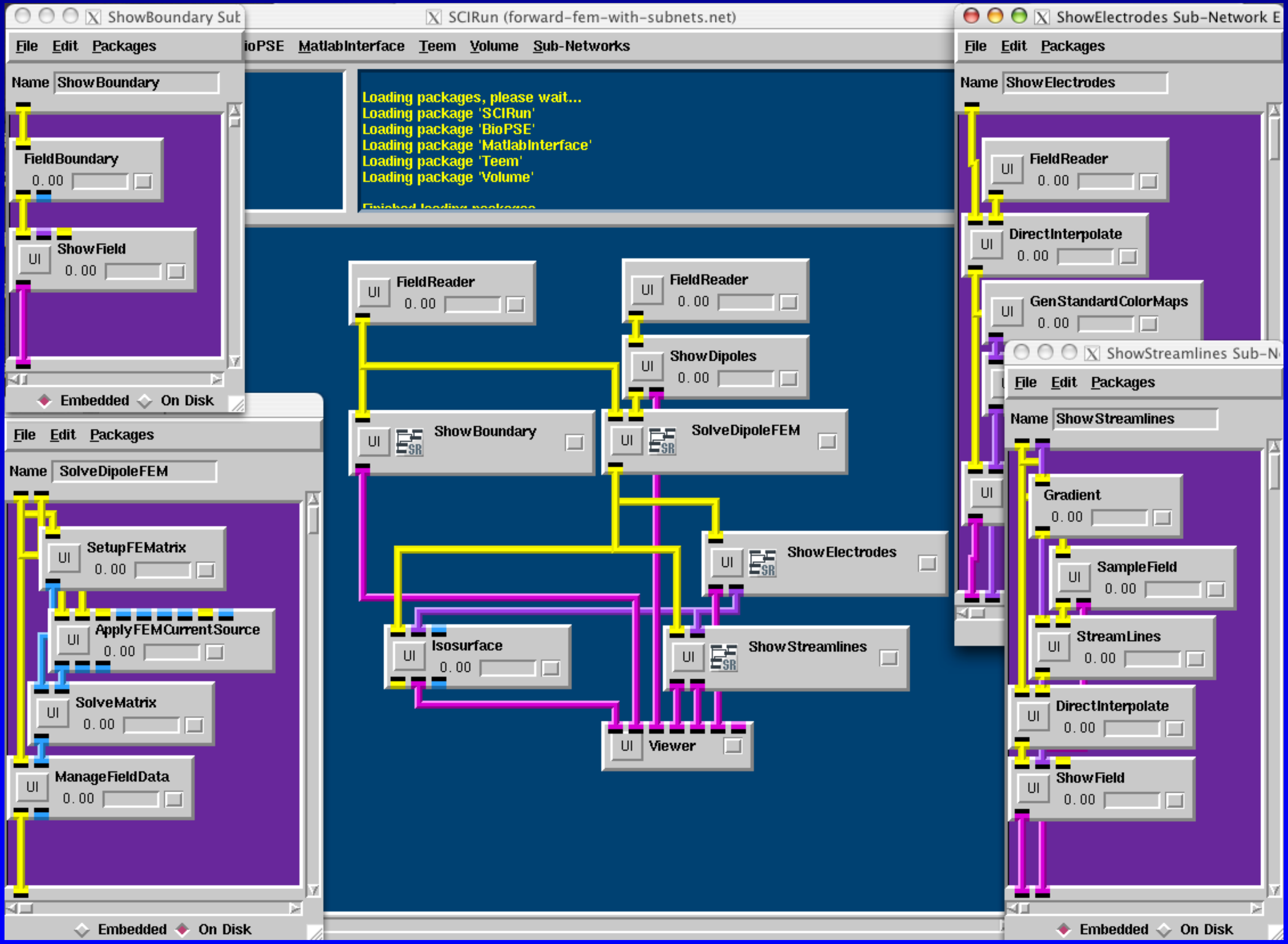
System Overview



```
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'

Finished loading packages.
*** Using SCIRUN_DATA /usr/sci/data/SCIRunData/1.20.0
*** Using DATASET utahtorso-lowres
```

Managing Complexity: Subnets

System Overview



```
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'
Loading package 'Volume'
Finished loading packages
```

Name ShowBoundary

Name SolveDipoleFEM

Name ShowElectrodes

Name ShowStreamlines

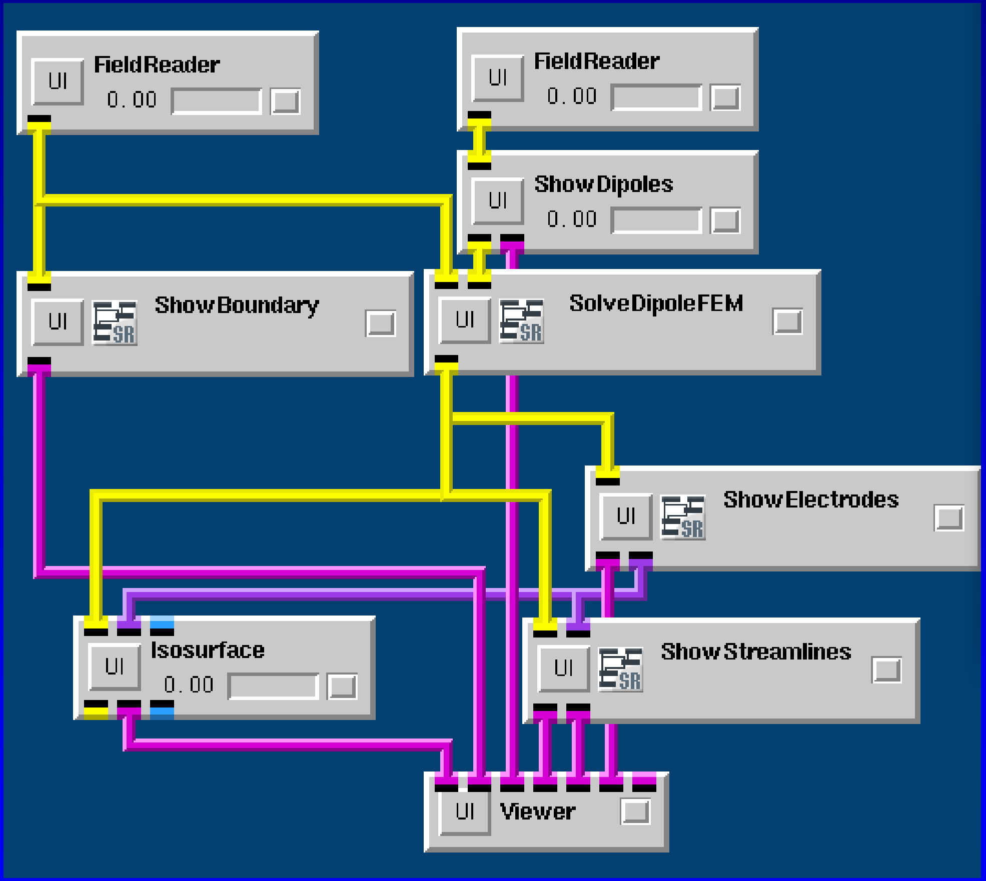
◆ Embedded ◇ On Disk

◇ Embedded ◆ On Disk

◆ Embedded ◇ On Disk

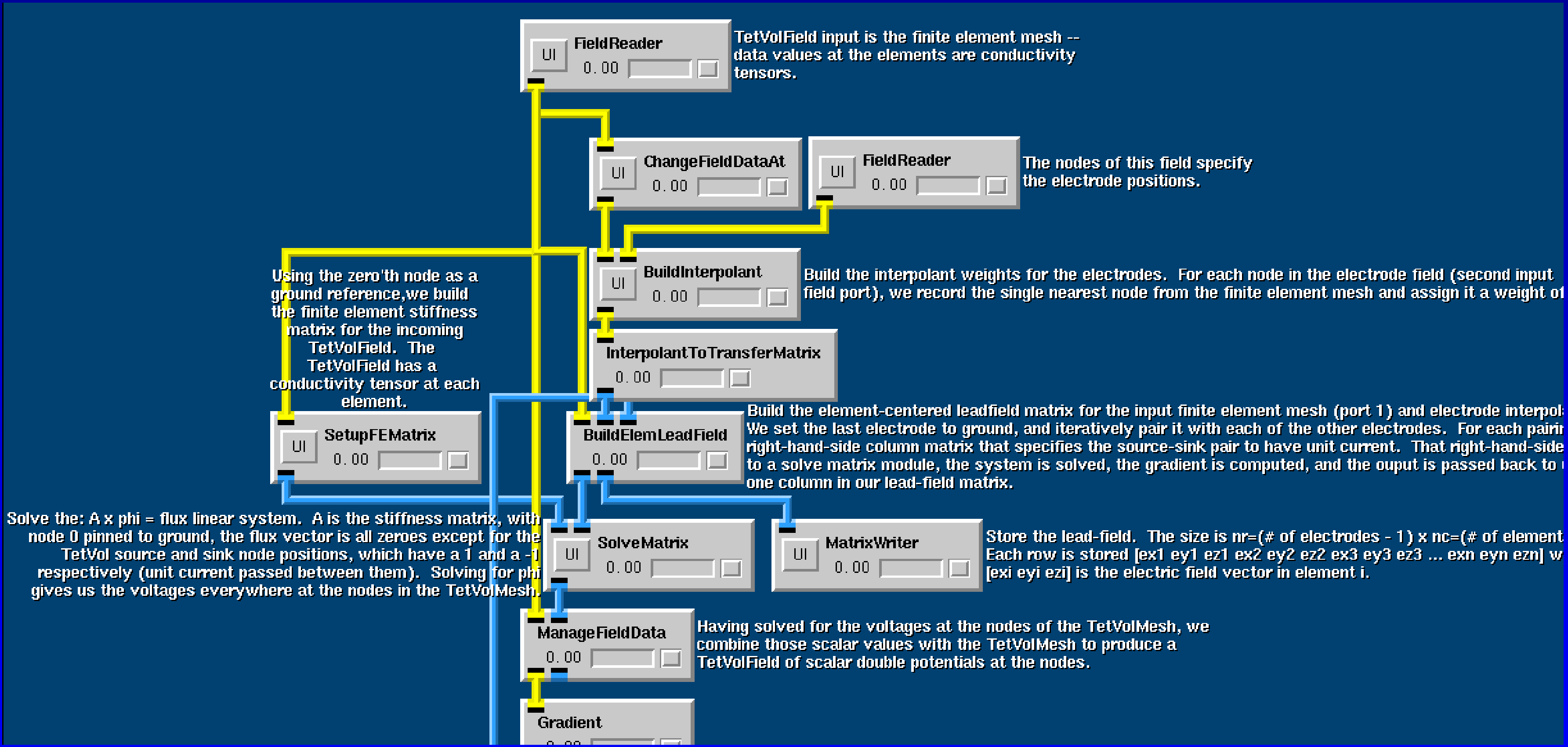
CIBC

Managing Complexity: Subnets



Managing Complexity: Annotations

System Overview



TetVolField input is the finite element mesh -- data values at the elements are conductivity tensors.

The nodes of this field specify the electrode positions.

Build the interpolant weights for the electrodes. For each node in the electrode field (second input
field port), we record the single nearest node from the finite element mesh and assign it a weight of

Using the zero'th node as a ground reference,we build the finite element stiffness matrix for the incoming TetVolField. The TetVolField has a conductivity tensor at each element.

Build the element-centered leadfield matrix for the input finite element mesh (port 1) and electrode interpol
We set the last electrode to ground, and iteratively pair it with each of the other electrodes. For each pairin
right-hand-side column matrix that specifies the source-sink pair to have unit current. That right-hand-side
to a solve matrix module, the system is solved, the gradient is computed, and the ouput is passed back to
one column in our lead-field matrix.

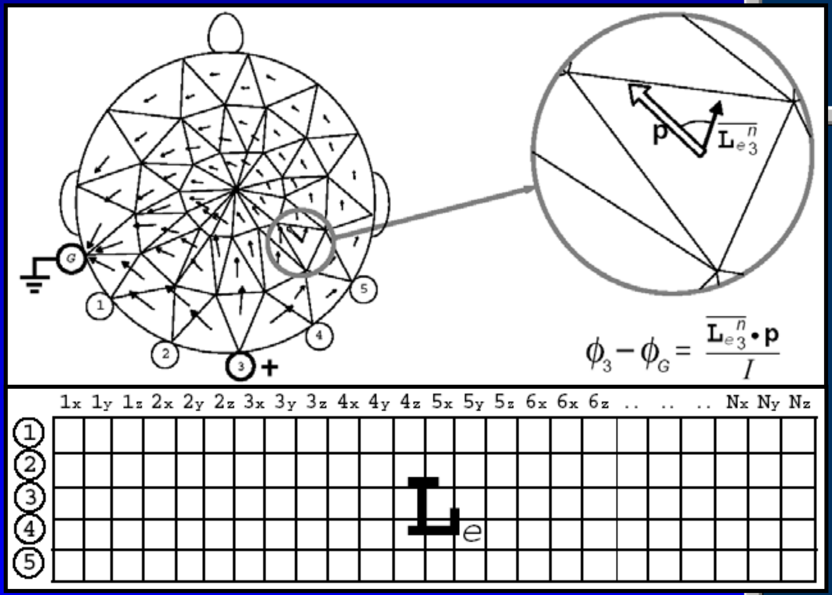
Solve the: A x phi = flux linear system. A is the stiffness matrix, with
node 0 pinned to ground, the flux vector is all zeroes except for the
TetVol source and sink node positions, which have a 1 and a -1
respectively (unit current passed between them). Solving for phi
gives us the voltages everywhere at the nodes in the TetVolMesh.

Store the lead-field. The size is nr=(# of electrodes - 1) x nc=(# of element
Each row is stored [ex1 ey1 ez1 ex2 ey2 ez2 ex3 ey3 ez3 ... exn eyn ezn] w
[exi eyi ezi] is the electric field vector in element i.

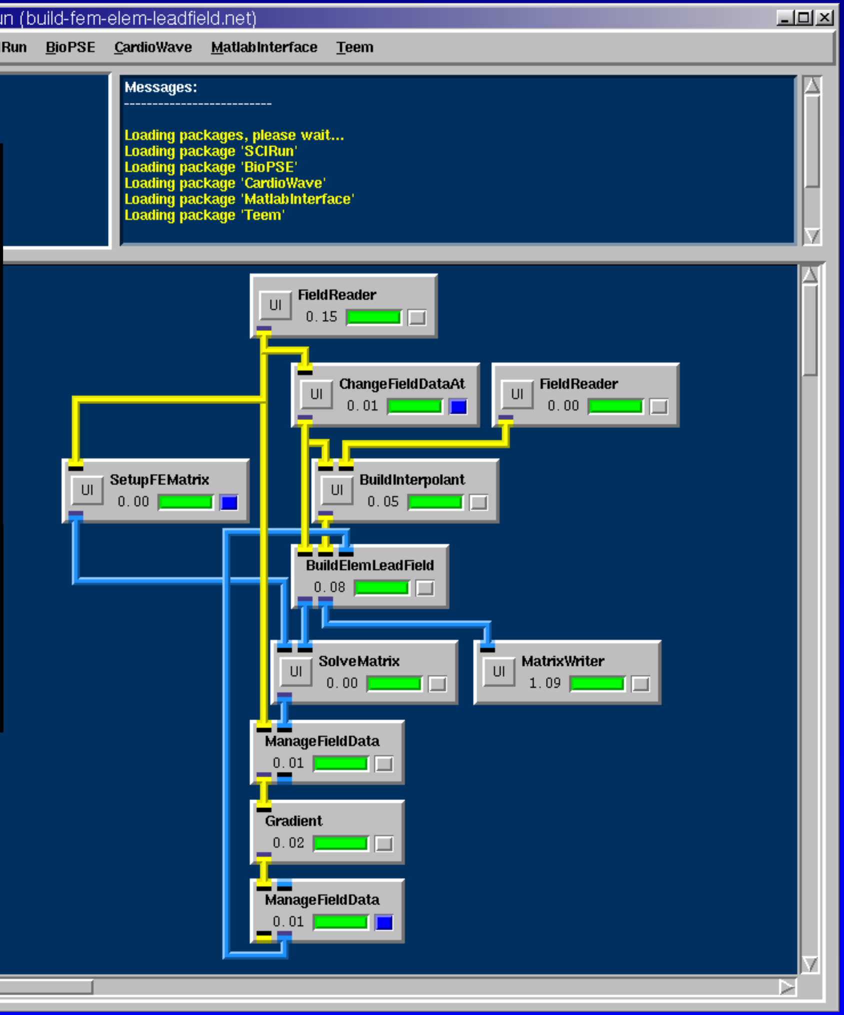
Having solved for the voltages at the nodes of the TetVolMesh, we combine those scalar values with the TetVolMesh to produce a TetVolField of scalar double potentials at the nodes.

build-fem-elem-leadfield.net

System Overview


G
1
2
3
4
5
+
p
$\overline{\mathbf{L}}_{e_3}^{n}$
1x 1y 1z 2x 2y 2z 3x 3y 3z 4x 4y 4z 5x 5y 5z 6x 6x 6z .. .. .. Nx Ny Nz
1
2
3
4
5
$\mathbf{L}_e$

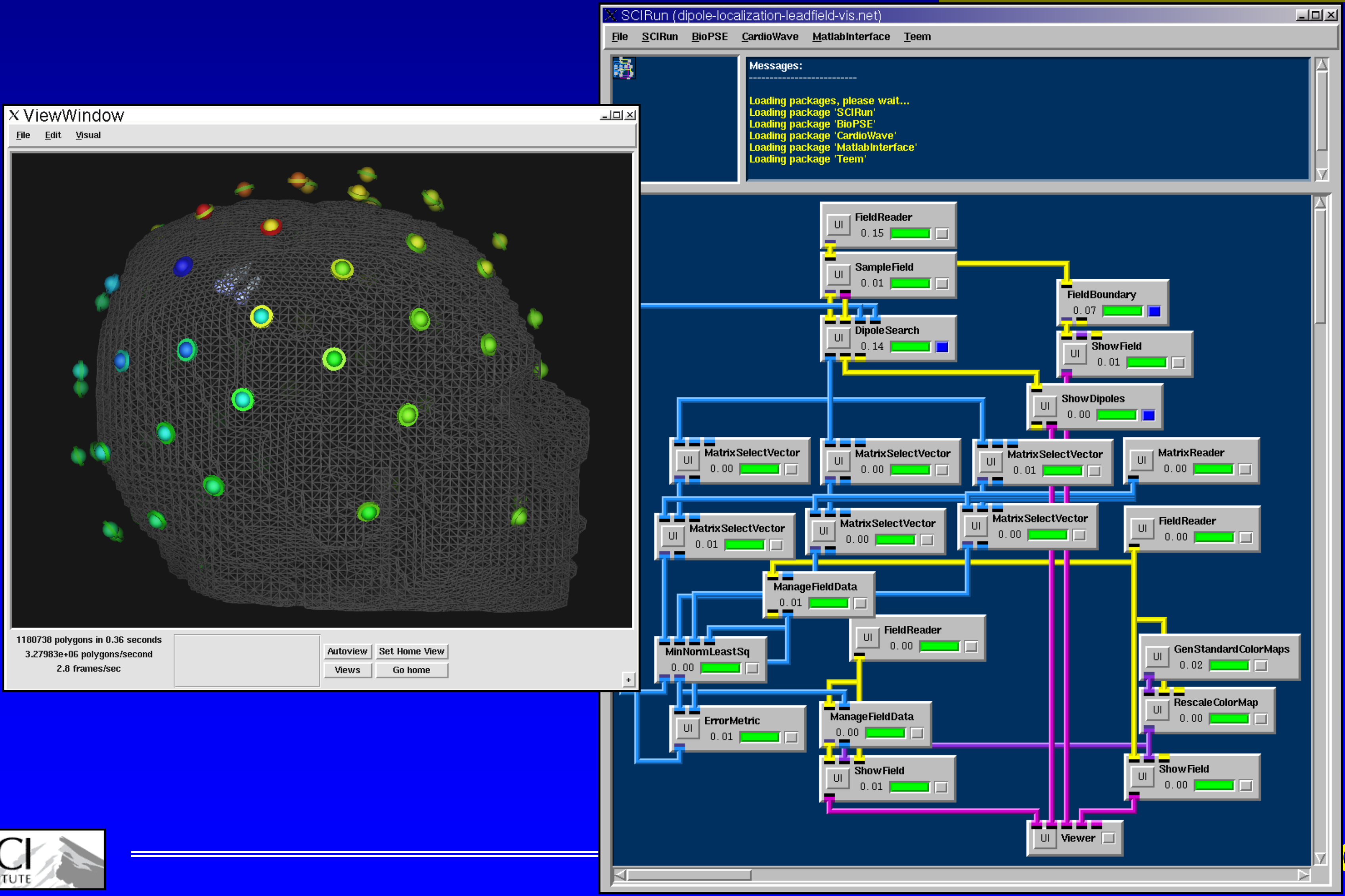
$$\phi_3 - \phi_G = \frac{\overline{\mathbf{L}}_{e_3}^{n} \bullet \mathbf{p}}{I}$$



```
Messages:
--------------------------

Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'CardioWave'
Loading package 'MatlabInterface'
Loading package 'Teem'
```

dipole-localization-leadfield-vis.net

System Overview

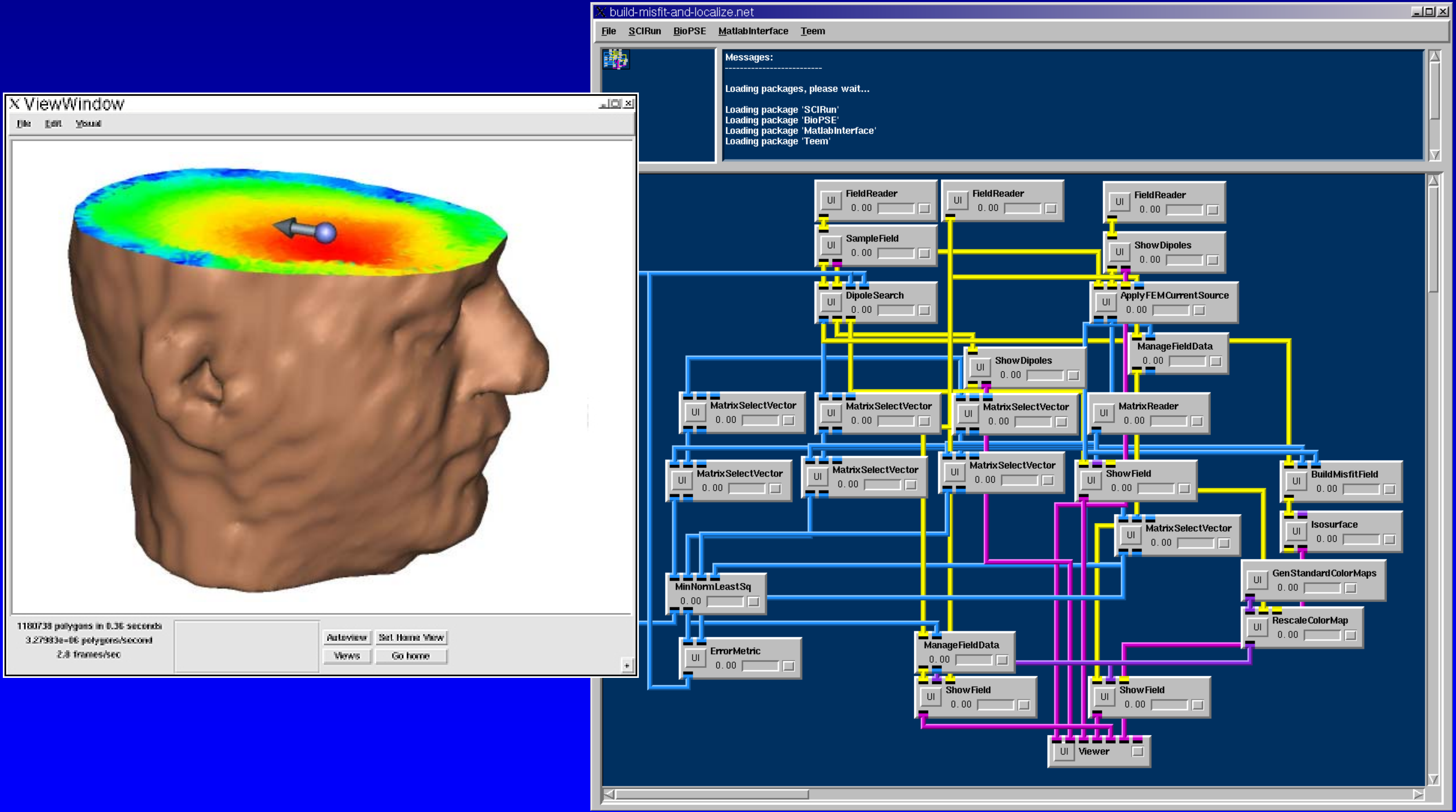


```
Messages:
---------------------------

Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'CardioWave'
Loading package 'MatlabInterface'
Loading package 'Teem'
```

```
1180738 polygons in 0.36 seconds
3.27983e+06 polygons/second
2.8 frames/sec
```

build-misfit-and-localize.net

System Overview

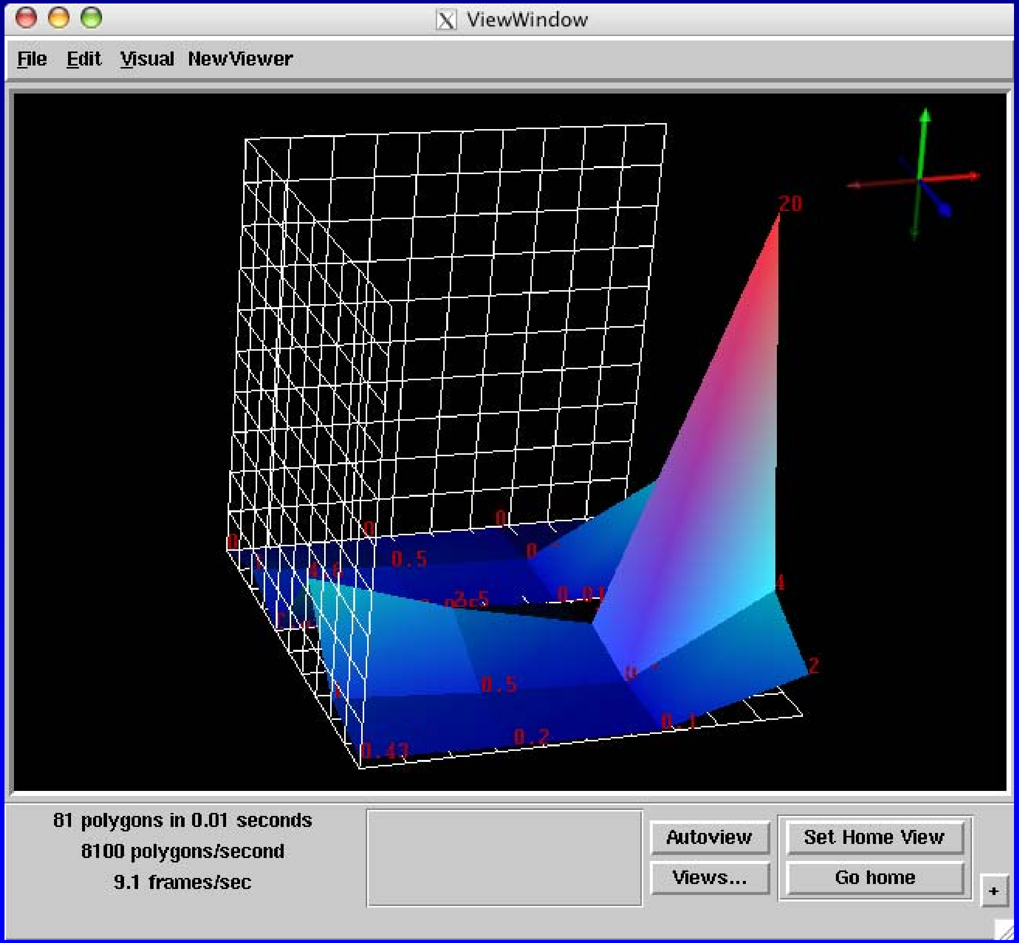


```
Messages:
--------------------------

Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'
```

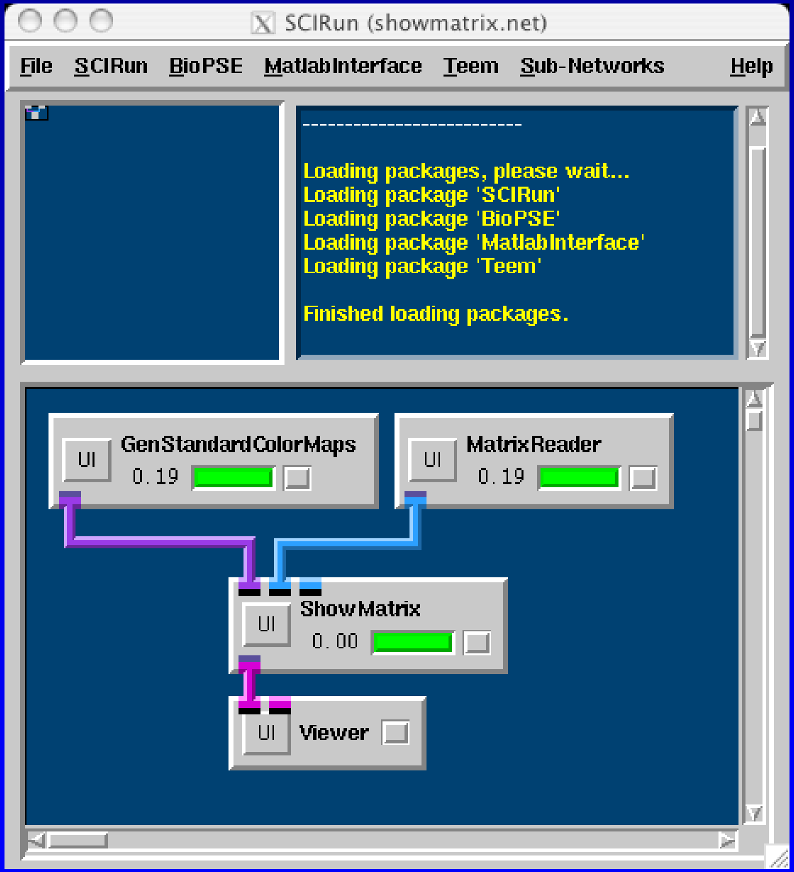
```
1180738 polygons in 0.36 seconds
3.27983e+06 polygons/second
2.8 frames/sec
```

showmatrix.net

System Overview



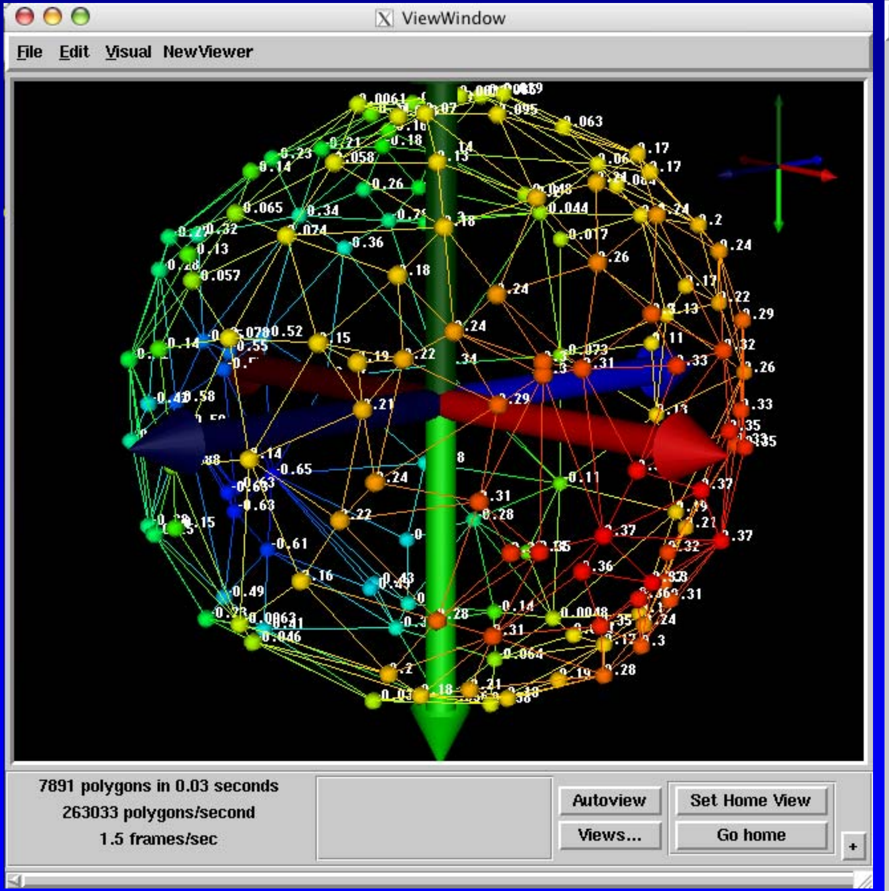
```
81 polygons in 0.01 seconds
8100 polygons/second
9.1 frames/sec
```



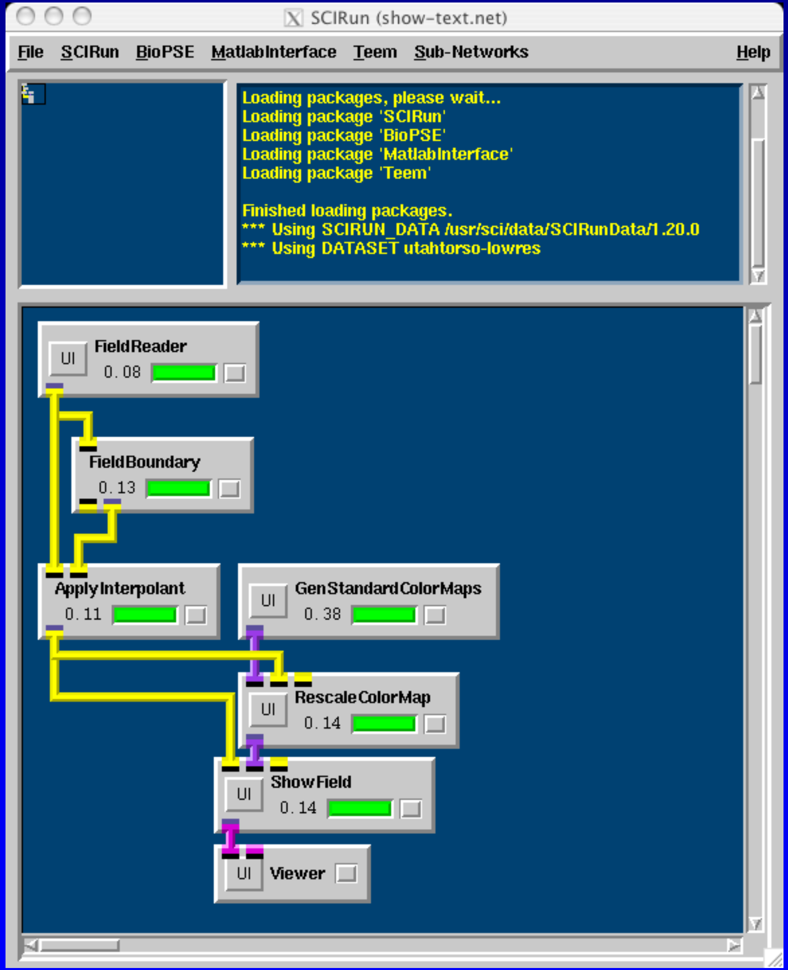
```
-------------------------
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'

Finished loading packages.
```

show-text.net

System Overview



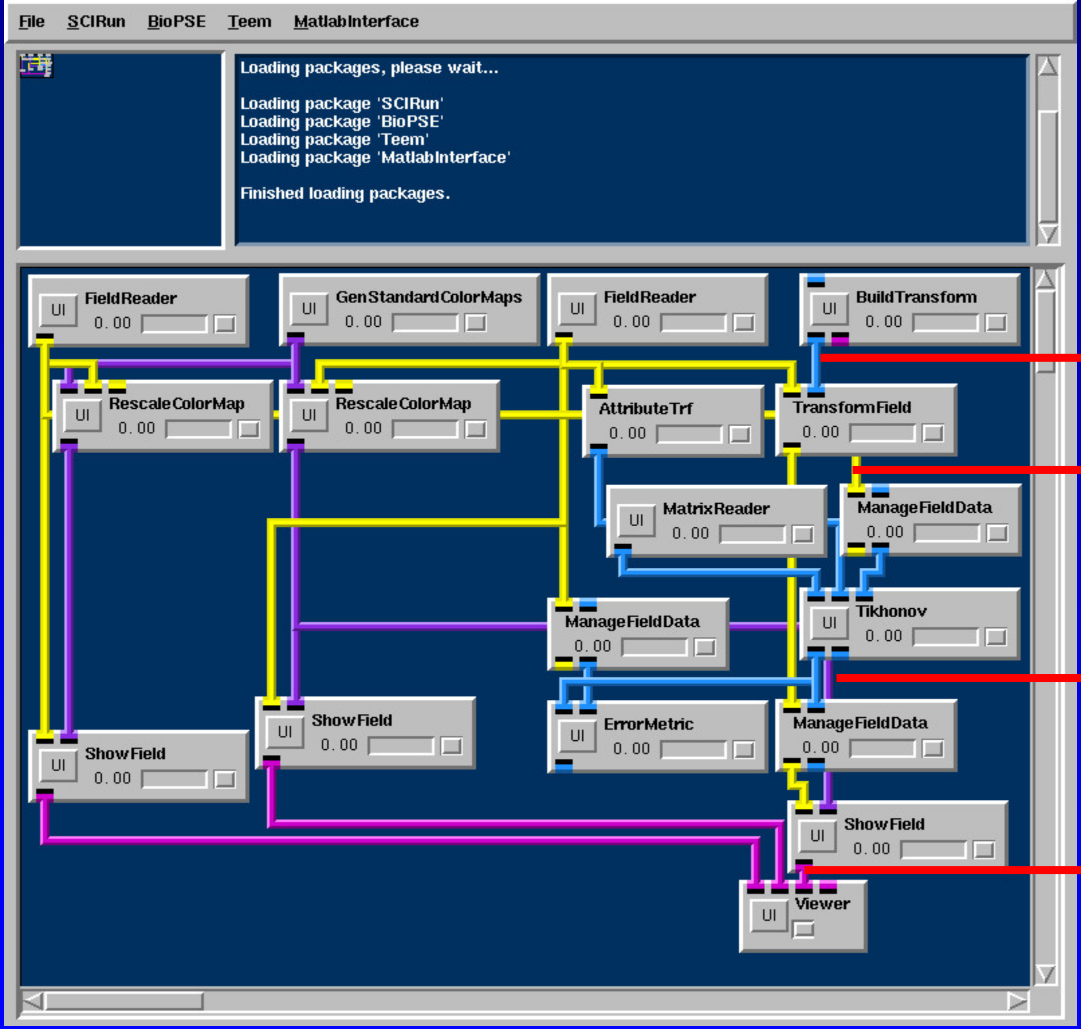
```
7891 polygons in 0.03 seconds
263033 polygons/second
1.5 frames/sec
```



```
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'

Finished loading packages.
*** Using SCIRUN_DATA /usr/sci/data/SCIRunData/1.20.0
*** Using DATASET utahtorso-lowres
```

Dataflow Datatypes Revisited

System Overview



```
Loading packages, please wait...

Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'Teem'
Loading package 'MatlabInterface'

Finished loading packages.
```

Matrix

Field

ColorMap

Geometry

Matrices: Class Hierarchy

- Matrix: base class
  - get, put, [ ], nrows, ncols, get_row, get_col, get_val, zero, mult, mult_transpose, print, {is_,as_,}{sparse,dense,column}, cg_solve, bicg_solve, scalar_multiply
- SparseRowMatrix
  - int *rows, int *cols, double *a, int nnz;
- ColumnMatrix
  - double *data;
- DenseMatrix
  - double **data;

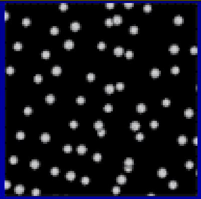
Matrices: External Libraries

- PETSc
  - Preconditioners: jacobi, bijacobi, sor, eisenstat, icc, ilu, asm, sles, lu, mg, spai, milu, nn, cholesky, ramg
  - Solvers: KSRICHARDSON, PSPCHEBYCHEV, KSPGG, KSPGMRES, KSPTCQMR, KSPBCGS, KSPBGS, KSPTFQMR, KSPCR, KSPLSQR, KSPBICG, KSPPREONLY

- BLAS and Atlas
  - Faster linear-algebra via loop unrolling

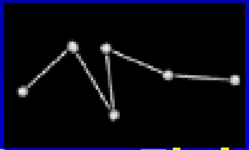
Fields: Mesh + Data

- Geometry
  - Regular
  - Irregular (basis)
- Data
  - int, float, double, ...
  - Vector, Tensor, ...
  - basis
- Properties

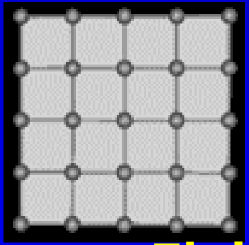


PointCloudField

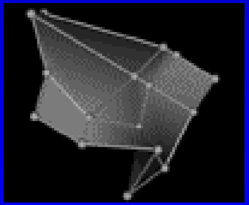
ScanlineField



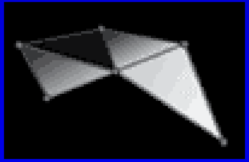
CurveField



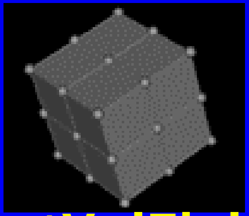
ImageField



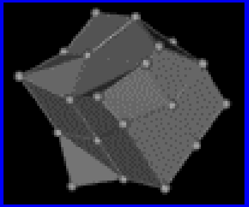
QuadSurfField



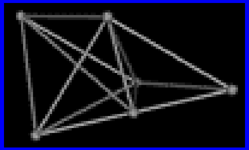
TriSurfField



LatVolField



HexVolField



TetVolField

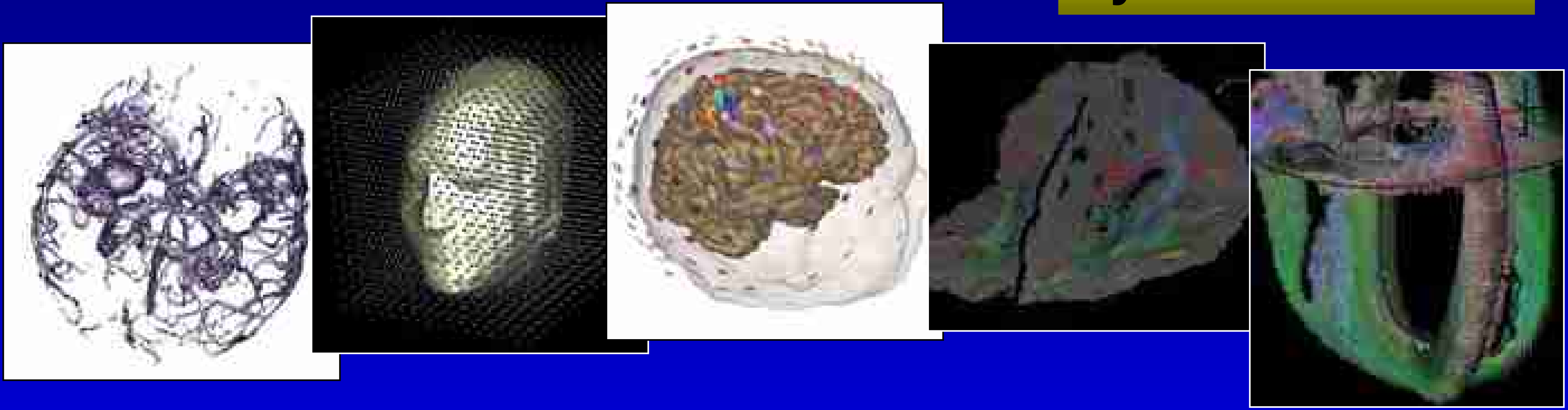
Persistence

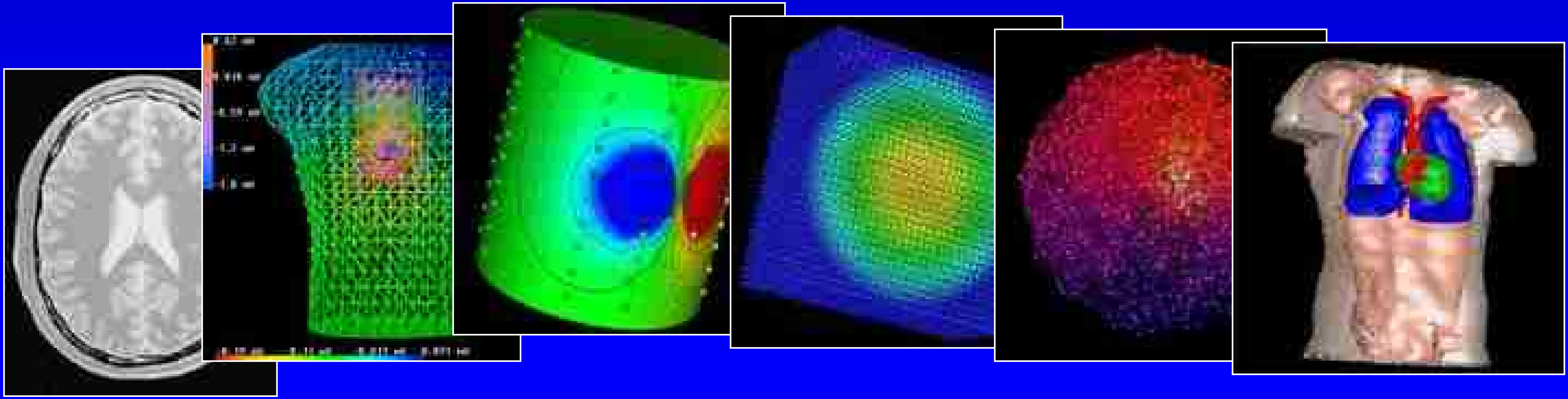
- Networks
- Serialize data for disk I/O
- Architecture independent
  - Smart pointers
  - Byte swapping
- Data files are (somewhat) human readable, but should ~not~ be generated / edited by anything other than SCIRun
  - Use “convert” programs

Persistent

```
void
Matrix::io(Piostream& stream)
{
  /* int version = */ stream.begin_class("Matrix", MATRIX_VERSION);
  PropertyManager::io(stream);
  stream.end_class();
}

void ColumnMatrix::io(Piostream& stream)
{
    /* int version = */stream.begin_class("ColumnMatrix", COLUMNMATRIX_VERSION);
    Matrix::io(stream);

    stream.io(rows);
    if(stream.reading()) {
      data=scinew double[rows];
    }
    int i;
    for(i=0;i<rows;i++)
      stream.io(data[i]);
    stream.end_class();
}
```

Example Datasets



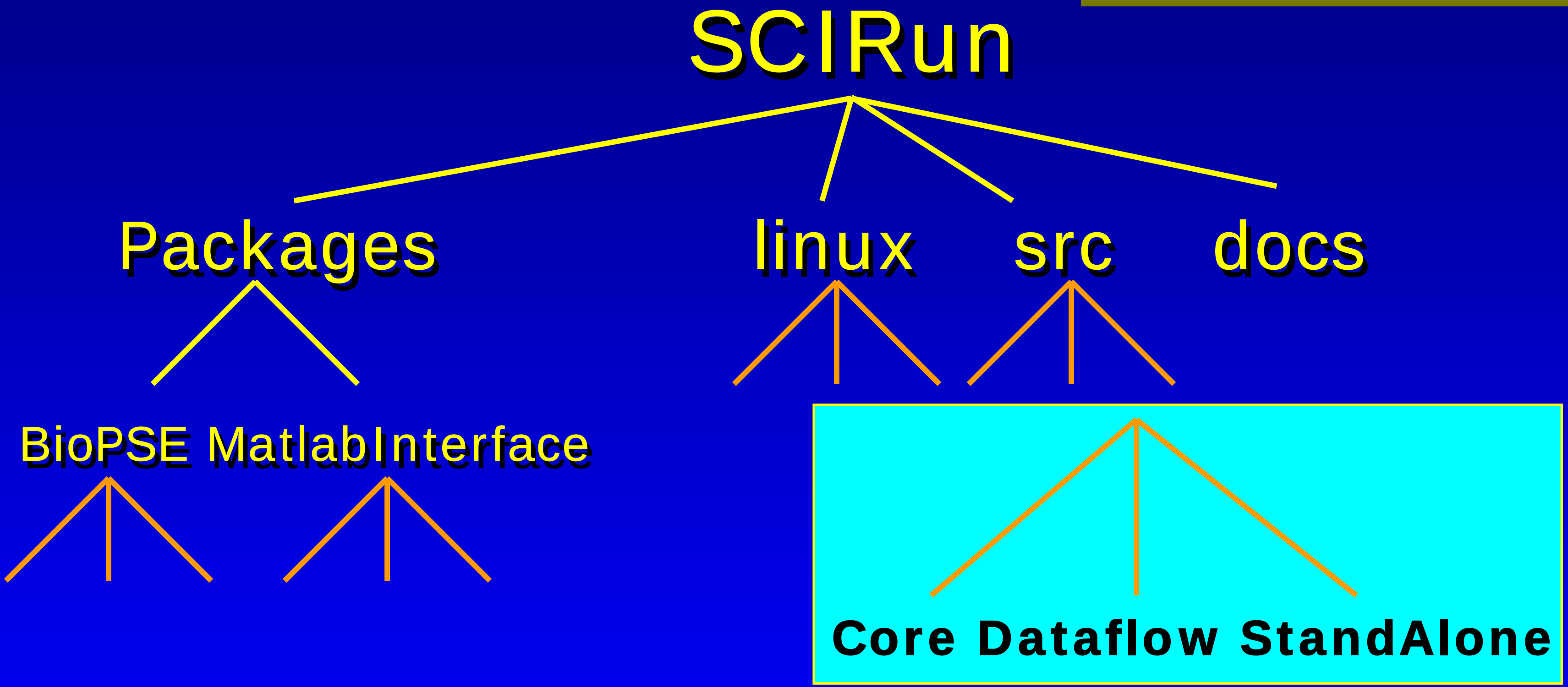


Overview

- Computational Science
- Problem Solving Environments
- Dataflow
- Datatypes
- Software Organization
- Extensibility
- PowerApps

Source Tree Organization

System Overview



SCIRun

Packages linux src docs

BioPSE MatlabInterface

Core Dataflow StandAlone

Core: algorithms, datatypes, math, threads
Dataflow: network, modules, ports, scheduler
StandAlone: converters, utilities

SCIRun Categories

Fields

- FieldsCreate
  - "sources" for new Fields
  - e.g. SampleLattice, FieldBoundary, ClipByFunction
- FieldsData
  - Just change data for an existing Field (Mesh untouched)
  - TransformFieldData, ManageFieldData, DirectMapping / ApplyMappingMatrix
- FieldsGeometry
  - Just change geometry for an existing Field (Data untouched)
  - Unstructure, HexToTet, QuadToTri
  - TransformField
- FieldsOther
  - Miscellaneous (FieldInfo, ChooseField, FieldMeasures, …)

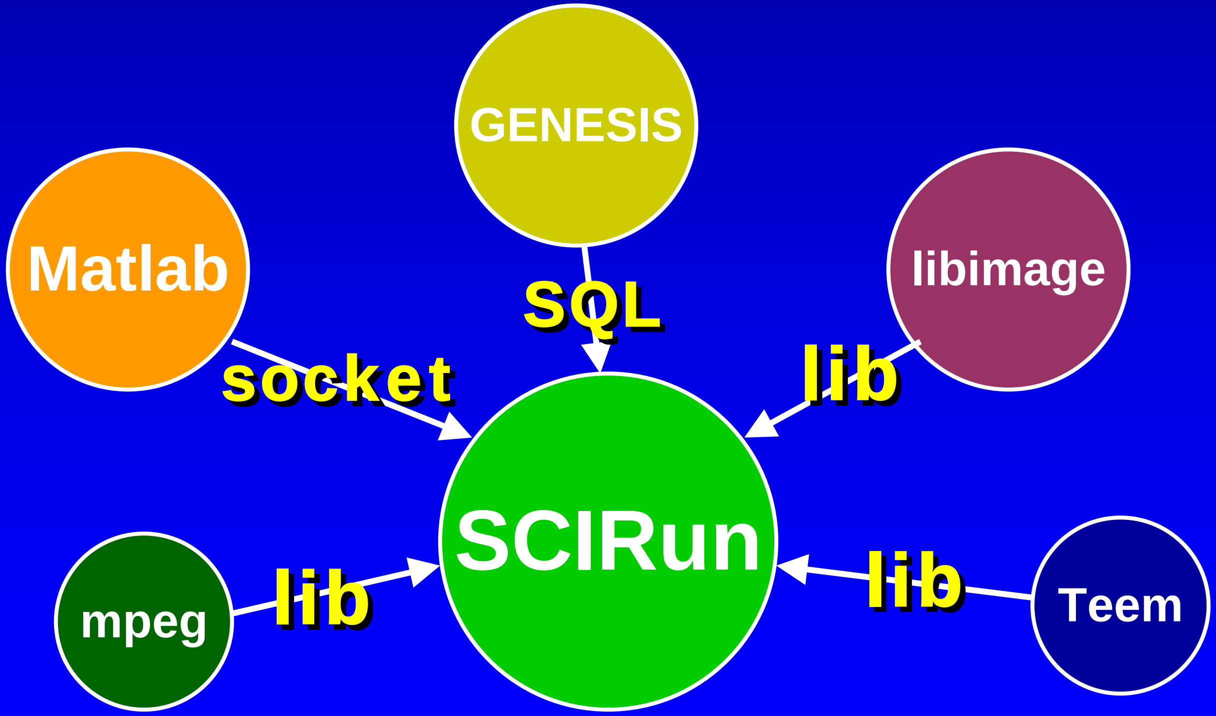
Visualization

- ColorMaps
- Isosurfaces

Extensibility

System Overview

- Leverage existing utilities
- Extensibility through *bridges*



Three Approaches

- Data Level
  - Command line tools to convert files
  - Communicating data across sockets
- Library Level
  - Teem, BLAS, ITK
- Application Level
  - Rewrite algorithms natively in SCIRun

Converters

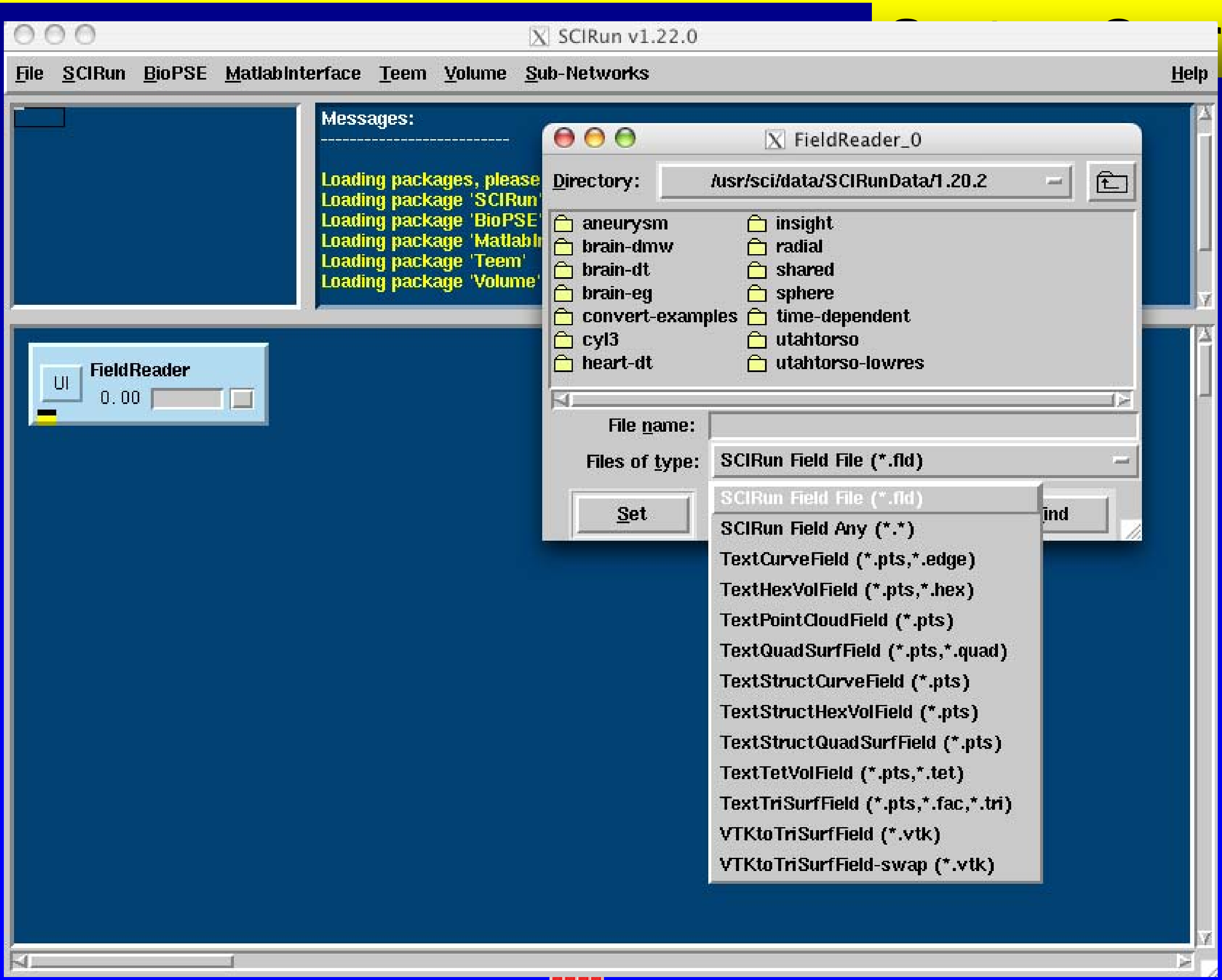
- Convert between human-editable text (e.g. CVRTI .pts, .dat files) and SCIRun Persistent objects
- See examples in SCIRunData/convert-examples/
- Each converter gives you usage info if invoked without arguments:

```
dmw stitch% TextToHexVolField

 Usage: TextToHexVolField pts hexes HexVolMesh [-noPtsCount] [-noElementsCount] [-oneBasedIndexing] [-binOutput] [debug]

    This program will read in a .pts (specifying the x/y/z coords of each point, one per line, entries separated by
    white space, file can have an optional one line header specifying number of points... and if it doesn't, you have
    to use the -noPtsCount command-line argument) and a .hex file (specifying i/j/k/l/m/n/o/p indices for each hex, also
    one per line, again with an optional one line header (use -noElementsCount if it's not there).  The hex entries are
    assumed to be zero-based, unless you specify -oneBasedIndexing.  And the SCIRun output file is written
    in ASCII, unless you specify -binOutput.
```

- Plug-ins for Readers / Writers

Data Import / Export

view



Messages:

Loading packages, please
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabIn
Loading package 'Teem'
Loading package 'Volume'

Directory: /usr/sci/data/SCIRunData/1.20.2

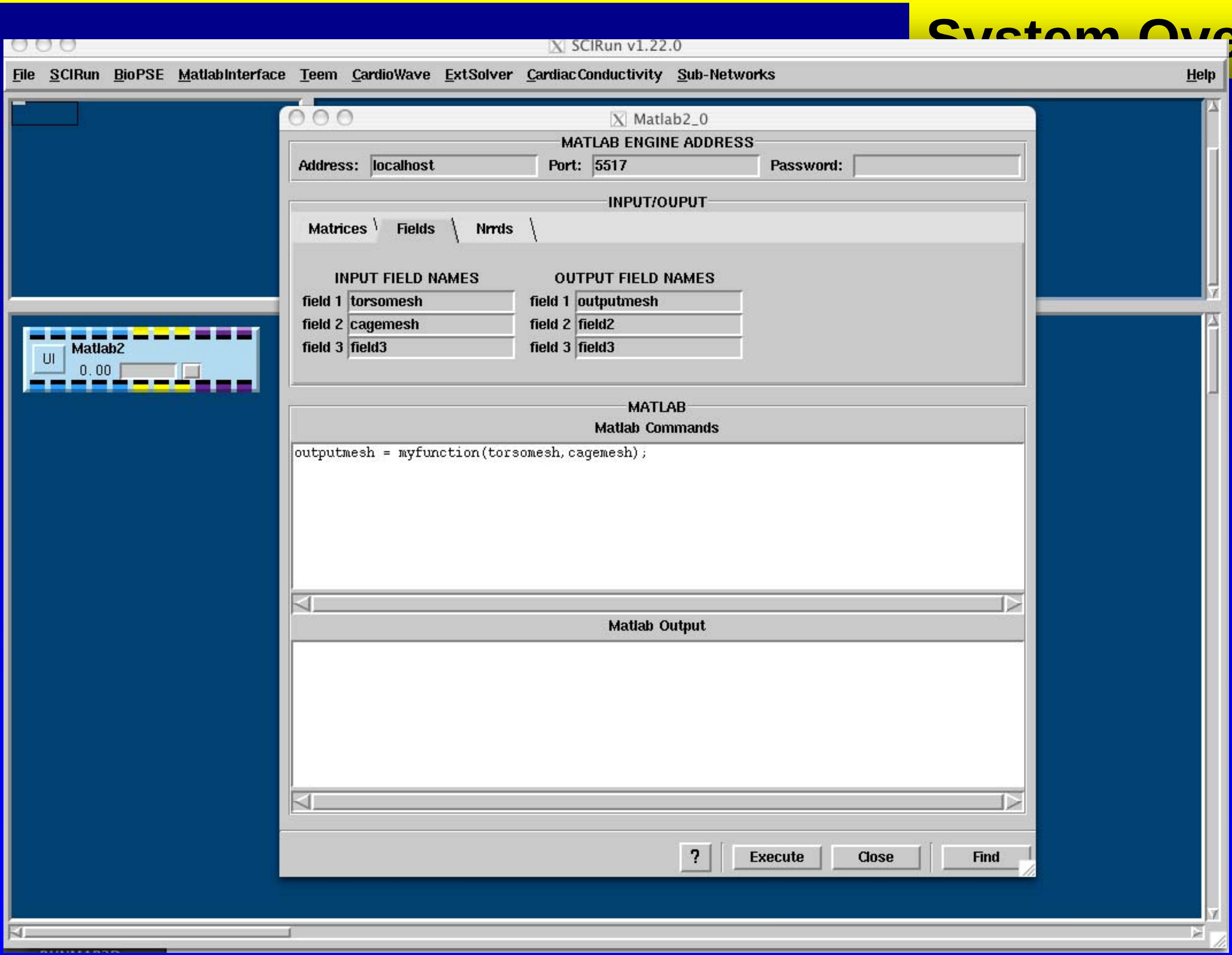
File name:

Files of type: SCIRun Field File (*.fld)

SCIRun v1.22.0
File
SCIRun
BioPSE
MatlabInterface
Teem
Volume
Sub-Networks
Help
FieldReader
UI
0.00
FieldReader_0
aneurysm
brain-dmw
brain-dt
brain-eg
convert-examples
cyl3
heart-dt
insight
radial
shared
sphere
time-dependent
utahtorso
utahtorso-lowres
Set
ind
SCIRun Field File (*.fld)
SCIRun Field Any (*.*)
TextCurveField (*.pts,*.edge)
TextHexVolField (*.pts,*.hex)
TextPointCloudField (*.pts)
TextQuadSurfField (*.pts,*.quad)
TextStructCurveField (*.pts)
TextStructHexVolField (*.pts)
TextStructQuadSurfField (*.pts)
TextTetVolField (*.pts,*.tet)
TextTriSurfField (*.pts,*.fac,*.tri)
VTKtoTriSurfField (*.vtk)
VTKtoTriSurfField-swap (*.vtk)

MatlabInterface

System Overview



Address: localhost
Port: 5517
Password:

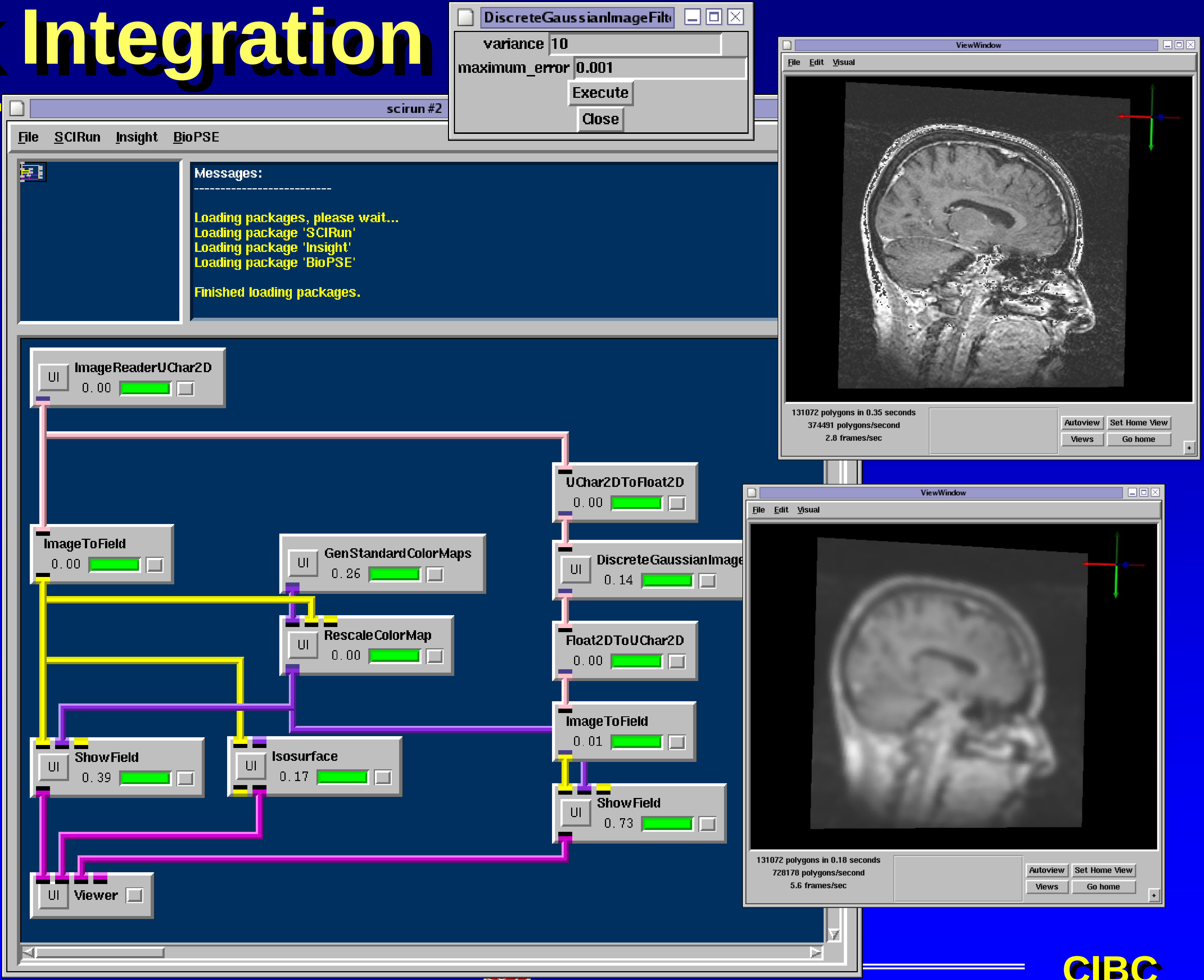
INPUT FIELD NAMES		OUTPUT FIELD NAMES	
field 1	torsomesh	field 1	outputmesh
field 2	cagemesh	field 2	field2
field 3	field3	field 3	field3

```
outputmesh = myfunction(torsomesh,cagemesh);
```

Three Approaches

- Data Level
  - Command line tools to convert files
- Library Level
  - Teem, BLAS, ITK
- Application Level
  - Rewrite algorithms natively in SCIRun

ITK Integration



DiscreteGaussianImageFilt

variance 10

maximum_error 0.001

Execute

Close

scirun #2

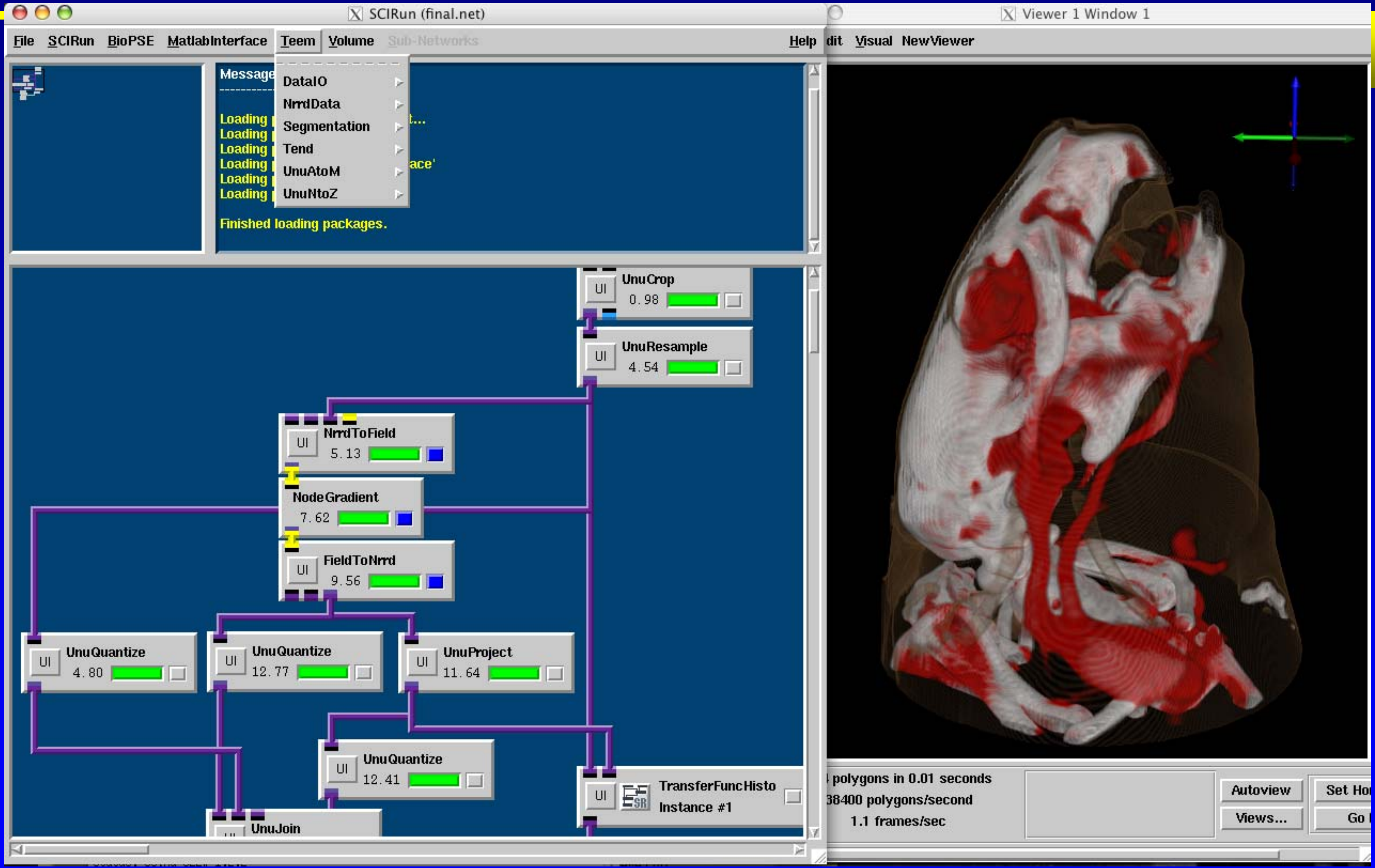
```
Messages:
---------------------------

Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'Insight'
Loading package 'BioPSE'

Finished loading packages.
```

```
131072 polygons in 0.35 seconds
374491 polygons/second
2.8 frames/sec
```

```
131072 polygons in 0.18 seconds
728178 polygons/second
5.6 frames/sec
```

CIBC

Teem



Loading
Loading
Loading
Loading
Loading
Loading

Finished loading packages.

polygons in 0.01 seconds
38400 polygons/second
1.1 frames/sec

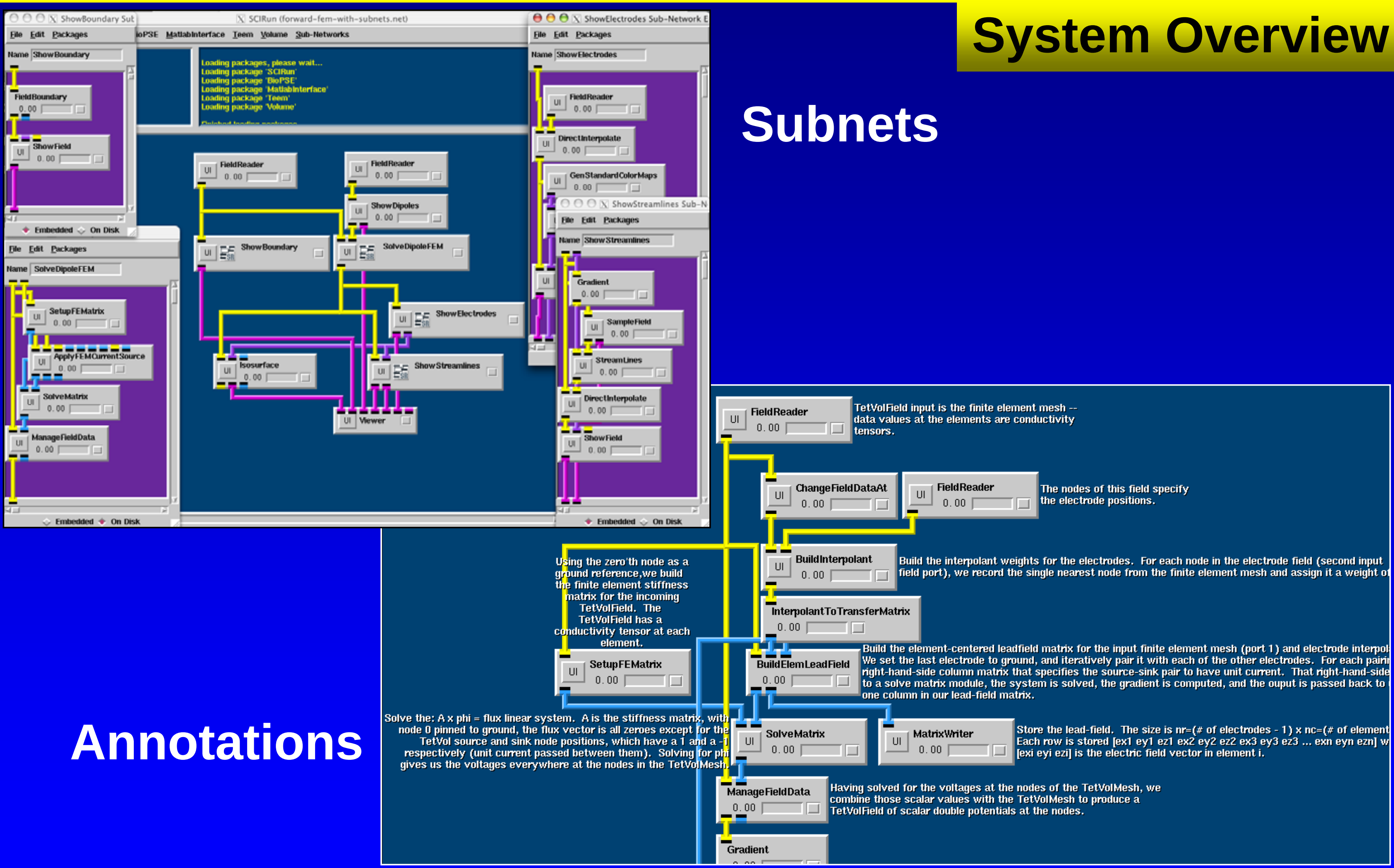
CIBC

Overview

- Computational Science
- Problem Solving Environments
- Dataflow
- Datatypes
- Software Organization
- Extensibility
- **PowerApps**

Managing Complexity: UIs

System Overview



```
Loading packages, please wait...
Loading package 'SCIRun'
Loading package 'BioPSE'
Loading package 'MatlabInterface'
Loading package 'Teem'
Loading package 'Volume'
```

TetVolField input is the finite element mesh -- data values at the elements are conductivity tensors.

The nodes of this field specify the electrode positions.

Build the interpolant weights for the electrodes. For each node in the electrode field (second input field port), we record the single nearest node from the finite element mesh and assign it a weight o

Using the zero'th node as a ground reference,we build the finite element stiffness matrix for the incoming TetVolField. The TetVolField has a conductivity tensor at each element.

Build the element-centered leadfield matrix for the input finite element mesh (port 1) and electrode interpol We set the last electrode to ground, and iteratively pair it with each of the other electrodes. For each pairi right-hand-side column matrix that specifies the source-sink pair to have unit current. That right-hand-side to a solve matrix module, the system is solved, the gradient is computed, and the ouput is passed back to one column in our lead-field matrix.

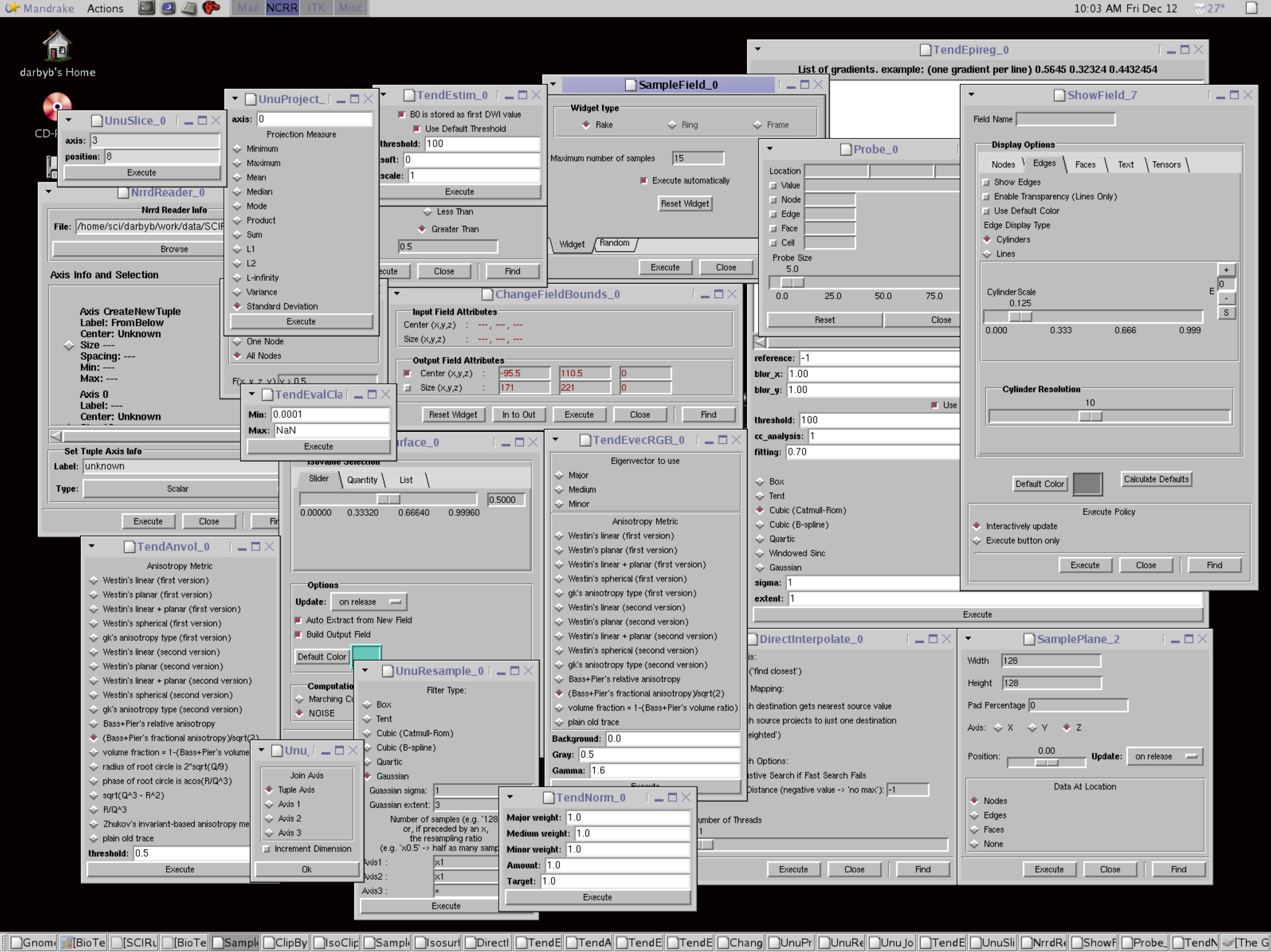
Solve the: A x phi = flux linear system. A is the stiffness matrix, with node 0 pinned to ground, the flux vector is all zeroes except for the TetVol source and sink node positions, which have a 1 and a -1 respectively (unit current passed between them). Solving for phi gives us the voltages everywhere at the nodes in the TetVolMesh.

Store the lead-field. The size is nr=(# of electrodes - 1) x nc=(# of element Each row is stored [ex1 ey1 ez1 ex2 ey2 ez2 ex3 ey3 ez3 ... exn eyn ezn] w [exi eyi ezi] is the electric field vector in element i.

Having solved for the voltages at the nodes of the TetVolMesh, we combine those scalar values with the TetVolMesh to produce a TetVolField of scalar double potentials at the nodes.

Subnets

Annotations



UnuSlice_0
axis: 3
position: 8

UnuProject_
axis: 0
Projection Measure: ● Standard Deviation

TendEstim_0
☑ B0 is stored as first DWI value
☑ Use Default Threshold
threshold: 100
soft: 0
scale: 1
● Greater Than
0.5

SampleField_0
Widget type: ● Rake
Maximum number of samples 15
☑ Execute automatically

TendEpireg_0
List of gradients. example: (one gradient per line) 0.5645 0.32324 0.4432454

ShowField_7
Field Name:
Edge Display Type: ● Cylinders
Cylinder Scale 0.125
Cylinder Resolution 10
Execute Policy: ● Interactively update

Probe_0
Probe Size 5.0

NrrdReader_0
File: /home/sci/darbyb/work/data/SCIF

Axis CreateNewTuple
Label: FromBelow
Center: Unknown
Size ---
Spacing: ---
Min: ---
Max: ---

Axis 0
Label: ---
Center: Unknown

Set Tuple Axis Info
Label: unknown
Type: Scalar

● All Nodes
F(x,y,z,v) v > 0.5

ChangeFieldBounds_0
Input Field Attributes
Center (x,y,z) : --- , --- , ---
Size (x,y,z) : --- , --- , ---

Output Field Attributes
☑ Center (x,y,z) : -95.5 110.5 0
□ Size (x,y,z) : 171 221 0

TendEvalCla
Min: 0.0001
Max: NaN

Isosurface_0
0.5000
Update: on release
☑ Auto Extract from New Field
☑ Build Output Field
Computation: ● NOISE

TendEvecRGB_0
Anisotropy Metric: ● (Bass+Pier's fractional anisotropy)/sqrt(2)
Background: 0.0
Gray: 0.5
Gamma: 1.6

TendAnvol_0
Anisotropy Metric: ● (Bass+Pier's fractional anisotropy)/sqrt(2)
threshold: 0.5

UnuJoin
Join Axis: ● Tuple Axis
□ Increment Dimension

UnuResample_0
Filter Type: ● Gaussian
Gaussian sigma: 1
Gaussian extent: 3
Number of samples (e.g. `128') or, if preceded by an x, the resampling ratio (e.g. `x0.5' -> half as many samp
Axis1 : x1
Axis2 : x1
Axis3 : =

TendNorm_0
Major weight: 1.0
Medium weight: 1.0
Minor weight: 1.0
Amount: 1.0
Target: 1.0

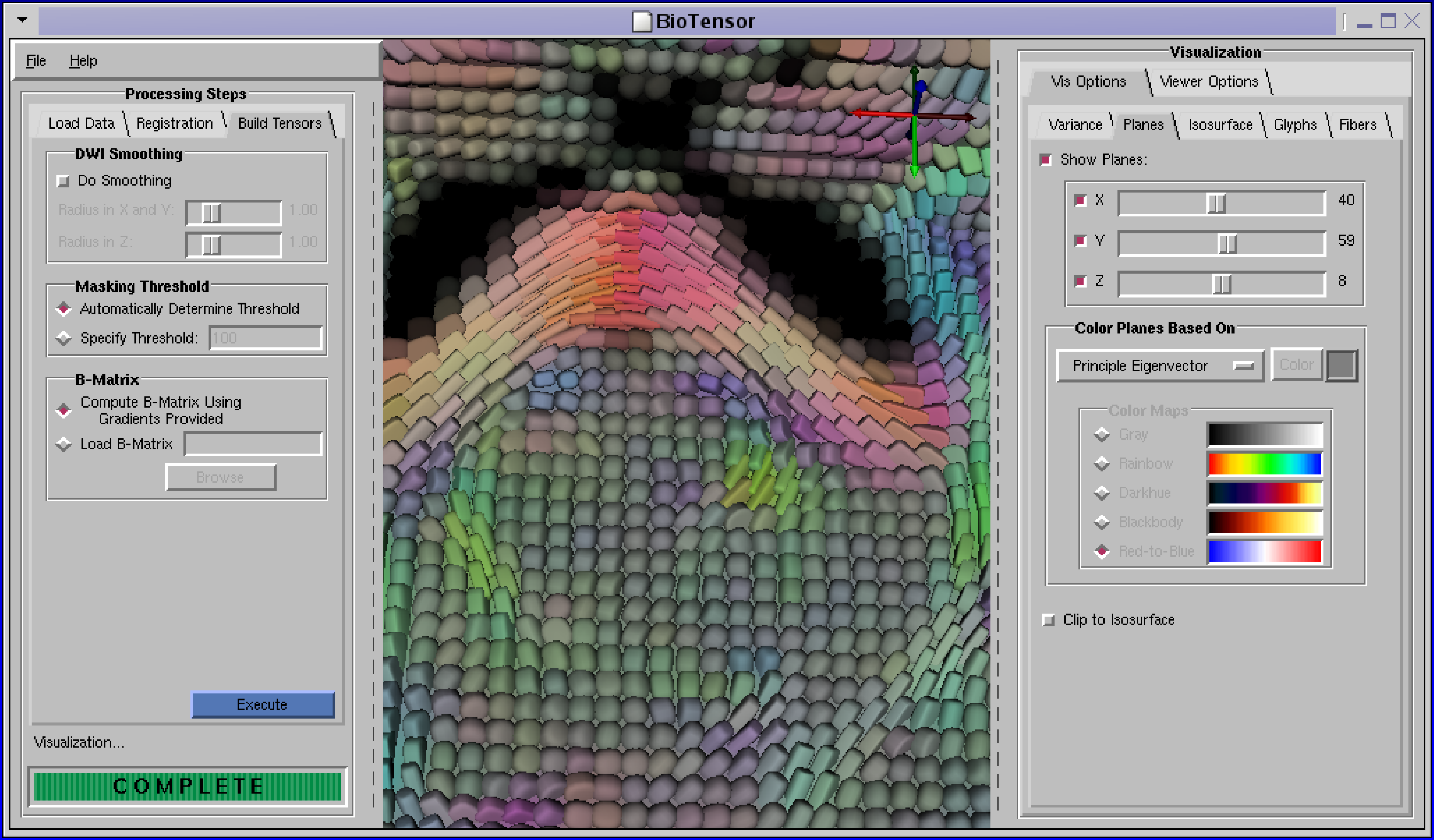
reference: -1
blur_x: 1.00
blur_y: 1.00
☑ Use
threshold: 100
cc_analysis: 1
fitting: 0.70
● Cubic (Catmull-Rom)
sigma: 1
extent: 1

DirectInterpolate_0
('find closest')
Mapping:
h destination gets nearest source value
h source projects to just one destination
eighted')
h Options:
stive Search if Fast Search Fails
Distance (negative value -> 'no max'): -1
umber of Threads 1

SamplePlane_2
Width 128
Height 128
Pad Percentage 0
Axis: ● Z
Position: 0.00
Update: on release
Data At Location: ● Nodes

PowerApps: User-Friendly, Domain-Specific

System Overview



DWI Smoothing

☐ Do Smoothing

Radius in X and Y: 1.00

Radius in Z: 1.00

Masking Threshold

● Automatically Determine Threshold

○ Specify Threshold: 100

B-Matrix

● Compute B-Matrix Using Gradients Provided

○ Load B-Matrix

Visualization...

COMPLETE

☒ Show Planes:

☒ X 40

☒ Y 59

☒ Z 8

Color Planes Based On

Principle Eigenvector

Color Maps

○ Gray

○ Rainbow

○ Darkhue

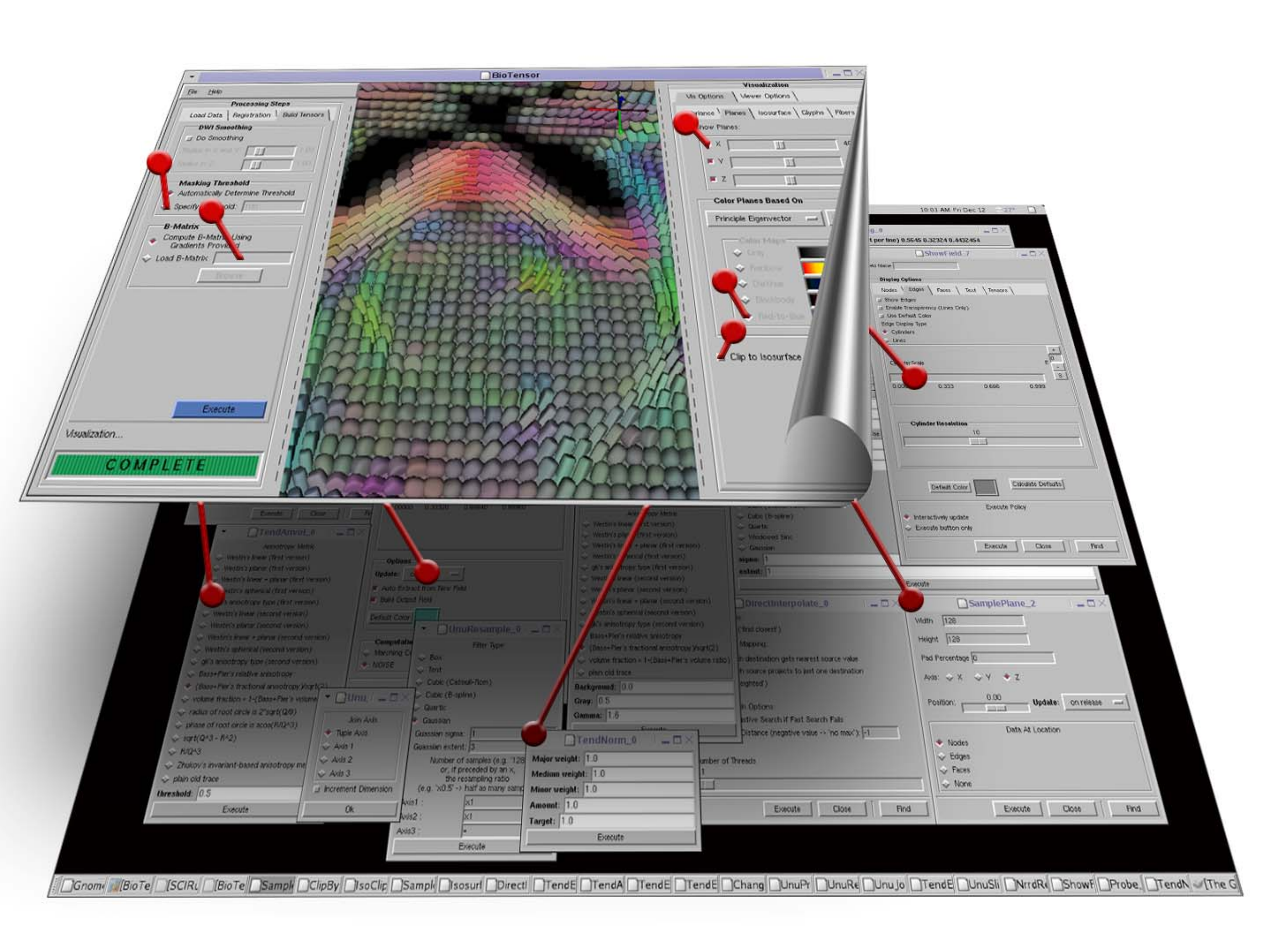
○ Blackbody

● Red-to-Blue

☐ Clip to Isosurface

Power Apps

System Overview

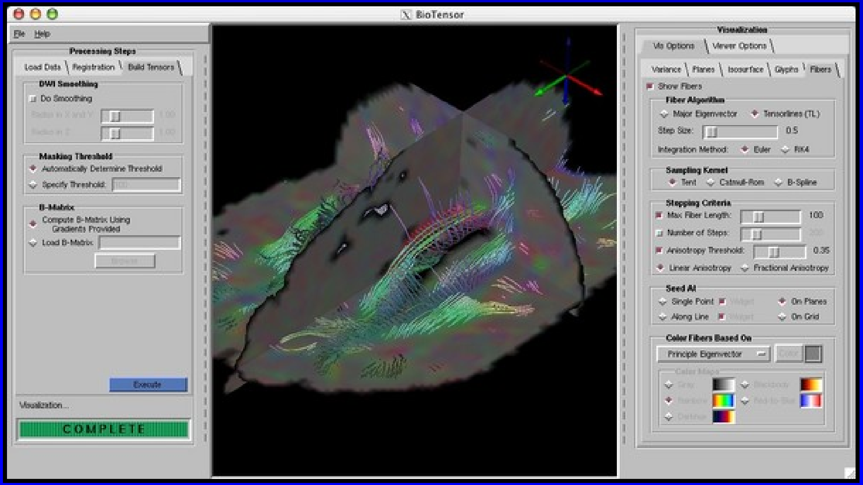


Power Apps

System Overview

Problem specific applications

- •Hide the complexities of dataflow
- •Provide a simplified graphical user interface
- •Focus on a specific task



DWI Smoothing
□ Do Smoothing
Radius in X and Y 1.00
Radius in Z 1.00

Masking Threshold
● Automatically Determine Threshold
○ Specify Threshold: 100

B-Matrix
● Compute B-Matrix Using Gradients Provided
○ Load B-Matrix

Visualization...
COMPLETE

☒ Show Fibers

Fiber Algorithm
○ Major Eigenvector ● Tensorlines (TL)
Step Size: 0.5
Integration Method: ● Euler ○ RK4

Sampling Kernel
● Tent ○ Catmull-Rom ○ B-Spline

Stopping Criteria
☒ Max Fiber Length: 100
□ Number of Steps: 200
☒ Anisotropy Threshold: 0.35
● Linear Anisotropy ○ Fractional Anisotropy

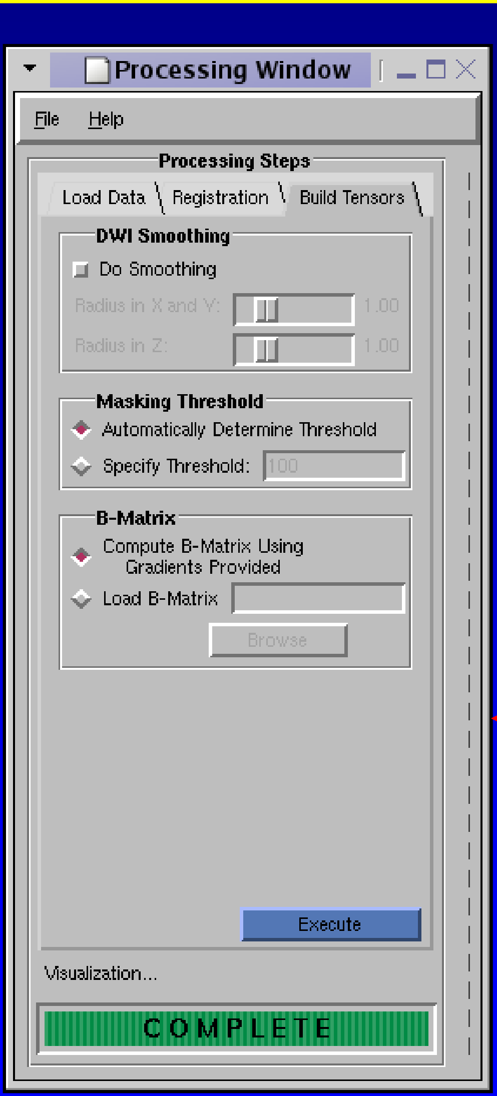
Seed At
○ Single Point ☒ Widget ● On Planes
○ Along Line ☒ Widget ○ On Grid

Color Fibers Based On
Principle Eigenvector

Color Maps
○ Gray ○ Blackbody
● Rainbow ○ Red-to-Blue
○ Darkhue

Power Apps

System Overview



Processing Window

Processing Steps

DWI Smoothing

□ Do Smoothing

Radius in X and Y: 1.00

Radius in Z: 1.00

Masking Threshold

● Automatically Determine Threshold

○ Specify Threshold: 100

B-Matrix

● Compute B-Matrix Using Gradients Provided

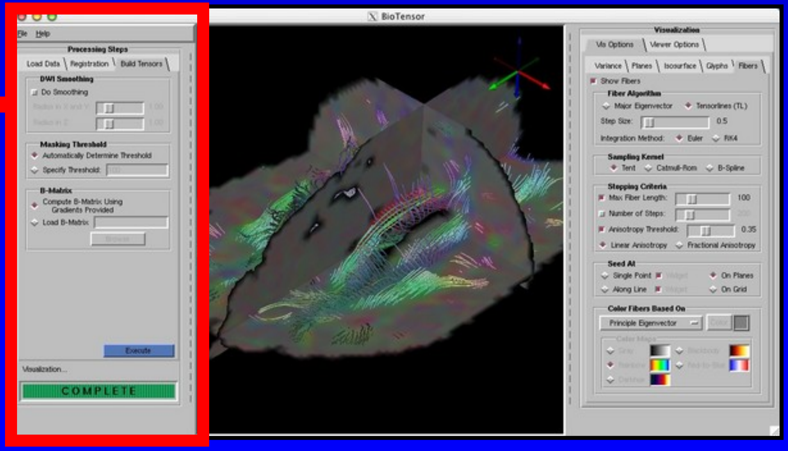
○ Load B-Matrix

Visualization...

COMPLETE

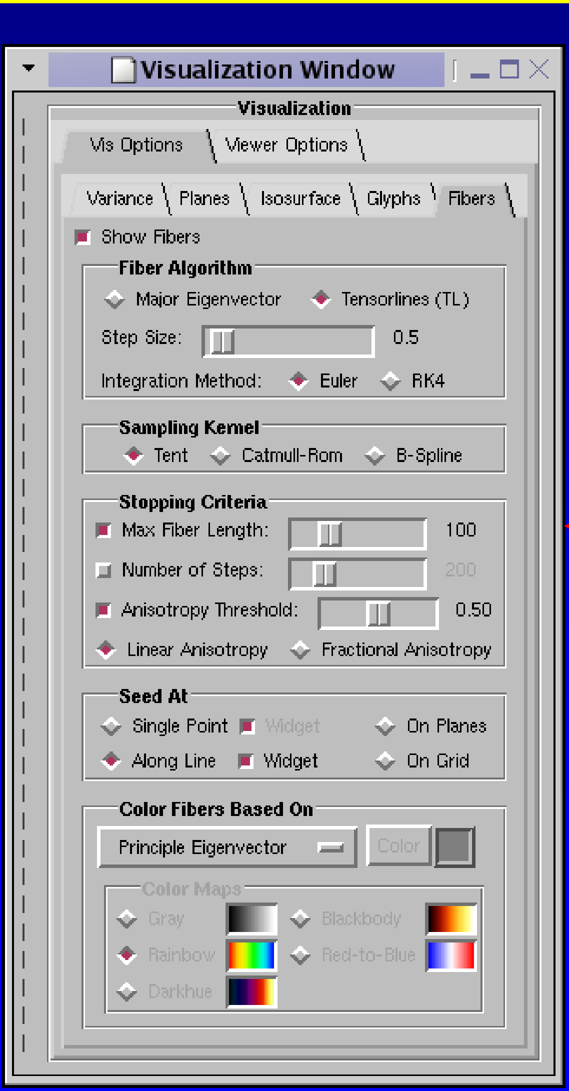
Processing Pane

Guide the user through specific processing steps



Power Apps

System Overview



Visualization Window

Visualization

☒ Show Fibers

Fiber Algorithm

○ Major Eigenvector ● Tensorlines (TL)

Step Size: 0.5

Integration Method: ● Euler ○ RK4

Sampling Kernel

● Tent ○ Catmull-Rom ○ B-Spline

Stopping Criteria

☒ Max Fiber Length: 100

□ Number of Steps: 200

☒ Anisotropy Threshold: 0.50

● Linear Anisotropy ○ Fractional Anisotropy

Seed At

○ Single Point ☒ Widget ○ On Planes

● Along Line ☒ Widget ○ On Grid

Color Fibers Based On

Principle Eigenvector

Color Maps

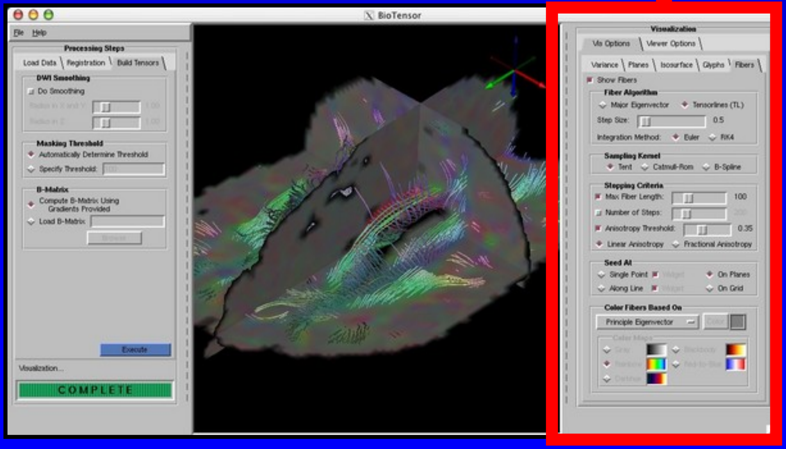
○ Gray ○ Blackbody

● Rainbow ○ Red-to-Blue

○ Darkhue

Visualization Pane

Provide different visualization options



Processing Steps

DWI Smoothing

□ Do Smoothing

Radius in X and Y: 1.00

Radius in Z: 1.00

Masking Threshold

● Automatically Determine Threshold

○ Specify Threshold:

B-Matrix

● Compute B-Matrix Using Gradients Provided

○ Load B-Matrix:

Visualization...

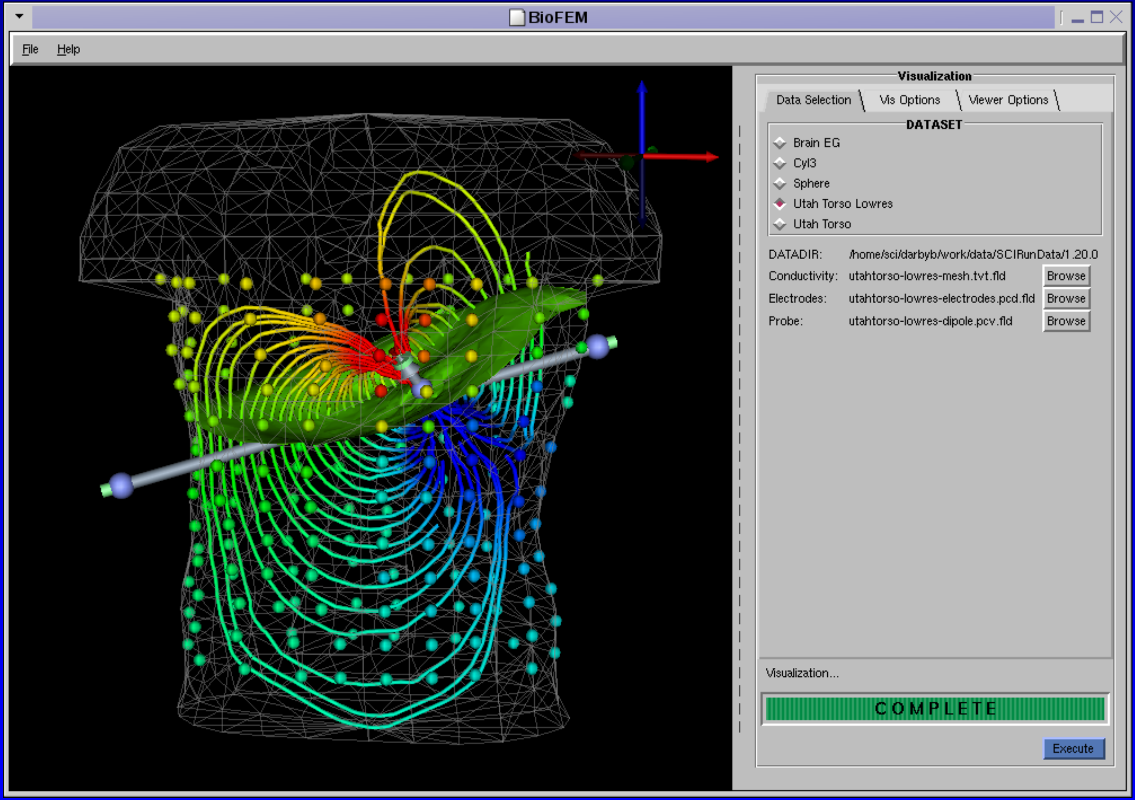
COMPLETE

BioFEM

System Overview

Encapsulation of the forward-fem network

- Change datasets
- Streamlines
- Isosurfaces
- Electrodes



DATASET

◇ Brain EG
◇ Cyl3
◇ Sphere
◆ Utah Torso Lowres
◇ Utah Torso

DATADIR: /home/sci/darbyb/work/data/SCIRunData/1.20.0
Conductivity: utahtorso-lowres-mesh.tvt.fld
Electrodes: utahtorso-lowres-electrodes.pcd.fld
Probe: utahtorso-lowres-dipole.pcv.fld

Visualization...

COMPLETE

http://software.sci.utah.edu/doc/User/Tutorials/BioFEM/BioFEM.html

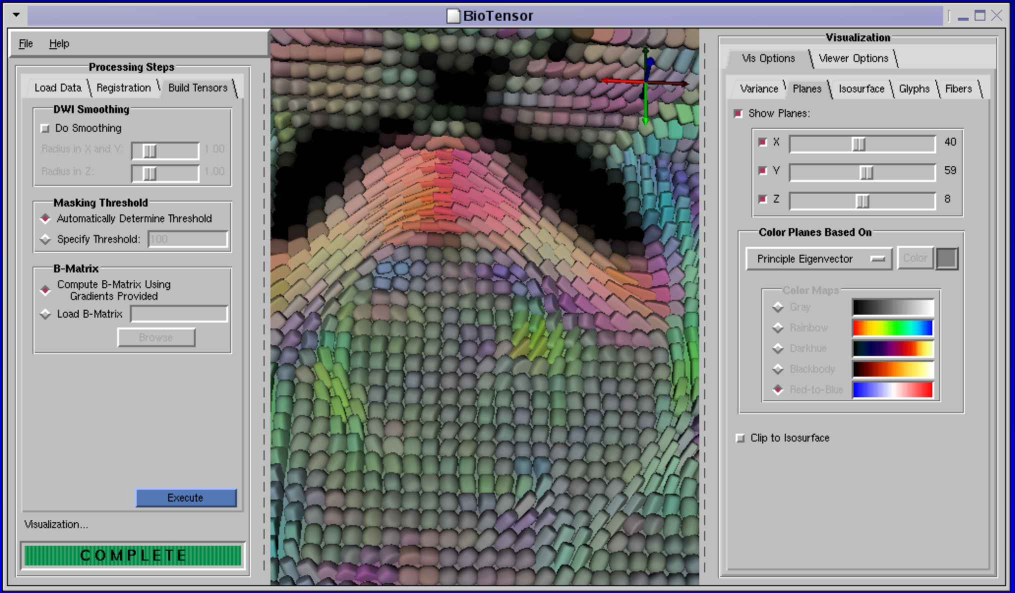
BioTensor

System Overview

Diffusion Tensor Imaging

Processing Steps

- Data Acquisition
- Registration
- Building Tensors



DWI Smoothing
□ Do Smoothing
Radius in X and Y: 1.00
Radius in Z: 1.00

Masking Threshold
● Automatically Determine Threshold
○ Specify Threshold: 100

B-Matrix
● Compute B-Matrix Using Gradients Provided
○ Load B-Matrix

☒ Show Planes:
☒ X 40
☒ Y 59
☒ Z 8

Color Planes Based On
Principle Eigenvector

Color Maps
○ Gray
○ Rainbow
○ Darkhue
○ Blackbody
● Red-to-Blue

□ Clip to Isosurface

Visualization Options

- Planes
- Isosurfaces
- Glyphs
- Fibers

http://software.sci.utah.edu/doc/User/Tutorials/BioTensor/BioTensor.html

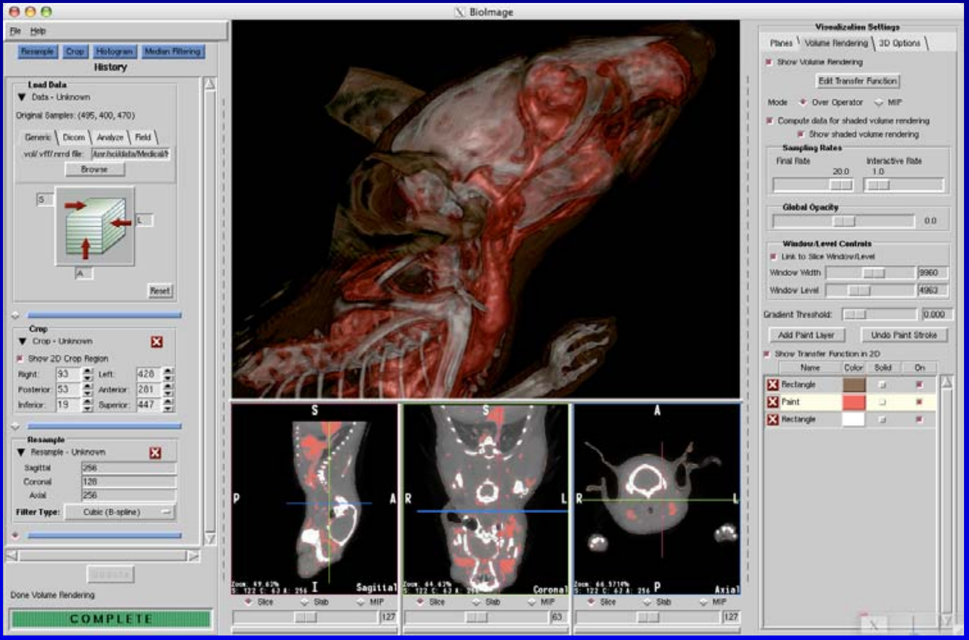
BioImage

System Overview

Volume Rendering

Processing Steps

- •Crop
- •Resample
- •Histogram Eq



Data - Unknown

Original Samples: (495, 400, 470)

vol/ vff/ nrrd file: /usr/sci/data/Medical/

Crop - Unknown

☒ Show 2D Crop Region

Right: 93 Left: 428

Posterior: 53 Anterior: 281

Inferior: 19 Superior: 447

Resample - Unknown

Sagittal 256

Coronal 128

Axial 256

Filter Type: Cubic (B-spline)

Done Volume Rendering

127 63 127

☒ Show Volume Rendering

Mode ● Over Operator ○ MIP

☒ Compute data for shaded volume rendering

☒ Show shaded volume rendering

Final Rate 20.0 Interactive Rate 1.0

Global Opacity 0.0

☒ Link to Slice Window/Level

Window Width 9960

Window Level 4963

Gradient Threshold: 0.000

☒ Show Transfer Function in 2D

Name	Color	Solid	On
Rectangle	🟫	□	☒
Paint	🟥	□	☒
Rectangle	⬜	□	☒

Visualization Options

- •Slices
- •Window Width / Level
- •MIPs
- •Multi-dimensional Transfer Functions

http://software.sci.utah.edu/doc/User/Tutorials/BioImage/BioImage.html