

User FAQ (v. 1.24.2)

Revision History

Revision 001 8/9/05

1. I get link errors when compiling ITK 2.0.1 OS X 10.3 to use with SCIRun.

If building ITK 2.0.1 on OS X 10.3, users may see the following errors:

```
InsightToolkit-2.0.1/bin/libitkvnl.dylib...
ld: vnl_math.o illegal reference for -dynamic code (section
difference reference from section (__TEXT,__eh_frame) relocation
entry (0) to symbol: __isnan defined in dylib: /usr/lib/libm.dylib)
/usr/bin/libtool: internal link edit command failed
make[9]: *** [/Users/blah/Code/C++/ITK/InsightToolkit-2.0.1/
bin/ libitkvnl.dylib] Error 1.
```

The solution is to either checkout a recent CVS copy of ITK (directions are on the ITK download page), or edit the file: `INSIGHT_ROOT/Utilities/vx1/core/vnl/vnl_math.cxx`, changing line 62 from:

```
# define isnan __isnan
to
# define isnan(x) __isnanand((double)x)
```

This simple fix will allow ITK 2.0.1 to compile on OS X.

Revision History

Revision 001 3/7/05

2. On a Linux system, what video cards and drivers work with SCIRun's advanced volume rendering code?

Nvidia FX class or better and ATI Radeon 9500 or better video cards will work.

An accelerated graphics card driver must also be installed. An accelerated graphics card driver offloads graphics computations to the graphics card hardware and results in faster graphics. Accelerated drivers enable scientific imaging modalities, such as volume rendering, to happen on the graphics card.

A later FAQ shows how to determine the type of graphics card installed.

Accelerated Nvidia drivers can be downloaded¹ from Nvidia's web site.

Accelerated ATI drivers can be downloaded² from ATI's web site.

Note that a non-accelerated driver is normally installed in a typical Linux installation. A later FAQ shows how to determine if an accelerated driver is installed.

Revision History

Revision 001 3/7/05

3. On a Linux system, how do I determine the type of installed graphics card?

There are two commands that can be used: `lspci` and `glxinfo`. The `lspci` command can be used to identify the card even when no graphics drivers are installed, but it may not report the exact model of the card correctly.

The `glxinfo` command will report the exact model of the card installed, but it will only work if the graphics drivers are properly installed and Xwindows is up and running. The `glxinfo` command must be run from an xterm that is being displayed on the machine's local monitor (it cannot be run from a remote ssh login or from a text-only console).

Here is a sample run of `lspci` and `glxinfo`:

```
$ /sbin/lspci | grep VGA
01:00.0 VGA compatible controller: nVidia Corporation NV35GL [GeForce FX 5900]
$
$ cat /var/log/XFree86.0.log |grep -i GPU
(II) NVIDIA Unified Driver for all NVIDIA GPUs
(-- ) Chipset NVIDIA GPU found
(II) NVIDIA(0): NVIDIA GPU detected as: GeForce FX 5900 Ultra
(-- ) NVIDIA(0): Interlaced video modes are supported on this GPU
$
$ glxinfo |grep renderer
OpenGL renderer string: GeForce FX 5900 Ultra/AGP/SSE
```

If your card was detected when linux was loaded on the machine, then a section in `/etc/X11/XFree86Config`, similar to the following, will be found:

```
Section "Device"
    Identifier   "Videocard0"
    Driver       "nvidia"
    VendorName   "Videocard vendor"
    BoardName    "NVIDIA GeForce 4 (generic)"
EndSection
```

If there are multiple "Device" sections, look towards the end of the file for a section named "Screen" to determine which "Device" is currently being used.

Please note that there are multiple X11 implementations, and the exact configuration file names, locations and formats may vary slightly depending on your linux distribution. Please see XFree86³ and X.org⁴ for an up to date description of the configuration files.

Revision History

Revision 001 3/7/05

4. On a Linux system, how do I determine if an accelerated graphics card driver is installed?

Look in `/etc/X11/XF86Config` or `/etc/X11/xorg.conf` for a section named "Device". The acceler-

ated ATI driver is called "fglrx":

```
Section "Device"
:
Driver      "fglrx"  <== accelerated
Driver      "radeon" <== non-accelerated
Driver      "ati"    <== non-accelerated
```

The Accelerated Nvidia driver is called "nvidia"

```
Section "Device"
:
Driver      "nvidia" <== accelerated
Driver      "nv"     <== non-accelerated
```

Revision History

Revision 001 3/7/05

5. On a Linux system, how do I know which Nvidia driver is currently installed?

Look in /proc/driver/nvidia:

```
$ cat /proc/driver/nvidia/version
NVRM version: NVIDIA Linux x86 NVIDIA Kernel Module 1.0-5336 Wed Jan 14 18:29:26 PST 2004
```

Above, the driver version is 5336.

Or, run glxinfo

```
$ glxinfo | grep version
server glx version string: 1.3
client glx version string: 1.3
OpenGL version string: 1.4.1 NVIDIA 53.36
glu version: 1.3
```

Revision History

Revision 001 3/7/05

6. I installed the latest Nvidia drivers, why won't SCIRun compile with advanced volume rendering?

You need to install the Nvidia OpenGL header files (they don't get installed by default). In order to install the headers, you need to give the --opengl-headers option to the install script, for example:

```
./NVIDIA-Linux-x86-1.0-6111-pkg1.run --opengl-headers
```

For more help, type

```
./NVIDIA-Linux-x86-1.0-6111-pkg1.run -A --help
```

After installing the Nvidia OpenGL headers, you should find files `gl.h`, `glx.h`, `glxtokens.h` in directory `/usr/include/GL`. Also check to make sure that those files are the Nvidia versions and not the Mesa version (Mesa is a software-only OpenGL implementation that comes packaged with linux):

```
$ pwd
/usr/include/GL
$ head gl.h

* Mesa 3-D graphics library
```

The above output indicates the presence of Mesa headers. Install the Nvidia headers.

```
$ head gl.h

** Copyright 1998-2002, NVIDIA Corporation.
```

The above output shows that Nvidia headers are installed.

Revision History

Revision 001 3/7/05

7. How do I tell if the Nvidia headers are installed? How do I know if the Nvidia headers match the version of Nvidia driver I have installed?

If in doubt, reinstall the driver. See the previous FAQ entry.

Revision History

Revision 001 02/22/05

8. What are the units associated with the bioelectric field simulations in BioPSE?

Here are the quantities that we're interested in and the units that they carry:

```
conductivity [sigma] = (amps / volts) / meter = siemens / meter
potentials [phi] = volts
electric field [E] = volts / meter
dipole source [p] = amps / meter
current density [J] = amps / (meter^2)
current source density [I] = amps / (meter^3)
```

Recall that:

```
J = sigma x E
and
E = - gradient (phi)
and
```

I = divergence (J)

As for the scales of those units (e.g. centi-, milli-, etc), those are up to the user—SCIRun doesn't actually keep track of them all that well. SCIRun assumes that the dipole source are in amps / meter, that the conductivities are in siemens / meter, that the model geometry is in meters, and it therefore reports its results in volts. If this isn't true (e.g. you know that your model is in mm), then you have to carry those scale factors through your computation (e.g. know that the results you get out are in kv).

The rule of thumb is that if we *increase* the conductivity, then we *decrease* the potentials by that same scale factor. Conversely, if we *increase* the dipole source moment, then we *increase* the potentials by that same scale factor. i.e. $V = I / \sigma$. Similarly, if we hold everything else constant, but *increase* the size of the domain, then we *decrease* the potentials by that same scale factor.

For example, the SCIRun Utah Torso model has a length scale of centimeters (10^{-2} meters) and conductivity units of (siemens / meter), so our output potentials are in hectovolts (10^2 volts).

Revision History

Revision 001 01/27/05

9. I just upgraded SCIRun and I'm experiencing a number of bad behaviors. Any ideas?

Try this: Rename `~/.scirunrc` to `~/.scirunrc.0`. Run SCIRun again. If the problems resolve then merge any changes you made in `~/.scirunrc.0` into the new `~/.scirunrc` created by SCIRun and delete `~/.scirunrc.0`.

Revision History

Revision 1.0 7/29/01

10. What systems are compatible with SCIRun?

SCIRun should be compatible with any SGI machine running Irix 6.5.

SCIRun has been tested on the following Linux distributions: (With past versions we have run on RedHat 7 and 8, and Mandrake 8. While these systems should still work, all local systems have been updated to Redhat 9 and Mandrake 9.2.)

- Mandrake 9.2
- Redhat 9.0

SCIRun has been tested on the following PC processor configurations:

- Dual Intel Pentium II
- Single Intel Pentium III
- Dual Intel Pentium III
- Single Intel Pentium 4
- Single AMD Athlon

SCIRun has been tested with the following PC graphics cards:

- NVIDIA GeForce & FX
- ATI Radeon 9700

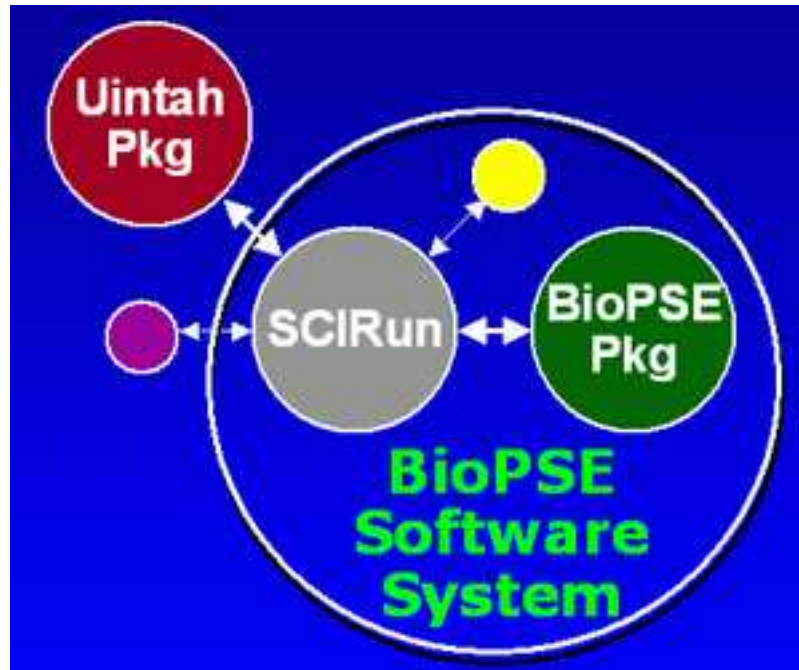
Revision History

Revision 1.0 7/29/01

11. What is the relationship between SCIRun, BioPSE, and other SCI Institute software?

It is important to understand the hierarchy of computational problem solving environments developed at the SCI Institute. From a historical perspective, SCIRun, which started development in 1992, was the original implementation of the computational framework. Since then, SCIRun and its computational workbench infrastructure has been the origin of many significant application-specific projects. Two major examples are the DOE sponsored Uintah system and the NIH sponsored BioPSE system (from the National Center for Research Resources⁵ (NCRR) Center at Utah⁶). The target applications of the Uintah project are combustion, computational fluid dynamics, and mechanical modeling implemented on large-scale, distributed, shared memory architectures. The goal of the BioPSE project is to create software for geometric modeling, simulation, and visualization for solving bioelectric field problems. A secondary goal of the SCIRun system is to make source code for problem solving environments publicly available to the scientific community.

To realize these significant projects, the SCIRun infrastructure has required significant reorganization, extension, and enhancement. Even with these changes, SCIRun remains the core infrastructure for problem solving environments, and the name used to refer to the entire ensemble of software. Thus, a user may install and operate the core SCIRun software and also augment its functionality with one or more of the “packages” such as BioPSE. SCI anticipates that the collection of packages will grow as the advantages of the SCIRun infrastructure become available to scientists and engineers of all disciplines.

Figure 1. BioPSE Software System

This figure shows the relationship among SCIRun and its packages. BioPSE consists of the basic SCIRun software together with the BioPSE modules and support libraries.

In addition to major projects that have both leveraged and advanced SCIRun, there exist a number of smaller packages that extend SCIRun's utility. Examples include the Teem package for raster data processing, the NetSolve package for linear algebra subroutines (developed by researchers at the University of Tennessee and Knoxville), and a communications interface recently introduced to the Matlab program. SCI has developed various forms of software wrappers or interfaces that allow SCIRun to leverage the strengths of third party tools, links referred to as "bridges."

There are instances when a tighter level of integration than a bridge between SCIRun and third-party software is necessary. One example is the addition of mpeg support for capturing animations from the SCIRun Viewer module. SCI uses the Berkeley and Alex Knowles' mpeg encoding tools. Another example is the set of image generation and manipulation tools from Paul Haeberli called libimage. To indicate if such tools are available, the configure scripts for SCIRun contain optional control flags.

The combination of a robust infrastructure and modular extensibility through packages and third-party libraries allows SCIRun to grow and adapt to changing needs and opportunities.

Revision History

Revision 1.0 3/15/03

12. What citation should be used when referring to SCIRun and BioPSE in a paper or grant application?

“BibTeX” and “plain text” citations can be used. For SCIRun and BioPSE citations go to:

http://software.sci.utah.edu/scirun-biopse_citation.bib

Thank you for the citation(s). Use of SCIRun/BioPSE citations in projects and publications helps ensure the continued funding of the SCIRun/BioPSE project. Please send citations to macleod@sci.utah.edu.

13. How do I get my data into SCIRun?

A set of command line utilities, called *converters*, convert “foreign” data into SCIRun file objects (and vice-versa). See Section *Importing and Exporting SCIRun Data*⁷ in the *SCIRun User's Guide* for information on the use of converter programs.

See also Appendix A⁸ of the BioFEM tutorial for information about getting finite element models imported into BioFEM.

Revision History

Revision 1.0 7/29/01

14. By default, what directions do the positive x,y,z axis point to in the viewer module?

By default, the negative-z axis points down, positive-x points to right, and positive-y points up. If the Axes is turned on, arrows point in +/-{x,y,z}. To remember which is which: (R,G,B) = (X,Y,Z). Arrows pointing in positive directions are brighter than arrows pointing in negative directions. ???One last note, click on the "Views" button at the botton-right of the ViewWindow and snap to a "canonical" view (e.g. "Look down +Z axis, Up vector +Y").???

Revision History

Revision 1.0 7/29/01

15. Is there a way to scale up the size of the axes in the viewer window to make the size of the axes comparable to the size of other objects?

Currently, everything must be scaled down to the size of unit-axes, by using the `Math::BuildTransform` and `Field::TransformField` modules.

Revision History

Revision 1.0 3/25/04

16. What 64bit hardware/OS is recommended? Will SCIRun compile on 64bit Opteron systems?

SCIRun does not yet (support in being investigated) run on Opteron. SGI Irix is the only supported 64 bit platform.

Revision History

Revision 001 03/29/04

17. Does SCIRun handle anisotropy in FEM/FDM forward calculations?

SCIRun/BioPSE fully supports inhomogeneous, anisotropic conductivities for FEM and FDM simulations; an $N \times 6$ matrix can be built that provides a unique tensor for every element in the domain. See Appendix A⁹ of the BioFEM tutorial for more information about getting finite element models imported into BioPSE.

Revision History

Revision 001 03/29/04

18. Can SCIRun compile under Windows XP using a Cygwin Interface?

No. There has been discussion about creating a native Windows port of SCIRun, however, SCI has not committed to this project.

Revision History

Revision 001 03/29/29

19. I built SCIRun under the latest release of Panther but the SCIRun executable doesn't do anything. Why?

This problem appeared with the Mac OSX 10.3.2 system update. To fix this problem, manually edit line 54 of file `SCIRun/src/scripts/program.mk`, inserting `"-bind_at_load"` after `"$(CXX)"`. Then remove the SCIRun executable and type `gmake`.

This problem has been resolved in SCIRun release 1.20.2.

Revision History

Revision 001 03/29/04

20. The same descriptions are given for the ApplyFEMCurrentSource module and the ApplyFEMVoltageSource module. To which module does the description apply?

The difference between these modules is that the ApplyFEMCurrentSource module is used to apply Neumann boundary conditions; known values related to the first spatial derivative of the potential, (e.g. flux, current density, dipoles).

The ApplyFEMVoltageSource module is used to apply Dirichlet boundary conditions; known values for the potential at specific locations. In both cases, boundary conditions affect the right side of the linear system, which is why both modules take an optional RHS ColumnMatrix as input, and produce a modified RHS ColumnMatrix as output. In the case of a Dirichlet BC, the stiffness matrix must also be modified, which is why ApplyFEMVoltageSource requires the stiffness matrix as input, and produces a modified stiffness matrix as output.

Typically, ApplyFEMCurrentSource takes two Fields as input: a TetVolField that specifies the geometry and conductivity information for the volume (e.g. `brain-eg-mesh.tvt.fld`), and a collection of dipole sources (`PointCloudField<Vector>`).

In contrast, the ApplyFEMVoltageSource applies Dirichlet condition at location in the mesh where potentials are known. Unlike the ApplyFEMCurrentSource, the ApplyFEMVoltageSource requires a second upstream module. Specifically, an InsertVoltageSource module is required. The user passes the TetvolField

of conductivity (e.g. brain-eg-mesh.tvt.fld) into the first Field input port of InsertVoltageSource, and a PointCloudField<double> specifying the positions and voltages of the known potentials into the second Field input port. The module identifies which nodes of the mesh the Dirichlet conditions will be applied, and stores that information with the output TetvolField. The output TetVolField, which now has the Dirichlet BC information stored as a Property of the field, is passed into the first input port of ApplyFEM-VoltageSource.

Revision History

Revision 001 03/29/04

21. Following the SCIRun/BioPSE tutorial, I have set up several SCIRun networks. SCIRun, however, produces the following error messages. What do they mean?

```
DynamicLoader::compile_so() syscal error 256:
command was 'cd/usr/local/SCIRun/linux/on-the-fly-libs;
/usr/bin/gmake SFInterfaceMaker.TetVolFieldint.TetVolMeshCell.so>
SFInterfaceMakerTetVolFieldint.TetVolMeshCell.log 2>&1'
DynamicLoader::create_cc(empty=true ) ' Could not create file
/usr/local/SCIRun/linux/on-the-fly-libs/SFInterfaceMaker.TetVolFieldint.TetVolMeshCell.cc
```

One feature of SCIRun/BioPSE is that it dynamically compiles some parts of the code at run-time based on the data passed through the network. If installed from an RPM (and unless instructed otherwise) SCIRun will try to generate code in /usr/local/SCIRun/linux/on-the-fly-libs/. SCIRun won't (usually) have privileges to write to this directory. The issue is fixed by creating a directory in your home directory, and setting the SCIRUN_ON_THE_FLY_LIBS environment variable to point to the new directory. For example:

```
mkdir /home/dmw/on-the-fly-libs/
setenv SCIRUN_ON_THE_FLY_LIBS /home/dmw/on-the-fly-libs/
```

SCIRun must be restarted to effect these changes.

Revision History

Revision 001 03/29/04

22. When I remotely display SCIRun, it sometimes hangs and sometimes crashes the X server, depending on if it is running on sgi/linux, and displayed on sgi/linux. What causes this?

Problems with the 4191 Nvidia drivers cause GL programs to misbehave. There has been success using the 3xxx Drivers (except 3D texturing). Determine what drivers are being used on the linux box by typing "rpm -qa grep NVIDIA".

Revision History

Revision 001 03/29/04

23. In the GenStandardColorMaps module, I can not change the alpha value of the applied color map. Documentation claims the default alpha value for every map is 50%, but I see no transparency with the default setting. Changing settings has no visible effect. Should I enable another setting for the alpha value in the color map?

In order for alpha to be applied, the downstream module needs to have the "Enable Transparency" box selected under the "Faces" tab.

Revision History

Revision 001 03/29/04

24. Is there an easy way to find the second spatial derivative in a volume?

No.

Revision History

Revision 001 03/29/04

25. Does SCIRun support 2D visualization?

Yes. The ShowSlices module will display orthogonal slices of a 3D nrrd in a 2D OpenGL window.

Revision History

Revision 1.0 8/27/03

26. I've installed SCIRun from its RPM. I'm running the networks in the tutorial and I'm getting these error messages and others like them:

```
REMARK: Maybe dynamically compiling some code, ignore failure here.
DynamicLoader::create_cc(empty = false) - Could not create file
/usr/local/SCIRun/linux/on-the-fly-libs/VFInterfaceMaker.TetVolFieldint.Te
tVolMeshCell.cc
DynamicLoader - Executing: cd /usr/local/SCIRun/linux/on-the-fly-libs;
/usr/bin/gmake VFInterfaceMaker.TetVolFieldint.TetVolMeshCell.so
DynamicLoader::compile_so() syscal error 256: command was 'cd
/usr/local/SCIRun/linux/on-the-fly-libs; /usr/bin/gmake
VFInterfaceMaker.TetVolFieldint.TetVolMeshCell.so >
VFInterfaceMaker.TetVolFieldint.TetVolMeshCell.log 2>&1'
DynamicLoader::create_cc(empty = true) - Could not create file
/usr/local/SCIRun/linux/on-the-fly-libs/VFInterfaceMaker.TetVolFieldint.Te
tVolMeshCell.cc
DynamicLoader - Executing: cd /usr/local/SCIRun/linux/on-the-fly-libs;
/usr/bin/gmake VFInterfaceMaker.TetVolFieldint.TetVolMeshCell.so
DynamicLoader::compile_so() syscal error 256: command was 'cd
/usr/local/SCIRun/linux/on-the-fly-libs; /usr/bin/gmake
VFInterfaceMaker.TetVolFieldint.TetVolMeshCell.so >
VFInterfaceMaker.TetVolFieldint.TetVolMeshCell.log 2>&1'
DYNAMIC COMPILATION ERROR:
/usr/local/SCIRun/linux/on-the-fly-libs/VFInterfaceMaker.TetVolFieldint.Te
tVolMeshCell.so does not compile!!
/usr/local/SCIRun/linux/on-the-fly-libs/VFInterfaceMaker.TetVolFieldint.Te
```

```
tVolMeshCell.so: cannot open shared object file: No such file or directory
REMARK: Dynamic compilation completed.
```

One of the features of SCIRun/BioPSE is that it dynamically compiles some parts of the code at run-time based on the data that you're passing through your network. In order for this to work, the software needs to be able to dynamically create files. However, because you have installed the software from RPM, the directory that the dynamic files are written to by default, `/usr/local/SCIRun/linux/on-the-fly-libs/`, is owned by root—which is why the program is having problems. You can fix this by creating a different directory that you own, and setting your `SCIRUN_ON_THE_FLY_LIBS` environment variable to point at that new directory. This environment variable overrides the default location, so that should fix the problem you're having. For example:

```
mkdir /home/dmw/on-the-fly-libs/
setenv SCIRUN_ON_THE_FLY_LIBS /home/dmw/on-the-fly-libs/
```

Revision History

Revision 1.0 3/18/03

27. Can a scirun net automatically execute as soon as it loads?

Add the following line to the end of the net file:

```
$m1-c needexecute
```

Adding the above line causes the execution of module `$m1`, plus the execution of all of modules that `$m1` depends on, and the execution of all modules that depend on `$m1`.

Revision History

Revision 1.0 2/20/03

28. When SCIRun is remotely displayed, it sometimes hangs and sometimes crashes the X server (depending on whether it is running on `sgi/linux` and being displayed on `sgi/linux`.) What causes this?

There are problems with the 4191 Nvidia drivers, causing GL programs to behave badly. There has been success using the 3123 drivers (except for 3D texturing). Determine what drivers are being used on the linux box by typing `"rpm -qa | grep NVIDIA"`.

Since 4191 is the most recent driver on nvidia's web site¹⁰, go back and use the 3123 drivers. NVIDIA does not have prebuilt rpms for RedHat 8.0, but it is easy to build from the source rpms:

```
# Removes the old installation. The actual number may need to be changed
rpm -e NVIDIA_GLX-1.0-4191 NVIDIA_kernel-1.0-4191

# Build the rpm from the source
rpmbuild --rebuild NVIDIA_kernel-1.0-3123.src.rpm

# Install the rpm. Note: the actual path may differ from system to system.
```

```
rpm -ivh /usr/src/redhat/RPMS/i386/NVIDIA_kernel-1.0-3123.i386.rpm

# The GLX rpm does not have to build from source (not kernel dependant),
# but I did anyway.
rpmbuild --rebuild NVIDIA_GLX-1.0-3123.src.rpm
rpm -ivh /usr/src/redhat/RPMS/i386/NVIDIA_GLX-1.0-3123.i386.rpm
```

Revision History

Revision 1.0 1/31/03

29. SCIRun dies with a memory allocation error. Specifically:

```
Error allocating memory (32833536 bytes requested) mmap: errno=12 Thread
```

If SCIRun is not configured with `--enable-64bit`, the program will not use more than approximately 2G of memory.

Revision History

Revision 1.0 9/15/02

30. How are inverse problems in electrocardiography solved in SCIRUN/BIOPSE. The so-called transfer matrix T is built and then a least-squares problem is solved. The transfer matrix is expressed using inverses of submatrices. Is this matrix T effectively computed? Are inverses really computed? What is the method implemented? In which modules can the source code be seen?

There are two general solutions to the bioelectric inverse problem. One formulation tries to recover equivalent dipole sources. The other tries to recover the voltages on an interior surface that is assumed to encompass any source (i.e. there are no sources located between the measurement surface and the interior surface).

In the first formulation (surface-to-source inversion), the inverse problem can be over-constrained (searching for a single dipole that accounts for the outer surface measurements), or under-constrained (searching for a large number of dipoles that are distributed through the domain). The over-constrained case is called parameterized inversion, The under-constrained case is called non-parameterized. In the parameterized case, a search algorithm locates the dipole that best reproduces the measured data. In the non-parameterized case, find the minimum-norm solution that best fits some a-priori information about the data (e.g. the solution should be spatially focused).

The inverse problem is ill-conditioned because of the poorly-specified boundary conditions on the inner surface. The formulation uses the transfer matrix built from a combination of sub-matrices from the stiffness matrix. SCIRun solves the resulting linear systems, but not by computing an explicit inverse. Rather, an iterative (conjugate-gradient) algorithm is used. There is a preliminary version of this code, unfortunately, it has not yet been released in BioPSE. For the moment, see this SPIE '95 paper¹¹, which describes this technique in more detail. This algorithm will be part of BioPSE in early Spring.

Revision History

Revision 1.0 7/29/01

31. When running SCIRun, one or more messages appear in the message window indicating a problem with a package and/or module. The message(s) is/are similar to the following:

```
Loading package 'SCIRun' Unable to load module 'CastField' :  
- can't find symbol 'make_CastField'
```

or

```
Unable to load all of package 'Teem' (category 'DataIO'  
failed) : - libPackages_Teem_Dataflow.so: cannot open  
shared object file: No such file or directory -  
libPackages_Teem_Dataflow_Modules_DataIO.so: cannot open  
shared object file: No such file or directory
```

Each module for a given package has its own .xml file that describes it. When SCIRun starts, it parses all .xml files in the packages (under Dataflow/XML) and tries to find the matching code within the related .so files. If the .so files cannot be found, the message “No such file or directory” is given. If the .so can be found, but the code for a particular module does not exist within the library, the message “can’t find symbol” is given.

The message(s) may or may not indicate a problem with SCIRun. For some modules, the .xml file may be listed, but the code has not been completed (this may be common for module developers). For other modules, the SCIRun installation is some how corrupt (.so files have been deleted, moved, etc.)

The solution is to build libraries the .xml files need or remove the offending .xml files.

Revision History

Revision 1.0.1 4/30/04

32. I am seeing the error “Xlib: sequence lost. . .”when running SCIRun

What does it mean and how do I fix it?

The most likely reason for seeing this is that you have found a bug in SCIRun with the locking of the X display. You should report this problem to scirun-develop@sci.utah.edu. The last time this error occurred it was in `Dataflow/Modules/Render/OpenGL.cc` and required that a `glGetIntegerv()` call be placed within a `gui->lock()/unlock()` section.

Notes

1. <http://www.nvidia.com/content/drivers/drivers.asp>
2. <https://support.ati.com/ics/support/KBAnswer.asp?questionID=3380>

3. <http://www.xfree86.org>
4. <http://www.x.org>
5. <http://www.ncrr.nih.gov/>
6. <http://www.sci.utah.edu/ncrr/>
7. <http://software.sci.utah.edu/doc/User/Guide/usersguide/srug7.html>
8. http://software.sci.utah.edu/doc/User/Tutorials/BioFem/BioFem.html#appendix_a
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