

SCIRun (*BioPSE/PowerApps*)

SCIRun/Installation

Download, Installation, and Support

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Two Places to Get SCIRun

SCIRun/Installation

- **Latest Release - SCI Website (Version 1.24.2)**
http://software.sci.utah.edu/scirun_1_24.html
 - **Binaries**
 - Mac (10.3 and 10.4, but NOT Intel based macs)
 - Linux (RedHat 9, Mandrake 9)
 - **Source**
 - Compile it yourself
- **Subversion Code Repository**
 - **Latest version (1.25...)**
 - Only source available, so you have to compile it.
 - **Not necessarily stable, but has the latest/greatest stuff**
 - **1.26 (Stabilized 1.25) due late 2006**

Getting Started

SCIRun/Installation

Compiler

- GNU C++ (gcc)
 - For the Mac: Recommend Version 4.0.1+
 - For Linux: Recommend Version 4.1+
 - Earlier compilers usually work, but some do have a few bugs in them depending on platform...
- To determine version, run: `gcc --version`

Support Libraries

- PNG, ZLIB, (LaPack, BLAS)
- In `/usr/lib` (or `/sw/lib` on the Mac) <- Usual locations
- If you don't have them, rpm them (linux), or Fink them (OSX)

SVN (Subversion)

- Subversion is a source code management and control system.
- Only necessary if you are not using the Release

Subversion (SVN)

SCIRun/Installation

- **Must have ssl support**
 - *svn --version*
 - Look for: *handles 'https' schema*
 - If not, then install “svn-client-ssl”
- **Currently we allow:**
 - **Anonymous check-out**
 - **But you must have an account to check-in**
 - Contact dav@sci.utah.edu if you need an account
- **More Info:**
 - <http://code.sci.utah.edu/SCIRunAndSubversionFAQ.html>
 - <http://subversion.tigris.org>

Basic SVN Commands

SCIRun/Installation

- **svn checkout**
`https://code.sci.utah.edu/svn/SCIRun/trunk/src SCIRun/src`
- **svn commit -m "log message here" [file(s)]**
 - Commits the changes you have made to the file(s).
- **svn diff file**
 - Shows the difference between your local copy of the file, and the unmodified version of the file.
- **svn update [file(s)]**
 - Brings your tree/file up to date with the repository
- **svn status [-u] [file(s)]**
 - Tells you the status of the file.
- **svn info [file(s)]**
 - Gives detailed information about the file.
- **svn blame [file]**
- **Dates must be of the form YYYY-MM-DD and must have {} around them... but you must escape the {} as seen here:**
 - `svn update --revision \{2006-01-19\} filename`

Necessary Thirdparty Software

SCIRun utilizes

SCIRun/Installation

- Tcl/tk and itcl/itk, Blt
- Xml
- Glew
- Teem
- Mpeg
- Freetype

Reasons for including libraries in SCIRun Thirdparty:

- **Required.** May use a specific version, and/or not (as) common, and/or not easy to install.

SCIRun & Thirdparty Installation

(From the SCI Website)

SCIRun/Installation

- <http://software.sci.utah.edu>
- Press the “Download” Button next to SCIRun
 - Or next to BioPSE, they will get you to the same place.
- First time you must Register
 - This allows us to see who is using SCIRun, and for what reason
- Login
- Choose Distribution (Source, Linux, Mac)
 - If you plan to build SCIRun from source, use SVN (Instructions coming on next slides)
 - Windows Port → In Beta

<http://software.sci.utah.edu>

SCI Institute Software and Data

...

Download

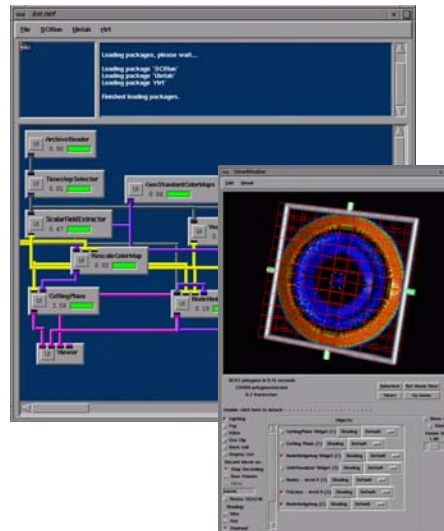
Overview

Documentation

Datasets

Mailing List

Report a Bug



SCIRun

SCIRun is a Problem Solving Environment (PSE) for simulation, modeling, and visualization of scientific problems.

SCIRun & Thirdparty Installation

(From Website (Cont.))

SCIRun/Installation

- Download
 - **SCIRunBioPSE-1.24.2-<distribution>**
 - Thirdparty and BioImage/BioTensor PowerApps come with SCIRunBioPSE
 - **SCIRunData.1.24.1.tar.gz** (*If building from source (SVN) you may still
 - **Optionally** want to download the SCIRunData in this way
 - SCIRunDocs
 - Insight.PKG
- Linux
 - **Distribution comes as an RPM**
 - su
 - rpm -ivh SCIRunBioPSE-1.24.2-<distribution>.rpm
 - Places SCIRun in /usr/local/SCIRun
- Mac (OSX)
 - **Distribution comes as a binary tarball (not a DMG)**
 - **Go to the directory you wish to place SCIRun in and then un-tar it:**
 - tar -zxf SCIRunBioPSE-1.24.2-OSX-bin.tar.gz

Thirdparty Installation

(Using Subversion (SVN))

SCIRun/Installation

- `cd /home/<user>/SCIRun`
- `svn co https://code.sci.utah.edu/svn/Thirdparty Thirdparty`
- `cd Thirdparty`
- `./install.sh /home/<user>/SCIRun/Thirdparty`
- [Note: the install script might tell you that it has found a copy of xml2 on your system and ask whether you still want to build a local version in your Thirdparty tree anyway -- tell it "yes", you do.]
- Creates `/home/<user>/SCIRun/Thirdparty/<scirun-version>/<compiler-version-bits>`
 - Eg: `SCIRun/Thirdparty/1.25.4/Linux/gcc-3.3.5-32bit/`

Getting and Building SCIRun

(Using SVN)

SCIRun/Installation

- `cd /home/<user>`
- `svn co https://code.sci.utah.edu/svn/SCIRun/trunk/src SCIRun/src`
- `svn co https://code.../svn/SCIRun/branches/cibc/src SCIRun/src`
- `cd SCIRun`
- `mkdir linux32opt` [or `darwin32dbg`, etc]
- `cd linux32opt`
- `../src/configure \`
 - `--enable-package="BioPSE Teem MatlabInterface" \`
 - `--enable-optimize --enable-32bit \`
 - `--with-thirdparty=</full/path/to/3p/1.25.4/Darwin/gcc-4.0.1-32bit \`
 - `--with-png=/sw` [<- for Mac]
- `make -j2` # Parallel makes are much faster (if you have the procs)
- At the end of this, you will have a "scirun" executable.

Common Problems

SCIRun/Installation

- **Missing/Bad system libraries**
 - **View/Send us “config.log” to help diagnose**
- **X11 development packages not installed**
- **Old and/or incorrect graphics drivers installed**
- **Old/bad compiler installed**

How To Get Help?

SCIRun/Installation

- General Information on SCI:
<http://www.sci.utah.edu>
- Mailing lists:
 - All SCIRun Users:
scirun@sci.utah.edu
 - SCIRun development team:
scirun-develop@sci.utah.edu
 - Subversion commit log: *(Don't send email directly to this list)*
scirun-cvs@sci.utah.edu
- Documentation
 - <http://software.sci.utah.edu/doc/>
- For best/quickest help for configure/compile issues, allow remote access to your machine

Documentation

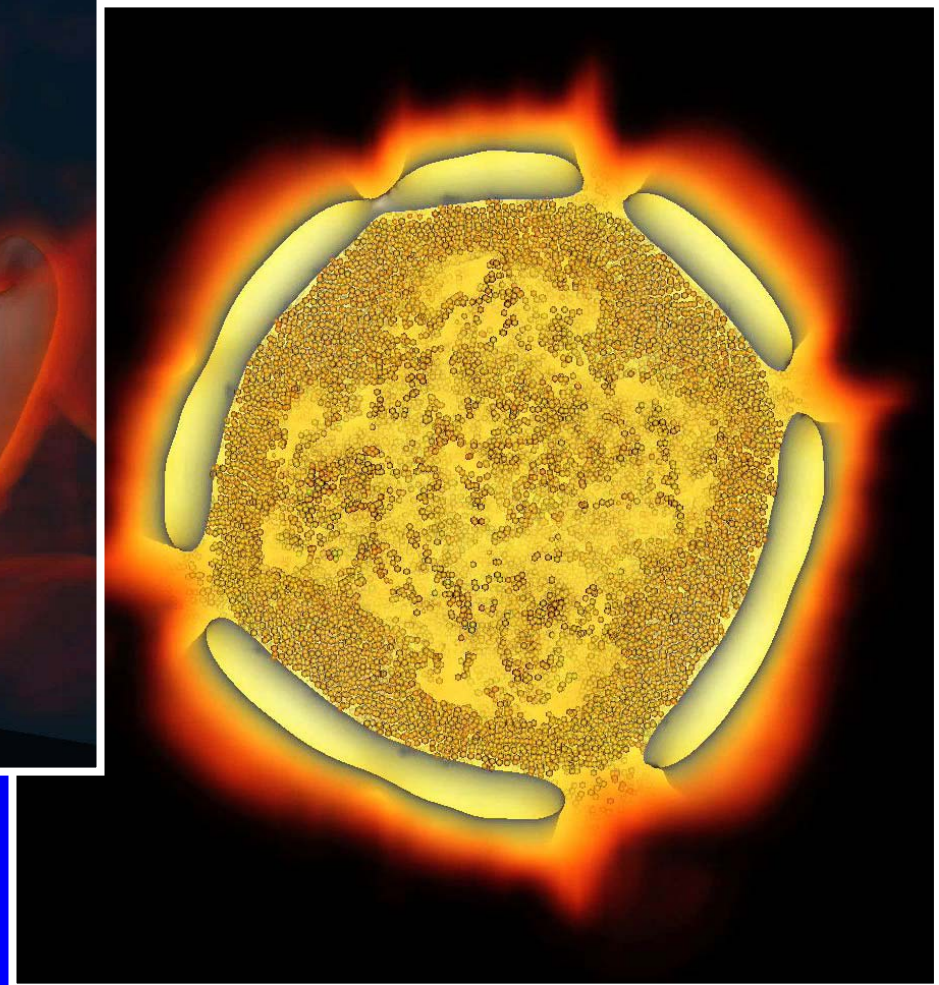
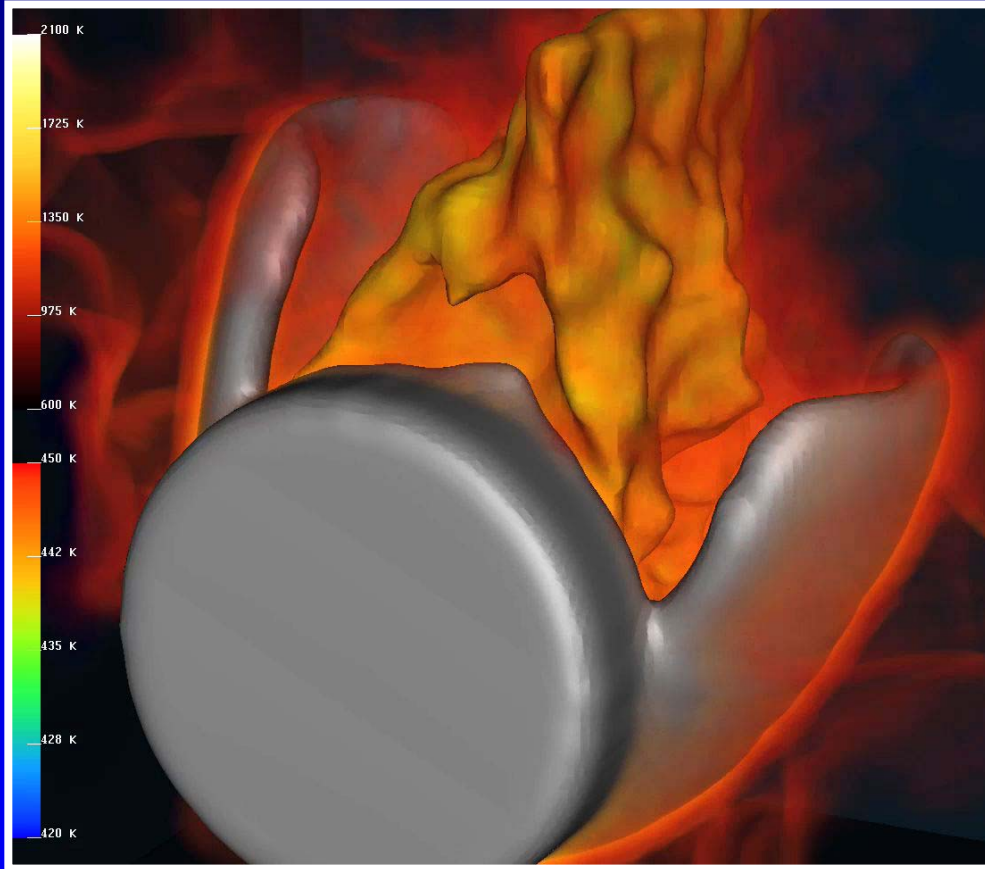
SCIRun/Installation

<http://software.sci.utah.edu/doc/>

- Tutorials
 - SCIRun
 - PowerApps
 - BioFEM, BioImage, BioTensor
- User
 - Guide
 - Module Reference
 - FAQ
- Installation
 - Linux/OSX/IRIX
 - FAQ
- Instructional Overview Videos
 - On: <http://software.sci.utah.edu>
 - In the [Video Overviews](#) section

Questions?

SCIRun/Installation



Coming Soon...

SCIRun/Installation

- ***CMake*** to replace *configure*
- In combination with DART, CMake will allow for better, more automated regression testing
- Individual users' systems can easily submit regression data to be viewed on a central webpage.

Creating a New Module

SCIRun/Installation

- **Source Code Layout:**

- **.../SCIRun/src/**

- **Core/**

- **Dataflow/**

- **GUI/**

<- TCL files

- **XML/**

<- Module descriptions

- **Modules/**

- **Category/**

<- C++ code

- **Packages/**

- **BioPSE/**

<- Duplicates SCIRun/src

- **Core/**

- **Dataflow/**

Module C++ Template

SCIRun/Installation

```
class StreamLines : public Module { // Inheritance from Module is the key.
public:
    virtual void execute();          // This routine does the work
private:
    GuiDouble    gui_step_size_; // Correlate with TCL file.
};                                   // GUI Vars automatically sync with TCL side

void StreamLines::execute() {
    // Verify inputs are correct
    FieldIPort *field_important = (FieldIPort *)get_important("Field"); // Correlate with XML
    FieldHandle fld_handle;

    if (!(field_important->get(fld_handle) && fld_handle.get_rep())) {

        // Do the modules work.

        // Send out any data that was computed.
    }
}
```

Module TCL File

SCIRun/Installation

- tcl is the GUI language
 - Tcl is for scripting,
 - Tk is for creating GUI elements
- See: <http://www.tcl.tk/man/tcl8.3/>
- Takes a little practice... use other modules as examples.
- Expert course on TCL is \$12,000/day, please contact me directly.