Highly Configurable Analysis:

Lessons From A Decade In Astrophysics

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Observation: All Science Is Interdisciplinary

Newton inextricably linked science with math

Turing inextricably linked science with computers

Biologists will write math & code



When Coding Or Data Exploration Is Hard

> When Easier

But Most Parents Will Say This Is More Accurate

Seem Familiar?

We all work hard, and have good intentions.

So, why does scientific data exploration & software sometimes feel harder than it need be?

A Tale of Two Coders

Software Engineer

<u>Researcher</u>

Careful, deliberate design Towards production deployment Must be fastidious Exploratory, open-ended analysis Towards publication Can be messy

Overlapping, But Not Identical, Aims

A Tale of Two Coders

Software Engineer

Careful design

Compiled/Binaries: C/C++/Java/etc

Static typing catches bugs earlier

Robust / predictable / clarity

OO is best

Creating **<u>new S/W</u>** is most fun/rewarding

Novice in science domain?

Version control, Makefiles, Regression tests

<u>Researcher</u>

Speed of obtaining result

Interpreted Scripts: compiling nuisance

Variable declaration a nuisance

Intuitive / flexible / contextual

Not if mandatory for common/simple case

Prefers trusted methods, vetted by years of research / publication use

Novice in CS domain?

What?

Classic Case : new / malloc Errors

ENOMEM is Fatal

isis>	load_data
isis>	fit_model

...WAIT 2 DAYS ...

isis> volview(3D_gas_cloud)

Out Of Memory! Aborted

linux%

assert() or exit() on error?

Not Necessarily

isis>	load data	

isis> fit_model

...WAIT 2 DAYS ...

isis> volview(3D_gas_cloud)

Out Of Memory: Close applications and retry.

isis> save_results
isis> volview(3D_gas_cloud)

Not if I lose days of analysis!

Human Context Trumps Dogma

What to do?

Claim

Given that science pushes boundaries of knowledge

And of technology to acquire / distill / analyze it

Scientific analysis S/W is never truly complete

Claim II

In our best interest, then, that it be EXTENSIBLE

<u>To Enable</u>

Researchers to incorporate custom/experimental codes

And drive system in directions not yet supported

Or perhaps even envisioned by its creators

Without programmer-army rewrite every few years

Claim III

Simply, but WLOG / power / flexibility

Biology

Math

Computing

Computing

Freeing practitioners to concentrate on

Scientific and algorithmic concerns

Rather than

Plumbing details of computational platform

(benefits developer, too: see modularity)

Case Study in Serendipity



MRIs in Astro Spectral Modeling S/W

10 Minutes of Goofing Around

• Series of 2D images in DICOM format



- On CD with Windows XP reader software
- Read as PNG, stacked as 3D & rendered on Linux
- With 120 Kb module wrapper of VOLPACK (1994)

Flexible S/W adapts for unintended uses OLD \Rightarrow BAD : volpack VERY FAST (Go NetLib!)

No Need To Convene Design-By-Committee



h5_write("mri.h5", vol)

volview(vol)

foreach i ([1:n]) vol [i-1, *, *] = png_read(...)

n = 73 vol = UInt_Type[n, 128, 128]







From 2D Slices Render volume Save as HDF5 for later ease Clean noise from sides Cut out quadrant to see interior

Create 3D

Real Science : Spatial+Spectral Fitting



Qualitative Visualizations Steer Quantitative Analyses

ND Arrays are Scientific Clay



DS9 visualizer showing ACIS CCD image & 3 regions of interest isis> image = ds9_get_array()
isis> image
Float_Type[1024, 1024]

To be shaped ...

isis> hist = sum(im, 0)
isis> range = [440:680]
isis> hplot(range-1, range, hist[range])
isis> xa = [440:680:4], ya = hist[xa]

isis> require("gsl")
isis> smooth = interp_cspline(range, xa, ya)
isis> oplot(range, smooth)

... and seen in arbitrary ways



Using a <u>numerical interpreter</u> as potter's wheel

Previous Example : So What?



DS9 single most widely used tool in astronomy

Mostly qualitative, though

Importing Controller Module

isis> import("ds9")

Merges DS9 imaging with ISIS numerics & extensibility

Without changing either app!

Modernity: Melange Of

File formats ...

... programming languages,

... monolithic GUIs

Given this complexity ...

More Concerned With How To

Load your data as ND array ...

... so <u>I can decide</u>

... how to best SHAPE & SEE it

- Quickly (by end-user / scientist)
- With little or no low-level coding
- Through ad-hoc mixtures of intrinsic functions,
- Plugin modules, scripts, interactive commands,
- Or even compiled code (dynamically loaded)

Pick Your Favorite: MatLab, R, S-Lang, Python, ...

10 Years In ISIS



Bulk of functionality provided by modules Most can be downloaded/used outside of ISIS

Spectral Modeling Innovations

- Programmable Atomic Database API
- Model == arbitrary interpreted math expression (not text)
- Model evaluation caching
- Hooks to customize nearly every aspect of fitting
- Natural multi-wavelength: X-ray, Radio, Visible, IR, Gamma
- Volume rendering : leading to spatial + spectral fitting
- Data Mining GUI-lets
- Nearly Transparent Parallelism: conf limits, model fit eval, etc
- Read/write access to FORTRAN common blocks
- Automated Vector-Parallel Bindings Generation
- HDF5 I/O

Years Ahead Of Other Groups : Very Small Team

Beyond XSPEC: Toward Highly Configurable Astrophysical Analysis (Noble & Nowak, 2008, PASP)

Modules: Evolutionary Advantage

Harder to extend venerable/monolithic app with arbitrary features than to add new modules to extensible system

Consider addition of HDF5 to Genome Workbench

Large C++ codebase; Long-ish NCBI institutional cycle

Design/write/test/document/release of ENTIRE APP?

Contrast With:

import("hdf5")

Leverages Internet: "All problems shallow" (Raymond/Torvalds) Someone, somewhere likely to have written a module ...



• Feature sets evolve MUCH more rapidly

Modules: Developer Advantage

Most of porting problem solved in interpreter, by someone else

Then the common refrain

"Small team, supported only on Linux"

begins to fade away.

JAVA Solves Portability, Too, BUT :

Anyone write interactive numerical interpreters in JAVA? (Byte) Compiled, static typing == not for itinerant bio coders

Modules: Yet More Advantages

More Stable: internal core of app unchanged as features added (better partition of test/doc/release workload)

Functional Orthogonality == needs smaller mental map (internal core need not be mastered by module developer)

More Nimble Schedule: modules released as ready, not app

More Nimble Response: modules can be loaded JIT, per use

Case Study: 2D + 2D Data Mining

Array Selection
With
where()

isis> arr = [1, 2, 3, 4, 1]
isis> i = where(arr < 2)
isis> print(i)
0, 4

Like R "subset()" but more concise?

Surprisingly Powerful Feature

Where : Visual Where Function

```
isis> table = read("cygnus_xI")
isis> table
Struct_Type with I7 fields
```

```
isis> points = vwhere(table)
```

GUI-let launched from interactive cmd line

VWhere 1.3.4		-=×
Plot Axes Expressions (vector length	n: 316)	
X time	Choose	Clear
Y Ichan + mchan	Choose	Clear
S-Lang> Plot OPlot Prompt	time mchan Ichan Ichan + m	ear chan ^{Quit}
S-Lang Namespace: vwpub		/



Create new axes on fly with arbitrary numerical expressions, including calls to C, C++, Fortran modules

Points selected via regions on plots of 2 axes



Effect instantly seen on plots of other axes



Returns same array of indices as where()

VWhere Benefits

Faster than file-based command-line tools (10x or more) Filters accumulated in memory, not files No file litter More intutive : no tool filter syntax needed Far more powerful, too (extensible math)

<u>Same Paradigm</u> ND arrays, shaped & seen in arbitrary ways Combines power of interactive analysis cmd line with GUI modules, where useful

Case Study: Parallel Model Fitting

You calculate p-value We calculate χ^2



Model components mathematically independent Embarrassingly parallel isis> require("pmodel") Evaluations farmed to independent CPUs / hosts ISIS unaware model is parallel: internals unchanged fit performed as if serial

Parallelism in ISIS: 5+ years before any others

Case Study: SLIRP Wrapper Generator

Dramatically reduce effort to call C/C++/Fortran from S-Lang.

Can vectorize funcs for natural S-Lang array usage.

Optionally with OpenMP for multicore.

Read / write access to Fortran common blocks.

Turnkey mechanism for scientists to include their custom models into modern analysis system.

Quick way for developer to generate wrapper modules for OTS libs being considered for use.

SLIRP Example : ASCII Volume

Problem: Visualize 320x320x320 cube of Doppler velocities, from ASCII file Solution: Convert to real-values with atof()

Problem II: Will be slow, atof() not vectorized Solution II : replace it with vector-parallel version

linux% slirp -make -openmp atof.h && make

SLIRP Example : Performance

Using only 100³ strings : 33x smaller dataset

```
isis> avol = array_map(String_Type, &sprintf, "%d", [1:100*100*100])
isis> tic; dvol = array_map(Double_Type, &atof, avol); toc
13.754
```

```
isis> import("atof")
isis> tic; pdvol = atof(avol); toc
0.1442
```

S-Lang intrinsic : 13.8 sec Vector-parallel replacement: 0.144 sec

95X faster on dual-core 1.8 GHz

Random Browse of Bio S/W

NCBI: CDTree, NCBI Toolbox, Genome Workbench Allen Brain Institute: Brain Explorer, etc Broad Institute: IGV, Arachne, ALLPATHS

... and many more ...

Overwhelmed by sheer volume of data

Impressed by maintenance of provenance

Layman's Concern With

Sense of qualitative, visualization orientation 3D molecules, 2D gene trees, Contig assemblies, ...

Then what? How does it lead to quantitative analysis?

Stated Differently: Difficult to see data flow between between disparate but similar tools

"Small team, supported only on Linux" Tough to swallow by R, MatLab, Python, etc crowd

Conclusion: Concern Turns To Joy



Deeply Resonant With Themes Of This Talk

Flexible, Modular, Extensible, Reproducible

Beautiful

But where is FireHose?

Why no (Bio)Python?