Thoughts on software for science

Steve Plimpton Sandia National Laboratories

ASCR Workshop on the Science of Scientific Software Development and Use December 2021







The Science of Scientific Software Development and Use

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- Second says our software is used by people who do science

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"Any field which has to have science in its name isn't one"

physics, chemistry, biology, mathematics, statistics

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- data science, information science, political science, ...

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So instead of asking:

How do we add more science to the process of making tools?

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Another way to **frame the challenge** for this workshop:

- (axiom 1) DOE's chief product is excellent domain science
- (axiom 2) Big computers and sci software are two (of many) tools used to that end
- Challenge: How do we make it as easy as possible for domain scientists to do excellent science with those 2 tools

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The rest of my talk takes that **point-of-view**: my bias != your bias

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- Faster and faster for Linpack flops:
 - 2 Gflop in 1988 Cray YMP
 - 1 Tflop in 1997 ASCI Red (Cray)
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 - 1 Eflop in 2022-3 Frontier (HP) and Aurora (Intel)
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Reasons:

- Moore's law
- 2 large-scale distributed parallelism
 - Summit = 5600 ft², 340 tons, 13 MW, 4000 gal H_2O/min
- GPUs for threaded parallelism

- Harder and harder to get good performance
- Fewer and fewer science apps achieve that performance
- Harder and harder to program the machines
 - hybrid nodes (CPU+GPU), imbalance in compute vs comm

Imbalance ratios over 30 years

- Local balance = flops to pay for 1 on-node word (8 bytes)
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- Thanks to Si Hammond at Sandia

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			Flops/	Flops/
Year	Machine	Linpack	local	remote
1988	Cray YMP	2.1 Gflops	0.5	0.5
1997	ASCI Red (SNL)	1.6 Tflops	8.3	20
2011	RoadRunner (LANL)	1.0 Pflops	6.7	170
2011	K-Computer (Japan)	11 Pflops	15	95
2012	Sequoia (LLNL)	17 Pflops	32	160
2013	Titan (ORNL)	18 Pflops	29	490
2016	Sunway TaihuLight (China)	93 Pflops	130	1500
2018	Summit (ORNL)	149 Pflops	45	10300
	, ,	_		
2021	Sunway Exascale (China)	$\sim 1.5 \text{ Eflops}$	350	9200
2022	Frontier (ORNL)	$\sim 1.5 \text{ Eflops}$	250	29400

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- Developing sci software requires larger and larger teams
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- Most of this is driven by hardware & chasing-flops mindset
- None of this is optimal for science and domain scientists

7 year project (2016-2023), total budget around \$4 billion

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A strategic **aside** for the workshop:

- DOE just spent \$1.2B on Scientific Software for exascale
- We're saying **now** we need to apply scientific methods?
- Challenge #1: What is this workshop proposing that wasn't included in ECP software \$\$ and why wasn't it?

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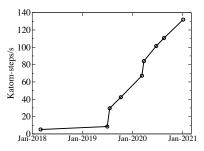
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Challenge #2: Can we exit this spending cycle of needing more and more \$\$ for software on new machines?

One example from within ECP

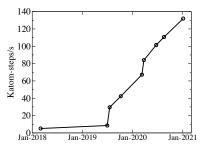
LAMMPS/SNAP performance on a NVIDIA V100 GPU



- LAMMPS = classical MD code for materials modeling
- SNAP = expensive, accurate ML potential
- Kokkos-ized for portable GPU performance
- Team: 2 ECP projects, NERSC, OLCF, ALCF, NVIDIA
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- Algorithm refactoring, code restructuring, opt, tuning
- Bottom line: **26x** speed-up in 3 years



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Success!

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- Optimized one model in one code in one science field yikes!
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Challenge #3:

Can our software efforts & tools have broader impact?

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- Challenge #4: To maximize impact on science, can we focus on customers in the much, much larger worldwide scientific computing community?

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- Sci software requires big teams of cross-disciplinary experts
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- **Challenge #5**: As toolmakers, can we write software so simple and good, we become **obsolete** (once the tool is deployed)?

Complex software is sub-optimal for domain science

Software **complexity** is not a **simple** issue (pun intended)

- Modern computers & science have unavoidable complexity
- One hand: shielding users from complexity is often good
- OTOH: domain scientists often need to know what's going on
- Payoff for hiding complexity varies with kind of software:
 - application vs library vs system software

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Sources of complexity for domain scientists:

- C++: templating, overloading, convoluted data structs, etc
- Hardware optimizations: compler directives, Cuda kernels, Kokkos abstractions, etc
- ML: perfectly designed to make path-to-results opaque to end users

Effects of sci software complexity on domain scientists

- Harder to understand what code is doing
- Harder to implement their new ideas w/out expert help
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David Parnas: "Complexity is not a goal. I don't want to be remembered as an engineer of complex systems."

Example of a scientific mistake due to software complexity

2018: Emails from Doug Kothe (head of ECP) and Mike Heroux (ECP Software), asking about this article:

PHYSICS TODAY

The war over supercooled water



- Sub-title: How a hidden coding error fueled a seven-year dispute between two of condensed matter's top theorists
- Article says group that made a mistake was using LAMMPS

Some details of controversy

- D Chandler (UC Berkeley) and P Debenedetti (Princeton)
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 - LAMMPS corrected for that ⇒ too-cold molecules
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- Bottom line: bug in their code, not LAMMPS
 - were clues in LAMMPS manual, but who reads the manual ?
- Key point: Our code was complicated enough that expert domain scientists got confused and made a science mistake

- New science often require new models and new code
 - different material (alloys, mixtures, interfaces, etc)
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Result: Contributions by 100s of users, some we never imagined

However we also learned this lesson

Child styles also used for CPU & GPU acceleration: variants for OpenMP, Intel, Cuda, Kokkos

Vanilla CPU	Accelerated CPU/GPU styles			
Pair+Fix styles	coverage	by developers	by users	
529	33%	275	23	

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Challenge #7: Can our tools enable average domain scientists to more easily write performant code ?

Examples of tool success stories

3 flavors

- Outside software
- Outside scientific software
- Within scientific software

Tool success story outside software

Experimental cell biology

- PCR (1983) = polymerase chain reaction, DNA replication
- Microarray chips (1995) = parallel gene expression (millions)
- DNA sequencing $(2001) = $10K/Mb \Rightarrow 2 \text{ dimes/Mb}$
- CRISPR (2012) = genome editing in living cells









- 3 Nobel prizes on this list
- All these technologies rapidly became ubiquitous
- Any lab, any grad student can use them

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- Challenge #8: Aspire to that ease-of-use for our software?

Tool success story outside scientific software

Google Mapreduce + Hadoop

- 2004 by Jeffrey Dean and Sanjay Ghemawat
- Goal: make it easy for anyone within Google to use their huge distributed computers to analyze big data
- Within a few years 1000s of MR codes running at Google
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Challenge #9: Can we make it similarly easy for **anyone** to write scientific software for big parallel computers?

Another tool success story outside scientific software





iPhone or Android apps

- 2.2M iOS apps at Apple store
- 3.5M Android apps at Google Play
- Ecosystem evolved ⇒ anyone can write a phone app
- Don't need an Apple employee or Android expert on your team

Challenge #10: Why not 10K or 1M apps on our big computers? **Challenge** #11: Create similar ecosystem for scientific software?

Tool success story #1 within scientific software



Python language

- Created around 1990 by Guido van Rossum
- Initial audience was not computational science
- Now ubiquitous in computational science and ML
- Easy to understand, easy to write, easy to extend

Tool success story #2 within scientific software



FFTW library for discrete Fourier transforms

- Late 1990s by Matteo Frigo and Steven Johnson
- Wilkinson prize for numerical software
- Example of a perfect black box (admittedly in narrow space)
- One of first auto-tuning numerical codes
- Hides the right amount of complexity: hardware, FFT size
- Easy for domain scientists to use, they know models amenable to solution via FFTs

Possible tool success story #3 within scientific software





PETSc and Trilinos sparse iterative solver packages

- Large teams at 2 DOE labs: Argonne and Sandia
- Goal: hide solver complexity from domain scientists
- Goal: enable use of complicated solvers as a black box
- Goal: make it easy to plug into any PDE model

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- How well are these goals met ?
- Are they easy for average domain scientists to use & extend ?

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Challenge #12:

Measure ease-of-use or learning curve for sci software ?

Challenge #13:

Measure for average domain scientists who both use & extend ?

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This workshop proposes to nurture how sci software is developed

- Need to recognize the nature of what is being nurtured
- Nature = domain scientists use our software to do science
- If we don't make it easier for them to do it,
 we're not nurturing sci software development effectively

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DOE labs are the perfect place to try and do this