

Enhancing Analysis Performance and Reproducibility

with Containers and the Cloud

Ricardo Rocha, CERN IT - ExaHealth 2021

<https://indico.cern.ch/event/1078121>

Ricardo Rocha

Computing Engineer - CERN Cloud Team

Kubernetes and Containers, Networking and SDN

GPUs and other Accelerators, Machine Learning

Cloud Native Computing Foundation (CNCF)

Representative of CERN in the CNCF and End User Community

Member of the CNCF Technical Oversight Committee (TOC)

<https://www.cncf.io/people/technical-oversight-committee/>

Lead of the CNCF Research User Group

<https://github.com/cncf/research-user-group>



@ahcorporto ricardo.rocha@cern.ch

Will the infrastructure run my software
in 10 years?

Machine	Default	Optimization off	Maximum	'Value' of -O
IBM/AIX	noopt		-03	-02
HP/UX	noopt		+03	+02
Solaris	noopt		-04	-03
Tru64 UNIX (Digital-UNIX)	-04	-00	-04	-04
SGI	-01	-00	-03	-02

7.3 Important Platform Dependent Differences

On most platforms at CERN the recommended Fortran compiler is called **f77**. The exception is HP/UX where you are recommended to use **fort77** rather than **f77** since it allows you to specify libraries in a way which is compatible with all the other platforms. For AIX on the RS/6000 the Fortran compiler is called **xlf**, but in more recent versions of AIX the name **f77** can also be used.

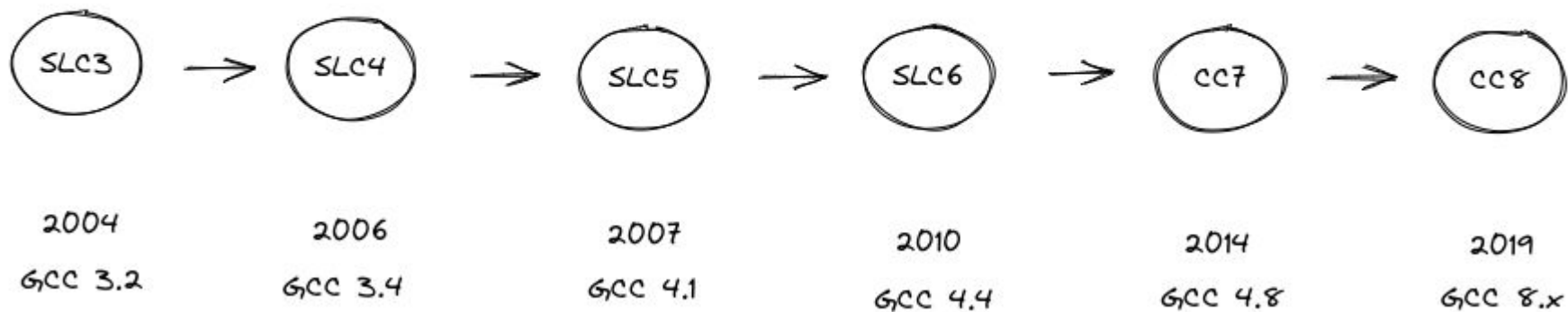
The table below shows the minimum command that should be used for compiling and linking in the CERN environment.

Machine	Compilation only	Compiling and/or Linking
IBM/AIX	xlf -c -qextname	xlf -qextname
HP/UX	fort77 -c +ppu	fort77 +ppu
Others	f77 -c	f77

As we saw in the section above, by default Unix compilers generate an executable module. The option “-c” (compile only) generates an object file but causes the linking phase to be suppressed.

The options -qextname on AIX and +ppu on HP/UX are explained in “Compiling and Linking Options” on page 50 and are ESSENTIAL for compatibility with the CERN Program Library.

Linux Era



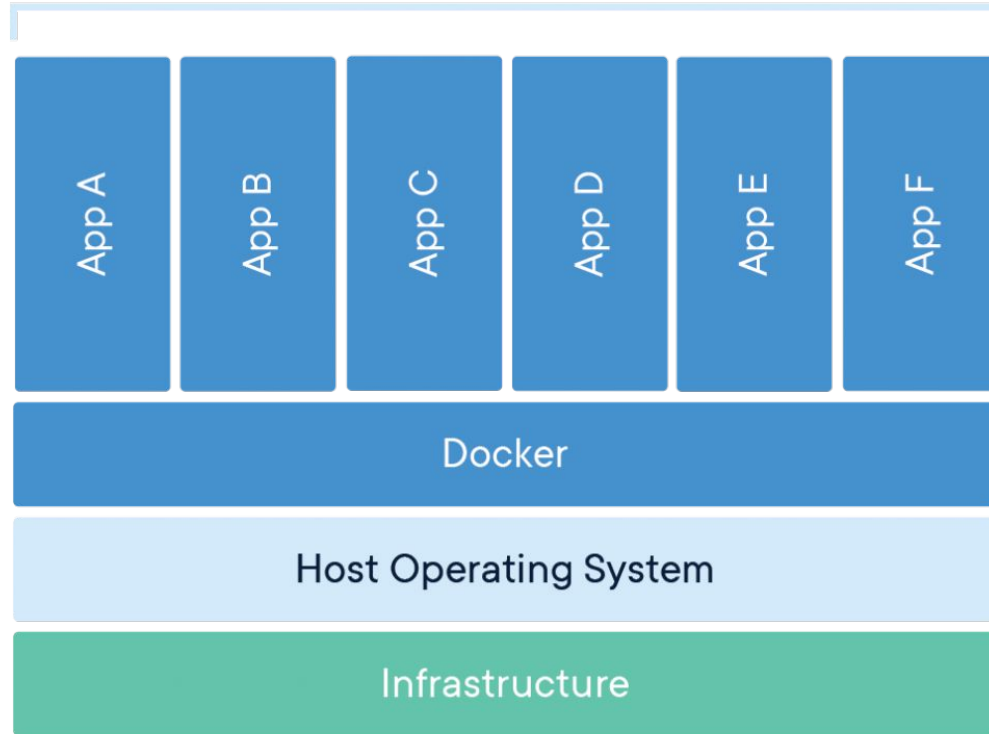
And we could go on...

Will i still be able to access my data?

Will my data format still be readable?

...

Containerized Applications

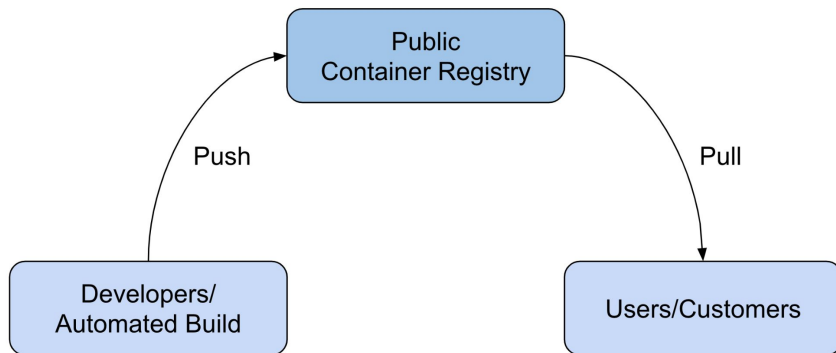


Evolve infrastructure and applications separately

Shared kernel, but distinct *operating systems*

Immutable, tagged images

Sharing using private and public registries



```
1 # Base image with explicit versioning
2 #
3 # Can be different from the host OS running the container,
4 # which could be running CentOS or other distribution
5 FROM ubuntu:16.04
6
7 # Trackback to image maintainer
8 MAINTAINER ricardo.rocha@cern.ch
9
10 # Dependencies with explicit versioning
11 RUN apt-get update
12 RUN apt-get install -y gcc:7.5.0 wget:1.12
13 RUN pip install scipy:0.18.1
14
15 # Any custom files, binaries, even data can be added
16 COPY ./specialfile /
17
18 # Anything else can be run as part of the image build
19 RUN wget http://domain/customscript -O /run.sh
20
21 # Default command being run on start
22 CMD ["/run.sh"]
```


In Depth: Linear Regression

Just as naive Bayes (discussed earlier in [In Depth: Naive Bayes Classification](#)) is a good starting point for classification tasks, linear regression models are a good starting point for regression tasks. Such models are popular because they can be fit very quickly, and are very interpretable. You are probably familiar with the simplest form of a linear regression model (i.e., fitting a straight line to data) but such models can be extended to model more complicated data behavior.

In this section we will start with a quick intuitive walk-through of the mathematics behind this well-known problem, before seeing how before moving on to see how linear models can be generalized to account for more complicated patterns in data.

```

[1]: %matplotlib inline
import numpy as np
import matplotlib.pyplot as plt

rng = np.random.RandomState(1)
x = 10 * rng.rand(50)
y = 2 * x + rng.rand(50)
plt.scatter(x, y)

[2]: from sklearn.linear_model import LinearRegression
model = LinearRegression().fit(x, y)
print('Coefficients: \n', model.coef_)
print('Intercept: \n', model.intercept_)

```

Simple

Slide Type

Raw NBConvert Format

Advanced Tools

Cell Metadata

```

{
  "kernelspec": {
    "display_name": "Python 3",
    "language": "python",
    "name": "python3"
  },
  "language_info": {
    "codemirror_mode": {
      "name": "ipython",
      "version": 3
    },
    "file_extension": ".py",
    "mimetype": "text/x-python",
    "name": "python",
    "nbconvert_exporter": "python",
    "pygments_lexer": "ipython3",
    "version": "3.6.7"
  }
}

```

Launcher

Notebook

Python 3, C++11, C++14, C++17, Julia 1.1.0, phylogenetics (Python 3.7), R

Console

Altair.ipynb

Seattle Weather: 2012-2015

Julia

```

[10]: using RDatasets, Gadfly
plot(dataset("datasets", "iris"), xs="Sepal.Length", ys="Petal.Length")

[8]: eigen(x)
Eigen{Complex{Float64}, Complex{Float64}, Array{Complex{Float64}, 2}, Array{Complex{Float64}, 12}}
eigenvalues:
10-element Array{Complex{Float64}, 1}:
 4.7433881566545466 + 0.0im
-0.4453896355895886 + 0.8im

```

python notebook

```

[1]: %matplotlib inline
from ipywidgets import interactive, fixed

We explore the Lorenz system of differential equations:
x-dot = sigma*(y - x)
y-dot = rho*x - y - x*z
z-dot = -beta + x*y

Let's change (sigma, beta, rho) with ipywidgets and examine the trajectories.

[2]: from lorenz import solve_lorenz
w = interactive(solve_lorenz, sigma=(0, 50, 50), rho=10, beta=2.6666666666666666)
w.interactive(children=(FloatSlider(value=10.0, description='sigma', max=50.0), FloatSlider(value=2.6666666666666666,

```

R

```

[3]: ggplot(data=iris, aes(x=Sepal.Length, y=Petal.Length)) +
  geom_point()

[1]: head(iris)
Sepal.Length Sepal.Width Petal.Length
1 5.1 3.5 1.4
2 4.9 3.0 1.4

```



Turn a GitHub repo into a collection of interactive notebooks

Have a repository full of Jupyter notebooks? With Binder, open those notebooks in an executable environment, making your code immediately reproducible by anyone, anywhere.

Build and launch a repository

GitHub repo or URL

Git branch, tag, or commit

Path to a notebook file (optional)

File ▾

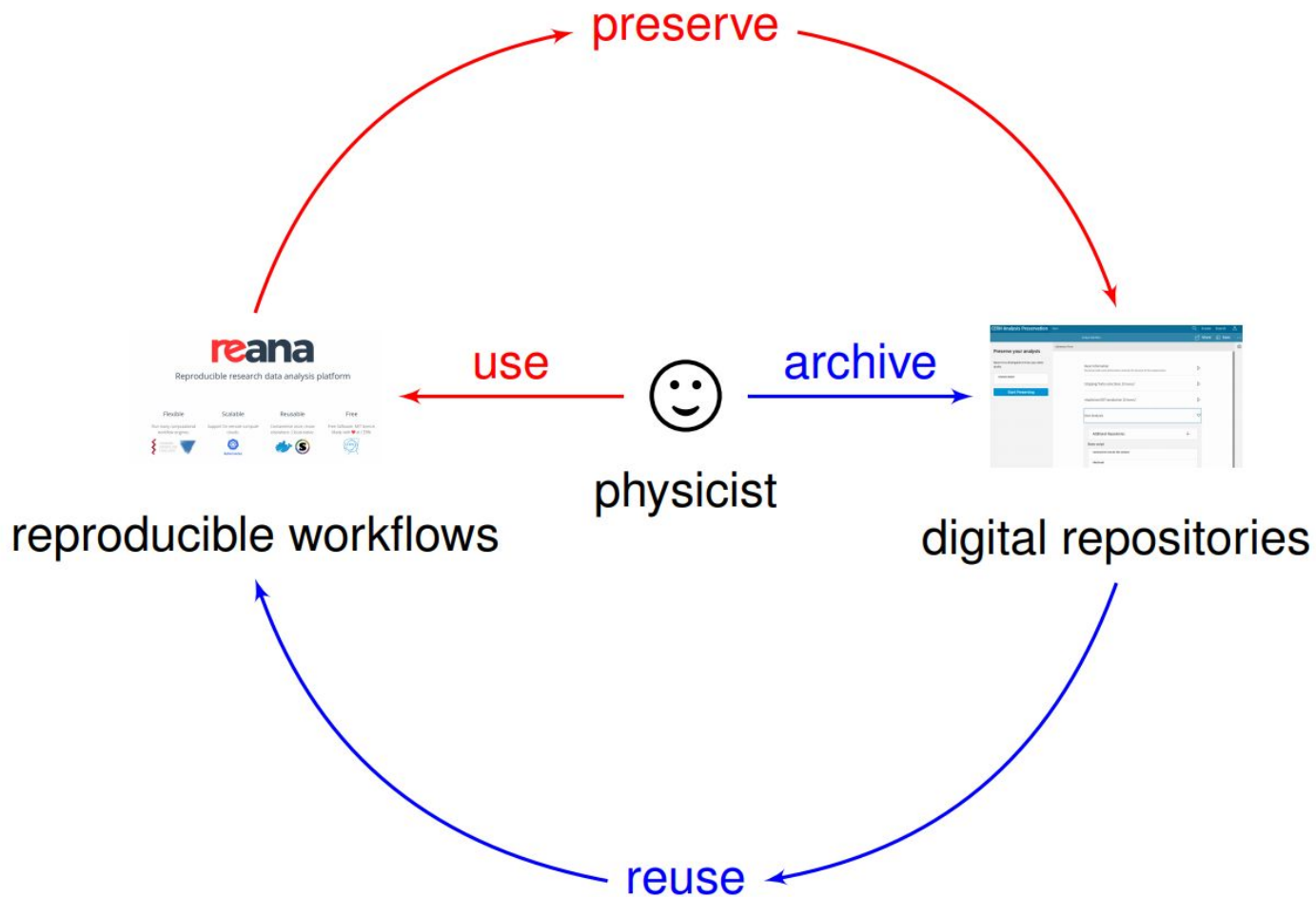
launch ▾

Already built!

Launching

Build logs

[show](#)



File Edit View Run Kernel Git Tabs Settings Help

Launcher us_data.pipeline

etl_us_census demographics_...

etl_us_data clean_us_data fit_us_data analyze_fit_us_...

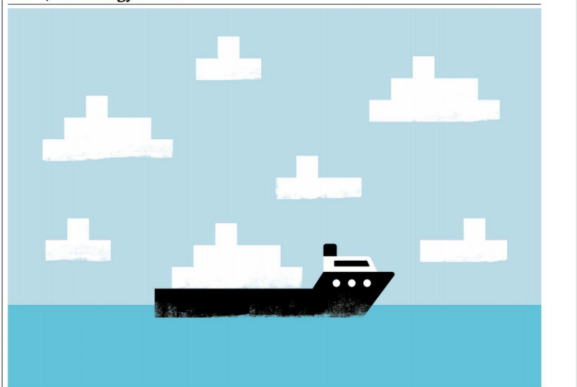
maps_us_data tables_us_data timeseries_us_d...

```
graph LR; etl_us_census --> clean_us_data; etl_us_data --> clean_us_data; clean_us_data --> demographics_...; clean_us_data --> fit_us_data; clean_us_data --> maps_us_data; clean_us_data --> tables_us_data; clean_us_data --> timeseries_us_d...; fit_us_data --> analyze_fit_us_...
```

0 0 us_data.pipeline

Containers & Open in Science

Work / Technology & tools



CONTAINERS IN THE CLOUD

Standardized platforms allow researchers to run each other's software — no installation required. By Jeffrey M. Perkel

Murphy's law for the digital age: anything that can go wrong, will go wrong during a live demonstration. For Ben Marwick, that happened in front of a roomful of landscape architecture students in Berlin. The topic: computational reproducibility using Docker. Docker is a software tool that generates 'containers' — standardized computational environments that can be shared and reused. Containers ensure that computational analyses always run on the same underlying infrastructure, fostering reproducibility. Docker thereby insulates researchers from the challenges of installing and updating research software. However, it can be difficult to use. Marwick, an archaeologist at the University of Washington in Seattle, had become

proficient in migrating Docker configuration files ('Dockerfiles') from one project to the next, making minor tweaks and getting them to work. Colleagues in Germany invited him to teach their students how to follow suit. But because every student had a slightly different set of hardware and software installed, each one required a customized configuration. The demo "was a complete disaster", Marwick says. Today, a growing collection of services allows researchers to sidestep such confusion. Using these services — which include Binder, Code Ocean, Colaboratory, Gigantum and Nextjournal — researchers can run code in the cloud without needing to install more software. They can click down their software configurations, migrate those environments from laptops to high-performance computing

clusters and share them with colleagues. Educators can create and share course materials with students, and journals can improve the reproducibility of results in published articles. It's never been easier to understand, evaluate, adopt and page the computational methods on which modern science depends. William Cono, a sleep researcher at Harvard Medical School in Boston, Massachusetts, spent weeks writing and debugging an algorithm, only to discover that a colleague's containerized code could have saved a lot of time. "I could have just gotten up and running, using all of the debugging work that he had already done, at the click of a button," he says. Scientific software often requires installing, navigating and troubleshooting a byzantine network of computational 'dependencies'

Work / Technology & tools

— the code libraries and tools on which each software module relies. Some have to be compiled from source code or configured just so, and an example of our code running on all five platforms can degenerate into a frustrating online odyssey through websites such as Stack Overflow and GitHub. "One of the hardest parts of reproducibility is getting your computer set up in exactly the same way as somebody else's computer is set up. That is just ridiculously difficult," says Kristin Whitaker, a neuroscientist at the Alan Turing Institute in London.

Easier evaluation

Docker reduces that to a single command. "Docker really provides reduced friction for that stage of the cycle of reproducing somebody else's work, in which you have to build the software from source and combine it with other external libraries," says Lorena Barba, a mechanical and aerospace engineer at George Washington University in Washington DC. "It facilitates that part, making it less error-prone, making it less onerous in researcher time." Barba's team does most of its work in Docker containers. But that is a computationally savvy research group; others might find the process daunting. A text-based 'command-line' application, Docker has dozens of options, and building a working Dockerfile can be an exercise in frustration.

That's where the cloud-based services come in. Binder is an open-source project that allows users to test-drive computational notebooks — documents such as Jupyter or R Markdown notebooks, which blend code, figures and text. Code Ocean, Gigantum and Nextjournal (the latter three have free and paid tiers) let users write code in the cloud as well as, and in some cases, bundle it with the data to be processed. These platforms also allow users to modify the code and apply it to other data sets, and provide version-control features for reviewing changes.

Such tools make it easier for researchers to evaluate their colleagues' work. "With Binder, you have taken that barrier [of software installation away], says Karthik Ram, a computational ecologist at the University of California, Berkeley. "If I can click that button and be dropped into a notebook where everything is installed, the environment is exactly the way you intended to be, then you may be more likely to take a look and give your feedback." Identifying required dependencies, and where to find them, varies with the platform. "Code Ocean and Gigantum, for example, have a one-click operation, whereas Binder requires a list of dependencies in a GitHub repository. Whitaker's advice: codify your computing environment as early as possible in a project, and stick with it. "If you try and do it at the end, then you are basically doing archaeology on your code, and it's really, really hard," she says. Ram developed a tool called Holopunch for

projects that use the statistical programming language R. Holopunch relieves the process of setting up Binder into four simple commands. (See <https://github.com/gigantum/all-five-platforms> at go.nature.com/2p9se1c.) The easiest way to try Binder is at mybinder.org, a free, albeit computationally limited, website. Or, for greater power and security, researchers can build private 'Binder hubs' instead. The Alan Turing Institute has two, including one called hub23 (a reference to Hub 23 at the Second World War code-breaking facility at Bletchley Park, UK), that provides

"Researchers can be confident that their code will remain usable, whichever platform they choose."

greater computational resources and the ability to work with data sets that cannot be publicly shared, Whitaker says. The Rango community, which promotes open, reproducible and scalable geoscience, built a dedicated BinderHub so that researchers can explore climate modelling and satellite data sets that can amount to tens of terabytes, says Joe Hamman, a computational hydroclimatologist at the National Center for Atmospheric Research in Boulder, Colorado. (Whitaker's team is building a tutorial on building a BinderHub at go.nature.com/3P95C.)

Languages and clouds

Google's Colaboratory is basically a cross between a Jupyter notebook and Google Docs, meaning users can share, comment on and jointly edit notebooks, which are stored on Google Drive. Users execute their code in the Google cloud — only the Python language is officially supported — on a standard cloud processing unit (CPU), a graphics processing unit (GPU) or a tensor processing unit (TPU), a specialized chip optimized for Google's TensorFlow deep-learning software. "You can open your notebook or someone else's notebook from GitHub, start playing around with it, and use your own GPU and CPU and GPU and CPU, and so on later," says Jake VanderPlas, a member of the Colaboratory team in Google in Seattle.

Nextjournal supports notebooks written in Python, R, Julia, Bash and Clojure, with more languages in development. According to Martin Kavalir, chief executive of Nextjournal, which is based in Berlin, the company has registered nearly 3,000 users since it launched the platform on 3 May. Code Ocean, a beta version of which launched last year, features a browser-based client that users can install on their own system or remotely, for cloud-based coding and execution in the Jupyter and RStudio coding environments. Cono and WhoSaidGigantum to

machine-learning algorithms in the Amazon cloud, says the service makes it easy for collaborators to do the ground running. "I can get my code running on Gigantum and push that cloud-to-cloud compute infrastructure to the training and learning," he explains. Then there's Code Ocean, which supports both notebooks and conventional scripts in Python, R, Julia, Matlab and C, among other languages. Several journals now use Code Ocean for publication and to promote computational reproducibility, including titles from Taylor & Francis, De Gruyter and SAGE. In 2018, Nature Technology, Nature Machine Intelligence and Nature Methods launched a pilot programme to use Code Ocean for peer review. Nature, Nature Protocols and BMC Bioinformatics subsequently joined the trial. More than 95 papers have now been included in the trial, according to Erika Patrana, editorial director of Nature Research's applied science and chemistry journals, and more than 20 of those have been published.

Felix Allen, a computer scientist at the Wellcome Sanger Institute in Hinxton, UK, co-authored one study in that trial, which analysed the types of mutation that can arise from CRISPR-based gene editing. (F. Allen et al. *Nature Biotechnol.* 37, 647–62, 2019). She estimates that it took a week to get the Code Ocean environment working. "I was surprised to really like it," Allen says. "And I think it was really nice that it made an example that someone could just press 'go' on and would work."

Although some worry about the long-term viability of commercial container-computing services, researchers do have options. Simon Adar, chief executive of Code Ocean, notes that Code Ocean 'compute capsules' are archived by the CLOCKSS project, which preserves digital copies of online scientific literature. And Code Ocean, Gigantum and Nextjournal allow Dockerfiles to be exported for use on other platforms. All of which means that researchers can be confident that their code will remain usable, whichever platform they choose.

Benjamin Habes Kains, a computational pharmacogenomics researcher at the Princess Margaret Cancer Centre in Toronto, Canada, also uses Python for his work. He has responded to critiques of an analysis he published in *Nature* (B. Habes Kains et al. *Nature* 504, 389–393, 2013). For him, Code Ocean provides a way to ensure his code can be used and evaluated by his team, peer reviewers and the broader scientific community. "It's not so much that an analysis is correct or incorrect," he says. "Nothing is really fully correct in this world. However, I've more transparent about it, you always communicate the level of confidence of criticism. You have nothing to hide — everything is there."

Jeffrey M. Perkel is technology Nature.

nature physics

Corrected: Publisher Correction

Open is not enough

Xiaoli Chen¹, Srinje Dalmeier-Tiessen^{1*}, Robin Dasler^{1,2}, Sebastian Feger^{1,3}, Parnfios Fokianos^{1,4}, Jose Benito Gonzalez¹, Harri Hirvonsalo^{1,5,6}, Dinos Koutris¹, Artemis Lavasa¹, Salvatore Mele¹, Diego Rodríguez Rodríguez¹, Tibor Šimko¹, Tim Smith¹, Ana Trisovic^{1,7}, Anna Trzcinska¹, Ioannis Tsanaktsidis¹, Markus Zimmermann¹, Kyle Cranmer¹, Lukas Heinrich¹, Gordon Watts¹, Michael Hildreth¹, Lara Lloret Iglesias⁸, Kati Lassila-Perini¹ and Sebastian Neubert^{1,9}

The solutions adopted by the high-energy physics community to foster reproducible research are examples of best practices that could be embraced more widely. This first experience suggests that reproducibility requires going beyond openness.

Open science and reproducible research have become pervasive goals across research communities, political circles and funding bodies¹. The understanding is that open and reproducible research practices enable scientific success, accelerating future progress and discoveries in any discipline. In the struggle to take concrete steps in pursuit of these aims there has been much discussion and awareness-raising, often accompanied by a push to make research products and scientific results open quickly. Although these are laudable and necessary first steps, they are not sufficient to bring about the transformation that would allow us to reap the benefits of open and reproducible research. It is time to move beyond the rhetoric and the trust in quick fixes and start designing and implementing tools to power a more profound change.

Our own experience from opening up vast volumes of data in particle physics cannot simply be taken on as an afterthought at the end of the scientific endeavour. In addition, openness alone does not guarantee reproducibility or reusability, so it should not be pursued as a goal in itself. Focusing on data is also not enough: it needs to be accompanied by software, workflows and explanations, all of which need to be captured throughout the usual iterative and closed research lifecycle, ready for a timely open release with the results. Thus, a graphics processing unit (GPU) or a graphics processing unit (GPU) is not having the reuse of research results as a goal requires the adoption of new research practices during the data analysis process. Such practices need to be tailored to the needs of each given discipline with its particular research environment, culture and idiosyncrasies. Services and tools should be developed with the idea of meshing seamlessly with existing research procedures, encouraging the pursuit of reusability as a natural part of researchers' daily work (Fig. 1). In this way, the generated research products are more likely to be useful when shared openly.

In tackling the challenge of enabling reusable research, we present these ideas as our guiding light when putting changes into practice in our community — high-energy physics (HEP). Here, we illustrate our approach, particularly through our work at CERN, and present our community's requirements and rationale. We hope that the explanation of our challenges and solutions will stimulate discussions around the practical implementation of work-

flows for reproducible and reusable research more widely in other scientific disciplines.

Approaching reproducibility and reuse in HEP

To set the stage for the rest of this piece, we first construct a more nuanced spectrum in pursuit of this place the various challenges facing HEP allowing us to better frame our ambitions and solutions. We choose to build on the descriptions introduced by Carol Goble² and Lorena A. Barba³ shown in Table 1. These concepts assume a research environment in which multiple labs have the equipment necessary to duplicate an experiment, which essentially makes the experiments portable. In the particle physics context, however, the immense cost and complexity of the experimental set-up essentially make the independent and complete replication of HEP experiments unfeasible and unhelpful. HEP experiments are set up with unique capabilities, often being the only facility or instrument of their kind in the world; they are also constantly being upgraded to satisfy requirements for higher energy precision and level of accuracy. The experiments at the Large Hadron Collider (LHC) are prominent examples. It is this uniqueness that makes the experimental data valuable for preservation so that it can be later reused with other measurements for comparison, confirmation or inspiration.

Our considerations here really begin after gathering the data. This means that we are more concerned with repeating or verifying the computational analysis performed over a given dataset rather than with data collection. Therefore, in Table 2 we present a variation of these definitions that takes into account a research environment in which 'experimental set-up' refers to the implementation of a computational analysis of a defined dataset, and a 'lab' can be thought of as an experimental collaboration or an analysis group.

In the case of computational processes, physics analyses themselves are intrinsically complex due to the large data volume and algorithms involved. In addition, the analysts typically study more than one physics process and consider data collected under different running conditions. Although comprehensive documentation on the analysis methods is maintained, the complexity of the software implementations often hides minute but crucial details,

PERSPECTIVE

<https://doi.org/10.1038/s41567-018-0342-2>

OPEN

Containers & (Open) Science

Work / Technology & tools



CONTAINERS IN THE CLOUD

Standardized platforms allow researchers to run each of their software – no installation required. By Jeffrey M. Perkel

Murphy's law for the digital age: anything that can go wrong, will go wrong during a live demonstration. For Ben Marwick, that happened in front of a roomful of landscape-archaeology students in Berlin. The topic: computational reproducibility using Docker.

Docker is a software tool that generates 'containers' – standardized computational environments that can be shared and reused. Containers ensure that computational analyses always run on the same underlying infrastructure, fostering reproducibility. Docker thereby insulates researchers from the challenges of installing and updating research software; however, it can be difficult to use.

Marwick, an archaeologist at the University of Washington in Seattle, had become

proficient in migrating Docker configuration files ('Dockerfiles') from one project to the next, making minor tweaks and getting them to work. Colleagues in Germany invited him to teach their students how to follow suit. But because every student had a slightly different set of hardware and software installed, each one required a customized configuration. The demo "was a complete disaster", Marwick says.

Today, a growing collection of services allows researchers to sidestep such confusion. Using these services – which include Binder, Code Ocean, Collaboratory, Gigantum and NextJournal – researchers can run code in the cloud without needing to install more software. They can lock down their software configurations, migrate those environments from laptops to high-performance computing

Somebody else's ridiculously different neuroscientist London.

single command. reduced friction for producing something you have to build combine it with Lorena Barba, a engineer at George Washington DC. "It's less error-prone, no developer time"

security, researchers can build private 'BinderHubs' instead. The Alan Turing Institute has two, including one called Hub23 (a reference to Hut 23 at the Second World War code-breaking facility at Bletchley Park, UK), that provides

"Researchers can be confident that their code will remain usable, whichever platform they choose."

greater computational resources and the ability to work with data sets that cannot be publicly shared, Whitaker says. The Pangaea

Work / Technology & tools

— the code libraries and tools on which each software module relies. Some have to be compiled from source code or configured just so, and an installation that should take a few minutes can degenerate into a frustrating online odyssey through websites such as Stack Overflow and GitHub. "One of the hardest parts of reproducibility is getting your computer set up exactly the same way as somebody else's computer was up. That is just ridiculously difficult," says the author. The Alan Turing Institute has

projects that use the statistical programming language R. Holopunch distils the process of setting up Binder into four simple commands. (See examples of our code running on all five platforms at go.nature.com/2p9v9e1.)

The easiest way to try Binder is at mybinder.org, a free, albeit computationally limited, website. Or, for greater power and security, researchers can build private 'BinderHubs' instead. The Alan Turing Institute has

machine-learning algorithms in the Amazon cloud, says the service makes it easy for collaborators to hit the ground running. "I think it can really transform the way we do research and use this cloud compute infrastructure to do the training and learning," he explains.

Then there's Code Ocean, which supports both notebooks and conventional scripts in Python, R, Julia, Matlab and C, among other languages. Several journals now use Code Ocean to review and to promote com-

putational reproducibility, including titles Francis, De Gruyter and SPIE. Bioinformatics, Nature Machine Learning Methods launched a not to use Code Ocean for peer review. Nature Protocols and BMC subsequently joined the club. Others have now been involved in linking to Erika Patrino, editorial are Research's applied science journals, and more than 20 of

one study in a paper of mutant genes (e.g. *medRxiv*, vol. 37, 64–72) a week to working. "The Allen says, "I've made an error, so I'm not too worried about the commercial context. I'm not too worried about the fact that their user platform is also Kalam, a physics researcher at the Center in analysis helps

(B. Harbo-Kain et al. *Nature* 2013). For him, Code Ocean to ensure this code can be by his team, peer reviewers' scientific community. "It's not so much that an analysis must be correct or wrong," he says. "Nothing is really fully correct in this world. However, if you're very transparent about it, you can always communicate efficiently in the face of criticism. You have nothing to hide."

Jeffrey M. Perkel is technology Nature.

nature physics

PERSPECTIVE

<https://doi.org/10.1038/s41567-018-0342-2>

OPEN

Corrected: Publisher Correction

Open is not enough

Xiaoli Chen¹, Sünje Dallmeier-Tiessen^{1*}, Robin Dasler^{1,2}, Sebastian Feger^{1,3}, Pamfilos Fokianos¹, Jose Benito Gonzalez¹, Harri Hirvonsalo^{4,5,6}, Dinos Koussidis¹, Artemis Lavasa¹, Salvatore Mele¹, Diego Rodriguez Rodriguez¹, Tibor Simkó⁷, Tim Smith¹, Ana Trisovic^{1,8,9}, Anna Trzcinska¹, Ioannis Tsanaktsidis¹, Markus Zimmermann¹, Kyle Cramer¹⁰, Lukas Heinrich¹, Gordon Watts¹, Michael Hildreth¹, Lara Lloret Igllesias¹, Kati Lassila-Perini¹¹ and Sebastian Neuber¹⁰

The solutions adopted by the high-energy physics community to foster reproducible research are examples of best practices that could be embraced more widely. This first experience suggests that reproducibility requires going beyond openness.

Open science and reproducible research have become pervasive goals across research communities, political circles and funding bodies¹. The understanding of what open and reproducible research more widely in other scientific disciplines.

Our own experience from opening up vast volumes of data is that openness cannot simply be tacked on as an afterthought at the end of the scientific endeavour. In addition, openness alone does not guarantee reproducibility or reusability, so it should not be pursued as a goal in itself. Focusing on data is also not enough: it needs to be accompanied by software, workflows and explanations, all of which need to be captured throughout the usual iterative and closed research lifecycle, ready for a timely open release with the results.

illustrate our approach, particularly through our work at CERN, and present our community's requirements and rationale. We hope that the explanation of our challenges and solutions will stimulate discussions around the practical implementation of work-

than one physics process and consider data collected under different running conditions. Although comprehensive documentation on the analysis method is maintained, the complexity of the software implementations often takes minutes but crucial details.

CERN, Geneva, Switzerland; ²Sheffield Hallam University, Sheffield, UK; ³Karlsruhe Institute of Technology, Karlsruhe, Germany; ⁴University of Cambridge, Cambridge, UK; ⁵NYU, New York, NY, USA; ⁶University of Washington, Seattle, WA, USA; ⁷University of Notre Dame, Notre Dame, IN, USA; ⁸Instituto de Física de Cantabria ICFAC, Santander, Spain; ⁹Heidelberg University, Heidelberg, Germany; ¹⁰Present address: DataCite, German National Library of Science and Technology, Hanover, Germany; ¹¹Present address: CSC, Espoo, Finland. *e-mail: sunja.dallmeier-tiessen@cern.ch; sebastian.neuber@cern.ch

Explore more than **two petabytes**
of open data from particle physics!

Start typing...

Search

search examples: [collision datasets](#), [keywords:education](#), [energy:7TeV](#)

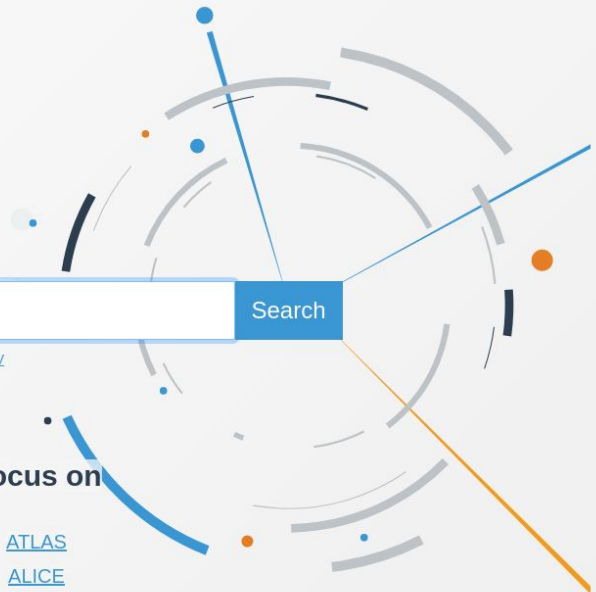
Explore

- [datasets](#)
- [software](#)
- [environments](#)
- [documentation](#)

Focus on

- [ATLAS](#)
- [ALICE](#)
- [CMS](#)
- [LHCb](#)
- [OPERA](#)
- [PHENIX](#)
- [Data Science](#)

⌵ Get started ⌵



Can we also build on this to
scale out our analysis?

Kubernetes

Spun out of Google as an open source
container orchestration project

Built on lessons from Borg and Omega

Loosely coupled collection of components to deploy, maintain and scale workloads

Declarative, Load Balancing, Self Healing, Auto Scaling

Service and Batch Workloads



Borg, Omega, and Kubernetes

BRENDAN BURNS,
BRIAN GRANT,
DAVID OPPENHEIMER,
ERIC BREWER, AND
JOHN WILKES,
GOOGLE INC.

Though widespread interest in software containers is a relatively recent phenomenon, at Google we have been managing Linux containers at scale for more than ten years and built three different container-management systems in that time. Each system was heavily

**LESSONS
LEARNED FROM
THREE CONTAINER-
MANAGEMENT
SYSTEMS OVER
A DECADE**

Kubernetes

Largest open source project after kernel

45.000 contributors, **148.000** code commits

83.000 pull requests, **1.1M** contributions

2000+ contributing companies

Google, RedHat, VMware, Huawei, Microsoft, IBM, Fujitsu, ...

Open community welcome to contributions

Special Interest Groups (SIGs) : Auto-Scaling, Multi-Cluster, Scheduling, ...

Largely used both in Research and Industry



Borg, Omega, and Kubernetes

BRENDAN BURNS,
BRIAN GRANT,
DAVID OPPENHEIMER,
ERIC BREWER, AND
JOHN WILKES,
GOOGLE INC.

Though widespread interest in software containers is a relatively recent phenomenon, at Google we have been managing Linux containers at scale for more than ten years and built three different container-management systems in that time. Each system was heavily

**LESSONS
LEARNED FROM
THREE CONTAINER-
MANAGEMENT
SYSTEMS OVER
A DECADE**

Kubernetes

Lingua franca of the cloud

Managed services offered by all major public clouds

Multiple options for on-premise or self-managed deployments

Common declarative API for basic infrastructure : compute, storage, networking

Healthy ecosystem of tools offering extended functionality



Rediscovering the Higgs

Like it's 2019...

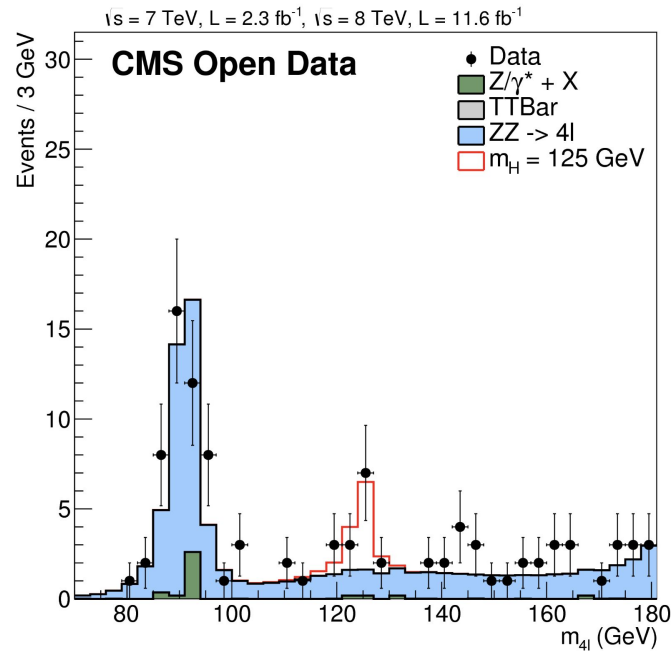
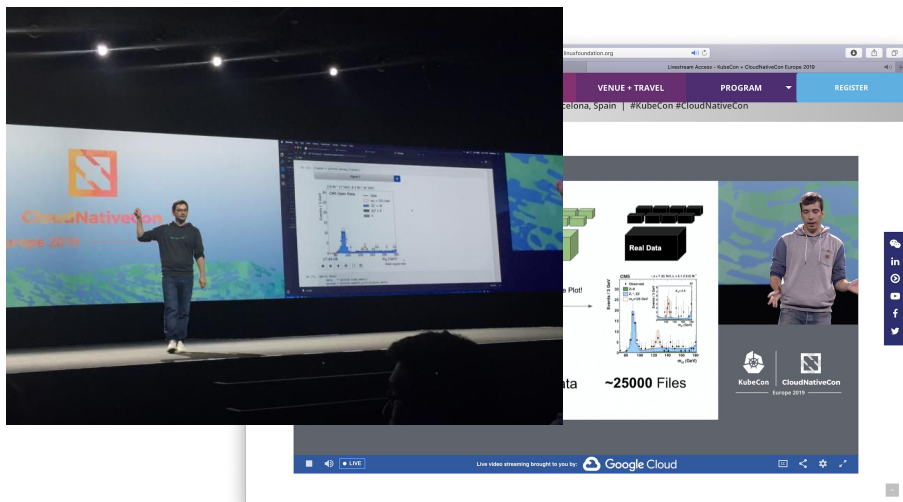
Challenge: $H \rightarrow 4l$ re-discovery on CMS Open Data

Benchmark analysis based on Open LHC Data.

Goal: Fit it within a live demo for 20-minute [Keynote at KubeCon EU 2019](#)

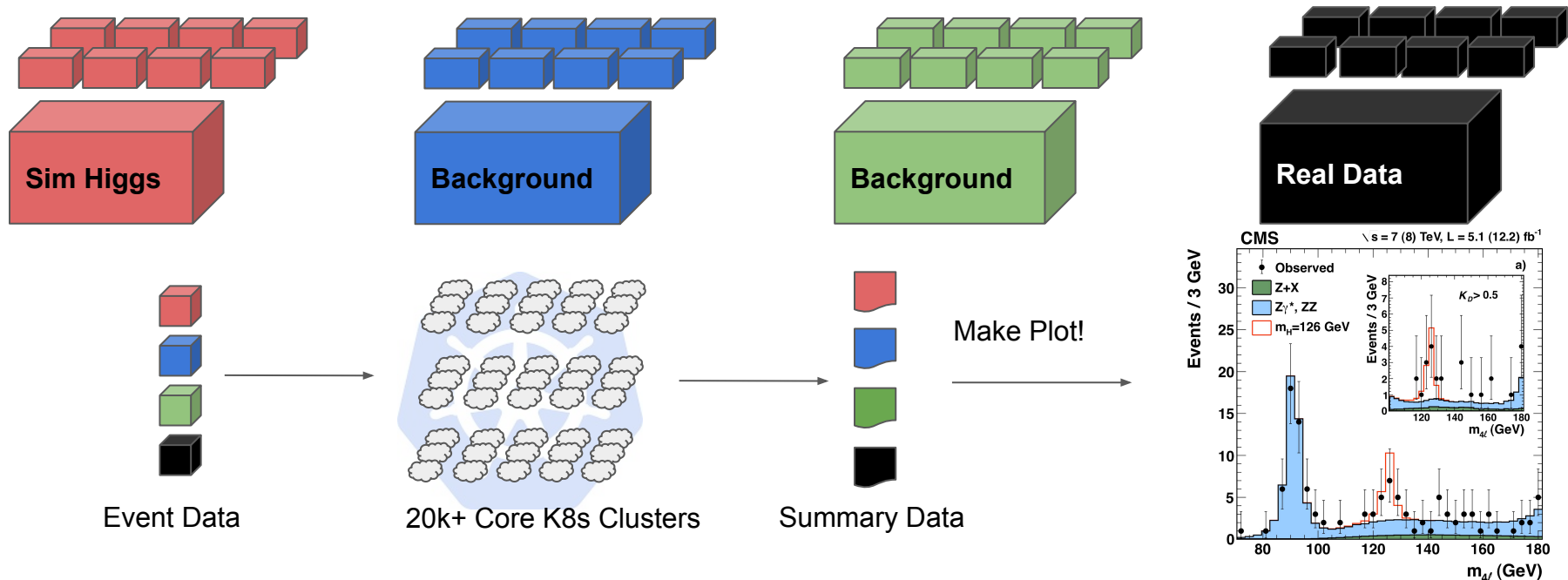
Learn something about cloud-native analysis, reproducibility, Open Data.

Have some Fun.



Challenge: $H \rightarrow 4l$ re-discovery on CMS Open Data

what would this look like in a cloud-native approach?



70 TB of Physics Data

~25000 Files

```
[16:01:21] cmsusr@e6f7bea2253e /Users/lukasheinrich/Code/awesomedemo/higgs-demo/CMSSW_5_3_32/src $ \root -b
```

```
*****  
*                                     *  
*      W E L C O M E  to  R O O T      *  
*                                     *  
*   Version   5.32/00   2 December 2011 *  
*                                     *  
* You are welcome to visit our Web site *  
*      http://root.cern.ch              *  
*                                     *  
*****
```

```
ROOT 5.32/00 (branches/v5-32-00-patches@42372, Jun 10 2014, 18:26:00 on linuxx8664gcc)
```

```
CINT/ROOT C/C++ Interpreter version 5.18.00, July 2, 2010
```



cmsopendata/cmssw_5_3_32 ☆

By [cmsopendata](#) • Updated 4 months ago

Container



70 TB Dataset



OpenStack Magnum

25000 Kubernetes Jobs



redis

Job Results



**Interactive
Visualization**

Aggregation



Google Cloud



Google Cloud
Storage



70 TB Dataset

Cluster on GKE

Job Results

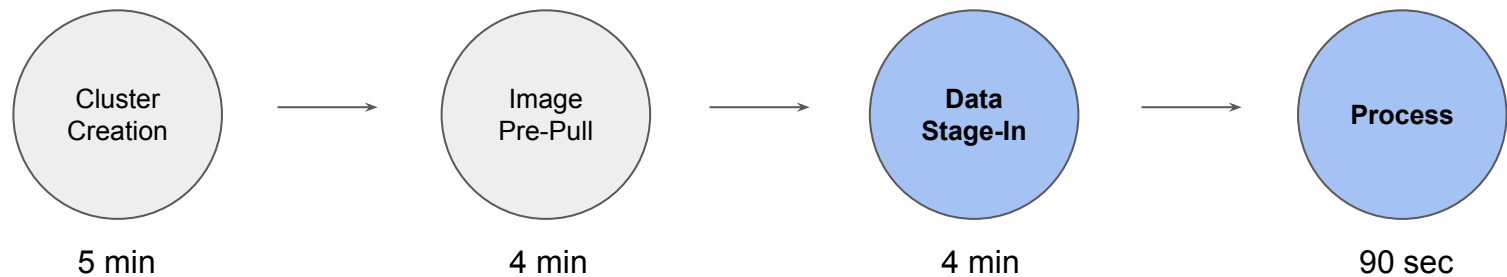
Interactive
Visualization

Max **25000 Cores**

Single Region, 3 Zones

25000 **Kubernetes Jobs**

Aggregation



vs ~24h for the original analysis

Machine Learning / Kubeflow

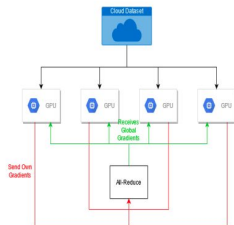
Scale out / distributed training, with CERN OpenLab

Example: Fast Simulation with 3D GANs

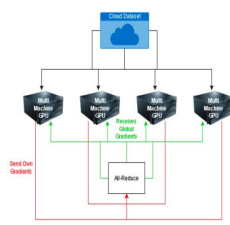
TensorFlow Based

Can benefit from (very) large numbers of GPUs, TPUs

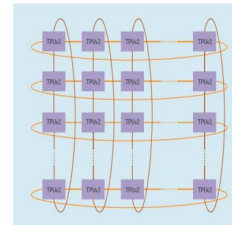
Mirrored Strategy



Multi Worker Mirrored Strategy



TPU Strategy

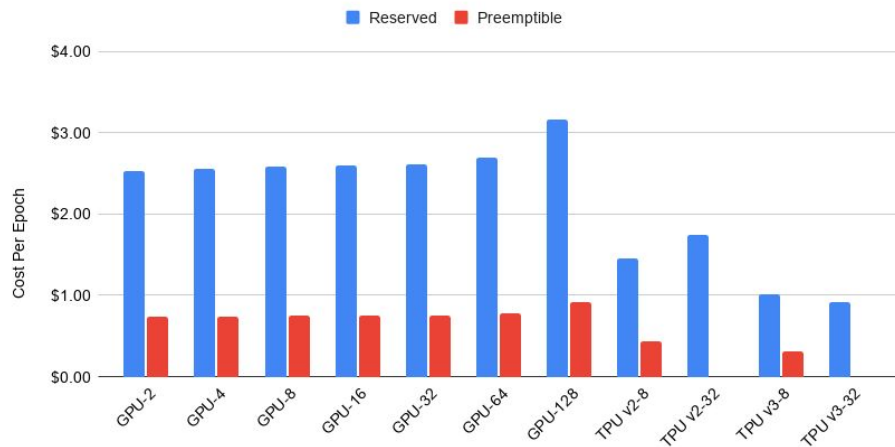
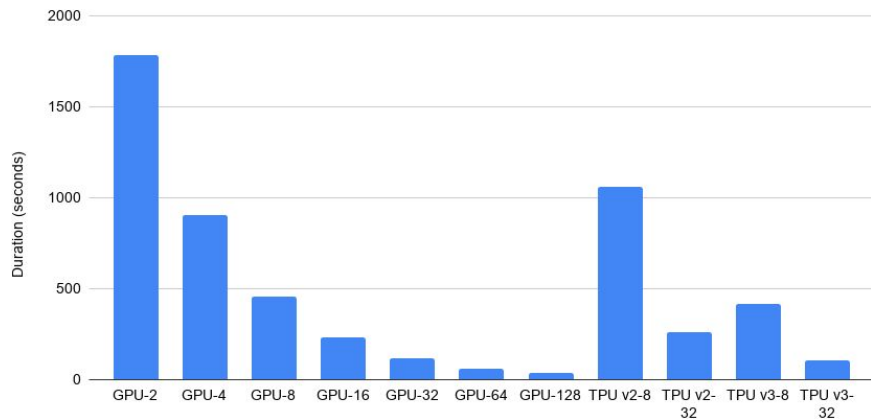


Results using the Google Cloud

From 1 to 128 GPUs: 3550 to 35 seconds per epoch

x100 speedup at the same total cost

TPUs seem to be particularly cost effective



Challenges Remaining

Data Movement

Data Gravity and Egress Costs

Avoiding lock-in to public cloud providers

Bridging with the HPC world

Questions?