

Workflow Enablement & AdVanced Environments (WEAVE)

AWS RADIUS Tutorial

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WEAVE aims to enable a focused WSC/CP effort in supporting user workflows and developing and maintaining production workflow tools

1. Dedicated support for workflow tools (orchestration, data, & analysis)
2. Single team to share user support and staff outreach, marketing efforts
3. Make workflow implementation in user-community a first-class objective
4. Centralized Workflow Tools Development Team
 - Shared knowledge base
 - Cross tool collaboration and co-design
 - Move toward common Python CI/CD infrastructure
5. Centralized project with clear organizational structure and responsibilities
 - WSC/CP takes responsibility for production workflow tools
 - Users know who to reach out to for help
 - Outside efforts know who to interface with

Our Vision: enhance user productivity and scientific quality through common infrastructure and tool integration

- Decrease human time from the posing of a problem to its answer
- Enable our users to take advantage of exascale computers like **El Capitan**
- Smooth integration and interoperation of **problem setup, simulation management, and analysis tools**
- Enable and support **code-agnostic inputs and outputs** for WSC/CP applications
- Allow users to work at a higher level than a **“Sea of Files”**
 - But let them **“see their files!”**
- Provide documentation and examples to enable **“tool builders”** in the user community to leverage a common workflow toolkit

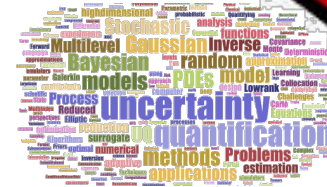
WEAVE Tools Components



Merlin



PyDV

The logo for KOSH 2.0, featuring a stylized 'K' composed of binary digits (0s and 1s) and a gear-like shape, followed by the text 'OSH 2.0' in a bold, sans-serif font.

Sina

{JSON}

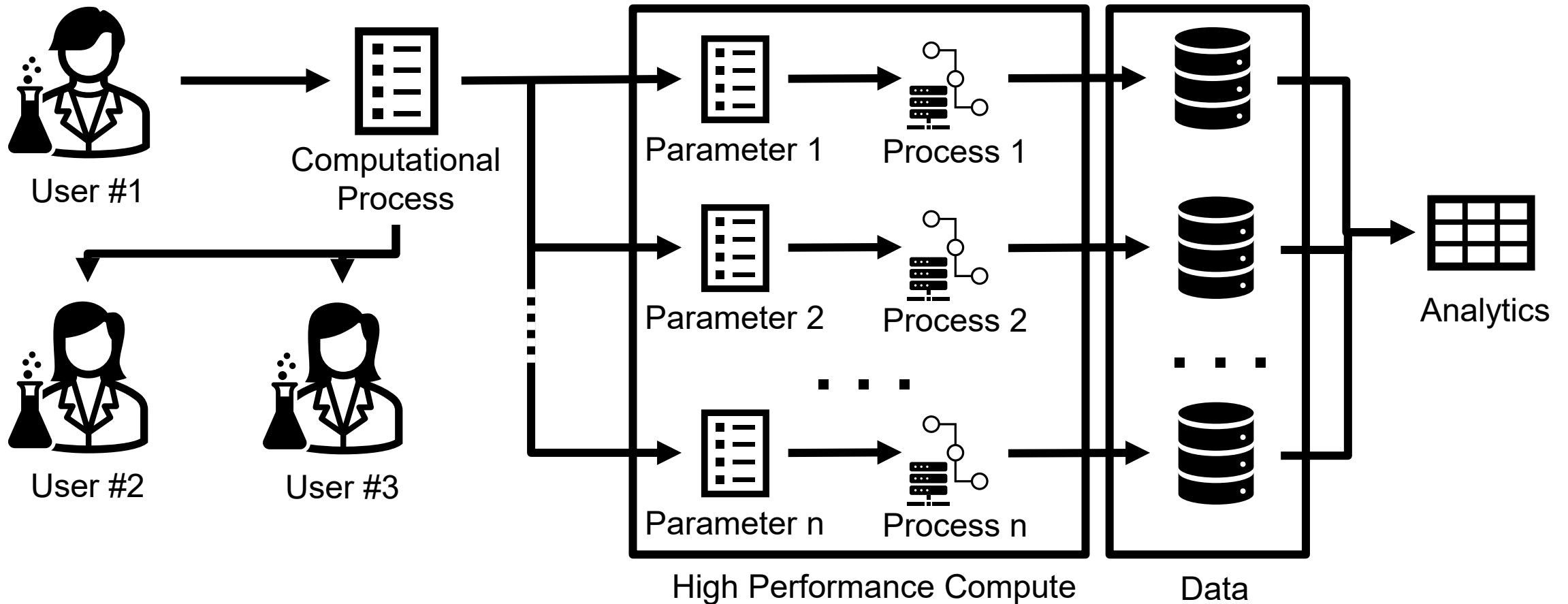


WSC's WEAVE team supports multiple tools for building complex HPC workflows

- **Maestro**
 - Provides minimal DSL for converting a task-graph of work into a human readable, machine agnostic specification
 - Manage execution on variety of HPC resources
 - Focus on shareability, repeatability, and provenance of what was run
 - Dependency lite for easier extendibility to enable an ecosystem of tools derived from it
- **Merlin**
 - Extension of Maestro to use distributed task queues for cross machine workflows
 - Tackle scaling problems with running many short jobs that overwhelm system level schedulers
- **Additional Workflow managers built on top of these tools:**
 - Encore: Developed in GS, is an extension of Maestro exploring addition of study level decision making and control flow for improved iterative/chained workflows

Orchestration: Maestro

Maestro aims to enable reproducible computational science following the model set by the experimental disciplines



Maestro's vision is to become a toolchain and ecosystem of tools adaptable to user's needs

Build up your workflow starting with the intent of the process

YAML Specification

```
description:
  name: physics_sim
  description: Run study using a parallel physics code.

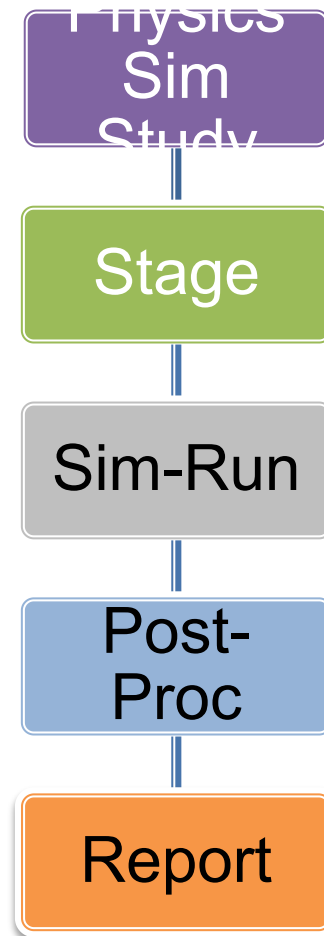
study:
  - name: stage
    description: Copy input decks and post-proc tools into study workspace.
    ...

  - name: sim-run
    description: run the simulation
    ...

  - name: post-proc-run
    description: processes the simulation outputs for a single run
    ...

  - name: report
    description: collects extracted data and performs summary analysis and reporting
    ...
```

Workflow Process



Minimal DSL enables a straightforward extension layer on top of familiar batch script based HPC workflows

- Turns your workflow description into a generic template that Maestro inflates at run time
 - Tokens: \$(TOKEN_NAME)
- Define variables and dependencies (path, git, ..) and insert in your workflow steps using tokens
- Launcher token for decoupling steps from schedulers: \$(LAUNCHER)
- Flexible definition of parameter tokens via user defined python functions for complex sampling
- Intuitive way to specify step dependencies
- Reference parent step workspaces in a portable way for sharing data between steps

```
env:
  variables:
    OUTPUT_PATH: ./phys_studies
    SIM_CODE: /path/to/physics/code/install/

  labels:
    INPUT_FILE: model.input
    INPUT_PATH: $(SPECROOT)/$(INPUT)

study:
  - name: sim-run
    description: run the simulation.
    run:
      cmd: |
        cp $(stage.workspace)/$(INPUT_FILE) .

        $(LAUNCHER) $(SIM_CODE)/sim_exe -in $(INPUT_FILE) -p 4 --res $(RES)
      procs: 4
      nodes: 1
      walltime: "00:10:00"
      depends: [stage] # Require stage step to complete before running this step

global.parameters:
  RES:
    values: [10, 20, 30]
    label: RES.%% # Expanded by Maestro to RES.10, RES.20, ...
```

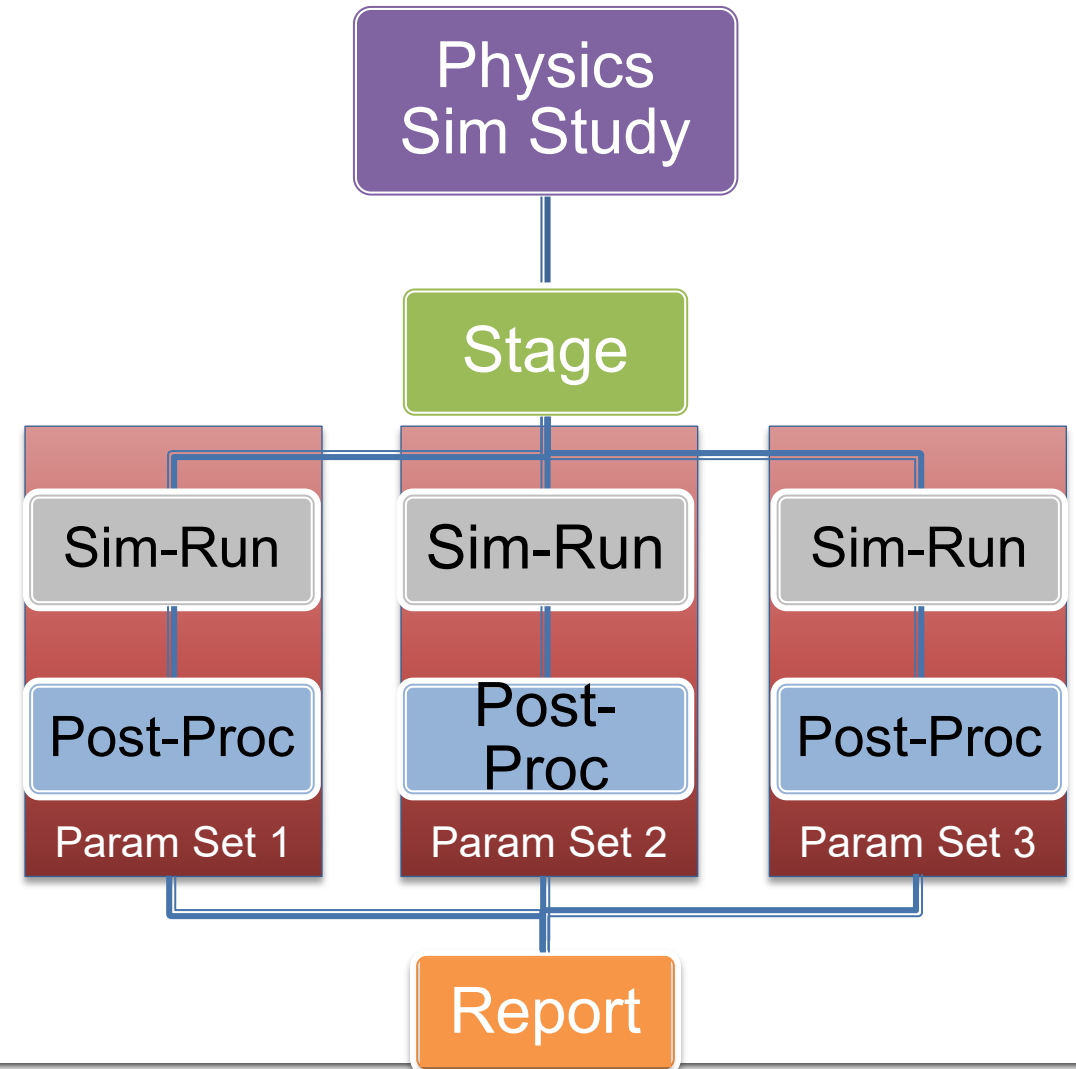

Having a complete, concrete, repeatable process, Maestro can run experiments with it by inflating the graph with parameters

YAML Specification

```
study:
  ...
  - name: sim-run
    description: run the simulation.
    run:
      cmd: |
        cp $(stage.workspace)/$(INPUT_FILE) .

        $(LAUNCHER) $(SIM_CODE)/sim_exe -in $(INPUT_FILE) -p 4 -res
$(RES)
      procs: 4
      nodes: 1
      walltime: "00:10:00"
    ...

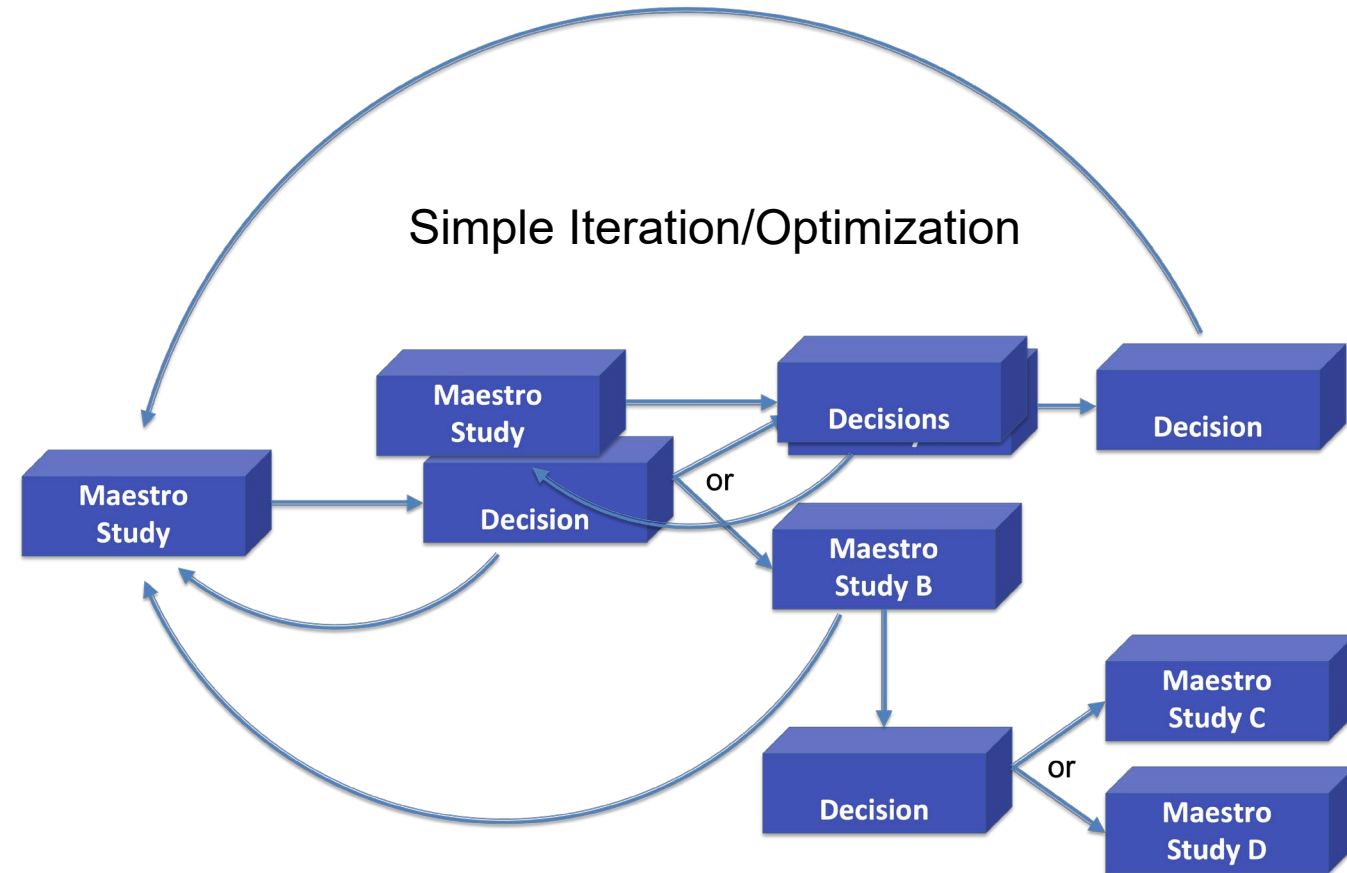
global.parameters:
  # Resolutions to run
  RES:
    values : [1, 2, 3]
    label  : RES.%%
  ...
```



Vision is to be a tool chain/ecosystem of orchestration tools for building complex workflows

- Two such examples already:
 - **Merlin**: exploring an implementation of distributed task queues and recursive type iterative workflows
 - **Encorewf**: adds outer layer with explicit decision-making steps and tracking of per-study iterations.
 - Simple single study spec based iterative and optimization type workflows
 - Chain disparate Maestro study spec's for more complex multi-phase workflows

Complex multi-phase iteration/optimization



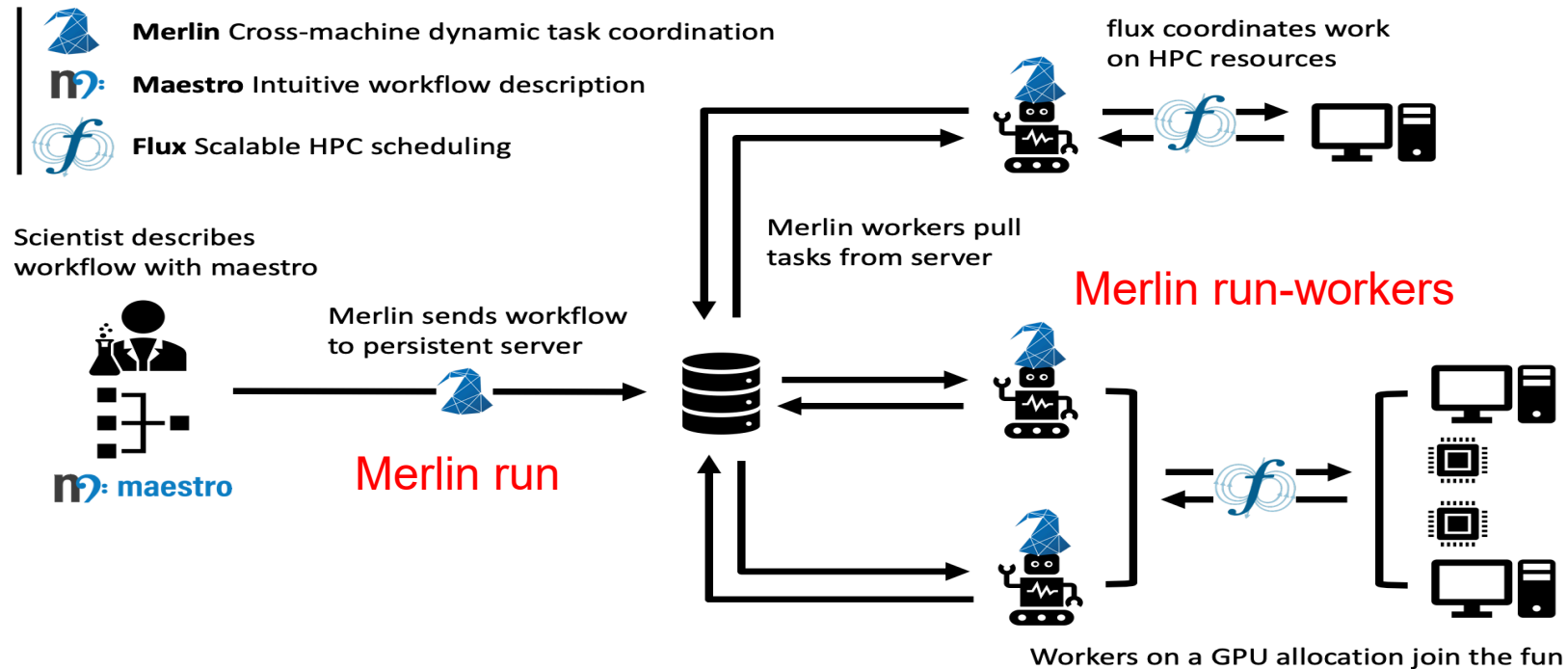
Merlin – Another workflow orchestration tool



- Merlin was created with the goal of making it easy to build, run, and process the kinds of large-scale HPC workflows needed for cognitive simulation
- Built as an extension of Maestro

Merlin runs its' workflows using a producer/consumer model

- Merlin uses the same YAML spec format as Maestro
- Central-server based system
- Two commands for the producer/consumer model
- HPC scheduling via Flux, Slurm, LSF, or PBS (untested w/ PBS so be wary)

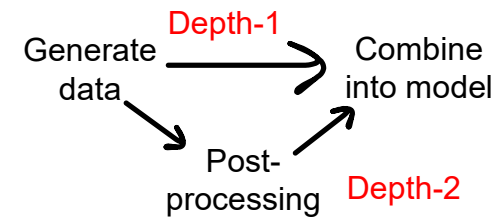


Differences From Maestro

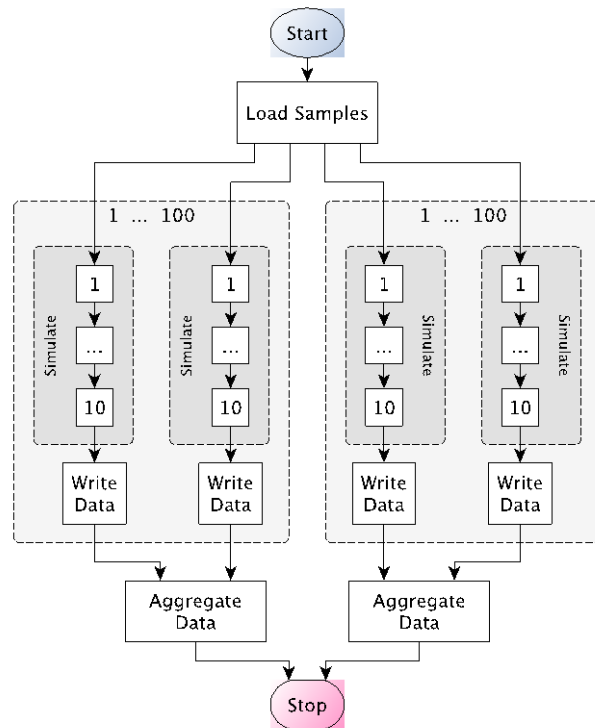
- CLI substitutions
 - e.g. variables, samples, etc.
- Merlin block in spec file
 - Samples (run for each set of parameters)
 - Work not tied to resources
 - Work can be shared across:
 - Batch jobs
 - Machines

```
merlin:
  resources:
    task_server: celery
    overlap: False
    workers:
      worker1:
        args: -l INFO --concurrency 3 --prefetch-multiplier 1 -Ofair
        steps: [step1]
        nodes: 1
        batch:
          type: slurm
          machines: [machine1, machine2]
  samples:
    generate:
      cmd: echo -en "sample\n1" > $(MERLIN_INFO)/samples.csv
    file: $(MERLIN_INFO)/samples.csv
    column_labels: [label1]
    level_max_dirs: 25
```

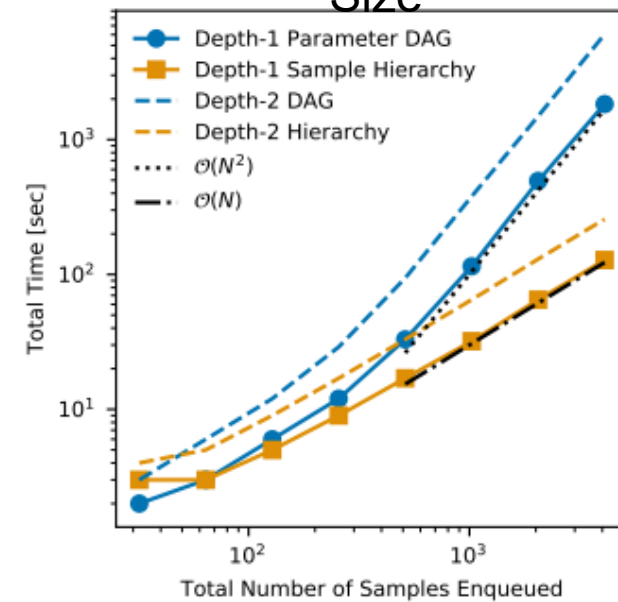

Scalability



Large-Scale Ensembles



Ideal Task Overhead – Independent of Ensemble Size



Maestro
DAG

Merlin
Hierarchy

J. L. Peterson *et al.* “Enabling Machine Learning-Ready HPC Ensembles with Merlin.” *Future Generation Computer Systems*. **131**:255-268 (2022).

J. L. Peterson, “Merlin Short Overview”, Lawrence Livermore National Laboratory, 2022.

Merlin allows for iterative workflow runs via recursive studies

- Allows for a base-case where you can do whatever is needed with the results of your iterative runs
 - E.g. running a post-processing script over all result files generated
- Once workers are started, they'll keep pulling tasks from their queues until they're stopped
 - This allows workers to keep completing work even if the work is queued from a different run of a study
 - i.e. no need to start the workers a second time

```
env:
  variables:
    ITER: 1
    MAX_ITER: 10
    PYTHON: <path to python>
    POST_PROC: <path to cumulative post processing script>
    ITER_OUTPUT: <path to iteration outputs>

study:
  <other steps>
  - name: iterate
    description: run another iteration or post process all iterations
    run:
      cmd: |
        if [ $(ITER) -ge $(MAX_ITER) ] ; then
          echo "done"
          $(PYTHON) $(POST_PROC) $(ITER_OUTPUT)/iter_*_results.json
        else
          next_iter=$(ITER)
          ((next_iter=next_iter+1))
          echo "Starting iteration " $next_iter
          cd $(SPECROOT)
          merlin run $(SPECROOT)/iterative_demo.yaml --vars ITER=$next_iter
        fi
    task_queue: iterative_queue
```

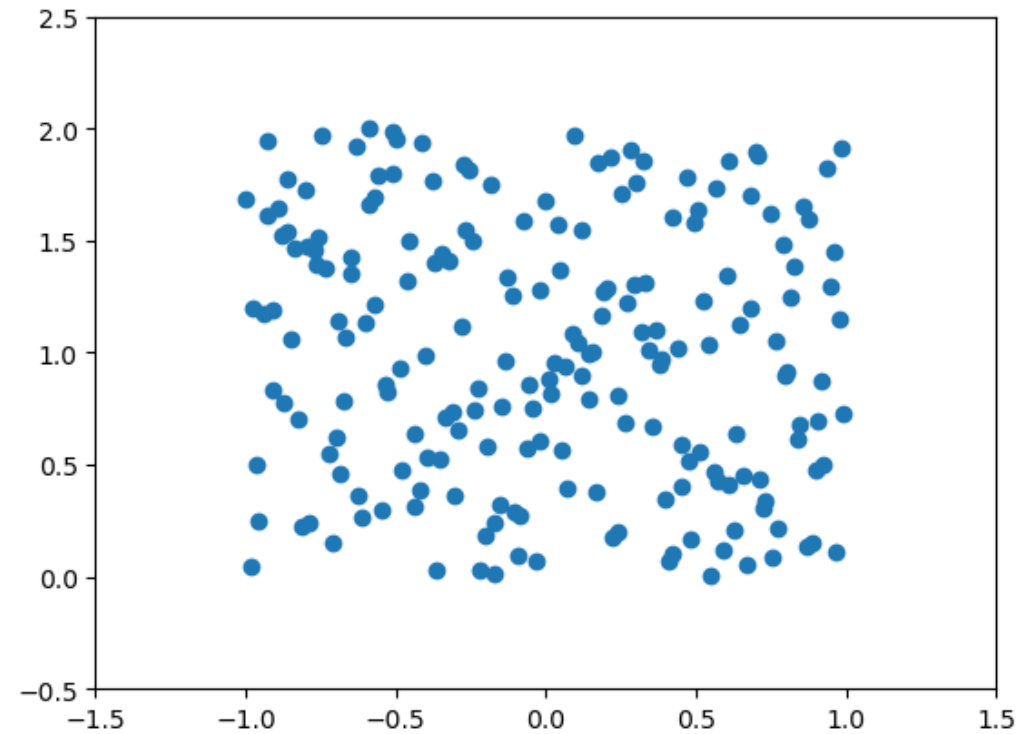


- Trata is a Bayesian sampling package designed to allow users to explore a parameter space by generating sample points
- Trata is a Spanish word from the Latin *trahō* “to extract” and is used colloquially to mean “try” or “sample”
- Trata includes the following modules:
 - `composite_samples`
 - `sampler`
 - `adaptive_sampler`



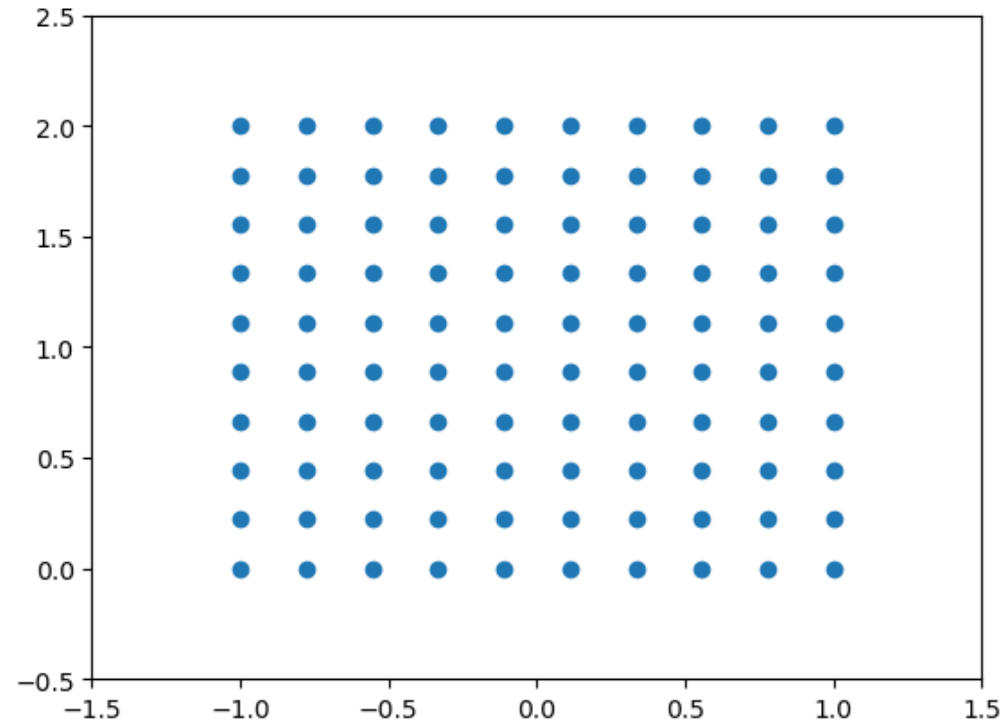


- The **sampler** module contains 16 sampling methods users can choose from to generate samples across a design parameter space
- Common methods include:
 - LatinHyperCube



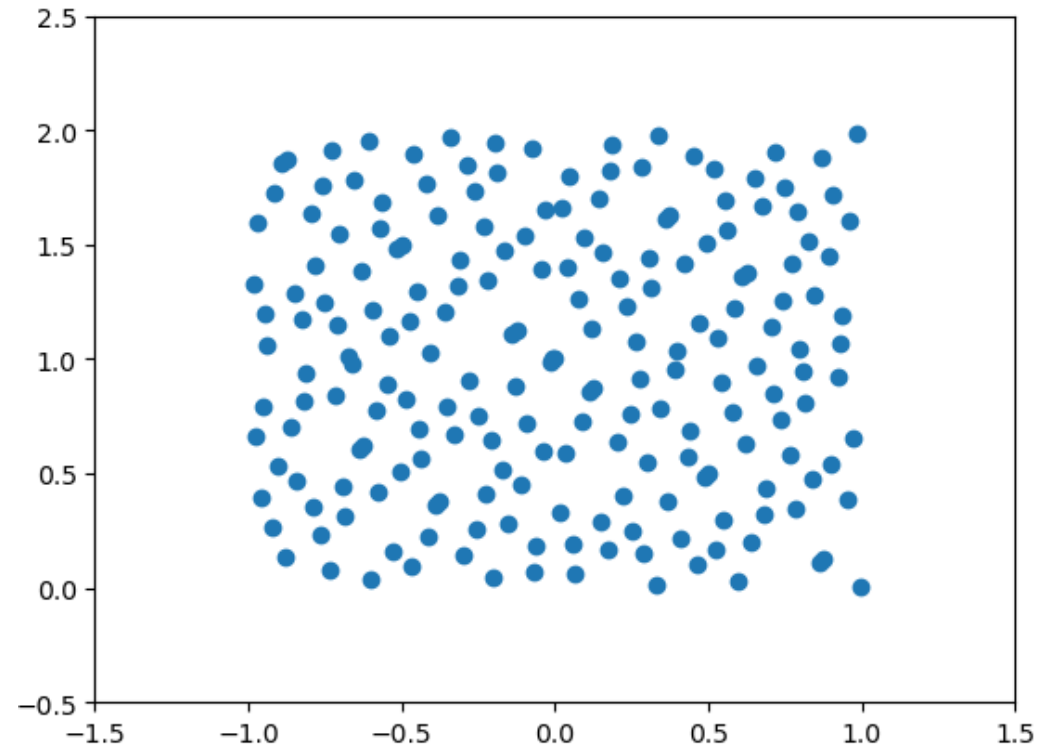


- The **sampler** module contains 16 sampling methods users can choose from to generate samples across a design parameter space
- Common methods include:
 - LatinHyperCube
 - CartesianCross





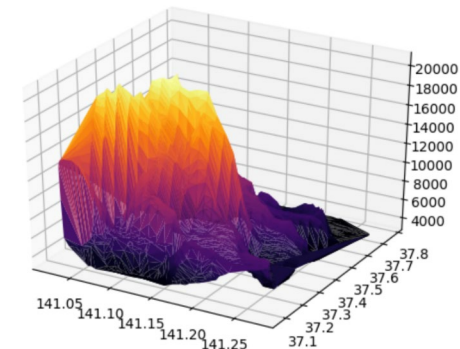
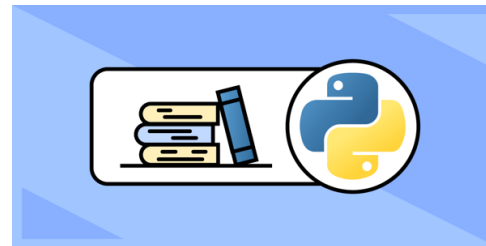
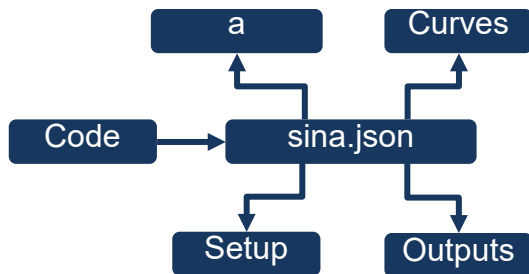
- The **sampler** module contains 16 sampling methods users can choose from to generate samples across a design parameter space
- Common methods include:
 - LatinHyperCube
 - CartesianCross
 - QuasiRandom



WEAVE's Sina Tool

Sina handles data munging

- Created to increase the availability of simulation data with minimal user effort
 - Integrates directly with codes to pull data
 - Outputs data into an easily-automated format
 - Provides tooling to render this data interactive (through Jupyter) and easily processed (through a Python API) across one run or many
- Intended especially for use with run metadata, allowing users to easily and efficiently find simulation runs that match their criteria.



Use cases and place in ecosystem

- Allow users to query and view hundreds, thousands, millions of result sets at once
- Drill down to “interesting” runs
- Targets data that **identify a run as interesting within the context of other runs**
- Does not orchestrate
- Does not replace VisIt or similar tools



Sina: Search API

- Queries are fast, terse, and flexible, ideally being intelligible without previous Sina experience

```
print("\n".join(recs.find_with_data(group_id="5cac5d")))
```

```
5cac5d_5  
5cac5d_10  
5cac5d_7  
5cac5d_3  
5cac5d_6  
5cac5d_0
```

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```
5cac5d_5  
5cac5d_10  
5cac5d_7  
5cac5d_3  
5cac5d_6  
5cac5d_0
```

- Because returned objects are pure Python (rather than db-specific), further manipulation is easy

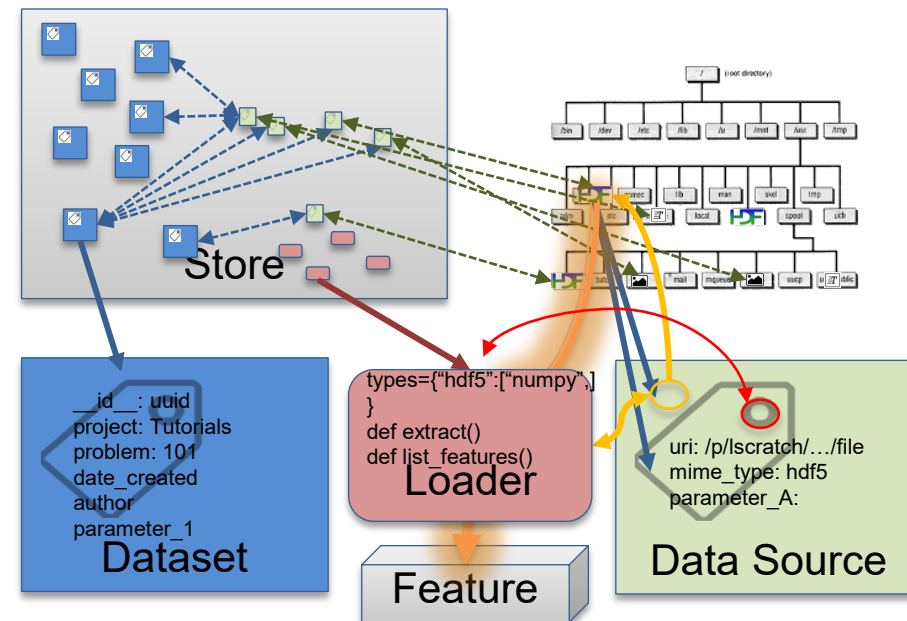
```
groups = set(x["group_id"]["value"] for x in recs.get_data(["group_id"]).values())  
print("Found the following groups: {}".format(groups))
```

```
Found the following groups: {'bdbe96', '01a014'}
```


WEAVE's Kosh Tool

Why use Kosh?

- Kosh is built on top of Sina:
 - Kosh can load a Sina store. Sina can query a Kosh store.
 - Sina is being integrated with Physics Codes.
 - Lots of Data and Metadata Accessible out of the box.
 - Multiple Database backends
 - Includes LC's Kubernetes deployed MySQL and Cassandra DB.
 - Optimized query search
- Kosh has unique features:
 - Kosh can access and process data in a consistent fashion, decoupled from data format and location via
 - "loaders"
 - "transformers"
 - "operators"



Features

- Locating and sharing data

- Once data is in the store, end user doesn't need to know where it is.
- Very easy to extend and add your own "loaders".

```
dataset.associate("/pth/to/some/file", mime_type="hdf5")
```

- Moving data

- Kosh can move data as it typically won't sit in one place.
- Can be done after the fact as well with re-associate function

```
kosh mv -store mystore.sql -sources file1.hdf5 movies/*.mp4 dir1 -destination some_dest_dir
```

- Metadata validation

- Kosh schemas help enforce consistency in your store

```
required = {"valid": [True, False]}  
optional = {"training": [1, "yes", 0, "y", "n", "no", True, False]}  
schema = kosh.KoshSchema(required, optional)  
dataset.valid = 1  
schema.validate(dataset) # -> Error  
dataset.valid = True  
dataset.schema = schema # -> goes into store and will be enforced  
dataset.valid = 1 # -> Error
```

Features (cont.)

- Data manipulation

- “Transformers”: allow data to be further post-processed after extraction from it's original URI and they can be chained

Post-process single feature (crop, etc...)

```
shuffle = kosh.transformers.npy.Shuffle()
data = ds.get_execution_graph("feature", transformers=[shuffle,])
```

- “Operators”: allow data to be further post-processed coming from different features either from the same source or not.

Combine multiple features from one or many datasets, will find loader for each features so that the data comes in compatible.

```
class ADD(kosh.KoshOperators):
    types = {"numpy":["numpy",]} # mime types supported
    def operate(*inputs, **kargs):
        [some code to add inputs]
        return new_result
twice = ADD(data, data)[:]
```



IBIS

- IBIS (**I**nteractive **B**ayesian **I**nference and **S**ensitivity) is designed to allow users to generate statistical models after physics simulations have run to completion
- These models can be used to predict the results of future simulation runs, and to perform sensitivity and uncertainty quantification analyses
- *Ibis* comes from the Egyptian word for the long-legged wading bird associated with the ancient Egyptian deity Thoth, god of science and magic



IBIS

- Markov chain Monte Carlo (MCMC) methods are commonly used in uncertainty quantification to assign probability distributions to uncertain design parameters
- Polynomial chaos expansion (PCE) models are an alternative to MCMC and provide the statistical characteristics of results with greatly reduced computational cost
- IBIS includes the following modules:
 - `filter`
 - `likelihoods`
 - `mcmc`
 - `mcmc_diagnostics`
 - `pce_model`
 - `sensitivity`
 - `plots`



IBIS and Trata

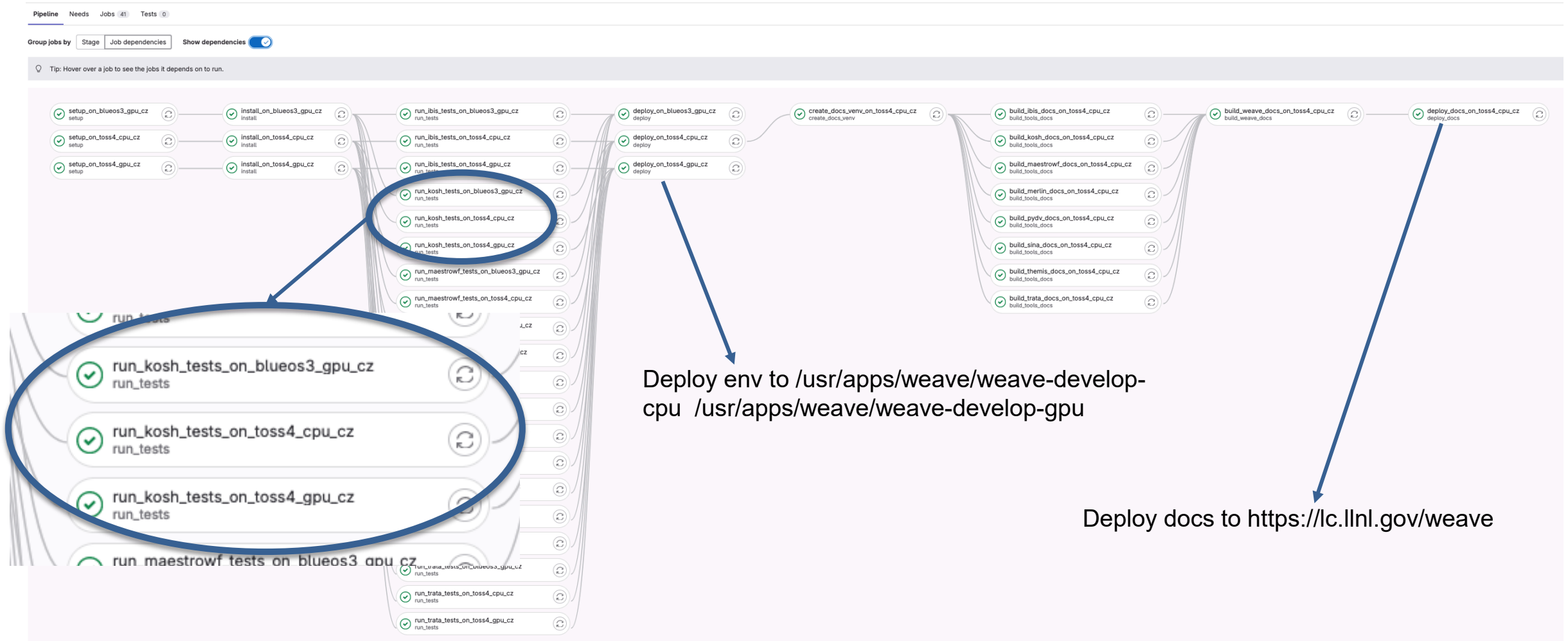


- Trata and IBIS are often used jointly as sampling is largely a pre-req to any UQ analysis
- The following example shows how sensitivity analysis can be used on a polynomial function that only acts on the first 10 variables
- Mutual information rankings order the measured amount of information obtained about one random variable by observing another
 - Recall a high mutual information indicates a large reduction in uncertainty; low mutual information indicates a small reduction; and zero mutual information between two random variables means the variables are independent

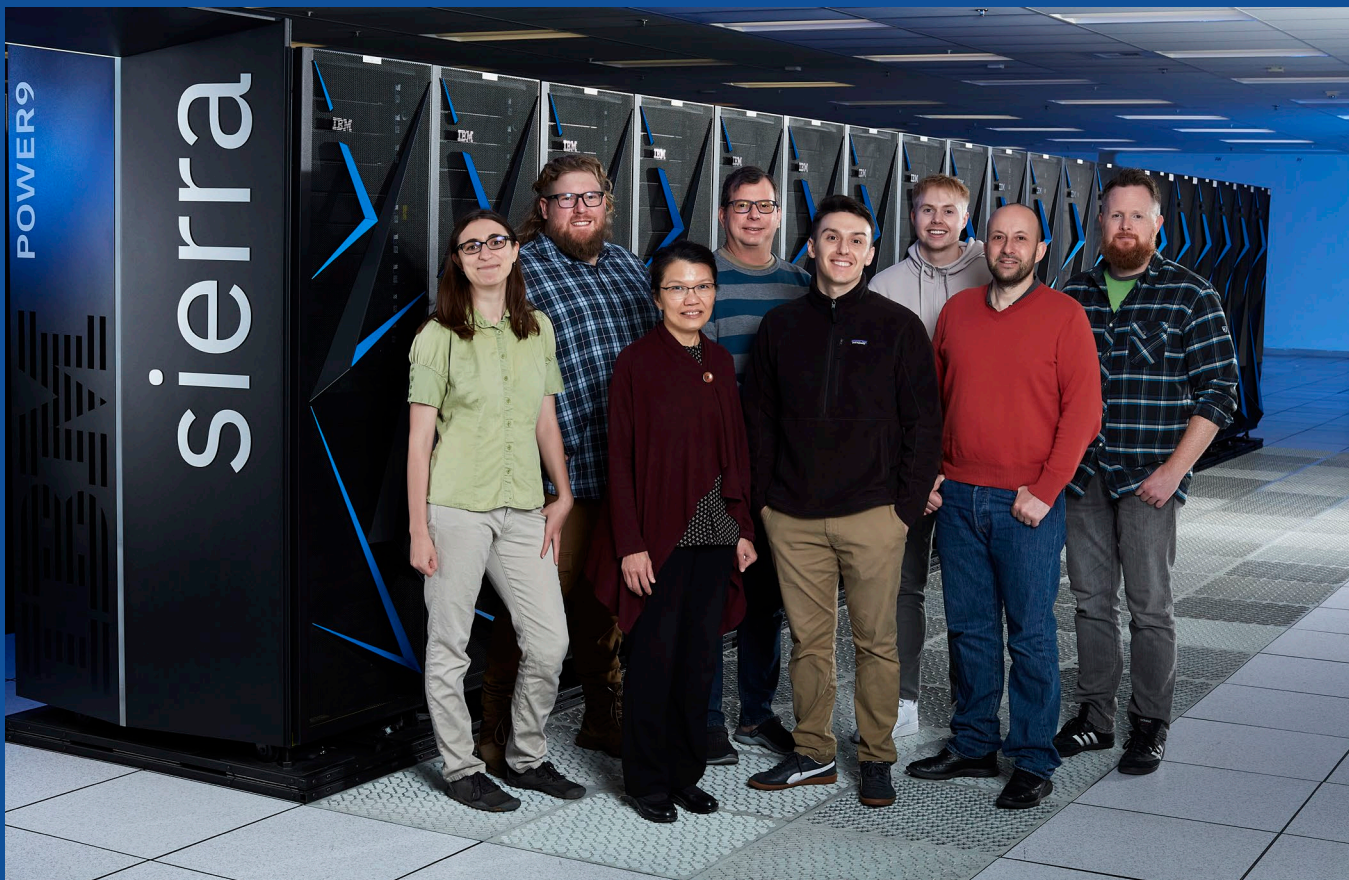
Where can I get these tools? And can I trust they work?

- Everything is under LLNL's Github umbrellla at:
- <http://github.com/LLNL/maestrowf>
- <http://github.com/LLNL/merlin>
- <http://github.com/LLNL/sina>
- <http://github.com/LLNL/kosh>
- <http://github.com/LLNL/trata>
- <http://github.com/LLNL/ibis>

WEAVE CI – automates documentation build and deployment



All tools are systematically tested together in various environments



Thank You!

**We look forward to
helping you now and
in the future.**

**Let's move on to the
tutorial. Led by Jorge
Moreno.**

Toy Tutorial Getting Started Steps

These are your login credentials (you should have received an email)

Instance IP: {ip_address}

SSH Username: radius{number}

SSH Password: {password}

You can connect to this instance by running this command:

```
ssh {username}@{ip_address}
```

then, enter the password when prompted.

Toy Tutorial Getting Started Steps

- micromamba activate
- micromamba activate /usr/apps/weave/weave-develop/
- cd weave-demos/CZ/ball_bounce/
- google-chrome &
- jupyter-lab &
 - Copy paste url from Jupyter-Lab into Google Chrome
- Follow README.md "WEAVE Workflow Example: How to run" section but skip Step 2 activate environment.
- Notebooks change: `%matplotlib notebook` to `%matplotlib inline`