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Flux:

A Fully Hierarchical Workload Manager for Supercomputing Workflows

1. PRODUCT/SERVICES CATEGORIES

A. Title

Flux: A Fully Hierarchical Workload Manager for Supercomputing Workflows

B. Product category

Software/Services | Special Recognition: Battling COVID-19

2. R&D 100 PRODUCT/SERVICE DETAILS

A. Primary submitting organization

Lawrence Livermore National Laboratory

B. Co-developing organization

University of Tennessee, Knoxville

C. Product brand name

Flux: Next-Generation Workload Management Software Framework



D. Product introduction

This product was introduced to the market between January 1, 2020, and March 31, 2021. This product is not subject to regulatory approval.

E. Price in U.S. Dollars

Free. Flux is open source and free to users.

F. Short description

Flux is a next-generation workload management software framework for high-performance computing (HPC). It combines fully hierarchical resource management with graph-based scheduling to improve the performance, portability, flexibility, and manageability of scheduling and execution of complex scientific workflows on HPC systems both at the system and user level.

G. Type of institution represented

Government or Independent Lab/Institute University/Academic

H. Submitter's relationship to product

Product developer

I. Photos



Flux product information, documentation, and other details are available at <u>flux-framework.org</u>.

J. Video

youtu.be/Ylwt51dyXOE





3. PRODUCT/SERVICE DESCRIPTION

A. What does the product or technology do?

Flux [1] is a next-generation workload management framework for supercomputers, high-performance computing (HPC) clusters, servers in the cloud and laptops.

Flux manages massive numbers of processors, memory and other resources of a computing system and assigns the work requested by users—also known as jobs or workloads—to one or more available resources that complete the work, a method known as scheduling. A job is typically expressed in a script that contains a formal specification that requests resources, identifies applications (e.g., multiphysics simulation software to run simultaneously across resources) along with their input data and environment, and describes how to deliver the output data. Modern science computing campaigns of sufficient complexity require many such jobs that contain numerous interconnected computational and other tasks [2]. The composition of numerous interdependent tasks that are spread across many jobs as well as within each job is often referred to as a scientific or computing workflow, distinguishing itself from a single job or workload.

Workload management software like Flux is critical for HPC users because it enables efficient execution of user-level applications while simultaneously providing the HPC facility with tools to maximize overall resource utilization [4]. HPC centers typically provide a wide range of computing systems on which scientific applications perform computations. The workload manager is responsible for efficiently delivering compute cycles of these systems to multiple users while considering their diverse resource types—e.g., compute racks and nodes, central and graphics processing units (CPUs and GPUs), multi-tiered disk storage [5]. Figure 1 depicts how Flux enables extreme-scale science.

However, two broad technical trends are making even the best-in-class products significantly ineffective. The first trend is the evolution of workloads for HPC. With the convergence of conventional HPC with new simulation, data analysis, machine learning (ML), and artificial intelligence (AI) approaches, researchers are ushering in new scientific discoveries, addressing our society's most pressing challenges. But this evolution also produces computing workflows—often comprising many distinct tasks interacting with one another [6–9]—that are far more complex than traditional products can sufficiently manage. Second, hardware vendors have steadily introduced new resource types and constraints into HPC systems. Multi-tiered disk storage, CPUs and GPUs, power efficiency advancements, and other hardware

components have gained traction in an era in which no single configuration reigns. Many HPC architectures push the frontiers of compute power with hybrid (or heterogeneous) combinations of processors [10], as in LLNL's Sierra supercomputer [11] and other pre-exascale systems [12].¹ The workload management software must manage and consider *extremely heterogeneous* computing resources and their relationships for scheduling in order to realize a system's full potential.

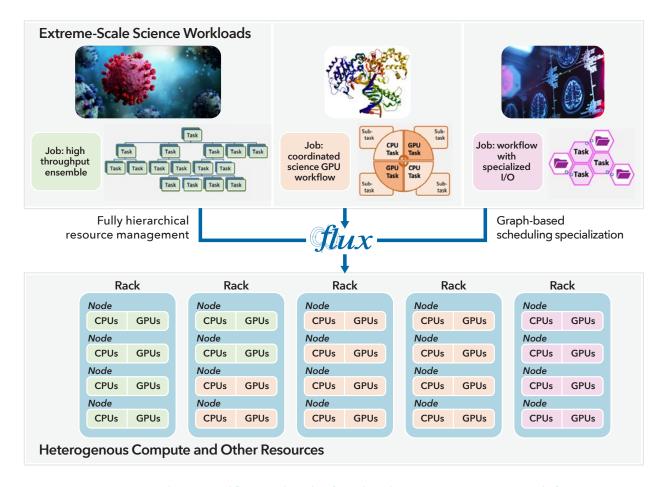


Figure 1: A complex HPC workflow—such as that for a drug discovery project—is composed of numerous interconnected tasks that are allocated and assigned to diverse sets of resources (e.g., racks, nodes, CPUs, GPUs, disk storage). Complex workflows can have varying resource requirements, interdependences, and interaction patterns. With a growing trend toward higher complexity in modern workflows, HPC workload managers must effectively enable the scheduling and execution of their tasks and direct them to run on specific areas of the computing hardware. Flux provides a flexible and customizable framework for workflows, both for HPC and the cloud [3]. With its unique features, such as fully hierarchical resource management and graph-based scheduling, Flux enables extreme-scale science.

^{1.} Exascale computers will be capable of at least a quintillion (10¹⁸) calculations persecond.





Flux solves the key technical problems that emerge from these trends. It combines *fully hierarchical resource management* with *graph-based scheduling* to improve the performance, portability, flexibility, and manageability of the scheduling and execution of both standard and complex scientific workflows on a wide range of HPC systems.

Fully Hierarchical Resource Management

Flux's fully hierarchical approach to resource management solves three primary deficiencies of existing workload manager products [13–16] in enabling emerging HPC workflows.

First, every product provides its own interface to workflows, each of which is incompatible with the interface provided by the others. Every user of a workflow must support every popular product, resulting in a multiplicative development effort. Instead, Flux is capable of managing resources from almost anywhere, including on bare metal resources, virtual machines in the cloud, HPC resources allocated by another workload manager product, or even on a single laptop. In practice, this means a workflow can create its own Flux instance to manage and to schedule allocated resources as if they were its personal supercomputer. Workflows can avoid having to support all of the various products and instead be programmed directly in Flux, leveraging Flux's flexibility to provide portability across multiple systems.

Second, most products only provide minimal support for a workflow when it needs to divide its allocated resources among smaller tasks—a common requirement of today's computing workflows. Specifically, these products allow a user to execute multiple jobs within a workflow, but if those jobs contain many tasks, these solutions make the user pay the cost of scheduling and executing those tasks. The limited support for arbitrary sub-division of work within a job adds much higher complexity to users' workflow software, slows its rate of development, and significantly limits its robustness and execution performance.

By contrast, Flux can recursively create nested instances of itself, which in turn aid in managing and scheduling a subset of the parent instance's resources. This means that large, complex workflows can easily and automatically sub-divide their jobs into arbitrarily small tasks and still rely on the workload manager to schedule their work efficiently and scalably. This capability greatly simplifies workflows, reducing their code maintenance burden while also improving their performance.

Third, traditional solutions assume that tasks within a workflow are independent and require little to no coordination or communication, creating an artificial barrier between different tasks. Modern HPC workflows are increasingly coupling





simulations with *in situ* analyses or machine-learning and AI models, where the results of a simulation are analyzed in real time in a separate task. In order for a task to coordinate with another task within the same workflow (e.g., *in situ* analyses) it must often resort to solutions with many side effects [6] to overcome this barrier.

With the innovation of Flux, jobs or tasks can connect to one another through messaging overlays and datastores built directly into Flux—a feature that significantly facilitates communication between jobs, breaking down the coordination barrier. In addition, Flux lets users configure and monitor all jobs and instances related to their workflow through the command-line and programming interfaces.

Figure 2 visually contrasts the complexity of the conventional and new or emerging HPC paradigms in terms of how they utilize the resources allocated by the system's workload manager. Nearly all existing products were designed when the workflows were much simpler as shown in Figure 2a. Yet, these solutions have significant difficulties with the emerging paradigm exemplified by Figure 2b, as well as with connecting and coordinating jobs. These problems have led users to develop their own *ad hoc* custom scheduling and resource management software or use tools that perform only workflow management or only scheduling. However, accomplishing sufficient job coordination *without* first-class support from a workload manager like Flux has already proven to be difficult for either approach. Perhaps more importantly, developing and maintaining *ad hoc* management software—especially

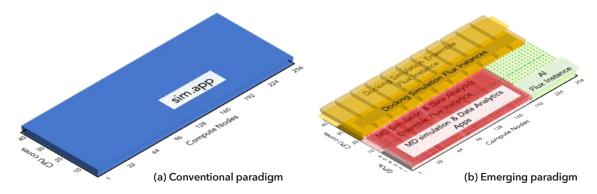


Figure 2: An illustration of how the computing resources allocated to a job—as granted by the HPC workload manager—differs between conventional and emerging scientific workflows. The notional x-axes depict the compute node IDs allocated to the job and y-axes depict the IDs of computing resources in each of these nodes. (a) The conventional paradigm requires only a single parallel simulation application to run. (b) The emerging paradigm often requires many different types of tasks such as an ensemble of molecular dynamics (MD) parallel simulation applications and another ensemble of docking simulation applications along with in situ data analysis for the MD ensemble while these tasks are driven by an Al.



in this era of ever-evolving HPC hardware architectures—has quickly become prohibitively expensive for supercomputing application teams.

Illustrative Batch Script Examples

In a job script used by a simpler workflow, the user enters line 1 in Figure 3a to submit a job script (line 2) to the system-level workload manager, requesting 256 compute nodes with 42 CPU cores each. This job script uses the allocated resources under the conventional workflow paradigm (see Figure 2a), where the application (i.e., sim.app) is executed across 256 compute nodes simultaneously, which then work together to perform a computationally challenging problem such as a physics simulation. More specifically, 42 copies of the sim.app software will be launched and run on each of the 256 compute nodes, with one copy per CPU core.²

Figure 3b shows a job script with multiple tasks submitted on a heterogeneous HPC system. Notice this script still remains simple with Flux, requiring only a few more lines within the script. Similar to the previous example, at line 1, the user submits a job script (through lines 2-5) with a request of 256 compute nodes each with 42 CPU cores—now also with 6 GPU resources (-g6). When this request is granted, Flux automatically creates a child instance that manages the requested resources. This job script then uses this instance as, in effect, a dedicated supercomputer and submits a series of sub-batch scripts to it. At line 2, the command run.dock.sh is again submitted, requesting a subset of the resources: 254 compute nodes with 24 CPU cores each, and no GPU resources. When this script is assigned to this subset, it will again spin up an even smaller Flux instance and run many smaller docking simulation applications under it. Similarly, at line 3, another sub-job script is submitted to this instance with a request of 192 nodes each with 18 CPU-core and all of the GPU resources—this time to execute a combined set of molecular dynamics (MD) simulations along with data analytics applications. Line 4 initiates the third sub-job script that runs AI applications to accelerate certain part of this computation with a request of 64 nodes, again each with 18 CPU-core and all of the requested GPU resources. At line 5, flux queue drain directs the top-level batch script to wait until all three sub-jobs will complete. To accomplish this under other more traditional products, each different workflow team either develops its own ad hoc software or relies on a separate workflow management software. The efficiency, robustness, and scalability of these software solutions vary wildly; the user of each workflow would need to find and read the documentation, learn about new interfaces, then install and deploy them. These examples can become even more complex. What if

^{2. -}n specifies the number of copies to be launched. 10,752 is equal to 42 times 256 and therefore requests one process per CPU core in the allocation.

the first job needed to connect to, and remotely submit tasks to, the second job? However, with Flux, such communication and coordination between distinct batch jobs can be easily accomplished using the same interfaces—in fact, the user needs only make a single line change to the first script in order to submit a new task such as an AI re-training task remotely into the Flux instance managing the second job: e.g., inserting FLUX_URI=\$(JobID_3b_AI.sh) flux mini batch retrain.sh into a line between 2 and 3 of Figure 3a.³ Based on this request, the first job uses the connector built into the Flux instance of the second job, then channels the same Flux commands to batch additional tasks or retrieve the status of the simulation run.

```
1 flux mini batch -N256 -n256 -c42 --wrap <<SCRIPT
2  flux mini run -N256 -n10752 sim.app
3 SCRIPT

1 flux mini batch -N256 -n256 -c42 -g6 --wrap <<SCRIPT
2  flux mini batch -N252 -c24 run.dock.sh
3  flux mini batch -N192 -c18 -g6 run.MD.sh
4  flux mini batch -N64 -c12 -g6 run.AI.sh
5  flux queue drain
6 SCRIPT</pre>
(a) Conventional batch job script

(b) Emerging batch job script
```

Figure 3: Compared to a conventional request (a), a job request for an emerging HPC workflow (b) that divides up heterogeneous resources—10,752 CPU cores and 1,536 GPUs—into multiple tasks still remains quite simple under Flux as each task is recursively managed by a child Flux instance and a sub-job script.

Graph-Based Scheduling in Each Flux Instance

Workflow complexity quickly multiplies as distinct tasks of today's scientific workflows often have vastly different requirements in resource types (e.g., CPU or GPU), duration of resource usage, and the relationships among resources. Furthermore, to satisfy new resource demands made by ambitious scientific studies and interdisciplinary research, HPC systems continue to increase in size and integrate numerous types of processing elements situated locally and in the cloud. As systems become larger and more diverse, they also become dynamic: Hardware and software components can vary as they are disused, fail, or change price. Managing complex combinations of resources that change over time requires elevating resource *relationships* to an equal footing with resources themselves.

^{3.} JobID_3b_AI.sh is a simple custom script that returns the job ID of the Flux instance running docking simulation applications within the second job.





Current-generation workload management products are designed to manage static, homogeneous HPC systems of the past, and their representation of resources reflects this rigid thinking. Data management and storage structures designed for efficiently representing compute-node-centric hardware resources do not encode complex and changing relationships (e.g., power capping, network flows, location), which makes them incapable of representing important components of newer heterogeneous, dynamic systems. Flux overcomes the limitations of current products by basing its resource representation (a model for characterizing resources) on a directed graph—a powerful and expressive structure capable of dynamically defining arbitrary resource types [17].

A directed graph is an abstract mathematical structure that associates objects (vertices) via directed relationships (edges). For example, a social media network is a directed graph; users are vertices, and communications between two users are edges where direction can be defined by the user who first contacts the other. In the case of Flux, a vertex can be a hardware resource (e.g., a CPU or compute node), and an edge can indicate containment (i.e., a server contains a CPU). Figure 4 is a visual representation of resource vertices and edges in a system with multi-tiered disk storage that can be allocated as a global pool or with respect to the distance (measured in number of edges) from other resources (e.g., a core). Matching a resource request consists of descending into the graph and checking vertices for suitability. Specifying different vertex and edge structure allows for tremendous request flexibility: Selecting solid-state drives in Figure 4 via a path through a rack (e.g., purple vertex rack0 to green vertex mtl1 0) versus through mtl2 0 (orange vertex near the graph center) permits priority based on proximity which is extremely difficult for current-generation schedulers to replicate. The ability to allocate resources in different ways based on paths is a unique capability of Flux, and one that is necessary for the upcoming El Capitan exascale system at LLNL.

Using a directed graph as a foundation for resource representation provides Flux with several key capabilities. The abstract model facilitates tremendous flexibility: Any type of resources (e.g., hardware, software, power distribution units) can be a vertex, and relationships between vertices are well-defined. Hierarchical scheduling assumes an elegant form when based on a directed graph model. Each Flux instance manages and schedules a *subgraph* (subset of the vertices and edges) of the resource graph, where a child instance's purview is a subgraph of its parent. Furthermore, a tremendous number of algorithmic techniques and optimized software libraries exist for performing fast operations on directed graphs. By basing its resource model on a directed graph, Flux integrates the fruits of algorithmic development to perform many required operations: e.g., quickly checking resource states, scheduling allocations, adding/removing resources, and transforming representations.





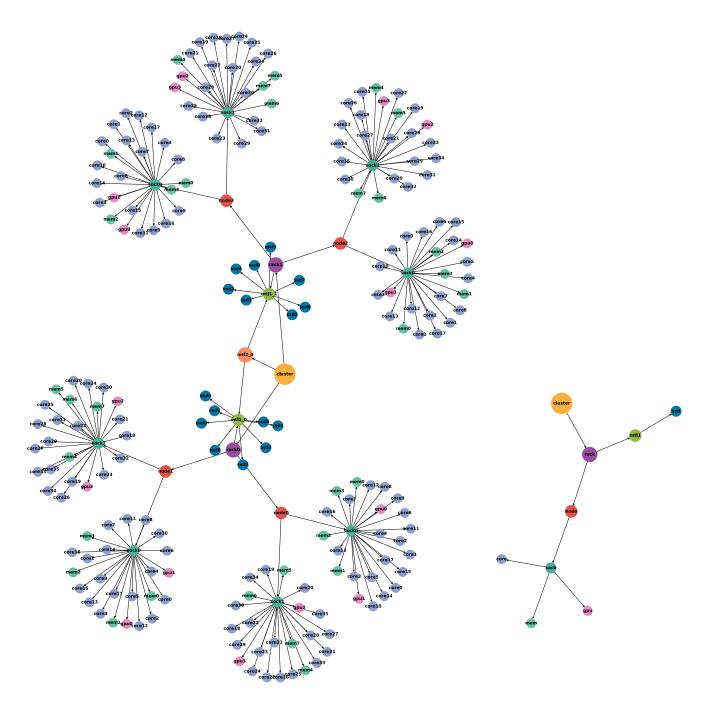


Figure 4: A directed graph of the multi-tiered storage test system's vertices and edges shows relationships between different resources such as disk storage nodes and GPU processors. Flux uses this mathematical model to coordinate job allocation among resources, ultimately ensuring an HPC workflow executes in the most resource-efficient way. The smaller graph on the right is an example of a resource request that is matched in the resource graph.





Scheduling operations are basic procedures in the context of directed graphs. To request a resource allocation, users specify their needs in a common markup language. Flux transforms the request into a directed graph, which it uses as a template to find matching resources in the system resource model. Finding resources amounts to checking resource vertices for availability, which Flux performs with its highly optimized implementation of *depth-first graph search*. Depth-first search is a ubiquitous technique for traversing each graph edge to the end (i.e., depth) before searching other edges.

The future of computing requires flexibility and dynamism, and the ability to change the graph model in any way at any time is one of Flux's primary features. Adding or removing resources is a straightforward matter of graph editing through well-known techniques for inserting or deleting subgraphs. Unlike existing products, Flux permits dynamic transformation of its resource model without manual reconfiguration and restart of the scheduler, which enables automated changes in resource relationships and addition or removal of resources. Mutability at-will is essential for supporting dynamic systems, as the traditional approach of accounting for every possible type of resource in each conceivable configuration is intractable. Complete flexibility of expression coupled with true dynamism and efficient resource allocation allows Flux to integrate and manage any resource representable by a directed graph at any time.

Flux Enables Extreme-Scale Science and Engineering

Spurred by the growing convergence of conventional HPC and new simulation, data analysis, and ML/AI techniques, the computational science community has been embracing much more diverse workflow solutions than ever before. These trends are already pushing the limits of the existing workload management products. Flux has been able to provide innovative solutions. Furthermore, our development team brought a co-design strategy to early scientific use cases, resulting in feature enrichments and further performance and scalability improvements. With the first-class workflow-enabling support of Flux, the software complexity of domain-specific workflow management software was greatly reduced, often to just a thin wrapper around Flux, and the overall end-to-end performance and scalability of workflows were significantly improved. This section highlights some of the representative scientific and engineering breakthroughs that Flux has enabled.

Cancer Research

The JDACS4C program—Joint Design of Advanced Computing Solutions for Cancer—is a partnership between the Department of Energy (DOE) and the National Cancer Institute to advance cancer research using emerging exascale HPC capabilities. The





Pilot 2 project within JDACS4C seeks to develop effective HPC simulation methods to uncover the detailed characterizations of the behavior of RAS proteins on cellular membranes. The RAS protein family are small GTPase-signaling proteins involved with the control of cell division and growth. Mutations leading to increased RAS activity contribute to a wide range of cancers, and up to 30% of human cancers are linked to mutations in the RAS gene family [19]. RAS proteins typically signal their downstream effectors when bound to the lipid bilayer of cellular membranes, and drugs that inhibit RAS activity do not exist yet.

Resolving RAS membrane dynamics and aggregation is a difficult task as macroscale length and time scales are needed; yet micro-scale molecule-level details are also required to capture protein–protein and protein–lipid interactions. To resolve RAS structure and dynamics on cellular membranes, the Pilot 2 team developed the Multiscale Machine-Learned Modeling Infrastructure (MuMMI) [7], which can sample data at the macro-scale with effective micro-scale resolution. This process is depicted in Figure 5.

A macro model is simulated at the membrane level with 300 RAS molecules, which is then coupled with an ML module that drives the sampling of patches, small neighborhoods around an RAS molecule. These patches are then used to instantiate and run corresponding MD simulations.

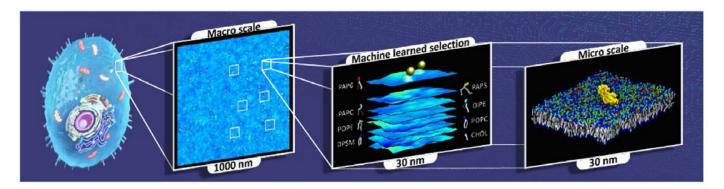


Figure 5: Addressing many important biological questions requires large length- and time-scales, yet at the same time molecular level details. Flux scalably and portably enables the MuMMI workflow to simulate protein–lipid dynamics for a 1 μ m \times 1 μ m membrane subsection at near-atomistic resolution.

The MuMMI workflow reveals many workload management challenges for workload managers on pre-exascale machines. These difficulties include needing to coschedule and to coordinate coupled simulation applications at different scales in a highly sophisticated manner. Specifically, it co-schedules macro models with several thousand MD simulations along with an ML module that prioritizes simulations





dynamically at a high rate and a data store to coordinate the data flow between different tasks running on CPUs and GPUs. Figure 6 shows how the MuMMI workflow used Flux to help schedule and execute various types of applications at large scale.

Owing to Flux, MuMMI's multi-layered, high-throughput simulation workflow could efficiently and effectively proceed by thin domain-specific workflow-management software tools, a combination of LLNL-developed software system called Maestro [20] and an ML-based tool that is coupled closely to the macro simulations. Specifically, the ML-based tool processes simulation frames and decomposes each frame into hundreds of patches, one for each RAS. These patches are scored by its pre-trained machine-learned model. The most "interesting" candidate patches—ones with highest scores—are fed to micro-scale MD simulation tasks, which are submitted, scheduled and executed by Flux.

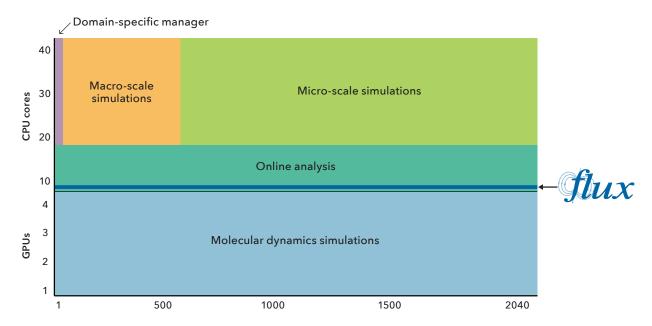


Figure 6: The award-winning MuMMI project utilizes heterogeneous CPU/GPU resources to perform different complex simulation and decomposition jobs simultaneously. Shown here are the number of processors used for a typical MuMMI run of 2,040 nodes on LLNL's Sierra supercomputer. Flux and complementary workflow software tools have a small footprint, taking up only a small fraction of the compute resources allocated to a MuMMI run (e.g., a single CPU core on each node).

In a departure from the traditional products, Flux provides many knobs to specialize and tune its scheduling policies so that it can deliver the best performance for each different type of workload. In the case of MuMMI, Flux's job-queuing capability is first specialized to a first-come, first-served (FCFS) policy.



A typical facility-wide workload manager's scheduling policy requires the scheduler to look ahead at all later jobs to find backfilling opportunities when the current job cannot be scheduled, which is computationally expensive and time consuming. With Flux, the queue depth is easily set to 1; the scheduler only looks ahead to the next job. This FCFS policy with a single-unit queue-depth parameter keeps the scheduling performance overhead at bay—an optimization well-suited for MuMMI's high-throughput workload. Considering only a few jobs when making a decision of what to run would be inappropriate for center-wide scheduling that must maintain fairness among many users.⁴

Flux is further specialized to perform its scheduling at the granularity of CPU/GPU level instead of at the exclusive node level—again a typical center-wide scheduling policy—to fulfill MuMMI's complex scheduling requirements. Additionally, to accelerate scheduling and reduce the number of waiting jobs maintained by a single Flux instance, Flux's hierarchical policy is specialized to launch a child instance on every compute node. The eight jobs related to the four micro-scale simulations running on each node are managed through this local instance. Overall, running on all of Sierra's 4,000 nodes, Flux allows MuMMI to utilize 16,000 GPUs and 176,000 CPUs efficiently at peak, simultaneously running 16,000 micro-scale MD simulations.

In November 2019, the MuMMI team won the SC19 Best Paper Award⁵ for this innovative computing workflow approach that enables a new genre of cancer research. The research team has continued to adopt Flux's newer features, and they successfully ran the next version of MuMMI on the full scale of the Summit supercomputer at Oak Ridge National Laboratory (ORNL) in March 2021.

Combating the COVID-19 Pandemic

Near Real-Time Scenario Modeling

Amid the COVID-19 pandemic, scientists have demanded complex scientific workflows to a greater degree than ever before. Combating the new global crisis has required U.S. computing leaders at federal agencies and within the DOE complex to partner with leading universities and technology firms worldwide. As a result, large computing facilities have seen an unprecedented surge of diverse and complex workflows. Many multi-disciplinary research teams have been successfully using Flux to enable major COVID-19 research workflows.

^{4.} Jobs belonging to multiple users must be considered to be reordered in accordance with the past resource usage of users relative to their shares, and to run later jobs if resources cannot currently be utilized by high-priority jobs.

^{5.} The annual Supercomputing Conference (SC) is one of the most prestigious conferences in the field of supercomputing. Only one research paper is selected as the best paper of the year.





COVID-19 spread modeling is an important class of scientific computing workflows as nations urgently need to predict the spread of this virus under various scenarios and inform decision makers. For example, a collaboration among LLNL, Los Alamos National Laboratory, and the National Energy Research Scientific Computing Center (NERSC) in which a large workflow consisting of an ensemble of EpiCast epidemiology simulations is employed to model COVID-19 spread patterns and to inform federal agencies like FEMA of the prediction. As part of the National Virtual Biotechnology Laboratory (NVBL), their workflow taps into U.S. census data to model scenarios such as how the virus will spread if schools are open two days a week.

Flux is playing a central role in providing high job throughput performance and portability required for urgent decision making. Flux's fully hierarchical resource management allows this class of workflows to run many modeling application tasks, each with a different scenario, efficiently at once on a large resource allocation. With strict deadline requirements, these workflows must also portably leverage computing resources from multiple institutions including the world's most powerful supercomputers at ORNL, LLNL, and NERSC. Existing software tools (e.g., SLURM [13] and IBM LSF [14]) fall short of meeting all of the project's requirements—high job throughput, co-scheduling ability, and portability between different HPC systems. Luc Peterson, software architect of a main tool used for the NVBL team reported, "With Flux, we can model one scenario with UQ [uncertainty quantification] for the entire country in about five minutes on a few [Lassen supercomputer] nodes—that is, near real-time feedback." This allowed U.S. policy decision makers to be informed of the results of COVID-19 spread modeling including confidence levels with no delay.

Fast ML-Based COVID-19 Antiviral Drug Design

In May 2020, a multidisciplinary LLNL team set out to develop a new highly scalable, end-to-end antiviral drug design workflow that could expediently produce potential COVID-19 drug molecules for further clinical testing. This team brought together multiple scientific experts:

- LBANN [21] (Livermore Big Artificial Neural Network Toolkit) researchers focused on developing a scalable ML technique to construct a high-quality ML model using 1.6 billion chemical compounds.
- ATOM [22] (Accelerating Therapeutics for Opportunities in Medicine)
 researchers coupled this ML model with a generative molecular design (GMD)
 pipeline to increase the probability of creating new COVID-19 antiviral drug
 molecules with desired properties (e.g., diversity, validity, efficacy, safety).
- ConveyorLC [23] researchers focused on coupling the above with their HPC



simulations that evaluate the docking properties of the newly generated drug candidate molecules—that is, searching for an appropriate ligand that both energetically and geometrically fits the target protein's binding site.

 Workflow infrastructure researchers devised workflow management techniques to ensure the scalability of this newly envisioned coupled workflow.

The team quickly discovered that creating an end-to-end solution based on existing components could present two workflow issues—and that Flux could comprehensively solve them. First, the ConveyorLC docking simulation implements its own *ad hoc* task scheduling on top of message passing interface (MPI) functionality, which is not scalable. The team discovered that the scalability of this scheme indeed led to a significant resource utilization loss starting at 50 nodes. At 200 nodes, the highest scale evaluated this scheduling scheme, resource utilization had already dropped to 45.5%. The second workflow challenge was that the GMD pipeline, a domain-specific workflow management tool, has never been scaled to a few compute nodes and beyond. Taken together, the ideal solution must be capable of utilizing large numbers of compute nodes by flexibly running many ConveyorLC tasks simultaneously each at a small scale (25 nodes) but still exposing this ensemble of tasks as a single unit to GMD to overcome its scalability.

Flux's fully hierarchical resource management has proven to be sufficiently scalable and flexible to solve both of the project's key workflow problems. For example, a large Flux instance managed ConveyorLC docking simulations as an ensemble, then submitted each docking simulation as sub-batch jobs running on their own small Flux instance to the parent instance. Using this hierarchical scheme, the team showed that docking achieved 98.98% resource utilization in the composite workflow context on 2,950 nodes of LLNL's Quartz supercomputer.

Overall, Flux enabled the scalable end-to-end workflow architecture that is used for massive ML training. This team's massive training work [24] was nominated for a special category of the 2020 ACM Gordon Bell Prize,⁶ and was named one of the four finalists. The team plans to submit the workflow-focused work to the same category of the ACM Gordon Bell Prize in 2021.

^{6.} Often called the Nobel Prize of supercomputing, the Association for Computing Machinery (ACM) Gordon Bell Prize is one of the most prestigious awards that recognizes outstanding achievement in HPC applications.





Engineering & Design Optimization

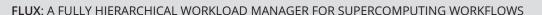
Uncertainty Quantification (UQ); Verification & Validation (V&V)

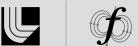
UQ is the science of quantitative characterization and reduction of uncertainties in both computational and real-world applications. Its goal is to determine the likelihood of certain outcomes if some aspects of the system are not precisely known. V&V are independent procedures used together to check that a product, service, or system meets requirements and specifications and that it fulfills its intended purpose. In the context of HPC workflows, these methods often share a common pattern: They must run a large ensemble of physics and other simulations on a supercomputer.

The traditional approach is to write a simple script that iterates through the many necessary job scripts and submits each as a job to the system workload manager. However, this approach has several drawbacks. First, system workload managers often impose limits on the number of concurrently running jobs that a single user can have, so throughput will be low and the user will have to wait a long time for their jobs to complete. Second, users with a large number of jobs will quickly be inconvenienced by submitting and monitoring all of the jobs, resubmitting them if they fail, and then running the post-processing script once they have all completed.

Domain-specific workflow management software tools such as LLNL's UQ Pipeline (UQP) [25] offer an alternative approach. UQP's main advantage is provisioning a resource allocation consisting of N nodes much more quickly than provisioning N resource allocations, each with one node, from the system workload manager. UQP then subdivides the remaining allocated nodes into N uniform "slots." Each slot executes one of N ensemble simulations. Unfortunately, domain-specific tools such as UQP require that the information contained in the batch-job submission script (written for the system workload manager) be re-implemented into the particular workflow management tool and subsequently submitted to the *ad hoc* scheduler within these tools. As a consequence, users must learn and port their code to each different tool whose performance and robustness vary widely. These redundant implementations within each of these tools are becoming prohibitively expensive to develop and support.

Flux recently allowed UQP, one of the most important tools for UQ and V&V workflows at LLNL, to overcome its disadvantages. The team's design extended Flux's fully hierarchical resource management and graph-based scheduling capability to provide the requisite job throughput performance without relying on their *ad hoc* solution. Based on this unified approach, they created a domain-specific workflow tool component called Themis as a thin wrapper around Flux. With Flux, Themis was





demonstrated to complete a 1-million-member ensemble simulation, which was not possible before.

Additive Manufacturing (AM)

AM is revolutionizing the manufacturing industry, allowing construction of complex machine and material parts not readily fabricated by traditional techniques. Although the industry has had significant interest and investment in AM, the fraction of this investment devoted to computer modeling and simulation is relatively small and focused on reduced-order models for industry use instead of the development of high-fidelity predictive models. As part of the DOE's Exascale Computing Project, the Exascale Additive Manufacturing Project (ExaAM) [26] represents a unique opportunity to use exascale computer simulations to enable the design of AM components with location-specific properties and acceleration of performance certification. ExaAM aims to incorporate microstructure evolution and the effects of microstructure within AM process simulations directly into an end-to-end HPC workflow.

The ExaAM team expressed interest in Flux and met with us in September 2020 to co-design the project's overall workflow using Flux. Flux's hierarchical resource management capabilities were tested on a portion of the workflow called ExaConstit to evaluate potential benefits. By November, the ExaAM team was able to integrate Flux into ExaConstit and reported a *4x job throughput performance improvement* with simple scripting changes—namely, submitting multiple batch-job scripts into a Flux instance on a large allocation instead of using the system's native workload manager. ExaAM team member Robert Carson noted, "The workflow change [to integrate Flux] is surprisingly small. In my Python script that generates all of these things, I only had to add about five additional lines for the Flux path."

Large AI on HPC

Flux has enabled extremely large AI workflows for LLNL's Machine Learning Strategic Initiative (MLSI) project. As part of LLNL's Laboratory Directed Research and Development Strategic Initiative portfolio, MLSI aims to combine simulations with experiments using ML to optimize the design of key devices used in National Ignition Facility. Similar to MuMMI and UQ workflows, the MLSI ML workflow requires extremely high job throughput, co-scheduling capabilities, and dynamism. To overcome these workflow challenges, a new workflow tool called Merlin [27] was developed under MLSI.

Merlin provides an adaptable, efficient Python-based workflow that runs an ensemble of simulations and records the results while concurrently running ML on the results as they become available. The ML model then helps steer the ensemble





of simulations as it improves (or learns) with more data. The workflow executes a variety of tasks to generate and analyze the data. The first of these is defining the ensemble of simulations. This ensemble consists of a set of samples spanning the spatial domain needed for creating a unique set of data describing the domain. An executable task will accept the sample set as input parameters and produce data for the ML model. The simulation can range from a simple ordinary differential equation to a massively parallel hydrodynamics simulation. These simulations may also be run on many different platforms with different workload managers, where scheduling and launching the simulations in a general manner becomes difficult.

The first version of the Merlin MPI parallel job launcher used a simple Python-based subprocess call to map a set of MPI parameters (e.g., number of nodes and CPU cores) onto the commands needed for launching under the system workload manager such as SLURM or IBM LSF. A maintenance issue arose when each new workload manager required a set of runtime parameters that do not map 1:1 between the various launch systems. Moreover, IBM LSF does not handle nested launches where there is one subprocess call for the allocation and a subsequent call for the simulation. Some parallel runs need CPU/GPU support, while others require only CPU cores. This requirement puts the onus on the workload manager to schedule resources for the various types of parallel jobs.

In Merlin, Flux solves both the nesting issue and co-scheduling issue through the use of a single Flux instance. Jobs can be concurrently scheduled because the single Flux instance tracks all available resources with a GPU/CPU-level scheduling policy. Nesting is not an issue with this single instance. The initial Flux-Merlin integration was designed and implemented on an LLNL Linux cluster. Porting it to other platforms, such as Sierra and Lassen supercomputers, was straightforward. Overall, the integration team was able to generate massive amounts of simulation data from 100 million short-running jobs, thanks to Flux.

Broad Applicability and Adoption

Because the workload manager is among the most critical software elements for large supercomputers, computing centers must often undertake a multi-year, phased effort to adopt a new *system-level, multi-user* workload manager to replace their existing solutions on large HPC systems. Flux can be run in both multi-user and single-user modes to facilitate a smoother, incremental adoption: Specifically, Flux's user-level capability called *single-user mode* interoperates easily with other traditional solutions and this has proven to be essential for enabling time-critical workflow



problems on the world's largest and most powerful supercomputers even before *multi-user mode* is deployed.

Figures 3a and 3b provide simple examples. We first note that the first lines of these scripts are nearly identical to that of traditional solutions. Exploiting this property, Flux can easily be adapted and used with a computing center's existing system workload managers with just a few keystrokes. For example, Figure 7 shows how Flux can enable the complex workflow in Figure 3b under SLURM, a traditional HPC workload manager, with just a two-line change in commands. This feature has proven to be critical in helping combat time-critical workflow problems such as in COVID-19 research. Thanks to this easy-to-adapt feature, Flux has enabled HPC users, research and industry collaborators, and computing centers to be able to respond to the needs of emerging workflows without having to adopt the full system-instance technology of Flux.

Figure 7: Enabling Flux under another workload manager like SLURM is as simple as executing this two-line command.

Flux's adaptability to different use cases, along with being open source, has spurred wide adoption outside of LLNL. Flux has users worldwide including our collaborators in both U.S. and European academic institutions; U.S. national labs; U.S. military and federal agencies; and prominent domestic and international scientific computing and HPC centers like NERSC in California and RIKEN in Japan, home of the top-ranked Fugaku supercomputer. Figure 8 shows the geological distribution of these institutions.







Figure 8: Users and collaborators of Flux are quickly expanding around the world.

B. How does the product operate?

Fully Hierarchical Resource Management Techniques

Flux's innovative fully hierarchical resource management capabilities drastically improve *scalability* and *flexibility* through a divide-and-conquer approach (Figure 9). Jobs and resources are divided among the schedulers in the hierarchy and managed in parallel. Figure 10 shows how this approach drastically increases the scalability of Flux over traditional schedulers that rely on a single, centralized process.

Three distinct principles underpin Flux's hierarchical design:

- **Hierarchical Bounding Principle:** A parent Flux instance grants job and resource allocations to its children.
- Instance Effectiveness Principle: Each Flux instance can be configured independently and is solely responsible for the most effective use of its HPC resource set.





 Arbitrary Recursion Principle: The first two principles apply recursively from the top of the resource hierarchy (e.g., the entire HPC center) down to any arbitrarily small subset of resources.

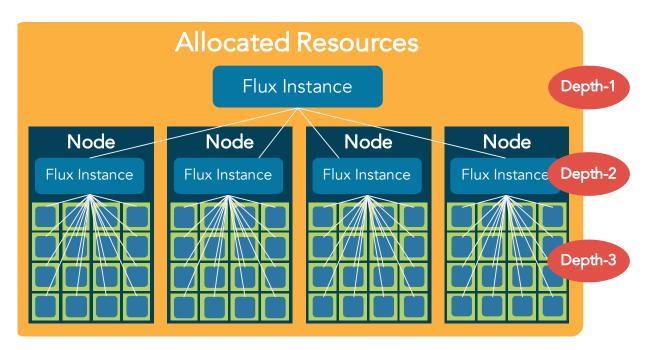


Figure 9: As a fully hierarchical workload manager, any Flux instance can spawn child instances to aid in scheduling, launching, and managing complex sequences of compute jobs. A top-level Flux instance (parent) is created within a 4-node resource allocation; the top-level instance then spawns additional levels of Flux instances (children), each of which manages a smaller subset of jobs and resources. The hierarchy of Flux instances extends down until the lowest-level instances each manage a single core—a maximal example of fully hierarchical capabilities.

Hierarchical bounding improves scalability in two ways. First, it reduces the number of resources that each Flux instance must consider, which improves the performance of each individual instance. Second, it enables Flux instances to delegate work to child instances, spreading the load across many independent instances and ultimately improving their collective performance.

Instance effectiveness enables the customization of Flux instances for specific workflows. The top-level Flux instance may be a system-wide, multi-user workload manager instance with expensive scheduling policies, but it can create a child single-user instance for each new workflow which enables the workflows to customize the scheduling and other policies to their exact needs. This customization includes not





only the scheduling policies and configuration scheduling parameters, but also the number of children that the Flux instance creates.

Arbitrary recursion amplifies the scalability and flexibility provided by the previous two principles. It allows for the creation of the appropriate number of Flux instances for each workflow. Specifically, this principle enables large ensemble workflows to create more Flux instances and thus improve job throughput with minimum performance overhead needed for parallelization. Flux instances within a hierarchy can even be dynamically created and removed depending on how workloads change over time.

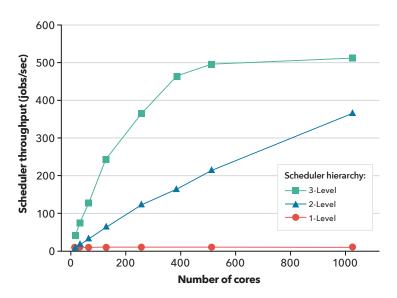


Figure 10: For multiple runs on between 1 and 1,152 cores of LLNL's Quartz supercomputer, three different configurations of schedulers are benchmarked on a 4,096-job workload. First, a traditional workload manager (red) schedules the workload at the same rate regardless of the number of cores. Second, two levels of Flux instances (blue), with the second level instances each managing 32 cores, schedules the workload 45x faster than the traditional workload manager (red) and scales well with the number of cores. Finally, three levels of Flux instances (green), with each third-level instance managing a single core, maximizes throughput at 60x faster than traditional techniques (red) and scales excellently with the number of cores.

Scalable Graph-Based Scheduling Techniques

Once instantiated, Flux effectively carries out many complicated operations, ranging from monitoring the health of resources, to enqueuing submitted tasks, to scheduling and executing these tasks. Flux uses a graph-based approach to scheduling as described on pp. 8–11. Flux's scheduler component, called Fluxion, is represented in Figure 11. During Flux instance initialization, Fluxion first populates an in-memory resource graph store (A) comprising vertices that represent the HPC system's various compute resources and edges that represent the relationships among those resources. The initialization process also includes the selection of the graph resource's representation granularity and traversal type if users decided to use non-default. Once initialization is complete, Fluxion is ready to receive the jobs' resource requests from Flux's core framework.





Flux first constructs a job's resource request in the form of an abstract resource request graph (B). The abstract request graph generally specifies the job's resource requirements in terms of both node-local resources (e.g., amount of compute cores and memory to be used) and higher level or even global resources (e.g., compute racks, network switches, power, parallel filesystem bandwidth). The abstract request graph then becomes the input for the selected graph traverser (A) to find its best-matching resource vertices and edges. The traverser "walks" the concrete resource graph store in this pre-defined walking order and matches the abstract request graph to the concrete resource graph.

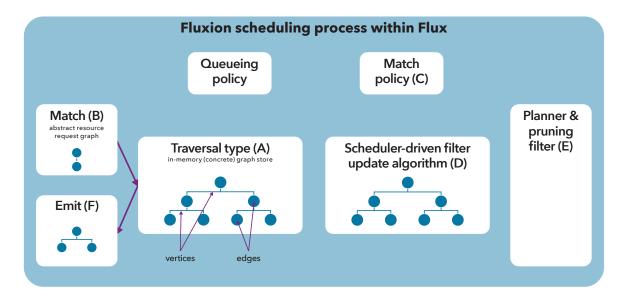


Figure 11: Fluxion, Flux's scheduler component, automatically performs multiple steps when a Flux instance is initialized. See text for a description of each lettered process.

As shown at (C), the best-matching criteria is determined by the match policy within Flux's traverser. The policy is invoked every time the traverser visits a vertex. The policy then evaluates how well a given resource vertex matches with the abstract request graph and scores it accordingly. Flux's resource model must also efficiently keep track of the status changes of resources over time in order to support various queuing and backfilling policies common to HPC job scheduling (e.g., EASY [28] and conservative [29] backfilling policies). Thus, the model directly integrates a highly efficient resource-time state tracking and search mechanism into every resource vertex. This mechanism (and a simple abstraction) is called Planner (E) [18].

After judicious selection of the appropriate representation granularity for the concrete resource graph—striking a balance between performance and scheduling





effectiveness—the resulting graph can still be quite large when modeling highend systems. Thus, the Fluxion scheduler includes other scalability strategies in its model, such as pruning filters (E). For example, pruning filters can be installed at high-level resource vertices (e.g., compute racks) to track the amount of available lower-level resources (e.g., compute cores) in aggregate, which reside somewhere in the subgraph rooted at that vertex. Fluxion also introduces a novel schedulerdriven filter update algorithm (D) that updates and maintains these filters without incurring high performance overhead. This filter significantly improves performance by pruning the required graph search. Finally, once Fluxion determines the best matching resource subgraph, this is emitted as a selected resource set representation at (F). Flux's core framework can then make use of this resource set to contain, bind and execute the target program(s) within those resources. As discussed on pp. 8-11, our graph-based techniques stray away from the traditional workload managers, helping usher in the era of extreme resource heterogeneity [10] for HPC. The existing solutions use rather simple, compute-node centric data model and scheduling schemes.

User Interfaces

Existing workload manager products typically provide only a command-line interface (CLI) as their primary user interface. Some of the more popular workload managers are bolstered by community efforts to support application programming interfaces (APIs) so that other software can more efficiently interoperate with them, but these community efforts are *ad hoc*, poorly supported, and thus usually short-lived. On the other hand, Flux provides both a CLI as well as first-class API support for the common programming languages C, C++, Python, and Lua. Work-in-progress support for the programming languages Rust and Julia has also been added. These APIs enable developers from many programming backgrounds to interoperate easily and efficiently with Flux. Furthermore, because these interfaces are provided as a core part of Flux, users can rely on their continued support.

Flux's Python support is particularly important due to the proliferation of Python-based workflow management systems. Many of them leverage Flux's Python API to directly integrate with Flux, including Maestro [20], Themis [25] and GMD [22] as described on p. 16, Radical Pilot [30], and Parsl [31]. As a workflow management system, integrating via an API as opposed to a CLI is both significantly easier—accessing the functionality is a direct call to Flux as opposed to an indirect call—and more performant—there is no need to create a new program for the CLI command or to perform any string parsing of the CLI output.



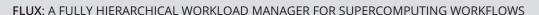


Single-User Mode

A unique and novel feature of Flux is that it allows for both single-user and multiuser modes. Most HPC users are familiar with the multi-user mode when interacting with the workload manager. Similar to a traditional solution, in this mode, decisions are made at the system-level, and requests from multiple users are honored through individual allocations based on priorities, accounts, and well-known scheduling policies such as EASY [28] and conservative [29] backfilling and fair sharing. Authentication between users as well as exclusive access to resources are important criteria in this mode. Here, the goal is to ensure that the resources from the entire cluster are shared among users in a fair and equitable manner, that user requests for allocations are met without starving any job, and while optimizing for high node utilization and low fragmentation. Conventional workload managers do not provide users with the comprehensive ability to manage resources within their own allocation. Traditionally, users are assumed to rely on the policies set by the system administrators within their allocation. The consequences of this limitation include the emergence of ad hoc scripting; "glue" code (i.e., written solely for the purpose of filling a gap or overcoming a limitation); and various workflow managers that attempt to streamline the complexity of scientific applications that need coupling, coordination, and dependency management, as discussed on pp. 5-8.

Flux provides a *single-user mode*, where users have the flexibility to manage resources and tasks within their allocation. This allows users to set up their own customized hierarchies as well as policies based on the graph-based resource model. This also allows users to tune additional scheduling options such as queue depths and throttling of jobs. For example, an ensemble-based workflow that encompasses thousands of short-duration, single-core jobs can spin up a network of nested Flux instances each with an FCFS policy, instead of relying on the system's default policy of FCFS plus backfilling, which may not be necessary for the user's workflow. Such a network of child Flux instances is also more scalable and fault tolerant, as it can easily absorb the stream of thousands of incoming jobs without becoming overwhelmed.

Similarly, for complex workflows with many dependencies and steps, users can set up a customized, coordinated network of Flux instances to facilitate communication between various tasks in the workflow in a scalable manner. Users could choose to divide their node in a manner where some tasks run on the heterogeneous components such as GPUs while other tasks of the application can utilize the CPUs, thus leveraging co-scheduling techniques.





Flux's single-user mode enables such customization with ease and supports diverse workflows and resources, which is not possible to accomplish with traditional solutions. The single-user mode is a distinguishing feature of Flux that gives enormous flexibility to the users, allowing them to derive maximal performance and utilization within their allocation for their specific use case.

Multi-User Mode

Like traditional workload managers, Flux also provides a multi-user mode. In this mode, Flux runs as a privileged account, accepts jobs from multiple users, sorts and schedules the jobs based on user's priorities, and finally executes each job as the submitting user. Similar to other products, Flux includes an accounting component to keep track of users' resource usage relative to their priority and job prologue and epilogue scripts that enable admins to customize Flux to their sites.

Unlike traditional solutions, Flux has three key architectural designs that make its multi-user mode very secure. The first is which parts of Flux run as root—the highest level of privilege on a computer. Typical workload managers run their entire software as root, meaning that any security vulnerability in the solution can be used to easily gain total control of the system. Flux breaks this mold with its Independent Minister of Privileges (IMP), which is the only component of Flux that runs as root. Every other Flux component runs as a dedicated system account with significantly fewer privileges than root. The IMP represents less than 2% of the total lines of code in the Flux project, making a security audit of Flux's root-privileged code much easier and exploiting flaws in Flux much harder.

The second key architectural difference between Flux and other products is that every communication with and within Flux is encrypted. Encrypted communication between users and the workload manager is particularly important in classified computing, where national security information cannot be exposed to users without need-to-know, and medical computing, where U.S. HIPAA laws require that medical information not be exposed to other users. Flux is also designed to take extra precautions with the user's submitted job specifications, which are the main input to Flux's IMP. Each job specification is cryptographically signed, and before executing the job, Flux's IMP verifies the signature to ensure a forged job submissions has not occurred. This additional level of validation cryptographically ensures that users cannot impersonate other users, preventing leaks of classified or sensitive information.

The third key architectural difference is Flux's modular design, which enables the extensive use of plugins. No existing approach can provide a one-size-fits-all solution;





each site will want to customize the workload manager to meet their specific needs, adapt to their unique environments, and enforce their local policies. Flux provides multiple points for site administrators to integrate with Flux via plugins. These plugins include a job ingest plugin for rejecting jobs that do not adhere to local policies, an accounting plugin to calculate each user's fair share of the system based on site-specific priorities, job-shell plugins that run as the user to apply site-local customizations to the job environment before the job runs, and the aforementioned prologue and epilogue scripts that run as root before and after the user's job. The combination of these plugins gives site administrators significantly more control to customize Flux versus other products.

C. Product comparison

As described earlier, Flux is capable of operating at either the system level in multiuser mode or the user level in single-user mode. This capability is unique to Flux, as other technologies fall into one category or the other.

Multi-User Competitors

Flux's multi-user competitors can be broken down into centralized, limited hierarchical, and decentralized workload managers. Centralized ones use a single, global scheduler that maintains and tracks the full knowledge of jobs and resources to make scheduling decisions. This model is simple and effective for moderate-size clusters, making it the state of the practice in most cloud-based and HPC centers today. Cloud workload managers (or often called container orchestration solutions) such as Swarm [33] and Kubernetes [34] and HPC workload managers such as SLURM [13], MOAB [16], IBM LSF [14], and PBSPro (OpenPBS) [15] are centralized. The cloud products—Kubernetes in particular—can achieve high job throughput, but they are incapable of efficient batch job scheduling and rely on overly simplistic resource models, resulting in poor performance for HPC workloads. On the other hand, centralized HPC solutions are capped at tens of jobs per second [35], provide limited to no support for co-scheduling of heterogeneous tasks [36], have limited APIs, and also rely on simple resource models. Both types of centralized workload managers, by design, suffer from an inability to nest within or integrate with other system workload managers. However, Flux is more flexible than centralized solutions because it can scale to the largest systems and workloads, be adapted to different types of system hardware and configurations, has more robust options, and does not impose job throughput quotas.



Limited hierarchical workload managers have emerged predominantly in grid (i.e., non-cluster) and cloud computing. This model's fixed-depth hierarchy typically consists of two statically configured levels of independent workload manager frameworks stacked together, relying on custom-made interfaces to facilitate interoperability. Example implementations include the cloud computing solutions like Mesos [37] and YARN [38] as well as the grid solutions like Globus [39] and HTCondor [40]. Efforts to achieve better scalability in HPC have resulted in this model's implementation at some large HPC centers. For example, in the past LLNL managed multiple clusters with a limited hierarchical workload manager that used the MOAB grid meta-scheduler on top of several SLURM workload managers, each of which managed a single cluster in the facility [41]. While this type of solution increases scalability over centralized scheduling, it is ultimately limited by its shallow (and therefore inflexible) hierarchy and the capabilities of the scheduling frameworks used at the lowest levels. Compared to these solutions, Flux is *fully* hierarchical and thus has no fixed-depth or artificial limits on its flexibility or scalability.

Decentralized workload management is a model studied in the academic literature, but unlike centralized ones, it has not gained traction. To the best of our knowledge, decentralized solutions are not in use in any HPC center's production environment. The cloud computing software like Sparrow [42] and HPC's SLURM++ [43] are examples of decentralized schedulers. In decentralized workload management, multiple workload manager instances each manage a disjointed subset of jobs and resources, yet they are fully connected and can communicate with each other. In this model, an instance communicates with other instances when performing work "stealing" (i.e., scheduling jobs initially allocated to another instance) and when allocating resources outside of its resource set (i.e., resources managed by another workload management instance). Despite providing higher job throughput, decentralized solutions suffer from many of the same problems as centralized ones. First, they have little to no support for co-scheduling of heterogeneous tasks and limited APIs. Second, these products commonly make assumptions about the types of applications being run to improve performance.

For example, Sparrow assumes that a common computational framework, such as Hadoop or Spark, is used by most of the jobs, limiting Sparrow's applicability to HPC workloads [42]. In contrast, Flux's hierarchical communication among its instances can scale to large systems, workloads and scheduler configurations, and it supports a broad range of workloads—including both loud and HPC—better than decentralized workload manager technologies can.





Single-User Competitors

Flux's single-user competitors can be divided into user-level runtimes and workflow managers. User-level runtimes offload a majority of task ingestion, scheduling, and launching from the batch job scheduler onto a user-level runtime. This means that users have to manage all of their workload scheduling instead of the workload manager managing it for them. These user-level runtimes are typically much simpler and less sophisticated than Flux and the other multi-user workload managers described above, but in exchange provide extremely high throughput. For example, CRAM provides no support for scheduling or queueing (i.e., there can only be one task per processor and once a task completes, the resources remain idle until all other tasks have completed), tasks requiring GPUs, or an API to query the status of tasks, but it can launch ~1.5 million tasks with an average job throughput of ~1,200 jobs per second [44]. Flux, in contrast, does not allow resources to sit idle and slow the overall execution of the workflow, even a workflow with 1.5 million tasks.

Workflow managers are designed to ease the composition and execution of complex workflows on various computing infrastructures, including HPC, grid, and cloud resources [45]. Example workflow managers include Pegasus [46], DAGMan [47], and the UQP [25]. Workflows can be represented as a directed acyclic graph (DAG), as is the case with Pegasus and DAGMan, or a parameter sweep, as is the case with the UQP. Once users specify a workflow, the workflow manager resolves the dependencies through the DAG, submits tasks to the various computing resources and handles moving data between the dependent tasks. Workflow managers provide an interface for users to track the status of their workflow in a portable fashion across many types of computing infrastructures. Although a workflow manager can improve the overall workflow throughput by taking advantage of multiple independent computing resources (e.g., clusters), it does not improve the job throughput or concurrent scheduling capabilities of any individual computing resource. Additionally, to submit and manage jobs in a portable way across different HPC systems, many workflow managers incur expensive side effects, such as the creation of millions of job status files [48], which can cripple modern parallel filesystems. Flux enables workflow managers to avoid these crippling side-effects with efficient, portable APIs for submitting, tracking, and coordinating jobs.

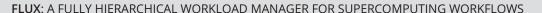
Overall, many of these single-user technologies are not in competition with Flux but instead are complementary to Flux. In fact, Flux has been integrated and leveraged by many workflow systems, including UQP and Themis [25], Radical Pilot [30], Swift/T [49], and Parsl [31], providing them with better scalability, usability, and portability.



D. Comparison Summary

Table 1: Comparison Matrix for Both Multi-User and Single-User Competitors

Features	Flux	SLURM	PBSPro (OpenPBS)	LSF	Moab	RadicalPilot	Balsam	Parsl	Nitro
Open source	Yes	Yes	Yes	No	No	Yes	Yes	Yes	No
MULTI-USER MODE									
Multi-user workload management	Yes	Yes	Yes	Yes	Yes	No	Yes	No	No
Fully hierarchical resource management	Yes	No	No	No	No	N/A	N/A	N/A	N/A
Graph-based advanced resource scheduling	Yes	No	No	No	No	N/A	N/A	N/A	N/A
Scheduling specialization	Yes	No	No	No	No	N/A	N/A	N/A	N/A
Security: only a small isolated layer running in privileged mode for tighten security	Yes	No	No	No	No	N/A	N/A	N/A	N/A
Modern command-line interface (CLI) design [16]	Yes	Outdated CLI	Outdated CLI	Outdated CLI	Outdated CLI	N/A	N/A	N/A	N/A
Application programming interfaces (APIs) for job management, job monitoring, resource monitoring, low-level messaging	Yes (4/4)	Some (3/4)	Some (2/4)	Some (2/4)	Some (3/4)	N/A	N/A	N/A	N/A
Language bindings	Yes (6)	C, REST	C, Python	C, Python	С	N/A	N/A	N/A	N/A
Bulk job submission	Yes	Only uniform jobs	Only uniform jobs	Only uniform jobs	Only uniform jobs	N/A	N/A	N/A	N/A
High-speed streaming job submission	Yes	No	No	No	No	N/A	N/A	N/A	N/A
SINGLE-USER MODE									
User-level workload management instance	Yes	No	No	No	No	Yes	Yes	Yes	Yes
Support for nesting within foreign resource manager	Yes	N/A	N/A	N/A	N/A	Yes	Yes	Yes	Yes
Fully hierarchical management of instances	Yes	N/A	N/A	N/A	N/A	No (two level)	No	No (two level)	No (two level)
Scheduler specialization for user level	Yes	N/A	N/A	N/A	N/A	Yes	No	Yes	No
Graph-based advanced scheduling for user level	Yes	N/A	N/A	N/A	N/A	No	No	No	No
Built-in facilities for inter-job communication and coordination	Yes	N/A	N/A	N/A	N/A	No	No	No	No
Modern CLI design [16]	Yes	N/A	N/A	N/A	N/A	No	Yes	No	Outdated CLI
APIs for job management, job monitoring, resource monitoring, low-level messaging	Yes (4/4)	N/A	N/A	N/A	N/A	Yes (4/4)	Some (2/4)	Some (2/4)	No
Language bindings	Yes (6)	N/A	N/A	N/A	N/A	Python	Python	Python	No
Bulk job submission	Yes	N/A	N/A	N/A	N/A	Limited support	No	Limited support	Only single-core jobs
High-speed streaming job submission	Yes	N/A	N/A	N/A	N/A	Yes	No	Yes	No
Support to launch MPI jobs	Yes	N/A	N/A	N/A	N/A	Yes	Yes	Limited support	No





Limitations

As with other high-end system software that targets the next generations of the world's largest supercomputers, development of the system instance of Flux, which will enable it to be the primary system workload manager on exascale-computing-class supercomputers by 2023, is actively being pursued as additional features and performance/scalability tuning, commensurate with the capabilities of then the world's fastest supercomputers, are required. It is important to note that existing workload managers in HPC (such as SLURM or LSF) have been developed and stabilized over a span of decades, until many HPC sites across the world adopted and deployed them, and they continue to add features. Similar expectations apply to the Flux framework as development effort and feature enhancements continue.

A key challenge for Flux includes the effort required for users to port their legacy applications and workflows to the flexible and modern Flux framework. Although the Flux framework is designed to be extremely user-friendly and easy to understand, the transition of legacy applications still requires some amounts of effort and developer bandwidth. This is because of the complex dependencies that could exist in some of the scientific workflows making them challenging to untangle and port. Additionally, the ideas of fully hierarchical resource management, graph-based scheduling, and customization of policies in the user's resource allocation are relatively new, and users need well-written documents, training and tutorials to realize the full potential of these novel capabilities. The Flux team provides detailed and up-to-date documentation, regularly holds tutorials at major venues, and engages with developers early on to help them design their workflow infrastructure on top of Flux. Additionally, the Flux team actively works with developers of workflow software to co-design and to provide the interfaces that streamline the porting of existing applications and workflows.





SUMMARY

Today's researchers require more computing applications than ever before in their scientific workflows. A single job may need to run multiple simulation applications at different scales along with in situ visualization, data analysis, machine learning, and artificial intelligence. These needs combined with hardware innovations (e.g., multitiered disk storage, combinations of processors, power efficiency advancements) have outpaced the capabilities of traditional workload management software, which cannot handle complicated workflows or adapt to emerging supercomputer architectures. Flux is an open-source software framework that manages and schedules computing workflows to maximize available resources to run applications faster and more efficiently. Flux's fully hierarchical resource management and graphbased scheduling features improve the performance, portability, flexibility, and manageability of both traditional and complex scientific workflows on many types of computing systems—in the cloud, at remote locations, on a laptop, or on nextgeneration architectures. Users can kick off a Flux-managed workload and monitor its progress with just a few commands. Researchers at LLNL and around the world are realizing that using Flux is like having your own personal supercomputer.

5. REFERENCES

- 1. Flux Framework Community, "Flux Framework: A flexible framework for resource management customized for your HPC site," <u>flux-framework.org</u>, Apr. 2021, (Retrieved Apr. 18, 2021).
- E. Deelman, T. Peterka, I. Altintas, C. D. Carothers, K. K. van Dam, K. Moreland, M. Parashar, L. Ramakrishnan, M. Taufer, and J. Vetter, "The future of scientific workflows," The International Journal of High Performance Computing Applications, vol. 32, no. 1, pp. 159–175, 2018.
 [Online]. Available: doi.org/10.1177/1094342017704893.
- HPCwire, "LLNL, IBM and Red Hat to Explore Standardized HPC Resource Management Interface," hpc-resource-management-interface/, Apr. 2021, (Retrieved Apr. 30, 2021).
- 4. D. H. Ahn, J. Garlick, M. Grondona, D. Lipari, B. Springmeyer, and M. Schulz, "Flux: A Next-Generation Resource Management Framework for Large HPC Centers," in 2014 43rd International Conference on Parallel Processing





Workshops, 2014, pp. 9–17.

[Online]. Available: doi.org/10.1109/ICPPW.2014.15.

- 5. Y. Georgiou, "Contributions for resource and job management in high performance computing," Ph.D. dissertation, Nov. 2010.
- D. H. Ahn, N. Bass, A. Chu, J. Garlick, M. Grondona, S. Herbein, H. I. Ingólfsson, J. Koning, T. Patki, T. R. Scogland, B. Springmeyer, and M. Taufer, "Flux: Overcoming scheduling challenges for exascale workflows," Future Generation Computer Systems, vol. 110, pp. 202–213, 2020.
 [Online]. Available: doi.org/10.1016/j.future.2020.04.006.
- F. Di Natale, H. Bhatia, T. S. Carpenter, C. Neale, S. K. Schumacher, T.
 Oppelstrup, L. Stanton, X. Zhang, S. Sundram, T. R. W. Scogland, G. Dharuman,
 M. P. Surh, Y. Yang, C. Misale, L. Schneidenbach, C. Costa, C. Kim, B. D'Amora,
 S. Gnanakaran, D. V. Nissley, F. Streitz, F. C. Lightstone, P.-T. Bremer, J. N.
 Glosli, and H. I. Ingólfsson, "A massively parallel infrastructure for adaptive
 multiscale simulations: modeling RAS initiation pathway for cancer," in
 Proceedings of Supercomputing '19: The International Conference for High
 Performance Computing, ser. SC '19, 2019.
 [Online]. Available: doi.org/10.1145/3295500.3356197.
- 8. C.-C. Yang, G. Domeniconi, L. Zhang, and G. Cong, "Design of Al-enhanced drug lead optimization workflow for HPC and cloud," in IEEE International Conference on Big Data, Dec. 2020, pp. 5861–5863. [Online]. Available: doi:org/10.1109/BigData50022.2020.9378387.
- 9. J. Minnich, K. McLoughlin, M. Tse, J. Deng, A. Weber, N. Murad, B. D. Madej, B. Ramsundar, T. Rush, S. Calad-Thomson, J. Brase, and J. E. Allen, "AMPL: A Data-Driven Modeling Pipeline for Drug Discovery," Journal of Chemical Information and Modeling, vol. 60, no. 4, pp. 1955–1968, 2020, PMID: 32243153. [Online]. Available: doi:org/10.1021/acs.jcim.9b01053.
- 10. J. S. Vetter et al., "Extreme Heterogeneity 2018 Productive computational science in the era of extreme heterogeneity: report for DOE ASCR Workshop on Extreme Heterogeneity," Dec. 2018.
- 11. Lawrence Livermore National Laboratory, "Sierra," hpc.llnl.gov/hardware/platforms/sierra, Lawrence Livermore National Laboratory, Apr. 2021, (Retrieved Apr. 18, 2021).





- 12. Oak Ridge National Laboratory, "Summit," <u>olcf.ornl.gov/summit/</u>, Oak Ridge National Laboratory, Apr. 2021, (Retrieved Apr. 18, 2021).
- B. Yoo, M. A. Jette, and M. Grondona, "SLURM: Simple Linux Utility for Resource Management," in Job Scheduling Strategies for Parallel Processing, D. Feitelson, L. Rudolph, and U. Schwiegelshohn, Eds. Berlin, Heidelberg: Springer Berlin Heidelberg, 2003, p. 44–60. [Online]. Available: doi.org/10.1007/10968987_3.
- 14. IBM Spectrum LSF, "Using the IBM Spectrum LSF Resource Connector," <u>ibm.</u> <u>com/support/knowledgecenter/SSWRJV_10.1.0/lsf_welcome/lsf_kc_resource_connector.html</u>, Apr. 2021, (Retrieved Apr. 30, 2021).
- 15. OpenPBS, "OpenPBS: Industry-leading workload manager and job scheduler for high-performance computing," openpbs.org, Altair, Apr. 2021, (Retrieved Apr. 30, 2021).
- 16. Adaptive Computing, "MOAB HPC SUITE," <u>adaptivecomputing.com/cherry-services/moab-hpc-suite/</u>, Adaptive Computing, Apr. 2021, (Retrieved Apr. 17, 2021).
- 17. Flux Framework Community, "Fluxion: An advanced graph-based scheduler for HPC," github.com/flux-framework/flux-sched, Apr. 2021, (Retrieved Apr. 19, 2021).
- 18. Flux Framework Community, "PLANNER API," <u>github.com/flux-framework/flux-sched/blob/master/resource/planner/README.md</u>, Apr. 2021, (Retrieved Apr. 18, 2021).
- 19. I. A. Prior, P. D. Lewis, and C. Mattos, "A Comprehensive Survey of Ras Mutations in Cancer," Cancer Research, vol. 72, no. 10, pp. 2457–2467, 2012. [Online]. Available: doi.org/10.1158/0008-5472.CAN-11-2612.
- 20. F. Di Natale, "Maestro Workflow Conductor," github.com/LLNL/maestrowf, Apr. 2021, (Retrieved Apr. 26, 2021).
- 21. B. Van Essen, H. Kim, R. Pearce, K. Boakye, and B. Chen, "LBANN: Livermore Big Artificial Neural Network HPC Toolkit," in Proceedings of the Workshop on Machine Learning in High-Performance Computing Environments, ser. MLHPC'15. New York, NY, USA: Association for Computing Machinery, 2015. [Online]. Available: doi:org/10.1145/2834892.2834897.





- 22. Lawrence Livermore National Laboratory, "Transforming drug discovery," <u>atomscience.org</u>, Apr. 2021, (Retrieved Apr. 19, 2021).
- 23. X. Zhang, S. Wong, and F. Lightstone, "Message passing interface and multithreading hybrid for parallel molecular docking of large databases on petascale high performance computing machines," Journal of Computational Chemistry, vol. 34, Apr. 2013.
 [Online]. Available: doi.org/10.1002/jcc.23214.
- 24. S. A. Jacobs, T. Moon, K. McLoughlin, D. Jones, D. Hysom, D. H. Ahn, J. Gyllenhaal, P. Watson, F. C. Lightstone, J. E. Allen, I. Karlin, and B. V. Essen, "Enabling rapid COVID-19 small molecule drug design through scalable deep learning of generative models," The International Journal of High Performance Computing Applications, May 2021. [Online]. Available: doi:10.1177/10943420211010930.
- 25. T. L. Dahlgren, D. Domyancic, S. Brandon, T. Gamblin, J. Gyllenhaal, R. Nimmakayala, and R. Klein, "Poster: Scaling uncertainty quantification studies to millions of jobs," in Proceedings of the 27th ACM/IEEE International Conference for High Performance Computing and Communications Conference (SC), Nov. 2015.
- 26. Exascale Computing Project, "ExaAM," <u>exascaleproject.org/research-project/exaam</u>, Apr. 2021, (Retrieved Apr. 19, 2021).
- L. Peterson, K. Athey, P. T. Bremer, V. Castillo, F. Di Natale, J. E. Field, D. Fox, J. Gaffney, D. Hysom, S. A. Jacobs, J. Koning, B. Kostowski, S. Langer, P. Robinson, J. Semler, B. Spears, B. Van Essen, J. S. Yeom, B. Kailkhura, and J. Thiagarajan, "Merlin: Enabling Machine Learning-Ready HPC Ensembles," 4 2019. [Online]. Available: osti.gov/biblio/1630805.
- 28. J. Skovira, W. Chan, H. Zhou, and D. Lifka, "The EASY LoadLeveler API project," in Job Scheduling Strategies for Parallel Processing, D. G. Feitelson and L. Rudolph, Eds. Berlin, Heidelberg: Springer Berlin Heidelberg, 1996, pp. 41–47. [Online]. Available: doi.org/10.1007/BFb0022286.
- 29. D. G. Feitelson, L. Rudolph, U. Schwiegelshohn, K. C. Sevcik, and P. Wong, "Theory and practice in parallel job scheduling," in Job Scheduling Strategies for Parallel Processing, ser. JSSPP 1997, vol. 1291. Berlin, Heidelberg: Springer Berlin Heidelberg, 1997, pp. 1–34, lecture Notes in Computer Science. [Online]. Available: doi.org/10.1007/3-540-63574-2_14.





- 30. A. Merzky, M. Turilli, M. Maldonado, M. Santcroos, and S. Jha, "Using Pilot Systems to Execute Many Task Workloads on Supercomputers," in Job Scheduling Strategies for Parallel Processing, D. Klusáček, W. Cirne, and N. Desai, Eds. Cham: Springer International Publishing, 2019, pp. 61–82. [Online]. Available: doi.org/10.1007/978-3-030-10632-4 4.
- 31. Y. Babuji, A. Woodard, Z. Li, D. S. Katz, B. Clifford, R. Kumar, L. Lacinski, Chard, J. M. Wozniak, I. Foster, M. Wilde, and K. Chard, "Parsl: pervasive parallel programming in python," in Proceedings of the 28th International Symposium on High-Performance Parallel and Distributed Computing, ser. HPDC '19. New York, NY, USA: Association for Computing Machinery, 2019, p. 25–36. [Online]. Available: doi.org/10.1145/3307681.3325400.
- 32. J. Dickey, "12 factor CLI apps," <u>medium.com/@jdxcode/12-factor-cli-apps-dd3c227a0e46</u>, Oct. 2018, (Retrieved May 7, 2021).
- 33. Docker Inc., "Swarm: a docker-native clustering system," github.com/docker/swarm, Docker Inc., Apr. 2021, (Retrieved Apr. 30, 2021).
- 34. Kubernetes, "Production-Grade Container Orchestration," <u>kubernetes.io</u>, Apr. 2021, (Retrieved Apr. 30, 2021).
- 35. K. Wang, "Slurm++: a distributed workload manager for extreme-scale high-performance computing systems," cs.iit.edu/~iraicu/teaching/CS554-S15/lecture06-SLURM++.pdf, Feb. 2015.
- 36. SchedMD, "Heterogeneous Job Support," slurm.schedmd.com/heterogeneous jobs.html, SchedMD, May 2021, (Retrieved May 3, 2021).
- 37. B. Hindman, A. Konwinski, M. Zaharia, A. Ghodsi, A. D. Joseph, R. Katz, Shenker, and I. Stoica, "Mesos: a platform for fine-grained resource sharing in the data center," in Proc. of the 8th USENIX Conference on Networked Systems Design and Implementation, ser. NSDI'11. Berkeley, CA, USA: USENIX Association, 2011, pp. 295–308.
 [Online]. Available: dl.acm.org/doi/10.5555/1972457.1972488.
- 38. V. K. Vavilapalli, A. C. Murthy, C. Douglas, S. Agarwal, M. Konar, R. Evans, Graves, J. Lowe, H. Shah, S. Seth, B. Saha, C. Curino, O. O'Malley, S. Radia, B. Reed, and E. Baldeschwieler, "Apache Hadoop YARN: Yet Another Resource Negotiator," in Proceedings of the 4th Annual Symposium on Cloud Computing, ser. SOCC '13. New York, NY, USA: ACM, 2013, pp. 5:1–5:16.





[Online]. Available: doi.org/10.1145/2523616.2523633.

- 39. I. Foster and C. Kesselman, "Globus: a Metacomputing Infrastructure Toolkit," International Journal of High Performance Computing Applications, vol. 11, no. 2, pp. 115–128, Jun. 1997. [Online]. Available: doi.org/10.1177/109434209701100205.
- 40. T. Tannenbaum, D. Wright, K. Miller, and M. Livny, "Condor A Distributed Job Scheduler," in Beowulf Cluster Computing with Linux, T. Sterling, Ed. MIT Press, Oct. 2001.
- 41. B. Barney, "SLURM and MOAB tutorial," hpc.llnl.gov/training/tutorials/slurm-and-moab, Lawrence Livermore National Laboratory, Aug. 2017, (Retrieved Apr. 22, 2021).
- 42. K. Ousterhout, P. Wendell, M. Zaharia, and I. Stoica, "Sparrow: Distributed, low latency scheduling," in Proceedings of the Twenty-Fourth ACM Symposium on Operating Systems Principles, ser. SOSP '13. New York, NY, USA: Association for Computing Machinery, 2013, p. 69–84. [Online]. Available: doi:org/10.1145/2517349.2522716.
- 43. X. Zhou, H. Chen, K. Wang, M. Lang, and I. Raicu, "Exploring distributed resource allocation techniques in the SLURM job management system," Illinois Institute of Technology, Department of Computer Science, Tech. Rep., 2013.
- 44. J. Gyllenhaal, T. Gamblin, A. Bertsch, and R. Musselman, "Enabling high job throughput for uncertainty quantification on BG/Q," in IBM HPC Systems Scientific Computing User Group (ScicomP), May 2014.
- 45. J. Yu and R. Buyya, "A Taxonomy of Workflow Management Systems for Grid Computing," Journal of Grid Computing, vol. 3, no. 3, pp. 171–200, Sep. 2005. [Online]. Available: doi.org/10.1007/s10723-005-9010-8.
- 46. E. Deelman, G. Singh, M. H. Su, J. Blythe, Y. Gil, C. Kesselman, G. Mehta, K. Vahi, G. B. Berriman, J. Good, A. Laity, J. C. Jacob, and D. S. Katz, "Pegasus: A framework for mapping complex scientific workflows onto distributed systems," Scientific Programming, vol. 13, no. 3, pp. 219–237, Dec. 2005. [Online]. Available: doi:org/10.1155/2005/128026.
- 47. P. Couvares, T. Kosar, A. Roy, J. Weber, and K. Wenger, Workflow Management in Condor. London: Springer London, 2007, pp. 357–375.



[Online]. Available: doi.org/10.1007/978-1-84628-757-2_22.

- 48. S. Herbein, T. Patki, D. H. Ahn, D. Lipari, T. Dahlgren, D. Domyancic, and M. Taufer, "Poster: Fully hierarchical scheduling: paving the way to exascale workloads," in Proceedings of the 29th ACM/IEEE International Conference for High Performance Computing and Communications Conference (SC), Nov 2017.
- 49. J. M. Wozniak, T. G. Armstrong, M. Wilde, D. Katz, E. Lusk, and I. T. Foster, "Swift/T: large-scale application composition via distributed-memory data flow processing." Proc CCGrid, 2013.

ADDITIONAL SUPPORTING INFORMATION

Flux website: flux-framework.org

Flux promo video: youtu.be/Ylwt51dyXOE

Flux documentation: flux-framework.readthedocs.io/en/latest/

Flux open-source code: github.com/flux-framework

Flux on Twitter: twitter.com/fluxframework

7. AFFIRMATION

I/we certify that all of the information within this submission entry is accurate and represents the most up-to-date information available for this entry.





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