# Makeflow: A Portable Abstraction for Data Intensive Computing on Clusters, Clouds, and Grids

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## ABSTRACT

*In recent years, there has been a renewed interest in languages and systems for large scale distributed computing. Unfortunately, most systems available to the end user use a custom description language tightly coupled to a specific runtime implementation, making it difficult to transfer applications between systems. To address this problem we introduce Makeflow, a simple system for expressing and running a data-intensive workflow across multiple execution engines without requiring changes to the application or workflow description. Makeflow allows any user familiar with basic Unix Make syntax to generate a workflow and run it on one of many supported execution systems. Furthermore, in order to assess the performance characteristics of the various execution engines available to users and assist them in selecting one for use we introduce Workbench, a suite of benchmarks designed for analyzing common workflow patterns. We evaluate Workbench on two physical architectures – the first a storage cluster with local disks and a slower network and the second a high performance computing cluster with a central parallel filesystem and fast network – using a variety of execution engines. We conclude by demonstrating three applications that use Makeflow to execute data intensive applications consisting of thousands of jobs.*[1]

## 1. INTRODUCTION

Many problems in both science and industry ranging from web indexing to genome analysis can be expressed as a graph of small sequential programs with a high degree of parallelism. A number of *workflow systems* [11, 17, 19, 22, 12, 9, 35] have been created to express and execute such programs. While these systems have many virtues, they typically couple a custom language to a custom runtime implementation, making it difficult to move applications across systems, or even to evaluate which system is most appropriate for a given application.

We argue that there has long existed a portable and effective language for data parallel computing. Traditional Make [13], although most commonly used for compiling and linking programs, is also very effective at expressing highly parallel data intensive applications. To this end, we present a new implementation called *Makeflow* (Make + Workflow) that can portably run the same applications across multicore processors, dedicated clusters (SGE), cycle scavenged grids (Condor), storage clouds (Hadoop), and combinations of the above (Work Queue), without requiring any changes to the application or the workflow description. This makes it possible to develop an application on a personal computer, and then seamlessly move it between institutional clusters and commercial clouds without any restructuring.

Of course there have been many *parallel* implementations of Make presented previously [5, 24, 4, 27]. These all assume a homogeneous set of reliable processors, all connected to a common shared filesystem. Makeflow goes beyond these previous systems with a truly *distributed* implementation that runs on heterogeneous, failure-prone distributed systems, taking advantage of data locality when the implementation allows it. To enable this, we require a small but important change to the semantics of Make: *data dependencies must be completely elaborated.* (To be clear, Makeflow is designed for data intensive scientific applications, and is not particularly suited for compiling and linking programs.)

Because Makeflow provides transparent portability of applications across systems with significantly different properties, it allows us to perform an objective comparison of the relative capabilities of each system for different types of workloads. To this end, we have created *Workbench*, a system-independent set of workflow benchmarks that measures dispatch latency, job throughput, I/O throughput, and interprocess communication. We evaluate Workbench on two distinct architectures – a storage cluster and a high performance computing cluster – using each of the execution engines supported by Makeflow. These results help the end user to select the right type of execution system for the workload at hand.

Makeflow is open source software that is currently in production use by a number of scientific communities. We conclude with a discussion of several bioinformatics and biometrics applications using Makeflow at Notre Dame.

Several previous publications have mentioned Makeflow in passing. A journal article [34] and a book chapter [29] briefly discuss Makeflow as an example of one of several kinds abstractions for distributed computing. This is the first publication to discuss Makeflow in detail, to present the Workbench benchmarks, and to evaluate workloads across multiple implementations.

## 2. THE MAKEFLOW LANGUAGE

The Makeflow language is very closely related to the traditional language of Make [13]. A valid Makeflow program consists of a sequence of assignments and rules. An **assignment** indicates the name and value of an environment variable, which applies to all

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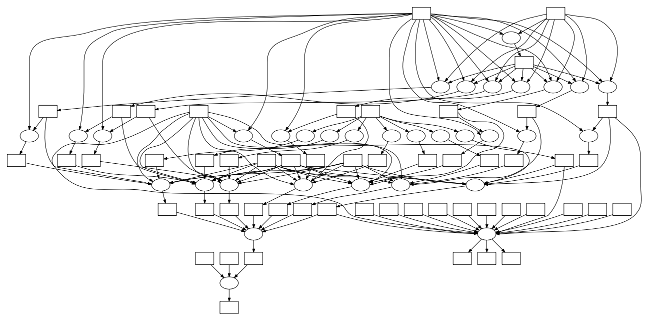


Figure 1: Example of a Bioinformatics Application in Makeflow

following items in the file. A **rule** indicates a command line to be executed, along with the input files required by that command, and the output files that it will create.

A Makeflow rule has slightly different semantics than traditional Make. Traditional Make simply requires that a rule state only the files that may have changed, but assumes that any other file in the filesystem is available for use by the command. In contrast, a Makeflow rule must accurately specify *all of the files* that a command requires as both input and output, because this is used to create the correct execution environment.

For example, this is an **incorrect** Makeflow rule:

```
out.dat:
   simulate.exe in.dat -o out.dat
```

In contrast the following rule is **correct**, because it specifies all of the input dependencies, including the executable and data file:

```
out.dat: simulate.exe in.dat
   simulate.exe in.dat -o out.dat
```

Figure 1 is a visualization of a relatively small bioinformatics job expressed in Makeflow, consisting of 33 jobs (circles) and the interdependent files (squares). In practice workflows are often very large, consisting of thousands to millions of jobs processing terabytes of data. (The largest are difficult to present in graphical form.) As seen in Figure 1, the graphs may be highly irregular and thus not easily expressed in a fixed abstraction such as Map-Reduce [11]. Once a workflow is expressed with fully elaborated data dependencies, a number of opportunities for executing the workflow efficiently and scalably become possible:

- **Job migration.** When the full dependencies of each job are known the single job may be moved to a remote execution site without requiring any particular runtime support on a shared filesystem. This enables harnessing of resources that are outside the immediate execution environment.

- **Workflow migration.** When the inputs and outputs of the whole workflow are known it becomes easy to move the entire workflow to another site. For example, one might allocate a cluster on a commercial cloud, send the inputs, execute the entire workflow remotely, and then retrieve the outputs.

- **Workflow decomposition.** Given sufficient information about jobs and data it may make more sense to partition the graph and run sub-graphs in distinct systems. As we show below, some execution systems are more effective at partitioned data and others are better at shared data.

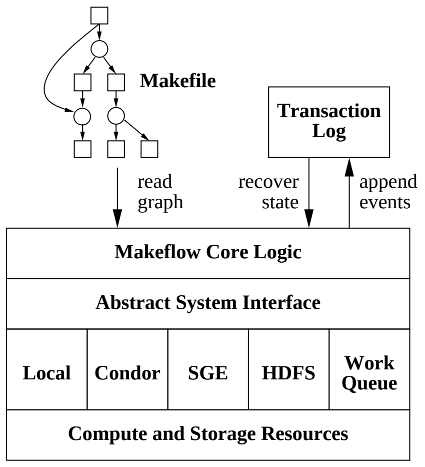


Figure 2: Architecture of Makeflow

- **Co-location of computation and data.** When operating on distributed data it is often beneficial to move computation to where the data is located or vice versa. With information about the data needs of each application an implementation of Makeflow can seek to put them together.

- **Resource management.** Cloud computing environments in particular require the user to make resource management decisions: allocating more machines always costs more money but may not necessarily improve performance. Accurate information about the computation and data needs of a workload makes it feasible to select appropriate resources for an execution.

In order to exploit these management and performance properties we have very deliberately chosen **not** to include any of the higher-order constructs found in other versions of Make, such as implicit and pattern rules. For example, if we include pattern rules then it is no longer possible to measure the width or depth of the graph without actually executing it. Makeflows must also be acyclic. Cycles introduce ambiguity into the correct execution and are only grudgingly permissible in traditional Make due to pattern rules, which Makeflow excludes. Furthermore, as in traditional Make there is no inherent facility for time-sensitive execution. Makeflow is a static declarative specification and nothing more.

We have not found any of these exclusions to be a serious limitation in practice: where more dynamic behavior is needed it is accomplished by writing a script which generates the desired workflow, which can then be processed as an independent step. (See our earlier paper on Weaver [6] for examples.) Essential non-infinite cycles can usually be accommodated with renaming and incremental names, and time-sensitive execution can be accomplished via `cron` or simple shell scripts. By analogy, HTML has achieved universal success by aiming simply to be a declarative statement of the structure of a web page; programmability has been obtained by a variety of languages that generate HTML.

## 3. IMPLEMENTATION

We have created an initial implementation of Makeflow that executes complex workflows effectively on several different execution platforms. Our implementation is open source software under active development, with a growing user community. [2] The work here

[2]http://www.nd.edu/~ccl/software

describes version 3.4.2 of the software, and exploits many (but not all) of the opportunities made possible by the graph representation.

Figure 2 shows the architecture of the current implementation. The user provides a workflow in the form of a Makefile, then executes the `makeflow` program. The Makeflow core logic manages the graph of processes and data, submits jobs to the abstract system interface, and records events in a transaction log. The abstract system interface provides an API for submitting a single job at a time, indicating input and output dependencies, and the ability to wait for the completion (or failure) of any previously submitted job. Drivers for multiple execution systems are hidden behind the abstract interface, and include Local execution, Condor, Sun/Oracle Grid Engine, Hadoop, and Work Queue, which we describe below. Events in the life of the workflow are recorded in a transaction log, which is used for both failure recovery and system monitoring.

## 3.1 System Drivers

Two details of the system drivers are worth noting. First, each driver is a combination of a computation environment with a tightly-coupled storage system. *Local* is actually *Local processes and a local filesystem*, while *Condor* is actually *Condor execution with file transfer*, and so forth. Each represents a significantly different method of accessing data at runtime. We will elaborate on these properties in each section below, but use the short name for clarity.

Second, we have found that many execution environments have poor support for monitoring the status and completion of many jobs asynchronously. All provide some interactive command or web page for observing system or job status, but this is unwieldy to access from within Makeflow because the information may be presented poorly, or the call may be very slow to invoke. Thus in each case we describe the method by which we monitor the status of executing jobs, and in many cases it involves a creative workaround to bypass the limitations of the system.

**Local Driver.** In Local execution mode, all jobs with satisfied data dependencies are forked as new processes that execute on the local machine. Makeflow then monitors the status of each child process and marks the job description as completed or failed once the child exits. The local engine uses the local filesystem as its storage component. Where multiple cores are available, multiple processes can run simultaneously. Local execution is often used for testing workflow descriptions to ensure they are constructed properly before scaling up.

Users can recommend local execution for specific jobs even when executing on a distributed system by prefixing the rule with the `LOCAL` keyword. This informs Makeflow that a particular command is optimally run locally, due to filesize, permissions, or configuration constraints, while still allowing the command to be managed as part of the workflow.

**Condor Driver.** Condor [30] is a distributed batch computing system that can be used across hardware ranging from desktop machines to high performance clusters. Condor provides a comprehensive matchmaking system to match jobs to their hardware requirements as well as to ensure fair usage of shared resources without inconveniencing their owners.

Figure 3 shows the interaction between Makeflow and Condor. For each job to be executed, Makeflow creates a job submission file and invokes `condor_submit`, which queues the job with the local `condor_schedd` daemon. The job submission file indicates the input and output files required for the job. `condor_schedd` communicates with the matchmaker to find a compatible execution machine. At the execution site, the input files are retrieved from the submission site, the job is executed, and output files are moved back. When multiple jobs execute simultaneously, the trans-

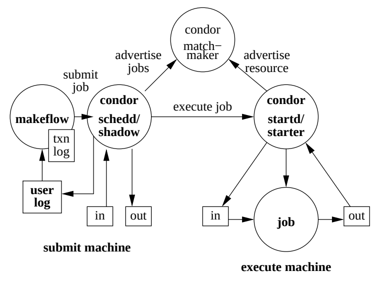


Figure 3: Makeflow on Condor

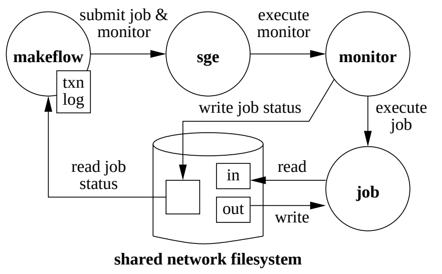


Figure 4: Makeflow on SGE

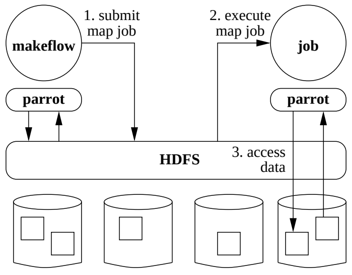


Figure 5: Makeflow on Hadoop

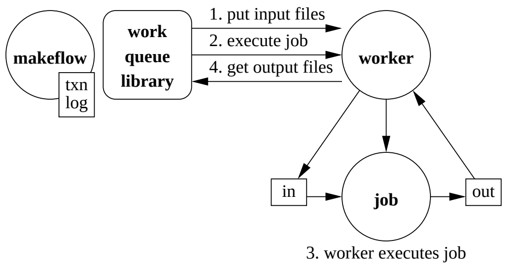


Figure 6: Makeflow on Work Queue

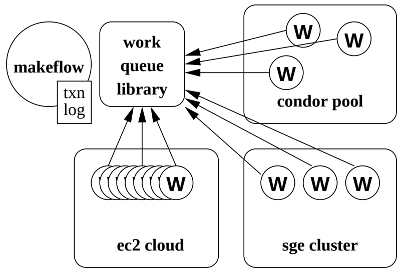


Figure 7: Building a Private Cloud with Work Queue

fers may happen concurrently.

To provide lightweight notification of job status Condor produces a *user log file* that indicates when a job starts, completes, migrates, and so forth. Makeflow monitors job status by periodically looking for new data appended to the file.

**SGE Driver.** Sun/Oracle Grid Engine (SGE) [14] is a batch system for managing large clusters. SGE schedules jobs across the nodes in a cluster, typically requiring the use of a shared filesystem such as NFS or AFS to provide uniform data access across the cluster. Unlike Condor, the queue of jobs in SGE is stored in a centralized location, which exercises absolute control over each node in the cluster.

Figure 4 shows the interaction between Makeflow and SGE. To submit a job, Makeflow invokes the `qsub` command, indicating a `wrapper` script and an executable. No information about required data is communicated. The job is run in the shared filesystem where the `wrapper` script can be accessed and executed by the node. The job's executable and its data are also accessed through the shared filesystem. The `wrapper` script writes to a log file the job's start time, completion time, and exit status. Makeflow monitors the log files of all running jobs to observe completion events.

**Hadoop Driver.** Hadoop [17] is an open source implementation of the Map-Reduce [11] distributed computing concept. HDFS is the file system component, corresponding to Google GFS [15]. Normally, to interact with Hadoop, one submits a Java program with a Map component and a Reduce component. This program is distributed to all nodes simultaneously and used to construct the graph of communicating processes.

It can be challenging to convert an existing application to a Map-Reduce form. A native Map-Reduce translation must accept input data via the `RecordReader` class, which may return records from any arbitrary point in the input file. The programmer writing the translation must decide how to divide program logic among the Map and the Reduce components and how to partition data horizontally, neither of which may have obvious solutions. Finally, many translated applications will require multiple invocations of Map-Reduce to complete the computation, adding overhead on each pass.

Legacy applications can be run using the Hadoop streaming wrapper. However, Hadoop streaming passes its input data to the wrapped command via standard input and assumes that the application can handle arbitrary splits in the input file. For applications that rely on accessing whole files the most common workarounds either ignore any data locality or run the risk of repeating jobs, potentially corrupting any output files. Furthermore, this still requires a potentially brand-new user to construct a wrapper script and learn the appropriate Hadoop and HDFS commands.

With Makeflow our objective is to make it possible to run existing, unmodified applications within the Hadoop environment, achieving acceptable parallelism and performance with minimal effort by the user. If all the user's code and data are already in Hadoop, Makeflow provides a way to execute applications that are not obviously of a Map-Reduce form.

Figure 5 shows how this is achieved. Makeflow passes its jobs to Hadoop as single-node Map-only jobs. Each job consists of the streaming wrapper program, the desired executable and the name of its input dependencies. Hadoop will then execute the job, ideally on a node close to the input data. The job is completely unaware of the Map-Reduce framework and will attempt to access files in the normal way through the filesystem. To enable this, we rely on the Parrot [28] interposition agent to transparently convert the application's system calls into the analogous HDFS library calls. (FUSE [1] can also be used for the same purpose but may require administrator permissions to install.) Makeflow spawns individual streaming commands for each job and tracks the exit codes to determine success or failure.

**Work Queue Driver.** Most of the available job execution engines are managed via a queue system, where jobs are submitted to a central manager which then dispatches jobs based on the available resources and system policies. As we show below this can result in long dispatch times with jobs sitting in a queue for minutes or longer. For long-running or data-intensive jobs this dispatch time may be subsumed by the computation time of the job itself; for a job which consists of huge numbers of short-running independent jobs the problem can be mitigated by batching many together; but for a workflow containing many small jobs, where most are dependent on the output of one or more previous jobs, this type of system may impose 10-100 or more seconds of wait time for each second of computation.

To address this problem we have created Work Queue, a master-worker framework designed to work natively with Makeflow. Work Queue provides fast invocation times, local storage management, and a means to rapidly deploy an execution environment for the user that is not already invested in a batch system.

Figure 6 shows the relationship between Makeflow and Work Queue. The system consists of a lightweight worker process and a master library which is linked into Makeflow. Workers may be submitted as jobs to one or more distributed systems (such as Condor or SGE), or run by hand on machines accessible to the user. As the workers are run, each initiates a TCP connection to the Makeflow process. The tasks for execution are stored in an internal queue within Makeflow, and executed as resources become available. To execute a job, the master simply transmits the required input files, tells the worker to execute a command line, and then retrieves the outputs. Both inputs and outputs can be cached at the worker with the knowledge of the master, so that commonly used data does not need to be re-transmitted.

The Work Queue system achieves fault tolerance in the following manner: The connection between each worker and the master is via TCP. If the worker or the network fails the master drops its internal record of the worker, assumes any running job failed, and reschedules it for another worker. If the master or the network fails the worker stops the running job, cleans up any cached data, and then attempts to connect again, up to a configurable timeout. The system safely accepts workers joining and leaving at runtime, albeit with some performance penalty.

By having the Makeflow process manage the individual tasks the negotiation or matchmaking time required by many underlying execution systems can be amortized across all of the tasks executed by a worker rather than incurring that cost on each individual task. Additionally, Figure 7 shows how Work Queue can be used to combine resources from multiple sources into a single "private cloud". The Worker process can be submitted as a batch job to systems such as Condor and SGE or executed on resources allocated from a commercial cloud. Regardless of how the worker is started, it contacts the master process and begins to execute jobs and cache data. From the perspective of Makeflow the set of workers forms a cloud of both computation and storage resources.

## 3.2 Transaction Log

As Makeflow processes a workflow it produces a transaction log. This is a complete description of the life of the workflow, including all job submissions, completions, and failures. The log file serves two purposes: it facilitates recovery from failures and it provides data for troubleshooting and performance analysis. The log is kept by Makeflow at the submission site, and is independent of the various logs produced by the batch systems.

Fault tolerance is critical in a distributed computing environment. Makeflow must operate with multiple distributed computing systems over the wide area, each with their own peculiar failure modes. It is not uncommon for the network or a batch system to fail during a job execution. A job within a workflow might run for hours or days, during which time Makeflow may become disconnected from the batch system or killed outright. A careless approach to job submission may result in multiple jobs being submitted unnecessarily, or orphaned jobs left running in the system with no corresponding record in Makeflow.

To address these problems, every event in the lifetime of a job is recorded in the transaction log. Rather than rely on the presence of files (as traditional Make would), Makeflow examines the transaction log to recover the state of running jobs. This allows Makeflow to crash and restart while its jobs continue to run. If Makeflow receives a signal to abort it works to remove jobs from the batch system, logging as it goes. Interacting with the batch system can take time, so if Makeflow crashes and restarts during an abort it will pick up the current state and then continue to abort cleanly.

Ideally, batch systems would facilitate this by providing an interface for *two-phase commit*. This would allow Makeflow to first request a job number from the batch system, record it to the transaction log, and then commit the job within the system. To our knowledge, no batch system provides this through a public interface. (Condor does this internally, but does not expose an API.) As such, our implementation has a short time window in which a failure could result in duplicate job submission.

The use of the log has the side effect that Makeflow can be killed and moved to a completely different machine, and as long as the corresponding workflow, transaction log, and dependencies are available, the workflow can be restarted without duplicating work. It also allows the user to switch execution engines mid-workflow. If the initial execution engine bogs down under external strain or part of the system fails permanently the user can stop the workflow and restart it using a different engine while preserving all of the work done up to that point.

The provenance information provided by the transaction log also makes debugging, performance analysis, and job status monitoring much easier. By maintaining the logs of which jobs fail, how many times they are retried, and what times the failures occur, it makes tracking down the problem easier. The details of the log file allow users to keep track of which jobs are unexpected bottlenecks or how close to completion the workflow is. The real-time timestamps allow the user to correlate job events with the logs maintained by many of the Makeflow subsystems in order to identify problems with the subsystem as well as to correctly identify which failures are due to the application itself and which are caused by the execution engine.

## 4. WORKBENCH

Makeflow allows one to run workflows across several different execution engines and physical architectures, including multicore systems, shared-nothing clusters, shared-filesystem clusters, and distributed transient caches. As a result, one would expect that different kinds of workflows would be better suited to different kinds of architectures.

To evaluate the essential performance characteristics of a system, we created Workbench, a set of simple workflow benchmarks implemented using Makeflow. Figure 8 shows the basic patterns, which are parameterized to run at various scales. Of course, none of these patterns is representative of a complete workflow; each exercises a different aspect of the system, including dispatch overhead, job throughput, I/O throughput, and interprocess communication. By understanding these basic parameters we can better judge the expected performance of a real workflow, which consists of many of these patterns put together.

We note that Workbench very deliberately exercises the *pathological cases* in workflow performance. We expect that any execution system would be effective at running a large number of independent processes that each run for hours with minimal input and output. The differences between systems are apparent only in the cases that stress I/O and/or large numbers of short jobs.

The five Workbench patterns are:

**Chained(J,T)** consists of a chain of $J$ jobs running for $T$ time, each producing one empty output file that is consumed by the next. When $T = 0$ the chained benchmark measures the average latency to submit a job, which puts a lower bound on the execution of any job. As we show below, many systems have a surprisingly high job latency.

**Concurrent(J,T)** consists of a set of $J$ independent running for $T$ time and producing no input or output. This benchmark measures the throughput of job dispatch and completion. If $T > 0$ then the throughput is likely to vary with the number of available processors.

**FanIn(J,T,F,S)** consists of a set of $J$ jobs running for $T$ time, each reading $F$ files of size $S$ as input. This benchmark measures the ability of the system to deliver input data. At large $F$ but small $S$ it stresses the number of file transactions, while at small $F$ and large $S$ it stresses the total data throughput.

**FanOut(J,T,S)** consists of a set of $J$ jobs running for $T$ time, with a common file of size $S$ as an input and independent files of size $S$ as outputs. This type of workflow is common in simulations, where the input file represents the starting data and each job is one run of the simulator with varying input parameters. The benchmark measures how well a system can exploit commonality of input data, typically when $S$ is large and $J$ is less than the number of cores.

**Map(J,T,S)** consists of $J$ independent jobs running for $T$ time, each of which reads one input file of size $S$ and writes one output file of size $S$. Maps occur in many transformative workflows, where a series of operations are performed on each of many input files, such as video transcoding or data exploration workflows. The Map benchmark also allows us to measure the aggregate I/O capacity of the system on independent tasks.

## 5. EVALUATION

We evaluate the Workbench benchmarks on two different physical architectures and four software systems.

The first architecture is a Storage Cluster (SC) that reflects the hardware philosophy of commercial clouds: large numbers of shared-nothing machines with large local disks, cost-effective commodity processors, and inexpensive mid-speed network interlinks. The

| | **Storage Cluster** (SC) | **High-Performance Cluster** (HPC) |
|---:|:---:|:---:|
| Size | 26 Machines | hundreds |
| CPU | 2.4 GHz 16-core Intel Xeon | 2.6 GHz 6-core AMD Opteron |
| RAM | 2GB per core | 2GB per core |
| Local Storage | 20TB SATA | 160GB SATA |
| Network Bandwidth | 1 Gb/s Ethernet | 10 Gb/s Ethernet |

Table 1: Cluster Statistics

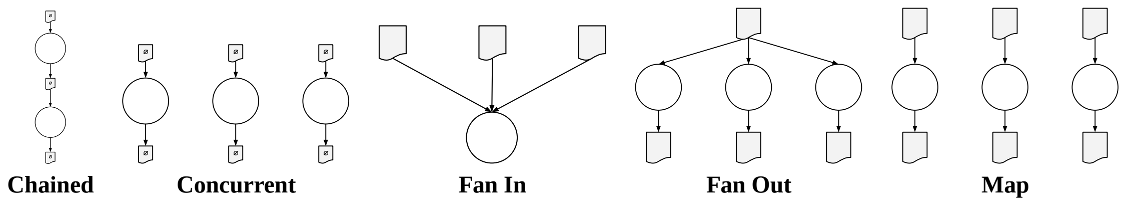


Figure 8: The Five Workflow Benchmark Patterns

second architecture is a High Performance Cluster (HPC) that reflects a more traditional cluster architecture: large numbers of machines that share a common high-performance filesystem and have minimal scratch disk on each machine, along with a high-speed network connection for communication. The capabilities of the two systems can be seen in Table 1. We evaluated the Condor and Hadoop systems installed on the Storage Cluster and SGE on the High-Performance Cluster. Work Queue was able to be run on both.

The results of these benchmarks are a function of both the physical architecture of the clusters available to us and the design of the software system in use. As such, we caution the reader not to compare the absolute results across clusters. Rather, the results reveal to what extent each software system can exploit the unique properties of each cluster.

To establish a baseline for I/O operations, we measured the maximum throughput achievable by a single client on each cluster, shown in Table 2.

| System | Storage | Read (MB/s) | Write (MB/s) |
|---|---|---|---|
| SC | Local | 137.24 | 549.24 |
| SC | HDFS | 19.78 | 55.94 |
| HPC | Local | 110.73 | 290.50 |
| HPC | NFS | 93.14 | 133.29 |

Table 2: Basic I/O Throughput

**Job Latency and Throughput**. To measure the latency of job submission we ran `Chained`$(128, 0)$ and to measure the throughput of job submission we ran `Concurrent`$(128, 0)$ on all configurations. The results are shown in Table 3.

| System | Engine | Latency | Throughput |
|---|---|---|---|
| | | Sec/Job | Jobs/Sec |
| SC | Local | 0.006 | 227.928 |
| SC | Condor | 28.065 | 1.940 |
| SC | Hadoop | 23.340 | 0.417 |
| SC | WorkQueue | 0.060 | 11.424 |
| HPC | WorkQueue | 0.016 | 115.711 |
| HPC | SGE | 7.659 | 6.261 |
| HPC | Local | 0.016 | 229.688 |

Table 3: Chained and Concurrent Results

The results of these tests demonstrate that the real bound on job throughput is the submission time of the system. Systems like Work Queue that are controlled and scheduled directly by Makeflow have relatively short dispatch times and can push out 100+ jobs/second. In contrast, systems like Condor and Hadoop that use an external scheduler have dispatch times orders of magnitude larger. Constrained as they are by the speed of the system's native dispatcher these drivers can only start at best a few jobs each second.

**File Transfer**. To measure the whole file throughput of each system we run `FanIn`$(1, 0, 1-256, \text{1MB})$ and varied the number of files in powers of two. The results are shown in Table 4.

In this test we see significant differences in the ability of each system to complete small file transactions. The distributed execution systems are all at least an order of magnitude worse than local storage, as they must transfer any files over a network. Work Queue's simple file transfer protocol manages to transfer files slightly faster than Condor or Hadoop to the Storage Cluster, but is handily beaten by the high-speed central fileserver utilized by SGE on the High Performance Cluster. Condor and Hadoop end up with similar performance numbers, reflecting the slower dispatch times required by negotiating job placement or packaging and setting up the Hadoop streaming jobs, balanced by the increased parallelism in file transfer.

**Aggregate I/O**. To measure aggregate I/O performance on large workflows, we ran `FanOut`(128, 0, 1MB/16MB/64MB) and `Map`(128, 0, 1MB/16MB/64MB) on both clusters. The SC results are shown in Figure 9 and the HPC results are shown in Figure 10.

For the Storage Cluster architecture the results indicate that when dealing with small files (a few MB or less) systems with minimal overhead and short dispatch times like Work Queue will likely dominate, achieving remarkably steady throughput regardless of the number of workers used. As the size of the files increases this gap closes. Work Queue's caching behavior provides a natural advantage for computing Fan-Out patterns, allowing it to maintain its performance lead up through 64MB files.

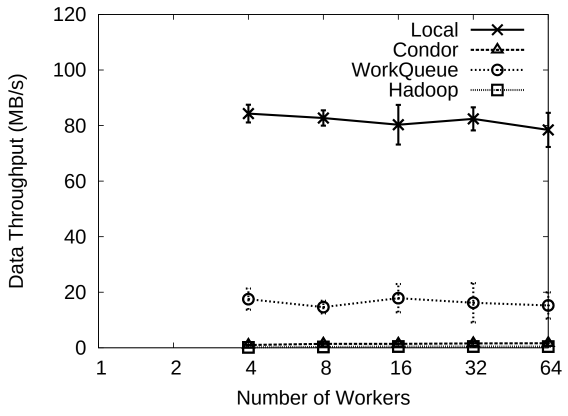
For Map patterns, where each file must be transferred fresh across the network, both Condor and Hadoop begin to catch up. At filesizes around 16MB Condor consistently achieves better performance than Hadoop, reflecting Condor's substantially better job throughput for independent jobs. At 64MB Condor catches up to Work Queue, as the time taken to transfer the data begins to substantially outweigh the submission times of each system.

The results on the HPC also demonstrate the dominance of short submission times when working with low file sizes. Even compared to SGE, which is supported by a large, fast, parallel filesystem, Work Queue still performs the best at small filesizes.

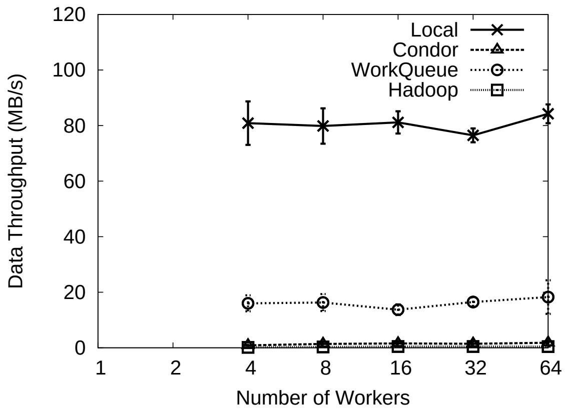
SGE's advantage in parallel acquisition of files begins to emerge earlier than Condor or Hadoop. At large numbers of workers for even 16MB files SGE begins to perform better than WorkQueue,

| System | Engine | Files / s |
|---|---|---|
| SC | Local | 911.54 |
| SC | Condor | 7.37 |
| SC | WorkQueue | 8.54 |
| SC | Hadoop | 6.18 |
| HPC | SGE | 23.53 |
| HPC | Local | 475.75 |
| HPC | WorkQueue | 13.00 |

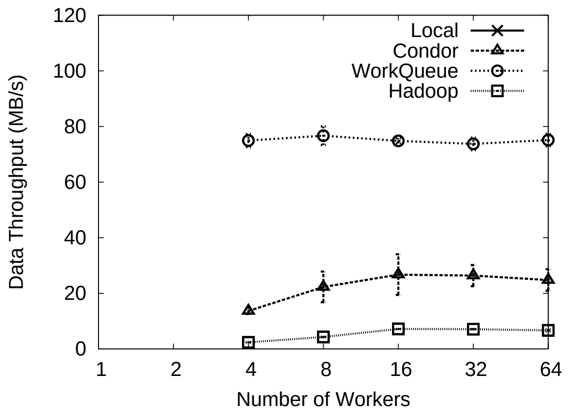
Table 4: FanIn 256 1MB Files



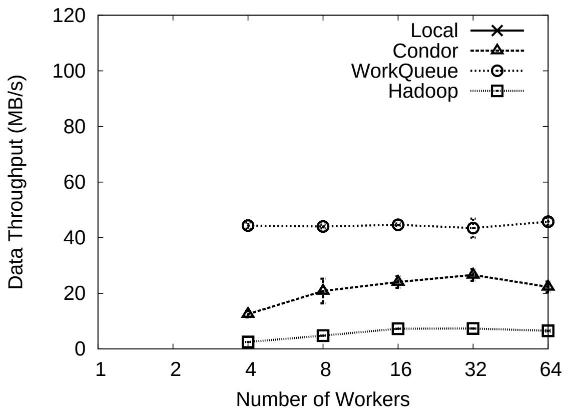
(a) FanOut 1MB



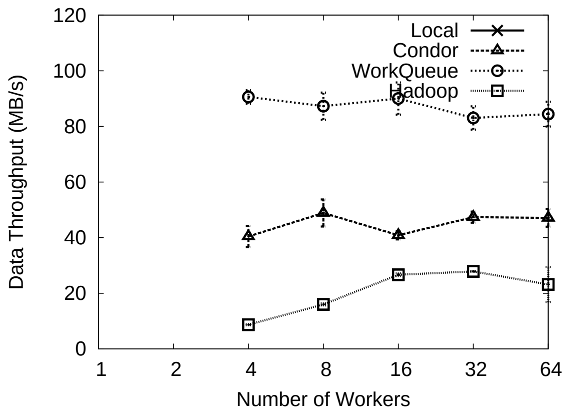
(b) Map 1MB



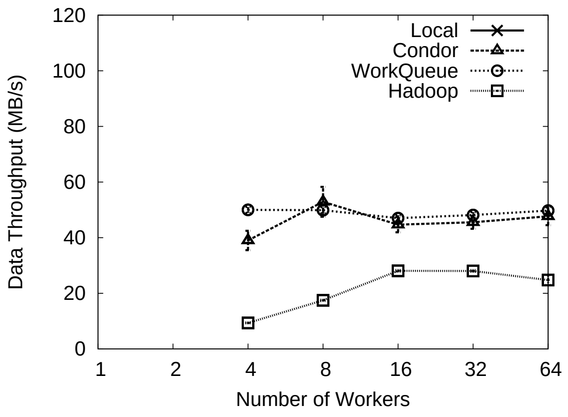
(c) FanOut 16MB



(d) Map 16MB

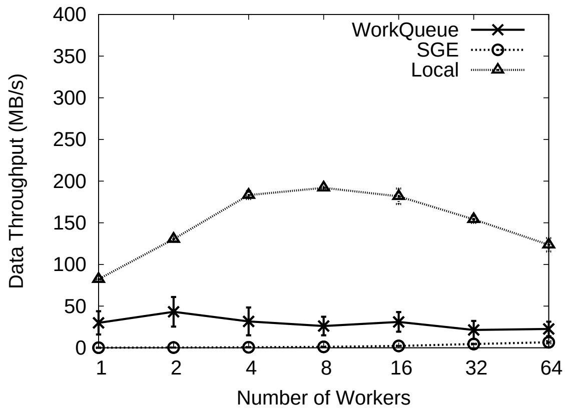


(e) FanOut 64MB

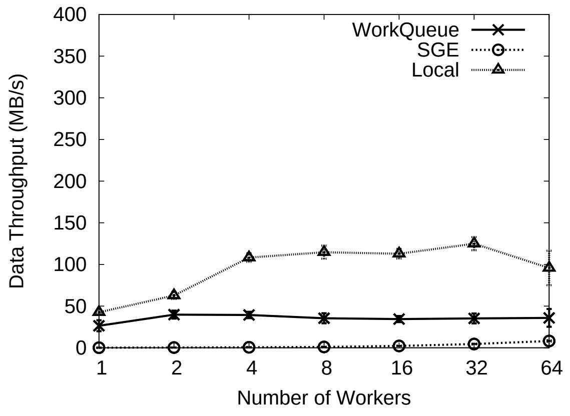


(f) Map 64MB

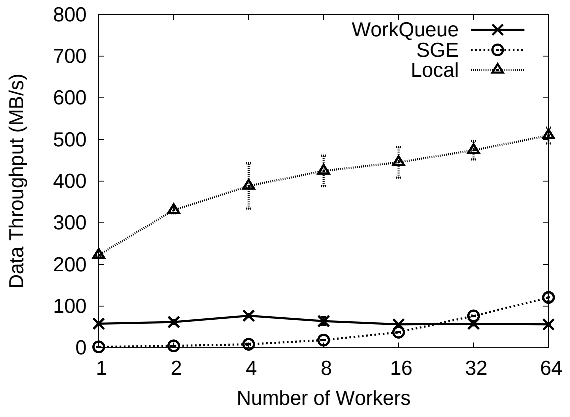
Figure 9: **Storage Cluster: Fan-Out and Map** These graphs display the average and standard deviation of data throughput for data intensive workflows, Map and FanOut. The workers execute the *cat* function on the input to create a copy output file. The data throughput is calculated based on the size of the input data being *read*. The time used to calculate this value also includes the time taken to return output, that is, *write* data. To keep runtimes reasonable, the benchmarks omit numbers for 1-2 workers on Condor and Hadoop.



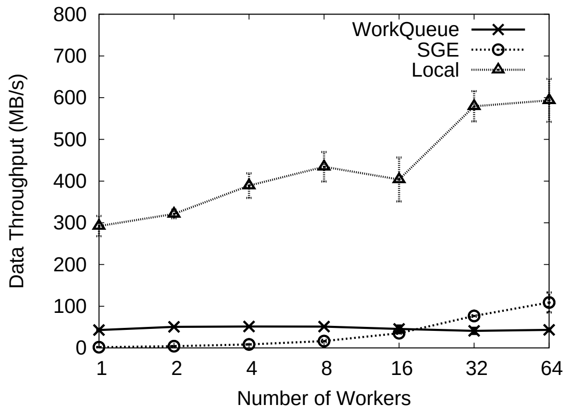
(a) FanOut 1MB



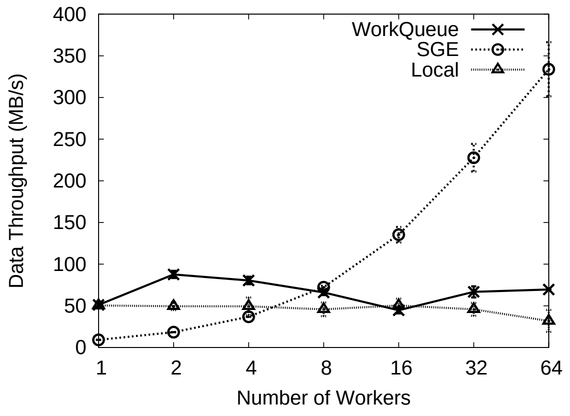
(b) Map 1MB



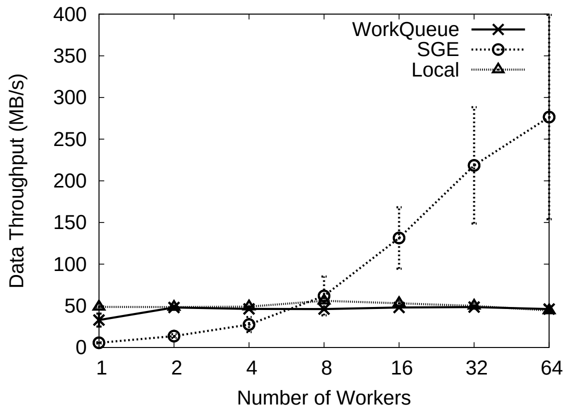
(c) FanOut 16MB



(d) Map 16MB



(e) FanOut 64MB



(f) Map 64MB

Figure 10: **High Performance Cluster: Fan-Out and Map** These graphs display the average and standard deviation of data throughput for data intensive workflows, Map and FanOut. The workers execute the *cat* function on the input to create a copy output file. The data throughput is calculated based on the size of the input data being *read* . The time used to calculate this value also includes the time taken to return output, that is, *write* data.

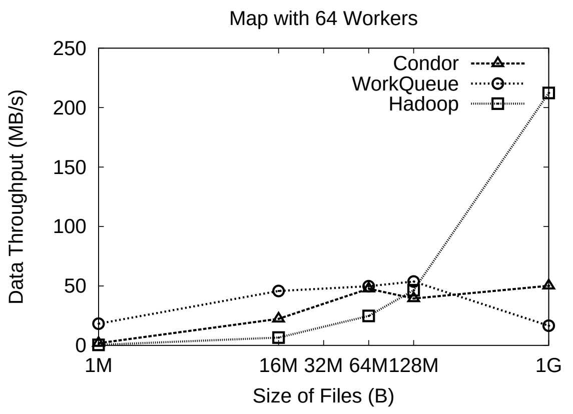


Figure 11: Large File Transfer

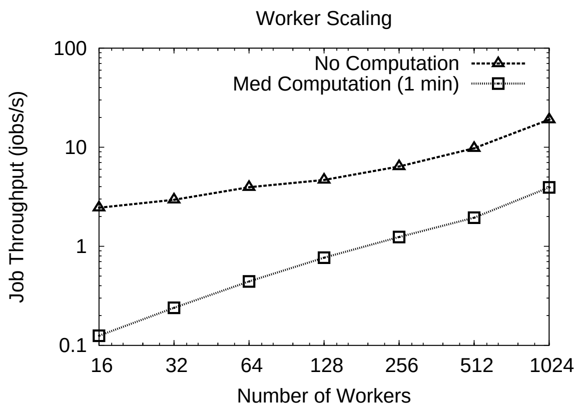


Figure 12: Worker Scaling

reaching twice the data throughput with `Map`$(128, 64, 0, 16\text{MB})$.

At the largest filesizes SGE quickly dominates both other systems. Lacking the bottleneck of sending all of the requisite data through a single master process, SGE is able to satisfy each worker's data dependencies faster and thus achieve much better performance than Work Queue.

**Large File Transfer**. Given Hadoop's bias towards working with large data sizes we were curious to see how well it scaled. We ran additional tests `FanOut`(128, 64, 0, 128MB/1GB) and `Map`(128, 64, 0, 128MB/1GB) on Hadoop, Condor and Work Queue. The results can be found in Figure 11.

As previously demonstrated, both Work Queue and Condor perform substantially better for small file sizes. For the 128MB test the three systems perform approximately the same, each obtaining a throughput of about 40-50MB/sec. Once the filesize grows to 1GB, Condor's performance seems to have plateaued, likely due to network saturation across the slower campus links. Work Queue, due to its need to transfer files serially, obtains very little parallelism and thus ends up reducing performance.

Hadoop's performance, on the other hand, dwarfs that of Condor and Work Queue by at least a factor of four. This is in large part due to the ability to harness the disk output of an entire cluster combined with the cluster's relatively high-speed internal network.

**Work Scaling** In order to examine Makeflow's ability to scale to large worker pools we ran some additional concurrency tests at relatively high worker count. We ran `Concurrent`$(2048, 0)$ and `Concurrent`$(2048, 60)$ on worker pools of various sizes (between 16 and 1024 simultaneous workers). The results are shown in Figure 12. The job throughput numbers scale directly with the number of workers, in proportion to the amount of computation time for each individual job.

## 6. APPLICATIONS

Makeflow is available as an open source project and has a growing community of users building scalable applications in fields such as bioinformatics, image processing, data mining, and molecular dynamics. In this section we will give some examples of non-trivial makeflows and our experience in executing them at large scale.

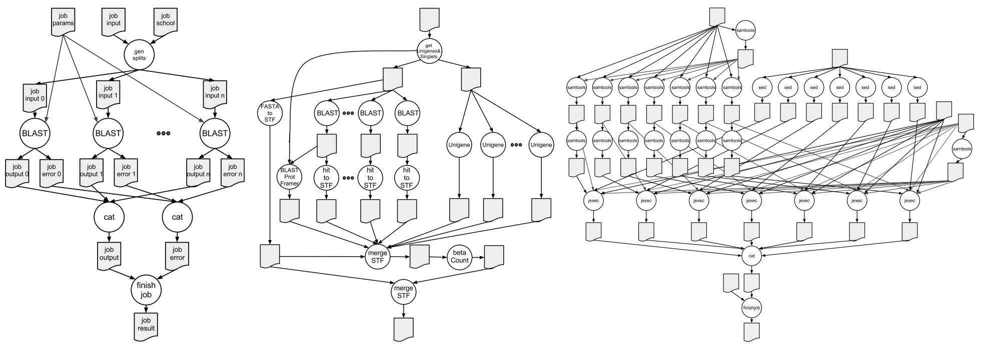
While Makeflow's simplicity makes it useful as a prototyping tool or a mechanism for domain scientists to write their own distributed applications, it is also useful for running large workflows in an efficient manner. Regularly, Makeflows will run harnessing hundreds or thousands of workers to process hundreds of gigabytes of image, video, and/or genomic data in support of biometrics research, bioinformatics research, and more. Some of the more extreme examples of these workflows can be seen in Figure 13.

**Biocompute**. An early adopter of Makeflow was Biocompute [7], a bioinformatics data analysis facility at the University of Notre Dame. Users interact with the system via a web portal to select various applications, choose parameters and input files, and then run various data analysis jobs.

The first implementation of Biocompute ran only BLAST [3] jobs, required custom-designed scripts for each stage of the backend processing, and only ran on the Notre Dame Condor pool. It was complex to implement, difficult to modify, and very failure prone because of the large number of component parts that interlocked in complex ways. The second implementation of Biocompute was developed using Makeflow for expressing these workloads. Instead of writing, testing, and debugging custom scripts to handle data management and fault tolerance for each basic module, these tasks could be delegated to Makeflow itself. Furthermore it became easy to implement more complicated workflows harnessing bioinformatics tools such as SHRiMP, SSAHA, or SNPexp. The same infrastructure for submitting, running, monitoring and reporting the status of each BLAST job could be reused and maintained independently of each workflow, and new types of workflows can be introduced by merely setting up an interface page and writing a module to generate the necessary workflow. Figure 13 shows a selection of these applications.

**BLAST***(Fig 13a)*. The primary use of Biocompute is to allow users to run their BLAST jobs against large reference databases in a reasonable amount of time. Most attempts to parallelize BLAST take one of two approaches. The first approach, taken most famously by mpiBLAST [10], is to segment the database and run the entire set of query sequences against each segment in parallel. The second approach, used by AzureBLAST [20] among others, is to distribute multiple copies of the reference database(s) and split up the set of query sequences, running each query sequence against the entire reference database in parallel.

Biocompute takes the second approach to distributed BLAST. Query sequences are provided by users via a web portal and partitioned for processing. The tasks are then coded into a makeflow and run by the Biocompute server. Due to the frequency of requests the large reference databases have been prestaged to known nodes, and the execution of the Makeflow is limited to only those nodes with databases present. While this somewhat limits the achievable parallelism, we've found the time savings for data transfer to outweigh those limitations.



(a) BLAST Diagram (b) EST Diagram (c) SNPExp Diagram

Figure 13: Biocompute Workflows

Biocompute runs an average of 785 BLAST subtasks per day against reference datasets totaling up to 128 GB of unique genetics data per task. It has been operating without major interruption for three years, marshaling approximately 23 CPU days of useful computation per day of real time.

For practical reasons the BLAST workflows are constrained by the number of nodes to which we have prestaged the large BLAST databases. Replication is based on frequency of use, and has resulted in replicated reference database size upwards of 2.8 TB in total. This limits the number of workers potentially available to any BLAST makeflows in theory but prevents the campus network and storage systems from being overwhelmed.

The limit imposed by our prestaging requirement also means that the largest BLAST workflows can run for days or even weeks, subjecting them to system disturbances like network or filesystem failure. Figure 14a provides a good example with hiccups on days 4, 8, 12, and 16 causing the number of workers running to drop to zero. Makeflow recovers from these disruptions, returns quickly to full operating capacity and completes the job without losing much, if any, work.

**EST Pipeline***(Fig 13b)*. One of Makeflow's major advantages is that it is easy for researchers who are experts in a field other than distributed systems to pick up and use. One example of this is the work done by Thrasher, et al. [31] in developing a pipeline for the analysis of Expressed Sequence Tags, or ESTs.

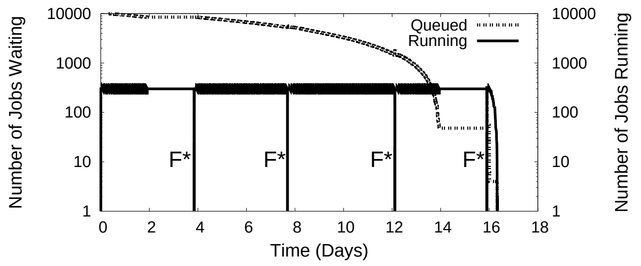
The EST Pipeline was originally developed as a series of scripts with multiple dependencies on uncommon and custom-built libraries. The pipeline was designed to be run by hand on a single machine with all of the relevant dependencies preinstalled. Makeflow, with its ease-of-use and integral dependency tracking, was able to exploit a fair amount of natural parallelism within the EST pipeline and provide a scalable solution portable between the Condor, SGE, and Work-Queue based systems available at Notre Dame.

The EST Pipeline workflow is dynamically generated by the Weaver workflow compiler [6] based on user-provided input data. The workflow is typical of many bioinformatics applications. Input data is initially split for parallel processing, followed with a chain of intermediate steps massaging data into readable forms and processing it with the desired bioinformatics tools. After processing is complete the results are then usually combined into a single report for the scientist to examine.

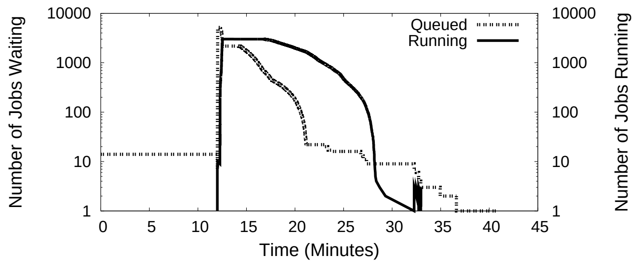
Figure 14b provides a good example of an EST Pipeline workflow taxing the boundaries of the systems we have available. The EST pipeline shows a reasonable queuing period before jumping to well over 2000 concurrently running jobs, a number that slowly degrades as the remaining work in the queue is exhausted. By harnessing an extreme amount of parallelism the EST Pipeline manages to complete within an hour and avoids any system failures or interruptions.

**SNP Exploration***(Fig 13c)*. Another example of a bioinformatics analysis pipeline made easily distributable by Makeflow is the SNP Exploration [26] (SNPExp) pipeline. SNPExp is used to help researchers identify interesting regions of assembled genomes through analysis of Single Nucleotide Polymorphisms, or SNP's.

The SNPExp pipeline is similar in nature to the EST pipeline. The data to be analyzed is preparsed and split into subsets. These are then distributed for individual analysis and the results are combined into a single report for the researcher. The complexity of this



(a) **BLAST Example**: This is an example of a typical large blast job. The job runs for over 16 days, computing tens of thousands of subtasks. The job also experiences major communication failures every four days or so (marked by `F*`). Each time the job recovered and continued running automatically.



(b) **EST Example**: This EST Pipeline run demonstrates a single makeflow simultaneously making use of nearly 3000 cores, enabling it to rapidly complete the massively parallel portion of the EST workflow.

Figure 14: Example jobs from Biocompute

workflow stems primarily from the preparation steps necessary to make the data readable by the analysis package.

The SNPExp is a good example of how Makeflow can allow researchers to rapidly prototype complicated workflows for solving intermediate-sized problems. The SNPExp pipeline is of a moderate size, small enough that it could theoretically be run on a single core in a manageable amount of time, but large enough that each test run could take an hour or longer. By using Makeflow to exploit the nascent parallelism this turnaround time was reduced to minutes, allowing the researcher to quickly test and refine the bioinformatics algorithms while leaving most of the complications imposed by distributed systems to be handled automatically by Makeflow.

## 7. RELATED WORK

Stu Feldman presented the original Make [13] as a means for maintaining dependencies in compilation. In the years since there have been many variations on Make that exploit *parallel* computing systems which assume a fault-free environment and a global filesystem namespace, which is required for the traditional Make semantics. For example, Amoeba pmake [5] made minimal modifications to make to allow jobs to be distributed across an Amoeba [21] cluster, relying on the central fileserver for a common namespace. ISIS pmake [24] took the unusual approach of forking commands for all rules simultaneously, relying on a object space similar to Linda [2] to block rules whose dependencies were not yet satisfied. PGMAKE [4] employed PVM to fork processes on a large cluster, and NFS to provide access to data files. The SGE batch system provides qmake [14], which dispatches each rule as an SGE job, again relying on a shared filesystem. GXP make [27] uses the standard GNU make [13], but interposes on the `SHELL` variable to dispatch commands to various remote filesystems, relying on a shared filesystem for data access. Makeflow builds upon this body of work by showing how a slight twist to the semantics allow Make to function correctly on fault-prone, shared-nothing distributed systems constructed from clusters, clouds, and grids.

Explicit statement of dependencies is not the only way of managing workflows. DAGMan [9], the workflow engine provided with Condor [30], states the control dependencies between batch jobs, and has no direct information about data needs. This can be useful if the jobs have side effects that are reflected in some external device such as a database or a physical actuator. Another technique is transparent result caching [33], in which the actual dependencies of a program are observed by interposition on file operations. This is useful for accelerating the performance of a repeated and highly uniform job, but offers no assistance in resource management on the first execution of a workflow. In a cloud environment where data movement has real costs, we believe that explicit statement of dependencies is of greater utility.

In recent years, cloud computing systems have emphasized the Map-Reduce programming model, popularized by Google [11] and the Hadoop [17] open source implementation of the same ideas. Map-Reduce is, by design, less flexible than a generalized graph programming model, but this makes it much more tractable to solve problems of data partitioning, data locality, and fault tolerance. The concept of Map-Reduce is portable to other architectures such as multicore [25] and graphics processors [18]. Systems such as Dryad [19] and Sphere [16] provide a more generalized graph processing model than Map-Reduce, but also focus on the storage cluster architecture.

It is common to view Map-Reduce programs from the perspective of query processing. A number of small domain specific languages have been created to simplify multiple invocations of Map-Reduce for this purpose. For example, Pig [23] consists of a series of simple query-like operators that are all implemented as calls to Map-Reduce. Cascading [8] is a similar idea, but is able to pipeline multiple operations together for higher efficiency. Hive [32] layers a table structure on top of files within Hadoop, and then applies Map-Reduce programs to implement a query language.

## 8. CONCLUSIONS

**Makeflow.** Many common problems in science and industry can be easily expressed as a graph of small sequential programs exhibiting a high degree of natural parallelism. These can be run on a variety of dedicated systems, but each requires the user to have some expertise with a custom language and runtime system. This makes it difficult for users to learn new systems, limiting the resources available to them.

We address this problem with Makeflow: a scalable, fault tolerant workflow manager based on and using syntax nearly identical to that of Unix `Make`, a language familiar to many users.

Makeflow scales in size, allowing users to run workflows consisting of anywhere from a handful of jobs to millions. It can run thousands of jobs concurrently, automatically handling data dependencies and failure conditions. Makeflow can run anything from simulations that require a few kilobytes of data per job to genetic analyses that require gigabytes or more.

Makeflow scales in time. Depending on the execution driver chosen, Makeflow can efficiently run jobs that last anywhere from seconds to days. Makeflow can run for days at a time, efficiently handling remote node crashes, network disruptions, local machine crashes, resource allocation changes, and more, without losing substantial amounts of useful computation.

Makeflow scales across systems. A workflow can be initially developed on a single workstation, tested on a local cluster (SGE, Hadoop), scaled up using a global computational grid (Condor), and deployed for production using any combination of the above, plus whatever flexible commercial cloud resources are desired (Work Queue). The same workflow description can be moved between these resources without change.

Makeflow scales across user expertise. Makeflow has been successfully used as everything from an instructional tool in undergraduate courses to a platform on which production-level systems are developed. The language of `Make` without the pattern rules and other complex constructs is extremely simple and fairly intuitive, and a reasonably efficient workflow can be built and run on any system using only the default settings. At the same time, expert users can carefully tune their workflows to the execution systems available, establishing requirements or constraints on the remote resources used and employing the fairly extensive debug and logging system to identify bottlenecks and eliminate them.

**Workbench.** Makeflow's inherent portability makes it easy to run the same workflow on each of the supported systems. This prompted our development and introduction of Workbench, a workflow benchmark suite for measuring the performance characteristics of common workflow patterns on a variety of systems. We also expect that Workbench can be useful for profiling and improving bottlenecks in both new and existing distributed systems. When running Workbench we observed that workflows with small files are much more affected by dispatch latency than data throughput. We also found that asynchronous file transfer provides the greatest benefit to high-data reasonably-parallel workflows, but that for low-data jobs the infrastructure necessary to run the job can slow dispatch to the point of reducing performance.

**Future Work.** There are a variety of directions we can take this work. Makeflow's knowledge about the data dependencies of a workflow offers many exciting opportunities to optimize execution.

Data-local computation, resource management, and graph decomposition are three areas we've already begun investigating.

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