

# TaskVine: Managing In-Cluster Storage for High-Throughput Data-Intensive Workflows

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#### TaskVine Overview



**TaskVine** is a workflow executor for data intensive workflows that carefully manages data dependencies and resource utilization by utilizing in-cluster storage and bandwidth





#### **TaskVine Architecture Overview**





# **Evaluation: Managing Transfers**

Experiment: Introducing remote data into cluster. Left: each task independently downloads file. Middle: Uncontrolled peer transfers between workers. Right: Limited peer transfers between workers.



Limiting peertransfer concurrency improves performance.

# TaskVine Program

Three paradigms can be combined:

- Dynamic Workflow: submit multiple tasks, wait for completion, consider results, submit more.
- Static Workflow: define entire workflow up front, wait for complete results to be returned.
- Serverless Computing: define functions as services, then submit lightweight invocations of those services.



Task Definitions:

- Regular Task
- Python Task
- Mini Task
- Serverless Task

Data Definitions:

- LocalFile
- TempFile
- BufferFile
- URLFile
- Mini Task\*

# **Regular Task Definition**





import taskvine <mark>as</mark> vine

```
m = vine.Manager(9123)
```

doc = m.declareURL("https://www.gutenberg.org/files/1960/1960.txt")

```
task = vine.Task("grep chair doc.txt")
task.add_input(doc, "doc.txt")
```

```
taskid = m.submit(task)
task = queue.wait(VINE_FOREVER)
```

print task.output



#### **TaskVine Application**



**NCBI** 

blast.tar.gz landmark.tar.gz untar untar blast/ landmark/ query ENV blastp stdout

blast\_url="https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LA
TEST/ncbi-blast-2.13.0+-x64-linux.tar.gz"

landmark\_url = "https://ftp.ncbi.nlm.nih.gov/blast/db/landmark.tar.gz"

```
query_string = "GCTAATCCA.."
```

```
software = m.declareUntar(m.declareURL(blast_url))
landmark = m.declareUntar(m.declareURL(landmark_url))
```

```
task = vine.Task("blastp -db landmark -query query.file")
task.add_input(software, "blastdir")
task.add_input(database, "landmark")
task.add_input_buffer(query_string, "query.file")
task.set_env_var("BLASTDB", value="landmark")
```

m.submit(task)

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sandbox

#### Mini-Tasks

New capabilities are added to the system by defining mini-tasks that use the same task infrastructure to define dependencies and execute them reproducibly:

data = m.declareXRootD( "xrootd://host/path", "proxy" )

Which is defined as a mini-task like this:

t = vine.Task("xrdcp {} output.root".format(url)); t.add\_input(proxy,"proxy509.pem") t.set\_env\_var("X509\_USER\_PROXY","proxy509.pem") data = m.declareMiniTask(t,"output.root")



# CCTools

#### **Evaluation: Mini Tasks**

Experiment: Mini Tasks enable tasks to share staged data, even when it requires some transformation following transfer. Left: Each task expands the environment itself as part of its own task definition. Right: Each task shares an expanded environment defined by a shared mini-task.



Environments can be staged and re-used among tasks

#### **TaskVine Implementation**



**TaskVine Worker** url url temp file file wq73dv sd698d xyz123 r223cdf su3g2n data.tar.gz config input.txt  $T_1$  $T_2$ output.txt output.txt 10 Task 1 Sandbox Task 2 Sandbox

- Environment
   Management
- Storage Management and Naming
- Transfer Management
- Serverless Computing

#### **Consistent Naming**

Files have one of three lifetimes:

- single-task
- workflow (default)
- forever

"forever" cached objects are given content addressable names from a **Merkle Tree** of the file's provenance. If any inputs change, then so does the name of the output, and it's not the same file.



**CCTools** 

#### **Evaluation: Caching Through Consistent Naming**



Experiment: Execution a workflow from a worker's perspective. During a cold start, there is substantial overhead due to transferring and staging data. This overhead is removed on subsequent runs.



NOTE: consistent naming for various data types make caching possible across workflows!



#### **Serverless Execution**

# Define ordinary Python functions
def my\_sum(x, y):
 return x+y

def my\_mul(x, y):
 return x\*y

```
# Create a library object from functions
L = m.create_library_from_functions(
        "my_library", my_sum, my_mul)
```

# Install the library on all workers.
m.install\_library(L)

```
f = FunctionCall('my_library', 'my_mul', 2, 17)
m.submit(f)
```



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#### **TaskVine Integration: Parsl**



import parsl
from parsl import python\_app
from parsl.configs.vineex\_local import config

parsl.load(config)

@python\_app
def double(x):
 return x\*2

future = double(1)
assert future.result() == 2



#### TaskVine Integration: Dask



import ndcctools.taskvine as vine
import dask
import dask.array as da

# Create a new manager listening on port 9123
manager = vine.DaskVine(9123)

x = da.random.random((10000,10000),chunks=5000) y = x + x.T z = y[::2,500:].mean(axis=1)

result = z.compute(manager.get())

#### print(result);

#### **Thanks!**

- **TaskVine** is a component of the Cooperative Computing Tools (cctools) from Notre Dame alongside Makeflow, Work Queue, Resource Monitor, etc.
- Latest release in October 2023.

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TaskVine is a framework for building large scale data intensive dynamic workflows that run on HPC clusters, GPU clusters, and commercial clouds. As tasks access external data sources and produce their own outputs, more and more data is pulled into local storage on workers. This data is used to accelerate future tasks and avoid re-computing exisiting results. Data gradually grows "like a vine" through the cluster. TaskVine is our third-generation workflow system, built on our twenty years of experience creating scalable applications in fields such as high energy physics, bioinformatics, molecular dynamics, and machine learning.



#### conda install -c conda-forge ndcctools





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