

Use the UMassCS Swarm2 cluster
efficiently for your research!

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Objectives

- Learn the basic architecture of swarm
- Walk through how to parallelize and run a job
- Tips for optimizing
- Checkpointing
- Troubleshooting

Swarm v Gypsum

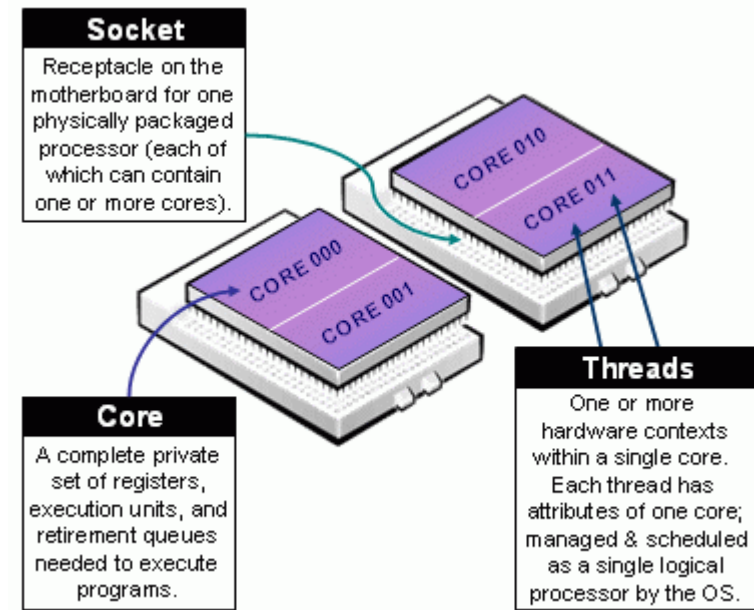
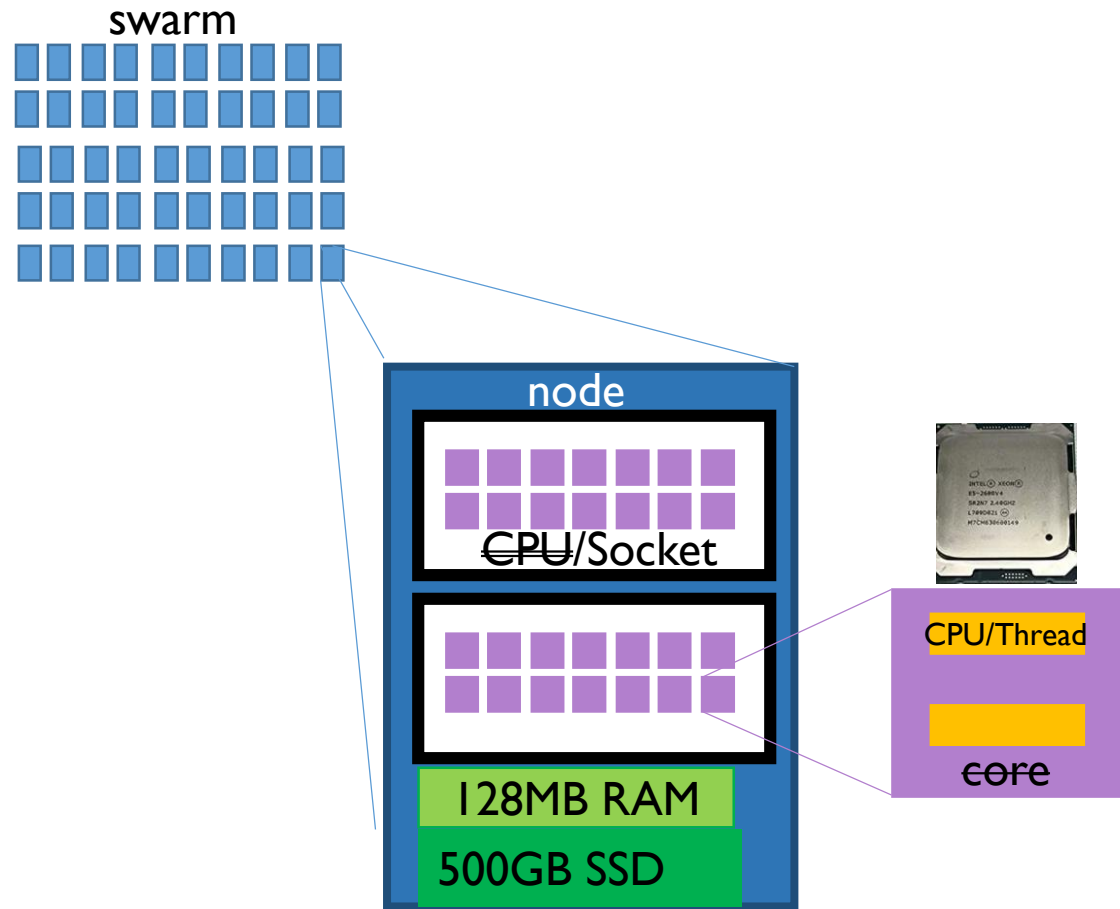
Swarm

- 50 nodes
 - 56 cores
 - 128 GB RAM
- Total
 - 2800 cores
 - 6.4TB RAM

Gypsum

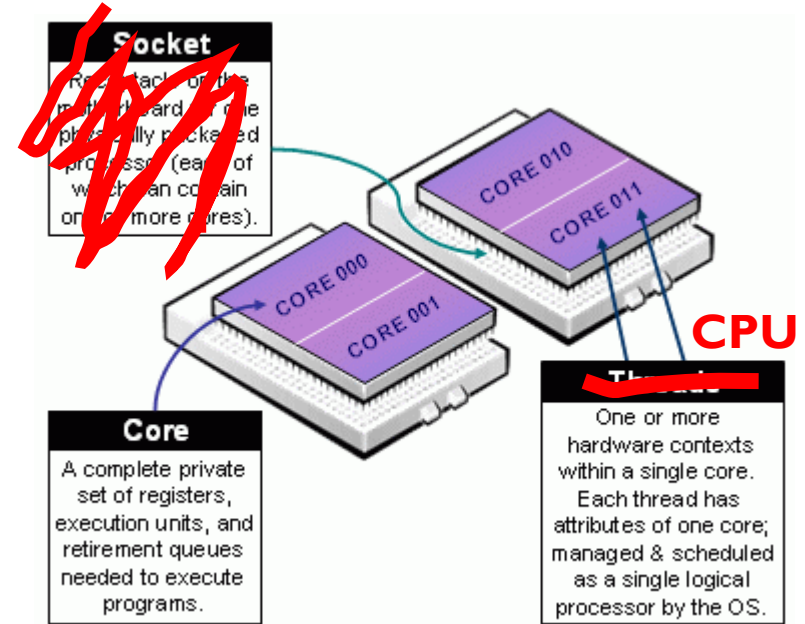
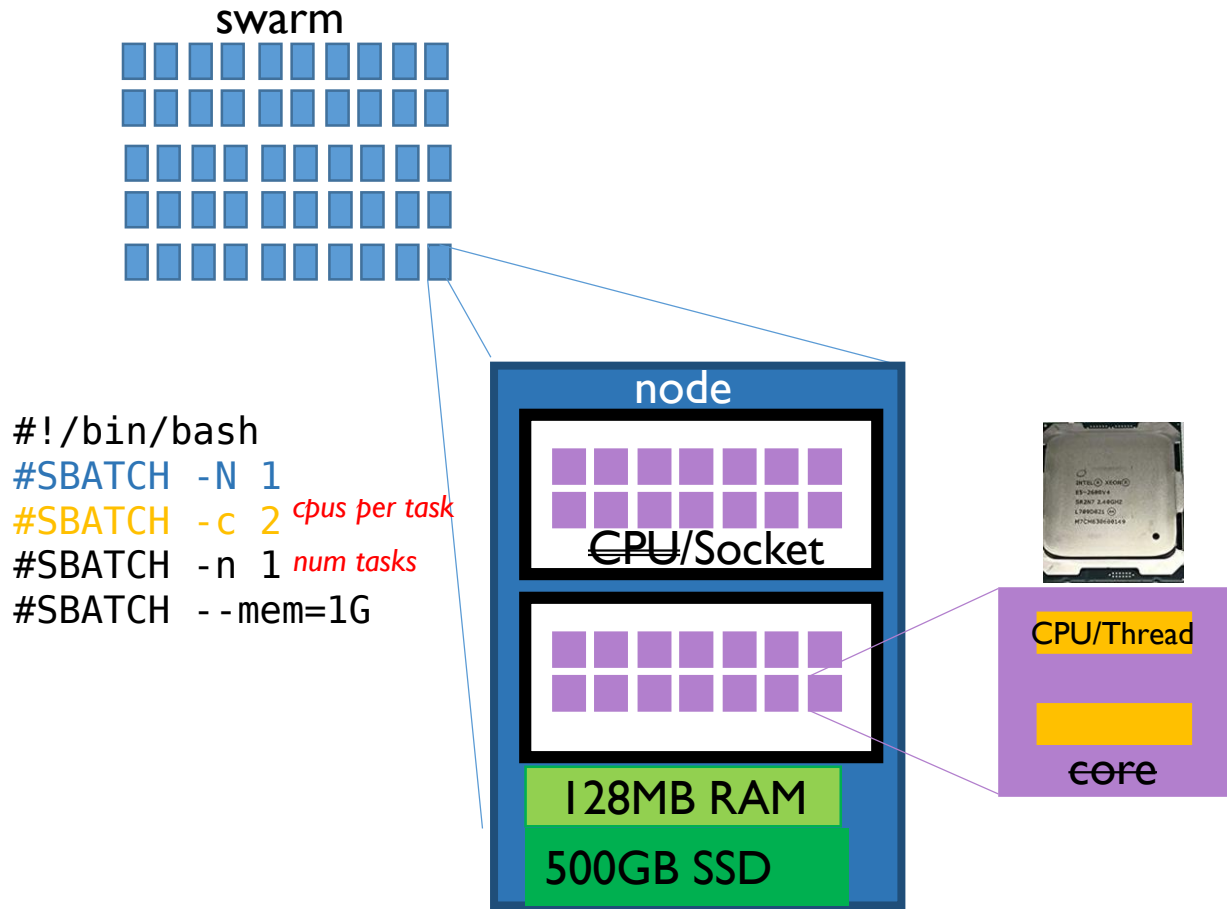
- 100 nodes
 - 4 GPU (25: M40, 75: TITAN X)
 - 24 cores
 - 256 GB RAM
- 53 nodes
 - 8 GPU (1080Ti)
 - 48 cores
 - 384 GB RAM
- Total
 - 4944 cores
 - 30.72TB RAM
 - 824 GPU

Clarifying ambiguous terminology



https://slurm.schedmd.com/mc_support.html

Clarifying ambiguous terminology



https://slurm.schedmd.com/mc_support.html

SLURM

- Queuing and scheduling system
- Tries to account for fairness
 - Priority queue based on a fairness score calculated by current and historical usage of **CPU** or **RAM** by you and your group, and the **age** of submission

Table 1. Backfill algorithm pseudocode.

-
1. Find the shadow time and extra nodes
 1. Sort the list of running jobs according to their expected termination time
 2. Loop over the list and collect nodes until the number of available nodes is sufficient for the first job in the queue
 3. The time at which this happens is the *shadow time*
 4. If at this time more nodes are available than needed by the first queued job, the ones left over are the extra nodes
 2. Find a backfill job
 1. Loop on the list of queued jobs in order of arrival
 2. For each one, check whether either of the following conditions hold:
 - It requires no more than the currently free nodes, and will terminate by the shadow time, or
 - It requires no more than the minimum of the currently free nodes and the extra nodes
 3. The first such job can be used for backfilling
-

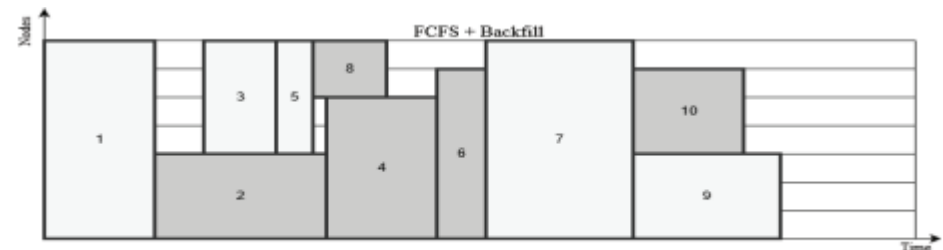


Fig. 1. Examples of FCFS and FCFS + Backfill.

Leonenkov and Zhumatiy (2015)

Introducing New Backfill-based Scheduler for SLURM Resource Manager

Resource Accounting and Limits

Swarm

Disk space:

- /home (10GB)
- /work1 (2TB)

User limits:

- 2240/2800 CPU limit
- ~~5.0~~1.0/6.4 TB RAM limit
- 10GB/allocated core (10GB/2 CPU)

Remember these rules

- **DO NOT** run anything on the head node --- always use srun or sbatch for anything computationally intensive
- DO NOT overallocate **time, memory, or CPU**
- **CHECK** your own jobs

BE RESPECTFUL!

First, you need an account

- Step 1. Get an account by having your advisor email CSCF
- Step 2. Log in with your CICS account

```
$ ssh ksung@swarm2.cs.umass.edu
ksung@swarm2.cs.umass.edu's password: hunter2

Last login: Sat Feb  2 23:11:24 2019 from c-66-31-41-74.hsd1.ma.comcast.net
Welcome to Bright release          7.3

                                     Based on CentOS Linux 7
                                     ID: #000002

Use the following commands to adjust your environment:

'module avail'           - show available modules
'module add <module>'   - adds a module to your environment for this session
'module initadd <module>' - configure module to be loaded at every login

-----

[ksung@swarm2 ~]$
```

SLURM commands

`sbatch` --- run an sbatch formatted file (normal way to run something)

`srun` --- run a command with specified resources. If within an sbatch file, it must be less than or equal to sbatch allocation. By default, the sbatch allocation will be used

`squeue` --- look at all submitted jobs by all users

Let's get something running!

- Example can be found in my home directory:

`/home/ksung/resources`

`/process_example`

Note: copy the whole directory to your own home directory before testing

Let's get something running!

Goal: parallelize the file on the right

Method 1: Make it runnable with command line arguments

Method 2: Parallelize it with a python library

```
import data {
1  from random import random
2  # baseline 8088k RSS
3  with open('data','r') as data_file:
4      data = data_file.readlines()
5      # 801988k RSS, 184MB filesize
6
7  def compute(x):
8      results_list = []
9      for i in range(int(1e7)):
10         v = data[(x+i)%len(data)]
11         result = v * v
12         results_list.append(result)
13     return sum(results_list)
14 # 1.86 sec baseline
15 all_results = []
16 for _ in range(100):
17     all_results = compute(int(rand()*1e7))
18 # 10.31 sec for 1 run / 1119096k RSS
19 with open('results','w') as results_file:
20     results_file.writelines(
21         [str(r) for r in all_results]
22     )
}
```

import data {

computation function {

run 100 times {

gather and write result {

process_serial.py

Let's get something running!

generate.py (generate example data to work with
--- shown here for replicability)

```
1  from random import random
2
3  def generate_data_file():
4      with open('data', 'w') as data_file:
5          for _ in range(int(1e7)):
6              data_file.write(str(random())+'\n')
7
8  generate_data_file()
```

```
[ksung@swarm2 swarmtest]$ srun python generate.py
[ksung@swarm2 swarmtest]$ ls -altrh data
-rw-r--r--+ 1 ksung brian 184M Feb  1 08:44 data
[ksung@swarm2 swarmtest]$ head data
0.6840357955948166
0.7258616689030184
0.8420618791853586
0.1869055299850192
0.6564391774778581
0.744592432297663
0.3576422277378445
0.5397177105307
0.9655819381147782
0.9031987970628081
```

Let's get something running --- profiling

process_serial.py

```
1 from random import random
2
```

Use **srun** and **time** to test and profile the script

```
[ksung@swarm2 swarmtest]$ srun time python process.py
0.02user 0.00system 0:00.04elapsed 90%CPU (0avgtext+0avgdata
8088maxresident)k
0inputs+0outputs (0major+2125minor)pagefaults 0swaps
```

0.04 sec runtime at
90% CPU

8M memory

Let's get something running!

process_serial.py

```
1  from random import random
2
3  with open('data','r') as data_file:
4      data = data_file.readlines()
5
```

```
[ksung@swarm2 swarmtest]$ srun time python process.py
1.20user 0.50system 0:01.75elapsed 97%CPU (0avgtext+0avgdata
802704maxresident)k
376376inputs+0outputs (0major+200857minor)pagefaults 0swaps
```

1.75 sec runtime at
97% CPU

803M memory

```

1  from random import random
2  # baseline 8088k RSS
3  with open('data','r') as data_file:
4      data = data_file.readlines()
5      # 801988k RSS, 184MB filesize
6
7  def compute(x):
8      results_list = []
9      for i in range(int(1e7)):
10         v = data[(x+i)%len(data)]
11         result = v * v
12         results_list.append(result)
13     return sum(results_list)
14 # 1.86 sec baseline
15 all_results = []
16 for _ in range(100):
17     all_results = compute(int(rand()*1e7))
18 # 10.31 sec for 1 run / 1119096k RSS
19 with open('results','w') as results_file:
20     results_file.writelines(
21         [str(r) for r in all_results]
22     )

```

```

[ksung@swarm2 swarmtest]$ srun time python serial_process.py
9.07user 1.07system 0:10.28elapsed 98%CPU (0avgtext+0avgdata
1119096maxresident)k
404200inputs+8outputs (5major+704966minor)pagefaults 0swaps

```

10.28 sec runtime at
98% CPU

1.2G memory

process_serial.py

Method 1 -- command line args

```
1 from random import random
2 # baseline 8088k RSS
3 with open('data','r') as data_file:
4     data = data_file.readlines()
5     # 801988k RSS, 184MB filesize
6
7 def compute(x):
8     results_list = []
9     for i in range(int(1e7)):
10         v = data[(x+i)%len(data)]
11         result = v * v
12         results_list.append(result)
13     return sum(results_list)
14 # 1.86 sec baseline
15 all_results = []
16 for _ in range(100):
17     all_results = compute(int(rand()*1e7))
18 # 10.31 sec for 1 run / 1119096k RSS
19 with open('results','w') as results_file:
20     results_file.writelines(
21         [str(r) for r in all_results]
22     )
```

process_serial.py

```
1 from random import random
2 import random,sys
3 run_number = sys.argv[1]
4 with open('data','r') as data_file:
5     data = data_file.readlines()
6
7 def compute(x): # profile this
8     results_list = []
9     for i in range(int(1e7)):
10         v = data[(x+i)%len(data)]
11         result = v * v
12         results_list.append(result)
13     return sum(results_list)
14
15 with open('results'+str(run_number),'w') as results_f:
16     results_f.write(
17         str(compute(int(rand()*1e7)))+'\n'
18     )
```

process_cmd.py

Anatomy of an sbatch file

```
#!/bin/bash
#SBATCH -j process_test # name
#SBATCH -N 1 # number of nodes
#SBATCH -n 1 # number of tasks
#SBATCH -c 2 # number of cpus per task
#SBATCH --mem=1G # memory per node
#SBATCH --mem-per-cpu=1G # memory per cpu
#SBATCH -a 0-99 # array
#SBATCH -t 00:01 # time allocated
#SBATCH -e process_test.err # error output file
#SBATCH -o process_out.out # stdout file

srun process.py ${SLURM_ARRAY_TASK_ID}
```

More info: <https://slurm.schedmd.com/sbatch.html>

run.sb

```
#!/bin/bash
#SBATCH -j process_test
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 2
#SBATCH --mem=1G
#SBATCH -a 0-99
#SBATCH -e process_test.err
#SBATCH -o process_out.out

srun process.py ${SLURM_ARRAY_TASK_ID}
```

process_cmd.py

```
from random import random
import random, sys
run_number = sys.argv[1]
with open('data', 'r') as data_file:
    data = data_file.readlines()

def compute(x): # profile this
    results_list = []
    for i in range(int(1e7)):
        v = data[(x+i)%len(data)]
        result = v * v
        results_list.append(result)
    return sum(results_list)

with open('results'+str(run_number), 'w') as results_f:
    results_f.write(
        str(compute(int(rand()*1e7)))+'\n'
    )
```

run.sb

```
#!/bin/bash
#SBATCH -j process_test
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 2
#SBATCH --mem=1G
```

```
#S[ksung@swarm2 swarmtest]$ sbatch run.sb
```

```
#SSubmitted batch job 9817176
```

```
#S[ksung@swarm2 swarmtest]$ squeue -u ksung
```

	JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
sru	9817176_0	defq	process_	ksung	R	0:04	1	swarm002
	9817176_1	defq	process_	ksung	R	0:04	1	swarm008

```
[ksung@swarm2 swarmtest]$ ~/sueff.py ksung
```

user	cpu eff	mem eff	alloc cpu	alloc mem
------	---------	---------	-----------	-----------

ksung	49.10%	≤ 0%	2	1G
-------	--------	------	---	----

ts_f:

process_cmd.py

```
from random import random
import random, sys
run_number = sys.argv[1]
with open('data', 'r') as data_file:
    data = data_file.readlines()
```

```
def compute(x): # profile this
```

```
    str(compute(int(rand()*1e7)))+'\n'
```

```
)
```

Post-hoc profiling

```
run.sb
#!/bin/bash
#SBATCH -j process_test
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 2
#SBATCH --mem=1G
#SBATCH --cpus-per-task=2
#SBATCH
#SBATCH
#SBATCH
```

```
[ksung@swarm2 swarmtest]$ sacct -j 9817176 -o Job,MaxRSS,TotalCPU,CPUTime,Elapsed
```

JobID	MaxRSS	TotalCPU	CPUTime	Elapsed
9817176_1		00:10.266	00:00:22	00:00:11
9817176_1.b+	726K	00:00.013	00:00:22	00:00:11
9817176_1.0	582K	00:10.252	00:00:20	00:00:10
9817176_0		00:11.203	00:00:24	00:00:12
9817176_0.b+	735K	00:00.014	00:00:24	00:00:12
9817176_0.0	588K	00:11.189	00:00:22	00:00:11

srun pro

```
process_cmd.py
from random import random
import random,sys
run_number = sys.argv[1]
with open('data','r') as data_file:
    data = data_file.readlines()

def compute(x): # profile this

with open('results'+str(run_number),'w') as results_f:
    results_f.write(
        str(compute(int(rand()*1e7)))+'\n'
    )
```

Post-hoc profiling (throttled result)

```
run.sb
#!/bin/bash
#SBATCH -j process_test
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 2
#SBATCH --mem=1G
#SBATCH
#SBATCH
#SBATCH
srun proc
```

```
process_cmd.py
from random import random
import random
run_number = sys.argv[1]
with open('data','r') as data_file:
    data = data_file.readlines()

def compute(x): # profile this
    with open("results"+str(run_number), "w") as results_f:
        results_f.write(
            str(compute(int(rand()*1e7)))+'\n'
        )
```

```
[ksung@swarm2 swarmtest]$ sacct -j 9817188 -o Job,MaxRSS,TotalCPU,CPUTime,Elapsed
```

JobID	MaxRSS	TotalCPU	CPUTime	Elapsed
9817188_1		00:09.913	00:02:20	00:01:10
9817188_1.b+	4696K	00:00.014	00:02:20	00:01:10
9817188_1.0	801932K	00:09.898	00:02:20	00:01:10
9817188_0		00:10.985	00:02:22	00:01:11
9817188_0.b+	4754K	00:00.014	00:02:22	00:01:11
9817188_0.0	800272K	00:10.971	00:02:22	00:01:11

Hyperthreading

- Non-MKL benchmark

```
[ksung@swarm2 ~]$ sacct -j 9826135 -o  
MaxRSS,TotalCPU,CPUTime,Elapsed  
-n 1  
-----  
MaxRSS  TotalCPU  CPUTime  Elapsed  
-----  
          00:09.680  00:00:26  00:00:13  
729K    00:09.680  00:00:26  00:00:13
```

```
[ksung@swarm2 ~]$ sacct -j 9826136 -o  
MaxRSS,TotalCPU,CPUTime,Elapsed  
-n 2  
-----  
MaxRSS  TotalCPU  CPUTime  Elapsed  
-----  
          00:35.875  00:00:38  00:00:19  
729K    00:35.875  00:00:38  00:00:19
```

- MKL benchmark

```
[ksung@swarm2 benches]$ sacct -j 9825685 -o  
MaxRSS,CPUTime,TotalCPU,Elapsed  
-n 1  
-----  
MaxRSS  CPUTime  TotalCPU  Elapsed  
-----  
          00:03:06  03:00.324  00:01:33  
5502K   00:03:06  00:00.014  00:01:33  
105819K 00:01:32  03:00.310  00:01:32
```

```
[ksung@swarm2 benches]$ sacct -j 9825304 -o  
MaxRSS,CPUTime,TotalCPU,Elapsed  
-n 2  
-----  
MaxRSS  CPUTime  TotalCPU  Elapsed  
-----  
          00:07:46  07:42.980  00:03:53  
4725K   00:07:46  00:00.014  00:03:53  
119065K 00:07:44  07:42.965  00:03:52
```

Hyperthreading

- Users can only book one whole core at a time (two threads with hyperthreading)
- Forcing your program to use both threads will probably not significantly increase your efficiency. It will however look like you're using only 50% of CPU
- Take advantage of libraries (like numpy) that optimize for hyperthreads! Python on swarm is compiled with Intel MKL support for hyperthreading. Anaconda's release should come with it, too.

Using a library is usually better

Pros

- Don't reinvent the wheel
- Can save memory and time
- Can consolidate (reduce) results more easily

Cons

- Libraries are language dependent
- It is sometimes harder to implement

Method 2 -- multiprocessing library

```
1 from random import random
2 # baseline 8088k RSS
3 with open('data','r') as data_file:
4     data = data_file.readlines()
5     # 801988k RSS, 184MB filesize
6
7 def compute(x):
8     results_list = []
9     for i in range(int(1e7)):
10        v = data[(x+i)%len(data)]
11        result = v * v
12        results_list.append(result)
13    return sum(results_list)
14 # 1.86 sec baseline
15 all_results = []
16 for _ in range(100):
17     all_results = compute(int(rand()*1e7))
18 # 10.31 sec for 1 run / 1119096k RSS
19 with open('results','w') as results_file:
20     results_file.writelines(
21         [str(r) for r in all_results]
22     )
```

process_multi.py

```
1 from random import random
2 from multiprocessing import Pool
3
4 with open('data','r') as data_file:
5     data = data_file.readlines()
6
7 def compute(x): # profile this
8     results_list = []
9     for i in range(int(1e7)):
10        v = data[(x+i)%len(data)]
11        result = v * v
12        results_list.append(result)
13    return sum(results_list)
14
15 p = Pool(20)
16 all_results = p.map(
17     compute,
18     [int(random()*1e7) for _ in range(100)]
19 )
20
21 with open('results','w') as results_file:
22     results_file.writelines(
23         [str(r) for r in all_results]
24     )
```

run.sb

```
#!/bin/bash
#SBATCH -J process_test
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 8
#SBATCH --mem=2G
#SBATCH -a 0
#SBATCH -e process_test.err
#SBATCH -o process_out.out
```

```
srun -c 8 python process_multi.py
```

(throttled result)

```
[ksung@swarm2 swarmtest]$ sacct -j 9838632 -o Job,MaxRSS,TotalCPU,
CPUtime,Elapsed
-----
JobID          MaxRSS      TotalCPU    CPUtime     Elapsed
-----
9838632_0      0           02:56.880  00:11:20   00:01:25
9838632_0.b+   4921K      00:00.015  00:11:20   00:01:25
9838632_0.0    800967K    02:56.865  00:11:20   00:01:25
```

Save memory with multiprocessing!

process_multi.py

```
1  from random import random
2  from multiprocessing import Pool
3
4  with open('data','r') as data_file:
5      data = data_file.readlines()
6
7  def compute(x): # profile this
8      results_list = []
9      for i in range(int(1e7)):
10         v = data[(x+i)%len(data)]
11         result = v * v
12         results_list.append(result)
13     return sum(results_list)
14
15  p = Pool(20)
16  all_results = p.map(
17      compute,
18      [int(random()*1e7) for _ in range(100)]
19  )
20
21  with open('results','w') as results_file:
22      results_file.writelines(
23          [str(r) for r in all_results]
24      )
```

run.sb

```
#!/bin/bash
#SBATCH -J process_test
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 8
#SBATCH --mem=2G
#SBATCH -a 0
#SBATCH -e process_test.err
#SBATCH -o process_out.out
```

```
srun -c 8 python process_multi.py
```

(throttled result)

```
[ksung@swarm2 swarmtest]$ sacct -j 9838647 -o Job,MaxRSS,TotalCPU,
CPUtime,Elapsed
-----
JobID          MaxRSS      TotalCPU    CPUtime     Elapsed
-----
9838647_0      06:27.126  00:14:56   00:01:52
9838647_0.b+   4779K      00:00.016  00:14:56   00:01:52
9838647_0.0    8991875K   06:27.110  00:14:56   00:01:52
```

Copy-on-write causes 8x memory usage

process_multi.py

```
1 from random import random
2 from multiprocessing import Pool
3
4 with open('data','r') as data_file:
5     data = data_file.readlines()
6
7 def compute(x): # profile this
8     results_list = []
9     for i in range(int(1e7)):
10        v = data[(x+i)%len(data)]
11        data[(x+i)%len(data)] = 0
12        result = v * v
13        results_list.append(result)
14    return sum(results_list)
15
16 p = Pool(20)
17 all_results = p.map(
18     compute,
19     [int(random()*1e7) for _ in range(100)]
20 )
21
22 with open('results','w') as results_file:
23     results_file.writelines(
24         [str(r) for r in all_results]
25     )
```

Don't commit these sins

- **DO NOT** run anything on the head node --- always use `srun` or `sbatch` for anything computationally intensive
- DO NOT overallocate **time, memory, or CPU**
- **CHECK** your own jobs

BE RESPECTFUL!

Other tips

- Minimize reads and writes to disk
- Write fault-tolerant code
 - Save “state” often so that code can restart if it fails for any reason
- Make your program as fragmentable as possible. It is easier to schedule a high number of low resource jobs than a lower number of resource intensive jobs

Checkpointing with DMTCP

- Example can be found in my home directory:

`/home/ksung/resources`

`/dmtcp_example`

Note: copy the whole directory to your own home directory before testing

Checkpointing with DMTCP (experimental)

- Any job with more than one node will be buggy
- Saves memory state to filesystem

Start a job: `sbatch slurm_launch.job`

Continue a job: `sbatch slurm_rstr.job`

- `/home/ksung/dmtcp_example`

```
-rw-----+ 1 ksung brian 29M Feb 2 23:38 ckpt_python3.5_471891ed5a75b2e2-45000-5b200cda64dd4.dmtcp
-rw-----+ 1 ksung brian 29M Feb 2 23:38 ckpt_python3.5_471891ed5a75b2e3-40000-5b203b8d6e72c.dmtcp
-rw-----+ 1 ksung brian 29M Feb 2 23:38 ckpt_python3.5_471891ed5a75b2e3-42000-5b203b8d74974.dmtcp
-rw-----+ 1 ksung brian 29M Feb 2 23:38 ckpt_python3.5_471891ed5a75b2e3-43000-5b203b8c96a52.dmtcp
-rwxr--r--+ 1 ksung brian 6.8K Feb 2 23:38 dmtcp_restart_script_471891ed5a75b2e3-40000-5b203b7babb47.sh
lrwxrwxrwx 1 ksung brian 60 Feb 2 23:38 dmtcp_restart_script.sh -> dmtcp_restart_script_471891ed5a75b2e3-40000-5b203b7babb47.sh
```


DMTCP

slurm_launch.out

slurm_rstr.out

```
[ksung@swarm2 dmtcp2]$ tail -30 dmtcp.out
swarm001 19
swarm001 19
swarm001 19
swarm002 19
swarm001 20
swarm001 20
swarm001 20
swarm002 20
swarm001 21
swarm001 21
swarm001 21
swarm002 21
swarm001 22
swarm001 22
swarm001 22
swarm002 22
swarm001 23
swarm001 23
swarm001 23
swarm002 23
swarm001 24
swarm001 24
swarm001 24
swarm002 24
slurmstepd: error: Step 9829757.0 exceeded memory limit (126337 > 102400), being killed
slurmstepd: error: *** STEP 9829757.0 ON swarm001 CANCELLED AT 2019-02-02T23:35:55 ***
slurmstepd: error: Exceeded job memory limit
srun: Job step aborted: Waiting up to 32 seconds for job step to finish.
srun: error: swarm002: task 7: Killed
srun: error: swarm001: tasks 0-1,3: Killed
```

```
swarm001 20
swarm001 20
swarm001 20
swarm001 20
swarm001 21
swarm001 21
swarm001 21
swarm001 21
swarm001 22
swarm001 22
swarm001 22
swarm001 22
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swarm001 26
swarm001 26
swarm001 26
swarm001 26
swarm001 27
swarm001 27
swarm001 27
swarm001 27
```

DMTCP

Excerpt from slurm_launch.job

```
#####  
# 1. Start DMTCP coordinator  
#####  
start_coordinator -i 10 # ... <put dmtcp coordinator options here>  
  
#####  
# 2. Launch application  
# 2.1. If you use mpiexec/mpirun to launch an application, use the following  
#       command line:  
#       $ dmtcp_launch --rm mpiexec <mpi-options> ./<app-binary> <app-options>  
# 2.2. If you use PMI1 to launch an application, use the following command line:  
#       $ srun dmtcp_launch --rm ./<app-binary> <app-options>  
# Note: PMI2 is not supported yet.  
# 2.3. If you use the Stampede supercomputer at Texas Advanced Computing Center  
#       (TACC), use ibrun command to launch the application (--rm is not required):  
#       $ ibrun dmtcp_launch ./<app-binary> <app-options>  
#####  
# dmtcp_launch --rm mpirun --mca btl self,tcp ./<your binary>  
srun dmtcp_launch --rm python count.py  
~
```

Excerpt from slurm_rstr.job

```
#####  
# 1. Start DMTCP coordinator  
#####  
start_coordinator # -i 120 ... <put dmtcp coordinator options here>  
  
#####  
# 2. Restart application  
#####  
/bin/bash ./dmtcp_restart_script.sh -h $DMTCP_COORD_HOST -p $DMTCP_COORD_PORT  
  
#####  
# If you use the Stampede supercomputer at Texas Advanced Computing Center  
# (TACC), add the --hostfile option:  
# /bin/bash ./dmtcp_restart_script.sh -h $DMTCP_COORD_HOST -p $DMTCP_COORD_PORT\  
#                                     --hostfile $HOSTFILE  
#####
```

Troubleshooting

- Memory error

```
slurmstepd: error: Step 9829757.0 exceeded memory limit  
(126337 > 102400), being killed  
slurmstepd: error: *** STEP 9829757.0 ON swarm001  
CANCELLED AT 2019-02-02T23:35:55 ***  
slurmstepd: error: Exceeded job memory limit  
srun: Job step aborted: Waiting up to 32 seconds for job  
step to finish.  
srun: error: swarm002: task 7: Killed  
srun: error: swarm001: tasks 0-1,3: Killed
```

Troubleshooting

- Time expiry error
 - SIGTERM 32 sec before SIGKILL

```
import signal
import sys
from time import sleep

def sigterm_handler(_signo, _stack_frame):
    print('sorry', flush=True)
    for i in range(1000):
        print(i, flush=True)
        sleep(1)
    sys.exit(0)

signal.signal(signal.SIGTERM, sigterm_handler)

sleep(600)
```

```
[ksung@swarm2 dmtcp2]$ srun -t 00:00:01
python term_test.py
srun: Force Terminated job 9844110
srun: Job step aborted: Waiting up to
32 seconds for job step to finish.
slurmstepd: error: *** STEP 9844110.0
ON swarm002 CANCELLED AT 2019-02-
05T14:07:34 DUE TO TIME LIMIT ***
sorry
0
.
.
.
28
29
srun: error: swarm002: task 0: Killed
```

Troubleshooting

- Allocation error --- your allocation doesn't make sense
- Assoc Limit --- you or your group is currently already maxing out your resource limit
- Resource --- you are first in line but there are not enough resources for your job
- Priority --- you are waiting for the first in line (Resource) to be scheduled

Troubleshooting

```
[ksung@swarm2 swarmtest]$ ~/blame.py 1

Percent of resources allocated per user
      alloc      wasted
user    cpu    mem    cpu    mem    num_nodes    cpus_per_node    mem_per_node
[REDACTED] 6.9%  12.1%  2.0%  10.8%    15           14.1           61.0G
[REDACTED] 4.2%  13.5%  1.9%  3.8%    14           9.1            73.1G
[REDACTED] 1.0%  1.2%  0.8%  1.0%    1           30.0           93.0G
[REDACTED] 1.0%  0.7%  0.8%  0.6%    3           10.0           16.7G
[REDACTED] 0.6%  0.1%  0.3%  0.1%    5            3.6            2.2G
[REDACTED] 9.4%  3.8%  0.1%  1.0%    8           36.0           36.0G
[REDACTED] 3.2%  2.6%  0.0% -0.6%    2           50.0          100.0G

Total swarm allocation
cpu    mem
0.26   0.34

Resources available
cpu    mem
2274   4989.2G

Conflicts:
REASON  PRIORITY    CPUS    NODES    MIN_MEMORY    USER
Resources      5004    30      1        93000M [REDACTED] x1

Waiting:
REASON  PRIORITY    CPUS    NODES    MIN_MEMORY    USER
ReqNodeNotAvail  UnavailableNod 5004    30      1        93000M [REDACTED] x9
AssocGrpMemLimit      4150    1        1        16000M [REDACTED] x1697
JobArrayTaskLimit     4004    4        1        15000M [REDACTED] x1
```

/home/ksung/blame.py

```
[ksung@swarm2 ~]$ blame.py

Percent of resources allocated per user
      alloc      wasted
user   cpu    mem    cpu    mem    num_nodes    cpus_per_node    mem_per_node
-----
[redacted] 7.1%  12.5%  2.2%  11.2%     15             14.7             63.0G
[redacted] 4.2%  13.5%  1.9%   5.6%     14             9.1              73.1G
[redacted] 1.9%   1.3%  1.7%   1.3%     6             10.0             16.7G
[redacted] 1.0%   1.2%  0.8%   1.0%     1             30.0             93.0G
[redacted] 0.6%   0.1%  0.3%   0.1%     5              3.6              2.2G
[redacted] 0.1%   0.1%  0.1%   0.1%     1              2.0              4.0G
[redacted] 9.4%   3.8%  0.1%   1.0%     8             36.0             36.0G
[redacted] 3.2%   2.6%  0.0%  -0.6%     2             50.0            100.0G

Total swarm allocation

cpu    mem
0.27   0.35

Resources available

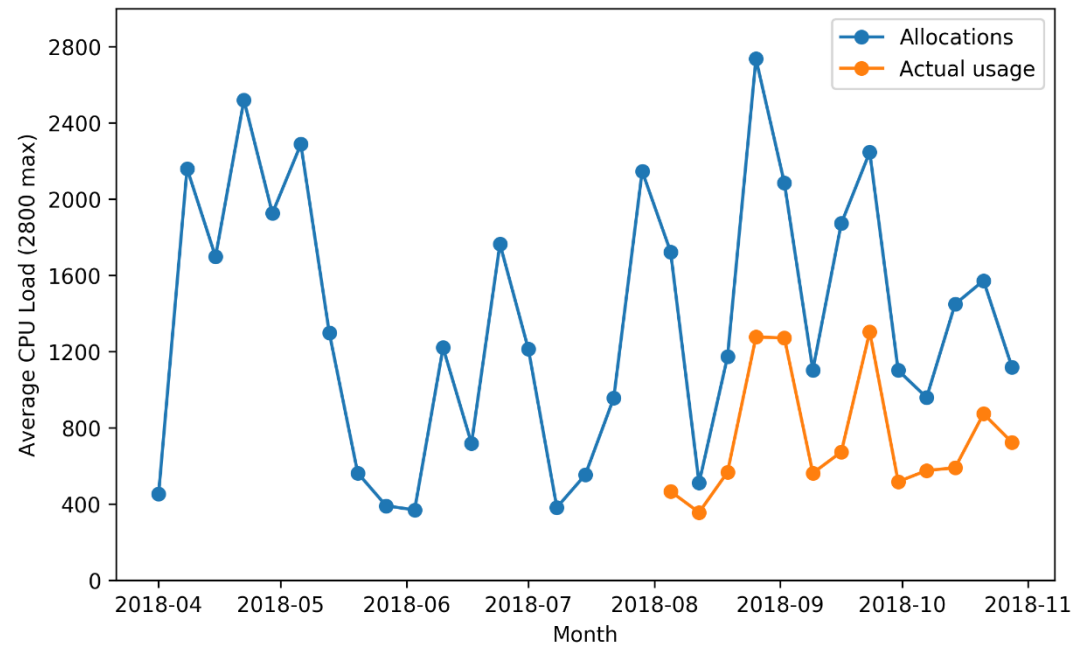
cpu    mem
2234   4905.2G
```

/home/ksung/sueff.py

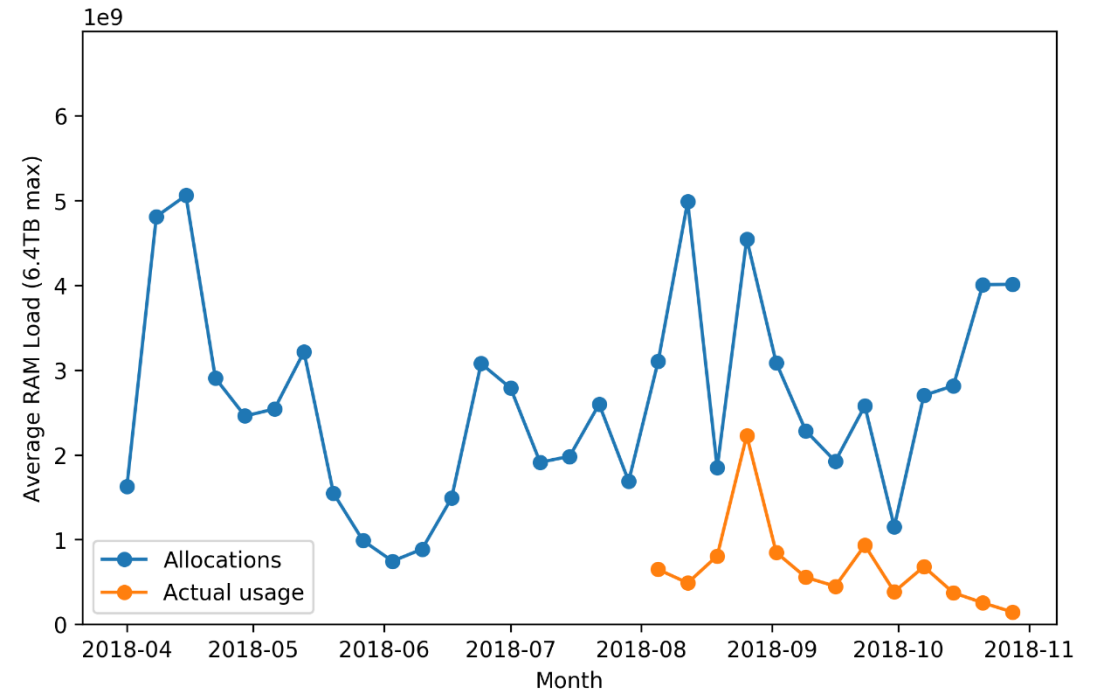
```
[ksung@swarm2 ~]$ sueff.py [redacted]
user   cpu eff    mem eff    alloc cpu    alloc mem
-----
[redacted] 69.70%    ≤ 10%      220         945G
```

Usage history

CPU (29%/50%)



Memory (11%/41%)



Policy changes to expect in the near future

Motivation: increase swarm efficiency, use, fairness, and turnover

- Shorter defq time and more defq-only nodes
- Changes in fairness calculation

Commands you should use often

`queue -u <user>`

`sbatch <sbatch file>`

`srun time <executable>`

`sacct -j <JobID> -o Job,MaxRSS,TotalCPU,CPUTime,Elapsed`

`blame (/home/ksung/resources/bin/blame)`

`sueff (/home/ksung/resources/bin/sueff)`

List of resources

- /home/ksung/resources/install --- install dmtcp, sueff, and blame

Examples:

- /home/ksung/resources/dmtcp_example
- /home/ksung/resources/process_example

<https://slurm.schedmd.com/sbatch.html>

<https://people.cs.umass.edu/~swarm/index.php?n=Main.NewSwarmDoc>

Summary

- **DO NOT** run anything on the head node --- always use srun or sbatch for anything computationally intensive
- Profile your program!
 - DO NOT overallocate **time, memory, or CPU**
- **CHECK** your own jobs when you run them

BE RESPECTFUL!

Install the tools:

```
$ /home/ksung/resources/install
```

Monitor the mailing list:

swarm-users@cs.umass.edu

Issues?

Email the mailing list or Keen: ksung@cs.umass.edu