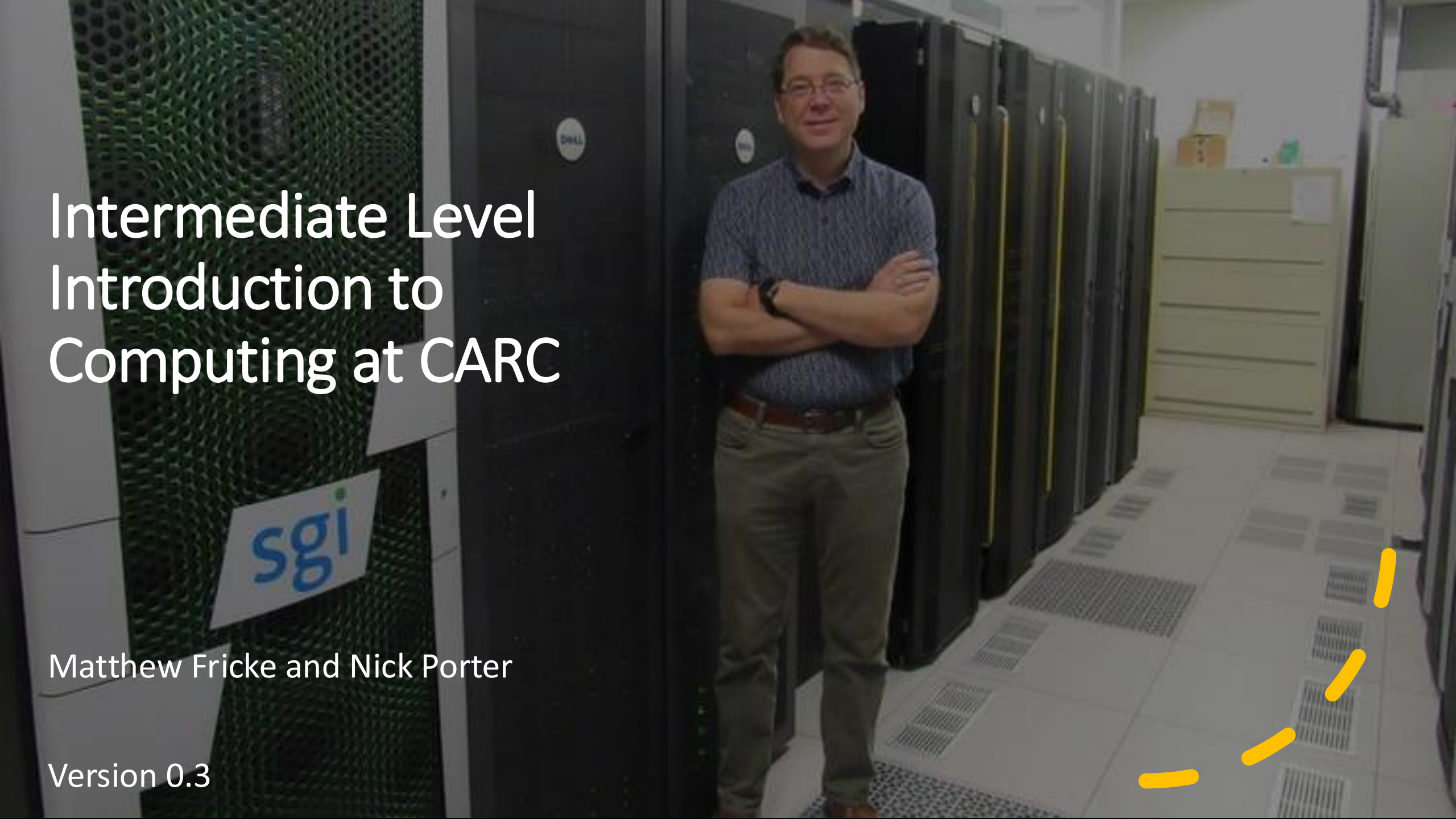


Intermediate Level Introduction to Computing at CARC

Matthew Fricke and Nick Porter

Version 0.3

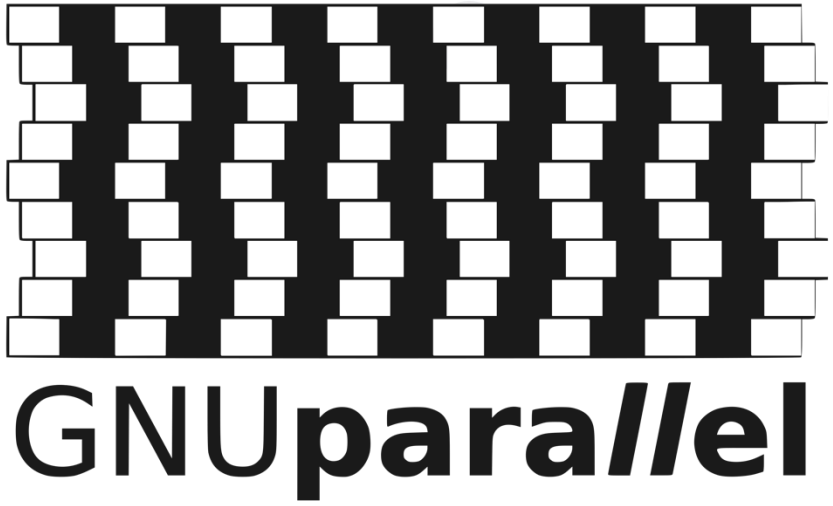
Goals

- 1) SLURM scheduler literacy
- 2) Ability to employ embarrassingly parallel solutions
- 3) Ability to employ coupled parallel solutions

NOTE: We won't cover file transfer, storage systems, module system, conda, PBS. (These are all covered in depth in the video tutorials)

Agenda

- HPC and Parallelism
- HPC Schedulers
- SLURM
- Embarrassingly Parallel
    - SLURM Arrays
    - GNU Parallel
- Coupled Parallelism
- MPI with MPI



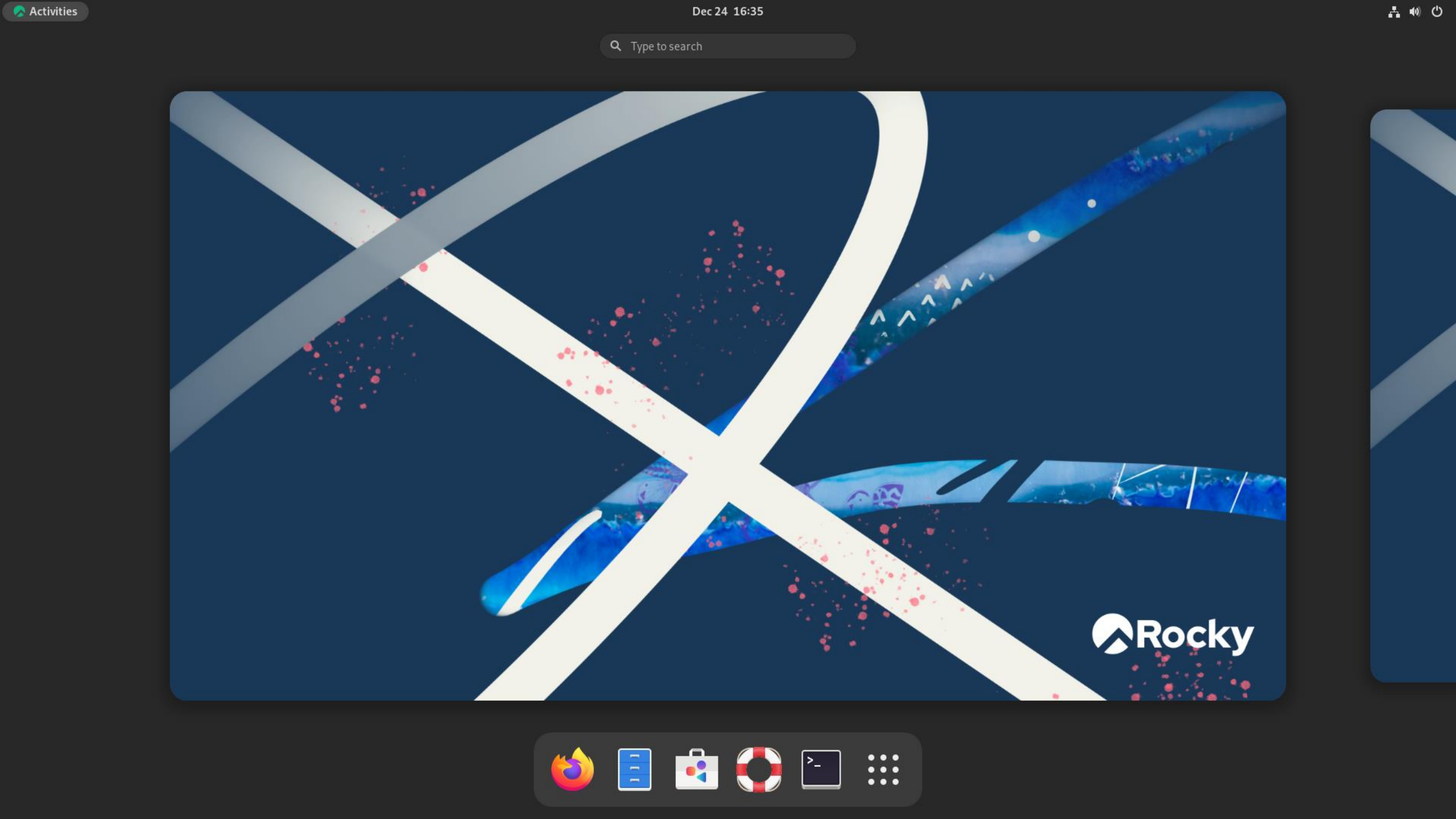
Logging into Hopper

First login to the Linux **workstation** in front of you.

Use your CARC username and password.

We are glad to help you login if you have trouble.

This is an “important step” so don’t let me move on until you have logged in


Activities
Dec 24 16:35
Type to search
Rocky

Logging into Hopper


```
ssh vanilla@hopper.alliance.unm.edu
```

You may be prompted for a password…

Don’t let me move on until you are able to login.

Logging into Hopper

```
--------------------------------------------------------------------------------
  Welcome to Hopper

  Be sure to review the "Acceptable Use" guidelines posted on the CARC website.

  For assistance using this system email help@carc.unm.edu.

  Tutorial videos can be accessed through the CARC website: Go to
    http://carc.unm.edu, select the "New Users" menu and then click
      "Introduction to Computing at CARC".

  Warning: By default home directories are world readable. Use the chmod command
    to restrict access.

  Don't forget to acknowledge CARC in publications, dissertations, theses and
    presentations that use CARC computational resources:

  "We would like to thank the UNM Center for Advanced Research Computing,
  supported in part by the National Science Foundation, for providing the
  research computing resources used in this work."

  Please send citations to publications@carc.unm.edu.

  Hopper is our newest general purpose cluster and member of the Taos/Hopper condo.

  There are four types of slurm partitions on Hopper:
  1) General - this partition is accessible by all CARC users.
  2) Debug - for testing your code and interactive jobs. Short time limits so that nodes are usually available right away.
  3) Condo - this partition is accessible by users who are members of the Hopper/Taos condo. Users with access to this partition also have access to the
community partition on the Taos cluster. Jobs run here may be interrupted by the hardware owner, so we recommend that your software support
checkpointing so it can recover.
  4) Private partitions - these partitions are dedicated to the condo grant/lab/center that purchased the associated hardware.

  Type "qgrok" to get information about the partitions to which you have access.
  Enter "quotas" to see your storage usage and limits.
  For a list of software installed on Hopper enter "module spider".
--------------------------------------------------------------------------------
  ******************************************************************************
  * Logging in under another person's account is strictly forbidden and will *
  * result in the account being          locked.                          *
  ******************************************************************************
```


ENJOY
Slurm
SODA
IT'S HIGHLY ADDICTIVE!
VOTED #1 SOFT DRINK OF THE 31ST CENTURY!
YOU WIN!
WHIMMY WHAM WHAM WOZZLE!
SLURMS McKENZIE

```
[vanilla@hopper ~]$ qgrok
partition      nodes nodes nodes total total free  total free  CPUs  RAM/node  time  CPU   GPU   RAM
name     jobs  free  busy  down  nodes CPUs  CPUs  GPUs  GPUs  /node       limit limit limit limit
---------- ----- ----- ----- ----- ----- ----- ----- ----- ----- --------- ----- ----- ----- -----
general   4    4    6    0    10   320  156  0    0    32   93G     2d   128   0    372G
debug     1    1    1    0    2    64   63   0    0    32   93G     4h   8     0    25G
totals:   5    5    7    0    12   384  219  0    0
```

```
[vanilla@hopper ~]$ qgrok
partition      nodes nodes nodes total total free  total free  CPUs  RAM/node  time  CPU   GPU   RAM
name     jobs  free  busy  down  nodes CPUs  CPUs  GPUs  GPUs  /node       limit limit limit limit
---------- ----- ----- ----- ----- ----- ----- ----- ----- ----- --------- ----- ----- ----- -----
general   4    4    6    0    10   320  156  0    0    32   93G     2d   128   0    372G
debug     1    1    1    0    2    64   63   0    0    32   93G     4h   8     0    25G
condo     29   30   25   0    55   1760 1060 37   8    32   94G-1.5T 2d   512   4    1.5T
bugs      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pcnc      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pathogen  0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
tc        8    1    9    0    10   320  104  0    0    32   93G-1.5T 1w   320   0
gold      0    2    0    0    2    64   64   0    0    32   93G     1w   64    0
fishgen   1    0    1    0    1    32   12   0    0    32   377G    1w   32    0
neuro-hsc 0    14   0    0    14   448  448  0    0    32   93G     1w   448   0
pna       0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
geodef    0    4    0    0    4    128  128  0    0    32   504G    1w   128   0
cup-ecs   0    0    2    0    2    64   0    13   8    32   188G    1w   64    13
tid       0    0    1    0    1    32   0    2    0    32   188G    1w   32    2
biocomp   0    1    0    0    1    32   32   1    0    32   188G    1w   32    1
chakra    0    0    1    0    1    32   0    1    0    32   188G    1w   32    1
quark     0    3    7    0    10   320  112  20   0    32   377G    1w3d 320   20
toadpole  0    1    0    0    1    32   32   0    0    32   94G     1w   32    0
insar     0    2    0    0    2    64   64   0    0    32   504G    1w   64    0
totals:   34   35   32   0    67   2144 1279 37   8
```

```
[vanilla@hopper ~]$ qgrok
partition      nodes nodes nodes total total free  total free  CPUs  RAM/node  time  CPU   GPU   RAM
name     jobs  free  busy  down  nodes CPUs  CPUs  GPUs  GPUs  /node       limit limit limit limit
---------- ----- ----- ----- ----- ----- ----- ----- ----- ----- --------- ----- ----- ----- -----
general   4    4    6    0    10   320  156  0    0    32   93G     2d   128   0    372G
debug     1    1    1    0    2    64   63   0    0    32   93G     4h   8     0    25G
condo     29   30   25   0    55   1760 1060 37   8    32   94G-1.5T 2d   512   4    1.5T
bugs      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pcnc      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pathogen  0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
tc        8    1    9    0    10   320  104  0    0    32   93G-1.5T 1w   320   0
gold      0    2    0    0    2    64   64   0    0    32   93G
fishgen   1    0    1    0    1    32   12   0    0    32   377
neuro-hsc 0    14   0    0    14   448  448  0    0    32
pna       0    1    0    0    1    32   32   0    0    32   93
geodef    0    4    0    0    4    128  128  0    0    32
cup-ecs   0    0    2    0    2    64   0    13   8    32   1
tid       0    0    1    0    1    32   0    2    0    32   188
biocomp   0    1    0    0    1    32   32   1    0    32
chakra    0    0    1    0    1    32   0    1    0    32   18
quark     0    3    7    0    10   320  112  20   0    32
toadpole  0    1    0    0    1    32   32   0    0    32
insar     0    2    0    0    2    64   64   0    0    32   50
totals:   34   35   32   0    67   2144 1279 37   8
```

Open partitions for use by everyone with a CARC account.

Purchased by the Office for the Vice President for Research.

```
[vanilla@hopper ~]$ qgrok
partition      nodes nodes nodes total total free  total free  CPUs  RAM/node  time  CPU   GPU   RAM
name     jobs  free  busy  down  nodes CPUs  CPUs  GPUs  GPUs  /node       limit limit limit limit
---------- ----- ----- ----- ----- ----- ----- ----- ----- ----- --------- ----- ----- ----- -----
general   4    4    6    0    10   320  156  0    0    32   93G     2d   128   0    372G
debug     1    1    1    0    2    64   63   0    0    32   93G     4h   8     0    25G
condo     29   30   25   0    55   1760 1060 37   8    32   94G-1.5T 2d   512   4    1.5T
bugs      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pcnc      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pathogen  0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
tc        8    1    9    0    10   320  104  0    0    32   93G-1.5T 1w   320   0
gold      0    2    0    0    2    64   64   0    0    32   93G     1w   64    0
fishgen   1    0    1    0    1    32   12   0    0    32   377G    1w   32    0
neuro-hsc 0    14   0    0    14   448  448  0    0    32   93G     1w   448   0
pna       0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
geodef    0    4    0    0    4    128  128  0    0    32   504G    1w   128   0
cup-ecs   0    0    2    0    2    64   0    13   8    32   188G    1w   64    13
tid       0    0    1    0    1    32   0    2    0    32   188G    1w   32    2
biocomp   0    1    0    0    1    32   32   1    0    32   188G    1w   32    1
chakra    0    0    1    0    1    32   0    1    0    32   188G    1w   32    1
quark     0    3    7    0    10   320  112  20   0    32   377G    1w3d 320   20
toadpole  0    1    0    0    1    32   32   0    0    32   94G     1w   32    0
insar     0    2    0    0    2    64   64   0    0    32   504G    1w   64    0
totals:   34   35   32   0    67   2144 1279 37   8
```

```
[vanilla@hopper ~]$ qgrok
partition      nodes nodes nodes total total free  total free  CPUs  RAM/node  time  CPU  GPU  RAM
name     jobs  free  busy  down  nodes CPUs  CPUs  GPUs  GPUs  /node       limit limit limit limit
---------- ----- ----- ----- ----- ----- ----- ----- ----- ----- --------- ----- ----- ----- -----
general   4    4    6    0    10   320  156  0    0    32   93G     2d   128   0    372G
debug     1    1    1    0    2    64   63   0    0    32   93G     4h   8     0    25G
condo     29   30   25   0    55   1760 1060 37   8    32   94G-1.5T 2d   512   4    1.5T
bugs      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pcnc      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pathogen  0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
tc        8    1    9    0    10   320  104  0    0    32   93G-1.5T 1w   320   0
gold      0    2    0    0    2    64   64   0    0    32   93G
fishgen   1    0    1    0    1    32   12   0    0    32   377
neuro-hsc 0    14   0    0    14   448  448  0    0    32
pna       0    1    0    0    1    32   32   0    0    32   93
geodef    0    4    0    0    4    128  128  0    0    32
cup-ecs   0    0    2    0    2    64   0    13   8    32   1
tid       0    0    1    0    1    32   0    2    0    32   188
biocomp   0    1    0    0    1    32   32   1    0    32
chakra    0    0    1    0    1    32   0    1    0    32   18
quark     0    3    7    0    10   320  112  20   0    32
toadpole  0    1    0    0    1    32   32   0    0    32
insar     0    2    0    0    2    64   64   0    0    32   50
totals:   34   35   32   0    67   2144 1279 37   8
```

Private partitions

- Reserved for use by the purchaser.
- Request access by emailing support@carc.unm.edu and CC the partition owner.

```
[vanilla@hopper ~]$ qgrok
partition      nodes nodes nodes total total free  total free  CPUs  RAM/node  time  CPU  GPU  RAM
name     jobs  free  busy  down  nodes CPUs  CPUs  GPUs  GPUs  /node       limit limit limit limit
---------- ----- ----- ----- ----- ----- ----- ----- ----- ----- --------- ----- ----- ----- -----
general   4    4    6    0    10   320  156  0    0    32   93G     2d   128   0    372G
debug     1    1    1    0    2    64   63   0    0    32   93G     4h   8     0    25G
condo     29   30   25   0    55   1760 1060 37   8    32   94G-1.5T 2d   512   4    1.5T
bugs      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pcnc      0    0    2    0    2    64   0    0    0    32   93G     1w   64    0
pathogen  0    1    0    0    1    32   32   0    0    32   93G     1w   32    0
tc        8    1    9    0    10   320  104  0    0    32   93G-1.5T 1w   320   0
gold      0    2    0    0    2    64   64   0    0    32   93G     1w
fishgen   1    0    1    0    1    32   12   0    0    32   377G
neuro-hsc 0    14   0    0    14   448  448  0    0    32   9
pna       0    1    0    0    1    32   32   0    0    32   93G
geodef    0    4    0    0    4    128  128  0    0    32   504
cup-ecs   0    0    2    0    2    64   0    13   8    32   188
tid       0    0    1    0    1    32   0    2    0    32   188G
biocomp   0    1    0    0    1    32   32   1    0    32   188
chakra    0    0    1    0    1    32   0    1    0    32   188G
quark     0    3    7    0    10   320  112  20   0    32   37
toadpole  0    1    0    0    1    32   32   0    0    32   94
insar     0    2    0    0    2    64   64   0    0    32   504G
totals:   34   35   32   0    67   2144 1279 37   8
```

Condo “scavenger” partition

- Allows you to use compute nodes purchased by another group that are currently idle.
- May be interrupted at any time if the owners start to use it.

```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug        up    4:00:00      1    mix hopper011
debug        up    4:00:00      1   idle hopper012
```

sinfo reports information about partitions

```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug        up    4:00:00      1    mix hopper011
debug        up    4:00:00      1   idle hopper012
```

The debug queues are intended for testing your programs.

And for interactive jobs.

```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug        up    4:00:00      1    mix hopper011
debug        up    4:00:00      1   idle hopper012
```

Name

```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug        up    4:00:00      1    mix hopper011
debug        up    4:00:00      1   idle hopper012
```

You can run a “job” for up to 4 hrs.

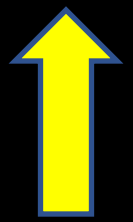
```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug        up    4:00:00      1    mix hopper011
debug        up    4:00:00      1   idle hopper012
```

There are two nodes in this partition.

```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug        up    4:00:00      1    mix hopper011
debug        up    4:00:00      1   idle hopper012
```

The state of the nodes in the partition

```
[vanilla@hopper ~]$ sinfo --partition debug
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug       up    4:00:00      1    mix hopper011
debug       up    4:00:00      1   idle hopper012
```



The name of the nodes in the partition

```
[vanilla@hopper ~]$ sinfo --partition general
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
general*     up 2-00:00:00      5  alloc hopper[001-009]
general*     up 2-00:00:00      4   idle hopper010
```

Hopper001 through 009 are running jobs.

Hopper010 is waiting to be used.

```
[vanilla@hopper ~]$ hostname
hopper
[vanilla@hopper ~]$
```

Running on the Head Node.
The head node's name is "hopper".

```
[vanilla@hopper ~]$ hostname
hopper
[vanilla@hopper ~]$ man hostname
```

```
[vanilla@hopper ~]$ hostname
hopper
[vanilla@hopper ~]$ man hostname
(‘q’ to quit)

[vanilla@hopper ~]$ man man
(‘q’ to quit)
```

[vanilla@hopper ~]$ man sinfo

sinfo(1) Slurm Commands sinfo(1)

NAME

sinfo - View information about Slurm nodes and partitions.

SYNOPSIS

sinfo [OPTIONS...]

DESCRIPTION

sinfo is used to view partition and node information for a system running Slurm

OPTIONS

-a, --all

Display information about all partitions. This causes information to be displayed about partitions that are configured as hidden and partitions that are unavailable to the user's group.

[vanilla@hopper ~]$ sinfo --all

```
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
general*     up 2-00:00:00      9  alloc hopper[001-009]
general*     up 2-00:00:00      1   idle hopper010
debug        up    4:00:00      2   idle hopper[011-012]
condo        up 2-00:00:00      1  down* hopper045
condo        up 2-00:00:00      3    mix hopper[018-020]
condo        up 2-00:00:00     16  alloc hopper[013-015,028-036,049-052]
condo        up 2-00:00:00     18   idle hopper[016-017,021-027,037-044,053]
bugs         up 7-00:00:00      2  alloc hopper[013-014]
pcnc         up 7-00:00:00      1  alloc hopper015
pcnc         up 7-00:00:00      1   idle hopper016
pathogen     up 7-00:00:00      1   idle hopper017
tc           up 7-00:00:00      3    mix hopper[018-020]
tc           up 7-00:00:00      2  alloc hopper[029-030]
tc           up 7-00:00:00      5   idle hopper[021-025]
gold         up 7-00:00:00      2   idle hopper[026-027]
fishgen      up 7-00:00:00      1  alloc hopper028
neuro-hsc    up 7-00:00:00      6  alloc hopper[031-036]
neuro-hsc    up 7-00:00:00      8   idle hopper[037-044]
cup-ecs      up 7-00:00:00      2  alloc hopper[049-050]
tid          up 7-00:00:00      1  alloc hopper051
biocomp      up 7-00:00:00      1  alloc hopper052
chakra       up 7-00:00:00      1   idle hopper053
pna          up 7-00:00:00      1  down* hopper045
```

```
[vanilla@hopper ~]$ srun --partition debug hostname
```

Tell slurm to run a program on a compute node…

```
[vanilla@hopper ~]$ srun --partition debug hostname
```

Run the program on a compute node in the debug partition.

```
[vanilla@hopper ~]$ srun --partition debug hostname
```

The program to run.

```
[vanilla@hopper ~]$ srun --partition debug hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
You have not been allocated GPUs. To request GPUs, use the -G option in your submission script.
hopper011
```

```
[vanilla@hopper ~]$ squeue
```

[vanilla@hopper ~]$ squeue

```
  JOBID PARTITION     NAME     USER ST       TIM
   4314   general      PRE erowland PD      0:00
   4315   general      PRE erowland PD      0:00
   4317   general      PRE erowland PD      0:00
   4318   general      PRE erowland PD      0:00
```

PD means programs that are waiting their turn.

Shows you what the slurm scheduler is doing right now.

Here we can see that user ’erowland’ has a lot of programs waiting to run.

```
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
2 (QOSMaxCpuPerUserLimit)
```

```
[vanilla@hopper ~]$ squeue
  JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
           4314   general      PRE erowland PD       0:00      2 (QOSMaxCpuPerUserLimit)
           4315   general      PRE erowland PD       0:00      2 (QOSMaxCpuPerUserLimit)
           4317   general      PRE erowland PD       0:00      2 (QOSMaxCpuPerUserLimit)
           4318   general      PRE erowland PD       0:00      2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
                                                                2 (QOSMaxCpuPerUserLimit)
           4337   general      PRE erowland PD       0:00      2 (QOSMaxCpuPerUserLimit)
```

The reason these jobs are not running is that ‘erowland’ is already using the maximum number of CPUs they are allowed.

```
[vanilla@hopper ~]$ squeue -t R --all
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
              4405     condo    2ndMA  mfricke  R 1-07:48:30      6 hopper[031-036]
              5208     condo       NN     kgu  R    5:48:49      1 hopper015
              5210     condo       NN     kgu  R    6:30:13      1 hopper014
              5209     condo       NN     kgu  R    6:31:13      1 hopper013
              5206     condo       NN     kgu  R    6:32:13      1 hopper051
              5207     condo       NN     kgu  R    6:32:13      1 hopper052
              5205     condo       NN     kgu  R    6:32:43      1 hopper028
              4595   cup-ecs golConfi aalasand  R 2-06:51:59      1 hopper050
              4594   cup-ecs golConfi aalasand  R 2-06:52:03      1 hopper049
              5120   general jupyterh   jacobm  R   11:45:47      1 hopper007
              4313   general      PRE erowland  R    1:17:29      2 hopper[003-004]
              5111   general    1stMA  mfricke  R   11:15:28      2 hopper[005-006]
              5025   general      c2n    jxzuo  R      1:50      1 hopper001
              5024   general      c2n    jxzuo  R     31:28      1 hopper002
              5203   general       NN     kgu  R    6:37:50      1 hopper009
              5201   general       NN     kgu  R    6:38:14      1 hopper008
              4390        tc UCsTpCyd lepluart  R 2-15:18:18      3 hopper[018-020]
              5198        tc       NN     kgu  R    6:40:19      1 hopper030
              5196        tc       NN     kgu  R    6:40:31      1 hopper029
```

```
[vanilla@hopper ~]$ srun --partition debug --ntasks 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
You have not been allocated GPUs. To request GPUs, use the -G option in your submission script.
hopper011
hopper011
```

```
[vanilla@hopper ~]$ srun --partition debug --ntasks 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
You have not been allocated GPUs. To request GPUs, use the -G option in your submission script.
hopper011
hopper011
```

You ran two copies of your program.

ntasks is the number of copies to run.

```
[vanilla@hopper ~]$ srun --partition debug --ntasks 8 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
hopper011
hopper011
hopper011
You have not been allocated GPUs. To request GPUs, use the -G option in your submission
script.
hopper011
hopper011
hopper011
hopper011
hopper011
hopper011
```

You ran eight copies of your program.

ntasks is the number of copies to run.

```
[vanilla@hopper ~]$ srun --partition debug --ntasks 8 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
hopper011
hopper011
hopper011
You have not been allocated GPUs. To request GPUs, use the -G option in your submission
script.
hopper011
hopper011
hopper011
hopper011
hopper011
hopper011
```

By default, each task (copy of your program) is allowed to use one CPU.

Many programs are able to use more than one CPU at a time.

```
[vanilla@hopper ~]$ srun --partition debug --ntasks 2 --cpus-per-task 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
You have not been allocated GPUs. To request GPUs, use the -G option in your submission script.
hopper011
hopper011
```

Here we are telling SLURM to run 2 copies of our program and let each copy of our program use 2 CPUs.

```
[vanilla@hopper ~]$ srun --partition debug --nodes 2 --ntasks-per-node 4 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest project
hopper012
You have not been allocated GPUs. To request GPUs, use the -G option in your submission script.
hopper012
hopper011
hopper011
hopper012
hopper012
hopper011
hopper011
```

Here we are telling SLURM to run 4 copies of our program on 2 different compute nodes.

This is useful when our programs need a bigger share of the compute node.

```
[vanilla@hopper ~]$ srun --partition debug --nodes 2
--ntasks-per-node 2 --cpus-per-task 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest
project
hopper011
You have not been allocated GPUs. To request GPUs, use the -G option in your
submission script.
hopper011
hopper012
hopper012
```

And we can combine all three.

```
[vanilla@hopper ~]$ srun --partition debug --mem 4G
--nodes 2 --ntasks-per-node 2 --cpus-per-task 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest
project
hopper012
hopper012
You have not been allo                                                    r
submission script.
hopper011
Hopper011
```

And we can specify how much memory we want.

--mem 4G means give me 4 gigabytes of memory per node.

```
[vanilla@hopper ~]$ srun --partition debug --mem 4G
--nodes 2 --ntasks-per-node 2 --cpus-per-task 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest
project
hopper012
hopper012
You have not been allo                                                    r
submission script.
hopper011
Hopper011
```

Why does all this matter?

The purpose of SLURM is to provide you the hardware your programs need.

So you have to understand what those requirements are really well.

```
[vanilla@hopper ~]$ srun --partition debug --mem 4G
--nodes 2 --ntasks-per-node 2 --cpus-per-task 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest
project
hopper012
hopper012
You have not been all                                                    r
submission script.
hopper011
Hopper011
```

1) **Can my program use multiple CPUs?**
2) **How much memory does my program need?**
3) **Can my program use multiple compute nodes (MPI*, GNU Parallel*)?**
4) **Can my program use GPUs?**

```
[vanilla@hopper ~]$ srun --partition debug --mem 4G
--nodes 2 --ntasks-per-node 2 --cpus-per-task 2 hostname
srun: Account not specified in script or ~/.default_slurm_account, using latest
project
hopper012
hopper012
You have not been alloca                                                    r
submission script.
hopper011
Hopper011
```

This command is getting pretty long.

We can use salloc to avoid asking for the same resources every time we use srun.

```
[vanilla@hopper ~]$ salloc --partition debug --nodes 2 --ntasks-per-node 2
salloc: Account not specified in script or ~/.default_slurm_account, using latest project
salloc: Granted job allocation 5251
salloc: Waiting for resource configuration
salloc: Nodes hopper[011-012] are ready for job
[vanilla@hopper ~]$
```

This command is getting pretty long.

We can use salloc to avoid asking for the same resources every time we use srun.

```
[vanilla@hopper ~]$ srun hostname
hopper012
hopper012
hopper011
You have not been allocated GPUs. To request GPUs, use the -G option in your
submission script.
hopper011
[vanilla@hopper ~]$ srun hostname
hopper012
hopper011
hopper012
hopper011
[vanilla@hopper ~]$
```

Now we can use srun over and over without having to ask for a new hardware allocation each time.

```
[vanilla@hopper ~]$ exit
exit
salloc: Relinquishing job allocation 5251
```

Always type exit when you are done with the hardware.
Running salloc inside an allocation gets very confusing.

BREAK

Interactive vs Batch Mode

Interactive Mode

- Everything so far has been interactive. You request hardware, run your program, and get the output on your screen right away.

Batch Mode

- Most programs at an HPC center are run in “batch” mode.
- Batch mode means we write a shell script that the SLURM scheduler runs for us. The script requests hardware just like we did with salloc and then runs the commands in the script.
- Whatever would have been written to the screen is saved to a file instead.

```
[vanilla@hopper ~]$ git clone https://lobogit.unm.edu/CARC/workshops.git
Cloning into 'workshops'...
remote: Enumerating objects: 132, done.
remote: Counting objects: 100% (75/75), done.
remote: Compressing objects: 100% (43/43), done.
remote: Total 132 (delta 33), reused 74 (delta 32), pack-reused 57
Receiving objects: 100% (132/132), 57.58 KiB | 3.60 MiB/s, done.
Resolving deltas: 100% (51/51), done.
```

Rather than make you write shell scripts lets just download some we wrote for this workshop…

[vanilla@hopper ~]$ **tree workshops**

```
workshops/
├── intro_workshop
│   ├── code
│   │   ├── calcPiMPI.py
│   │   ├── calcPiSerial.py
│   │   └── vecadd
│   │       ├── Makefile
│   │       ├── vecadd_gpu.cu
│   │       ├── vecadd_mpi_cpu
│   │       ├── vecadd_mpi_cpu.c
│   │       ├── vecaddmpi_cpu.sh
│   │       └── vecadd_mpi_gpu.c
│   ├── data
│   │   ├── H2O.gjf
│   │   └── step_sizes.txt
│   └── slurm
│       ├── calc_pi_array.sh
│       ├── calc_pi_mpi.sh
│       ├── calc_pi_parallel.sh
│       ├── calc_pi_serial.sh
│       ├── gaussian.sh
│       ├── hostname_mpi.sh
│       ├── vecadd_hopper.sh
│       ├── vecadd_xena.sh
│       ├── workshop_example2.sh
│       ├── workshop_example3.sh
│       └── workshop_example.sh
└── README.md
```

Run tree to see how the workshops directories are organized…

```
[vanilla@hopper ~]$ tree workshops
workshops/
├── intro_workshop
│   ├── code
│   │   ├── calcPiMPI.py
│   │   ├── calcPiSerial.py
│   │   └── vecadd
│   │       ├── Makefile
│   │       ├── vecadd_gpu.cu
│   │       ├── vecadd_mpi_cpu
│   │       ├── vecadd_mpi_cpu.c
│   │       ├── vecaddmpi_cpu.sh
│   │       └── vecadd_mpi_gpu.c
│   ├── data
│   │   ├── H2O.gjf
│   │   └── step_sizes.txt
│   └── slurm
│       ├── calc_pi_array.sh
│       ├── calc_pi_mpi.sh
│       ├── calc_pi_parallel.sh
│       ├── calc_pi_serial.sh
│       ├── gaussian.sh
│       ├── hostname_mpi.sh
│       ├── vecadd_hopper.sh
│       ├── vecadd_xena.sh
│       ├── workshop_example2.sh
│       ├── workshop_example3.sh
│       └── workshop_example.sh
└── README.md
```

Run tree to see how the workshops directories are organized…

The workshop files are divided into “code”, “slurm”, and “data” directories.

```
[vanilla@hopper intro_workshop]$ pwd
/users/vanilla/workshops/intro_workshop
[vanilla@hopper intro_workshop]$ cat slurm/workshop_example.sh
#!/bin/bash
#SBATCH --partition debug
#SBATCH --ntasks 4
#SBATCH --time 00:05:00
#SBATCH --job-name ws_example
#SBATCH --mail-user your_username@unm.edu
#SBATCH --mail-type ALL

srun hostname
```

Let's take a look at the workshop_example.sh script in the slurm directory…

```
[vanilla@hopper intro_workshop]$ sbatch slurm/workshop_example.sh
sbatch: Account not specified in script or ~/.default_slurm_account, using latest project
Submitted batch job 5252
[vanilla@hopper intro_workshop]$
```

We submit our slurm shell script with the sbatch command.

```
[vanilla@hopper intro_workshop]$ sbatch slurm/workshop_example1.sh
sbatch: Account not specified in script or ~/.default_slurm_account, using latest project
Submitted batch job 5252
[vanilla@hopper intro_workshop]$
```

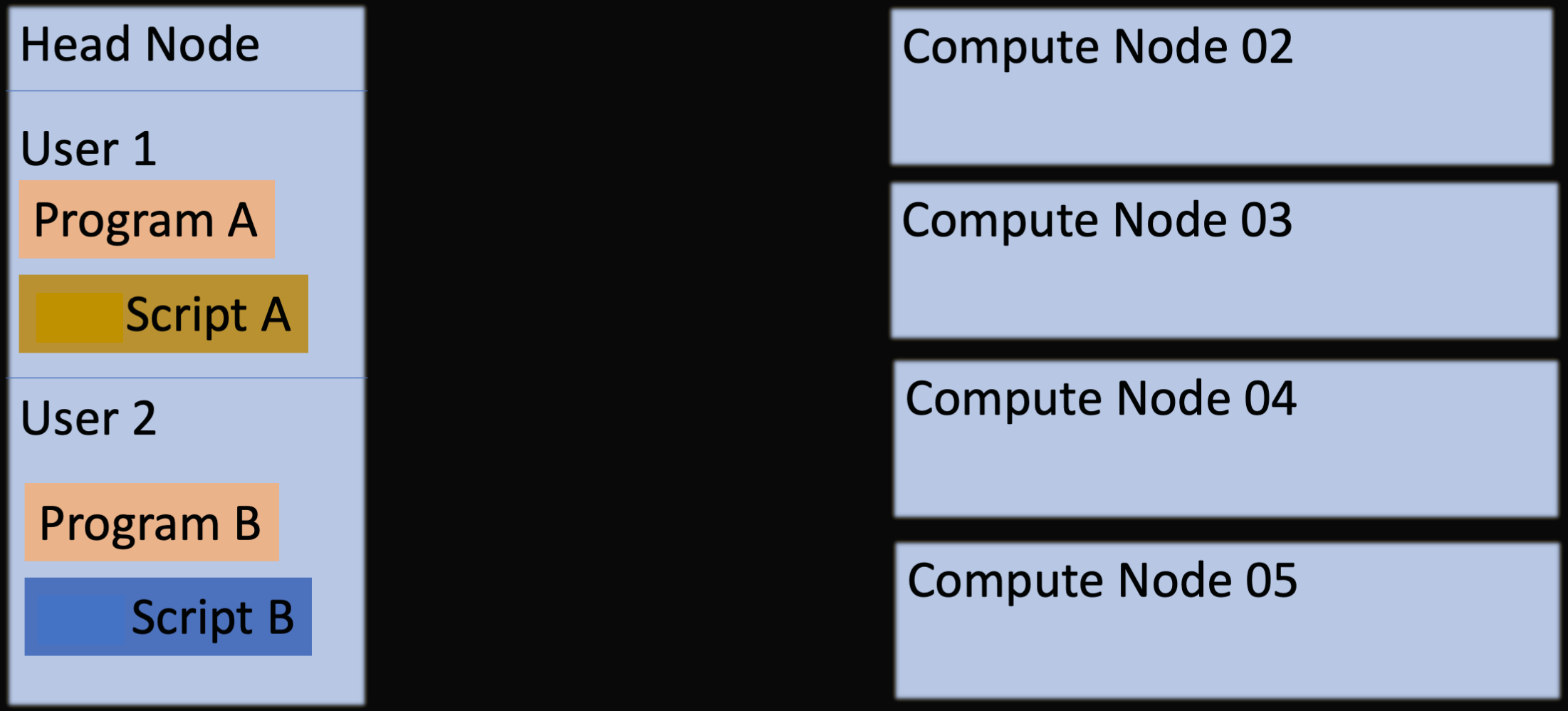
We submit our slurm shell script with the sbatch command.

Notice that the only output we get is a job id.

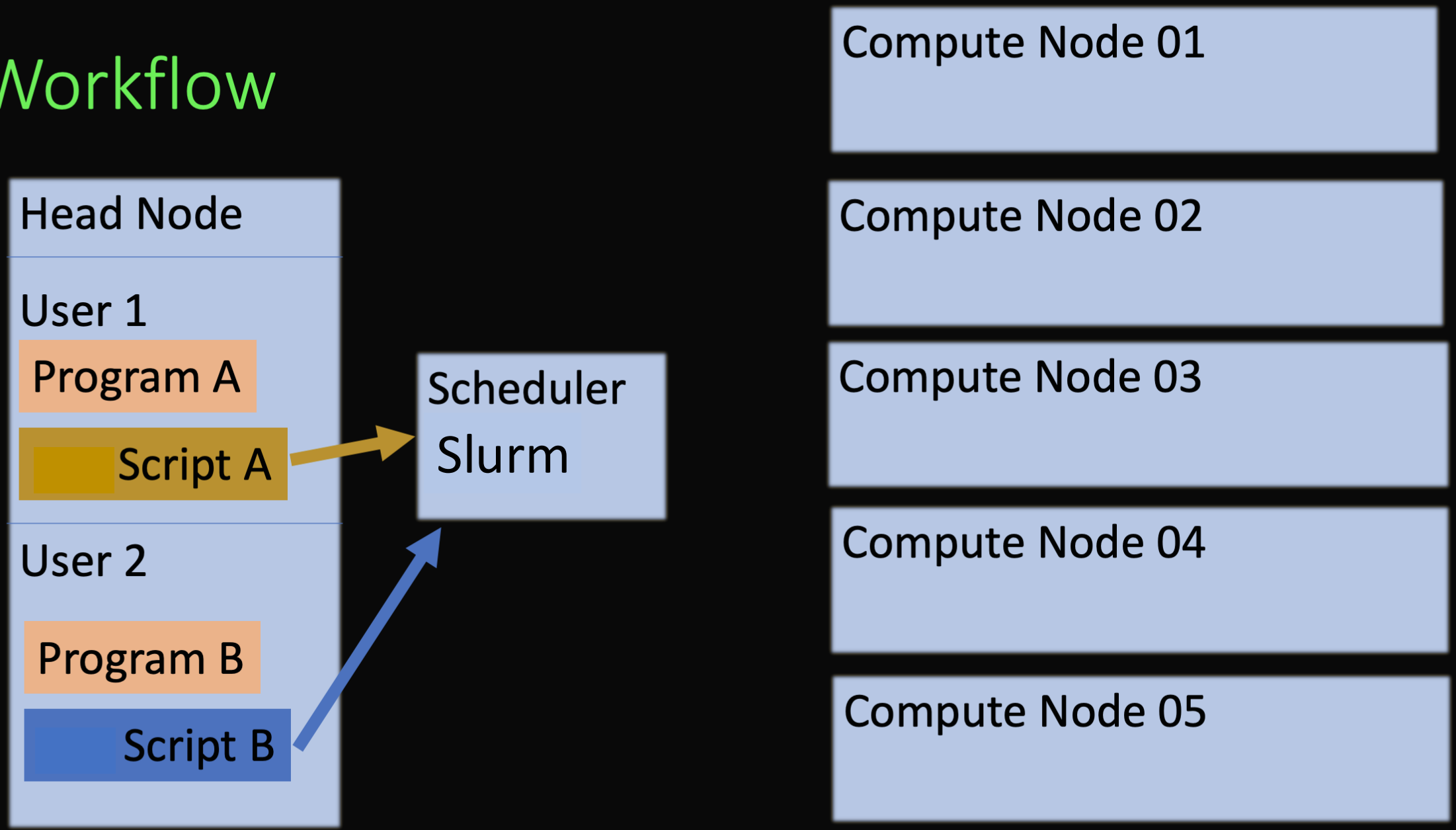
This indicates that the script was successfully sent to the scheduler.

The commands in the script will run as soon as the hardware requested is available.

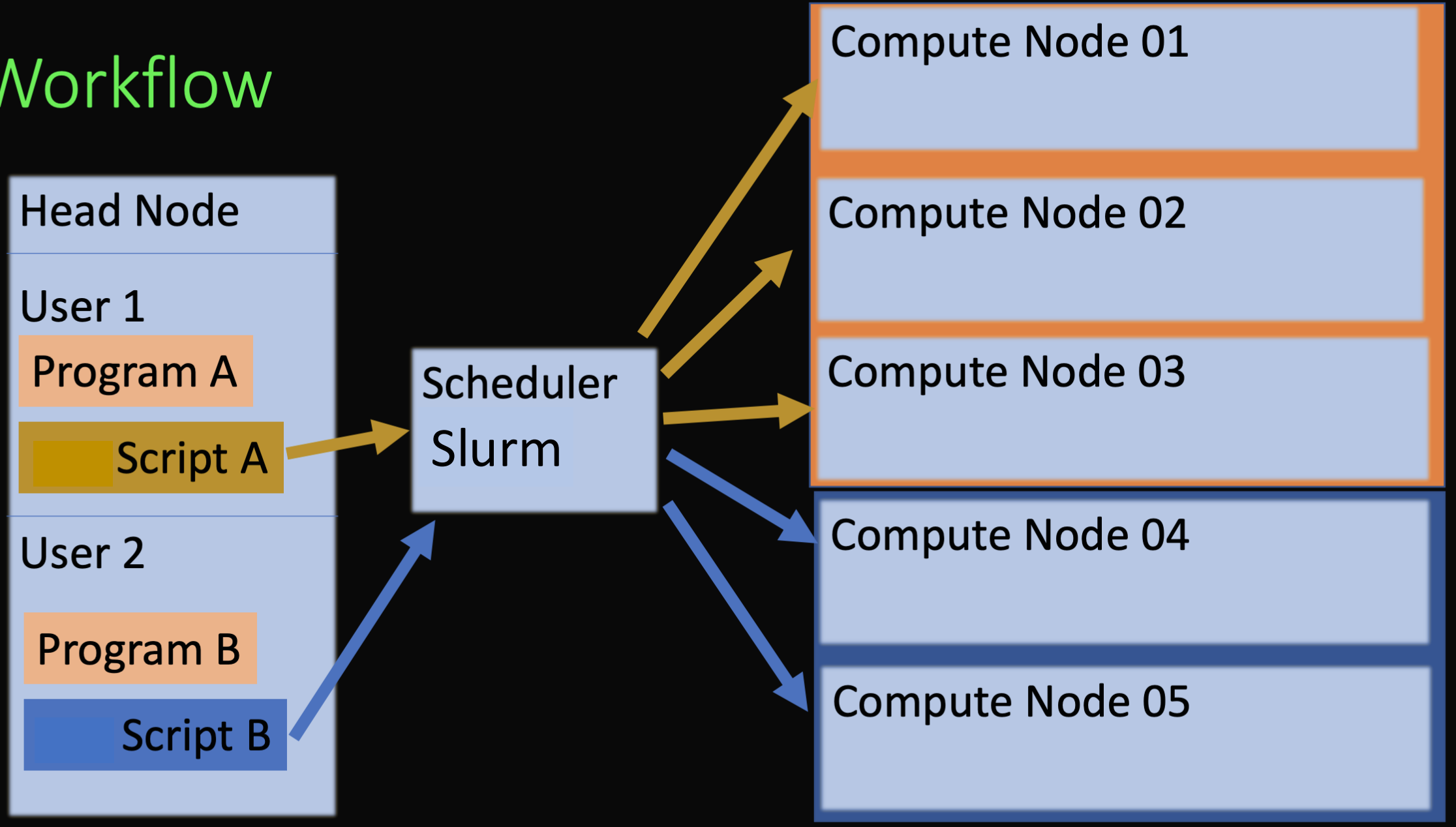
Workflow


Head Node
User 1
Program A
Script A
User 2
Program B
Script B
Compute Node 01
Compute Node 02
Compute Node 03
Compute Node 04
Compute Node 05
Shared filesystems – All nodes can access the same programs and write output

Workflow

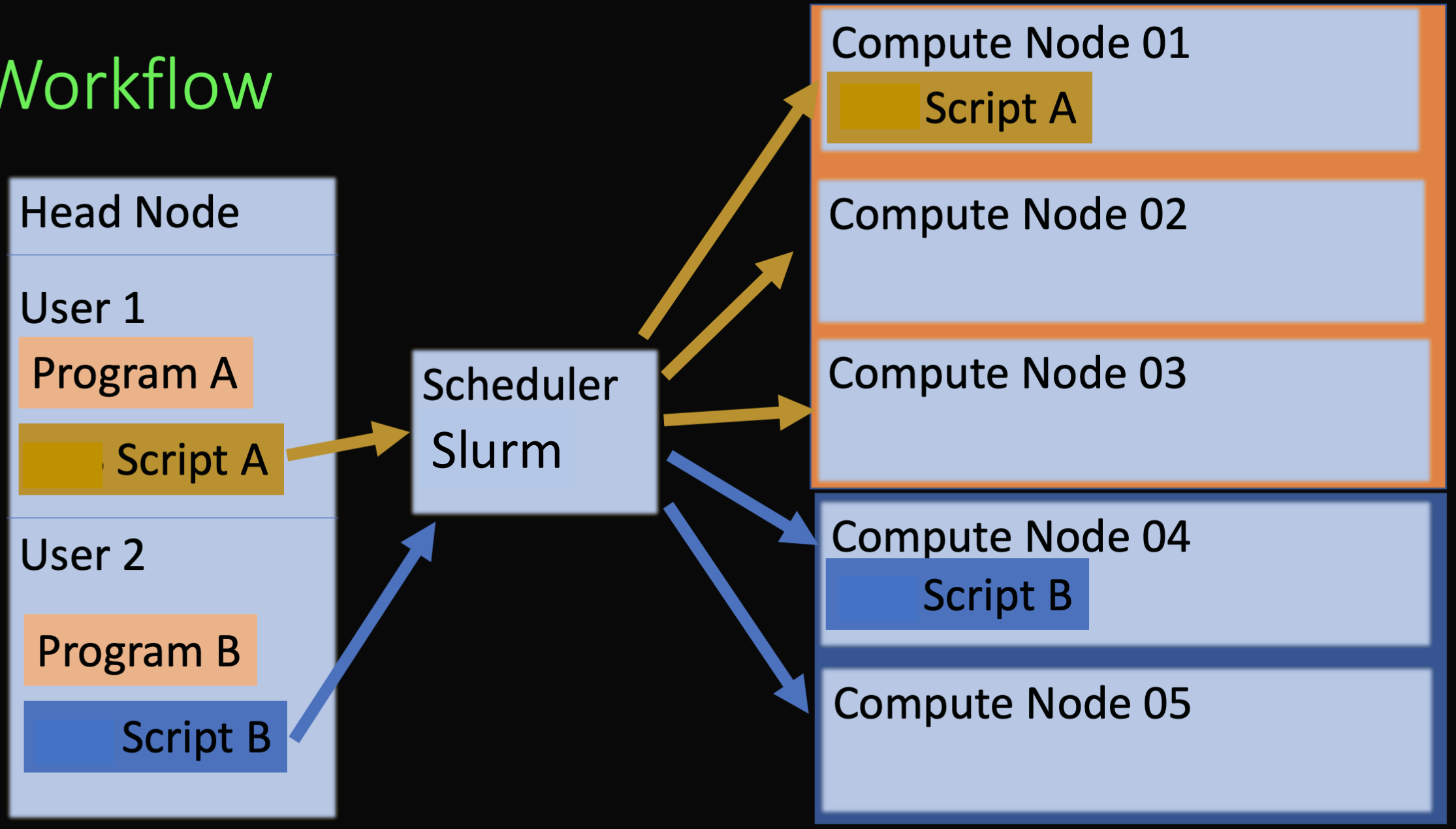

Head Node
User 1
Program A
Script A
User 2
Program B
Script B
Scheduler
Slurm
Compute Node 01
Compute Node 02
Compute Node 03
Compute Node 04
Compute Node 05
Shared filesystems – All nodes can access the same programs and write output

Workflow



Shared filesystems – All nodes can access the same programs and write output

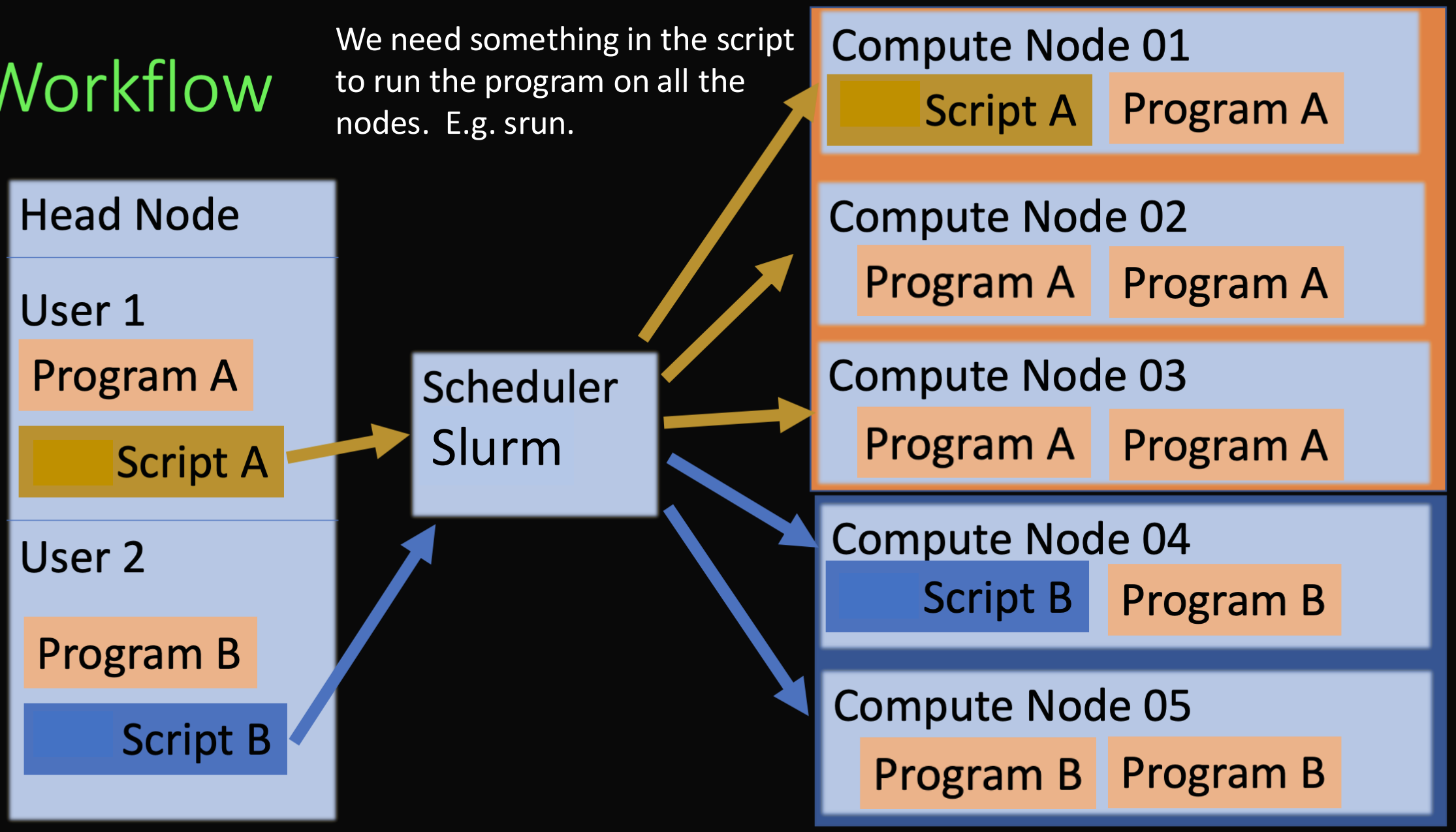
Workflow



Shared filesystems – All nodes can access the same programs and write output

Workflow

We need something in the script to run the program on all the nodes. E.g. srun.



Shared filesystems – All nodes can access the same programs and write output

```
[vanilla@hopper intro_workshop]$ ls
code  data  pbs  slurm  slurm-5252.out
```

The hostname command is very fast so everyone's job should finish in a few seconds.

When it is finished you will have a new file named slurm-{your job id}.out.

```
[vanilla@hopper intro_workshop]$ ls
code  data  pbs  slurm  slurm-5252.out
```

When it is finished you will have a new file named slurm-{your job id}.out.

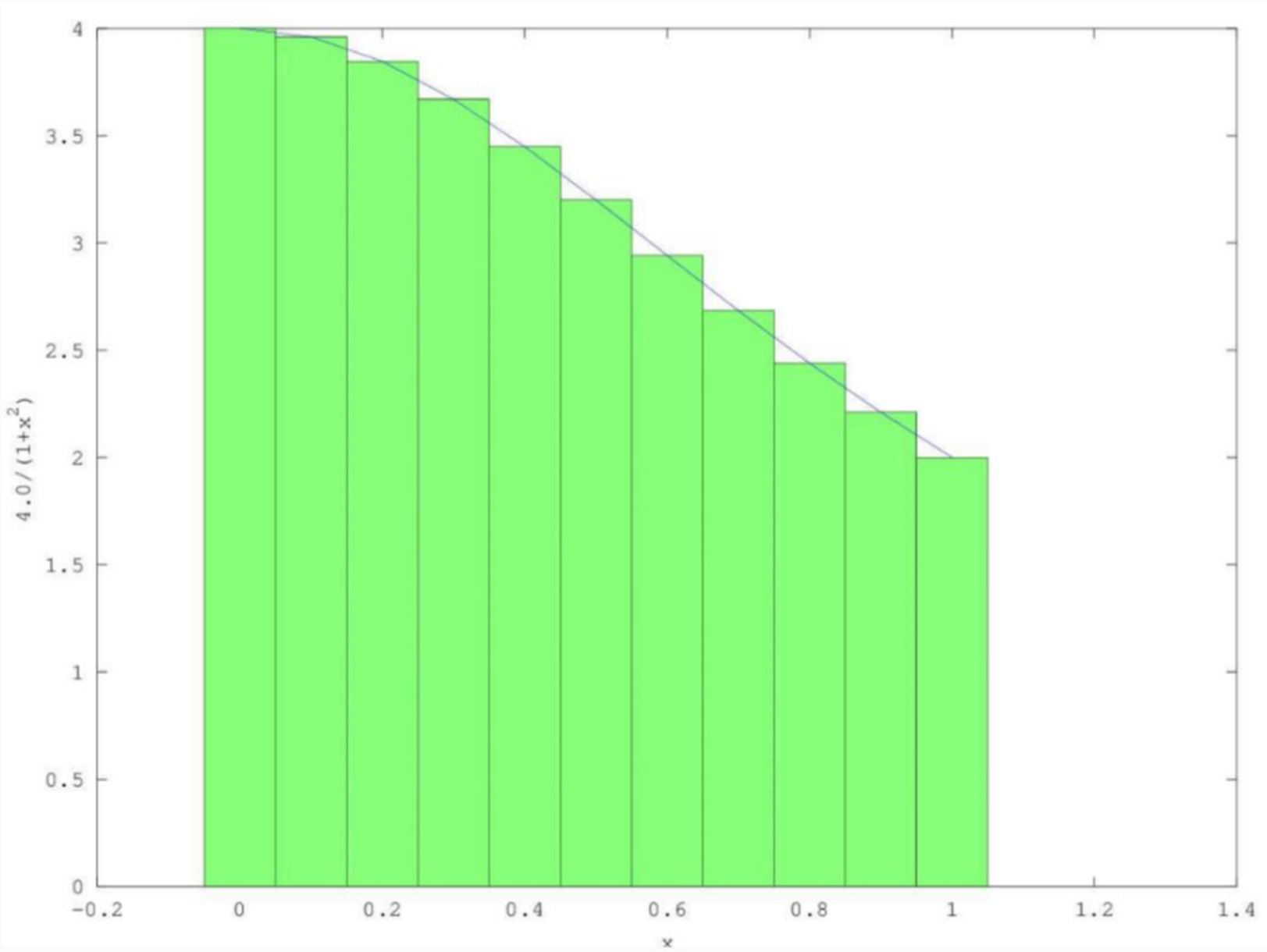
```
[vanilla@hopper intro_workshop]$ cat slurm-5252.out
hopper011
```

```
[vanilla@hopper intro_workshop]$ ls
code  data  pbs  slurm  slurm-5252.out
```

When it is finished you will have a new file named slurm-{your job id}.out.

```
[vanilla@hopper intro_workshop]$ cat slurm-5252.out
What do you see?
```

Serial Program to Calculate π



$$\int \frac{4}{1+x^2} = \pi$$

$$\Sigma_{i=1}^{N} \frac{4}{1+\left(\frac{i+\frac{1}{2}}{N}\right)^2} \approx \pi$$

```
[vanilla@hopper intro_workshop]$ module load miniconda3
[vanilla@hopper intro_workshop]$ conda create -n numpy numpy
```

Wait a while – introduce yourselves to your neighbor…

Conda allows you to install software into your home directory. In this case we need the numerical python libraries for calcPiSerial.py

Let's experiment with a program that does slightly more than print the hostname.

```
[vanilla@hopper intro_workshop]$ source activate numpy
[vanilla@hopper intro_workshop]$ srun --partition debug python code/calcPiSerial.py 10
srun: Using account 2016199 from ~/.default_slurm_account
You have not been allocated GPUs. To request GPUs, use the -G option in your submission
script.
Pi = 3.142425985001098709 40, (Diff=0.00083333141130559341) (calculated in 0.000005 secs
with 10 steps)
```

Activate the numpy environment and
Run calcPiSerial.py on a compute node.

For our example program the more steps it takes the more accurate it is, but the longer it takes.

```
[vanilla@hopper intro_workshop]$ sbatch slurm/calc_pi_serial.sh
 sbatch: Using account 2016199 from ~/.default_slurm_account
Submitted batch job 5263
vanilla@hopper:~/workshops/intro_workshop$ squeue –-me
JOBID PARTITION     NAME     USER ST      TIME  NODES NODELIST(REASON)
5263     debug calc_pi_  vanilla  R      0:44      1 hopper011
```

Edit slurm/calc_pi_serial.sh.
Change the email address to your address and submit the script.

Then enter squeue --me to see the job status.

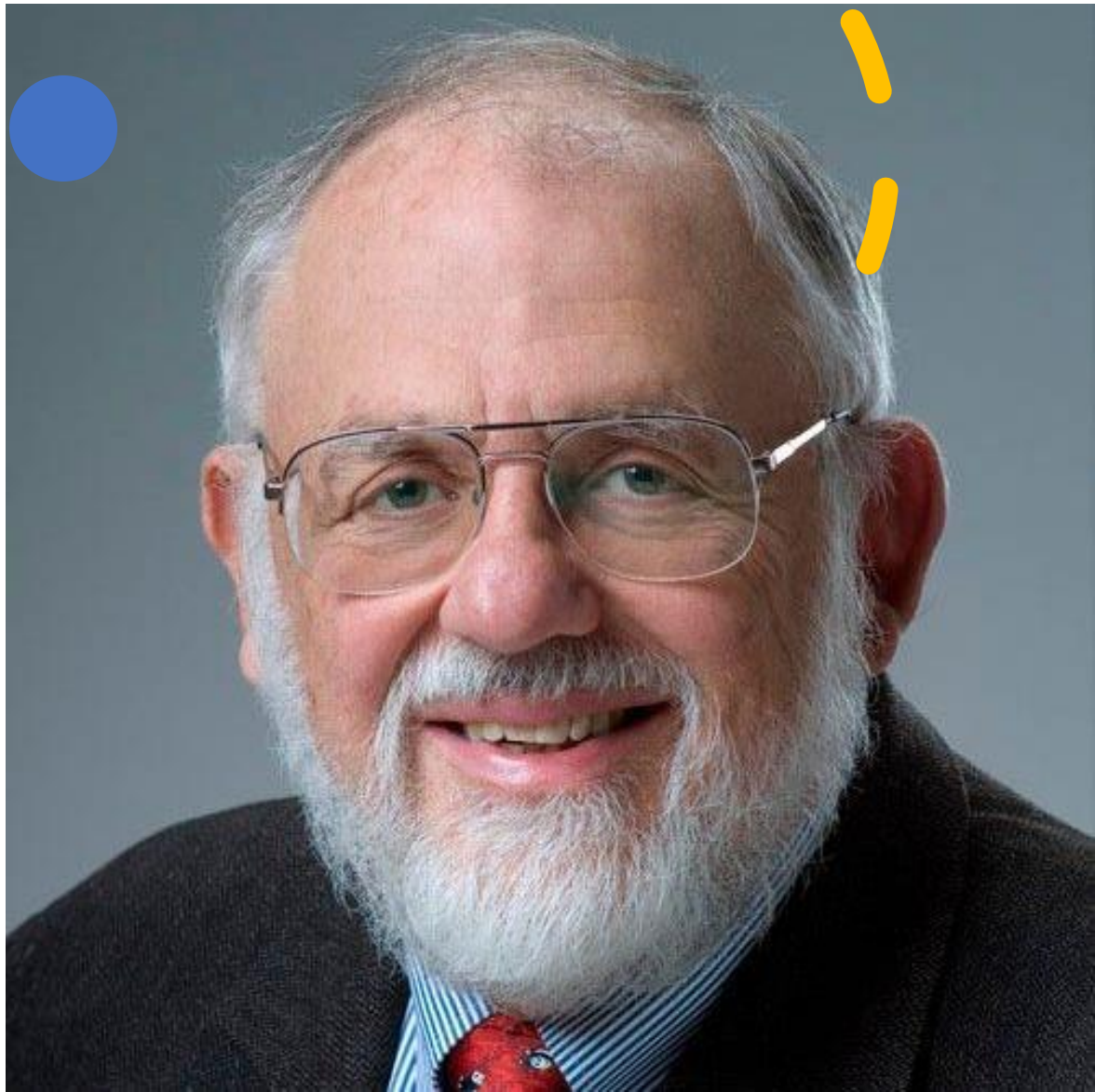
Take a look at the job output.

Parallelism – Embarrassingly Parallel

- Embarrassingly parallel (Cleve Moler) are problems that are really really easy to speed up with mode CPUs.

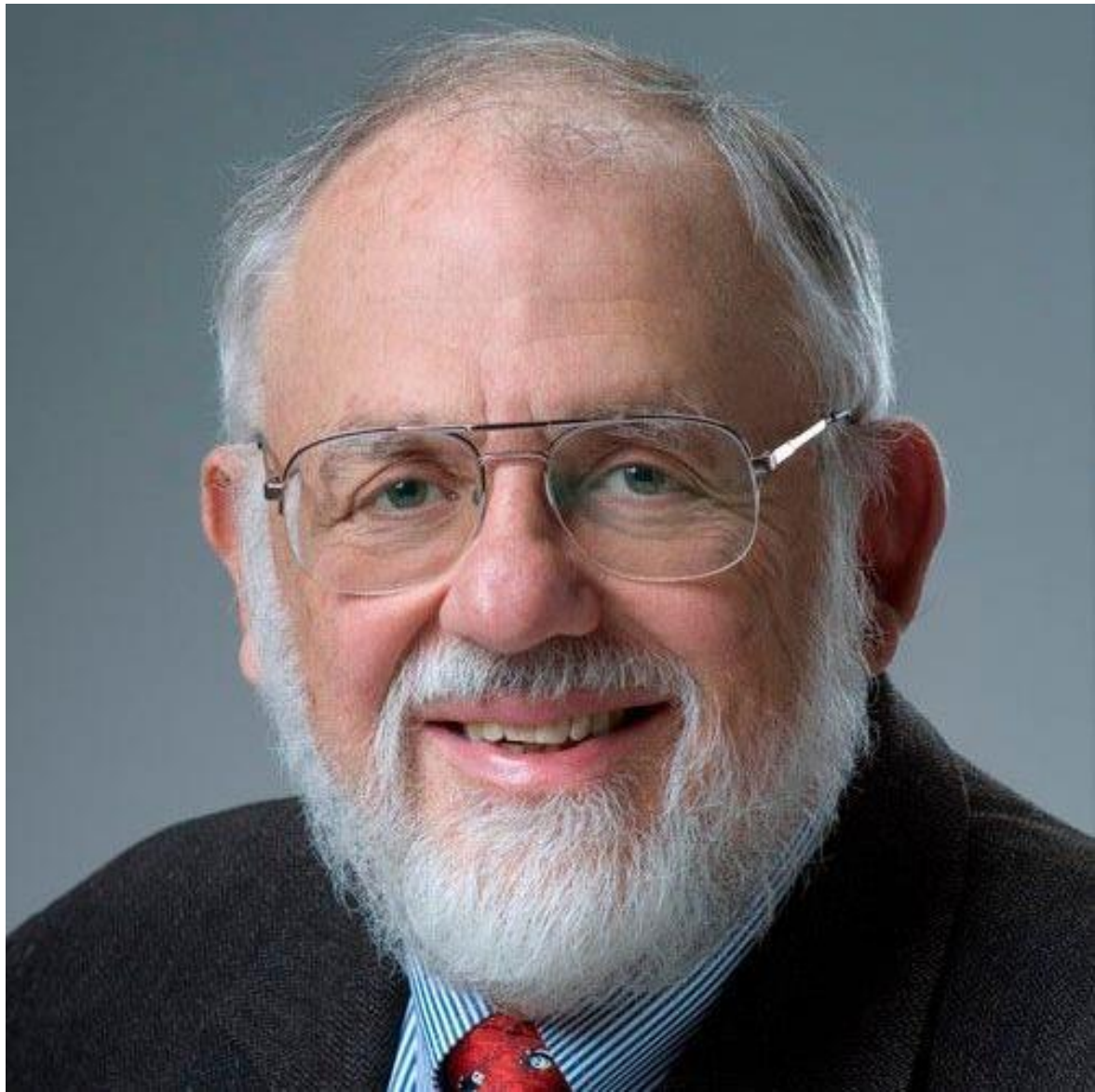
- The most common example is that you have a program that runs in serial and takes some input file, processes it, and produces some output.

- The problem is that you have 1,000 of the input files and want to run your program on each one.



Parallelism – Embarrassingly Parallel

This is ”embarrassing” because all you have to do is run 1,000 copies of your program on 1,000 CPUs each with a different input file and you are done.



SLURM ARRAYS

- One way to run the 1,000 copies of your program on 1,000 different inputs would be to write 1,000 slurm scripts each specifying a different input to your program and then sbatch submit them all. (this would work but there are better ways).

- SLURM arrays are used to schedule a lot of jobs with one slurm script.

```
[vanilla@hopper intro_workshop]$ nano slurm/calc_pi_array.sh
#!/bin/bash
#SBATCH --partition debug
#SBATCH --ntasks 1
#SBATCH --time 00:05:00
#SBATCH --job-name calc_pi_array
#SBATCH --mail-user your_username@unm.edu
#SBATCH --mail-type ALL
#SBATCH --array=1-12%3

echo "$HOSTNAME - $SLURM_ARRAY_TASK_ID"

module load miniconda3
source activate numpy

NUM_STEPS="${SLURM_ARRAY_TASK_ID}0000"
echo "Calculating pi with $NUM_STEPS..."
cd $SLURM_SUBMIT_DIR
python code/calcPiSerial.py $NUM_STEPS
```

Requires some annoying bash scripting.

$something means get the value of the variable "something"

--array says

1) **run 12 separate jobs**
2) **Store the count of the job in the variable SLURM_ARRAY_TASK_ID**

```
[vanilla@hopper intro_workshop]$ cat slurm/calc_pi_array.sh
#!/bin/bash
#SBATCH --partition debug
#SBATCH --ntasks 1
#SBATCH --cpus-per-task 3
#SBATCH --time 00:05:00
#SBATCH --job-name calc_pi_array
#SBATCH --mail-user your_username@unm.edu
#SBATCH --mail-type ALL
#SBATCH --array=1-12%3

echo "$HOSTNAME - $SLURM_ARRAY_TASK_ID"

module load miniconda3
source activate numpy

NUM_STEPS="${SLURM_ARRAY_TASK_ID}0000"
echo "Calculating pi with $NUM_STEPS..."
cd $SLURM_SUBMIT_DIR
python code/calcPiSerial.py $NUM_STEPS
```

```
[vanilla@hopper intro_workshop]$ sbatch slurm/calc_pi_array.sh
 sbatch: Using account 2016199 from ~/.default_slurm_account
Submitted batch job 5263
vanilla@hopper:~/workshops/intro_workshop$ squeue --me
JOBID PARTITION     NAME     USER ST      TIME  NODES NODELIST(REASON)
5263     debug calc_pi_  vanilla  R      0:44      1 hopper011
```

Submit the array script.
Then enter squeue --me to see the job status.
Take a look at the job output. (How many output files do you have?)

JOB arrays are OK or very simple inputs like programs that take a single file as input. But even passing in a value takes some annoying variable manipulation.

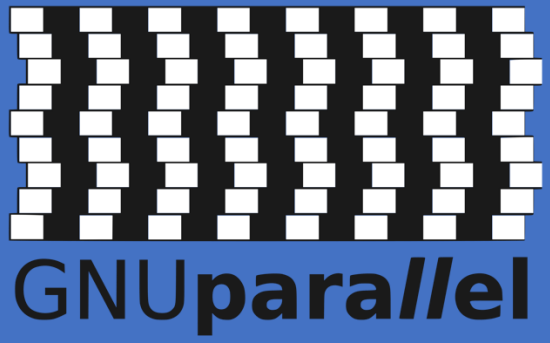
GNU Parallel is much more sophisticated it can take inputs in all sorts of ways. We will look at just 3 ways.

To access GNU parallel enter **module load parallel**

Let's experiment with parallel interactively…

***NOTE: we don't use srun to run parallel.**

GNU Parallel



Has been around for a very long time and has lots and lots of great features.

But basically it creates a job for every input it receives. The inputs can be specified in the command, read from a file, or be the output of another program.

It also remembers which jobs have finished and which still need to be run. So when you run out of time and resubmit it will automatically pick up where it left off.

```
[vanilla@hopper intro_workshop]$ salloc --partition debug --ntasks 2
salloc: Using account 2016199 from ~/.default_slurm_account
salloc: Granted job allocation 5275
salloc: Waiting for resource configuration
salloc: Nodes hopper011 are ready for job

$ LANG=C
$ parallel python code/calcPiSerial.py ::: 10 20 30 40

Pi = 3.141800986893094282 95, (Diff=0.000208333330330116695) (calculated in 0.000006 secs
with 20 steps)
Pi = 3.141644736922657443 76, (Diff=0.000052083333286432776) (calculated in 0.000008 secs
with 40 steps)
Pi = 3.142425985001098709 40, (Diff=0.000833331411305593 41) (calculated in 0.000006 secs
with 10 steps)
Pi = 3.141685246179748425 28, (Diff=0.000092592589955309 28) (calculated in 0.000012 secs
with 30 steps)
```

```
[vanilla@hopper intro_workshop]$ seq 10 10 100
10
20
30
40
50
60
70
80
90
100
```

GNU Parallel can read the output of other programs and use them as inputs to your program.
Here a copy of calc pi is run for each row in the output of seq

```
[vanilla@hopper intro_workshop]$ seq 10 10 100 | parallel python code/calcPiSerial.py
Pi = 3.141800986893094282 95, (Diff=0.00020833330330116695) (calculated in 0.000007 secs with 20 steps)
Pi = 3.142425985001098709 40, (Diff=0.00083333141130559341) (calculated in 0.000006 secs with 10 steps)
Pi = 3.141685246179748425 28, (Diff=0.00009259258995530928) (calculated in 0.000007 secs with 30 steps)
etc
```

```
[vanilla@hopper intro_workshop]$ find -name *.sh
./slurm/calc_pi_array.sh
./slurm/calc_pi_mpi.sh
./slurm/calc_pi_parallel.sh
./slurm/calc_pi_serial.sh
./slurm/gaussian.sh
./slurm/hostname_mpi.sh
etc

$ find -name *.sh | parallel wc -l
7 ./code/vecadd/vecaddmpi_cpu.sh
19 ./slurm/calc_pi_array.sh
15 ./slurm/calc_pi_mpi.sh
20 ./slurm/calc_pi_parallel.sh
14 ./slurm/calc_pi_serial.sh
16 ./slurm/gaussian.sh
15 ./slurm/hostname_mpi.sh
etc
```

A common application is to use find to produce a list of paths with some extension.

Then parallel runs some program on each path.

In this case wc -l counts the lines in a file. In some real CARC examples the input files are phylogenetic trees, graphs, neuroimages, or CT scans.

```
[vanilla@hopper intro_workshop]$ exit
exit
salloc: Relinquishing job allocation 5275
```

Don’t forget to exit your salloc allocation.

```
(numpy)[vanilla@hopper intro_workshop]$ cat slurm/calc_pi_parallel.sh
#!/bin/bash
#SBATCH --partition debug
#SBATCH --nodes 2
#SBATCH --ntasks-per-node 4
#SBATCH --time 00:05:00
#SBATCH --job-name calc_pi_parallel
#SBATCH --mail-user your_username@unm.edu
#SBATCH --mail-type ALL

module load parallel
module load miniconda3
source activate numpy

LANG=C
cd $SLURM_SUBMIT_DIR
parallel --sshloginfile $PBS_NODEFILE \
--env PATH \
--workdir $SLURM_SUBMIT_DIR \
"hostname; python code/calcPiSerial.py {}" :::: data/step_sizes.txt
```

Take a look at slurm/calc_pi_parallel.sh.

In this example parallel reads the parameters from a file and runs a copy of calcPiSerial.py on each row.

```
(numpy)$sbatch slurm/calc_pi_parallel.sh
sbatch: Using account 2016199 from ~/.default_slurm_account
Submitted batch job 5276
```

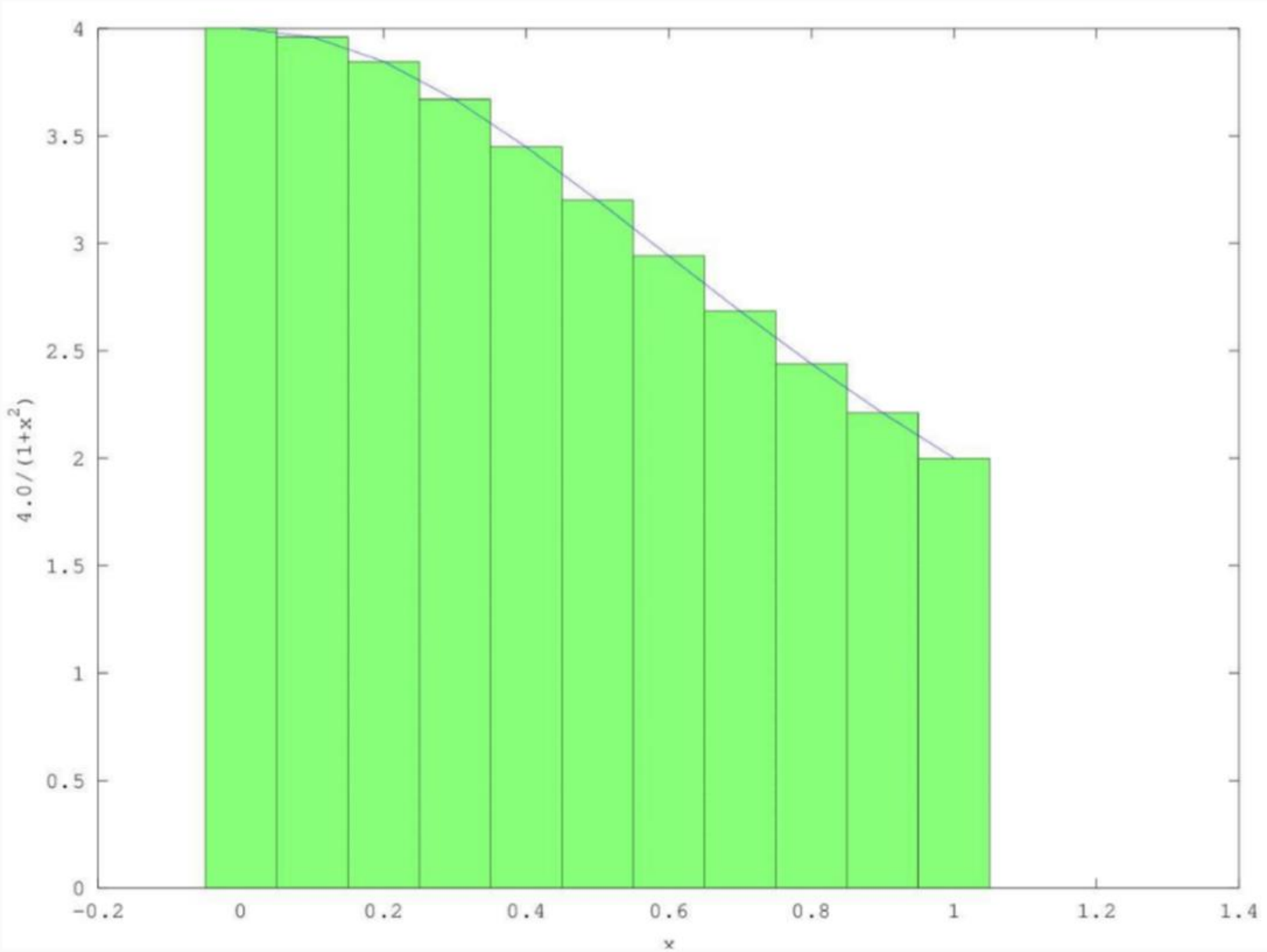
Submit the job, check it's progress with squeue --me, and take a look at the output.

Parallelism – Coupled Parallelism

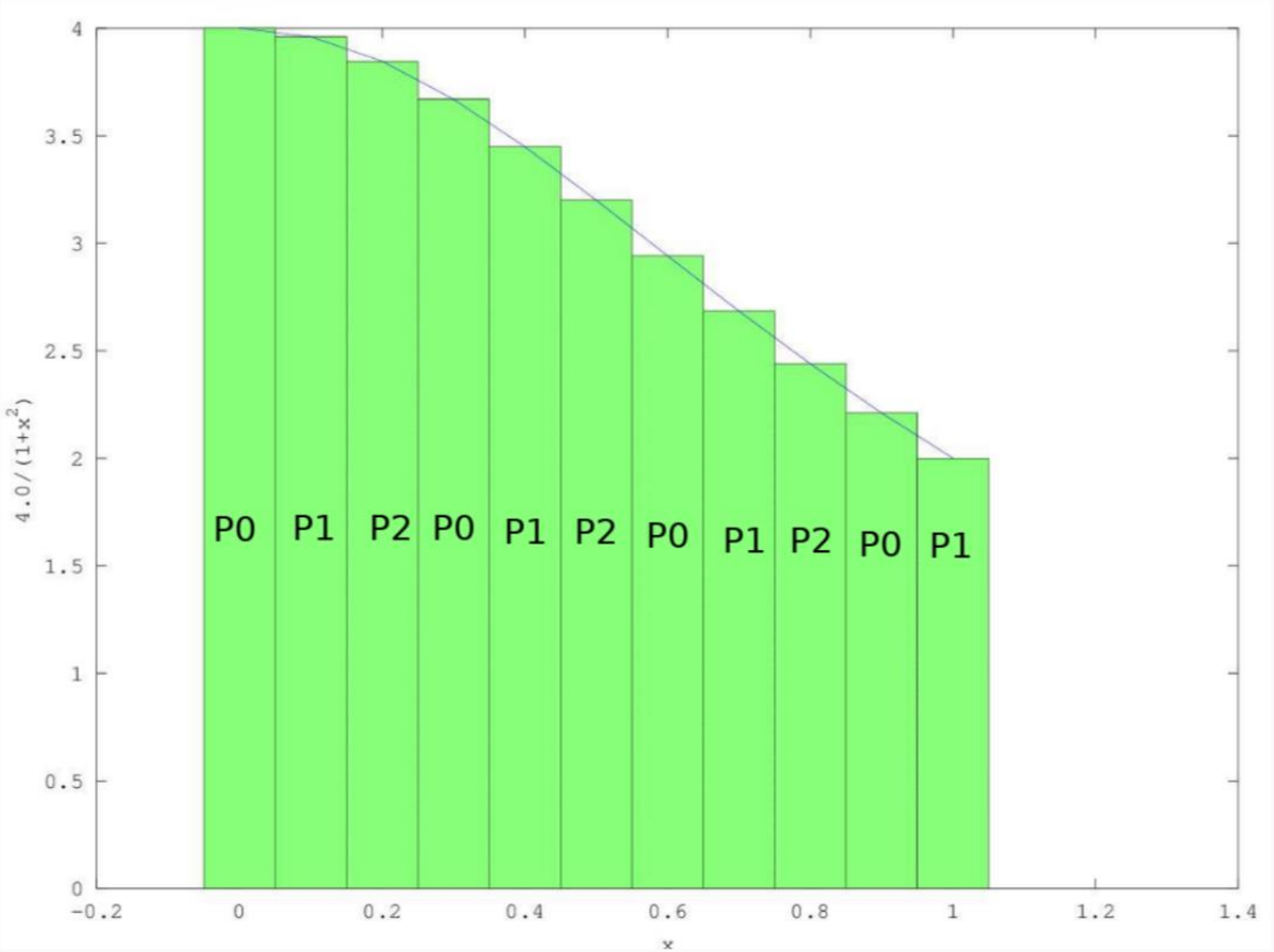
- Coupled problems are those where the CPUs need to work together to solve a problem by communicating with each other.
- Many commercial and research programs designed to run on HPC systems like CARC use a library called the message passing interface (MPI) to do this.

- We have written an MPI version of our python pi calculator to demonstrate.

Serial Program to Calculate π



Parallel Program to Calculate π



MPI: Message Passing Interface

When programs need to run on many processors but also communicate with one another.

Here the parallel version of calcPi needs to communicate the partial sums computed by each process so they can all be added up.
To communicate we will use the MPI library.

Make sure you are in the ~/workshops/intro_workshops directory.
Install your mpi conda environment from file:

```
conda env create –f conda_env/mpi_numpy.yml
```

```
import time
import sys
import numpy as np # Value of PI to compare to

##################### SETUP MPI - START ####################
from mpi4py import MPI        #Import the MPI library
comm = MPI.COMM_WORLD         #Communication framework
root = 0                      #Root process
rank = comm.Get_rank()        #Rank of this process
num_procs = comm.Get_size()   #Total number of processes
############################## END ##############################

#Distributed function to calculate pi
def Pi(num_steps):
    step = 1.0 / num_steps
    sum = 0
    for i in range(rank, num_steps, num_procs): # Divide sum among
processes
        x = (i + 0.5) * step
        sum = sum + 4.0 / (1.0 + x * x)
    mypi = step * sum

    # Get that partial sums from all the processes, add them up, and give
to the root process
    pi = comm.reduce(mypi, MPI.SUM, root)
    return pi
```

```
#Main function
# Check that the caller gave us the number of steps to use
if len(sys.argv) != 2:
    print("Usage: ", sys.argv[0], " <number of steps>")
    sys.exit(1)

num_steps = int(sys.argv[1],10);

#Broadcast number of steps to use to the other processes
comm.bcast(num_steps, root)

# Call function to calculate pi
start = time.time() #Start timing
pi = Pi(num_steps) # Call the function that calculates pi
end = time.time() # End timing

# If we are the root process then print our estimation of pi,
# the difference from numpy's value, and how long it took
print("Pi = %.20f, (Diff=%.20f) (calculated in %f secs with %d
steps)" %(pi, pi-np.pi, end - start, num_steps))
```

```
#!/bin/bash
#SBATCH --partition debug
#SBATCH --nodes 2
#SBATCH --ntasks-per-node 4
#SBATCH --time 00:05:00
#SBATCH --job-name calc_pi_mpi
#SBATCH --mail-user your_username@unm.edu
#SBATCH --mail-type ALL

module load miniconda3
source activate mpi_numpy

cd $SLURM_SUBMIT_DIR
srun --mpi=pmi2 python code/calcPiMPI.py 1000000000
```

sbatch slurm/calc_pi_mpi.sh

```
srun --mpi=pmi2 python code/calcPiMPI.py 1000000000
```

srun understands MPI programs!

If you ever used mpirun or mpiexec you had to provide a lot of parameters to describe how many compute nodes you had and what their names are, etc.

But srun is part of SLURM so it already knows all that.

The only thing you have to specify is the communication library to use. In our case “pmi2”.

Experiment

Run calc_pi_mpi.sh.

Vary the number of tasks it uses.

Use squeue to monitor the state of your job,

Look at your output files.

What is the relationship between the number of tasks and how cast it calculates pi?

Useful Slurm Commands

squeue --me --long	shows information about jobs you submitted
squeue --me --start	shows when slurm expects your job to start
scancel jobid	cancels a job
scancel --u $USER	cancels all your jobs
sacct	shows your job history
seff jobid	shows how efficiently the hardware was used