

High Performance Computing

Running code on giant computing clusters

COMPASS 2024

Image credit: Owen Stanley, SDSC/UC San Diego

What Is HPC?



Laptop



Supercomputer

What Is HPC?



Laptop

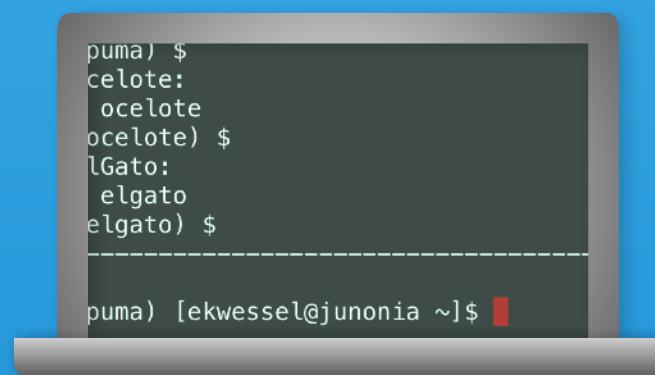


Supercomputer

Computing Cluster

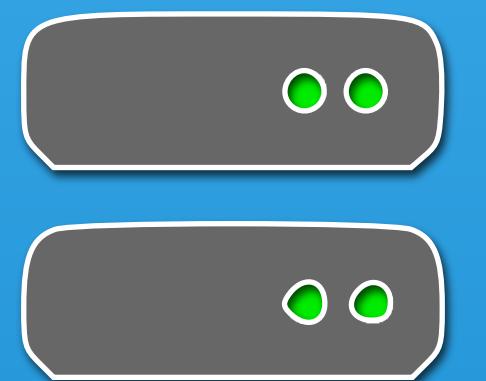
You are here

Your computer

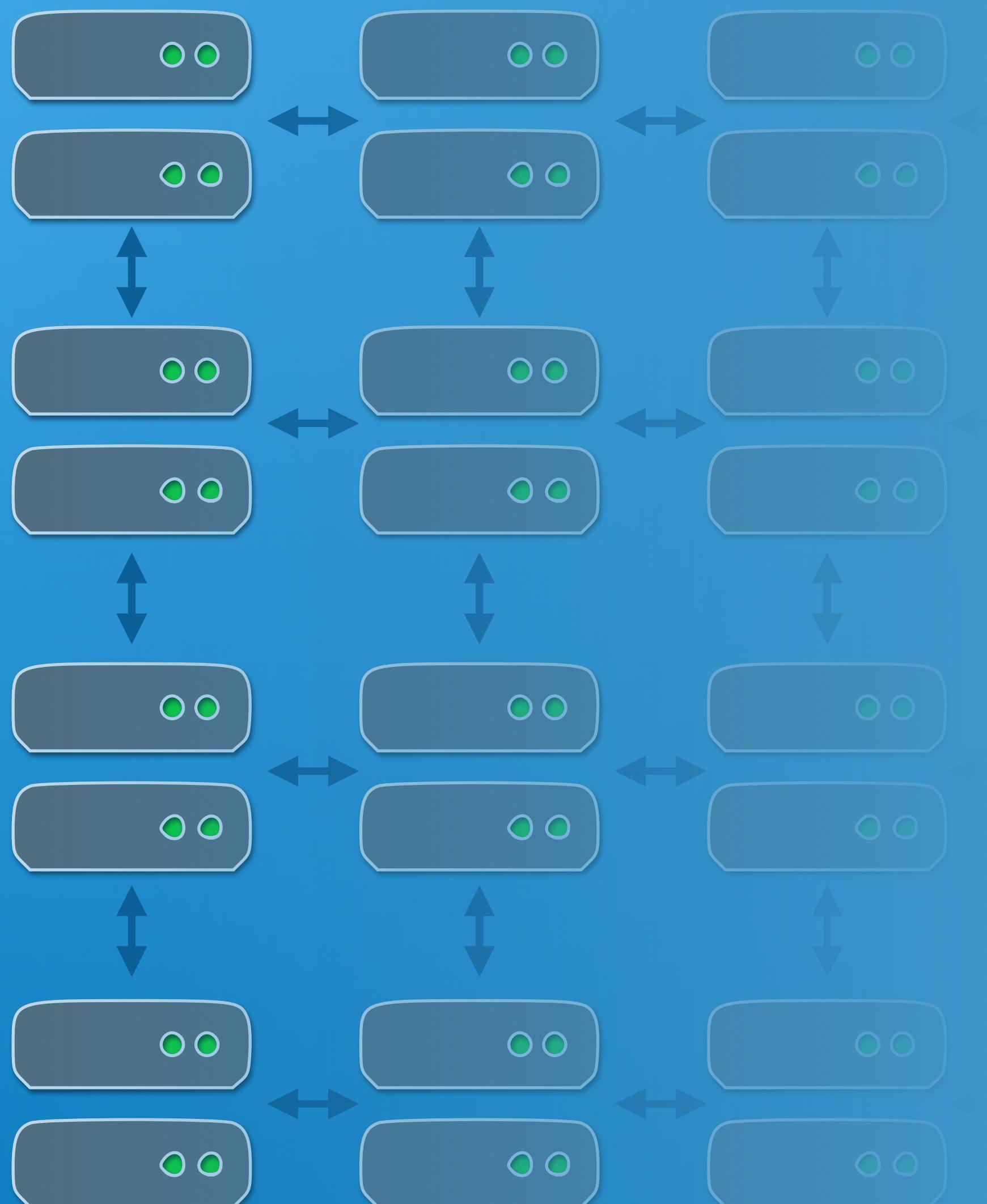


Internet

Log-in node



Local connections



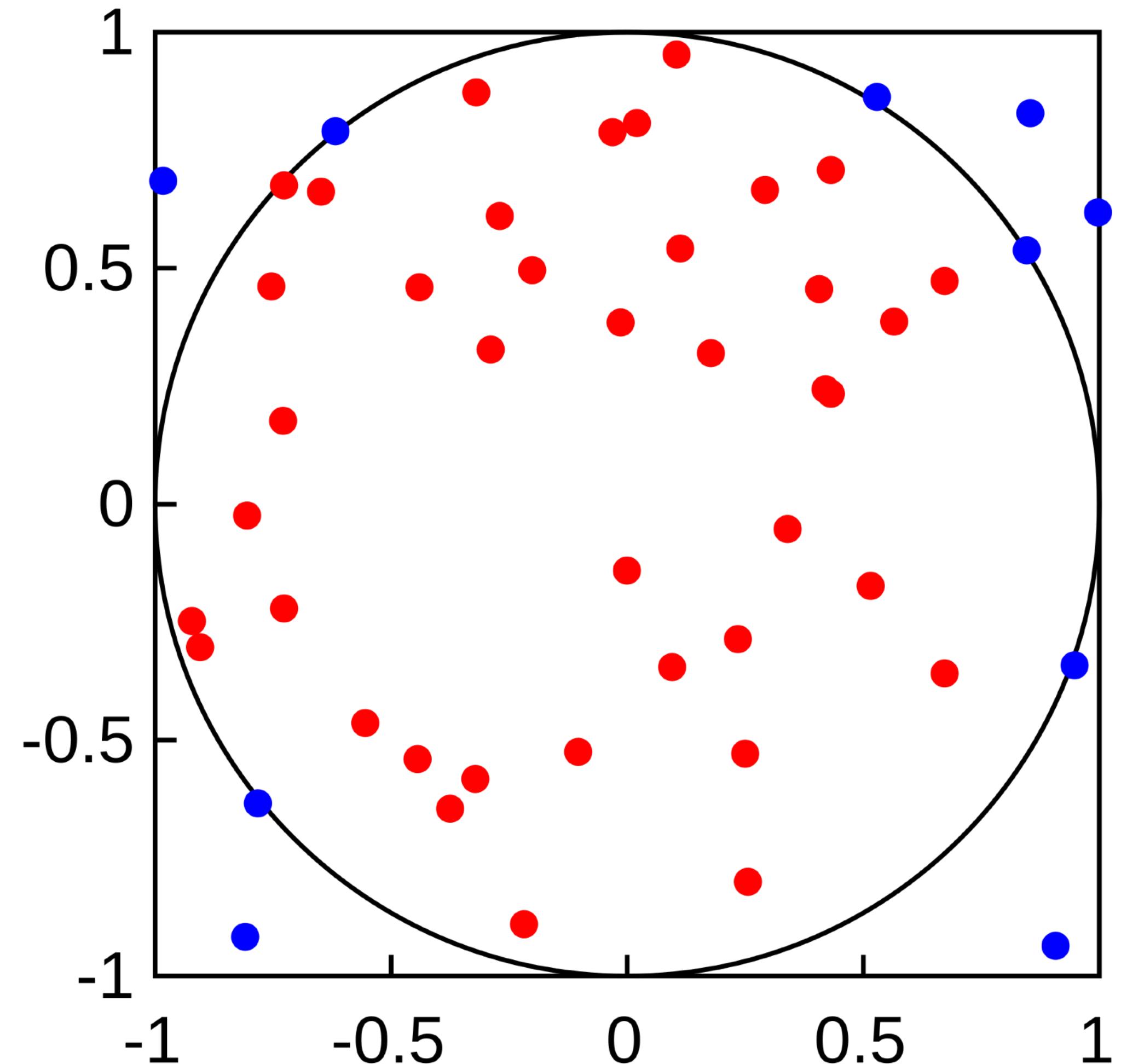
Part I: Writing some code

Part II: Running it on the HPC Cluster

Computing the value of π

(In the worst way...)

- Randomly place a dot in the square
- What is the probability of it landing inside the circle?
- Average number red dots / blue dots =... ?

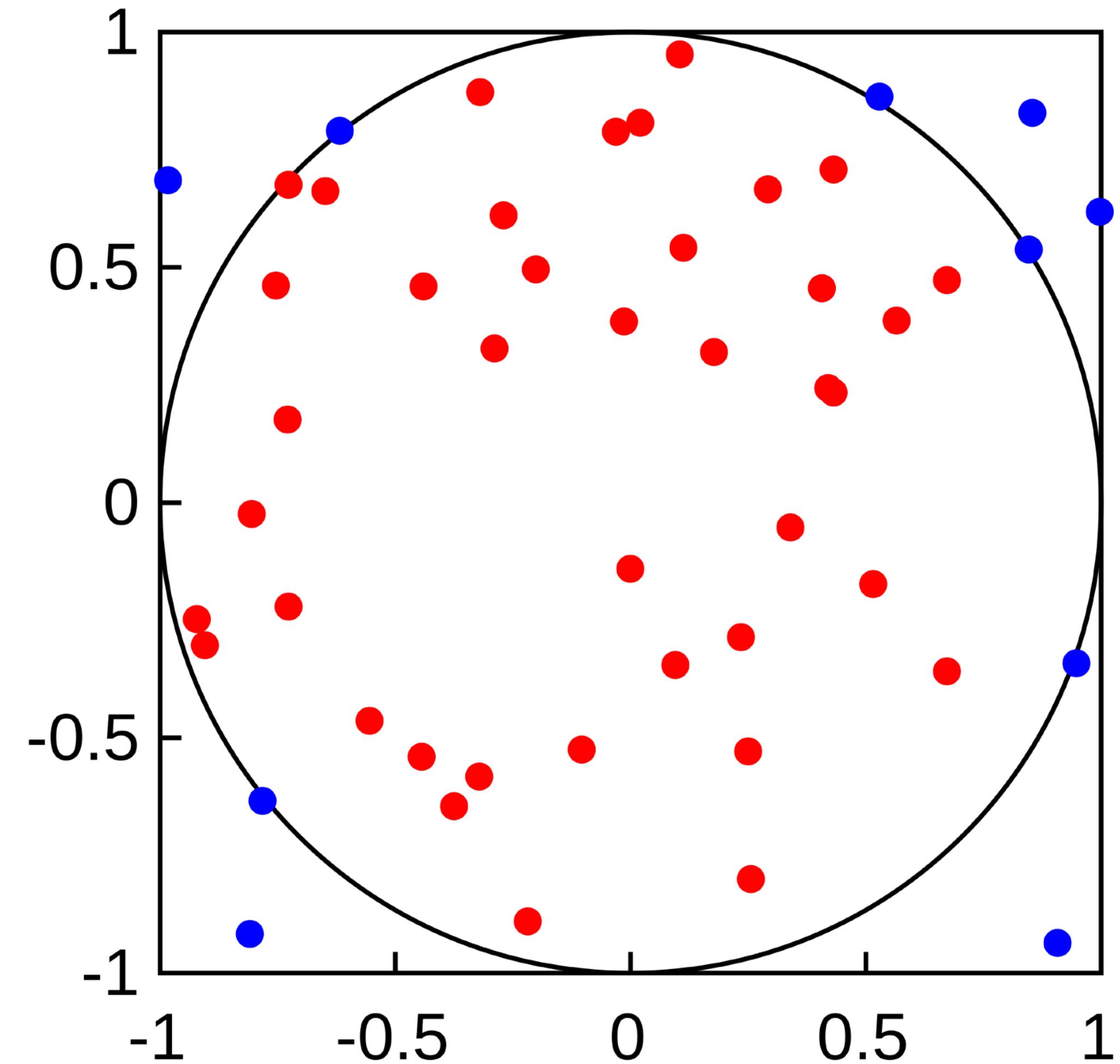


Computing the value of π

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$$\frac{\pi r^2}{4r^2} = \frac{\pi}{4}$$



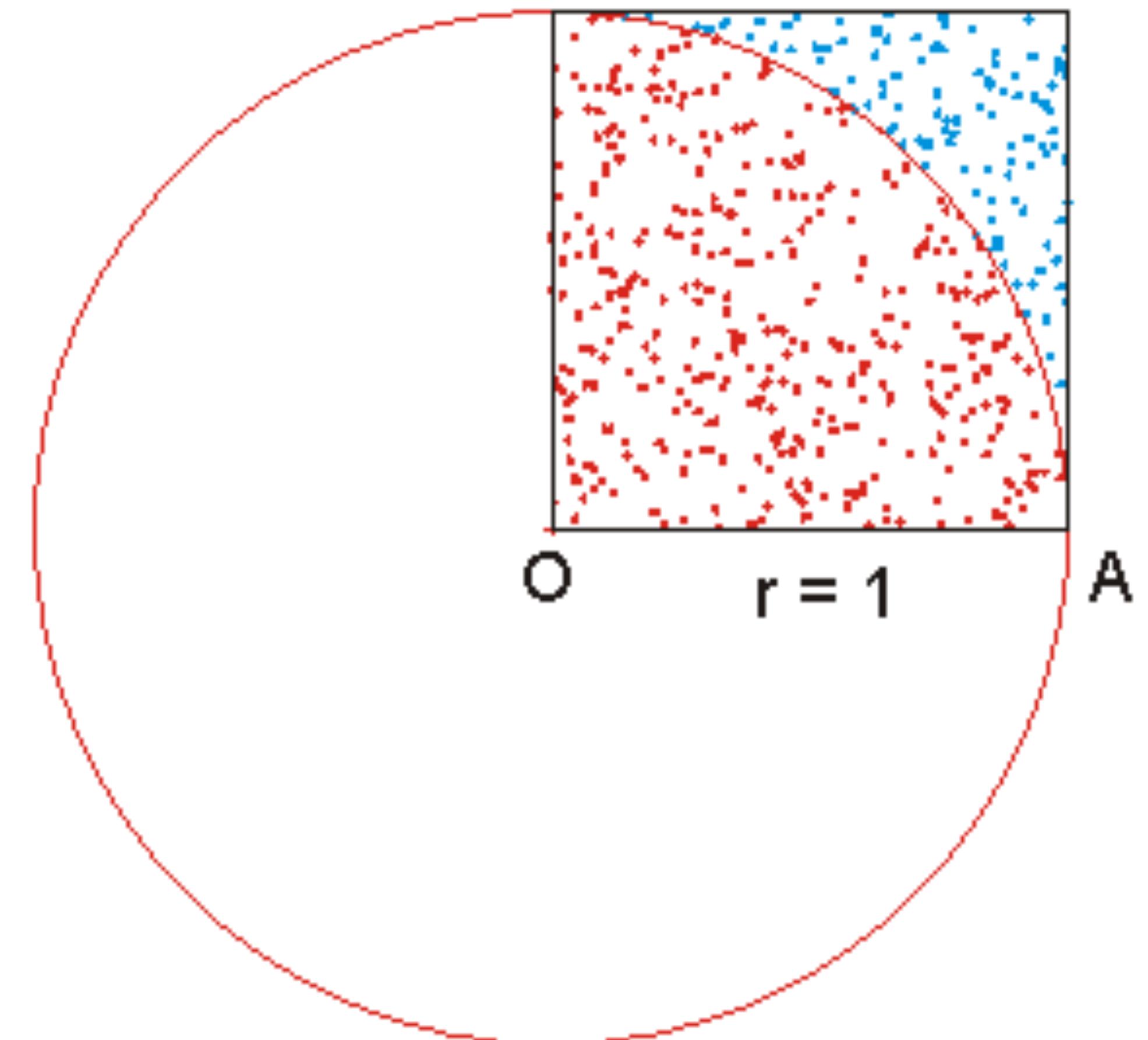
Computing the value of π

(In the worst way...)

I have written a program that:

- Randomly places a points in a square
- Counts how many are within a circle
- Estimates π from the ratio
- We save effort by only doing this for one quarter of the square

This is called “Monte Carlo” integration



1. Make a “COMPASS” folder

2. Upload the monte_carlo_pi.py script

This is the UArizona *Open OnDemand* server.

Please NOTE: "windfall" jobs will be restarted or terminated without notice if pre-empted by a "standard" job in queue.

The screenshot shows a file browser interface with the following elements:

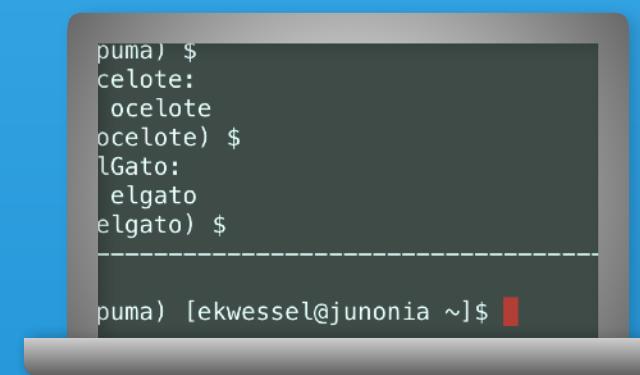
- Top Bar:** Includes links for Apps, Files, Jobs, Clusters, Interactive Apps, My Interactive Sessions, Help, and Log Out.
- Toolbar:** Buttons for Open in Terminal, Refresh, New File, New Directory, Upload (circled in red), Download, Globus, Copy/Move, and Delete.
- Left Sidebar:** Home Directory, /groups, and /xdisk.
- Path Bar:** Shows the current path: / home / u27 / ekwessel /.
- File List:** Shows 48 of 106 rows selected. The columns are Type, Name, Size, and Modified at. A single folder named "ApparentHorizonFinderTest2D" is listed under the "athenak" directory.

monte_carlo_pi.py

```
1 #!/usr/bin/env python3
2 import sys
3 import random
4
5 # First, we check that our script was called with the correct number of arguments
6 # If not, we print a usage message and exit:
7 if len(sys.argv) != 3:
8     print("Usage: monte_carlo_pi.py n_points seed_value")
9     sys.exit()
10
11 # Next, we get the two input arguments that our script was called with.
12 # These are the number of points to generate and the seed value for the random number generator.
13 n_points = int(sys.argv[1])
14 seed_value = int(sys.argv[2])
15
16 # Using the seed value, we initialize a random number generator
17 random.seed(seed_value)
18
19 # Count the number of points that fall within the unit circle
20 count = 0
21 for i in range(n_points):
22     x_point = random.random()
23     y_point = random.random()
24     if x_point**2 + y_point**2 <= 1:
25         count = count + 1
26
27 # The ratio of the area of the unit circle to the area of the unit square is pi/4
28 pi_estimate = 4*count/n_points
29
30 print(f"{pi_estimate:.20f}") # Print the estimate with 20 decimal places
--
```

You are here

Your computer



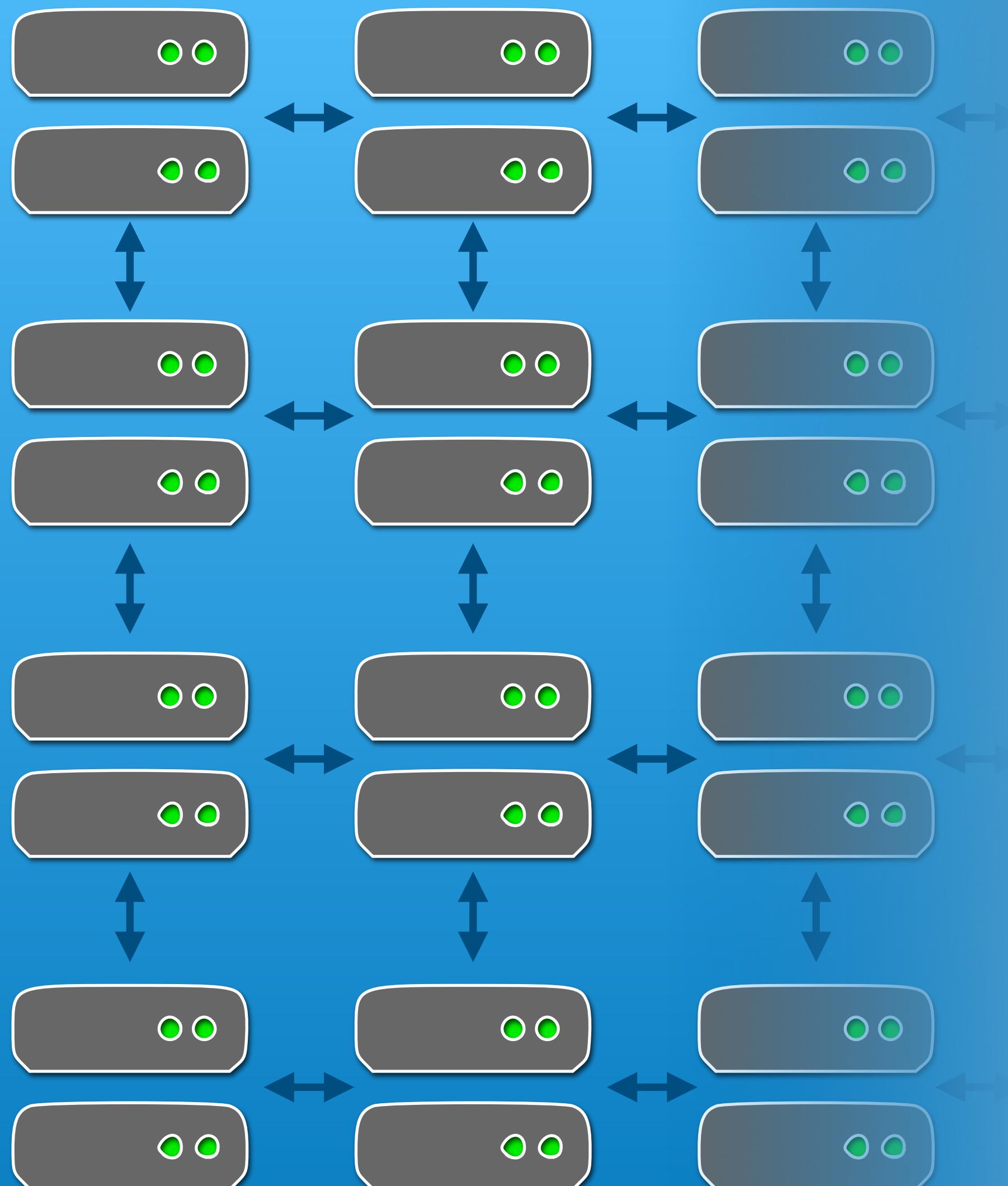
Your code belongs here

Log-in node

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Computing Cluster



Part I: Writing some code

Part II: Running it on the HPC Cluster

The HPC Job Scheduling Queue

- Every program users want to run is a **job**
- Users can add **jobs** to the **scheduling queue**
- The **scheduler** keeps track of the queue, decides when & where jobs run
- On UA's HPC the scheduler software is “Slurm”



Creating a job script

We use bash scripts to tell the scheduler what we want our jobs to do.

Makes this run as a bash script

Directives to the queue system

Commands to run when job starts

**Based on this template,
create your own
job submission script:
`job_sub.sh`**

```
#!/bin/bash

# -----
### Directives Section
# -----
#$SBATCH --job-name=hello_world
#$SBATCH --account=<your_group>
#$SBATCH --partition=standard
#$SBATCH --nodes=1
#$SBATCH --ntasks=1
#$SBATCH --time=00:01:00

# -----
### Code Section
# -----
echo "Hello world, I am running on compute node $HOSTNAME"
# sleep only used for demonstration purposes
sleep 30
```

Submitting a job to the queue

- To submit your job, use the **sbatch** command

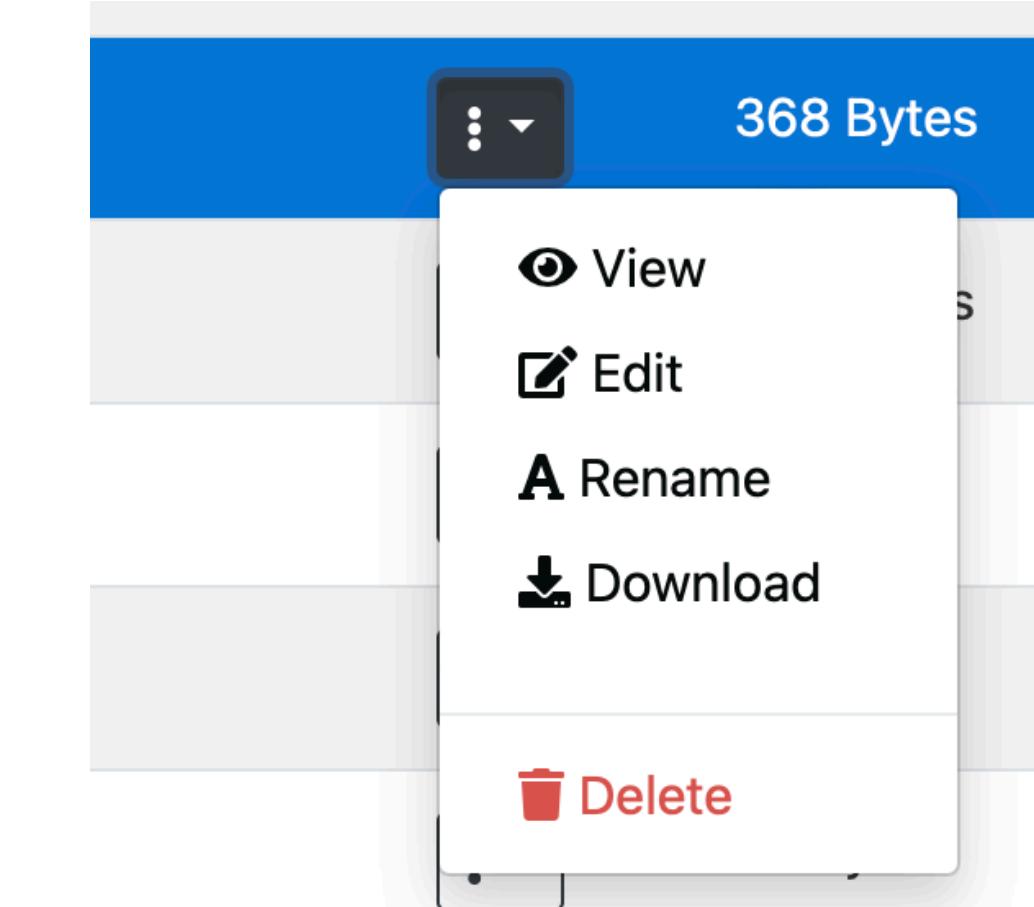
```
$ sbatch job_sub.sh
```

- To check on your job, use the **qstat** command

```
$ qstat -u <username>
```

Submitting a bunch of jobs to the queue

- To estimate π , we need many copies of `monte_carlo_pi.py` to run on the cluster
- The best way to do this is with a **job array**
- Make a new job submission script called `job_array_sub.sh`
- Edit it, and type the following:
- Submit using `sbatch`:
 \$ `sbatch job_array_sub.sh`



```
1 #!/bin/bash
2
3 #SBATCH -J monte_carlo_pi  # Job Name
4 #SBATCH -o monte_carlo_pi_%a.o%j
5 #SBATCH --partition=windfall
6 #SBATCH -N 1 -n 1
7 #SBATCH --mem-per-cpu=4gb
8 #SBATCH --cpus-per-task=1
9 #SBATCH -t 0:30:00      # Run time (hh:mm:ss)
10 #SBATCH --array 0-10
11
12 module load python
13
14 ./monte_carlo_pi.py 1000000000 $RANDOM
15 |
```

Viewing the results

- The files `monte_carlo_pi_*.o*` contain the output
- What output did you get?
- **Exercise: How can we combine the outputs?**
- How accurate was our estimate of π ?

One way to average the estimates

Save

/home/u27/ekwessel/COMPASS_2024/average.py

```
1 #!/usr/bin/env python3
2
3 import sys
4 import numpy as np
5
6 # First, we check that our script was called with the correct number of arguments
7 # If not, we print a usage message and exit:
8 if len(sys.argv) != 2:
9     print("Usage: average.py filename")
10    sys.exit()
11
12 filename = sys.argv[1]
13
14 estimate_array = np.genfromtxt(filename)
15
16 print(f"{np.mean(estimate_array):0.20f}")
```

UA HPC Resources

HPC Documentation:

<https://hpcdocs.hpc.arizona.edu/>

A wonderful introductory presentation by our HPC center staff:

[https://hpcdocs.hpc.arizona.edu/events/workshop materials/
intro to hpc/files/IntrotoHPC.ResBaz2024.pdf](https://hpcdocs.hpc.arizona.edu/events/workshop_materials/intro_to_hpc/files/IntrotoHPC.ResBaz2024.pdf)