INTRODUCTION TO CLUSTER COMPUTING

Carlos Teijeiro Barjas (HPC Advisor) Maxim Masterov (HPC Advisor)

UvA – Amsterdam (remote) – 31/03/2020

Outline

- Introduction to High Performance Computing
 - Definitions
 - Parallel programming
- SURFsara facilities
 - Presentation
 - Systems and specifications
 - Running jobs
- Hands-on exercises
 - Exercise available in your home directories (LisaGPUTutorials.txt)



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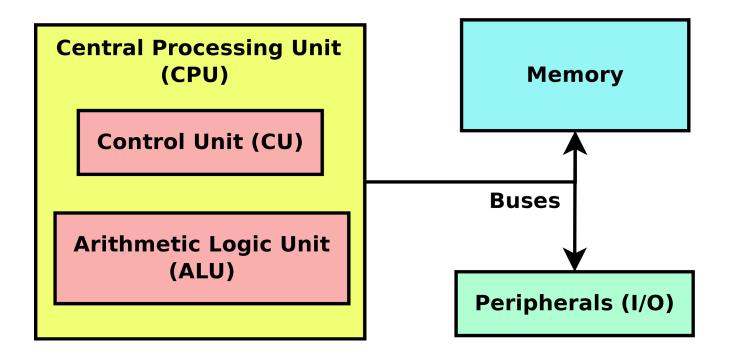
High-performance computing (HPC) is ...

- ... an area of computer-based computation. It includes all computing work that requires a high computing capacity or storage capacity.
- ... the use of parallel processing for running advanced application programs efficiently, reliably and fast.
- ... the practice of aggregating computing power in a way that delivers much higher performance than one could get out of a typical desktop computer or workstation in order to solve large problems in science, engineering, or business.
- ... the use of super computers and parallel processing techniques for solving complex computational problems.

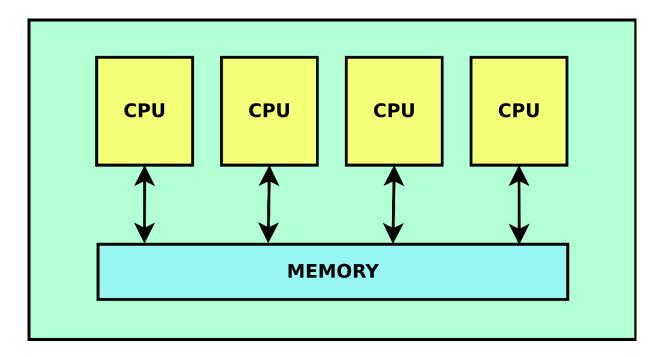
A computer is ...



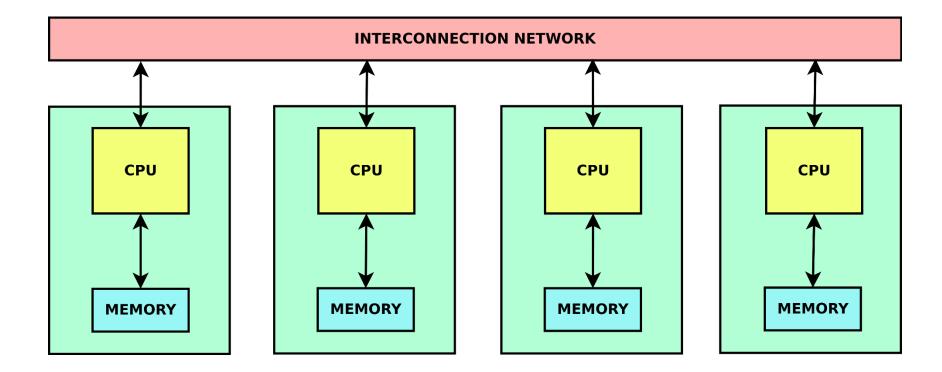
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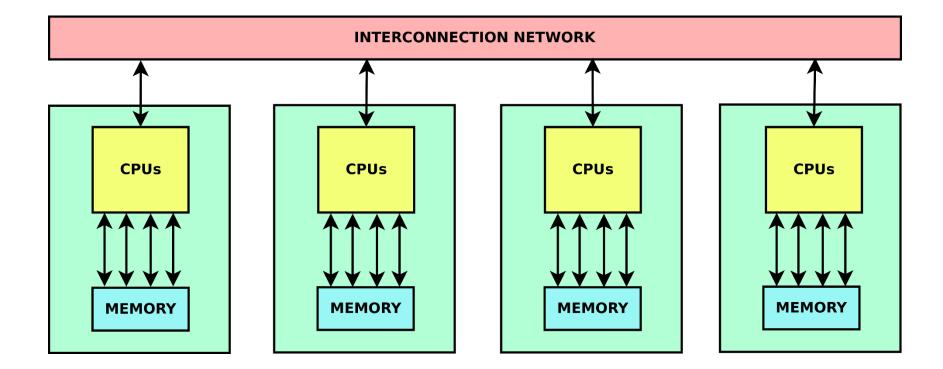




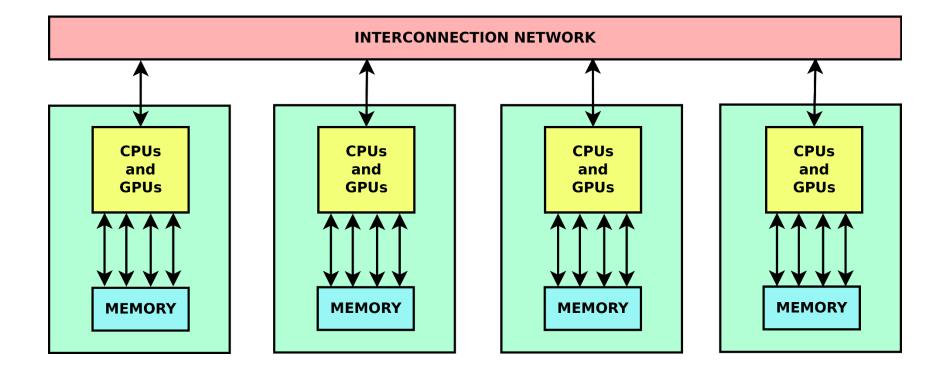














High-performance computing (HPC) ...

- ... is an area of computer-based computation. It includes all computing work that requires a high computing capacity or storage capacity.
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- ... is the part of computing focused on making computers collaborate efficiently up to very large scales
- ... is optimized and scalable computer coordination (hardware and software)

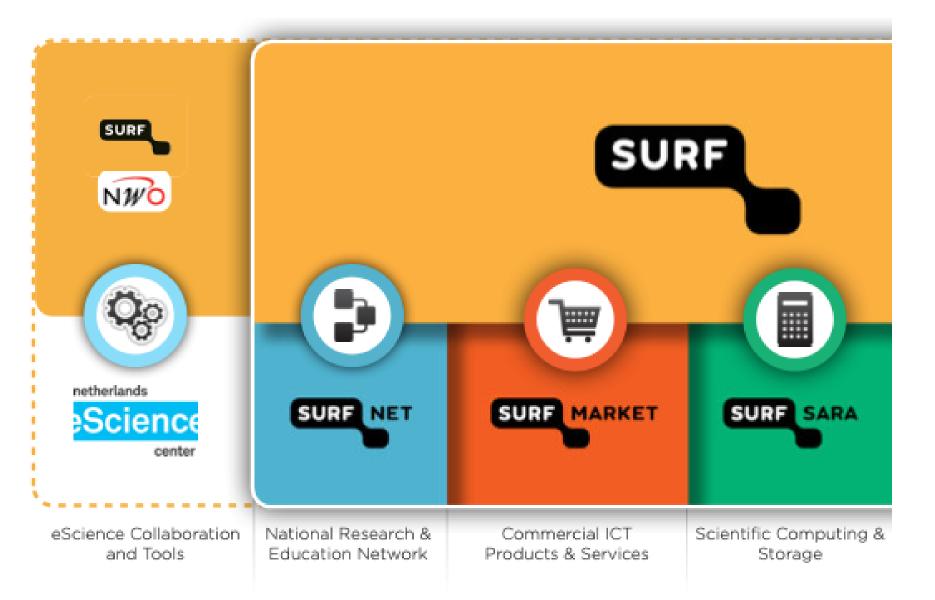


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SURFsara is part of SURF





Location of SURFsara





Activities at SURFsara

- Regular user support: from a few minutes to a couple of days
- Application enabling for Dutch Compute Challenge Projects
 - Potential effort by SURFsara staff: 1 to 6 person months per project
- Performance improvement of applications
 - Typically meant for promising user applications
 - Potential effort by SURFsara staff: 3 to 6 person months per project
- Support for PRACE applications: access to European systems
- Visualization projects
- Training and workshops (regular and on demand)
- Please contact SURFsara at <u>helpdesk@surfsara.nl</u>



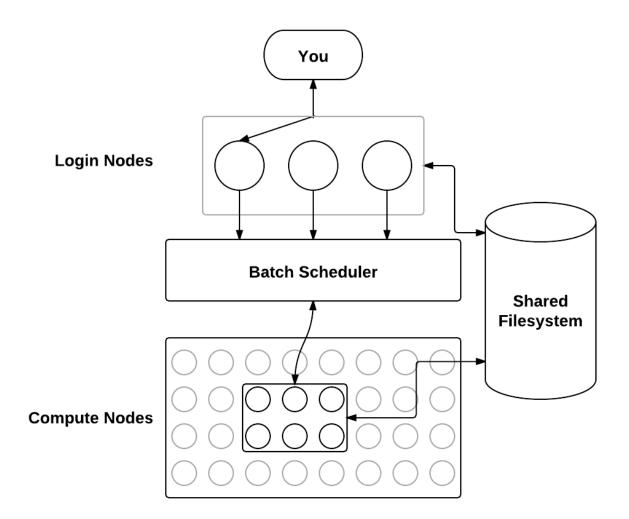
Dutch national supercomputers: performance increase

Year	Machine	R _{peak} (GFlop/s)	kW	GFlop/s/ kW
1984	CDC Cyber 205 1-pipe	0.1	250	0.0004
1988	CDC Cyber 205 2-pipe	0.2	250	0.0008
1991	Cray Y-MP/4128	1.33	200	0.0067
1994	Cray C98/4256	4	300	0.0133
1997	Cray C916/121024	12	500	0.024
2000	SGI Origin 3800	1,024	300	3.4
2004	SGI Origin 3800 +SGI Altix 3700	3,200	500	6.4
2007	IBM p575 Power5+	14,592	375	40
2008	IBM p575 Power6	62,566	540	116
2009	IBM p575 Power6	64,973	560	116
2013	Bull bullx DLC	250,000	260	962
2014	Bull bullx DLC	>1,000,000	>520	1923
2017	Bull bullx DLC + KNL	> 1,800,000		
2016	Raspberry PI 3 (35 euro)	0.44	0.004	110



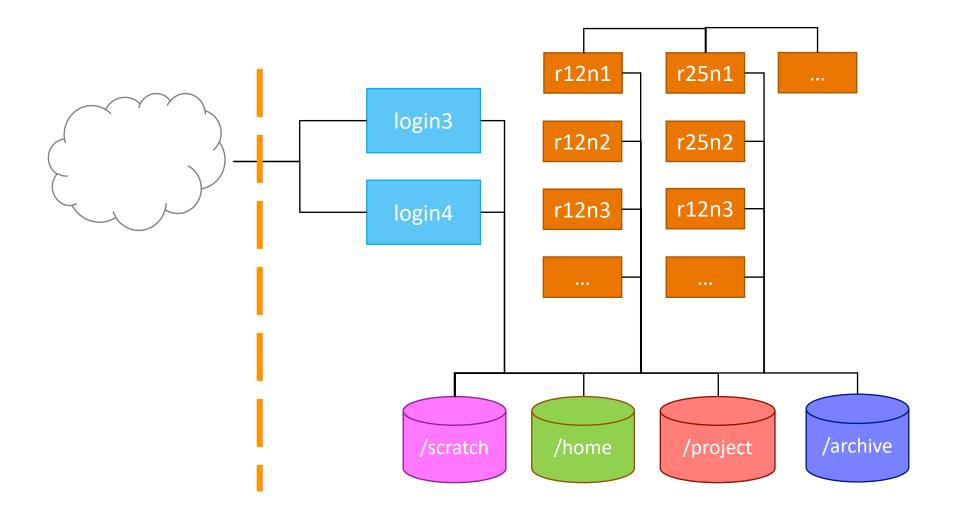


Schematic overview of a supercomputer

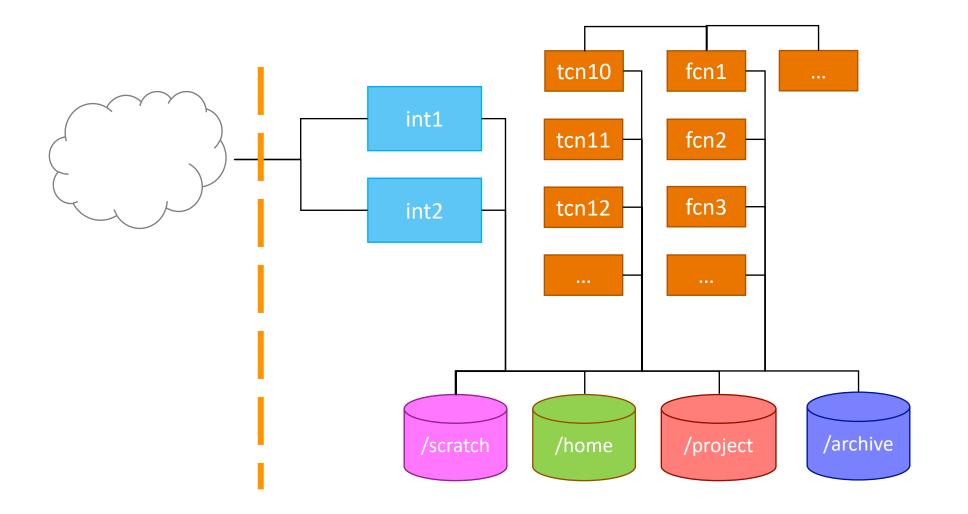




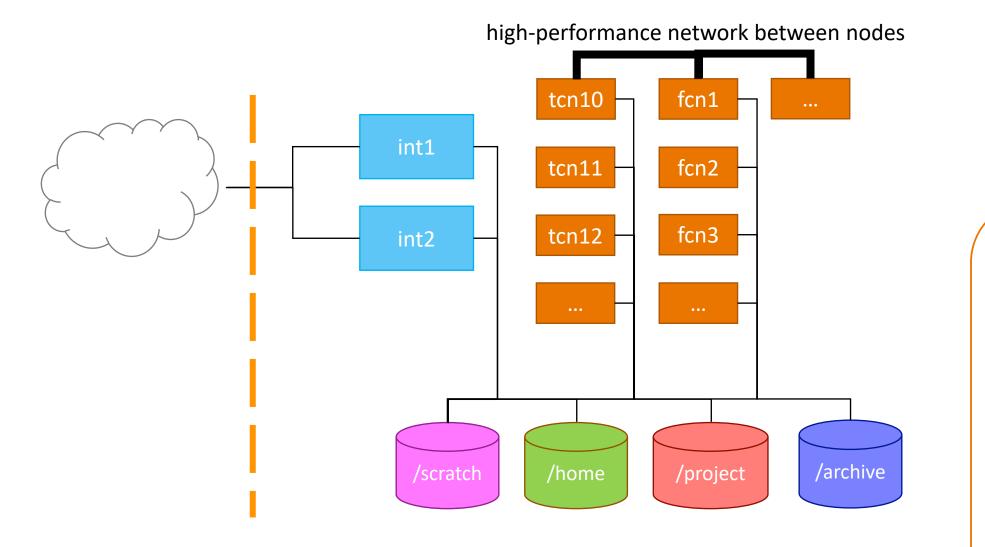
Specific example: Lisa architecture



Specific example: Cartesius architecture



Specific example: Cartesius architecture



1 thin node island, a so-called Bull sequana X1000 cell

 177 sequana X1110 thin nodes, each with 2 × 16-core 2.6 GHz Intel Xeon E5-2697A v4 and 64 GB memory

3 thin node islands

- 360 bullx B720 thin nodes, each with 2 × 12-core 2.6 GHz Intel Xeon E5-2690 v3 and 64 GB memory
- 2 thin node islands
 - 360 + 180 bullx B710 thin nodes, each with 2 × 12-core 2.4 GHz Intel Xeon E5-2695 v2 and 64 GB memory



- 1 fat node island
 - 32 bullx R428 E3 fat nodes with 4 × 8-core 2.7 GHz Intel Xeon E5-4650 and 256 GB memory
- 18 sequana X1210 Xeon Phi nodes
 - 64-core 1.3 GHz Intel Xeon Phi 7230 (Knights Landing) with 96 GB memory
- 1 accelerator island with 66 bullx B515 GPGPU accelerated nodes
 - 2 × 8-core 2.5 GHz Intel Xeon E5-2450 v2 with 96 GB memory
 - 2 × NVIDIA Tesla K40m GPGPUs/node

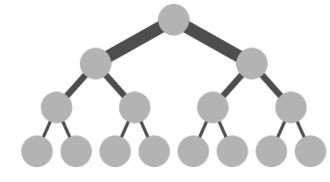


- 2 bullx R423-E3 interactive front end nodes
 - 2 × 8-core 2.9 GHz Intel Xeon E5-2690 with 128 GB memory
- 5 bullx R423-E3 service nodes
 - 2 × 8-core 2.9 GHz Intel Xeon E5-2690 with 32 GB memory

- Global summary
 - 47,776 cores + 132 GPUs: 1.843 Pflop/s (peak performance)
 - 130 TB memory



- Low-latency network: 4x FDR14 InfiniBand
 - Non-blocking within fat- and thin-node islands and 3.3 : 1 inter-island pruning factor
 - 56 Gbit/s inter-node bandwidth
 - 2.4 μs inter-island latency
 - Maximum 700 nodes per job
- File systems and I/O
 - 180 TB NFS file system (home)
 - 7.7 PB Lustre file system (scratch and project)
- bullx GNU/Linux OS, compatible with Red Hat Enterprise Linux
- Specific policy for software installation and maintenance



Compute power on Lisa

Number	Processor Type	Clock	Scratch	Memory	Sockets	Cache	Cores	GPUs	Interconne ct
23	<u>Bronze</u> <u>3104</u>	1.70 GHz	1.5 TB NVME	256 GB UPI 10.4 GT/s	2	8.25 MB	12	4 x GeForce 1080Ti, 11 GB GDDR5X	40 Gbit/s Ethernet
2	<u>Bronze</u> <u>3104</u>	1.70 GHz	1.5 TB NVME	256 GB UPI 10.4 GT/s	2	8.25 MB	12	4 x Titan V, 12GB HBM2	40 Gbit/s Ethernet
8	<u>Gold 5118</u>	2.30 GHz	1.5 TB NVME	192 GB UPI 10.4 GT/s	2	16.5 MB	24	4 x Titan RTX, 24 GB GDDR6	40 Gbit/s Ethernet
192	<u>Gold 6130</u>	2.10 GHz	1.7 TB	96 GB UPI 10.4 GT/s	1	22 MB	16	-	10 Gbit/s Ethernet
96	<u>Silver 4110</u>	2.10 GHz	1.8 TB	64 GB UPI 9.6 GT/s	2	11 MB	16	-	10 Gbit/s Ethernet
1	<u>E7-8857</u> <u>v2</u>	3.00 GHz	13 TB	1 TB QPI 8.00 GT/s	4	30 MB	48	-	10 Gbit/s Ethernet
1	<u>Gold 6126</u>	2.60 GHz	11 TB	2 TB UPI 10.4 GT/s	4	19.25 MB	48	-	40 Gbit/s Ethernet

Compute power on Lisa

CPU nodes

Total number of CPU cores: Total amount of memory: Total peak performance: Disk space: Operating System:

GPU nodes

Total number of CPU cores: Total number of CUDA cores: Total number of Tensor cores: Total amount of memory: Total peak performance (SP): Total peak performance (DP): 4704
30 TB
263 TFlop/sec
400 TB for the home file systems
Debian Linux

492 376832 1280 6.3 TB 1,576.8 TFlop/sec 52.9 TFlop/sec



File systems on Cartesius and Lisa

- /home/user
 - User home directory (quota currently 200GB)
 - Storage of important files (sources, scripts, input and output data)
 - Backed up
 - Based on NFS: not the fastest file system
- /scratch (/scratch-local & /scratch-shared on Cartesius)
 - Variable quota depending on disk (currently 8 TB on Cartesius)
 - Temporary storage (during running of a job and shortly thereafter)
 - Not backed up: any data is removed after 14 days !!!
 - Based on Lustre: the fastest file systems on Cartesius & Lisa



File systems on Cartesius and Lisa

/archive

- Connected to the tape robot (quota virtually unlimited)
- Given upon request for long term storage of files (in compressed format)
- Backed up
- Slow especially to retrieve "old" data and not available in compute nodes
- /project
 - Large and fast on Cartesius. On Lisa, large but not so fast
 - Given upon request for special projects requiring lots of space
 - Not backed up, but permanent until the end of the associated project
 - Comparable in speed with /scratch on Caratesius. On Lisa, comparable to /home



Running jobs: first change your password

SURFsara user portal × +				
(i) SURFsara B.V. (NL) https://portal.surfsara.nl/login/?next=/home/	C Search	☆自♥	+ ^ /	
Username sdemo001 Password Submit				
<u>https://pc</u>	ortal.surfsara.nl	<u> </u>		

SURF

SARA



User portal

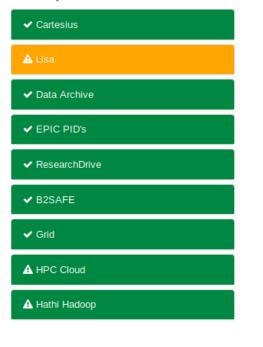


Welcome, you are currently logged in as Carlos Teijeiro (uid: carlost)

A Home	
A Your Profile	SURFsara user portal
E Accounting	
🗟 Public ssh keys	Welcome to the SURFsara user Portal
Q Change password	SURFsara supports researchers in the Netherlands and works closely together with the academic community and industry.
Helpdesk	The SURFsara user portal allows you to:
-	View your login profile
🕞 Logout	 Check your accounting details (if applicable)
	Change your password

Contact the helpdesk

Current system status



User portal



Welcome, you are currently logged in as Carlos Teijeiro (uid: carlost)

🕋 Home SURFsara user portal A Your Profile Accounting 🗂 Public ssh keys **Q** Change password Helpdesk ► Logout

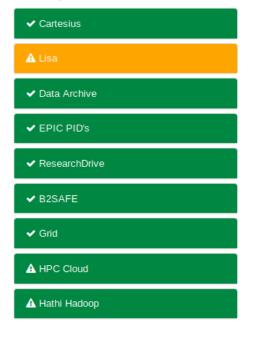
Welcome to the SURFsara user Portal

SURFsara supports researchers in the Netherlands and works closely together with the academic community and industry.

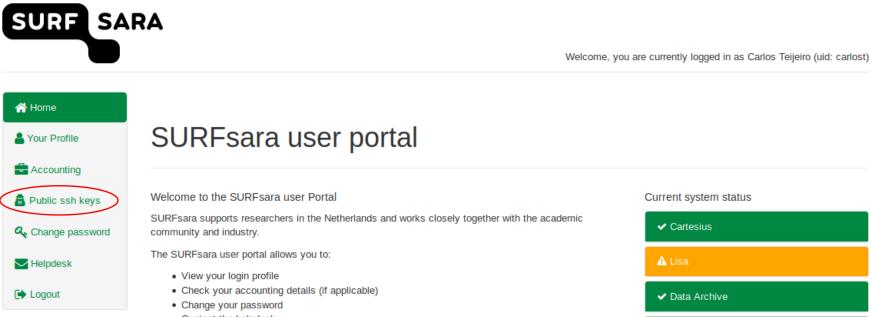
The SURFsara user portal allows you to:

- View your login profile
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- Change your password
- Contact the helpdesk

Current system status



User portal



Contact the helpdesk

✓ EPIC PID's

✓ ResearchDrive

✓ B2SAFE

🗸 Grid

A HPC Cloud

\Lambda Hathi Hadoop

Connecting to Cartesius or Lisa

- Windows operating system
 - MobaXterm (recommended): <u>https://mobaxterm.mobatek.net/</u>
 - PLEASE DOWNLOAD THE PORTABLE EDITION !!!
 - Putty
- MacOS
 - Terminal (preinstalled)
 - XQuartz (<u>http://www.xquartz.org</u>)
- Linux
 - You are already well equipped!



Connecting to Lisa

When you log in with ssh, you access the login nodes

```
user@local:~$ ssh lgpu0000@lisa.surfsara.nl
sdemo000@lisa.surfsara.nl's password:
sdemo000@login4:~$ ls
lisa-file.txt
```

With scp you can transfer files to/from your local machine

```
user@local:~$ ls
local-file.txt
user@local:~$ scp local file.txt lgpu0000@lisa.surfsara.nl:
user@local:~$ scp lgpu0000@lisa.surfsara.nl:lisa_file.txt .
user@local:~$ ls
lisa-file.txt local-file.txt
user@local:~$ ssh lgpu0000@lisa.surfsara.nl
lgpu0000@lisa.surfsara.nl's password:
lgpu0000@login4:~$ ls
lisa-file.txt local-file.txt
```



Running jobs: how-to guide

- Schedulers distribute work to batch nodes
- Workflow:
 - 1. You upload your data from your computer to the cluster system
 - 2. You create a job script with the work steps
 - 3. **You** submit the job script to the scheduler
 - 4. The scheduler looks for available computers to run your work
 - 5. When a batch node with the requirements you specified becomes available, your work runs
 - 6. When the job is finished, you download the results to your computer
- Batch scheduler on Cartesius and Lisa: SLURM

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Running jobs: useful commands of the SLURM scheduler

- sbatch <jobscript> submit a job to the scheduler
- squeue -j <job_id> inspect the status of job <job_id>

squeue -u <user_id> - inspect all jobs of user <user_id>

scancel <job_id> - cancel job <job_id> before it runs

scontrol show job <job_id>

- show estimated job start



Running jobs: first example

```
#!/bin/bash
#SBATCH --job-name="firsttest"
#SBATCH --nodes=1
#SBATCH --ntasks=10
#SBATCH --time=00:01:00
#SBATCH --partition=normal
echo "Who am I?"
whoami
echo
echo "Where ?"
srun hostname
echo
sleep 120
date
```

 Create a text file with *exactly* the first lines; name the file "job.sh"

- Submit this job with "sbatch job.sh" and look the status with "squeue –u login_id"
- Use "scontrol show job job_id" to find out when your job will run
- Look at your home-directory to see what happens there; look at the files.
- Which files were created? Look at those files.
- Try to play with email notifications!
 - #SBATCH -- mail-type=BEGIN, END
 - #SBATCH --mail-user=<your_email_address>

echo "DONE"

Running jobs: best practices

Give the scheduler a realistic walltime estimate

• Your home directory is slow. Use \$TMPDIR.

 Load software modules as part of your job script – this improves reproducibility

 Run parallel versions of your programs (and use "srun" to ask SLURM to run multi-process applications)



Anatomy of a job script

- Job scripts consist of:
 - the "shebang" line: #!/bin/bash
 - scheduler directives
 - command(s) that load software modules and set the environment
 - command(s) to prepare the input
 - command(s) that run your main task(s)
 - command(s) to save your output

Module management: useful commands

module avail

- available modules in the system
- module load <mod> - load <mod> in the shell environment
- module list - show a list of all loaded modules
- module unload <mod> - remove <mod> from the environment
- unload all modules module purge
- module what is < mod>
- show information about <mod>

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Example: a real job script

#!/bin/bash
#SBATCH -t 0:20:00
#SBATCH -N 1 -c 24

module load 2019
module load Python/2.7.14-foss-2017b

cp -r \$HOME/run3 \$TMPDIR

cd \$TMPDIR/run3 python myscript.py input.dat

mkdir -p \$HOME/run3/results
cp result.dat run3.log \$HOME/run3/results



Running jobs: second example

#!/bin/bash
#SBATCH --job-name="python"
#SBATCH --nodes=1
#SBATCH --cpus-per-node=10
#SBATCH --time=00:10:00
#SBATCH --partition=normal

module purge module load 2019 module load GCC

echo "OpenMP parallelism"

for ncores in {1..10}

do

export OMP_NUM_THREADS=\$ncores echo "CPUS: " \$OMP_NUM_THREADS echo "CPUS: " \$OMP_NUM_THREADS >&2 ./pi echo "DONE " done

- Check the file "python.sh" in your home directory:
 - linux-cluster-computing/cluster/batch
- Submit this job with "sbatch python.sh" and look the status with "squeue –u login_id"
- If you needed to use some input file or you would generate an output file... where would you put the copy commands for scratch?
- Now try the same with "pi.sh"... but first compile the code! (./compilepi)
- Can you play around with the variable 'ncores' and see some parallel efficiency?

Everything about jobs: user info pages

Go to:

https://userinfo.surfsara.nl

Click on the corresponding system:

Cartesius: Usage → Batch Usage (jobs)

- Lisa: User guide \rightarrow Creating and running jobs



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THANK YOU FOR YOUR ATTENTION

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helpdesk@surfsara.nl

www.surf.nl

@SURF_onderzoek

Driving innovation together