

High-Performance Computing & Biology

Paul Johnston

paul.johnston@fu-berlin.de

Berlin Center for Genomics in Biodiversity Research |
Leibniz-Institut für Gewässerökologie und Binnenfischerei |
Freie Universität Berlin

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slides: <https://github.com/perugolate/hpc>

I might use terms interchangeably but:

- a computing cluster is a type of HPC
- bioinformatics is type of data science

sorry if I confuse anyone

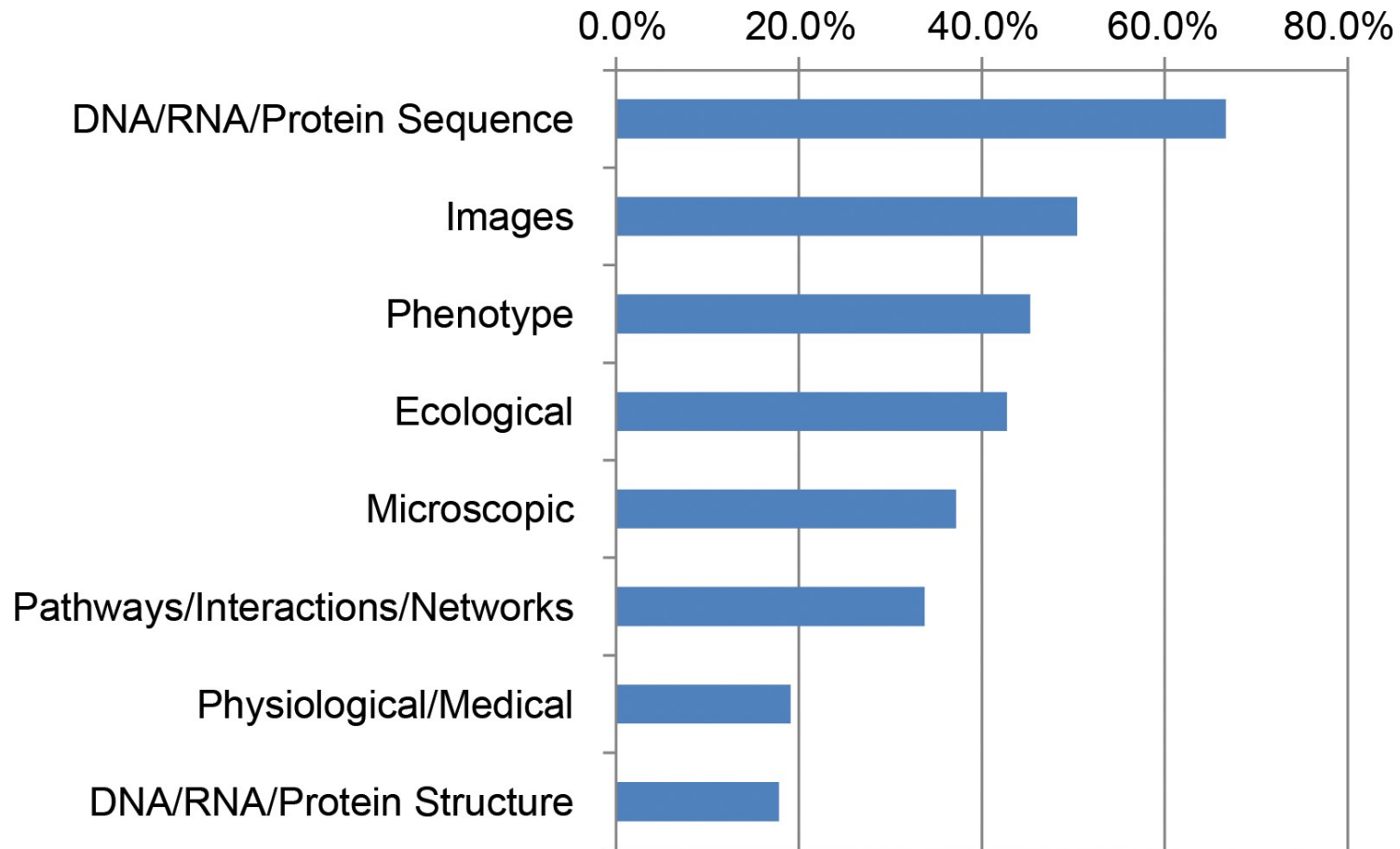
94% of students/faculty/researchers use large data sets or will in the near future (n = 1,097)

47% rated their bioinformatics skill level as “beginner,” (n = 608)

58% felt their institutions do not provide all the computational resources needed for their research (n = 1,024)

<https://doi.org/10.1371/journal.pcbi.1005755>

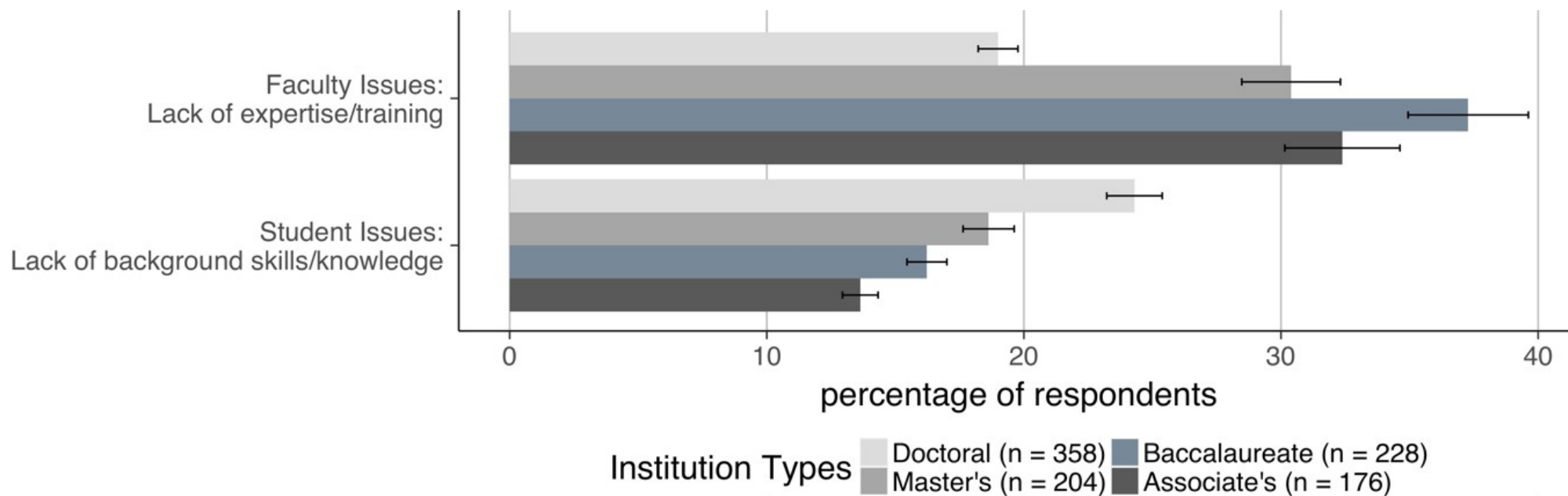
Biologists receive little training in data science...



but most projects require it..

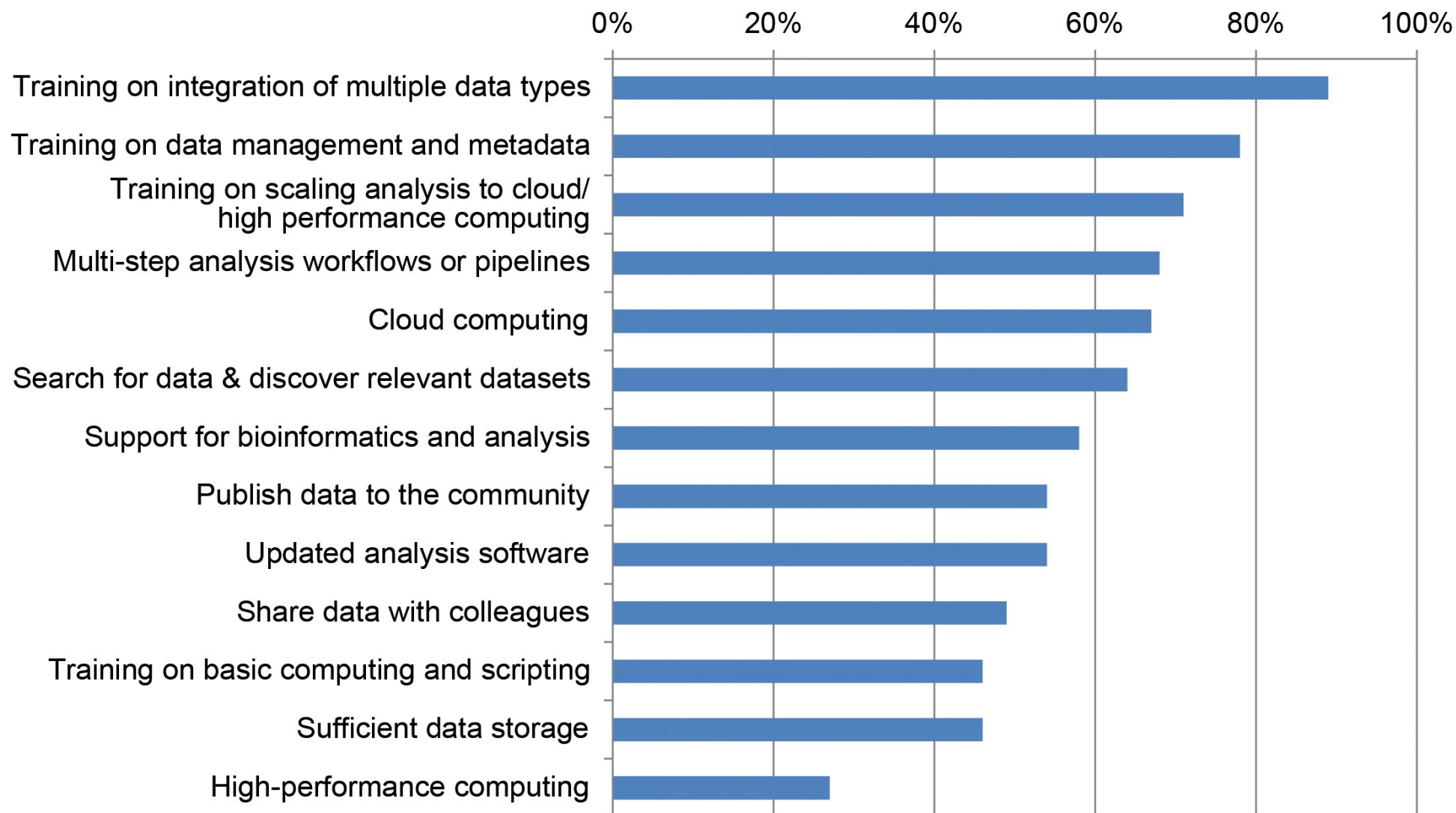
Barriers to teaching bioinformatics

Decade of Highest Degree Earned	Formal Bioinformatics Training (%)	Faculty Integrating Bioinformatics (%)
1980–1989	8.4	35.4
1990–1999	11.3	41.9
2000–2009	35.1	41.7
2010–2016	48.3	25.2



<https://doi.org/10.1371/journal.pone.0224288>

Unmet needs in bioinformatics



<https://doi.org/10.1371/journal.pcbi.1005755>

“These studies suggest a scenario of big data
inundating unprepared biologists.”

<https://doi.org/10.1371/journal.pcbi.1005755>

(d) *De novo* assembly and annotation

Assemblies for both species were produced using Trinity v. 2.8.4 [29], incorporating quality and adapter filtering via Trimmomatic [30] and subsequent *in silico* normalization. Assemblies were annotated with the Trinotate annotation pipeline [31].

(e) Inference of orthologous gene groups

OrthoFinder v. 2.2.7 [32] was used to infer orthology between predicted peptide sequences from *Gr. bimaculatus*, *G. mellonella* and the proteomes of other insect species with sequenced genomes. These included *Acyrtosiphon pisum*, *Apis mellifera*, *Drosophila melanogaster*, *Tribolium castaneum*, *Zootermopsis nevadensis*, as well as all Lepidopteran genomes from lepbases release 4 [33].

(f) Immune effector gene identification

Immune effectors of *Gr. bimaculatus* and *G. mellonella* were identified from orthologue groups containing annotated immune genes from previously published insect genome projects. Additionally, blast and HMM homology searches were performed using previously described insect immune effector proteins as queries against each *de novo* assembly.

(g) Differential gene expression

For both species, transcript abundances were quantified by pseudo-aligning RNAseq reads to *de novo* assemblies using Salmon v. 0.12.0 [34]. tximport [35] was used in conjunction with DESeq2 [36] to model gene-level estimated counts while correcting for changes in transcript usage across samples. Specifically, to identify differential expression as a function of developmental stage, likelihood-ratio tests were performed between full and intercept-only negative binomial GLMs. Differential expression was considered to be significant when fold changes were greater than 2 for pairwise Wald contrasts of developmental stages, with a false discovery rate (FDR)-corrected *p*-value of less than 0.05. The mean of the normalized counts for each gene was used as the informative covariate for indepen-

- The fine details of the computation aren't reported (memory, storage, time etc)
- it's easy for others to underestimate the required resources
- computing skill set is also unclear

Storage problems

RNAseq of 35 samples

- one lane of NovaSeq
- 35 compressed fastq files
- >400 GB (compressed)



The storage
is full before
I've even started!

Time problems

alignment of 35 RNAseq samples to genome

- Each alignment takes 5 hours
- Will run for 7 days
- Will use all resources



My laptop is
melting

Memory problems

Quantification of 35 RNAseq samples gives

- a matrix of 10,000s of counts x 35
- need to fit 10,000s of models
- needs 20-100 GB of RAM



I only have 16 GB
of RAM !

Lots of problems

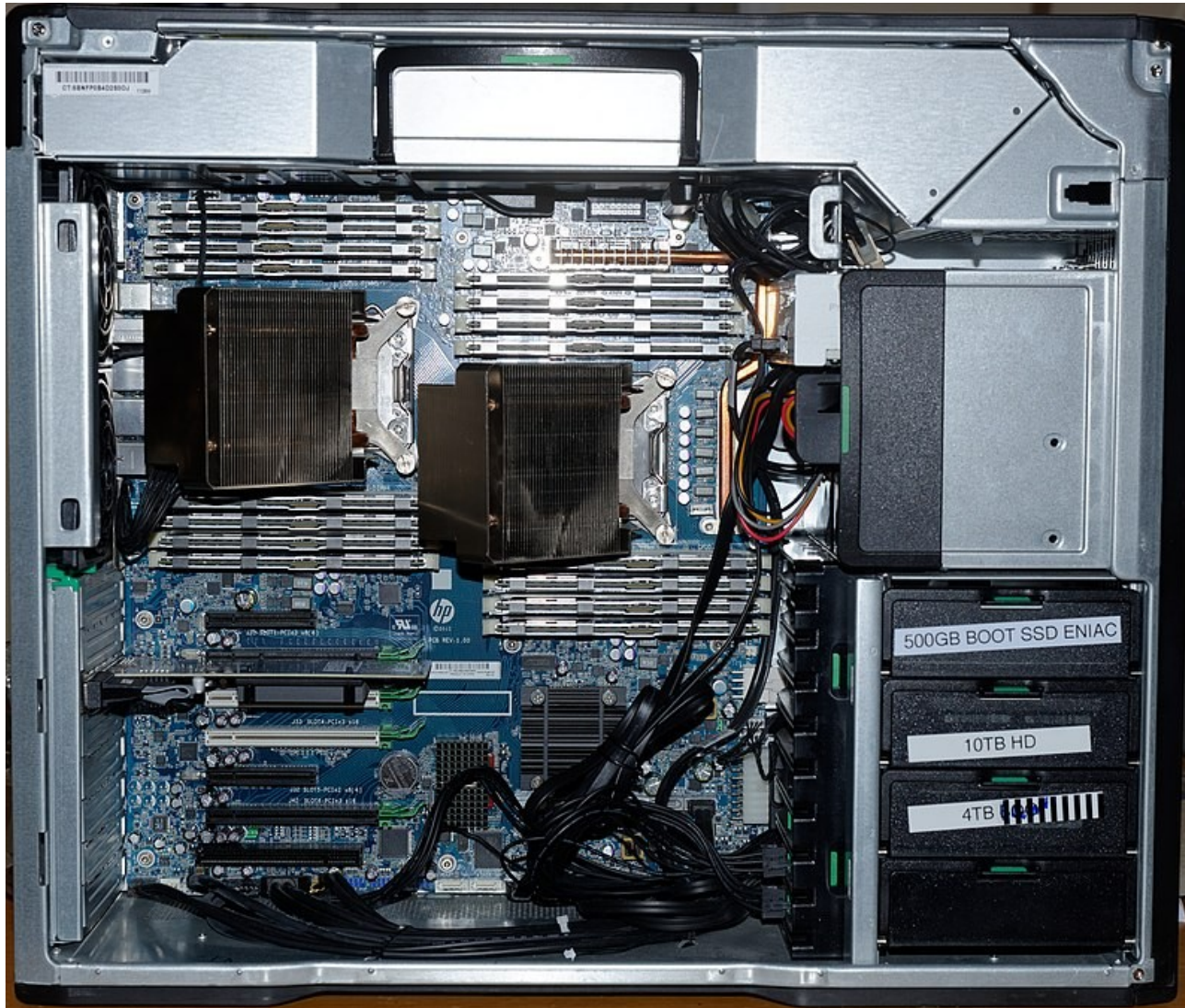
de novo assembly of 35 RNAseq samples

- needs >100 GB RAM, runs for many days
- needs many CPUs, generates TBs of files
- repeat the assembly many times with different parameters



This will
take months !

Workstation (1,000s €)



Server (10,000s €)



- e.g. 36,000€
 - 1.5 TB RAM
 - 40 cores
 - 48 TB storage
- Plus energy, cooling, rack etc.

Computing cluster (HPC)

100,000s €



Important points

Every university has (access to) a cluster

Usage is generally free or extremely cheap

There are university employees to provide support

The system is highly robust and stable

i.e. it's there and it works now

Search

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List of results

Projects
People
Institutions

Your Projects query is

Keyword(s): **boris proppe**

■ Include projects without final report

[start new search](#)
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More Results

Based on your query, more matches were found in the following areas





→ People (1)

→ Institutions (1)

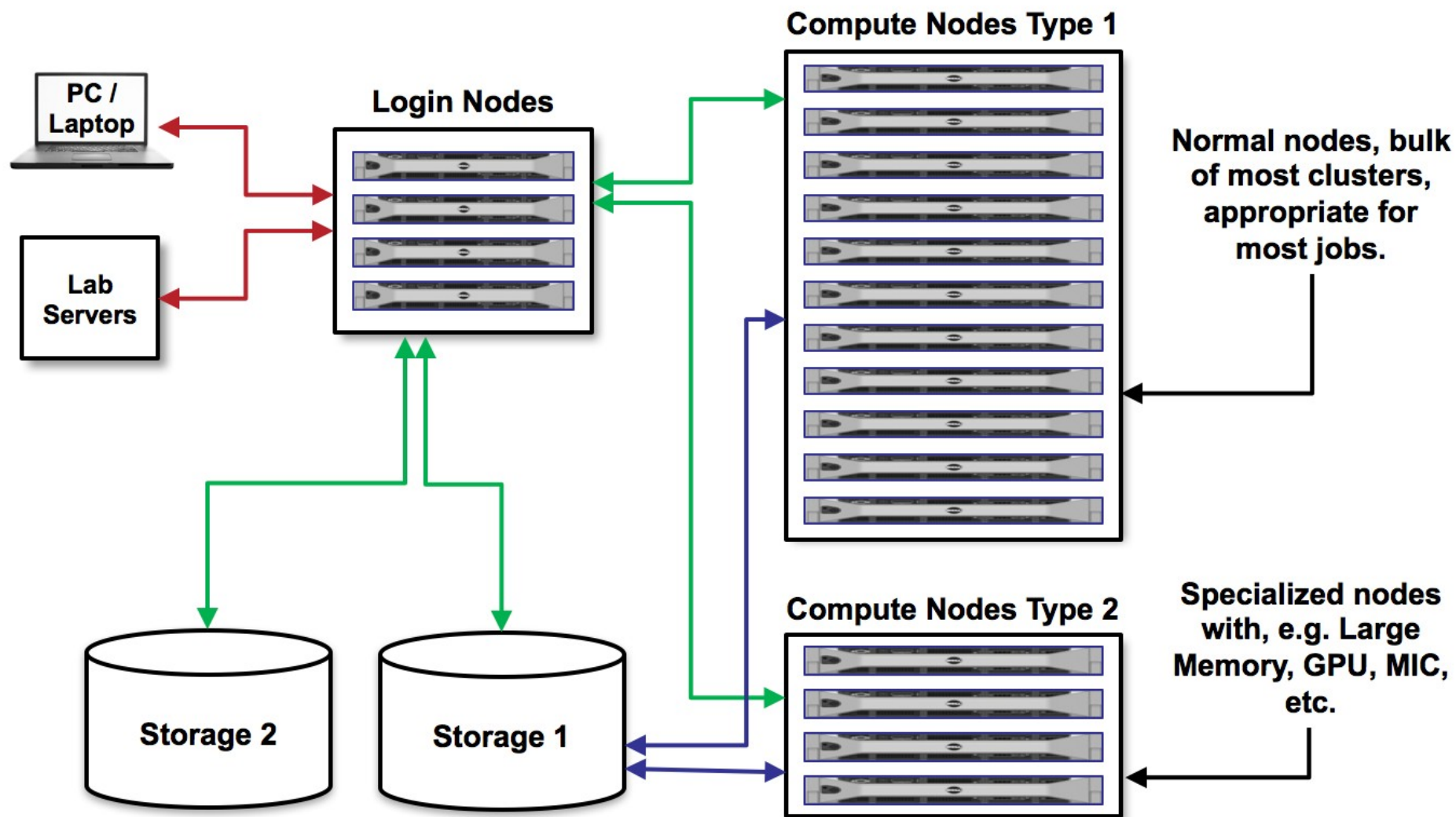
results per page: 5 | 10 | 25 | 50

Order by: **Relevance** | Name | GZ ⓘ

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Results 1 to 2 out of 2 on 1 page
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	High-Performance-Computing-Cluster und Speichersystem			
Leader	Boris Proppe			
DFG Programme	Major Research Instrumentation	Term	In 2010	
<hr/>				
	High-Performance-Computing-Cluster und Speichersystem			
Leader	Boris Proppe			
DFG Programme	Major Research Instrumentation	Term	In 2017	
<p>Das Hochschulrechenzentrum (ZEDAT) und die IT-Dienste der Fachbereiche Mathematik/Informatik und Physik der Freien Universität Berlin beantragen gemeinsam die ...</p> <p>→ more</p>				

Typical cluster



Terminology

Job: reservation to run commands

Node: physical machine, part of cluster

Core/CPU: processing unit, nodes contain many CPUs

Partition: nodes may be organized into partition
e.g. begendiv bought large-memory nodes

Curta specifications

Specifications

Nodes	170x Intel CPUs only, 12x Asus with GPUs
Processors	2x Xeon Skylake 6130 (2.1 GHz, 16 cores, 22 MB Cache) per node
GPUs	24x NVIDIA GTX1080Ti
RAM	3/6/12/24 GB per core (96/192/384/768 GB per node) 103/50/8/4 nodes
File System	1.8 PB /scratch with Lustre
Network	10 Gigabit-Ethernet - TCP/IP
Interconnect	Omnipath
Operating System	CentOS 7
Batch-System	Slurm

The DOI [10.17169/refubium-26754](https://doi.org/10.17169/refubium-26754) refers to a more complete description of the system and should be referred to in any publications.

<http://dx.doi.org/10.17169/refubium-26754>

Connecting to the cluster

```
# remember to use your zedat username  
ssh USERNAME@curta.zedat.fu-berlin.de
```

Connecting to the cluster


```
# remember to use your zedat username  
ssh USERNAME@curta.zedat.fu-berlin.de
```

- must be inside FU network (or use VPN)
- if the VPN doesn't work on your system
then you can first connect to the zedat login
server




```
# connect to login server  
ssh USERNAME@login.zedat.fu-berlin.de  
# you are now connected to the login server  
# from here you can connect to the cluster  
ssh USERNAME@curta.zedat.fu-berlin.de  
# you should now be connected to the cluster (curta)
```

Connecting to the cluster

- zedat also provides a shell here:
<https://www.zedat.fu-berlin.de/Shell>


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Startseite Beschäftigte Kontakt Impressum





Direktzugang  Suchbegriff  


ZEDAT Das Hochschulrechenzentrum der Freien Universität Berlin

AKTUELLES	SERVICES	HILFE	SCHULUNG	WIR ÜBER UNS
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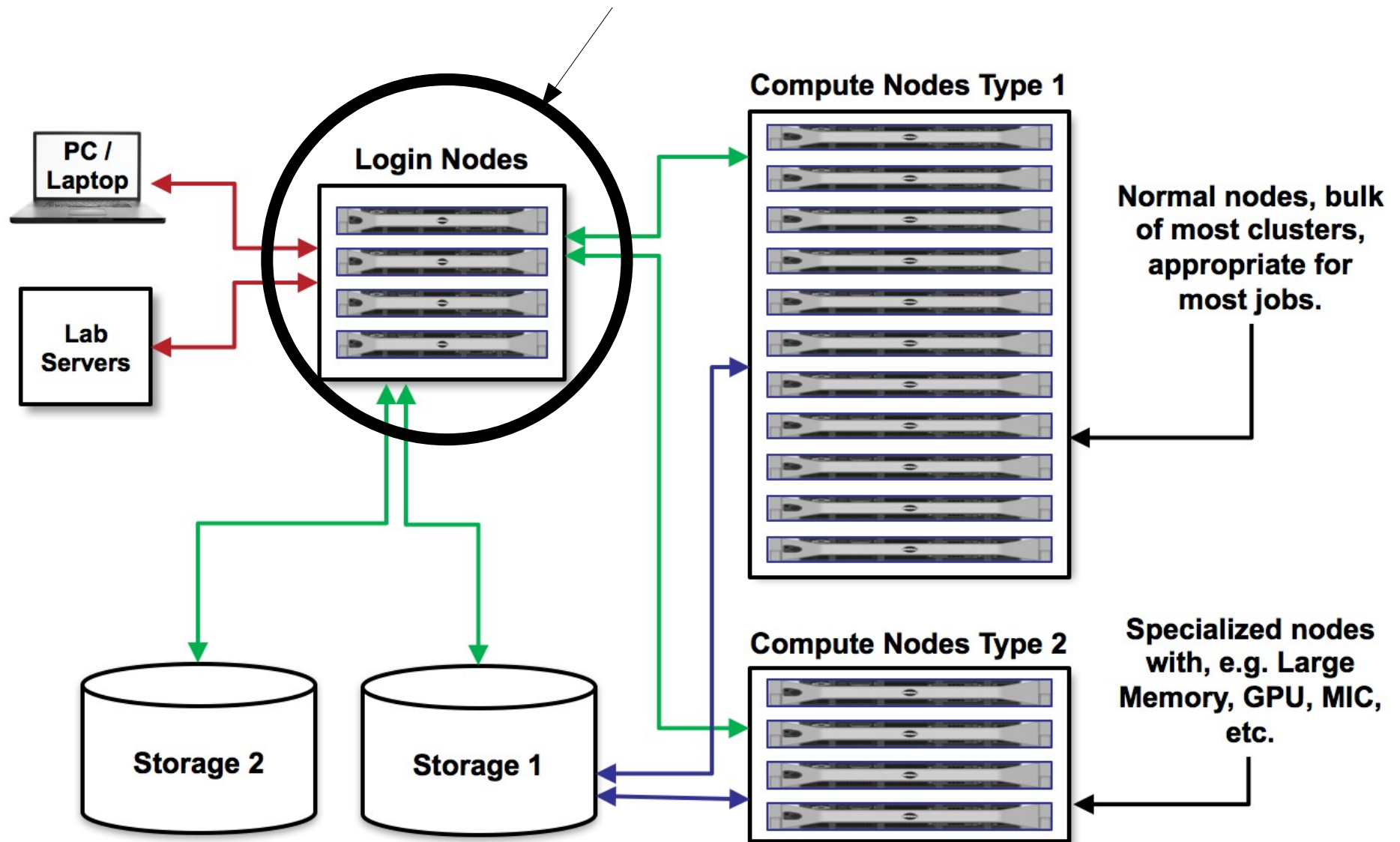
 ZEDAT » Shell

ZEDAT login:

 Webmail
 Portal
 Datenablage
 Shell



You are now on one of these nodes



Login nodes

These are for basic tasks:

- Uploading data `# scp, rsync, wget, etc`
- Managing files `# cp, mv, gunzip`
- Compiling software `# configure, make`
- Editing scripts `# nano, vim`
- Checking/managing jobs `# queue`

Important note

The login nodes are for setting things up and submitting jobs to the compute nodes

Running commands on the login nodes is bad

- You would get an annoyed email from admin
- It slows/crashes the node for other users

Compute nodes

Job scripts are sent here to run

- resources allocated by workload manager (Slurm)
- other workload managers/schedulers exist
e.g. PBS, SGE, LFS
- resources are allocated according to:
system load
fair share algorithms

Basic conventions

```
# remember to use your zedat username  
ssh USERNAME@curta.zedat.fu-berlin.de
```

- | | |
|------------------|--|
| /home/\$USER/ | <ul style="list-style-type: none">- limited space- backed up nightly- store software, config files |
| /scratch/\$USER/ | <ul style="list-style-type: none">- lots of storage space- no backup- default working space |

Different cultures exist in different clusters
e.g. precise location of scratch, backup policy

First job on the cluster

```
# remember to use your zedat username  
ssh USERNAME@curta.zedat.fu-berlin.de
```

```
# enter the following command
```

```
echo "Hello World"
```

```
# "Hello World" should print to your screen (the standard output)
```

First job on the cluster

```
# remember to use your zedat username  
ssh USERNAME@curta.zedat.fu-berlin.de  
# enter the following command  
echo "Hello World"  
# "Hello World" should print to your screen (the standard output)
```

We just ran a command on the login node
(this is OK because it is not intensive)

Now lets submit it as a job to a compute node

First job on the cluster

```
# we should work in our scratch directory
# so navigate to your scratch directory
cd /scratch/$USER/
# now make a directory with a sensible name to work in
# yearmonthday_sensible_name is a good naming convention
mkdir 20221130_lvdatascieeb
# navigate inside the new directory
cd 20221130_lvdatascieeb
# copy the example job script from my scratch directory to yours
cp /scratch/perugolate/20221130_lvdatascieeb/20221130_hello_world.sh .
# have a look at the script
cat 20221130_hello_world.sh
```

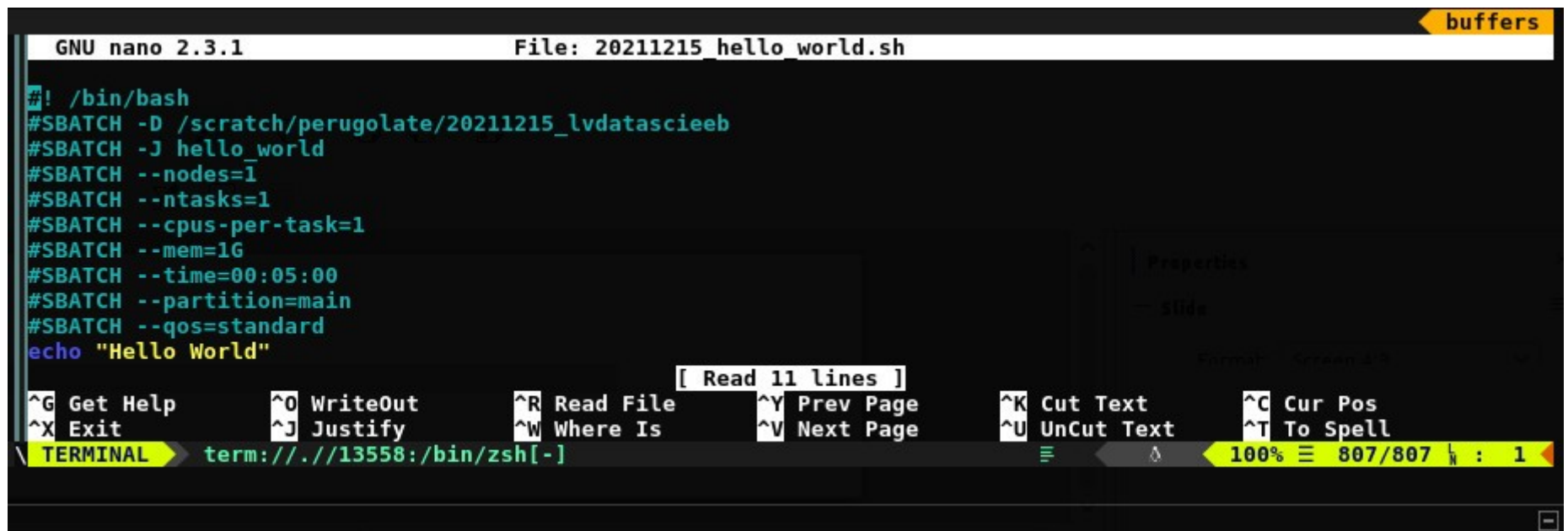
Example job script

```
#!/bin/bash
#SBATCH -D /scratch/USERNAME/20221130_lvdatascieeb    # directory
#SBATCH -J hello_world                                # name of job
#SBATCH --nodes=1                                     # requested nodes
#SBATCH --ntasks=1                                    # number of tasks in job
#SBATCH --cpus-per-task=1                             # requested CPUs
#SBATCH --mem=1G                                       # requested RAM
#SBATCH --time=00:05:00                               # requested time
#SBATCH --partition=main                              # partition where job will run
#SBATCH --qos=standard                                # complicated
echo "Hello World"
```

- line 2 specifies the directory where the job will run
- we need to edit it

Example job script

```
# open the job script in the text editor 'nano'
nano 20221130_hello_world.sh
# navigate with arrow keys to USERNAME on line 2
# delete and enter your username
# when finished editing, press control+X to exit
# then press shift+Y to save changes
# (or maybe shift+J if your language is set to german, I'm not sure)
```



```
GNU nano 2.3.1                               File: 20211215_hello_world.sh
```

```
#!/bin/bash
#SBATCH -D /scratch/perugolate/20211215_lvdatascieeb
#SBATCH -J hello_world
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH --mem=1G
#SBATCH --time=00:05:00
#SBATCH --partition=main
#SBATCH --qos=standard
echo "Hello World"
```

[Read 11 lines]

^G Get Help	^O WriteOut	^R Read File	^Y Prev Page	^K Cut Text	^C Cur Pos
^X Exit	^J Justify	^W Where Is	^V Next Page	^U UnCut Text	^T To Spell

TERMINAL term://./13558:/bin/zsh[-]

100% 807/807 : 1

buffers

Submit the job

```
# submit the job script using  
sbatch 20221130_hello_world.sh
```

sbatch is a command from the slurm workload/schedule managing software

squeue is used to monitor the queue (or squeue --me)

squeue

JOBID	PARTITION	NAME	USER	ST	TIME	NODES
NODELIST(REASON)						
8695474	agkeller	KF-2	heif89	R	1-06:23:29	1 g014
8694500	agkeller	Lil-3	heif89	R	1-06:50:38	1 g013
8717240	begendiv	jamesTes	james94	R	3:07:30	1 b004
8717994	begendiv	GEP.merq	ddepanis	R	6:30	1 b002
8717993	begendiv	GEP.merq	ddepanis	R	34:32	1 b003
8717992	begendiv	GEP.merq	ddepanis	R	37:32	1 b004
8717991	begendiv	GEP.merq	ddepanis	R	46:58	1 b001
8717989	begendiv	GEP.busc	ddepanis	R	53:25	1 b002
8717983	begendiv	GEP.busc	ddepanis	R	1:36:20	1 b003

Submit the job

```
# submit the job script using  
sbatch 20221130_hello_world.sh
```

The job should complete instantly

You will notice “Hello World” was not printed to your screen

The standard output was redirected to a file slurm-[jobID].out

Job output

```
# slurm has also added some usage stats to the end of the file
```

```
cat slurm-*.out
```

```
Hello World
```

```
== Epilog Slurmctld
```

```
=====
```

```
Job ID: 8722119
```

```
Cluster: curta
```

```
User/Group: perugolate/agrolff
```

```
State: COMPLETED (exit code 0)
```

```
Cores: 1
```

```
CPU Utilized: 00:00:00
```

```
CPU Efficiency: 0.00% of 00:00:01 core-walltime
```

```
Job Wall-clock time: 00:00:01
```

```
Memory Utilized: 0.00 MB (estimated maximum)
```

```
Memory Efficiency: 0.00% of 1.00 GB (1.00 GB/node)
```

```
=====
```

```
=====
```

Software

The cluster works just like a linux computer

- you can download/compile software
- you can install a package manager e.g. conda
- the HPC staff can help/advise on installation
- common software is available via “module load”
multiple versions of python/perl/R
bioinformatics software

Second job

Let's adapt one of your R exercises to the cluster

We need to:

- upload your R script and data
- make some edits to the R script
- create a job script to run the R script

Upload your script/data

transfer your R script / data to the the cluster

open a new terminal/shell on your computer and run:

```
# the command should be a single line
scp Exercises_Statistics2_Solutions.R username@curta.zedat.fu-berlin.de:/scratch/USERNAME/20221130_lvdatascieeb
# and the data
scp data_files_08.12.21.zip username@curta.zedat.fu-berlin.de:/scratch/USERNAME/20221130_lvdatascieeb
```

If you don't have your R script / data from last week, then copy them from my scratch directory:

```
# copy script from my scratch
cp /scratch/perugolate/Exercises_Statistics2_Solutions.R ./
# copy data from my scratch
cp /scratch/perugolate/data_files_08.12.21.zip ./
```

Prepare the data/script

```
# unzip the uploaded data  
unzip data_files_08.12.21.zip
```

We are going to prepare exercise 1 (the first 62 lines) from Exercises_Statistics2_Solutions.R as a script

the file paths (C:\\Users\\Lynn\\) show the script was likely not prepared on a unix computer. Lets fix the line endings first:

```
# if a file was prepared on windows or Mac (prior to OS X) the line endings  
# will be (invisibly) different, which can cause all sorts of problems  
dos2unix Exercises_Statistics2_Solutions.R
```

```
# copy first 62 lines to a new file with a sensible name  
head -n 62 Exercises_Statistics2_Solutions.R > 20221130_exercise_01.R
```


Modify script

```
# open the script in nano to edit  
nano 20221130_exercise_01.R
```

We are not using windows so change line 3 from:

```
filestem <- 'C:\\Users\\Lynn\\'
```

to:

```
#filestem <- 'C:\\Users\\Lynn\\'
```

the hash character ensures that this line is ignored

Next we modify line 9 to read:

```
dat <- read.table("LG_Data_Phytoplankton_Species1.txt", header=T)
```

Save the changes

Make a job script

We can reuse the sbatch parameters from the first job script

Lets copy the first 10 lines to a new script file:

```
# copy the sbatch parameter lines from first job script
head -n10 20221130_hello_world.sh > 20221130_exercise_01.sh
# open the new file in nano for editing
nano 20221130_exercise_01.sh
```

Make a job script

I have made the following edits in nano

- changed job name on line 3 from “hello_world” to “ex_1”
- added 2 commands to the bottom (in bold)

```
#!/bin/bash
#SBATCH -D /scratch/perugolate/20221130_lvdatascieeb
#SBATCH -J ex_1
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH --mem=1G
#SBATCH --time=00:05:00
#SBATCH --partition=main
#SBATCH --qos=standard
module load R/4.1.0-foss-2021a
Rscript 20221130_exercise_01.R
```

Make a job script

Many versions of R are already installed on the cluster

It is also possible to

- download and compile it yourself
- install it using a package manager such as conda

Here, we have loaded R using:

```
module load R/4.1.0-foss-2021a
```

This is a safe option because it has been compiled properly by the HPC staff

You can see the other software available by using:

```
module avail
```

Submit the job script

```
sbatch 20221130_exercise_01.sh
```

The job should complete within a few seconds

Again nothing is printed to the screen. This has been redirected to a text file `slurm-[jobID].txt`

```
head slurm-8726728.out
```

```
Call:
```

```
lm(formula = Size ~ TP * Trans, data = dat)
```

```
Residuals:
```

```
  Min      1Q  Median      3Q      Max
-4.0573 -0.9617  0.0516  0.9243  3.1775
```

```
Coefficients:
```

```
      Estimate Std. Error t value Pr(>|t|)
```

Job output

R was not run in interactive mode

- i.e. there was no window to display the plots

In this case Rscript redirects the plots to Rplots.pdf

You will need to transfer the file to your computer in order to view it

Open a terminal on your computer and type:

```
# replace USERNAME with your username
```

```
# the command should be a single line
```

```
scp username@curta.zedat.fu-berlin.de:/scratch/USERNAME/20221130_lvdatascieeb/  
Rplots.pdf ./
```