# Hey look we have a cluster now isn't that cool what does it do does it do stuff yes it does it's cool

## Doing cluster stuff for fun and ~~profit~~ science

**Lukas Burk**

Leibniz Institute for Prevention Research and Epidemiology — BIPS

2026-04-07

BioWiMium

# We have a new cluster

## You might have *heard*



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- What is this cluster thing
- How does it work (using R / Python, Slurm)
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> 😭 I know it's noisy and no I don't know when that is fixed

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- Access via *head node*
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> 💡 There’s a learning curve, but the payoff is huge

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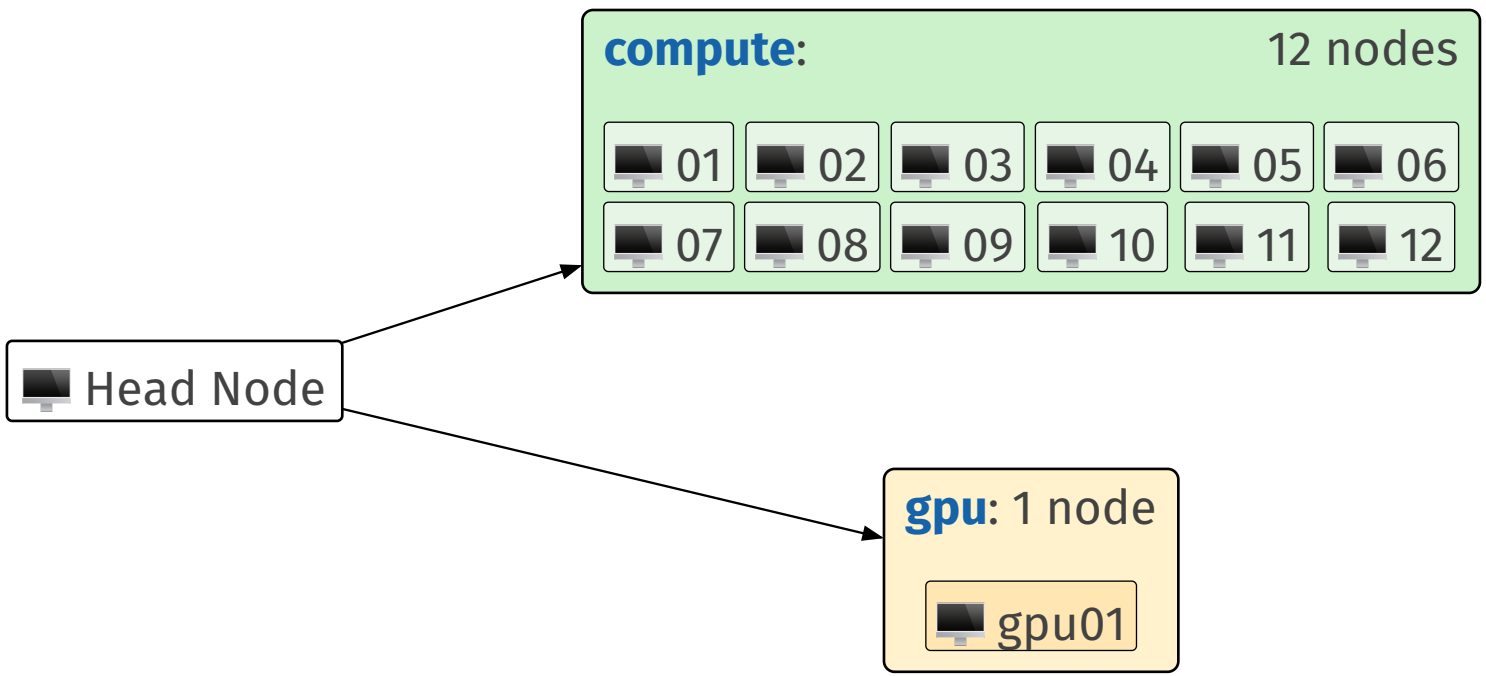
8. Repeat until ~~insane~~ done

# Cluster topology

## Partitions

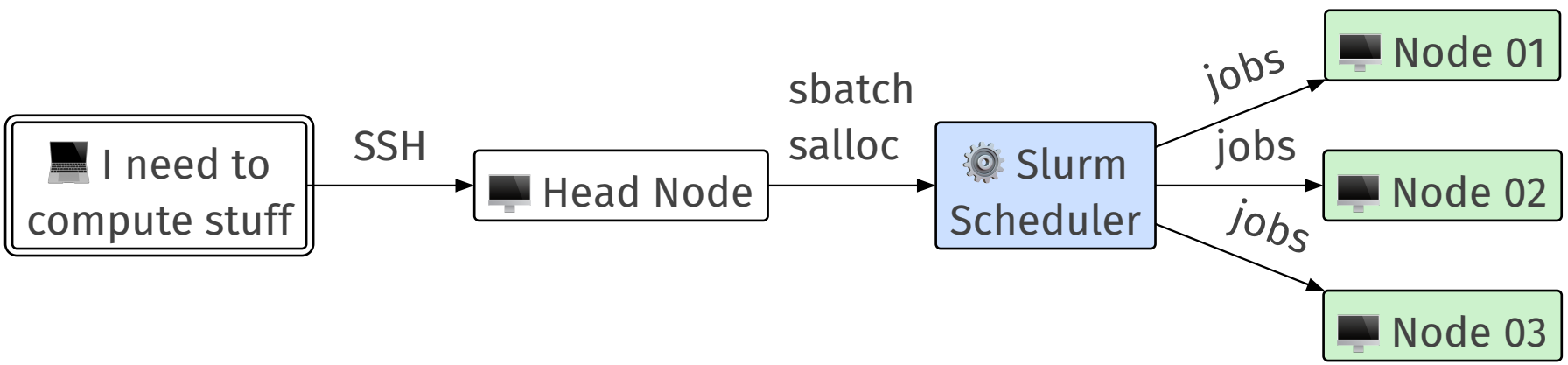




# Cluster topology

## It only looks weird because it is





# The head node

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⚠ The head node is shared by *everyone*. Heavy processes will be *terminated*.

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## Just to make sure you're confused



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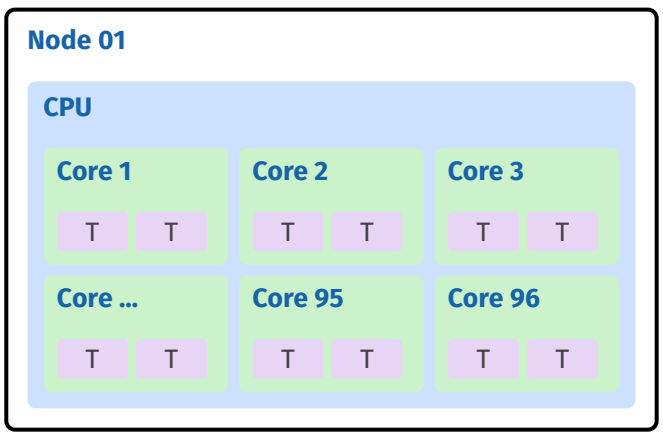

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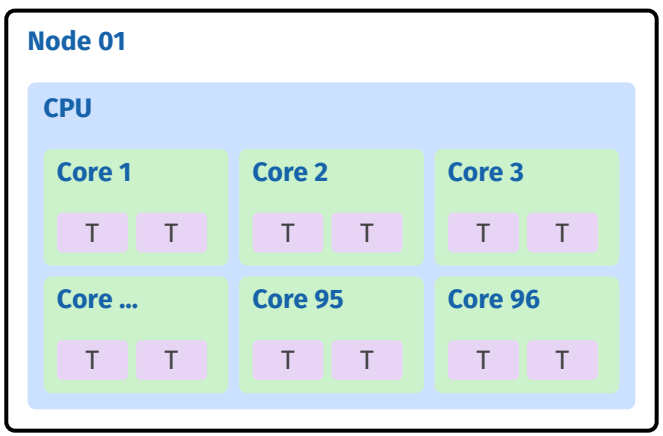

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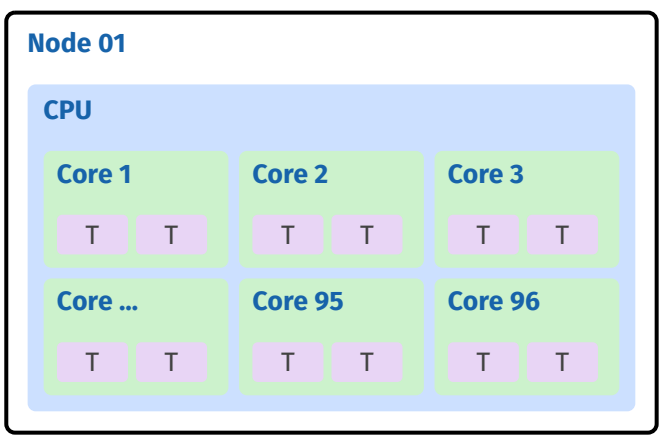

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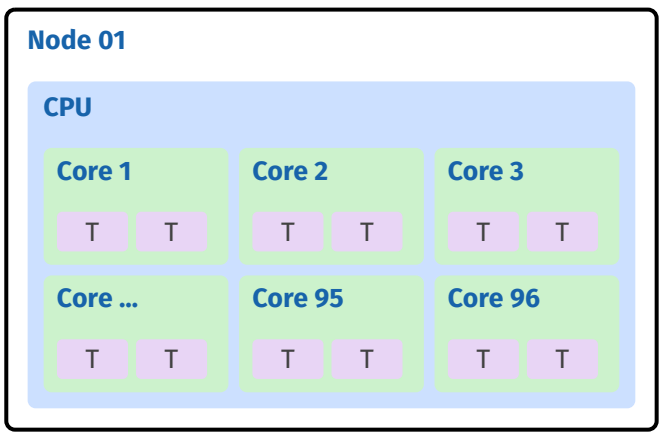

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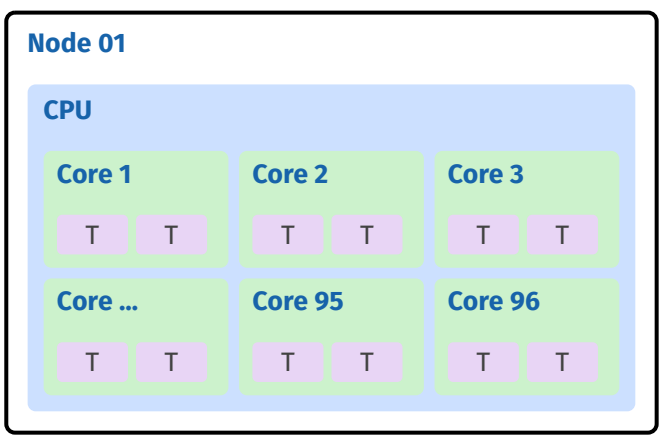

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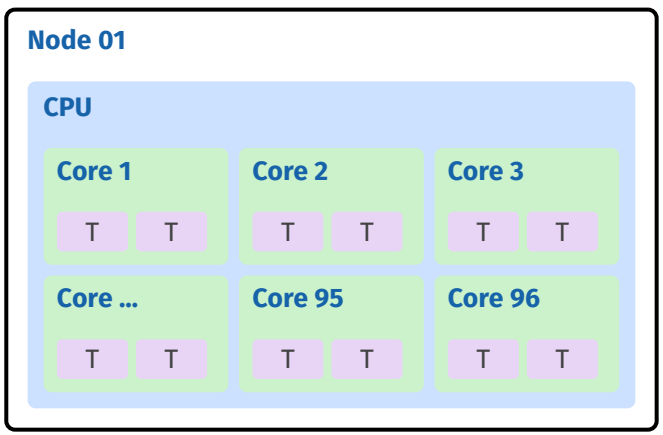

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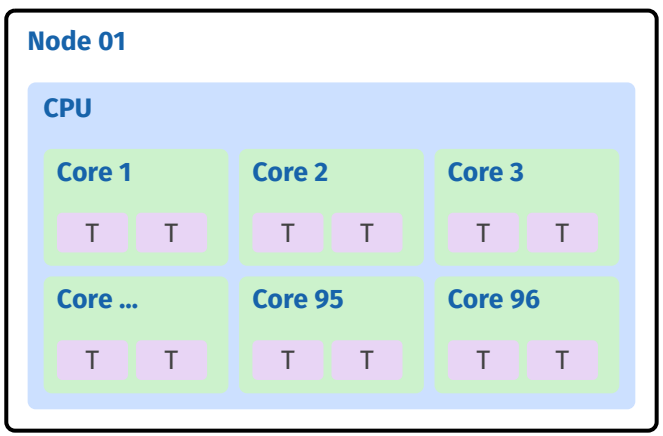

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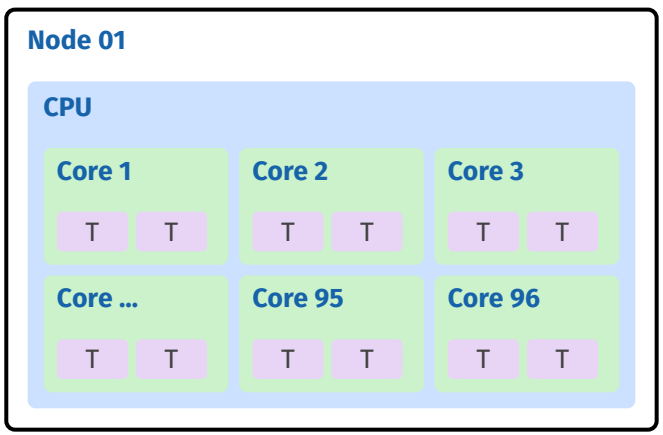

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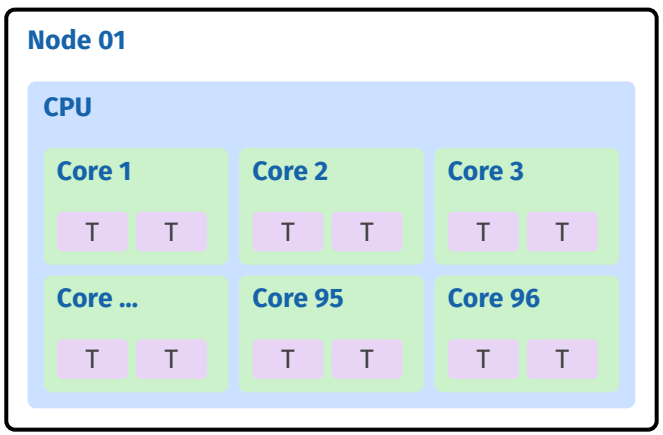


⚠ **Slurm**: You need 10 **threads** → you request 10 **“cpus”**

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→ It’s impossible to “endanger” other people’s compute jobs

# Logging in

## Different environments for different tasks



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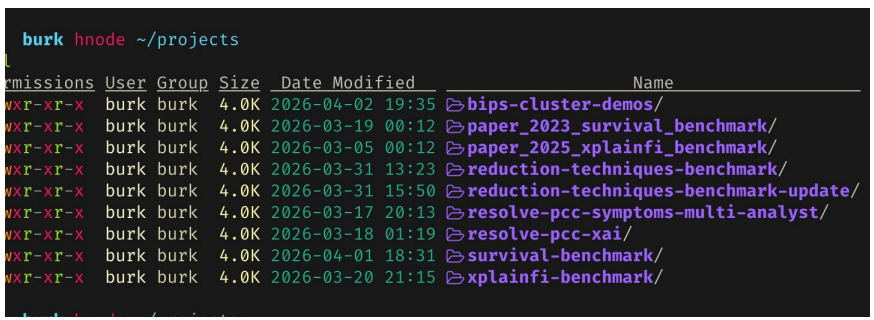

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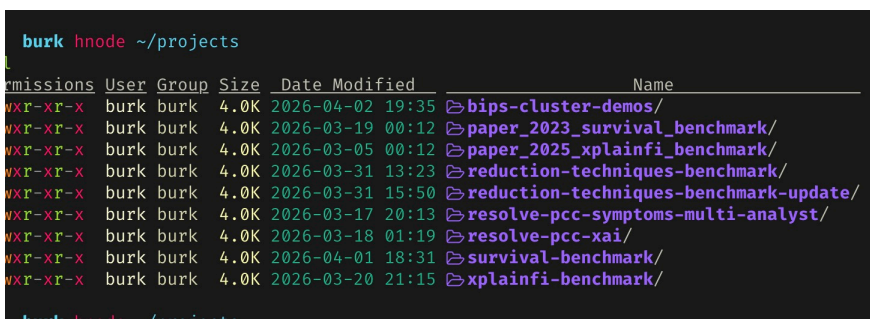


### Positron (VScode)

- Uses SSH for communication with head node
- GUI on your own device (PC, laptop)
- Terminal / R console runs **on head node**
- All files you see are on the head node
- 😎 Edit files conveniently

# The first thing you see when you log in

## Trying to point you in the right direction



# Software is managed differently

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- (Python: Use `uv`, no need for modules: (docs.astral.sh/uv))

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## Interactive: `salloc`

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salloc --cpus-per-task=20 --mem=4G --time=06:00:00
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salloc: Granted job allocation 137031
salloc: Nodes node01 are ready for job

# start R session
R

# Do work or run script
ranger::ranger(foo ~ ., data = bar)
source("analysis.R")
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## Batch job: `sbatch`

- Write an `analysis.sh` wrapper script

```
#!/bin/bash
#SBATCH --job-name=my-analysis
#SBATCH --output=logs/%x_%j.out
#SBATCH --cpus-per-task=20
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#SBATCH --time=06:00:00

Rscript analysis.R
```

- Run `sbatch analysis.sh` and go home

# Slurm resource allocation

## Partitions and QoS



- Slurm groups hardware in *partitions*
- 2 partitions: `compute` (12 nodes, *default*) and `gpu` (1 node)
- Prioritization is done in *Quality of Service* (QoS) queues:

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- For `sbatch` or `#SBATCH --qos=<name>`:

**short**: 1 hour **medium** (default): 1 day **long**: 7 days

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- You need 1 thread, you ask for `cpus-per-task=`**1**, you get **1** core reserved
- → More efficient to just ask for 2 “cpus” and 1 full core

# Example: Efficiently using a node

If your goal is to fully utilize 1 node (96 cores, 192 threads)



## What works

- 1 job with 192 threads ✅

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## What works

- 1 job with 192 threads ✅
- 96 jobs with 2 threads ✅

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- 1 job with 192 threads ✅
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## What works

- 1 job with 192 threads ✅
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## What does not work

- 192 jobs with 1 thread ❌

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## What works

- 1 job with 192 threads ✅
- 96 jobs with 2 threads ✅
- 8 jobs with 24 threads ✅

## What does not work

- 192 jobs with 1 thread ❌
- Each job reserves 1 **core**
- → 192 jobs allocate 192 cores, but a node only has 96!

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⚠️ If you're used to `batchtools`, you probably default to single-threaded jobs

# Did it work?

## Checking on your jobs



While running:

- `squeue --me`: list your jobs
- `tail -f logs/job_12345.out`: watch output
- `scancel <jobid>`: cancel a job

After completion:

- Check your output files (e.g. `logs/`)
- `sacct --starttime=today`: job history
- `sacct -j <jobid> --format=JobID,State,Elapsed,MaxRSS`

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Common failure modes

- **TIMEOUT**: job ran out of time, request more with `--time`
- **OUT_OF_MEMORY**: request more RAM with `--mem`
- **FAILED**: your script has a bug, check the log output (*did you load modules?*)

# Where does your stuff live?

## Two storage tiers



### Home directory

`/srv/home/<user>`

- Fast
- Limited space, also shared with software
- Scripts, code, *active* projects

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- Large capacity
- Slower
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- Compute nodes also have fast **local scratch** (`$TMPDIR`, auto-cleaned after job)

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> ⚠ There are **no backups**. Use `git` for code, be careful with data.

# User utilities

## Command-line aliases/functions



- I have prepared a few shorthand tools based on things I need often
- On head node, get info with `slurm_user_help`:

```
❯ slurm_user_help
=== Slurm User Helper Functions ===

JOB MONITORING:
  sq              - Enhanced squeue with better formatting
  sqm             - My jobs queue
  sqs             - Job status summary with colors
[...]

JOB ACCOUNTING:
  slac              - Enhanced sacct
  slac1h/1d/3d/1w   - Jobs from last hour/day/3days/week (excludes PENDING)
    State filters:  -a (all), -p (pending), -c (completed), -f (failed), -r (running)
  sltoday           - Jobs submitted today
```

# Getting started

## And further reading material



1. Ask me for an account, I will send you login credentials
2. Read (and bookmark) the docs:
   - cluster.bips.coffee (public)
3. Bookmark the dashboard (current cluster usage):
   - http://srvcluster.bips.de/ (no https!)
4. Try demos / usage examples for `batchtools`, `mirai`, `targets`:
   - srvgit.bips.eu/bips/bips-cluster-demos