




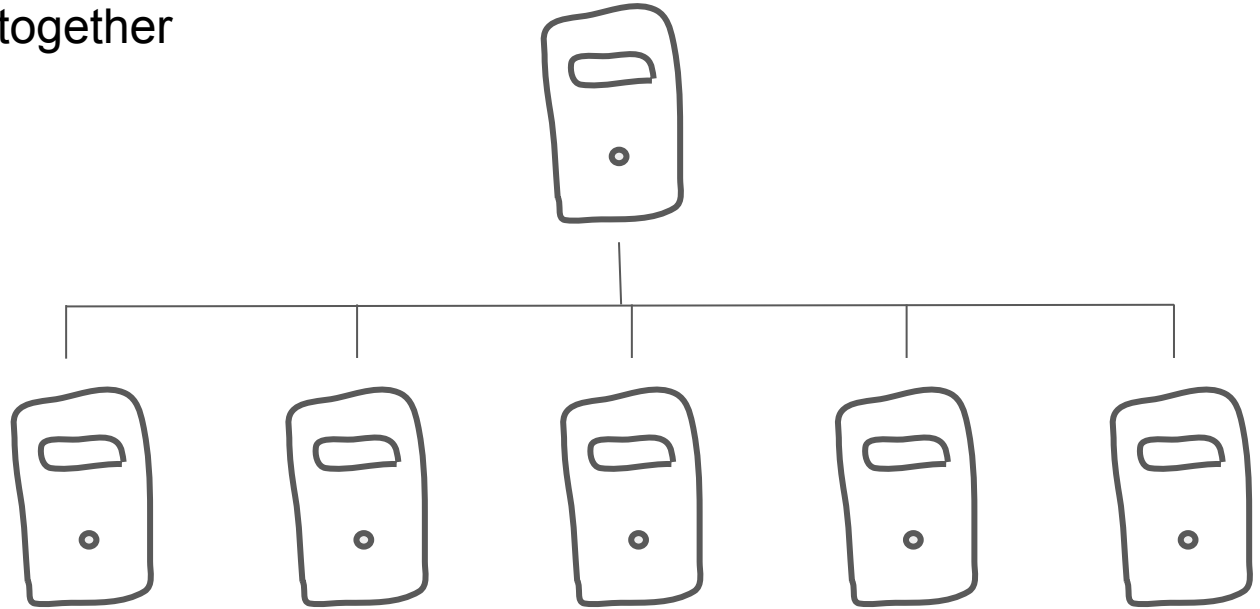
Before starting...



During this course, you are going to run analyses on a computer cluster

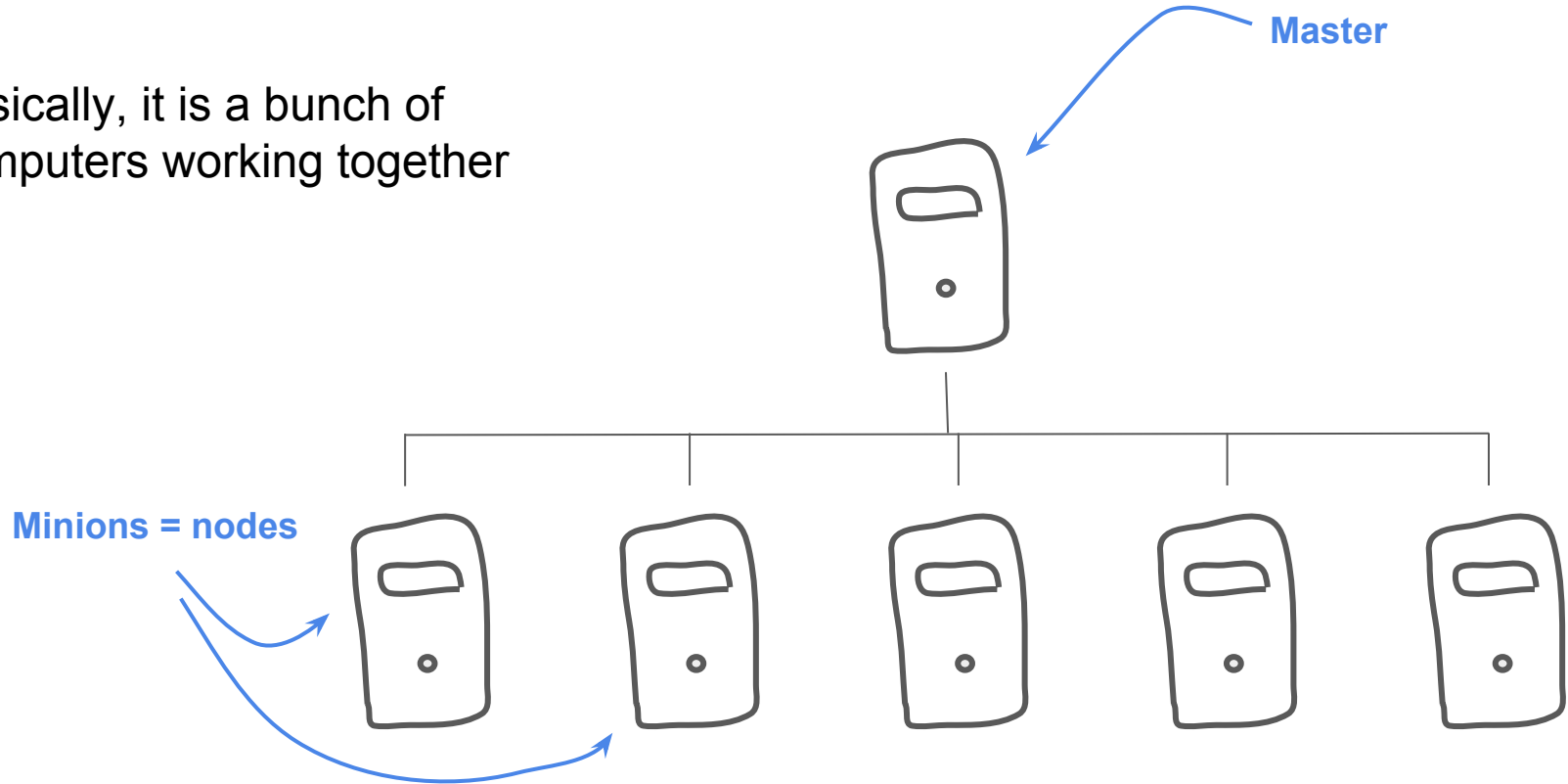
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Basically, it is a bunch of computers working together



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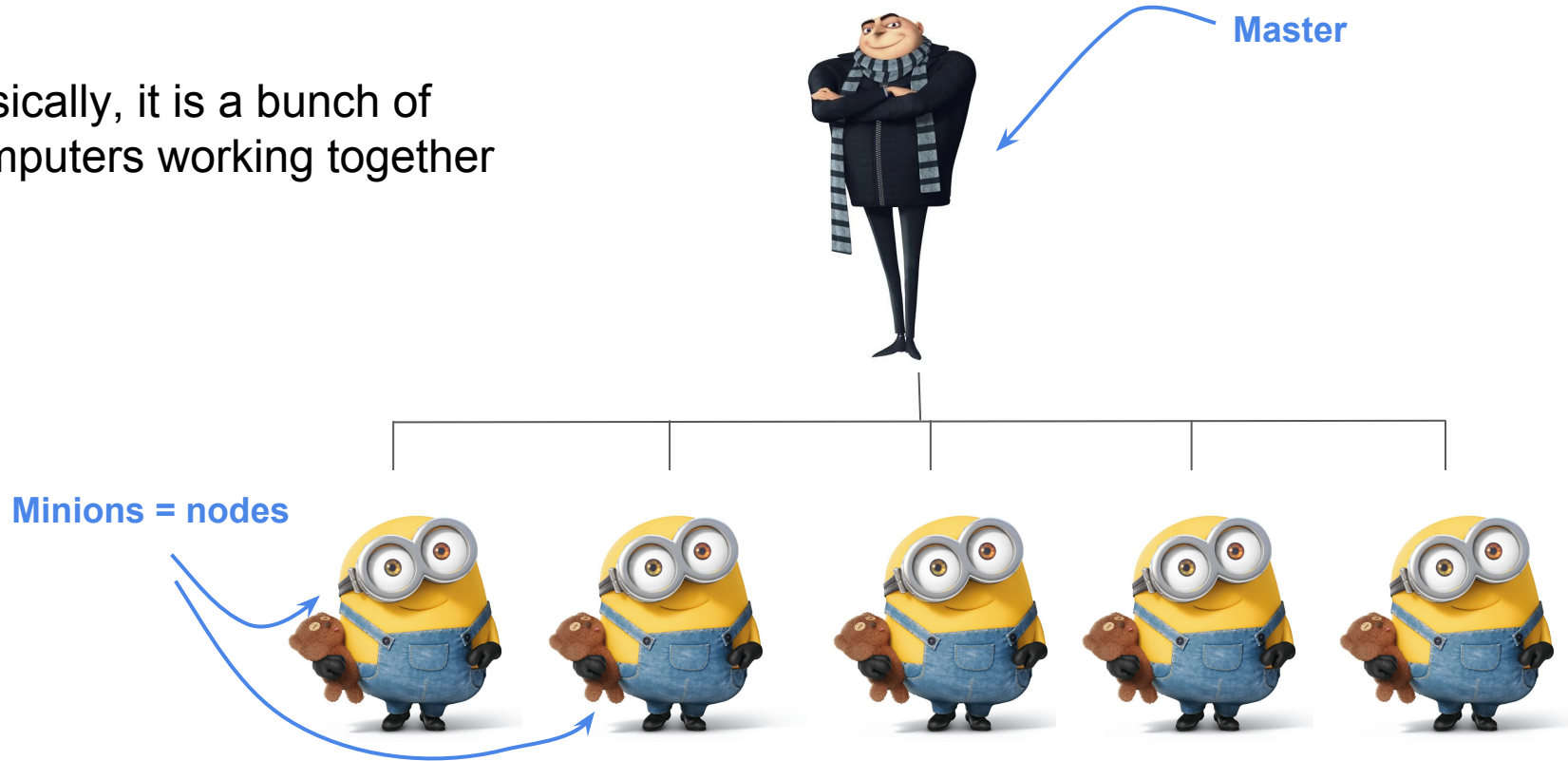




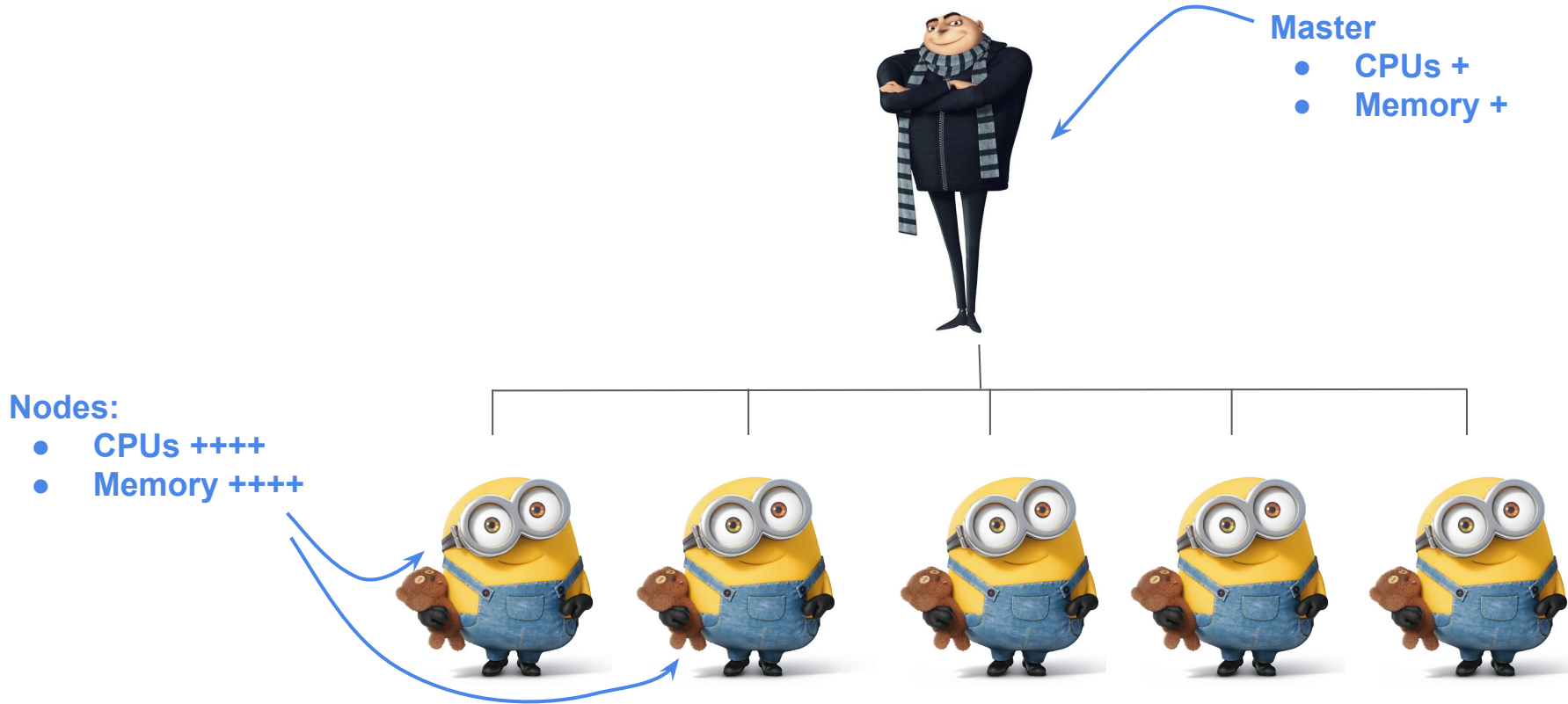
Hum... Wait...

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Master:

- Executes light bash command lines. Ex: cd, mv, ls...
- Is used to send big jobs to Minions

Nodes:

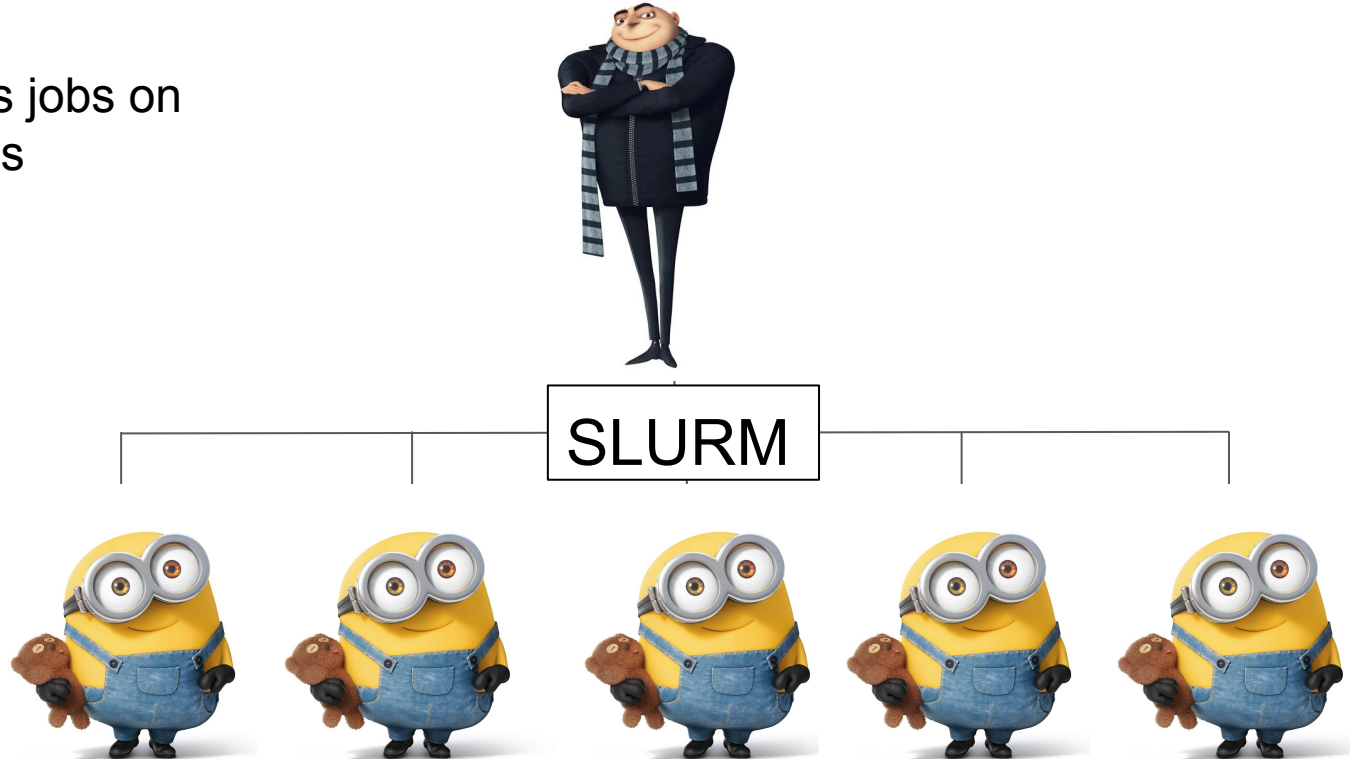
- Executes master's jobs





# A computer cluster: how to send jobs to minions?

**Slurm** dispatches jobs on the nodes/minions



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```
srun fastqc file.fastq
```



SLURM



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```
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```

- Command line to run
- Prepend the command line with **srun**



SLURM



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```
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```

Job 1

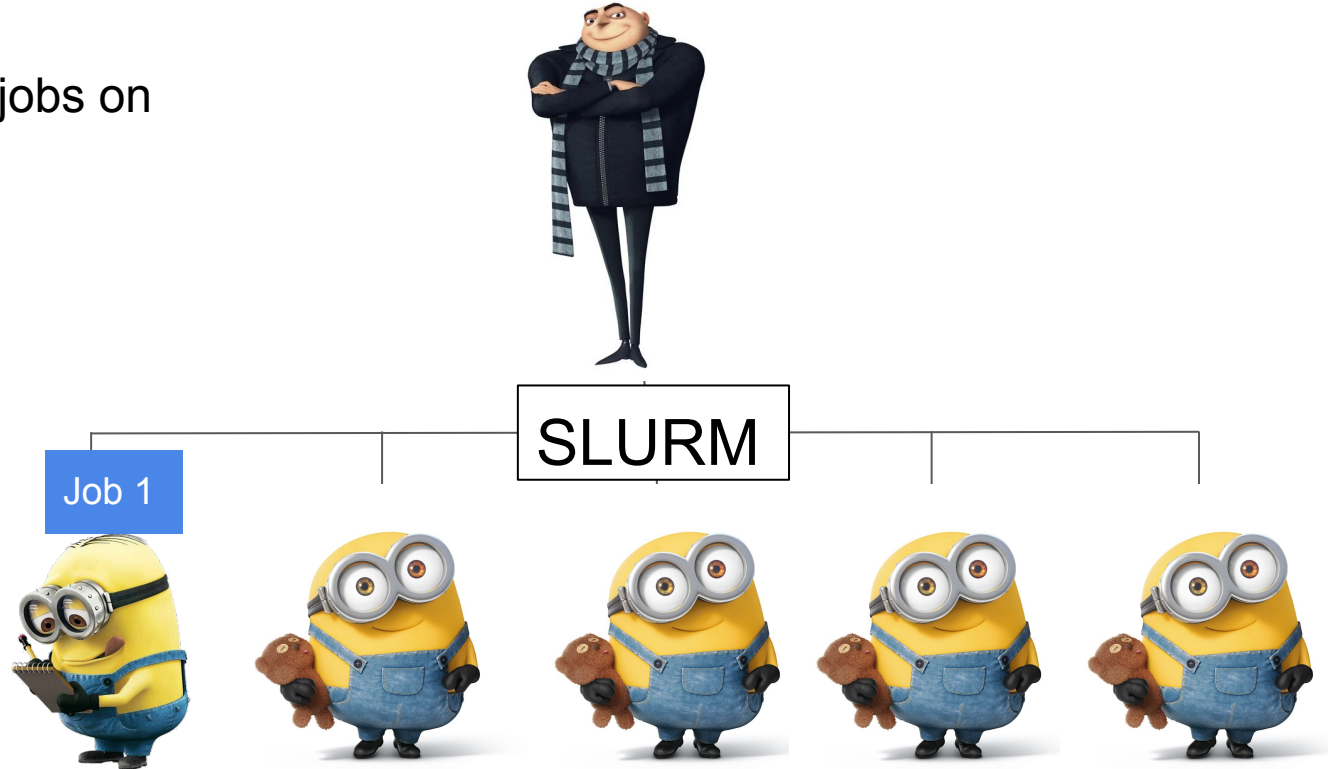


SLURM



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```
srun fastqc file2.fastq
```

Job 2



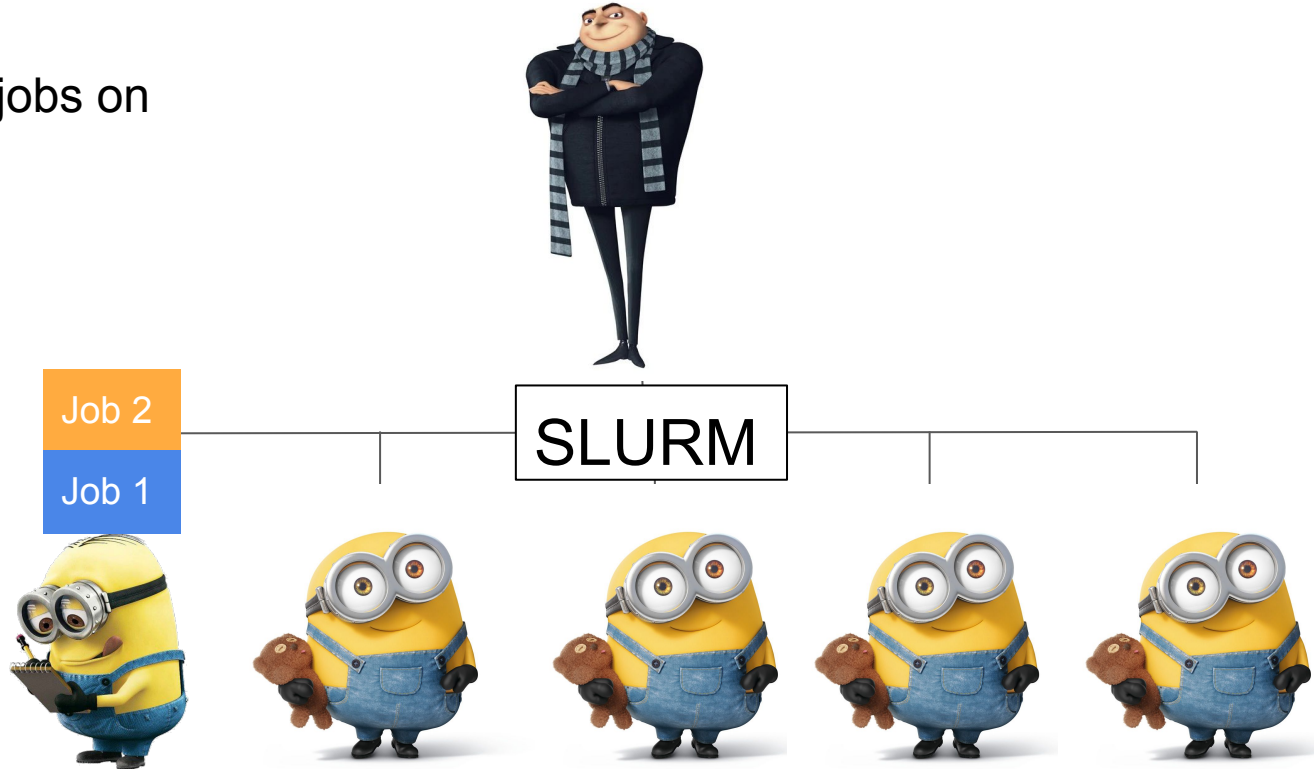
SLURM

Job 1



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```
srun fastqc file3.fastq
```

Job 3



Job 2

Job 1

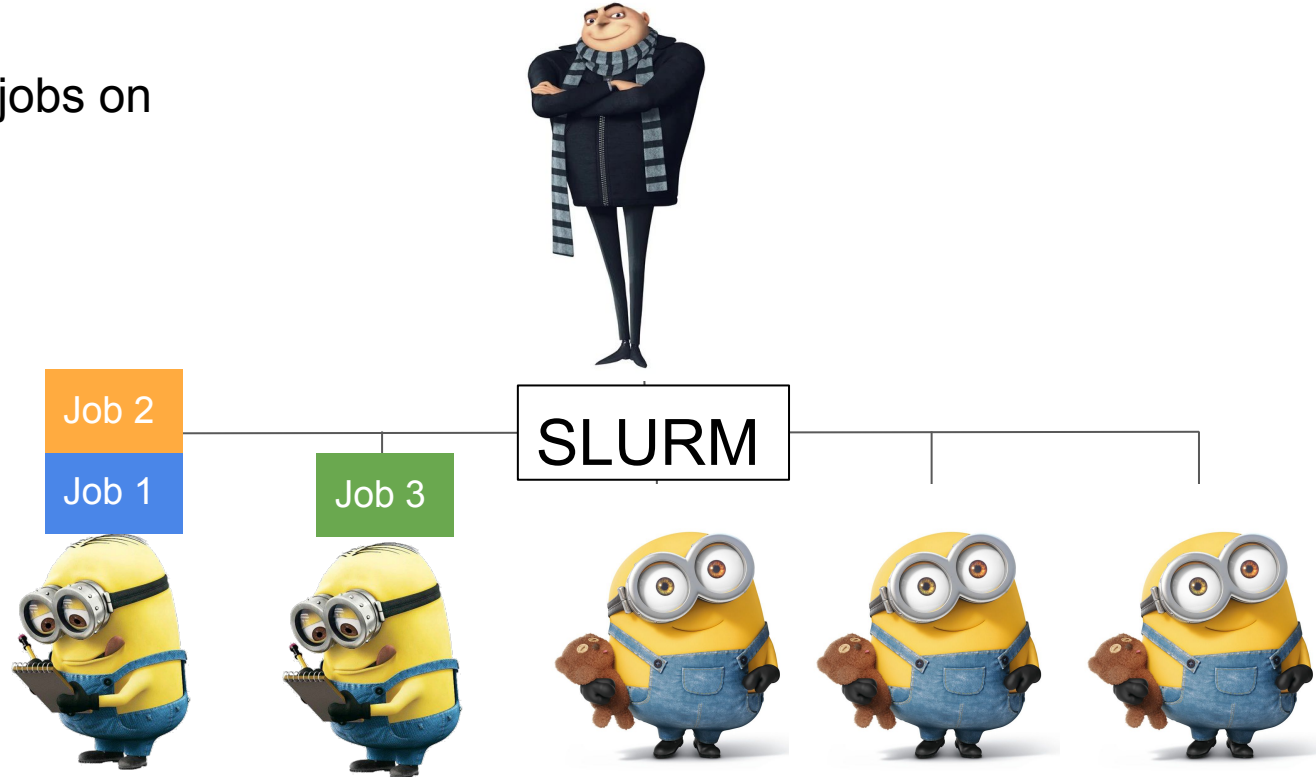
SLURM





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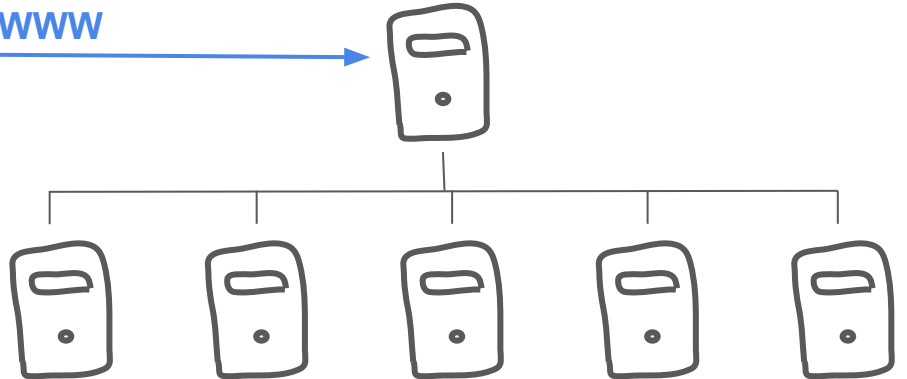


# A computer cluster: how to use it?

```
ssh <login>@hpc.igbmc.fr
```



www



You are connected to the “master” of the server!



# How to use a computer cluster: summary

- Get connected to the master and keep working on it
- For **basic command** (cd, ls, mv, mkdir...), run it directly on the “**master**”
- For all the rest, including **bioinformatics tools**, prepend all command lines by **srun** so that your job will run on a **node** of the cluster
  
- You're freaking out? Don't worry, you'll be guided all over the practical sessions.

# Your turn! Get connected to the server

# On Windows with MobaXterm

Session : ssh

Host : hpc.igbmc.fr

Specify username : ticked and filled in

Advanced SSH settings : X11-Forwarding

# On MacOS and Linux

```
ssh -XY <login>@hpc.igbmc.fr
```



# TIPS

- **Keep track** of all command lines you run. You can for example, create a text file in which you write every commands you run.
- Give **content-explicit names** to the files you're generating.
- Give to files the **right extension**.
- **Create directories!!**
- **Compress** big files (with gzip for instance).