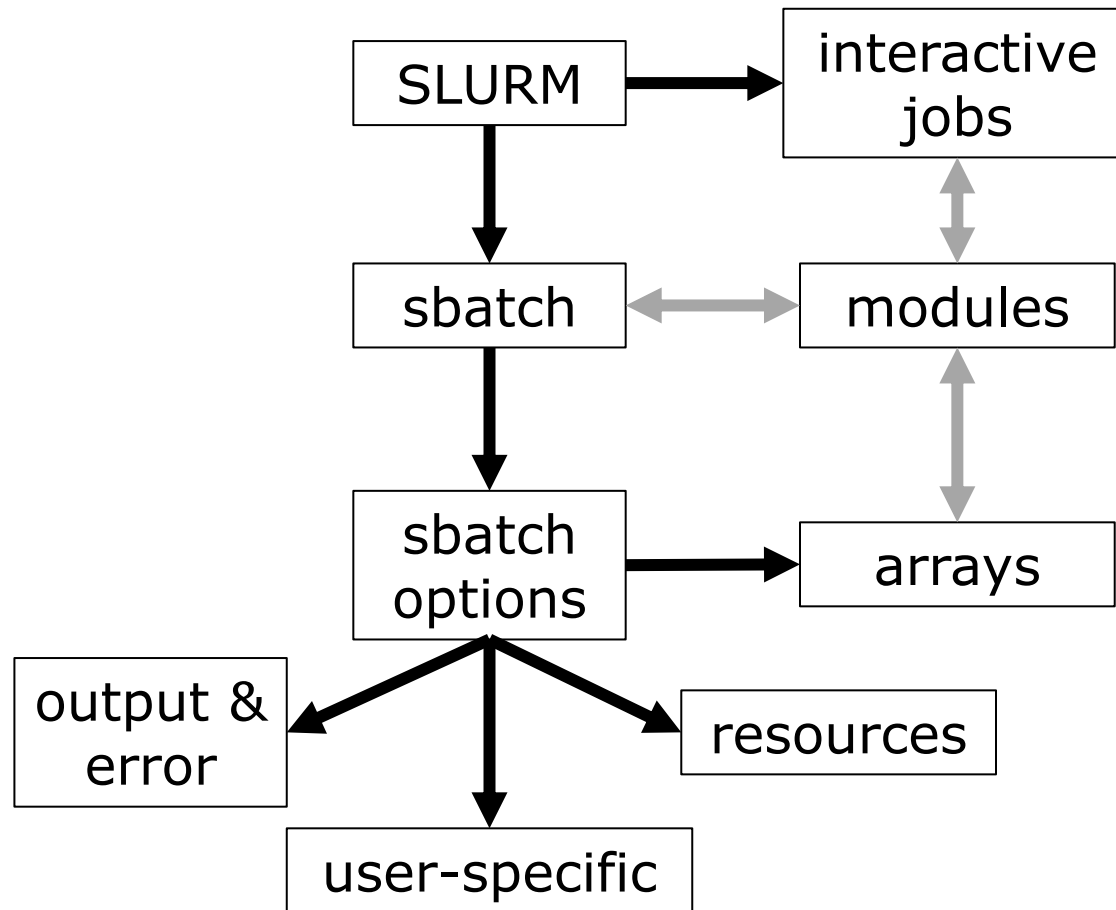


# Introduction to SLURM and modules

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# Outline



# **1. SLURM: introduction**

# Limited resources

- Cluster has many users wanting to run jobs, which limits:
  - CPU
  - Working memory
  - Time
- How to assign which resources to which job?

# Job scheduling

## Job (computing)

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From Wikipedia, the free encyclopedia

In [computing](#), a **job** is a unit of work or unit of execution (that performs said work).

## Job scheduler

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From Wikipedia, the free encyclopedia

A **job scheduler** is a computer application for controlling unattended background program execution of [jobs](#).<sup>[1]</sup>

# SLURM

- **S**imple **L**inux **U**tility for **R**esource **M**anagement
- Job scheduler on:
  - UBELIX
  - IBU cluster
  - and many more



# Resource allocation commands

- sbatch
- srun
- salloc

```
script.sh
```

```
#!/usr/bin/env bash
```

```
my_program \  
--cpu 32 \  
--memory 128G
```

```
sbatch [options] script
```

```
$ sbatch --cpus-per-task=32 --mem-per-cpu=4G ./script.sh
```



script.sh

```
#!/usr/bin/env bash

#SBATCH --cpus-per-task=32
#SBATCH --mem-per-cpu=4G

my_program \
--cpu 32 \
--memory 128G
```

\$ sbatch ./script.sh

```
$ sbatch ./script.sh
```

```
Submitted batch job 6245994
```

```
$ squeue --job 6245994
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
6245995	pall	script.sh	gvangees	R	0:07	1	binfservas01

```
$ squeue -A gvangeest
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
6245995	pall	script.sh	gvangees	R	0:07	1	binfservas01

## **2. Frequently used sbatch options**

## 2.1 Required resources

- CPU
  - `--cpus-per-task=2`
- Working memory
  - `--mem-per-cpu=4G`
- Time (days-hours:minutes:seconds)
  - `--time=1-05:00:00`

Conservative values will cause  
your job to start earlier  
**But:** job will fail if resources are  
overrequested!

## 2.2 user specific

- Job name:
  - `--job-name=my_job_name`
- e-mail
  - `--mail-user=user@students.unibe.ch`
  - `--mail-type=begin,end,fail`

## 2.3 output & error

- `--output=existing/path/output_%j.txt`
- `--error=existing/path/error_%j.txt`

Path should exist!  
Job will fail otherwise  
(without error message)

# **3. Interactive jobs**

# Why submit interactive job?

- **Interactive job:** allocated resources that are approachable with shell
- Head (login) node is not for computation
- Debugging and testing can be much more convenient if interactive



# srun

- Versatile command
- Used for job steps within sbatch (not treated in this course)
- Also for allocation of interactive job with pty (pseudo-terminal mode)

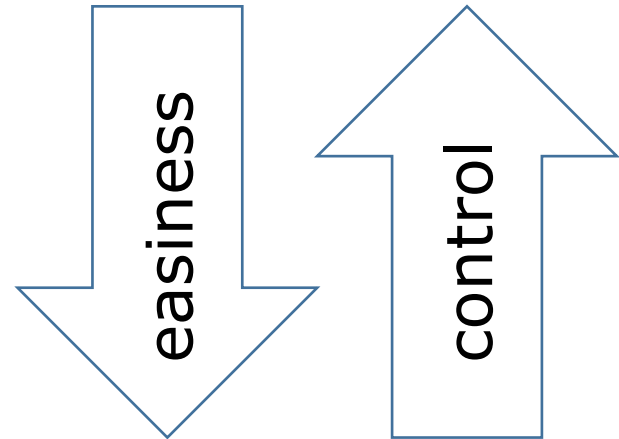
```
$ srun --cpus-per-task=1 --mem-per-cpu=4000 \  
> --time=00:05:00 --pty bash
```

Exit the interactive job  
with `exit`

# 4. Modules

# Software

- Install it yourself (at ~)
- Use a container
- Install with conda
- Use modules



# Modules

- Check for available modules:
  - `module avail`
- Add a module to environment:
  - `module add`
- Unload a module:
  - `module rm`
- Available modules:
  - <https://www.vital-it.ch/services>

# **5. Job arrays**

# 5.1 Jobs in parallel

- Run similar command with different parameters: parameter sweep
- E.g. alignment (e.g. with minimap2) on several files.

script.sh

```
#!/usr/bin/env bash
```

```
#SBATCH --array=0-3
```

```
#SBATCH --cpus-per-task=32
```

```
#SBATCH --mem-per-cpu=4G
```

```
my_program \
```

```
$SLURM_ARRAY_TASK_ID
```

--array=0-3

job\_0

SLURM\_ARRAY\_TASK\_ID=0

job\_1

SLURM\_ARRAY\_TASK\_ID=1

job\_2

SLURM\_ARRAY\_TASK\_ID=2

job\_3

SLURM\_ARRAY\_TASK\_ID=3

## 5.2 Using UNIX arrays

```
$ ls
file1.txt file2.txt file3.txt
$ FILES=(./*)
$ echo ${FILES[0]}
file1.txt
$ echo ${FILES[1]}
file2.txt
$ echo ${FILES[2]}
file3.txt
```

UNIX uses zero-based indexing



script.sh

```
#!/bin/bash
```

```
#SBATCH --cpus-per-task=32
```

```
#SBATCH --mem-per-cpu=4G
```

```
#SBATCH --array=0-7
```

```
FILES=(/path/to/input_data/*)
```

```
my_program ${FILES[$SLURM_ARRAY_TASK_ID]}
```