

# Compute Canada Tutorial



# Slurm Jobs

Salloc/Sbatch

Squeue

Sacct

# Salloc

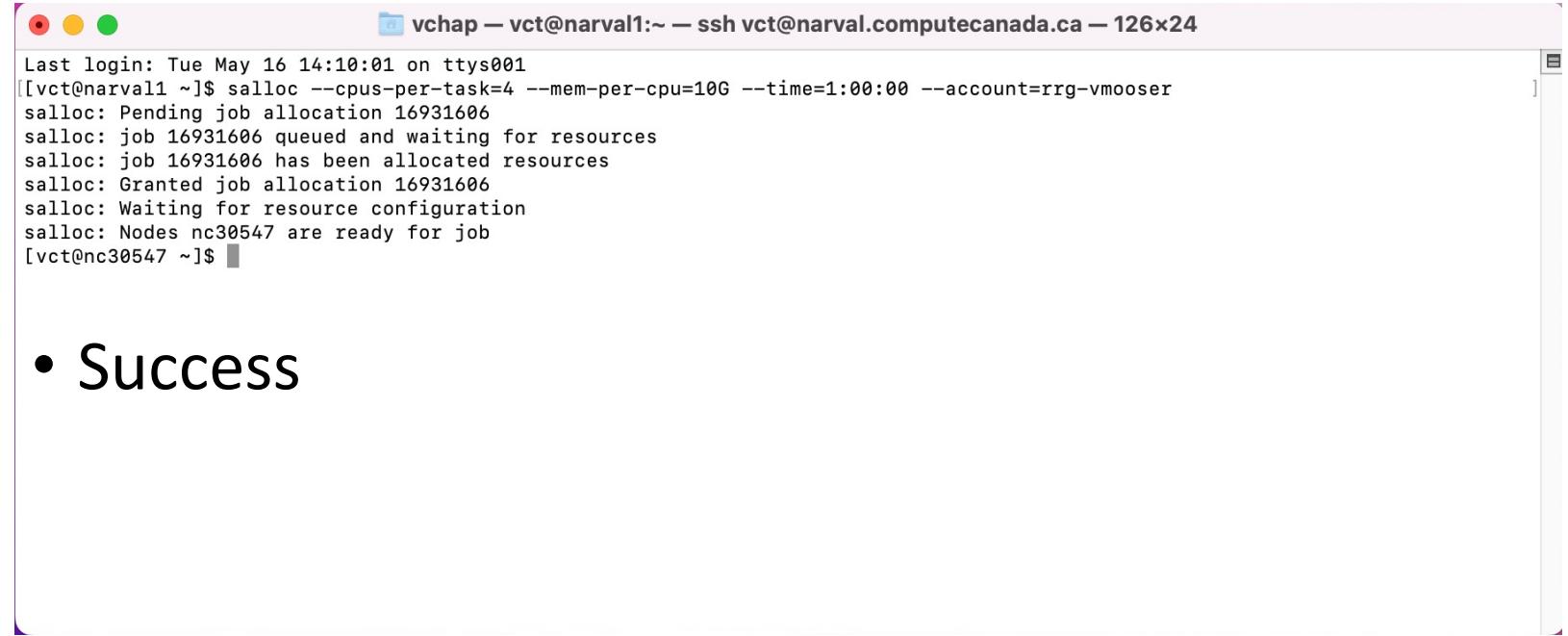


vchap — vct@narval1:~ — ssh vct@narval.computeCanada.ca — 126x24

```
Last login: Tue May 16 14:10:01 on ttys001
[vct@narval1 ~]$ salloc --cpus-per-task=4 --mem-per-cpu=10G --time=1:00:00 --account=rrg-vmooser
salloc: Pending job allocation 16931606
salloc: job 16931606 queued and waiting for resources
```

- Command breakdown:
  - Salloc -> interactive
  - cpus-per-task=4 -> 4 cpus for this job
  - Mem-per-cpu=10G -> each cpus is accompanied of 10G
  - Time=1:00:00 -> 1 hour
  - Account=rrg-vmooser -> use the allocation of the CERC
- We obtained a number : 16931606
  - This is the job ID (we will use it later)

# Salloc



A screenshot of a terminal window titled "vchap — vct@narval1:~ — ssh vct@narval.computeCanada.ca — 126x24". The terminal shows the following output:

```
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[vct@narval1 ~]$ salloc --cpus-per-task=4 --mem-per-cpu=10G --time=1:00:00 --account=rrg-vmooser
salloc: Pending job allocation 16931606
salloc: job 16931606 queued and waiting for resources
salloc: job 16931606 has been allocated resources
salloc: Granted job allocation 16931606
salloc: Waiting for resource configuration
salloc: Nodes nc30547 are ready for job
[vct@nc30547 ~]$ █
```

• Success

# Sbatch

- For the same options same options :

```
vchap — vct@narval1:~/scratch/CARTaGENE_V4 — ssh vct@narval.computeCanada.ca — 126x24
● ○ ●
#!/bin/bash
#SBATCH --cpus-per-task=4
#SBATCH --mem-per-cpu=10G
#SBATCH --time=1:00:00
#SBATCH --account=rrg-vmooser

plink2 ...
batch.sh (END)
```

```
vchap — vct@narval1:~/scratch/CARTaGENE_V4 — ssh vct@narval.computeCanada.ca — 126x24
[[vct@narval1 CARTaGENE_V4]$ sbatch batch.sh ]]
```

Sacct																	
Account	User	JobID	Start	End	AllocCPUS	Elapsed	AllocTRES	CPUTime	AveRSS	MaxRSS	MaxRSSTask	MaxRSSNode	NodeList	ExitCode		State	
rrg-vmoos+	vct	16889344	2023-05-15T10:06:09	Unknown	10	1-06:32:52	billing=62,cpu=10,mem=250G,no+1	12-17:28:40					n111001	0:0		RUNNING	
rrg-vmoos+		16889344.ba+	2023-05-15T10:06:09	Unknown	10	1-06:32:52	cpu=10,mem=250G,node=1	12-17:28:40					n111001	0:0		RUNNING	
rrg-vmoos+		16889344.ex+	2023-05-15T10:06:09	Unknown	10	1-06:32:52	billing=62,cpu=10,mem=250G,no+1	12-17:28:40					n111001	0:0		RUNNING	
rrg-vmoos+	vct	16929082	2023-05-16T14:48:08	2023-05-16T14:58:01	1	00:09:53	billing=3,cpu=1,mem=15G,node=1	00:09:53					nc20133	1:0		FAILED	
rrg-vmoos+		16929082.in+	2023-05-16T14:48:08	2023-05-16T14:58:01	1	00:09:53	cpu=1,mem=15G,node=1	00:09:53	156260K	156260K	0	nc20133	nc20133	1:0	FAILED		
rrg-vmoos+		16929082.ex+	2023-05-16T14:48:08	2023-05-16T14:58:01	1	00:09:53	billing=3,cpu=1,mem=15G,node=1	00:09:53	72K	72K	0	nc20133	nc20133	0:0	COMPLETED		
rrg-vmoos+	vct	16931606	2023-05-16T16:21:18	2023-05-16T16:24:47	4	00:03:29	billing=10,cpu=4,mem=40G,node+1	00:13:56					nc30547	0:0		COMPLETED	
rrg-vmoos+		16931606.in+	2023-05-16T16:21:18	2023-05-16T16:24:47	4	00:03:29	cpu=4,mem=40G,node=1	00:13:56	956K	956K	0	nc30547	nc30547	0:0	COMPLETED		
rrg-vmoos+		16931606.ex+	2023-05-16T16:21:18	2023-05-16T16:24:47	4	00:03:29	billing=10,cpu=4,mem=40G,node+1	00:13:56	0	0	0	nc30547	nc30547	0:0	COMPLETED		
rrg-vmoos+	vct	16932102	None	2023-05-16T16:37:42	4	00:00:00		00:00:00					None assigned	0:0	CANCELLED by 3057922		

# Sacct

- Breakdown

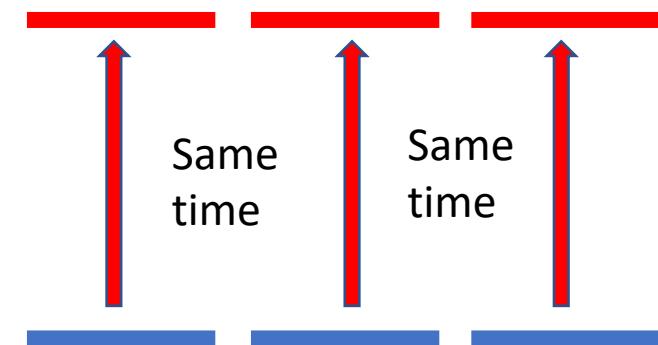
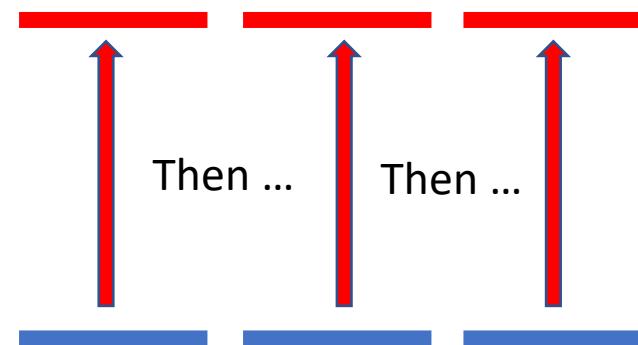
- Account = name of the allocation used
- User = your user name
- JobID = previously mentioned
- Start = Start Time
- End = End Time
- AllocCPUS = nb cpu used
- Elapsed = total time
- CPUTime = metric of time \* cpu
- RSS = memory (by polling, so it can miss spikes)
- Node = The node (s) used for that job
- State / Exit code = Job ending details (Successful, exited on an error etc...)

sq or queue

- Similar to sacct except less detailed and only the current job

```
vchap — vct@narval4:~ — ssh vct@narval.computeCanada.ca — 80x24
[vct@narval4 ~]$ sq
      JOBID      USER      ACCOUNT          NAME   ST TIME_LEFT NODES CPUS T
RES_PER_N MIN_MEM NODELIST (REASON)
      17073732    vct rrg-vmooser_ Association Te   R 3-05:42:50      1   10
      N/A     25G nl10101 (None)
[vct@narval4 ~]$
```

# Job Parallelization concept



# Job Parallelization Arrays

- Sbatch option
  - #SBATCH –array=1-20
    - - -> everything in between left and right
    - , -> nothing in between left and right
    - : -> step by variable on the right
    - % -> limit the number of submission by variable on the right

- Job Arrays
  - Parallelization
    - For each array the submitted batch file will be executed the same \*\*\* EXCEPT \*\*\*
    - \*\*\*EXCEPT\*\*\*  
\$SLURM\_ARRAY\_TASK\_ID takes a different value
    - Value of SLURM\_ARRAY\_TASK\_ID is define by the submission
      - Example array=1-5
        - 1 2 3 4 5

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# Job Parallelization Arrays

- Code Example
  - It will for each chromosome (file context)
  - run the plink2 freq command
  - The output will be named after the input

```
CellProfiler — vct@narval4:/scratch/vct/CARTaGENE_V4 — ssh vct@narval.com

#!/bin/bash
#SBATCH --cpus-per-task=4
#SBATCH --mem-per-cpu=10G
#SBATCH --time=1:00:00
#SBATCH --account=rrg-vmooser
#SBATCH --array=1-22

plink2 --vcf chr$SLURM_ARRAY_TASK_ID.vcf.gz --freq --out chr$SLURM_ARRAY_TASK_ID
batch.sh (END)
```