

**Navigation & help**

pwd	print working directory
ls -lh	list files with sizes
ls -lah	list including hidden files
cd <dir>	change directory
cd ~	home directory
cd ..	parent directory
man <command>	manual/help page (q to quit)
history   grep <word>	search your past commands

**File & directory operations**

mkdir <dir>	make a new directory
cp SRC DEST	copy file
cp -r DIR/ DEST/	copy directory recursively
mv SRC DEST	move or rename
rm <file>	remove file (use rm -i for safety)
touch <file>	create an empty file
ln -s TARGET LINK	make a symbolic link

**Viewing files**

less -S <file>	view file (no wrapping)
head -n 20 <file>	first 20 lines
tail -n 20 <file>	last 20 lines
zcat file.fastq.gz   head -n 8	peek into a compressed FASTQ
cat <file>	print file to terminal

**Search, count, sort**

grep -n "PATTERN" file	find pattern with line numbers
grep -i / -v / -o / -n	ignore case / invert match / only match / line numbers
zgrep "AGATCGGAAG" *.fastq.gz	search inside compressed FASTQs
wc -l file	count lines
sort -n file	numeric sort
uniq -c	unique lines with counts

**Pipes & redirects**

cmd1   cmd2	pipe output of one command into another
cmd > out.txt	write to file (overwrite)
cmd >> out.txt	append to file
cmd 2> err.txt	write errors to file
cmd &> all.txt	capture both stdout and stderr
cmd < in.txt	use file as input

**Compression & archives**

gzip file / gunzip file.gz	compress or decompress
tar -czvf out.tar.gz DIR/	archive and compress directory
tar -xf out.tar.gz	extract archive

**tmux essentials**

tmux new -s analysis	Start a new named session
Ctrl-b d	Detach from session
tmux ls	List sessions
tmux attach -t analysis	Reattach to session
tmux kill-session -t name	Kill a session
Ctrl-b %	Vertical split
Ctrl-b "	Horizontal split
Ctrl-b arrow-key	Move between panes
Ctrl-b c	Create new window
Ctrl-b n / Ctrl-b p	Next / previous window
Ctrl-b ,	Rename window

**Slurm essentials**

squeue -u \$USER	Show your jobs
sinfo	Show partitions/nodes
sbatch job.slurm	Submit batch job
scancel <jobid>	Cancel job
srun -t 30:00 -a <AC> -p cpu -c 2 script.sh	Run one-off job with resources
sinteractive -t 2:00:00 -a <AC> -p cpu -c 4	Start interactive job with resources
seff <jobid>	Show efficiency of a completed job

**Slurm sample job**

```
#!/bin/bash
#SBATCH --job-name=fastqc
#SBATCH --account=ACCOUNT
#SBATCH --partition=cpu
#SBATCH --nodes=1
#SBATCH --cpus-per-task=4
#SBATCH --output=fastqc.%j.out
#SBATCH --error=fastqc.%j.err

module --force purge
module load biocontainers
module load fastqc

for file in *fastq.gz; do
fastqc -t ${SLURM_CPUS_ON_NODE} ${file};
done
```

# Use Bash as the job's shell  
 # Job name shown by squeue/sacct  
 # Slurm account/allocation to charge  
 # Queue/partition to submit to  
 # Number of nodes requested  
 # CPU threads for \*each\* task (here 1 task)  
 # Stdout log file (%j = JobID)  
 # Stderr log file

# Start with a clean module environment  
 # Load site module providing containers  
 # Load FastQC (module or container wrapper)

# Run FastQC using Slurm-provided thread count