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1 Linux-commands and useful links
2 =====
3 pwd - where am I (which is the current directory)
4 ll - show the list of files (detailed information)
5 ls - short list of files
6 cp file1 file2 - copy files
7 use left mouse button to highlight filenames and then the right mouse button to paste filenames
8 use tab-key to finalize filenames (directory names)
9 example (for a file starting with letter "t"): ll t <tab>
10 cd - - goes back to the latest directory you have been
11 cp -Rp - copy directories (Recursively) preserving time stamps
12 du -h - how big is a directory (human readable format)
13 touch filename - creates a new file (empty)
14 chmod u+x programname - allow yourself (give permissions) to execute this program
15 ./programname - executes the program in/from the current dir
16 touch filename.dat - creates a new empty file with that name and extention
17 tail -f filename (ascii) - allows to see the last 10 lines of a file (quit with ctrl c)
18 useful for watching OpenFOAM-output on supercomputers (e.g. file slurm-20716755.out)
19 tail -f filename -n 500 - shows the last 500 lines on the screen (quit with ctrl c)
20 arrow up - shows the last command (you can press it several times to see also precious commands)
21 !mod - repeats the last command starting with "mod" (e.g. command "module available")
22 history - shows your last 1000 commands (earlier commands will be overwritten by the newest commands)
23 mkdir aaa_kurs - creates the directory for the (OpenFOAM-course) runs today
24 cp dirname/filename . - copies a file to the present dir
25 more filename - lists the contents of a file on the screen (continue with the space key)
26 cd .. - go one directory up
27 cp ../filename . - copies the file from the upper directory to the present directory
28 do not use Allrun (from the usual OpenFOAM-tutorials) on a login node - instead we should use sbatch (queues) - see below
29 sbatch my_jobsubmitfile.sh - submitting a job (may contain the command Allrun or an OpenFOAM-solvername to be executed)
30 sinfo -t idle - shows the names of the queues and the free resources
31 https://wiki.bwhpc.de/e/BwUniCluster\_2.0\_Batch\_Queuees - one can see all options for the queues on bwuniCluster (uc2)
32 https://www.nhr.kit.edu/userdocs/horeka/batch/ - all options for the queues on HoreKa supercomputer
33 scontrol show job - information of your active jobs in all queues
34 scancel job-number - cancels/stops your job
35 squeue - short version of the queues and jobs
36 blockMesh > fileFromBlockMesh.dat - writing output of the program to a file (redirecting the output)
37 reconstructPar -latestTime - reconstructs a parallel run (into a 1-processor run) - useful e.g. when changing the
38 number of cores between 2 consequent runs (or for postprocessing (optionlly for ParaView))
39 grep -in abcd filename - extracts the lines containing string abcd from file filename to the screen (showing also
40 the number of the line where the string appears). For additional information type "man grep" or
"grep --help"
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