basics

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1 Basics pre-requisites molecular modeling

1.1 New to HPC & Sigma2?

Read https://documentation.sigma2.no/getting started/getting started.html

1.2 TigerVNC

Remote desktop (mac/win) - tigerVNC (https://documentation.sigma2.no/getting_started/remote-desktop.html) - Download & install TigerVNC: https://tigervnc.org/ - Start TigerVNC and eneter as server to connect to: - desktop.saga.sigma2.no:5901 - Right click the desktop window and choose Open Terminal Here

1.3 Maneuvering the command line (cmd)

In short, bash is a command processor that runs in a text window where the user (you) types **commands** that causes **actions**. Since bash also can read and execute commands from files, it can be used to write scripts.

1.3.1 Some basic commands commands

```
ls — List directory contents
ls -ltr

cd — Change directory

cd path/to/some/place
cd ../

. and .. . means here where I am now

cp somestuff/from/somewhere/foo.txt .
.. means the previous directory. One level up.
cd ../
```

```
pwd — Print working directory Where am I? > pwd
echo — Prints text to the terminal window echo Hello world
touch — Creates a file touch readme.txt
less — view the contents of a text file
touch readme.txt
echo hello world >> readme.txt
less readme.txt
grep — search
grep hello readme.txt
mkdir — Create a directory
rmdir — Remove directory
1.4 Git
1.4.1 clone
git clone https://github.com/....
1.4.2 Update repo
git pull
1.4.3 Add changes (add - commit - push)
git add filename
git commit -m "did some changes in filename"
git push
1.5 REACT on Saga
module load chemREACT/REACT
```

REACT.py

1.6 Qgui on Saga

module load Qgui/Qgui

The Qgui module automatically loads Q6.

1.7 Gaussian on SAGA

A job scritp, g16run.sh, is in bin.

g16run.sh \$inputfile \$nodes \$hours

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