

High Performance Computing and software environments:

Install and/or use existing software and modules

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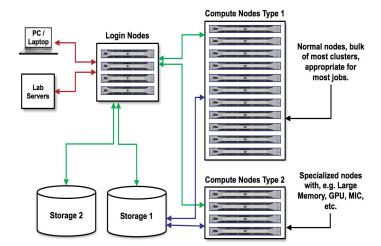


Outline

- Software distribution on HPC clusters
- ★ Why modules? How to find modules?
- Software stacks on Grex
- How to build software from sources
 - R packages
 - Python packages
 - Perl modules
 - configure/make
 - o cmake/make
- ★ Singularity/Apptainer

HPC Cluster:

- Hardware
- Network
- Software





Software distribution

Operating system package managers/repos:

- ★ Ubuntu: ~\$ sudo apt-get install <package>
- ★ CentOS: ~\$ sudo yum install <package>
- ★ On HPC: users do not have sudo!

On cloud and personal machines, users have a privilege access but not on HPC clusters.

Using a centralized HPC software stack:

- ★ Software distributed via CVMFS: CC software stack (CC clusters), ...
- ★ Local software: modules, legally restricted software (VASP, Gaussian, ...)

Local installation: usually to \$HOME {/home/\$USER} or \$PROJECT

- ★ Get the code: download the sources/binaries: wget, git clone, ... etc.
- ★ Settings: load dependencies, set environment variables, ... etc.
- ★ Build: ./configure {cmake ..} +opts; make; make test {check}; make install



Software layers

User layer: Python packages, Perl and R modules, home made codes, ...

User

Software stacks: modules for Intel, PGI, OpenMPI, CUDA, MKL, high-level applications. Multiple architectures (sse3, avx, avx2, avx512)

Nix or gentoo: GNU libc, autotools, make, bash, cat, ls, awk, grep, etc.

Gray area: Slurm, Lustre client libraries, IB/OmniPath/InfiniPath client libraries (all dependencies of OpenMPI) in Nix (or gentoo) layer, but can be overridden using PATH & LD_LIBRARY PATH.

OS: kernel, daemons, drivers, libcuda, anything privileged (e.g. the sudo command): always local. Some legally restricted software too (VASP).



Why modules?



Why modules?

https://docs.alliancecan.ca/wiki/Utiliser des modules/en

CCEnv(S)

Where:

- Control different versions of the same program.
- Avoid conflicts between different versions and libraries.

Set the right path to each program or library.



Useful commands for working with modules:

- module **spider** <soft>/<version>
- module list; module avail
- unload or purge L: Module is loaded

[someuser@bison]\$ module avail

GrexEnv (S,L)

S: Module is Sticky, requires --force to

- module **load** soft/version; module **unload** {rm} <soft>/<version>
- module **show** soft/version; module **help** <soft>/<version>
- module purge; module --force purge
- module use ~/modulefiles; module unuse ~/modulefiles



Software stacks on Grex

- ★ Grex environment [default]: GrexEnv
 - no module loaded by default.
 - use module spider <name of the software> to search for modules
 - Compilers: {GCC, Intel}, MKL, PETSc, ... etc.
 - Gaussian, ANSYS, MATLAB, ... etc.
- ★ The Alliance (Compute Canada) environment [optional]: CCEnv
 - Switch to CCEnv; load a standard environment; choose the architecture[sse3, avx2, avx512], use module spider <soft>
 - ~\$ module load CCEnv
 - ~\$ module load StdEnv/2020
 - ~\$ module load arch/avx512
 - ~\$ module load gcc/9.3.0 geant4/10.7.3

module load StdEnv/2016.4 module load arch/sse3 module load nixpkgs/16.09 gcc/5.4.0 geant4/10.05.p01



Modules on Grex

- → More than 500 modules:
 - Compilers: GCC [5,7,9,11]; Intel [2014 2020].
 - Libraries: HDF5, PETSc, GSL, MKL, Libxc, Boost, ...
 - Gaussian, ANSYS, MATLAB, VASP, ORCA, MCR, Java, Python, R, ... etc.
 - LAMMPS, GROMACS, ABINIT, QE, VMD, Molden, OpenBABEL, ... etc.
- → Software maintenance on Grex and Alliance clusters:
 - We install programs and update modules on request from users.
 - Search for a program using "module spider <name of your program>"
 - If not installed, ask for support "support@tech.alliancecan.ca"
 - We will install the module or update the version.
 - For commercial software, contact us before you purchase the code:
 - to check license type.
 - see if it will run under Linux environment, ... etc.



Modules on Grex: GrexEnv

		/o _l	pt/lmod	/grex/7.6/modulefiles/Co	re		
admixture/1.3.0		intel/14.0.2.144		ncl_ncarg/6.4.0		uofm/adf/2019.305-impi	
admixture/1.23	(D)	intel/15.0.5.223		ncl_ncarg/6.5.0		uofm/adf/2020-impi	
ant/1.10.11		intel/2017.8		nodejs/4.4.7		uofm/adf/2020.103-impi	
circos/0.69-6		intel/2019.5	(D)	nodejs/8.12.0		uofm/adf/2021-impi	
cmake/3.12.3		intel/2020.4		nodejs/13.2.0	(D)	uofm/adf/2021.102-impi	
cmake/3.14.0		j/j903		openbabel/2.3.2		uofm/adf/2021.106-impi	(D)
cmake/3.16.9		jags/3.4.0		openbabel/2.4.1		uofm/cfx/15.0	
cmake/3.23.2	(D)	jags/4.0.0		openbabel/3.0.0		uofm/cfx/16.2	
cns/1.3		jags/4.3.0	(D)	openbabel/3.1.1	(D)	uofm/cfx/18.2	
eigen/3.3.7		java/jdk7u25		ovito/2.9.0		uofm/cfx/19.2	
fastqc/0.11.9		java/jdk7u45		ovito/3.0.0-dev502	(D)	uofm/cfx/20.1	
gaussian/g09.b01.unlim		java/jdk8u5		pandoc/2.9.2.1		uofm/cfx/20.2	
gaussian/g09.b01		java/jdk8u66		per1/5.14.4		uofm/cfx/21.1	(D)
gaussian/g09.e01.unlim		java/jdk8u92	(D)	per1/5.22.1	(D)	uofm/feko/2021.2	
gaussian/g09.e01		java/jdk13.0.1		per1/5.28.1		uofm/gaussian/g03	
gaussian/g16.b01		julia/1.3.0-bin		php/5.6.40		uofm/gaussian/g09.e01	
gaussian/g16.c01.avx2.unlim		julia/1.5.4-bin		php/7.3.12	(D)	uofm/gaussian/g09	(D)
gaussian/g16.c01.avx2		julia/1.6.1-bin		python/2.7.12-miniconda		uofm/mathematica/11.0	
gaussian/g16.c01	(D)	julia/1.7.0-bin	(D)	python/3.6-miniconda	(D)	uofm/matlab/R2014A	
gcc/4.8		libcerf/1.4		settarg		uofm/matlab/R2015B	
gcc/5.2		lmod		singularity/3.5.2		uofm/matlab/R2017A	
gcc/7.4	(D)	ls-prepost/4.7.13		smrtlink/6.0.0.47841		uofm/matlab/R2019B	
gcc/9.2		mcr/mcr		stata/14.2-fagfs		uofm/matlab/R2020B2	(D)
gcc/11.2		mk1/10.3.11	(D)	stata/15.0-fagfs	(D)	uofm/starccm/16.06.010	
git-lfs/3.2.0		mkl/11.1.0		tbb/14		uofm/starccm/17.02.008-R8	(D)
git/2.21.0		mk1/2019.5		tbb/2019.5	(D)	uofm/umcfd/2.4	
gnuplot/5.2.7		molden/5.9		trimmomatic/0.39		vina/1.1.2	
go/1.10.4		multiwfn/3.8-gui		uofm/adf/2016-impi-test		vmd/1.9.3	
go/1.11.5		multiwfn/3.8-nogui	(D)	uofm/adf/2016-impi		vncworkspace/1.1	
go/1.12.12		nbo/6.0		uofm/adf/2017-impi		vtune/2019.4	
go/1.13		nbo/7.0	(D)	uofm/adf/2017.114-impi		vtune/2019.5	(D)
go/1.13.3	(D)	ncl_ncarg/6.2.1	(D)	uofm/adf/2018dev-impi		wine/3.0	
intel/12.1.5.339		ncl_ncarg/6.3.0		uofm/adf/2019-impi		xtb/6.5.0-bin	
				/opt/lmod/stacks			

module avail

module spider python module spider java

module load gcc ompi module avail

module spider <soft> module spider <soft>/<ver>

module show <soft> module purge

If not available:

→ contact support support@tech.alliancecan.ca



Find and load Gaussian

Gaussian: restricted software; requires a registration

https://docs.alliancecan.ca/wiki/Gaussian

https://um-grex.github.io/grex-docs/specific-soft/gaussian/

[someuser@bison]\$ module spider gaussian

gaussian:

Versions:

gaussian/g09.e01

gaussian/g16.b01

gaussian/g16.c01.avx2

gaussian/g16.c01

[someuser@tatanka ~]\$ module load gaussian/g16.c01 Loading Gaussian version 16.c01

Available: Grex [Also on Cedar and Graham]

For detailed information about a specific "gaussian" package (including how to load the modules) use the module's full name. Note that names that have a trailing (E) are extensions provided by other modules.

For example:

\$ module spider gaussian/g16.c01



Find and load ORCA

ORCA:

- restricted software
- requires a registration

[someuser@bison]\$ module spider orca

https://docs.alliancecan.ca/wiki/ORCA https://um-grex.github.io/grex-docs/specific-soft/orca/

[someuser@bison]\$ module spider orca/5.0.4

orca:

Versions:

orca/4.2.1

orca/5.0.1

orca/5.0.2

orca/5.0.4

[someuser@bison]\$ module load gcc/4.8 ompi/4.1.1 orca/5.0.4

Loading module: gcc/4.8

Loading module: ORCA/5.0.4

For detailed information about a specific "orca" package (including how to load the modules) use the module's full name. Note that names that have a trailing (E) are extensions provided by other modules.

For example:

\$ module spider orca/5.0.4

Available: Grex and all Alliance clusters



Find and load LAMMPS

[someuser@bison]\$ module spider lammps

lammps:

[someuser@bison]\$ module spider lammps/29Sep21

Versions:

lammps/5Jun19 lammps/5Nov16 lammps/11Aug17 lammps/23Jun22 lammps/29Sep21 lammps/30jul16

[~@tatanka ~]\$ module load intel/2019.5 ompi/3.1.4 lammps/29Sep21 Lmod is automatically replacing "gcc/7.4" with "intel/2019.5".

Unloading module: qcc/7.4.0

Loading module: LAMMPS/29Sep21

For detailed information about a specific "lammps" package (including how to load the modules) use the module's full name. Note that names that have a trailing (E) are extensions provided by other modules. For example:

\$ module spider lammps/29Sep21



MATLAB and MCR

This module can be loaded directly: module load mcr/mcr

[someuser@bison ~]\$ module s	pider matlab <u>nttps://um-grex.gitnub.io/grex-docs/specific-soft/matlab/</u>
uofm/matlab:	
Versions: uofm/matlab/R2014A	[someuser@bison ~]\$ module spider mcr
uofm/matlab/R2015B uofm/matlab/R2017A	mcr: mcr/mcr

For detailed information about a specific "uofm/matlab" package (including how to load the modules) use the module's full name. Note that names that have a trailing (E) are extensions provided by other modules.

For example:

uofm/matlab/R2019B

uofm/matlab/R2020B2

\$ module spider uofm/matlab/R2020B2



Modules from the Alliance software stack

abinit/9.2.2	(chem)	lammps-omp/20220623	(chem, D)	plumed/2.6.2	(chem)
abinit/9.6.2	(chem, D)	latte/1.2.1	(chem)	plumed/2.7.0	(chem)
adol-c/2.7.2		libcf/1.0.3		plumed/2.7.1	(chem)
apbs/1.3	(chem)	libgridxc-mpi/0.8.0		plumed/2.7.3	(chem)
berkeleygw/2.1.0	(phys)	met/9.1.1	(phys)	plumed/2.7.4	(chem)
berkeleygw/3.0.1	(phys, D)	mpas/7.0		plumed/2.8.1	(chem, D)
bigdft/1.8.3	(chem)	mpi4py/3.0.3	(<u>t</u>)	pnetcdf/1.9.0	(io)
boost-mpi/1.72.0	(*)	mpi4py/3.1.2	(t)	pnetcdf/1.10.0	(io)
boost-mpi/1.80.0	(t, D)	mpi4py/3.1.3	(t, D)	pnetcdf/1.12.2	(io, D)
cdo/1.9.8	(geo)	mrbayes/3.2.7	(bio)	psi4/1.3.2	(chem)
cdo/2.0.4	(geo)	mscg/1.7.3.1	(chem)	psi4/1.4	(chem)
cdo/2.0.5	(geo, D)	mumps-metis/5.2.1	(t)	psi4/1.5	(chem, D)
cfour-mpi/2.1	(chem)	mumps-parmetis/5.3.5	(t)	quantumespresso/6.5	(chem)
cgns/3.4.1	(phys)	ncl/6.6.2	(vis)	quantumespresso/6.6	(chem)
cgns/4.1.0	(phys)	ncview/2.1.8	(vis)	quantumespresso/6.7	(chem)
cgns/4.1.2	(phys, D)	nektar++/5.0.1	(math)	quantumespresso/6.8	(chem)
combblas/1.6.2		netcdf-c++-mpi/4.2	(io)	quantumespresso/7.0	(chem, D)
cp2k/7.1	(chem)	netcdf-c++4-mpi/4.3.1	(io)	raxm1/8.2.12	(bio)
cp2k/8.2	(chem)	netcdf-fortran-mpi/4.5.2	(io)	ray/3.0.1	(bio)
cp2k/9.1	(chem, D)	netcdf-fortran-mpi/4.6.0	(io, D)	repasthpc/2.2.0	(bio)
cpmd/4.3	(chem)	netcdf-mpi/4.7.4	(io)	repasthpc/2.3.0	(bio, D)
cslib/20180813		netcdf-mpi/4.9.0	(io, D)	rosetta/3.10	(chem)
dakota/6.13	(*)	neuron/7.8.2	(bio)	rosetta/3.12	(chem)
delft3d/62441	(chem)	neuron/8.0.0	(bio, D)	rosetta/3.13	(chem)
dl_poly4/4.10.0	(chem)	nwchem/6.8.1	(chem)	rosetta/2019.21.60746	(chem, D)
elpa/2020.05.001	(math)	nwchem/7.0.2-p1	(chem, D)	scalapack/2.1.0	(math)
esmf/8.0.1	(geo)	octopus/10.1	(chem)	scotch/6.0.9	(math)
esmf/8.2.0	(geo, D)	openfoam-extend/4.1	(phys)	shengbte/1.1.1	(phys)
etsf_io-mpi/1.0.4		openfoam/6	(phys)	shengbte/1.5.0	(phys, D)
fds/6.7.5		openmolcas/20.10	(chem)	siesta/4.0.1	(chem)
fds/6.7.6		openmx/3.9	(chem)	siesta/4.1-b4	(chem)
fds/6.7.7		openmx/3.9.9	(chem, D)	siesta/4.1-MaX-3.0	(chem)
fds/6.7.8		osu-micro-benchmarks/5.6.2	(t)	siesta/4.1.5	(chem, D)
fds/6.7.9	(D)	p4est/2.2	(math)	slepc/3.14.2	
fftw-mpi/3.3.8	(math)	parallelio/2.5.4		sundials/2.7.0	
ga/5.7.2	(t)	paraview-offscreen/5.8.0	(vis)	sundials/5.3.0	(D)

Software stacks:

- CCEnv (S)
- GrexEnv (S,L)

On Grex:

module load CCEnv module load arch/avx512 module load StdEnv/2020 module avail

Jobs:

- skylake partition
- largemem partition



Example of Geant4 from CCEnv

```
[~@yak ~]$ module spider geant4

Versions:
geant4/9.6.p04
geant4/10.02.p03
geant4/10.04.p02
geant4/10.06
geant4/10.7.3
geant4/11.1.0

Other possible modules matches:
geant4-data
```

```
[~@yak ~]$ module load CCEnv
[~@yak ~]$ module load arch/avx512
[~@yak ~]$ module load StdEnv/2020
[~@yak ~]$ module spider geant4
[~@yak ~]$ module spider geant4/11.1.0
[~@yak ~]$ module load gcc/9.3.0 geant4/11.1.0
```

To find other possible module matches execute:

```
$ module -r spider '.*geant4.*'
```

For detailed information about a specific "geant4" package (including how to load the modules) use the module's full name. Note that names that have a trailing (E) are extensions provided by other modules.

For example:

\$ module spider geant4/11.1.0



Installing a software

as user:

What are the programs you can install locally under your account?



Building software

- Local installation [user's directory: home, project]:
 - R packages; Julia packages, Perl modules
 - Python packages: virtual environment, conda
 - Home made programs and commercial software.
- Installation with:
 - make; make test {check}; make install
 - configure; make; make test {check}; make install
 - cmake; make; make test {check}; make install
- Java applications: jar files
- Singularity and/or Aptainer:
 - build the image and run the program from the container



Local installation

- R packages: minimal installation
 - R as modules: users can install the packages in their home directory.
- ★ Python as modules: python and scipy-stack
 - users can install the packages needed in their home directory.
- Perl and bioperl as modules:
 - users can install the packages needed in their home directory.
- Other software installed locally:
 - Home made programs {up to a user or a group}
 - Restricted and licensed software that can not be distributed via CVMFS.
 - Custom software: patch from a user, changing parts of the code, ... etc.
 https://docs.alliancecan.ca/wiki/Installing software in your home directory



Local installation: R packages

R packages: rgdal, adegenet, stats, rjags, dplyr, ... etc.

Choose a module version: module spider r

Load R and dependencies (gdal, geos, jags, gsl, udunits... etc):

module load gcc/7.3.0 r/3.6.0 gdal udunits

Launch R and install the packages:

~\$ R

> install.packages("sp")

'lib =/cvmfs/soft.computecanada.ca/easybuild/{..}/R/library''' is not writable

Would you like to use a personal library instead? (yes/No/cancel) **yes**Would you like to create a personal library '~/R/{...}' to install packages into? (yes/No/cancel) **yes**

--- Please select a CRAN mirror for use in this session ---

> install.packages("dplyr")

```
[~]$ module spider r

Versions:

r/4.0.0

r/4.0.2

r/4.0.5

r/4.1.0

r/4.1.2

r/4.2.1

r/4.2.2
```



Local installation: Python

- Load the modules:
 - module load python
- Create a virtual environment
 - virtualenv ~/my_venv
- Activate the virtual environment
 - source ~/my_venv/bin/activate
- Update pip
 - pip install --no-index --upgrade pip
- Install the packages
 - pip install pandas
 - pip install -r requirements.txt
 - python setup.py install

module load gcc gcc/11.2 python/3.11.2 virtualenv ~/my_venv source ~/my_venv/bin/activate pip install cutadapt deactivate

module load gcc/11.2 python/3.11.2 source ~/my_venv/bin/activate cutadapt [+options] deactivate

https://docs.alliancecan.ca/wiki/Python



Local installation: perl

Example: Hash::Merge; Logger::Simple; MCE::Mutex; threads ...

Load Perl module: module load perl

Install the the first package using cpan or cpanm:

~\$ cpan install YAML

Would you like to configure as much as possible automatically? [yes] yes

What approach do you want? (Choose 'local::lib', 'sudo' or 'manual')

[local::lib] local::lib

Would you like me to append that to /home/\$USER/.bashrc now? [yes] yes

Install the rest of the packages using cpan or cpanm:

~\$ cpan install Hash::Merge

~\$ cpan install Logger::Simple

~\$ cpan install MCE::Mutex

https://docs.alliancecan.ca/wiki/Perl



Installation with make: **STAR**

- ★ Download the code {wget; curl; git clone; ...}:
 wget https://github.com/alexdobin/STAR/archive/refs/tags/2.7.10b.tar.gz
- ★ Unpack the code: tar -xvf 2.7.10b.tar.gz
- ★ Load GCC compiler: module load gcc
- ★ Compile the code: cd STAR-2.7.10b/source make

~/.bash_profile

PATH=\$PATH:\$HOME/bin:\$HOME/software/star/2.7.10b/bin export PATH

★ Copy the binaries and set the path: mkdir -p ~/software/star/2.7.10b/bin cp STAR ~/software/star/2.7.10b/bin

PATHs/environment variables added to module files when the program is installed as a module. Possibility to add local modules as a user.

STAR: Spliced Transcripts
Alignment to a Reference

export PATH=\$PATH:\${HOME}/software/star/2.7.10b/bin



Installation with configure/make

- ★ Download and unpack the code: wget, ... gunzip, ... etc.
- ★ Load the modules and dependencies: module load gcc ompi fftw
- ★ Configure the program
 - If configure not included, run: autoreconf -fvi [to generate it].
 - ./configure --help [to see the different options].
 - ./configure --prefix=<path to install dir> {+other options}
- ★ Compile and test:
 - make; make -j4
 - make check; make test
- ★ Install the program:
 - make install



Installing: treemix

- ★ Download the source files: wget https://bitbucket.org/nygcresearch/treemix/downloads/treemix-1.13.tar.gz
- ★ Unpack the source files: tar -xvf treemix-1.13.tar.gz
- ★ Change the directory: cd treemix-1.13/
- ★ Load the modules: module load gcc boost
- ★ Configure: ./configure --prefix=/home/\$USER/software/treemix/1.13
- ★ Compile and install: make && make install
- ★ Set a path: export PATH=\$PATH:\$HOME/software/treemix/1.13/bin
- ★ Usage in a job script:

module load gcc boost export PATH=\$PATH:\$HOME/software/treemix/1.13/bin treemix {+options if any}



Example: ABINIT

module load intel ompi gsl netcdf instdir=<path to the installation directory>

```
../configure --prefix=$\{instdir\} --enable-mpi --enable-mpi-io --with-fft-flavor=fftw3-mkl
--with-linalg-flavor=mkl --with-math-flavor=gsl --enable-debug="no"
--enable-optim="standard" --enable-64bit-flags --with-linalg-libs="-L$MKLROOT/lib/intel64
-lmkl scalapack lp64 -lmkl blacs openmpi lp64 -lmkl intel lp64 -lmkl sequential
-lmkl_core -lm" --with-fft-incs="-l$MKLROOT/include/fftw -l$MKLROOT/interfaces/fftw3xf"
--with-fft-libs="-L$MKLROOT/interfaces/fftw3xf -lfftw3xf intel lp64"
--with-dft-flavor="atompaw+libxc+wannier90" --with-trio-flavor="netcdf" --enable-lotf
--enable-macroave --enable-gw-dpc CC=mpicc CXX=mpic++ FC=mpif90 F77=mpif77
F90=mpif90
```



Example: PETSc

```
./configure --with-blas-lapack-dir=$MKLROOT/lib/intel64 --prefix=${instdir} --with-cxx-dialect=C++11
--download-scalapack=yes --download-blacs=yes --download-superlu dist=yes
--download-mumps=yes --download-parmetis=yes --download-metis=yes --download-spooles=yes
--download-cproto=yes --download-prometheus=yes --with-mkl pardiso=1
--with-mkl pardiso-dir=$MKLROOT --with-mkl-sparse-optimize=1 --with-scalar-type=complex
--with-debugging=0 --with-hdf5=yes --with-hdf5-dir=$HDF5HOME --download-suitesparse=yes
--download-fftw=${fftsrc} --download-amd=yes --download-adifor=yes --download-superlu=yes
--download-triangle=yes --download-generator=yes --with-64-bit-pointers=no --with-cc=mpicc
--CFLAGS='-O2 -msse4.2 -xSSE4.2 -mp1 -I$MKLROOT/include -mkl -fPIC ' --with-cxx='mpicxx'
--CXXFLAGS='-O2 -msse4.2 -xSSE4.2 -mp1 -I$MKLROOT/include -mkl -std=c++11 -fPIC '
--with-fc='mpif90' --FFLAGS='-O2 -msse4.2 -xSSE4.2 -mp1 -I$MKLROOT/include -mkl -fPIC '
--with-single-library=yes --with-shared-libraries=yes --with-shared-ld=mpicc
--sharedLibraryFlags="-fpic -mkl -fPIC" --with-mpi=yes --with-mpi-shared=yes --with-mpirun=mpiexec
--with-mpi-compilers=yes --with-x=yes
```



Example with cmake/make

- ★ Download and unpack the code: wget, ... gunzip, ... etc.
- ★ Load the modules and dependencies: module load gcc ompi fftw
- ★ Configure the program: you may need to load cmake module
 - mkdir build && cd build
 - cmake .. --help [to see the different options].
 - cmake .. -DCMAKE_INSTALL_PREFIX=installdir {+other options}
- ★ Compile and test:
 - make; make -j8
 - make check; make test
- ★ Install the program:
 - make install

Using the GUI:

ccmake .. {+ options}



Cmake options for GROMACS

- Download and unpack the source files
- ★ Load modules: module load intel/15.0 ompi/3.1.4 fftw cmake
- configure; compile; install cd gromacs-5.1.4; mkdir build; cd build cmake -DCMAKE INSTALL PREFIX=<path to install dir> -DBUILD SHARED LIBS=off -DBUILD TESTING=off -DREGRESSIONTEST DOWNLOAD=off -DCMAKE C COMPILER='which mpicc' -DCMAKE CXX COMPILER='which mpicxx' -DGMX BUILD OWN FFTW=on -DGMX SIMD=SSE4.1 -DGMX DOUBLE=off -DGMX EXTERNAL BLAS=on -DGMX EXTERNAL LAPACK=on -DGMX FFT LIBRARY=fftw3 -DGMX GPU=off -DGMX MPI=on -DGMX OPENMP=off -DGMX X11=on ../gromacs-5.1.4 make -j4; make install



Cmake options for CERN-ROOT

- Download and unpack the source files
- Load modules:

module load gcc/9.2 tbb/2019.5 gsl/2.7.1 python/3.7.5 fftw/3.3.8 module load cfitsio/4.0.0 mkl/2019.5 cmake/3.16.9 git export FFTW DIR=/global/software/cent7/fftw/3.3.8-gcc92-ompi314

★ configure; compile; install

```
mkdir build && cd build
```

- cmake -DCMAKE_INSTALL_PREFIX=<path to install dir> -DGCC_INSTALL_PREFIX=/global/software/cent7/gcc-9.2.0-rpath-76/\
- -DPYTHON_EXECUTABLE=`which python` -DGSL_CONFIG_EXECUTABLE=/global/software/cent7/gsl/2.7.1-gcc92/bin/gsl-config \
- -DGSL INCLUDE DIR=/global/software/cent7/gsl/2.7.1-gcc92/include
- -DGSL_LIBRARY=/global/software/cent7/gsl/2.7.1-gcc92/lib/libgsl.so \
- -DGSL_ROOT_DIR=/global/software/cent7/gsl/2.7.1-gcc92/ -DCMAKE_C_COMPILER=`which gcc` \
- -DCMAKE_CXX_COMPILER=`which g++` -DCMAKE_FORTRAN_COMPIER=`which gfortran` \
- -DCFITSIO_INCLUDE_DIR=/global/software/cent7/cfitsio/4.0.0-gcc92/include \
- -DCFITSIO_LIBRARY=/global/software/cent7/cfitsio/4.0.0-gcc92/lib/libcfitsio.so \
- -DJEMALLOC ROOT DIR=/usr -Dpython3=ON -Dpcre=ON -Dzlib=ON Dunuran=ON -Dexplicitlink=ON -Dminuit2=ON -Droofit=ON \
- -DCMAKE_SKIP_RPATH=ON -Dxrootd=OFF -Dmysql=OFF -Dkrb5=OFF -Dodbc=OFF -Doracle=OFF \
- -DQT_QMAKE_EXECUTABLE=/usr/bin/qmake-qt4 <path to source directory>



Java applications

- Download and unpack the code
- ★ Load java module: module load java
- ★ Run the code
- ★ Example: Trimmomatic
 - wget http://www.usadellab.org/cms/uploads/supplementary/Trimmomatic/Trimmomatic-0.39.zip
 - unzip Trimmomatic-0.39.zip
- ★ Run the code module load java java -jar <path to>/trimmomatic-0.39.jar {+options if any}



Easybuild as package manager

All CC software stack is installed using easybuild

- ★ Software process:
 - A user request to install software: Ticket
 - Evaluation of the software: HPC analyst
 - Opening an internal ticket for software installation
 - An analyst will install the software
 - Local installation
 - Update the recipe on GitHub
 - Compile the program, push to dev and prod
 - An analyst will follow up with the user: original ticket



Using easybuild as a user

https://github.com/ComputeCanada/easybuild-easyconfigs/tree/computecanada-main/easybuild/easyconfigs

- → Search for the recipe: eb -S ont-guppy
- Copy the recipes:
 - eb ont-guppy-6.2.1.eb --try-software-version=6.4.8 --copy-ec
 - eb ont-guppy-6.2.1-gcccuda-2020a.eb --try-software-version=6.4.8 --copy-ec
- → Edit the recipes and change the checksums:
 - eb ont-guppy-6.4.8.eb --force --inject-checksums
 - eb ont-guppy-6.4.8-gcccuda-2020a.eb --force --inject-checksums
- → Install the modules:
 - eb ont-guppy-6.4.8.eb --force --sourcepath=./
 - eb ont-guppy-6.4.8-gcccuda-2020a.eb --force --sourcepath=./

eb <some recipe> [+options]



Singularity/Apptainer

Resources: Github, DockerHub, SingularityHub, Aptainer.

Singularity examples: https://github.com/singularity/ware/singularity/tree/master/examples

- Documentation: https://singularityware.github.io/user-guide.html
- ★ DockerHub: https://hub.docker.com/explore/
- ★ SingularityHub: https://www.singularity-hub.org/
- ★ Apptainer: https://apptainer.org/docs/

https://docs.alliancecan.ca/wiki/Singularity/en https://um-grex.github.io/grex-docs/

Access to Singularity:

- **Connect to cluster:** Grex, cedar, graham, beluga or narval:
- Load a module: module load singularity [or apptainer]
- ★ Build the image: convert the image from Docker to Singularity [Apptainer]
- ★ Note: You may need to use your own Linux machine or VM to build the image.



Singularity/Apptainer

- ★ Alternative for running software: difficult to build from source
- Possibilite to convert Docker images to singularity.
- ★ Singularity installed on all clusters {no Docker for security reasons}
- ★ Build the image:

module load singularity singularity build qiime2-2021.11.sif docker://quay.io/qiime2/core:2021.11

- ★ Run the code via singularity:
 - singularity exec -B \$PWD:/home -B /global/scratch/someuser:/outputs \
 - -B /global/scratch/someuser/path/to/inputs:/inputs <path to qiime2-2021.11.sif> \qiime feature-classifier fit-classifier-naive-bayes \
 - --i-reference-reads /outputs/some_output_feature.qza \
 - --i-reference-taxonomy /outputs/some_output_ref-taxonomy.qza \
 - --o-classifier /outputs/some_output_classifier.qza



More readings

- **★** FAQ:
 - https://docs.alliancecan.ca/wiki/Frequently Asked Questions
- ★ Software:
 - https://docs.alliancecan.ca/wiki/Available_software
 - https://docs.alliancecan.ca/wiki/Utiliser_des_modules/en
 - https://docs.alliancecan.ca/wiki/Installing_software_in_your_home_direct_ory
- ★ Grex: https://um-grex.github.io/grex-docs/



Thank you for your attention

Any question?