Exercises for the NorESM user workshop 2026

Hands-on session 1

Download the NorESM2.3 version:

1. $ ssh -Y username@betzy.sigma2.no
2. $ mkdir NorESMworkshop2026
3. $ cd NorESMworkshop2026
4. $ git clone https://github.com/NorESMhub/NorESM.git **NorESM2.3_b01**
5. $ cd NorESM2.3_b01
6. $ git checkout noresm2_3_beta01
7. $ ./manage_externals/checkout_externals

The "-Y" option enables X11 forwarding, e.g. for viewing model output on Betzy.

Optional re-naming of repository. Could be useful if you have many versions checked out.

Exercise: 1

Run compset **N1850frc2** with grid **f19_tn14** for 1 month

Step 1:- create experiment

mkdir cases

cd cases

../cime/scripts/create_newcase --case **n1850_f19_tn14_23beta3M** --compset N1850frc2 --res f19_tn14 --project nn9560k --machine betzy --run-unsupported --pecount=S

Step-2 setup and build

cd n1850_f19_tn14_23beta3M

./case.setup

./case.build

Before case.submit modify **.case.run**; add following lines:
#SBATCH --qos=noresm_course
#SBATCH --reserv=noresm_course

Step-3 set run length and submit

./xmlchange STOP_OPTION=nmonths

./xmlchange STOP_N=1

check file **CaseStatus**, **README.case** as those contain steps performed in experiments and experiment information

Exercise 2:

Remove lines from .case.run:

#SBATCH --qos=noresm_course
#SBATCH --reserv=noresm_course

Continue same run for next 23 months:

./xmlchange STOP_N=23

./xmlchange CONTINUE_RUN=TRUE

./xmlchange --subgroup case.run JOB_WALLCLOCK_TIME=10:00:00

./case.submit

Hands-on session 2

Create, setup, build and submit your (first?) NorESM2-LM piControl simulation running on 4 nodes by repeating these steps:

```
$ cd ~/NorESMworkshop2026/NorESM/cime/scripts/

$ ./create_newcase --case
~/NorESMworkshop2026/cases/N1850frc2_f19_tn14_test01_20260114 --mach betzy --res
f19_tn14 --compset N1850frc2 --project nn9560k --pecount=S --run-unsupported

$ cd ~/NorESMworkshop2026/cases/N1850frc2_f19_tn14_test01_20240114/

$ ./case.setup

$ ./case.build

$./case.submit
```

- Output will be available on $USERWORK/archive/N1850frc2_f19_tn14_test01_20260114

Hands-on session 2 : query_config

Use query_config to learn more about NorESM model options

1. Go to scripts directory: `cd cime/scripts`
2. Find details about compsets N1850frc, NorESM coupled, and blom
   - `./query_config --compsets | grep N1850frc2`
   - `./query_config --compsets | awk '$1 ~ /^N/'` ← NorESM compsets
   - `./query_config --compsets blom` ← OMIP compsets
   - `./query_config --compsets cam | awk '$1 ~ /^N/'` ← AMIP compsets
3. Find config options for a component or data replacement
   - `./query_config --components blom` ← Active ocean component
   - `./query_config --components docn` ← Data ocean component
4. Find details about grids
   - `./query_config --grids | grep -A 2 tn14` ← All grids using tn1v4 ocean grid

Hands-on session 3 -

A) piControl (N1850)
- create a new case with resolution f19_tn14
- Set --pecount=S
- make it a branch run
- reference case: N1850_f19_tn14_11062019
- reference date: 1600-01-01
- 1 month simulation time

For A,B we need to change only env_run.xml

B) historical (NHIST)
- create a new case with resolution f19_tn14
- Set --pecount=S
- make it a hybrid run
- reference case: N1850_f19_tn14_11062019
- reference date: 1600-01-01
- Start date: 1850-01-01
- 1 month + 1 month simulation time i.e.
  run for 1 month, resubmit simulation once and
  run for 1 more month
  (set RESUBMIT=1)
- Dump restart files every 10 days

https://noresm-docs.readthedocs.io/en/noresm2/configurations/cmip6_compsets.html#reproduce-cmip6-picontrol-historical-and-ssp5-8-5-experiments

- Check how xmlquery and xmlchange work together with the xml files:
  - Assuming you want to change the total run time for NorESM, but do not remember the exact keyword, find all keywords that include STOP or CLOCK:

    `./xmlquery --partial STOP`

    `./xmlquery --partial CLOCK`
  - STOP_N is defined in env_run.xml, view file with “less” or grep STOP_N in env_run.xml
  - Change STOP_N value

    `./xmlchange STOP_N=10`
  - Confirm change has been made in env_run.xml

- Create a clone case from (A), and add daily output for surface DMS flux from the ocean component
  - See “create_clone” from “setting up a clone case”
  - Modify “user_nl_blom”: daily output for surface DMS flux
    SRF_DMSFLUX=4, 2, 2
    (format for output is ‘daily, monthly, yearly’, default is ‘0, 2, 2’)

- Run case (A) on normal queue for 1 month with `--pecount=M` to run on 8 nodes. Compare model throughput in the log file with the previous run.

- Run NorESM with data component for either atmosphere or ocean for 1 month.
  Compare model throughput with fully coupled run.

- Run on development queue: Set `--pecount=128` when doing create_newcase ; In case:

```
./xmlchange NTASKS_OCN=123
./xmlchange JOB_QUEUE="devel" --subgroup case.run --force
./xmlchange JOB_WALLCLOCK_TIME=0:30:00 --subgroup case.run
./xmlchange JOB_WALLCLOCK_TIME=0:30:00 --subgroup case.st_archive
```

Hands-on session on compsets

1. Create an ocean-sea ice only case (e.g. compset = NOICPLHISTOC)
2. Look at the README.case file in your case directory. How can you tell that only the ocean and sea ice components are active?
3. What can you tell about the atmosphere and land components? Are those active, data-components, stubb?
4. Try the same with ./xmlquery. What additional information do you get?

1. ./xmlquery –p BLOM
2. ./xmlquery –p CICE
3. ./xmlquery –p CAM
4. ./xmlquery –p CLM

Repeat the steps with atmosphere-land only (e.g. compset = NF1850) and fully coupled (e.g. compset = N1850).

Hands-on session make a case using bash script - part 1

There are two sample scripts on Betzy:
/cluster/shared/noresm/WORKSHOP/scripts/ReproExperimentScriptSimple.sh
/cluster/shared/noresm/WORKSHOP/scripts/ReproExperimentScript.sh
–

1. make a copy and save it somewhere (e.g. in your NorESMWorkshop2024 directory)
2. make changes to suit your needs. In particular,review these four lines and at least replace xxUSERxx with your Betzy user ID.

```
COMPSET="N2000"
RES="f19_tn14"
SRCROOT="/cluster/projects/nn9039k/xxUSERxx/NorESM"
CASEDIR="/cluster/work/users/xxUSERxx/cases/${COMPSET}_${RES}"
```

Hands-on session make a case using bash script - part 2

There are two sample scripts on Betzy:
/cluster/shared/noresm/WORKSHOP/scripts/ReproExperimentScriptSimple.sh
/cluster/shared/noresm/WORKSHOP/scripts/ReproExperimentScript.sh
–

1. Make a copy and save it somewhere (e.g. in your NorESMWorkshop2024 directory)
2. Make a new script where you specify your run environment. E.g. Hands-on session 3B on slide 6

Hands-on session : checkout_externals

In release-noresm2.0.9 there is a second externals file:
Externals_continuous_development.cfg

This (now outdated) file was used to build NorESM with alternative development branches of model components. We can use this file to illustrate how to use “status checker”:

1. Look at differences between externals files:
   `diff -u Externals.cfg Externals_continuous_development.cfg`

2. Examine status for current and alternative externals file
   `./manage_externals/checkout_externals -S` ← for current externals
   `./manage_externals/checkout_externals -e Externals_continuous_development.cfg -S` ← for alternative externals

Symbols used by status checker:

: all is fine	s : out-of-sync	o : optional source
e : empty	? : unknown (no .git or .svn)	M : modified source