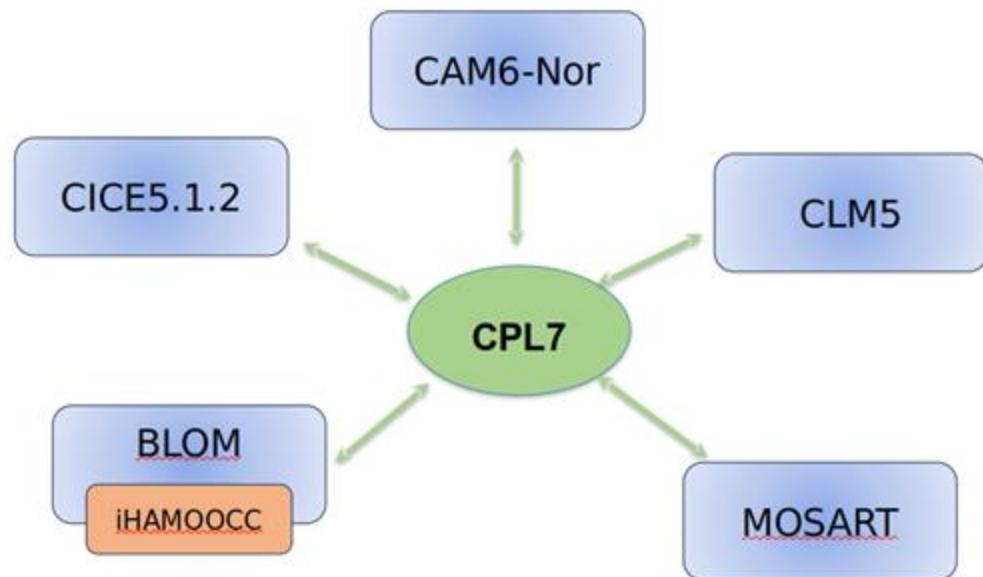


What is the NorESM2.1 architecture

# NorESM2 coupling and prognostic components



NorESM2 is based on the second version of the Community Earth System Model, CESM2, and share most of the CESM2 structure, but modifies model component.

Atmosphere model :

CAM6-Nor replaces standard CAM  
OsloAero6 atmospheric chemistry

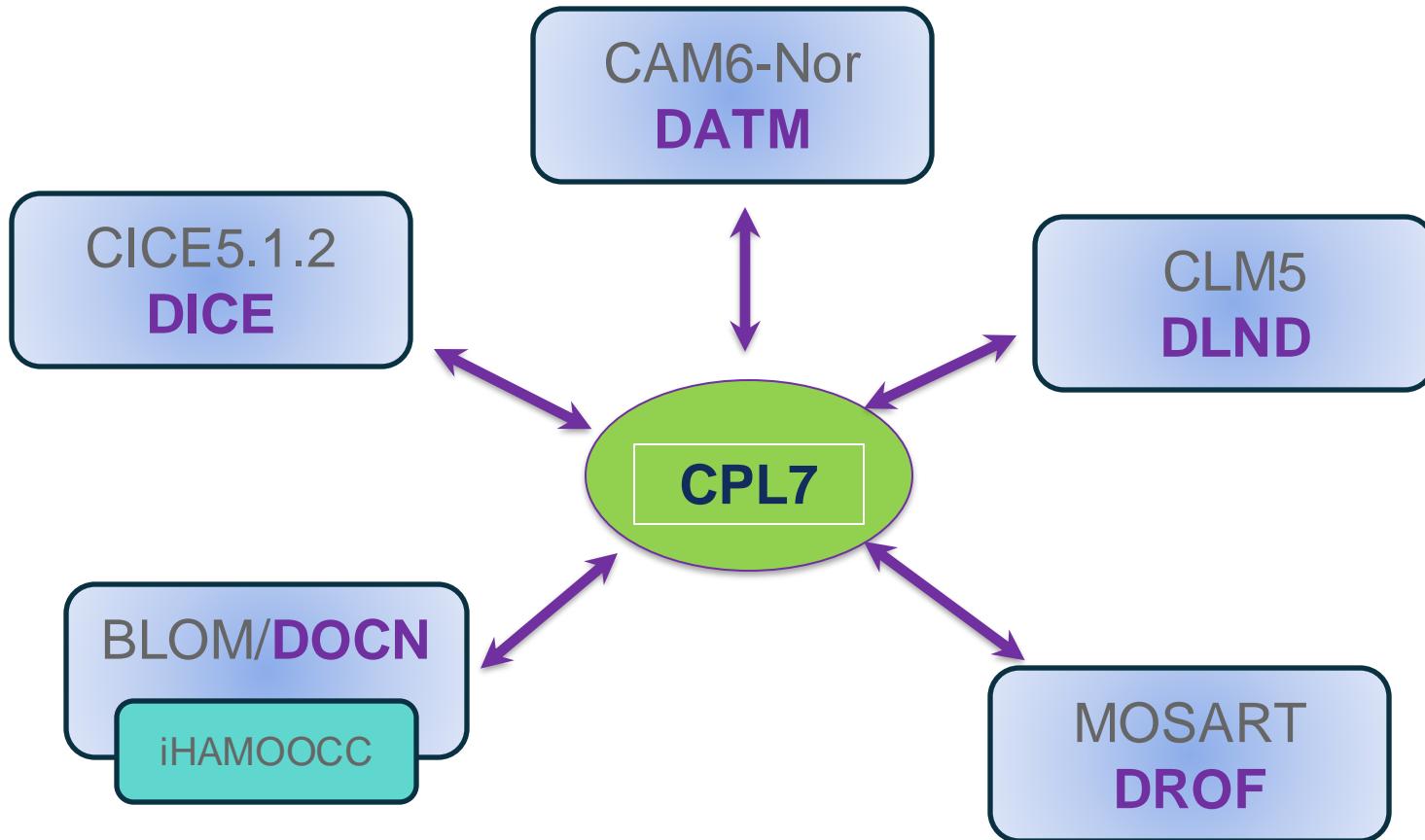
Ocean model :

BLOM Isopycnic coordinate model  
iHAMOCC ocean biogeochemical model

Sea-ice model:

Wind drift of snow

# NorESM2 data components



## Specifying the compset – first independent part of experiment definition

Compset specifies:

- Which components should be used
- What physics each component should have

# Creating a new case

A new case is created by running the script

**\$SRCROOT/cime/scripts/create\_newcase**

Where \$SRCROOT is your root directory for a NorESM checkout

```
./create_newcase  
-- case <fullpathname of case>  
-- compset <long compset name or alias>  
-- res <long resolution name or alias>  
-- machine <machine name>  
-- project <project name>  
-- pecount <label, e.g. M>  
--user_mod_dirs <path to user mods>  
--run-unsupported
```

Red is required  
Grey is optional

First part

Second part

# What is the compset longname syntax?

The compset longname has the specified order atm, lnd, ice, ocn, river, glc, wave, cesm-options

**TIME\_ATM[%phys]\_LND[%phys]\_ICE[%phys]\_OCN[%phys]\_ROF[%phys]\_GLC[%phys]\_WAV[%phys]/[\_BGC%phys]**

TIME = Time period (e.g. 1850, 2000, HIST, SSP126, SSP245, SSP370, SSP585)

ATM = [ **CAM60**, DATM] ;

LND = [**CLM50**, DLND, SLND] ;

CICE = [**CICE**, DICE, SICE]

OCN = [**BLOM**, DOCN, SOCN];

ROF = [**MOSART**, RTM, DROF, SROF] ;

GLC = [**CISM2**, SGLC]

WAV = [**WW3**, DWAV, SWAV];

BGC = optional BGC scenario

Stub components denote a component that does nothing

OPTIONAL %phys attributes specify submodes of the given system

For example DOCN%DOM is the mode of DOCN where specified SST files are read in  
ALL data models must have a %phys option that corresponds to the data model mode

# More on compset specification

Compset is which components will be used along with possible component physics options and associated forcing files (time period)

- Fully coupled: (compset aliases beginning with N or B)
  - **1850\_CAM60%NORESM\_CLM50%BGC\_CICE\_BLOM%ECO\_MOSART\_SGLC\_SWAV**
  - Run ./query\_config --compsets allactive
- CAM (atm) with prescribed docn/cice forcing (alias NF, F or Q)
  - **1850\_CAM60%NORESM\_CLM50%BGC\_CICE%PRES\_DOCN%DOM\_MOSART\_SGLC\_SWAV**
  - Run ./query\_config --compsets cam
- CLM (Ind) with prescribed datm forcing (alias I)
  - **1850\_DATM%GSWP3v1\_CLM40%BGC\_SICE\_SOCN\_MOSART\_SGLC\_SWAV**
  - Run ./query\_config --compsets clm
- BLOM with prescribed datm and rof forcing (alias G and C)
  - **1850\_DATM%NYF\_SLND\_CICE\_BLOM%ECO\_DROF%NYF\_SGLC\_SWAV**
  - Run ./query\_config --compsets blom

# Some NorESM2 fully coupled compsets

## N1850frc2: (piControl)

1850\_CAM60%NORESM%FRC2\_CLM50%BGC-CROP\_CICE%NORESM-  
CMIP6\_BLOM%ECO\_MOSART\_SGLC\_SWAV\_BGC%BDRDDMS

## NHISTfrc2: (historical)

HIST\_CAM60%NORESM%FRC2\_CLM50%BGC-CROP\_CICE%NORESM-  
CMIP6\_BLOM%ECO\_MOSART\_SGLC\_SWAV\_BGC%BDRDDMS

## NSSP126frc2: (CMIP6 scenario)

SSP126\_CAM60%NORESM%FRC2\_CLM50%BGC-  
CROP\_CICE%NORESMCMIP6\_BLOM%ECO\_MOSART\_SGLC\_SWAV\_BGC%BDRDDMS

Specifying the model resolution –

Second independent part of experiment definition

# Choosing the Model Grid

- Grid specification for each component
  - **a%name\_l%name\_oi%name\_r%name\_m%mask\_g%name\_w%name**
- Fully coupled:
  - a%1.9x2.5\_l%1.9x2.5\_oi%tnx1v4\_r%r05\_g%null\_w%null\_m%tnx1v4
  - alias is **f19\_tn14**
- CAM with prescribed docn/cice forcing
  - a%1.9x2.5\_l%1.9x2.5\_oi%1.9x2.5\_r%r05\_g%null\_w%null\_m%tnx1v4
  - alias is **f19\_f19\_mtn14**
- CLM with prescribed datm forcing
  - a%1.9x2.5\_l%1.9x2.5\_oi%null\_r%r05\_g%null\_w%null\_m%tnx1v4
  - alias is **f19\_f19\_mtn14**
- BLOM/CICE with prescribed datm and rof forcing
  - a%T62\_l%null\_oi%tnx1v4\_r%rx1\_g%null\_w%null\_m%tnx1v4
  - alias is **T62\_tn14**

If atm/lnd/cice/docn  
are on the same grid  
need to specify an  
ocean/land mask in  
alias (mtn14)

# Standard model grids for NorESM2

## In general:

- Ocean and Sea-ice always **MUST** have the same grid
- Atmosphere and land have the same grid - but usually different from active ocean/ice
- River, Glacier and Wave are on their own grids - and different from the above
- Coupler is used to interpolate/transfer fields from one grid to another grid

## Grids for scientifically supported NorESM2 experiments include:

### Atmosphere & land:

**f19** :  $1.9 \times 2.5 = 1.9$  degree latitude and 2.5 degree longitude resolution = 144x96

**f09** :  $0.9 \times 1.25 = 0.9$  degree latitude and 1.25 degree longitude resolution = 288x192

### Ocean & sea ice:

**tnx1v4** : tripolar 1 degree grid = 360x384

### Data atmosphere: (OMIP experiments)

**T62, TL319** : approx. 2 degree Gaussian and 0.5 degree spectral grid

## For experts:

All available grid definitions are in `$SRCROOT/cime/config/cesm/config_grids.xml`)

## Understanding your case

- README.case
- xmlquery
- pelsayout
- preview\_namelist
- preview\_run

# Understanding your case –

## README.case and xmlquery

> **./create\_newcase --case foo --compset N1850 --res f19\_tn14**

Compset is:

1850\_CAM60%NORESM\_CLM50%BGC-  
CROP\_CICE%NORESMCMIP6\_BLOM%ECO\_MOSART\_SGLC\_SWAV\_BGC%BDRDDMS

Model grid is:

a%1.9x2.5\_l%1.9x2.5\_oi%tnx1v4\_r%r05\_g%null\_w%null\_m%tnx1v4

- **What to do first – look README.case**
- **What are are the available xml variables, their definition and their values?**

Most information you need to know about the case is in **xmlquery!!!**

How does xmlquery work?

> **./xmlquery --help**

What are all the variables in the xml files (don't need to look inside)

> **./xmlquery --listall**

What if I want to look at particular xml variables but don't know the full name

> **./xmlquery --partial (or -p)**

> **./xmlquery --partial --full (or -p --full)**

# Example: query the BLOM configuration

> **./xmlquery -p BLOM**

Results in group build\_component\_bлом

BLOM\_TRACER\_MODULES: iage ecosys  
BLOM\_TURBULENT\_CLOSURE: oneeq advection  
BLOM\_UNIT: cgs

Results in group run\_component\_bлом

BLOM\_COUPLING: full  
BLOM\_NDEP\_SCENARIO: 1850  
BLOM\_N\_DEPOSITION: TRUE  
BLOM\_RIVER\_NUTRIENTS: TRUE  
BLOM\_VCOORD: isopyc\_bulkml

> **./xmlquery --full BLOM\_TRACER\_MODULES**

Results in group build\_component\_bлом

BLOM\_TRACER\_MODULES: value=iage ecosys  
type: c  
valid\_values: ['iage', 'iage ecosys']  
description: Optional ocean tracers.  
Valid values are a combination of: iage ecosys  
file: \$CASEROOT/foo/env\_build.xml

# Understanding your case – preview\_namelists

**What are my resolved namelists?**

**The namelists that actually get read by the components.**

> cd \$CASEROOT

> **./preview\_namelists**

- This must be run after ./case.setup
- Output namelists are in \$CASEROOT/CaseDocs as well as in \$RUNDIR/run
- **CaseDocs/ is where you can quickly see component namelists – this is ONLY used for documentation**
- **Customize:** You can customize namelists by editing the appropriate user\_nl\_XXX file and then run ./preview\_namelists again (DO NOT edit files in either CaseDocs or run – they will be overwritten) – more on this tomorrow from Matvey

# Understanding your case – payout

## What is my processor layout?

NOTE: this might not be optimal for your experiment out of the box!

>/payout

NTASKS: number of MPI tasks for each component

NTHRDS: number of OpenMP threads for each component

ROOTPE: first MPI task for each component

Comp	NTASKS	NTHRDS	ROOTPE
CPL :	256/	1;	0
ATM :	256/	1;	0
LND :	256/	1;	0
ICE :	256/	1;	0
OCN :	256/	1;	0
ROF :	256/	1;	0
GLC :	256/	1;	0
WAV :	256/	1;	0
ESP :	<u>256/</u>	1;	0

Comp	NTASKS	NTHRDS	ROOTPE
CPL :	256/	1;	0
ATM :	256/	1;	0
LND :	256/	1;	0
ICE :	256/	1;	0
OCN :	256/	1;	256
ROF :	256/	1;	512
GLC :	256/	1;	0
WAV :	256/	1;	0
ESP :	256/	1;	0

Comp	NTASKS	NTHRDS	ROOTPE
CPL :	768/	1;	0
ATM :	768/	1;	0
LND :	192/	1;	0
ICE :	544/	1;	224
OCN :	256/	1;	768
ROF :	128/	1;	0
GLC :	768/	1;	0
WAV :	32/	1;	192
ESP :	1/	1;	0

All components sharing  
the same MPI tasks –  
total tasks is 256

OCN and ROF on  
different tasks –  
total tasks is 768

Ind and ice running on  
different tasks but  
sharing those with atm

# Understanding your case

## preview\_run

- What batch information is being submitted?
- How is the short-term archiving used?
- What are the environment variables that are set?
- What are the batch queue settings?

➤ **./preview\_run**

```
CASE INFO:  
nodes: 8  
total tasks: 1024  
tasks per node: 128  
thread count: 1  
  
BATCH INFO:  
FOR JOB: case.run  
ENV:  
    module command is /cluster/installations/lmod/lmod/libexec/lmod python --quiet restore system  
    module command is /cluster/installations/lmod/lmod/libexec/lmod python load StdEnv intel/2020a  
    Setting Environment KMP_STACKSIZE=64M  
    Setting Environment MKL_DEBUG_CPU_TYPE=5  
    Setting Environment OMPI_MCA_mpi_leave_pinned=1  
    Setting Environment OMPI_MCA_btl=self,vader  
    Setting Environment OMPI_MCA_rmaps_rank_file_physical=1  
    Setting Environment OMPI_MCA_coll_hcoll_enable=1  
    Setting Environment OMPI_MCA_coll=^fca  
    Setting Environment OMPI_MCA_coll_hcoll_priority=95  
    Setting Environment OMPI_MCA_coll_hcoll_np=8  
    Setting Environment HCOLL_MAIN_IB=mlx5_0:1  
    Setting Environment HCOLL_ENABLE_MCAST_ALL=1  
    Setting Environment OMP_NUM_THREADS=1  
SUBMIT CMD:  
    sbatch --time 00:59:00 --account nn2345k .case.run --resubmit  
  
FOR JOB: case.st_archive  
ENV:  
    module command is /cluster/installations/lmod/lmod/libexec/lmod python --quiet restore system  
    module command is /cluster/installations/lmod/lmod/libexec/lmod python load StdEnv intel/2020a  
    Setting Environment KMP_STACKSIZE=64M  
    Setting Environment MKL_DEBUG_CPU_TYPE=5  
    Setting Environment OMPI_MCA_mpi_leave_pinned=1  
    Setting Environment OMPI_MCA_btl=self,vader  
    Setting Environment OMPI_MCA_rmaps_rank_file_physical=1  
    Setting Environment OMPI_MCA_coll_hcoll_enable=1  
    Setting Environment OMPI_MCA_coll=^fca  
    Setting Environment OMPI_MCA_coll_hcoll_priority=95  
    Setting Environment OMPI_MCA_coll_hcoll_np=8  
    Setting Environment HCOLL_MAIN_IB=mlx5_0:1  
    Setting Environment HCOLL_ENABLE_MCAST_ALL=1  
    Setting Environment OMP_NUM_THREADS=1  
SUBMIT CMD:  
    sbatch --time 0:59:00 --account nn2345k --dependency=afterok:0 case.st_archive --resubmit  
  
MPIRUN:  
    srun /cluster/work/users/mvertens/noresm/test_tutorial/bld/cesm.exe >> cesm.log.$LID 2>&1
```

Before you run – checking your case

# **xmlchange and check\_input\_data**

## **xmlchange**

use to change variables in xml files

```
> cd $CASEROOT  
> ./xmlchange STOP_OPTION=nmonths  
> ./xmlchange STOP_N=6
```

which will change the variables STOP\_OPTION and STOP\_N in the file env\_run.xml

## **check\_input\_data**

determines if the required data files for the case exist on local disk in the appropriate subdirectory of \$DIN\_LOC\_ROOT. If any of the required datasets do not exist locally, **check\_input\_data** will download them to the \$DIN\_LOC\_ROOT directory hierarchy via interaction with the input data server.

Will see more details in upcoming talks!

# Some steps to take **BEFORE** starting a long run

1. first build the case (`case.build`)
2. verify that input data is present – and download if not (`check_inputdata`)
3. perform a debug test (`xmlchange DEBUG=TRUE`) if you have changed to code or namelist
4. run a performance test and check timing file  
Determining best processor layout can be a huge benefit for performance!

# Why a debug test?

- Normally if the xml variable DEBUG is not enabled the compiler flags to check for floating point exceptions or array bound problems are not turned on. Its important to do this before you run a long run. You can do a 1 day test with debug on out of your \$CASEROOT.
- Simply do the following:
  - ./case.build – clean-all
  - ./xmlchange DEBUG=TRUE
  - ./xmlchange STOP\_OPTION=ndays
  - ./xmlchange STOP\_N=1
  - ./case.build
  - ./case.submit
- If this works – then simply reset the default values and build again
  - ./case.build –clean-all
  - ./xmlchange DEBUG=FALSE
  - ./case.build
- If it crashes – need to resolve the problem!

# How to validate performance

- Start with a simple case - clm, datm, rof, cpl

```
➤ ./create_newcase \
--case test_perf \
--compset 2000_DATM%GSWP3v1_CLM50%BGC-CROP_SICE_SOCN_MOSART_SGLC_SWAV \
--res f19_f19_mtn14
➤ cd test_perf
➤ ./xmlchange NTASKS=512
➤ ./xmlchange DIN_LOC_ROOT_CLMFORC=/cluster/shared/noresm/inputdata/atm/datm7
➤ ./payout
➤ ./case.setup
➤ ./case.build
➤ ./case.submit
```

Comp	NTASKS	NTHRDS	ROOTPE
CPL :	512/	1;	0
ATM :	512/	1;	0
LND :	512/	1;	0
ICE :	512/	1;	0
OCN :	512/	1;	0
ROF :	512/	1;	0
GLC :	512/	1;	0
WAV :	512/	1;	0
ESP :	512/	1;	0

However, we know that DATM and CLM run concurrently in time – so can place DATM on a separate processor set  
Let's start with a 5 day test and see the timing file

# How can we get better performance?

```
> cd timing/test_perf/  
> look at cesm_timing.test_perf.$id
```

## Overall Metrics:

Model Cost:	112.34	pe-hrs/simulated_year
Model Throughput:	109.39	simulated_years/day

```
Init Time : 27.490 seconds  
Run Time : 10.820 seconds 2.164 seconds/day  
Final Time : 0.002 seconds
```

```
Actual Ocn Init Wait Time : 0.000 seconds  
Estimated Ocn Init Run Time : 0.000 seconds  
Estimated Run Time Correction : 0.000 seconds  
(This correction has been applied to the ocean and total run times)
```

Runs Time in total seconds, seconds/model-day, and model-years/wall-day  
CPL Run Time represents time in CPL pes alone, not including time associated with data exchange

TOT Run Time:	10.820 seconds	2.164 seconds/mday	109.39 myears/wday
CPL Run Time:	0.486 seconds	0.097 seconds/mday	2435.31 myears/wday
ATM Run Time:	1.644 seconds	0.329 seconds/mday	719.93 myears/wday
LND Run Time:	8.402 seconds	1.680 seconds/mday	140.87 myears/wday
ICE Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myears/wday
OCN Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myears/wday
ROF Run Time:	0.815 seconds	0.163 seconds/mday	1452.22 myears/wday
GLC Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myears/wday
WAV Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myears/wday
ESP Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myears/wday
CPL COMM Time:	2.595 seconds	0.519 seconds/mday	456.09 myears/wday

Let's reset the PE-layout and  
Put the atm on its own pes –  
but with much fewer tasks

```
./xmlchange NTASKS=496  
./xmlchange NTASKS_ATM=16  
./xmlchange ROOTPE_ATM=496
```

./payout now gives

Comp	NTASKS	NTHRDS	ROOTPE
CPL	496/	1;	0
ATM	16/	1;	496
LND	496/	1;	0
ICE	496/	1;	0
OCN	496/	1;	0
ROF	496/	1;	0
GLC	496/	1;	0
WAV	496/	1;	0
ESP	496/	1;	0

# How can we get better performance? (cont)

Now let's look at the new timing file

## Overall Metrics:

Model Cost:	93.37	pe-hrs/simulated_year
Model Throughput:	131.61	simulated_years/day

Init Time : 136.563 seconds  
Run Time : 8.993 seconds      1.799 seconds/day  
Final Time : 0.002 seconds

Actual Ocn Init Wait Time : 0.000 seconds  
Estimated Ocn Init Run Time : 0.000 seconds  
Estimated Run Time Correction : 0.000 seconds  
(This correction has been applied to the ocean and total run times)

Runs Time in total seconds, seconds/model-day, and model-years/wall-day  
CPL Run Time represents time in CPL pes alone, not including time associated with data exchange

TOT Run Time:	8.993 seconds	1.799 seconds/mday	131.61 myears/wday
CPL Run Time:	5.070 seconds	1.014 seconds/mday	233.44 myears/wday
ATM Run Time:	2.137 seconds	0.427 seconds/mday	553.84 myears/wday
LND Run Time:	8.158 seconds	1.632 seconds/mday	145.08 myears/wday
ICE Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myyears/wday
OCN Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myyears/wday
ROF Run Time:	0.845 seconds	0.169 seconds/mday	1400.66 myyears/wday
GLC Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myyears/wday
WAV Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myyears/wday
ESP Run Time:	0.000 seconds	0.000 seconds/mday	0.00 myyears/wday
CPL COMM Time:	2.476 seconds	0.495 seconds/mday	478.01 myyears/wday

Throughput is increased by ~30% with the same number of total PES

Model cost is less

HUGE performance saving  
If you will run a long time!

# Questions?

# Reproducible Development with Scripts

# Reproducible Development with Scripts

- Most aspects of reproducible experiments can be included in a simple bash script
- A script is a single file that can be shared and stored.
  - In addition to creating all the settings found in the case documentation, it can (should) also control the exact code version used for the experiment.
- Elements of a script
  - 1) Make sure the model source (SRCROOT) has the correct version of the model (TAG) checked out (including infrastructure and component models)
  - 2) Call **create\_newcase** with a compset (COMPSET), model grid (RES), case (CASEDIR) and any other desired options
  - 3) Execute any need **xmlchange** commands
  - 4) Call **case.setup**
  - 5) Add any desired custom namelist settings
  - 6) Call **case.build** and **case.submit**
  - 7) Check for errors in any of these steps

# Sample Experiment Script ( part 1)

```
#! /bin/bash
## Run an out-of-the-box N2000 experiment for 3 months
##      but with reduced output.

## Experiment basics, modify these for your experiment
TAG="release-noresm2.0.9"
COMPSET="N2000"
RES="f19_tn14"
SRCROOT="/cluster/projects/nn9039k/xxUSERxx/NorESM"
CASEDIR="/cluster/work/users/xxUSERxx/cases/${COMPSET}_${RES}"
REPO="https://github.com/NorESMhub/NorESM"
PROJECT="nn9039k"

## (make sure that clone exists, otherwise, clone REPO)
if [ ! -d "${SRCROOT}" ]; then
    git clone -o NorESM ${REPO} ${SRCROOT}
fi

## Ensure correct source is checked out
cd ${SRCROOT}
git checkout ${TAG}
./manage_externals/checkout_externals
```

# Sample Experiment Script (part 2)

```
## Create your case
./cime/scripts/create_newcase --case ${CASEDIR} --compset ${COMPSET} --res ${RES}

## Any PE changes must go here

## Changes that affect the build go here
./xmlchange DEBUG=TRUE
./xmlchange STOP_OPTION=nmonths,STOP_N=3

## Build the model
./case.build

## Last chance to modify run-time settings
echo "history_chemistry      = .false." >> user_nl_cam
echo "history_chemspecies_srf = .false." >> user_nl_cam
echo "history_clubb           = .false." >> user_nl_cam

## Submit the job
./case.submit
```

# Sample Scripts on Betzy

There are two sample scripts on Betzy:

- **/cluster/shared/noresm/WORKSHOP/scripts/ReproExperimentScriptSimple.sh**
  - Just run the commands.
  - Is nearly the same as the example on the previous two pages
- **/cluster/shared/noresm/WORKSHOP/scripts/ReproExperimentScript.sh**
  - A more careful script that performs checks for success and also can skip some steps if they have already been done

To work with one of these scripts, make a copy and then make changes to suite 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}"

# Questions?

# **Model Development**

- Creating a GitHub Fork
- Working with multiple remotes in a git clone
- Model development – commits and pushes
- Adding a new model (e.g., BLOM, CAM, CLM) to NorESM.

# Model Development – Working with the code

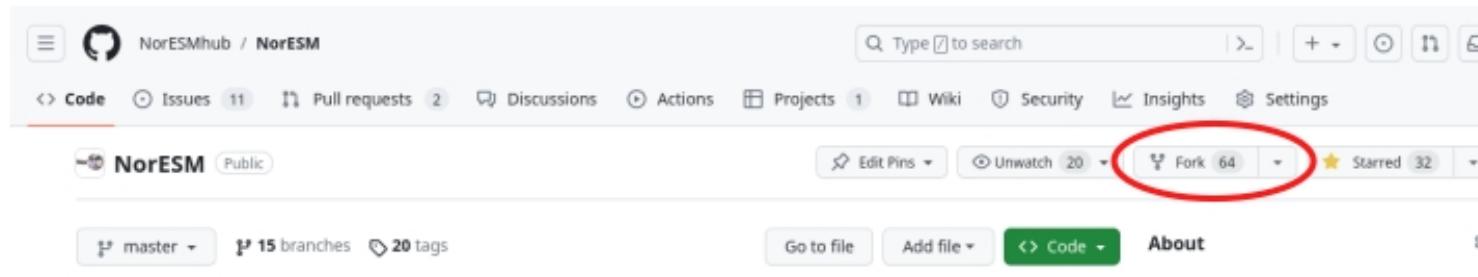
Steps to working with code modifications using git and GitHub

1. Create a personal fork of the repository where you want to make changes\*
2. Add that fork as a new remote in your clone\*
3. Create and checkout a branch to store your changes
4. Make any changes to your branch and run tests (experiments)
5. Commit early and often to make it easy to track what was changed when
6. Push your branch to your fork for backup and sharing

\* One time set-up

# Working with the code - create a personal fork

- A “fork” is a GitHub term for a repository that remembers where it came from.
- A fork is a standard GitHub repository with the added feature that you can see the other forks and open a Pull Request (PR) to one of them.
- From the main page of NorESMhub/NorESM (or NorESMhub/<component>):



# Working with the code – create a personal fork

- After you are satisfied with the settings, press the “Create Fork” button.

## Create a new fork

A *fork* is a copy of a repository. Forking a repository allows you to freely experiment with changes without affecting the original project. [View existing forks.](#)

Required fields are marked with an asterisk (\*).

Owner \*



gold2718

Repository name \*

/ NorESM

NorESM is available.

By default, forks are named the same as their upstream repository. You can customize the name to distinguish it further.

Description (optional)

Norwegian Earth System Model and Documentation

Copy the `master` branch only

Contribute back to NorESMhub/NorESM by adding your own branch. [Learn more.](#)

You are creating a fork in your personal account.

Create fork

# Working with the code - adding a new remote

- Copy the URL for your new fork

The screenshot shows a GitHub fork repository page for 'NorESM' (Public). The repository was forked from 'NorESMhub/NorESM'. The main navigation bar includes 'Pin' and 'Watch' buttons. Below the repository name, it shows 'master', '1 branch', and '0 tags'. A message indicates the 'master' branch is up to date with the original repository. On the right, there's a 'Code' dropdown menu with options for 'Local' and 'Codespaces'. Under 'Clone', there are three options: 'HTTPS' (selected), 'SSH', and 'GitHub CLI'. The 'HTTPS' URL is displayed as <https://github.com/gold2718/NorESM.git>. A red circle highlights the 'Code' dropdown, and a red arrow points to the copy icon (a clipboard with a plus sign) next to the URL.

# Working with the code - adding a new remote (cont.)

- Copy the URL for your new fork

```
$ git remote add <name> https://github.com/<name>/NorESM.git
```

```
$ git remote -v
```

```
origin https://github.com/NorESMhub/NorESM (fetch)
origin https://github.com/NorESMhub/NorESM (push)
<name> https://github.com/<name>/NorESM.git (fetch)
<name> https://github.com/<name>/NorESM.git (push)
```

# Working with the code – creating a new branch

- A branch in git is just a new pointer to the last commit.
- When creating a new branch, always declare where the branch will begin

```
$ git branch my_edit release-noresm2.0.7
```

```
$ git checkout my_edit
```

- You can combine the new branch creation and checkout

```
$ git checkout -b my_edit release-noresm2.0.7
```

# Working with the code - making code changes

- If you make changes to source code, you need to call `./case.build` again
- If you change any Fortran `use` statements, you should rebuild the model:

```
./case.build -clean <component>; ./case.build
```

- where `<component>` is a component type such as `atm` or `ocn`.
- The fastest way to force a rebuild is: `rm -r bld`
- If you change anything in `cime_config`, you should start with a new case

# Working with the code – using commits as a development tool

- Make sure your git environment is configured correctly
- For any machine you work on (e.g., Betzy), you need to have these settings:

```
git config --global user.name "Your Name"
```

```
git config --global user.email <GitHub email address>
```

- Useful introduction to git from Software Carpentry:  
<https://swcarpentry.github.io/git-novice/>
- Also, see the “contribute” section in the NorESM documentation
- If you like looking at code differences graphically, you can try git’s difftool:

```
git config --global diff.tool=meld
```

```
git config --global difftool.prompt=false
```

# Working with the code – using commits as a development tool

- Commit often! Commits help you track differences and find problems.
- Always enter a useful log message, future you will thank you.
- If you create a new source file, be sure to add it before making your commit:

```
$ git add <new_file>
```

- To commit all changes and type in a log message:

```
$ git commit -am 'Great log message here'
```

- To commit all changes and have an editor window open to enter your log message:

```
$ git commit -a
```

# Working with the code – interacting with your fork

- Push your branch to your fork. This serves both as a backup and as a means to share – with others or with yourself on other machines.
- Always specify the destination repository and the branch that you want to push.

```
git push <name> my_edit
```

# Working with the code – updating Externals.cfg

- If you are making edits to a branch of a component model and want to perform coupled runs with NorESM, you need to update the Externals.cfg file in NorESM. (Note that for most component models (e.g., CAM, CTSM), you can build and run non-coupled cases with just a clone of that component.)
- Make a branch of your NorESM clone and edit Externals.cfg (example below for CAM):

```
[cam]
tag = cam_cesm2_1_rel_05-Nor_v1.0.5
protocol = git
repo_url = https://github.com/NorESMhub/CAM
local_path = components/cam
required = True
```

```
[cam]
branch = my_edit
protocol = git
repo_url = https://github.com/<name>/CAM
local_path = components/cam
required = True
```