

Run CAM-Chem on Cheyenne

This example describes how to run CAM-chem out-of-the-box with specified dynamics on the NCAR cheyenne HPC. More information on running CESM is available from the CESM Tutorials (e.g., <http://www.cesm.ucar.edu/events/tutorials/2019/coursework.html>). However, this page includes specific instructions for chemistry simulations. The compset required for this setup is named "FCSD".

- Get a [Cheyenne account](#) for the NCAR High performance Computer system if you don't have one.

(A) Copy the model setup code to your own directory

1. Make a copy of the source code from the latest release in your own directory, the latest code can be downloaded following the instructions at: http://www.cesm.ucar.edu/models/cesm2/release_download.html

It is best to put this code in your 'home' or 'work' directory (not scratch). This directory is referred to as \$CESM_ROOT below. This should only need to be done once for each code base update of CESM. Note that when running on cheyenne you do not need to get any of the input data files.



Tip for New Users:

Having problems? Try the [Troubleshooting](#) page.

Downloading the source code will be completed by using the git clone feature. For example, first download the latest release (e.g. CESM2.2.0, with recent bug fixes):

```
> cd /glade/work/$USER/  
> git clone https://github.com/ESCOMP/CESM.git {my_cesm_sandbox}  
> cd {my_cesm_sandbox}  
> git fetch origin  
> git checkout cesm2.2-rcbranch
```

It is recommended to use a descriptive label, including the model version and perhaps the current date, for your local directory instead of "my_cesm_sandbox".

Download the model component source code.

```
> ./manage_externals/checkout_externals
```

And all the code to continue should be in the new sandbox folder. To use previous/other versions or to address errors, see instructions on the CESM page linked above.

(B) Create a new case

2. Use the code in the model directory \$CESM_ROOT to create a new case called \$CASENAME:

```
> $CESM_ROOT/cime/scripts/create_newcase --case <your_path/$CASENAME> --mach cheyenne --res f09_f09_mg17 --  
compset FCnudged
```

From section A, \$CESM_ROOT would be /glade/work/\$USER/my_cesm_sandbox

A new directory \$CASEROOT = <your_path+\$CASENAME> is created. You may need to add --run_unsupported to the call line if you are not running with a scientifically validated compset and resolution combination.

Note 1: For additional help and options, type ./create_newcase -h

Note 2: To find the possible compset types \$CESM_ROOT/cime/scripts/query_config --compsets cam.

Note 3: If you need to specify a project on cheyenne, the command is --project \$PROJECT_NUMBER.

Note 4: The above call uses the [new nudging scheme on 32 model layers](#), to use the old nudging scheme with 56 model layers use the compset: --compset FCSD, and [adjust met files accordingly](#).



Tip for New Users:

Information on the compsets can be found here: <http://www.cesm.ucar.edu/models/cesm2/config/compsets.html>

(C) Set up your case

3. From within `$CASEROOT`

```
> ./case.setup
```

4. Make changes to the model configuration using the `*.xml` files; you can edit the files directly or use the `xmlchange` tool (in your case directory).

Changes to `env_build.xml` must be made before building, or you will need to re-build.

See advanced pages to [change the chemistry source code](#).

(D) Build the Executable



Tip for New Users:

You can use script `xmlquery` to query a variable in the xml files before modifying a variable with `xmlchange` command. For example:

```
> ./xmlquery CALENDAR
```

5. Compile and build the model in `$CASEROOT`



Note

First address any current bug-fixes: [Bugs and Updates](#)

```
>qcmd -- ./case.build
```

Note: you cannot run `./case.build` interactively from the cheyenne prompt because it uses too much memory: you must use `'qcmd'`.

Note 1: You may need a project number to run `qcmd`: `qcmd -A $PROJECT_NUMBER -- ./case.build`

6. (Optional) Make changes to the model runtime setup: Changes to `env_run.xml` can be made at any time:

a. If not starting in the default 2005, change dates: see [Changing Dates of a Run](#) (also see relevant namelist changes)

b. The default option for biogeochemistry is "specified phenology" (satellite LAI) with CLM5 physics:

```
<entry id="CLM_BLDNML_OPTS" value="-bgc sp">
```

```
<entry id="CLM_PHYSICS_VERSION" value="clm5_0">
```

Other options are available, such as irrigated crops - please see the [CLM documentation](#).

c. The default simulation is a test run for 5 days. Change `STOP_OPTION` and `STOP_N` to alter this to desired values.

7. (Optional) Check namelist settings in the namelist files `user_nl_cam` and `user_nl_clm`. Most CAM-chem related namelist variables are in `CaseDocs/atm_in`, but MEGAN and drydep are in `CaseDocs/drv_flds_in` (these files are created during build). To modify any of these, copy the appropriate lines to `user_nl_cam` and edit there.

For example, if the startdate has been changed in `env_run.xml`, you have to also change the date of the initial meteorology file in `user_nl_cam` to start at the corresponding date.

For other changes see [namelist changes](#) or advanced options page.

After adding changes to `user_nl_*` files, optionally run:

```
> ./preview_namelists
```

NOTE: most changes in `user_nl_*` files do not require re-building. However, during a run (`CONTINUE_RUN = TRUE`) no changes can be made to history output (fincl lists). If you want to change history output, create a new or [branch](#) run.



Tip for New Users:

There are many namelist variables. You can find their definitions at: http://www.cesm.ucar.edu/models/cesm2/settings/current/cam_nml.html

8. Check the run setup. In the `env_batch.xml` file make sure to have your project added correctly: `<entry id="PROJECT" value=$YOUR_PROJECT_CODE>` Depending on the version of CESM, you may instead find the entry id for PROJECT in `env_workflow.xml`

Change your walltime if desired: `<entry id="JOB_WALLCLOCK_TIME" value="12:00:00">` (12 hours max)

9. If you make changes to `env_build.xml` variables or SourceMods after setting up and building, you may have to clean your setup and build again:

```
> ./case.setup --clean
> ./case.setup
```

OR

```
> ./case.setup --reset
```

(which cleans, then does setup)

followed by

```
> ./case.build --clean
> qcmd -- ./case.build
```

(E) Run the Model

10. Submit run to queue:

```
> ./case.submit
```

While running, output is written to `<run_dir>: /glade/scratch/<username>/$CASENAME/run`

After the run completes successfully, output files are moved to the short term archive: `/glade/scratch/<username>/archive/$CASENAME/atm/hist` (similar directories exist for other model components: Ind, etc.).

Restart and initial conditions files are written to: `/glade/scratch/<username>/archive/$CASENAME/rest`

Note: long term archiving is currently not working

**Tip for New Users:**

Default output is monthly, so if you run a test 5-day simulation with monthly output, you will not see any files in the `atm/hist` location. However, restart files will have been created.

11. Useful commands while model is running:

check your run progress:

```
>qstat -u <user>
```

If you find an issue and need to delete your run:

```
>qdel <JobID>
```

If your model run doesn't complete, try some of the suggestions on the troubleshooting page.

12. To continue a run from restart files, for example after an initial start up, change `CONTINUE_RUN` to `TRUE` in the `env_run.xml` file.

**Tip for New Users:**

High performance computing systems often have maximum wall times (e.g. `JOB_WALLCLOCK_TIME` = 12 hours), meaning a long run will need to be split into several smaller runs. In this case, change the "RESUBMIT" value in `env_run.xml` file to greater than zero. For example, you can simulate 10 years by changing `STOP_OPTION=nyears`, `STOP_N=1` and `RESUBMIT=9`. This will perform an initial run of 1 years + (9 resubmits x 1 years per job) = 10 years.