The Land (CLM5) Tutorial Session

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Notes:

- We will use the tutorial account code UESM0008

- For qcmd you can use -A UESM0008 to set your account code.

- You will need to change the account code and the queue in your cases:

  - ./xmlchange JOB_QUEUE=regular

  - ./xmlchange PROJECT=UESM0008

- To refer to using an editor we will say $EDITOR. This can be any editor of your choice and if you set the environment variable for it you can use the command as given (i.e. setenv EDITOR vim).

CLM5.0 Offline – "I" compsets

Compsets are shortcuts designed for specific cases… treat them as starting points for all cases

"I" compsets run the clm/datm/rof/cism and no sea-ice/ocean/atm/wave models

SP = Satellite Phenology;   BGC = Biogeochemistry

Short Name   Description

I2000Clm50Sp   CLM50SP, yr. 2000 pfts, CO_2, aerosol$_{dep}$

   Long Name: 2000_DATM%GSWP3v1_CLM50%SP_SICE_SOCN_MOSART_CISM2%NOEVOLVE_SWAV

I1850Clm50BgcCrop   CLM50BGC+Crop, yr 1850 pfts, CO_2, aerosol$_{dep}$

   Long Name: 1850_DATM%GSWP3v1_CLM50%BGC-CROP_SICE_SOCN_MOSART_CISM2%NOEVOLVE_SWAV

IHistClm50BgcCrop   CLM50BGC+Crop, 1850-2010 pfts, CO_2, aerosol$_{dep}$ + N$_{dep}$

   Long Name: HIST_DATM%GSWP3v1_CLM50%BGC-CROP_SICE_SOCN_MOSART_CISM2%NOEVOLVE_SWAV

/glade/p/cesm/tutorial/cesm2.1.1_tutorial/cime/scripts/query_config --compsets clm

Atmospheric forcing for these compsets are from Global Soil Wetness Project (GSWP3) for 1901-2014.

In exercise A, you will try the I2000Clm50Sp compset

In exercise B, you will try the IHistClm50BgcCrop compset

In exercise C, you will again use the I2000Clm50Sp compset and modify input data

Exercise A. Basic CLM5 usage

Goal: Run the CLM50SP at ~1° lat/lon horizontal resolution for five days

In this exercise you will try the I2000Clm50Sp compset.

Exercise B. Differences between compsets

Goal: Create a case with a different compset and see how settings change automatically for you. Contrast the history files from exercise (A) and (B).

In this exercise you will try the IHistClm50BgcCrop compset which is a 20th century transient run using GSWP3v1 atmospheric forcing and the biogeochemistry model including crops.

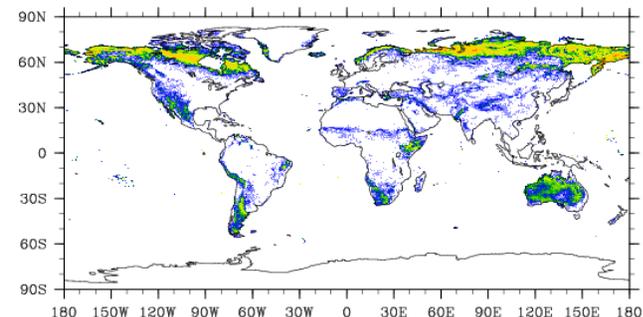# Exercise C. Understanding and modifying input data

Goal: Learn what inputs CLM needs and what they look like

Here we will again use the I2000Clm50Sp compset, modify one of the plant functional type properties, and compare results to exercise A.
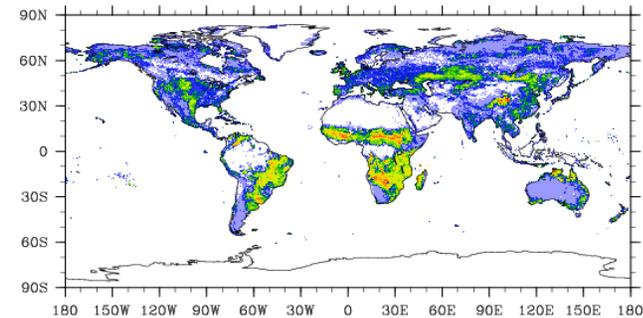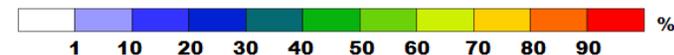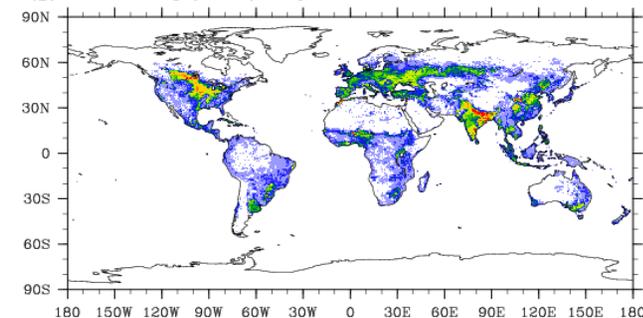

(a) Current Day (2000) Tree PFTs
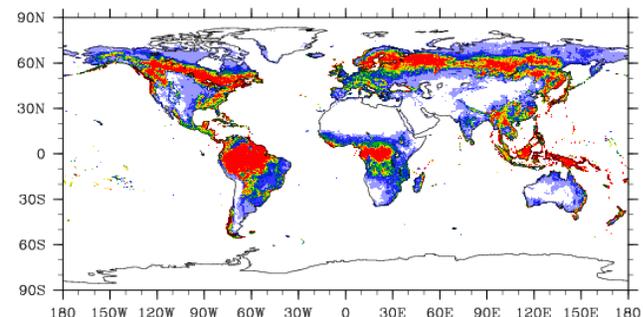
(c) Current Day (2000) Shrub PFTs

(e) Current Day (2000) Grass PFTs

(g) Current Day (2000) Crop PFT

Exercise A. detailed steps

1) Create the case…

cd /glade/p/cesm/tutorial/cesm2.1.1_tutorial/cime/scripts

./create_newcase --case ~/cases/i.day5.a --compset I2000Clm50Sp --res f09_g17_gl4 --run-unsupported

#./create_newcase --help   …for documentation

2) Setup the case…

cd ~/cases/i.day5.a

You need not change env_build.xml for this case to work, but now would be the time to make such changes

Execute setup

./case.setup

Exercise A. detailed steps

3) Change the clm namelist…

#Since we are running just five days and history output default is monthly averages, we will change the clm namelist to get daily average output

#Add hist_nhtfrq and set to -24 (i.e., 24 hrs, daily average) in the clm namelist

#Add hist_mfilt and set to 6 (i.e., 5 daily average time samples plus an initialization step) in the clm namelist

$EDITOR user_nl_clm

#Add these lines:

hist_nhtfrq = -24

hist_mfilt = 6

#Generate the namelists (look at lnd_in in CaseDocs directory once the following is done)

./preview_namelists

4) Shorten the requested run time (this may help your job to start sooner) and set the account number and queue

./xmlchange --subgroup case.run JOB_WALLCLOCK_TIME=0:15:00

./xmlchange JOB_QUEUE=regular

./xmlchange PROJECT=UESM0008

Exercise A. detailed steps

5) Build the case and compile the code…

qcmd –A UESM0008 -- ./case.build

6) Submit the run…

./case.submit

to see the $jobID and whether the job is pending or running

qstat -u $USER

to kill the job if necessary

qdel $jobID

run executes in /glade/scratch/$USER/i.day5.a/run

land history output at the end of the run will be moved to

/glade/scratch/$USER/archive/i.day5.a/lnd/hist

look at the history file in the archive directory, e.g., using ncview (module load ncview)

cd /glade/scratch/$USER/archive/i.day5.a/lnd/hist

ncview i.day5.a.clm2.h0.0001-01-01-00000.nc &

note that there will be six time samples in this file, ignore the first one, it is an initialization step
     and is not a daily average

Exercise B. detailed steps

1) Create the case…

cd /glade/p/cesm/tutorial/cesm2.1.1_tutorial/cime/scripts

./create_newcase --case ~/cases/i.day5.b --compset IHistClm50BgcCrop --res f09_g17_gl4 --run-unsupported

2) Setup the case…

cd ~/cases/i.day5.b

#Execute setup

./case.setup

3) Note differences between this case and the case created in exercise A

cd ~/cases

#For example,

diff i.day5.a/env_run.xml i.day5.b/env_run.xml

Exercise B. detailed steps

4) Change the clm namelist…

cd ~/cases/i.day5.b

#Since we are running just five days and history output default is monthly averages, we will change the clm namelist to get daily average output

#Add hist_nhtfrq and set to -24 (i.e., 24 hrs) in the clm namelist

#Add hist_mfilt and set to 6 (i.e., 5 daily average time samples plus an initialization step) in the clm namelist

$EDITOR user_nl_clm

#Add these lines:

hist_nhtfrq = -24

hist_mfilt = 6

#Generate the namelists (look at lnd_in in CaseDocs directory once the following is done)

./preview_namelists

5) Shorten the requested run time and set the account number and queue

./xmlchange --subgroup case.run JOB_WALLCLOCK_TIME=0:15:00

./xmlchange JOB_QUEUE=regular

./xmlchange PROJECT=UESM0008

6) Build the case and compile the code…

qcmd –A UESM0008 -- ./case.build

Exercise B. detailed steps

7) Now compare the CaseDocs directories in i.day5.b and i.day5.a (in particular you could compare lnd_in) and note the differences, e.g.,

diff CaseDocs/lnd_in ../i.day5.a/CaseDocs/lnd_in

8) Submit the run…

./case.submit

9) Compare the history files from these two runs (e.g., side by side using "ncview"). Note the extra variables in the file produced from exercise B (biogeochemistry variables). Specific fields to compare (leaf and stem area index [TLAI, TSAI], transpiration and canopy and ground evaporation [FCTR, FCEV, FGEV). What do you think negative values of FCEV and FGEV mean?

Exercise C. detailed steps

1) Look at lnd_in in the exercise A case

Find the parameter file specified by the "paramfile" namelist item. Look at variable "rholvis" in this file using ncview or ncdump –v rholvis. This is the visible leaf reflectance for every pft.

2) Create a case like the one in exercise A but with a different case name (i.e., i.day5.a_pft) by using create_clone, e.g.,

cd /glade/p/cesm/tutorial/cesm2.1.1_tutorial/cime/scripts

./create_clone --case ~/cases/i.day5.a_pft --clone ~/cases/i.day5.a

3) Modify the rholvis parameter in the pft-physiology file.

Use nco, python or ncl to modify the pft-physiology file. Change the visible leaf reflectance (variable rholvis) for pft #4 (tropical broadleaf evergreen tree).

First, make a copy of the file, e.g., in your scratch directory

cd /glade/scratch/$USER

cp /glade/p/cesmdata/cseg/inputdata/lnd/clm2/paramdata/clm5_params.c171117.nc ./

chmod u+w clm5_params.c171117.nc

Exercise C. detailed steps

There are many different ways to change NetCDF files. Because it's a binary format, you will need some type of script or interpreter to read the file and write it out again (such as ferret, IDL, NCL, NCO, Perl, Python, Matlab, Yorick). If you are familiar with any of these you should be able to figure out how to modify the NetCDF parameter file.

In the next few slides we will demonstrate how to do so using: NCO, Python (with the NetCDF4 module), and NCL.

NOTE: For any tasks other than setting up, building, submitting cases (e.g., using ncl or nco) you should probably do these tasks on the Data Visualization Cluster - - Casper, and not on the Cheyenne login nodes.

(use "execdav –a UESM0008" to get a Casper node).

Exercise C. changing NetCDF file -- NCO

Here we change the parameter file using the NetCDF Operators (NCO).

See http://nco.sourceforge.net/

Using ncap2:

```
module load nco
cp clm5_params.c171117.nc clm5_params.c171117.new.nc

ncap2 -A -v -s 'rholvis(4)=0.4' clm5_params.c171117.nc clm5_params.c171117.new.nc
```

Exercise C. changing NetCDF file -- Python

Here we change the parameter file using Python and the NetCDF4 module. See
https://unidata.github.io/netcdf4-python/netCDF4/index.html

Setup the python environment and make sure the NetCDF4 module is loaded

```
module load python
ncar_pylib
cp clm5_params.c171117.nc clm5_params.c171117.new.nc
```

Save the following into a small python script called filename.py:

```
from netCDF4 import Dataset
nc = Dataset( "clm5_params.c171117.new.nc", "a" )
nc["rholvis"][4] = 0.4
nc.close()
```


And then type

```
python filename.py
deactivate              # to remove NCAR python from the environment
```

Exercise C. changing NetCDF file -- NCL

Here we change the parameter file using NCL (NCAR Command Language), see
http://ncl.ucar.edu/

NOTE: NCL has moved to maintenance mode and won't be further developed. Use of Python and the NCL Python utilities (such as PyNGL) is now recommended.

Save the following ncl script to filename.ncl:

```
begin
a = addfile("clm5_params.c171117.new.nc","w")
rholvis = a->rholvis
rholvis(4) = 0.4d
a->rholvis = rholvis

end
```

and then type:

```
cp clm5_params.c171117.nc clm5_params.c171117.new.nc
ncl filename.ncl
```

Exercise C. changing NetCDF file

Regardless of the process you take to change the file, you'll want to examine it to make sure the change is correct. After you have created the new file, look at the new file to make sure your changes worked, e.g.,

ncdump –v rholvis clm5_params.c171117.new.nc

and compare it to the original file

ncdiff clm5_params.c171117.nc clm5_params.c171117.new.nc ncdiff.nc

ncdump –v rholvis ncdiff.nc

Exercise C. detailed steps

4) Follow the steps in exercise A to setup model (./case.setup) for i.day5.a_pft, change the clm namelist to point to new pft-physiology file (using user_nl_clm; paramfile = '/glade/scratch/$USER/clm5_params.c171117.new.nc'), then build (qcmd –A UESM0008 -- ./case.build) and run (./case.submit).

Compare history output against that generated in exercise A, e.g., use ncdiff. What differences do you see? Specific fields to compare (FSRVD, FSRVI, FSR, FSA, FSH, FCTR, TV, TSA).