Document for Homework 6: Running the Default Barotropic Model

User accounts

You will be running the model yourself. An account on my cluster "ozone" has already been made for you. Your long username is "ats601" plus your first initial and then your lastname (all lowercase). For example, Bruce Banner's username is "ats601bbanner". Wherever you see "ats601bbanner" throughout this document (and throughout the code), you should fill this in with your own username. Your default password is your 9-digit CSU ID number.[1] Your shortened username, which will be needed throughout, is just the first initial and your last name (drop the ats601).

Getting on the cluster

The GFDL FMS barotropic model has already been setup on my group's compute cluster (named "ozone", located at ozone.atmos.colostate.edu). Login to the cluster using ssh. You can ssh onto ozone from any computer on-campus[2] using a Unix/Linux/Mac *Terminal* with the following command:
>>ssh ats601bbanner@ozone.atmos.colostate.edu
where you should replace "ats601bbanner" with your username. You may be asked if you should allow the secure connection to ozone, type "yes" and hit enter. Then, enter your password and hit enter.

Your personal directory where you will run the model can be found at */home/ats601/bbanner* (where, you should replace *bbanner* with your shortened username of first initial plus last name). When you login, by default you should be in your home directory, but just in case you can type:
>> cd /home/ats601/bbanner
where once again you should replace "bbanner" with your shortened username.

Setting up the cluster the first time - bashrc and ssh keys

Before we get too far, we need to setup your account on ozone so that the correct modules load every time you log-in to ozone. To do this, you need to make a *.bashrc* file and a *.bash_profile*. I have made these files for you, and all you have to do is copy them over to your home directory. Type the following from within /home/ats601/bbanner/

[1] Come talk to me if you aren't sure what this is - I was given it when you signed-up for the course.

[2] For security reasons, logging into ozone from off campus requires quite a few more steps (i.e. VPN software) and I will not be discussing that. You will need to determine how to do this for your own system if this is of interest. In what follows, I will only describe how to access ozone from on-campus.

>> cp /home/eabarnes/courses/f17_601/barotropic_model_bashrc.sh .bashrc

>> cp /home/eabarnes/courses/f17_601/barotropic_model_bashprofile.sh .bash_profile

Note that the periods are very important in both lines.

The periods means that a normal *ls* will not show these files, that is, they are hidden. To check that the copy worked and the files are actually there, type:

>> ls -a

and look for the files. Now your modules will load correctly from now on every time you log-in to ozone.

If the *.bashrc* and *.bash_profile* files are not made correctly, the modules will not be loaded, you will get an error when you try and submit your runscript to the queue or try and check the status of your model simulation. The error will read something like "qsub: command not found". If you get this error, it means that your *.bashrc* and *.bash_profile* are not setup correctly.

To get your *.bashrc* file to take effect, exit ozone by typing

>> exit

Then, follow the steps above about "Getting on the cluster" to log back in.

The last setup thing you have to go is setup an ssh key so that the nodes can write files to your directory. To do this, follow the steps below.

1. move to your home directory if you aren't already there by typing

   >> cd /home/ats601/bbanner

2. then type

   >> ssh-keygen -t rsa

   hit <enter>

3. It will prompt you to answer three questions - don't type anything - just hit <enter> three times.

4. type

   >> cd ~/.ssh

5. then type

   >> cat id_rsa.pub ≫ authorized_keys

6. You're done. You should not have to follow these steps again.

Getting the model

The model code, and runscripts (files you "submit to the cluster queue" to tell it what files to run) have all been prepared for you. I want *each of you to copy the folder with the code to your own directory*. That is, each of you will have your own version of the code (that you can later modify). To copy the code to your directory do the following:

- Make sure you are in your own home directory (not the *.ssh* directory) by typing
  >> *pwd* (to show your current path).
  If you are not in your home directory, follow the previous step above to get there.

- Then, type the following:
  >> *cp -r /home/eabarnes/courses/f17_601/gfdl_spectral_core .*

Note that the period at the end is very important. The copying process will take a few seconds, be patient. Once the copying is complete, you have the model! From now on, only modify files that are within your own directory.

Compiling the model

The entire model is contained within the directory *gfdl_spectral_core*, and your next task is to compile the model. In essence, the compilation process puts all of the model code (in this case Fortran code) into one master executable file ("fms.x") that you then submit to the cluster's queue to be run. So, our next task is to compile the code to make this massive, all-inclusive fms.x file.

1. From within your directory, go to the compilation file folder. To do this, type:
   >> *cd gfdl_spectral_core/exp/spectral_barotropic/compile_scripts*

2. Open the file "compile_spectral_oz" using the text editor of your choice. I prefer to use "vim". To do this type
   >> *vim compile_spectral_oz*

3. You need to change the base directory path to be your path (rather than the path for "bbanner"). This is on line 4. Thus, where you see "bbanner" change it to your shortened username. If you don't know how to use vim, here is how to do this.

   - navigate using the arrow keys to the line you want to change

- hit the letter "i" key (this puts the editor into "text edit" mode)
- scroll over to "bbanner" and use the delete key to delete this shortened username and replace it with your own
- also scroll over the "eabarnes" and delete this, as this is not the path to your code anymore
- hit the "esc" key (this gets you out of "text edit" mode)
- type the following sequence to save and exit: ":wq" and then hit the enter key

Good, now that the file is pointing to the correct code, we are ready to compile! This is easy, just type:
>> *./compile_spectral_oz*
Then, just be very patient (will take a few minutes). A lot of text will flash across your screen, but don't worry, none of them are fatal errors, so let it run. Be patient and wait until the program is done compiling.

To be really sure that things compiled correctly, you can go and look to see if the "fms.x" file was created. To do this, type the following:
>> *cd ..* (this takes you to the previous, parent directory)
>> *ls exec.oz* (this lists the contents of the directory *exec.oz*)
Look and see if the fms.x file is in the exec.oz folder. If so, the code compiled!

Running the model in default mode

Now you are ready to setup the runscript and run the model. To do this, we will go into the working directory ("workdir") where you will prepare the runscripts, and where the data will actually be saved. To get there from the previous step, type:
>> *cd workdir*
Then, to get to the runscripts folder type:
>> *cd runscripts*
You should see a file called "runscript_default" - this is what you are going to modify now. Open the file in your favorite text editor (again, mine is vim). For example, type:
>> *vim runscript_default*
Now that the file is open, you should see a line (line 16) that says "set source_dir = ...". You will see that this points to bbanner's directory - you want it to point to yours. So, once again, we need to change the username "bbanner" to be your shortened username. To do this we will follow similar steps as we did before:

- navigate using the arrow keys to the line you want to change

- hit the letter "i" key (this puts the editor into "text edit" mode)
- scroll over to "bbanner" and use the delete key to delete this username and replace it with your own
- hit the "esc" key (this gets you out of "text edit" mode)
- type the following sequence to save and exit: ":wq" and then hit the enter key

You are now ready to run the model! To run the model, type the following (you should be inside the runscripts folder). You are going to submit the runscript to the queue, and then it should run

>> *qsub runscript_default*

To see if the model is running, type the following:

>> *qstat*

and you should see your username and the status of your run on the right hand side ("R" means running, "Q" means it is waiting for its turn, "C" means complete, and "E" means error.) The code should take less than 5 seconds if there is no one ahead of you in the queue.

When the code is done running, you can find the data located in the "workdir" folder. That is, from the runscript directory just type:

>> *cd ..* (takes you back one directory)

>> *ls* (lists everything in the current directory)

You should see a folder called "default" (if you don't, wait a few seconds then look again). This is your model output!

Navigate into the "default" folder by typing:

>> *cd default*

and then list the contents with

>> *ls* (lists everything in the current directory)

You should see a file called "default.1.nc" - this is your data file![3]

To exit out of ozone, type:

>> *exit*

Error and log files: If you run into issues, you will want to look in the log and data files. These files will appear wherever you were when you submitted your runscript to the queue (most likely, they will appear in your *runscript* directory). The files are named *out_def.out* and *out_def.err*. These files will often give you a

[3] If you want to visualize your data file (and have an x-windows application loaded on your local machine), you can then type

>> *ncview default.1.nc&*

and you should see a GUI pop-up that will show a movie of your data.

clue as to why your model crashed, and you can read the contents of the file by either opening them with your favorite editor (see examples above) or having their content print-to-screen by typing:

>> cat out_def.out

>> cat out_def.err

Getting the data to your local machine

The final step is to get the data from ozone to your local computer where you can analyze it with your software of choice. Here are the steps to do this:

1. Open a new terminal window on your local machine where you will be doing the analysis.
2. Navigate to where you want to save the data file (using the "cd" command).
3. Type the following to get the data off of ozone (all one line):

   >> scp ats601bbanner@ozone.atmos.colostate.edu:/home/ats601/bbanner/gfdl_spectral_core/exp/spectral_barotropic/workdir/default/default.1.nc .

   You will want to change the two occurrences of "bbanner" to your own shortened username. Also, note that the space and period at the end of this command is very important.
4. Finally, you will be prompted to enter your *ozone password* in order for the copying of the file to be complete (the default being your 9-digit CSU ID).
5. Once the file download is complete, the file is now sitting on your machine and you can analyze away!

Data overview

The netcdf file contains the following *daily*[4] fields.

- **ucomp**: zonal wind
- **vcomp**: meridional wind
- **vor**: relative vorticity
- **stream**: stream function

and dimensional fields:

- **time**: time count (in days)
- **lon**: longitude
- **lat**: latitude

[4]Unlike the reanalysis data you have analyzed thus far, this data is not output every 6 hours, but rather, it is being output once every 24 hours (i.e. once a day).