Tutorial 02 LiveCROCO: Manipulating NetCDF Files

1. Purpose

In this tutorial we will review basic instructions for creating and transforming NetCDF files in LiveCROCO virtual machine. CROCO input and output files are in NetCDF format, so it is very useful to learn how to transform these files.

1.1. Specific objectives

1. View the contents of a NetCDF file using *ncdump*.
2. Extract variables (without deleting them).
3. Add variables.
4. Delete variables.
5. Average the variables of a file.
6. Concatenate files chronologically.
7. Rename variables or dimensions.
8. Select time steps.
9. Select an area.
10. Calculate the difference between variables of two files.
11. Reduce the size of a file by manipulating the precision with which it is recorded.

2. Main Tools

Here we will see some Linux tools for handling NetCDF files. While it is possible to use Matlab/Octave/Python to accomplish the same thing, these tools have the advantage of being very fast and are easily integrated into a bash script.

2.1. ncdump

The **ncdump** tool is used to display the header and content of NetCDF files.

2.2. nco

The **nco** tools are used to manipulate the content of a NetCDF file.

2.3. ncview

The **ncview** tool is used to make simple graphs of different variables that a NetCDF file contains. The use of this tool is described in Tutorial 01 de LiveCROCO.

3. Exercises

Get the AVG files from

```
wget http://mosa.dgeo.udec.cl/CROCO2021/Tutorial02/ArchivosTutorial03_CROCO2021.tar.gz
gzip -d ArchivosTutorial02_CROCO2021.tar.gz
tar -xvf ArchivosTutorial02_CROCO2021.tar
```

and do the following operations

1. Extract a variable from the GRD file and save it to a file called dndx.nc.

   First we study the content of file that we are going to use

   ```
       ncdump -h croco_grd.nc | less
   ```

   From there we select, for example, *dndx* variable and extract it, saving it in another file named *dndx.nc*.

   ```
            ncks -v dndx croco_grd.nc dndx.nc
   ```

   You can verify what you get with command

   ```
       ncdump -h dndx.nc | less
   ```

2. Add that variable to an AVG file.
   We first verify that the variable does not exist.

   ```
       ncdump -h croco_avg_Y1M1.nc | grep dndx
   ```

   we add it

   ```
        ncks -h -A dndx.nc croco_avg_Y1M1.nc
   ```

   and then

   ```
       ncdump -h croco_avg_Y1M1.nc | grep dndx
   ```

3. It is also possible to remove a variable from a file

   ```
   ncks -C -O -x -v dndx croco_avg_Y1M1.nc croco_avg_Y1M1.nc

   ```

4. Average the content of each AVG files from year 1.

   ```
       ncra croco_avg_Y1M1.nc croco_Y1M1.nc
       ...
       ncra croco_avg_Y1M12.nc croco_Y1M12.nc
   ```

   You can verify that files have a single time step using

   ```
       ncdump -h croco_Y1M1.nc | less
   ```

5. Concatenate all files of monthly averages of year 1. The explicit form is

```
     ncrcat croco_Y1M1.nc croco_Y1M2.nc
     croco_Y1M3.nc  croco_Y1M4.nc  croco_Y1M5.nc
      croco_Y1M6.nc croco_Y1M7.nc croco_Y1M8.nc
       croco_Y1M9.nc croco_Y1M10.nc croco_Y1M11.nc
        croco_Y1M12.nc
     croco_Y1.nc
```

   or this way

```
    ncrcat croco_Y1M?.nc meses_1-9.nc
    ncrcat croco_Y1M1?.nc meses_10-12.nc
    ncrcat meses_1-9.nc meses_10-12.nc croco_Y1.nc
```

   You can verify that files have 12 time steps with

```
    ncdump -h croco_Y1.nc | less
```

6. Rename h variable to depth of GRD file.

```
     ncrename -v h,depth croco_grd.nc
ncrename: In total renamed 0 attributes, 0 dimensions, 0 groups, and 1 variable
```

7. Select the first 3 months of annual file.

```
     ncks -F -d time,1,3 croco_Y1.nc EFM.nc
```

   The -F option is required so that 1 is first time step, if not used index starts at zero.

8. Select southern half of study area.

```
     ncea -d eta_rho,8.0,14.0 croco_avg_Y1M7.nc croco_SUR_Y1.nc
```

   o

```
     ncks -d eta_rho,8.0,14.0 croco_avg_Y1M7.nc croco_SUR_Y1.nc
```

9. Create a new file containing the difference between months 1 and 2 of the first year.

```
    ncdiff croco_avg_Y1M1.nc croco_avg_Y1M2.nc diffM1M2.nc
```

10. Concatenate all the original monthly files and generate another yearly file with reduced precision.

    First we concatenate original files

```
    ncrcat croco_avg_Y1M?.nc meses_1-9.nc
    ncrcat croco_avg_Y1M1?.nc meses_10-12.nc
    ncrcat meses_1-9.nc meses_10-12.nc croco_avg_Y1.nc
```

    We now reduce file size by reducing results presicion

```
    ncpdq -L 5 -4 croco_avg_Y1.nc croco_avg_Y1_sml.nc
```

You may notice the size of files change from 177M to 43M.

4. Conclusion

In this tutorial you learned how to use tools to view the content and modify NetCDF files.

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5. References

```
Zender, C. S. (2016). Bit Grooming: statistically accurate
precision-preserving quantization with compression, evaluated in
the netCDF Operators (NCO, v4. 4.8+). Geoscientific Model
Development, 9(9), 3199-3211.
```

6. Helpful Links

`http://research.jisao.washington.edu/data/nco/`