Adding NAEI emissions into WRF-Chem

Please note sectors in NAEI and EDGAR don't match so this is only set up to use the totals currently – you will have to figure out the sector mapping by yourself if you want to do this

Overview of process:

1) download NAEI data from Github https://github.com/ailishgraham/NAEI_Emissions_WRF_Chem and add to emissions directory (I made a new directory called NAEI)

2) Download and use Doug's scripts to create netcdf for each species

3) Take copy of *anthro_emis_irregular_grid* (for NAEI emissions) and *anthro_emis_regular_grid* (for EDGAR emissions) and save to where your wrf_code is. (see more detailed guide on next page)

4) Run anthro_emis_irregular_grid and anthro_emis_regular_grid (I've automated this – see next page for what files to copy to use this automated version)

5) Combine both of the wrchemi files from anthro_emis to create a merged emission dataset where all UK emissions are from the NAEI (see below again)

6) Run main.bash and post.bash as usual

For people at Leeds we wouldn't need to run pre.bash, main.bash and post.bash separately – I've automated the run by adding the steps above into all of the .bash files required to automate the run. So just run . master.bash once you have made sure all of the filepaths in config.bash are correct (especially the top one and the output ones) and that you understand what is happening in pre.bash. The main part I have changed in pre.bash is:

```
# ------------------------------------------------------------------------

# 4) emissions

# ------------------------------------------------------------------------

 msg "Naei emissions"


ln -s ${WRFanthrodirNaei}/anthro_emis anthro_emis_naei

./anthro_emis_naei < anthro_emis_naei.inp > anthro_emis_naei.out


msg "Edgar emissions"


ln -s ${WRFanthrodirEdgar}/anthro_emis anthro_emis_edgar

./anthro_emis_edgar < anthro_emis_edgar.inp > anthro_emis_edgar.out
```

msg "Merging NAEI and EDGAR emissions together"

cp /nobackup/ee15amg/new_emis/wrf3.7.1_code/WRFotron_doug_NAEI/combine_emissions.py .

python combine_emissions.py

msg "Finished merging emissions"

cp wrfchemi_00z_d01 wrfchemi_12z_d01

But I had to adapt config.bash and master.bash, as well as anthro_emis, and created a new mapping input file to do this so make sure you copy the whole WRFotron directory over.

Steps in more detail:

1) I have put the NAEI data in my github repo (It's in *NAEI_emissions_scripts/raw_emissions*)

2) Doug's scripts are also in *NAEI_emissions_scripts*. There are 4 scripts in there:

The main script *NAEI_anthro_emiss_preparation.py* combines 3 other scripts:

A) *MODULE_bng_to_latlon_local.py* deals with converting the OS grid coordinates to lat/lon

B) *MODULE_convert_ascii_netcdf.py* saves the ASCII files as netcdf

C) MODULE_point_source_apportionment.py adds in the source points from the excel file

Running *NAEI_anthro_emiss_preparation.py* requires numba to be installed and this can only be done in python3. The filepaths in the scripts will need to be changed to your own but it should run after this is done. It creates a netcdf for each species.

3) I have uploaded my normal (*anthro_emis_regular_grid)* and NAEI version of anthro_emis (*anthro_emis_irregular_grid*). These both have slight changes in the fortran code to create wrfchemi files with NAEI and EDGAR in the names so I can keep a track of which have been made. This also means when I combine them in step 6 (above) I can name the file the usual 'wrfchemi_00z_d01', which saved me changing the source code for running the main part of WRF-Chem.

Compile new versions of anthro_emis (run user guide from ***./make_anthro.*** Read step 3 below for more details on the changes I've made to both of these.

Take a copy of *WRFotron_doug_NAEI*. *Master.bash, config.bash,* p*re.bash*, *emis_naei_mozmos.inp* and *combine_emissions.py* contain the changes/files needed to incorporate the NAEI emissions to your run. But make sure you change paths to your own. Also check settings in namelists against your own.

4) Run both anthro_emis versions with the input files from *WRFotron_doug_NAEI*

Pre.bash has been adapted to used new version anthro_emis for NAEI (*anthro_emis_irregular_grid)* with the mapping (*emis_naei_mozmos.inp)* I made (I've adapted my anthro_emis code to name the wrfchemi file wrfchemi_00/12z_naei)

Pre.bash also runs anthro_emis for EDGAR (*anthro_emis_regular_grid)* so you can then combine them with NAEI in the next step (again I've adapted my anthro_emis code to name the wrfchemi file wrfchemi_00/12z_edgar)

5) The python code to combine both of the WRFChemi files is also in *WRFotron_doug_NAEI* and should also be listed in *pre.bash.* This simply replaces any lat/lon value from the wrfchemi file where NAEI data is available (for any species) with NAEI data. You could adapt this to work with the Irish emissions too.

Pre.bash automatically runs the python code (*combine_emissions.py*) to combine the emissions from the wrfchemi files (naei and edgar in my case) and names it wrfchemi_00/12z_d01. But it does need numpy and netcdf libraries so make sure you have these in your version of ncl_nco_python3 – you can

add them using ***conda create -n ncl_nco_python3 -c conda-forge ncl nco python xarray netcdf4 scipy matplotlib*** *pandas* if you don't have it already

6) Feed this input file into your WRF-Chem run (I name the merged emissions *wrfchemi_00/12z_d01,* in the usual convention, to save me having to adapt any of the source code)

When main.bash runs it will read the merged emission wrfchemi file into main.bash (main.bash expects to receive: wrfchemi_00/12z_d01, which is the same name of the merged emission file made in pre.bash)

This should all work automatically from .master.bash but check if the pre.bash steps have worked using: *grep -i "success" *.out *.log; ls -ltr wrfchemi*d0**in the run directory.

It should look like this:

anthro_emis_edgar.out: anthro_emis completed successfully

anthro_emis_naei.out: anthro_emis completed successfully

exo_coldens.out: make_exo_coldens: completed successfully

fire_emis.out: fire_emis: Completed successfully

wesely.out: make_wes: completed successfully

geogrid.log:2019-11-19 18:16:00.847 --- *** Successful completion of program geogrid.exe ***

metgrid.log:2019-11-19 18:17:05.557 --- *** Successful completion of program metgrid.exe ***

mozbc_bc.log: successfully exited from module_wrfchem_lib ...

mozbc_bc.log: successfully exited from module_mozart_lib ...

mozbc_bc.log: bc_wrfchem completed successfully

ungrib.log:! Successful completion of ungrib. !

ungrib.log:2019-11-19 18:14:34.462 --- *** Successful completion of program ungrib.exe ***

-rw-r--r-- 1 ee15amg EAR 163417956 Nov 19 18:32 wrfchemi_naei_00z_d01

-rw-r--r-- 1 ee15amg EAR 163417956 Nov 19 18:32 wrfchemi_naei_12z_d01

-rw-r--r-- 1 ee15amg EAR 245975668 Nov 19 18:40 wrfchemi_edgar_00z_d01

-rw-r--r-- 1 ee15amg EAR 245975668 Nov 19 18:43 wrfchemi_edgar_12z_d01

-rw-r--r-- 1 ee15amg EAR 27044867 Nov 19 18:44 wrfchemi_00z_d01

-rw-r--r-- 1 ee15amg EAR 27044867 Nov 19 18:44 wrfchemi_12z_d01

If it's failed then work out where it and re-submit pre.bash from the run directory (you can make a copy and run it from where it failed by deleting the earlier steps which worked).