UKCA Emissions Discussion & Proposed Changes

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Background

The Design Document (Appendix 1) outlines 2 deficiencies in the current handling of emissions in UKCA, namely:

1. No check whether a particular file/field is duplicated
2. Restriction in combining interactive and prescribed BVOC emissions

Proposed Changes

For point 1. above, it was proposed that a duplicate check be added to the model by default (and *without* adding a new logical), whereby each file would have a *tracking_id* attribute, which would be unique to each file. The model would simply check that all the *tracking_id*s are unique and fail cleanly if not.

The *tracking_id* should be incorporated into emissions processing software. Although there would be benefits to having the *tracking_id* human readable, this should not be the case – *tracking_id* is part of the cf-standard and must be produced using the python uuid package. Backwards compatibility could be achieved for pre-existing files (e.g. CMIP6) by only checking if the field exists in the files metadata. If it doesn't exist, the file could be allowed by default.

For point 2. above, it was proposed to remove the current restriction such that prescribed and interactive emissions can be combined for species like methanol and acetone. Instead of having a UM warning, it was proposed that there be a pop-up warning from Rose when the coupling between iBVOC and UKCA is activated, so that users are prompted to remove the prescribed biogenic emissions file to avoid duplication.

Although fire emissions weren't discussed explicitly, if the recommendation is to remove the above restriction for biogenics, then it follows that no such restriction should be put in place for fire emissions although a similar pop-up warning would be desirable (when switching from prescribed fire emissions to interactive emissions).

Two other issues were also raised during the discussion:

3. NVOC/MeOH emissions
4. Biomass burning emissions

In relation to point 3., it was agreed that the use of the named NVOC file isn't very transparent and the user ought to be able to prescribe an MeOH file directly. We propose that users ought to be able to prescribe either an MeOH or an NVOC file in the near-term, but with a view to converging on all emissions files being species-specific in the longer term i.e. removing the use of the NVOC file. This would need to be done in such a way as to not break UKESM1, which uses the NVOC file with the meoh_factor.

For point 4. above, it was proposed to keep biomass burning files as 3D (not 4D due to size) but to add new capability to distribute them in the vertical if required/desirable. This could be defined in the code and activated through metadata. It could also allow for the future incorporation of a plume rise model.

Actions:

1. Mohit to open UM ticket for resolving NVOC/MeOH issue
2. Ashok to identify how vertical distribution of biomass burning emissions in handled in ACCESS

3. Fiona to make CMG aware of these proposed changes before any further action is taken

APPENDIX 1

Design Document

An enhancement of UKCA emissions with source/sector information

Version-1.0

Background

The UKCA NetCDF emissions processing system currently allows for emission values feeding to a given tracer to be split over any number of files. The critical attribute that governs this functionality is the *tracer_name* attribute in the NetCDF emission files. This is translated into the *emitted_tracer* attribute which is present for all the emission fields in the model. Thus, any emission data variables possessing attribute with value *emitted_tracer='X'* are added to the X chemical tracer in the model.

This leads to the following deficiencies in the current system:

1. There is no check in the system that a particular file or field is duplicated[#]
2. There is no check that a specified (fixed/ file based) emission field is being used at the same time as an interactive field for the same source. E.g. isoprene, acetone, monoterpene, methanol, NOx from soil, CH4 (wetlands, other terrestrial sources) etc..

#: Actually, this is a serious deficiency (confirmed by a simple test with same the file added twice to the ukca_em namelist item) and should be fixed immediately, irrespective of the source/ sector enhancement.

The issue at (2) currently has a work around such that certain species like Isoprene and Monoterpene permit only one type of source i.e. either *specified* (file) or *interactive*. However, for acetone and methanol, only *specified* values are permitted. It means that we cannot use interactive emissions from JULES (although available) in combination with prescribed anthropogenic emissions, for example. This is a limitation of the work around applied.

A similar potential problem will arise when interactive fire emissions are possible with INFERNO and coupled to UKCA (coming soon!) and will need to be combined with prescribed anthropogenic emissions. Without any checks, there's the potential for duplicating emissions but any workaround like that implemented for isoprene and monoterpene will present the same drawbacks as for acetone and methanol.

Hence, there is a need for the emission processing system to be improved such that it can handle multiple sources of emission for a given chemical field, with adequate checks to detect and prevent any duplication. At the same time, we recognise that flexibility is important.

Proposed Design Details

1. Emission fields – *offline (file-based)* as well as *online (interactive, or from other parts of model*) will have a new attribute e.g. *source_sector.*
2. Each of the emission species (i.e. tracers that need emissions) for that chemistry scheme will have a new attribute *l_check_sources,* which would be TRUE for species that have a likelihood of duplication.
3. Currently, to avoid adding more complexity to the Run_ukca namelist, the *l_check_sources* value will be hardwired in the code, again based on prior judgement regarding which of the species is likely to have this duplication.

4. For backward compatibility, the *source_sector* attribute will be an optional feature unless the *l_check_sources* is set to TRUE. For the same reason, the latter logical will be set to FALSE for all species by default.
5. If *l_check_sources* is set to TRUE for any species/ tracer then ALL emission fields (offline, online) feeding into that species/ tracer need to have the *source_sector* attribute specified.
6. Only a specified subset of *source_sector* values will be permitted, to avoid multiple or slightly varying descriptions of the same source (see below for proposed values).
7. During the initial stage of emissions processing -e.g. in *ukca_emiss_init*, after all files and fields have been looped through and attributes populated- extra code will be required to:
    - Loop over all the emission species/ tracers and find a tracer that requires source checks (*l_check_sources=TRUE)*
    - Loop over all emission fields and find those that feed into that tracer (*emitted_tracer=X)*
    - Temporarily store the *source_sector* values from these emission fields and check whether any value appears twice
    - If so, flag up an error, highlighting the tracer involved
    - Ideally, loop over all the tracers and perform this check, giving information on all duplicate sources *before aborting the model*

Emission Diagnostics

Once a standard set of source/ sectors is established, it would be possible to diagnose the contribution from each source to a given species, of course via addition of new diagnostics to Stash.

Exceptions/ complications

- Values of oceanic DMS, Chlorophyll-a and even iBVOCs, are actually passed to emissions processing from other parts of the model (Ancil reading/ Ocean model via STASH for former and via a module from JULES for the latter). The DMS/Chl-a fields do not have any indication if they are from Ancil or Ocean, while the presence of iBVOCs is dependent on logicals (both UKCA and JULES side). Some thought will be needed to allocate the *source_sector* attribute in a sensible way for these.
- Only the BC and OC GLOMAP-Mode emissions actually feed directly into aerosol tracers as mass. (Seasalt is also populated directly but does not have any specified source). The rest of the aerosol tracers are populated indirectly, with all the emission fields feeding into these currently labelled as ‘online’. Allocation of *source_sector* values to these will also need to be considered carefully.

Proposed values for *source_sector*

Note: ter = Terrestrial, oce = Oceanic

Option – A = Grouped:

ter-anthro (e.g. industrial, transport, biofuel, agri, crop burn-off, etc)

t*er-biogen* (e.g. vegetation, soil, wetlands),

ter-fires (natural fires)

oce-anthro (mostly shipping)

oce-biogen (DMS and Chl-a conc, isoprene?, acetone?, NH3)

Option – B: Partitioned:

ter-indus, ter-transp, ter-biofuel, ter-agri, ter-anthro-biomass

ter-vege, ter-soil-nat, ter-wetland,

ter-fire-nat, ter-fire-anthro

oce-ship, oce-vege,

oce-nat (e.g. CH4 from hydrates)

The 'Grouped' nomenclature would be useful when only combined data from different sources is available for emissions. This would not force the users to specify a 'partitioned' name even though enough information on source is not available.

On the other hand, use of 'Grouped' nomenclature would force the combining of different data to fit the categories even if source-wise details are available.