

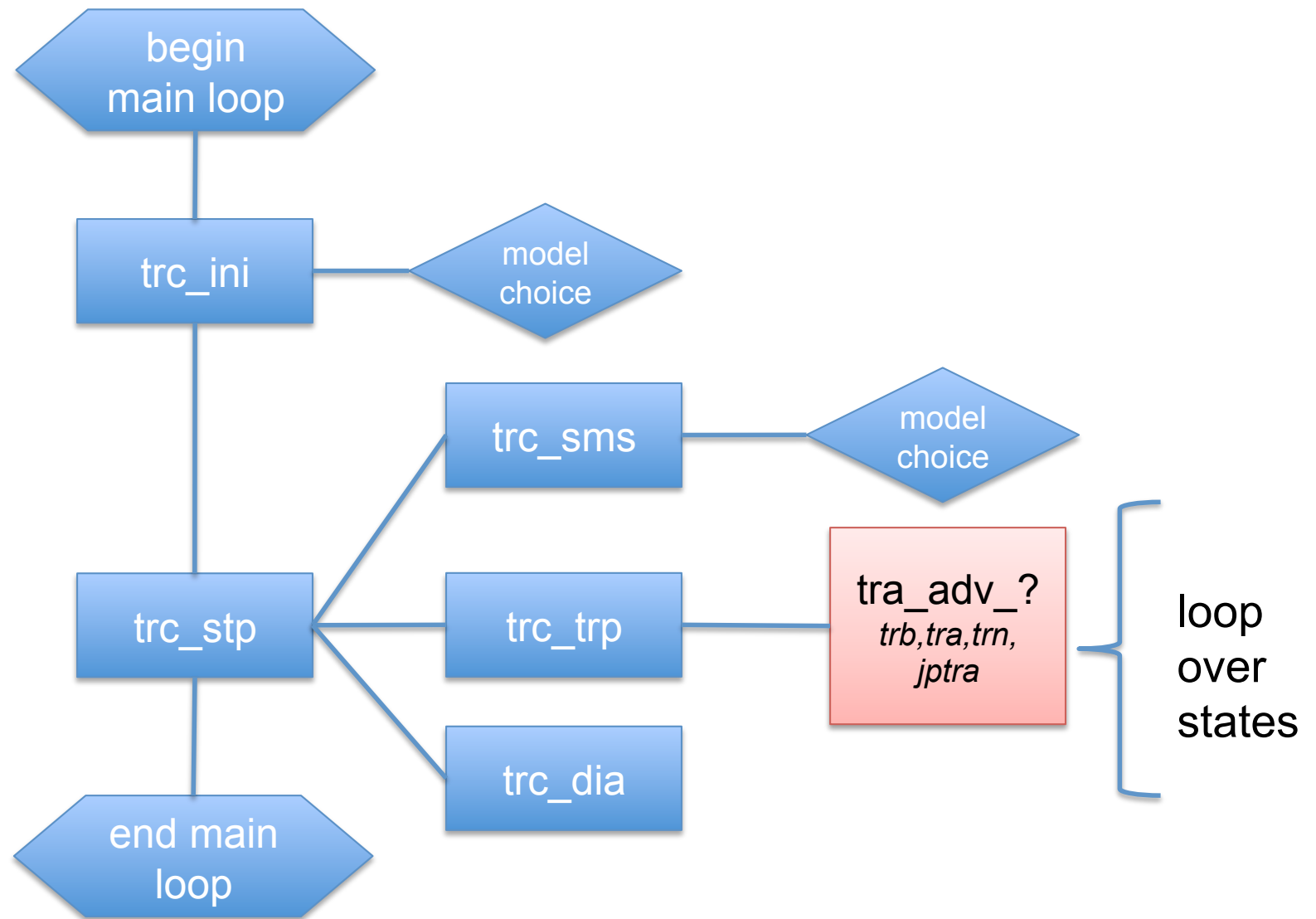
Extending TOP interface (Marcello Vichi, CMCC)

- <http://forge.ipsl.jussieu.fr/nemo/wiki/ticket/846>
- Interface for other biogeochemical/ecosystem models that have a a complex structure and separate development cycle
- ERSEM-like models (BFM, PML-ERSEM)
 - more realms (pelagic, benthic, sea ice ecosystems)
 - several components and constituents
 - autonomous output handling
- Allows for a generic treatment of boundary processes for the biogeochemical state variables
 - Surface (nutrient deposition)
 - Lateral (open boundaries; rivers)

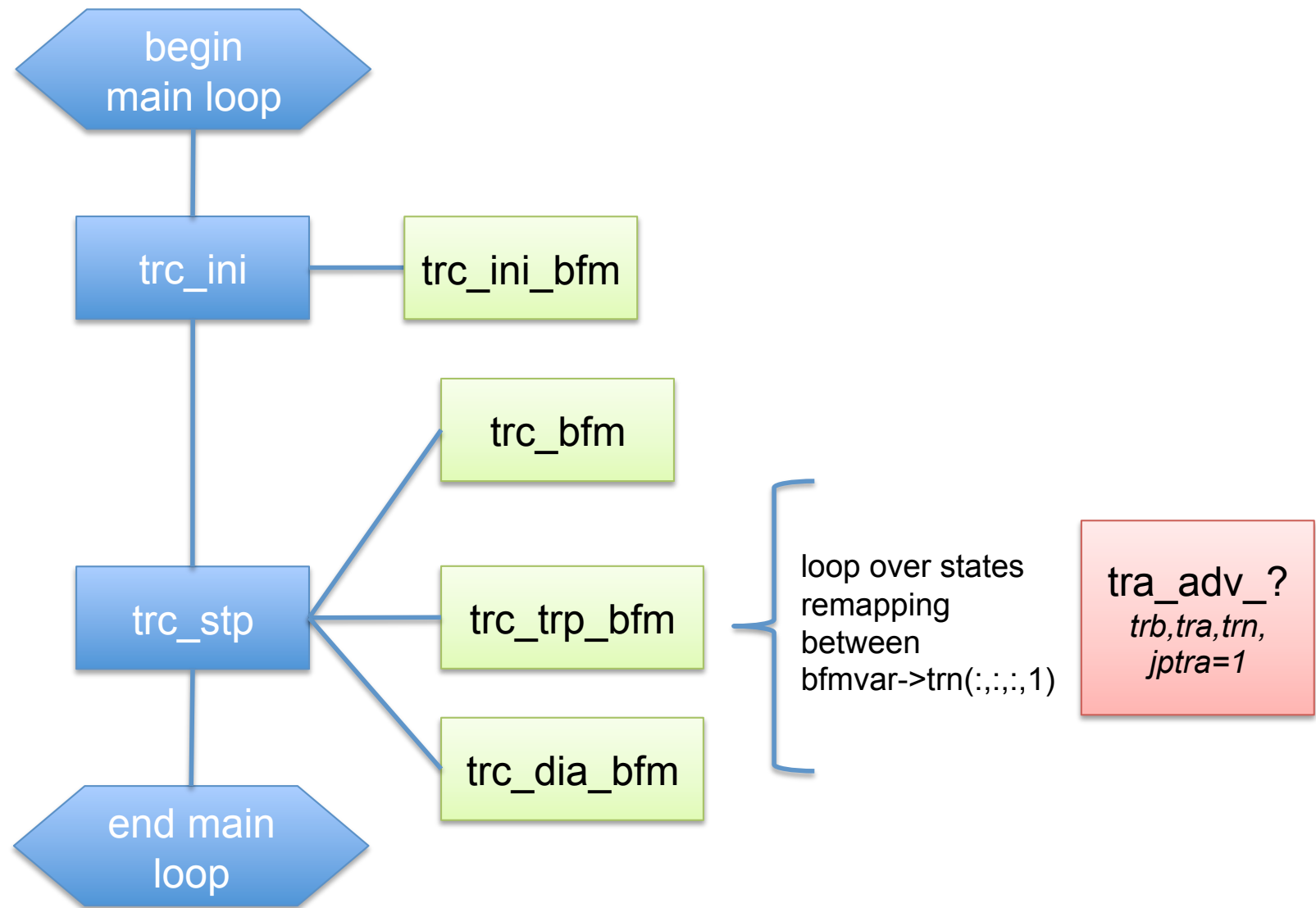
Issues

- more a matter of memory layout and variable handling than of coupling
- 2 different methods
 - BGC state variables are part of the NEMO memory (trn, tra, 1:jptr) and loops over state variables are usually included inside the functional routines (advection, diffusion, etc.)
 - BGS state variables have separated memory (with different dimensions) and they are mapped . Loops are outside

The current TOP interface



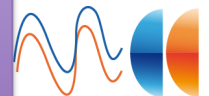
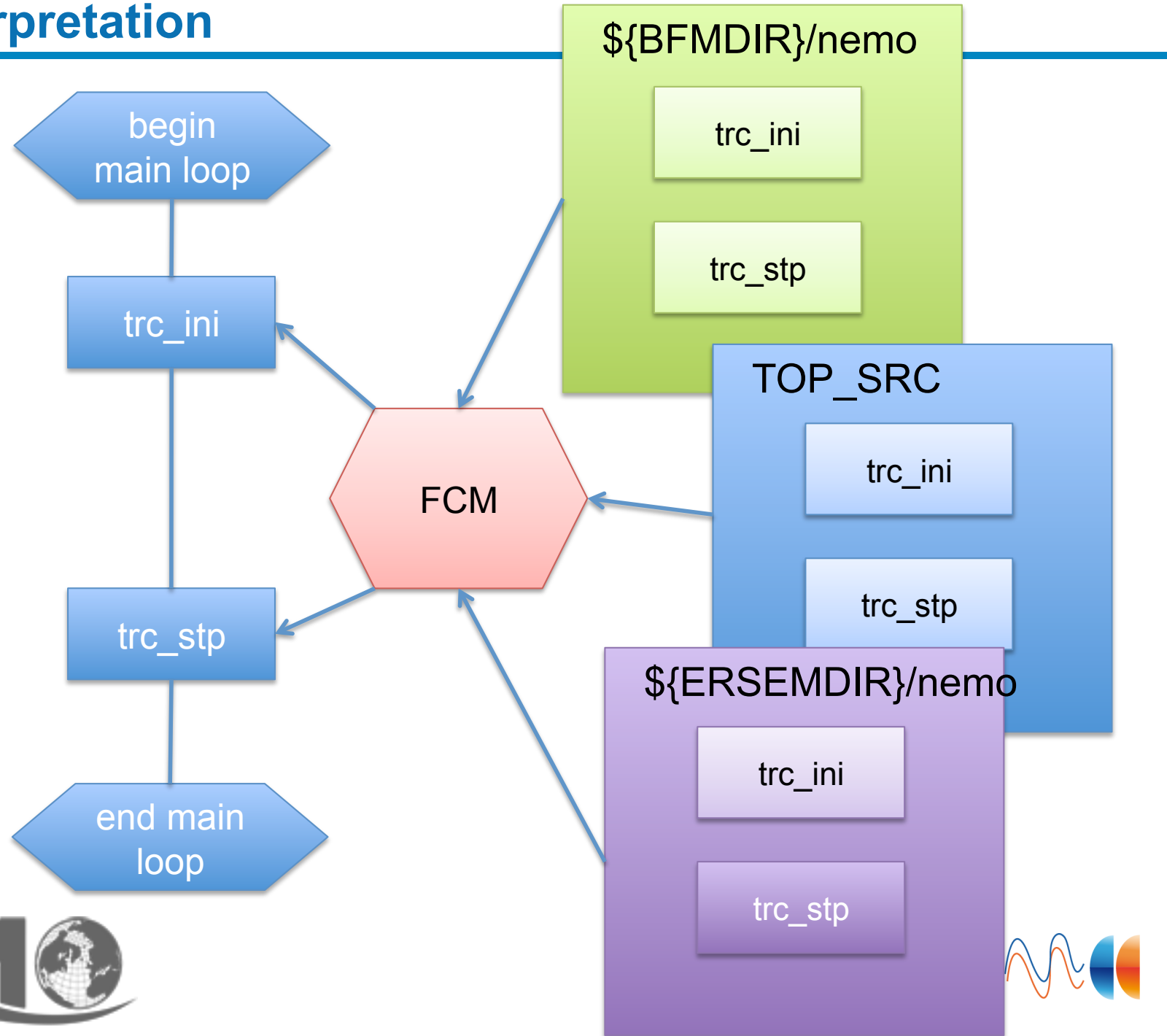
The current BFM interface



Christian's proposal

- To use FCM for providing the appropriate `trc_ini` and `trc_stp` subroutines in place of the standard ones
- The perfect solution!
- My comment on the wiki: The way we handle the coupling with the BFM now is to have a directory called `nemo` within the BFM tree that contains all needed routines. In our case, This directory is exactly what should go into `MY_SRC`. Extending on this method, the solution would be to totally substitute the main calling routines (`trcstp` and `trctrp`) with modified copies that will be maintained by each group in the tree of the biological model. In that case, I think we should be able to fit into the `MY_TRC` layout easily. As far as I can understand, FCM should consider the content of `MY_SRC` directory in place of the files with the same names in the `WORK` directory. My only concern is whether FCM can eventually put the content of an external directory into `MY_SRC`, without the need to do it manually.

My interpretation



Beyond...

- Provide generic interfaces for boundary conditions where state variables are accessed through interface arguments (just like advection, diffusion, etc.)

`trc_river_input(trn,tra,jptra,additional arguments)`

`trc_sbc_input(trn,tra,jptra,additional arguments)`

`trc_bbc_input(trn,tra,jptra,additional arguments)`
(for benthic nutrient flows)

