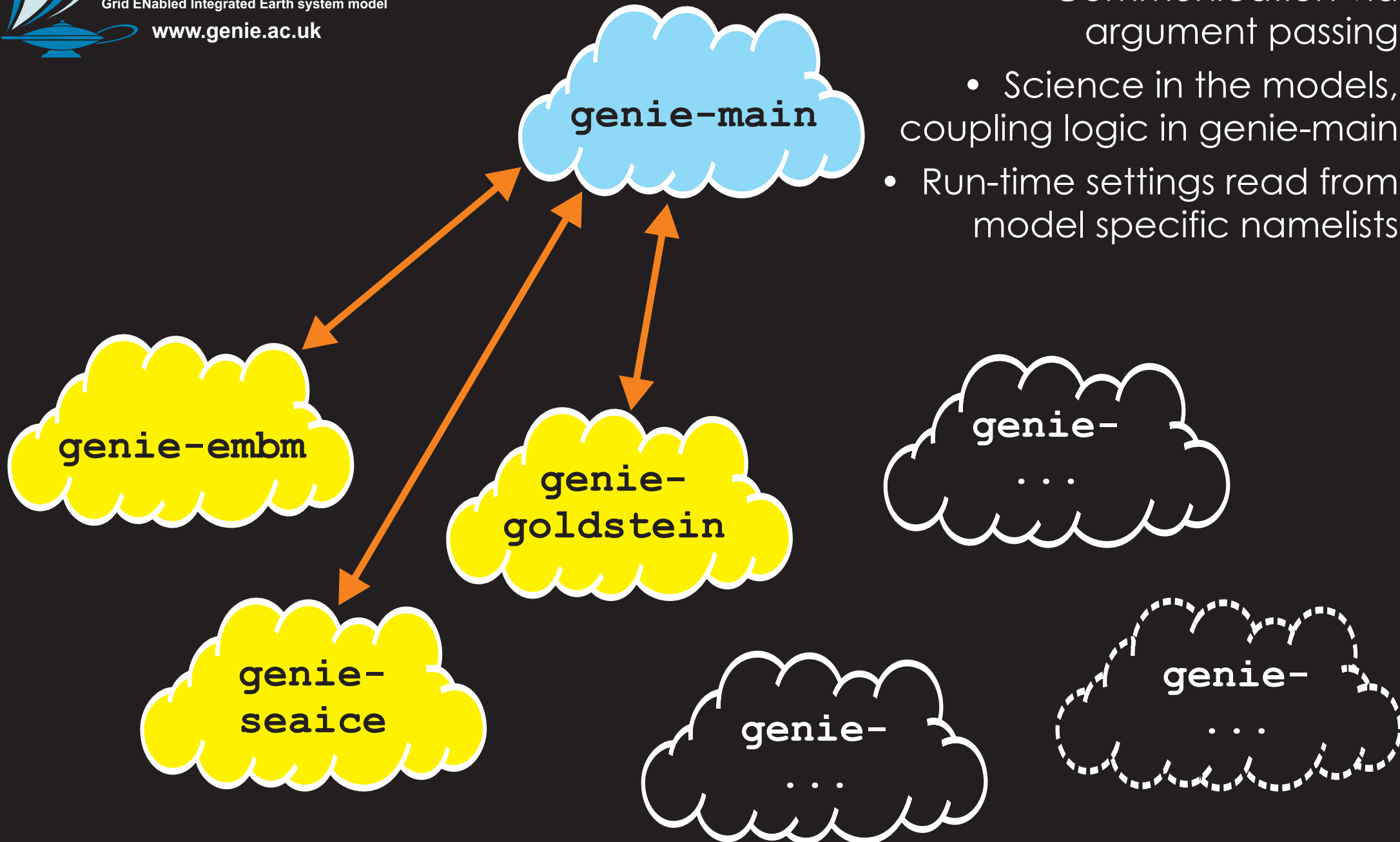


Andy Ridgwell (andy@seao2.org)

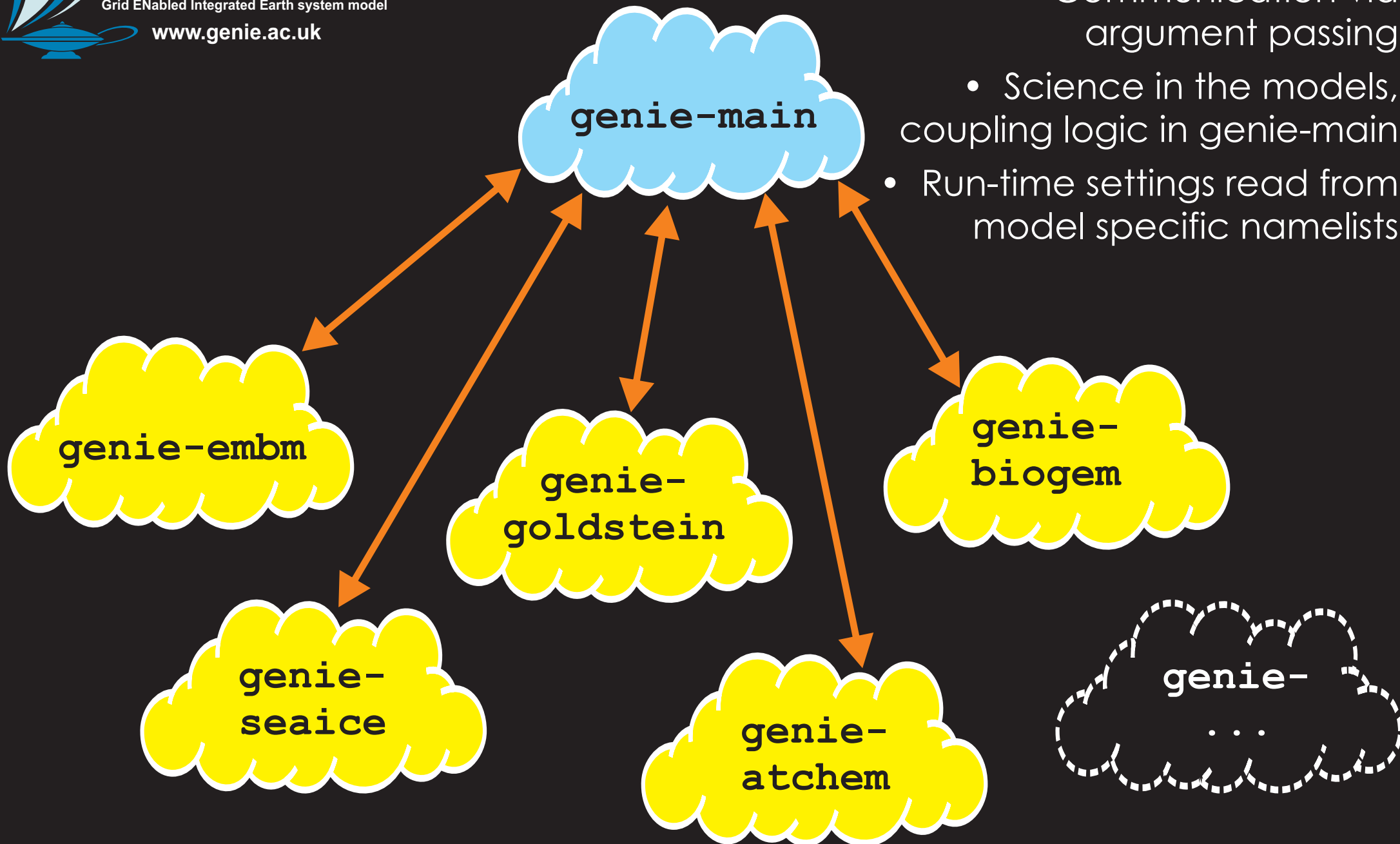
Modular, Hierarchical

- Communication via argument passing
- Science in the models, coupling logic in genie-main
- Run-time settings read from model specific namelists



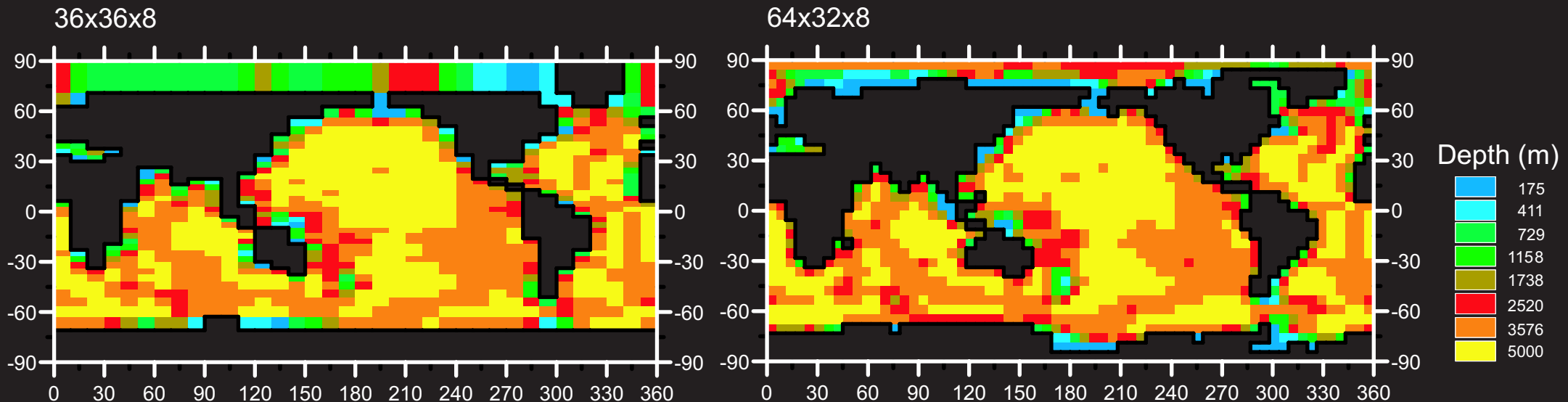
Modular, Hierarchical

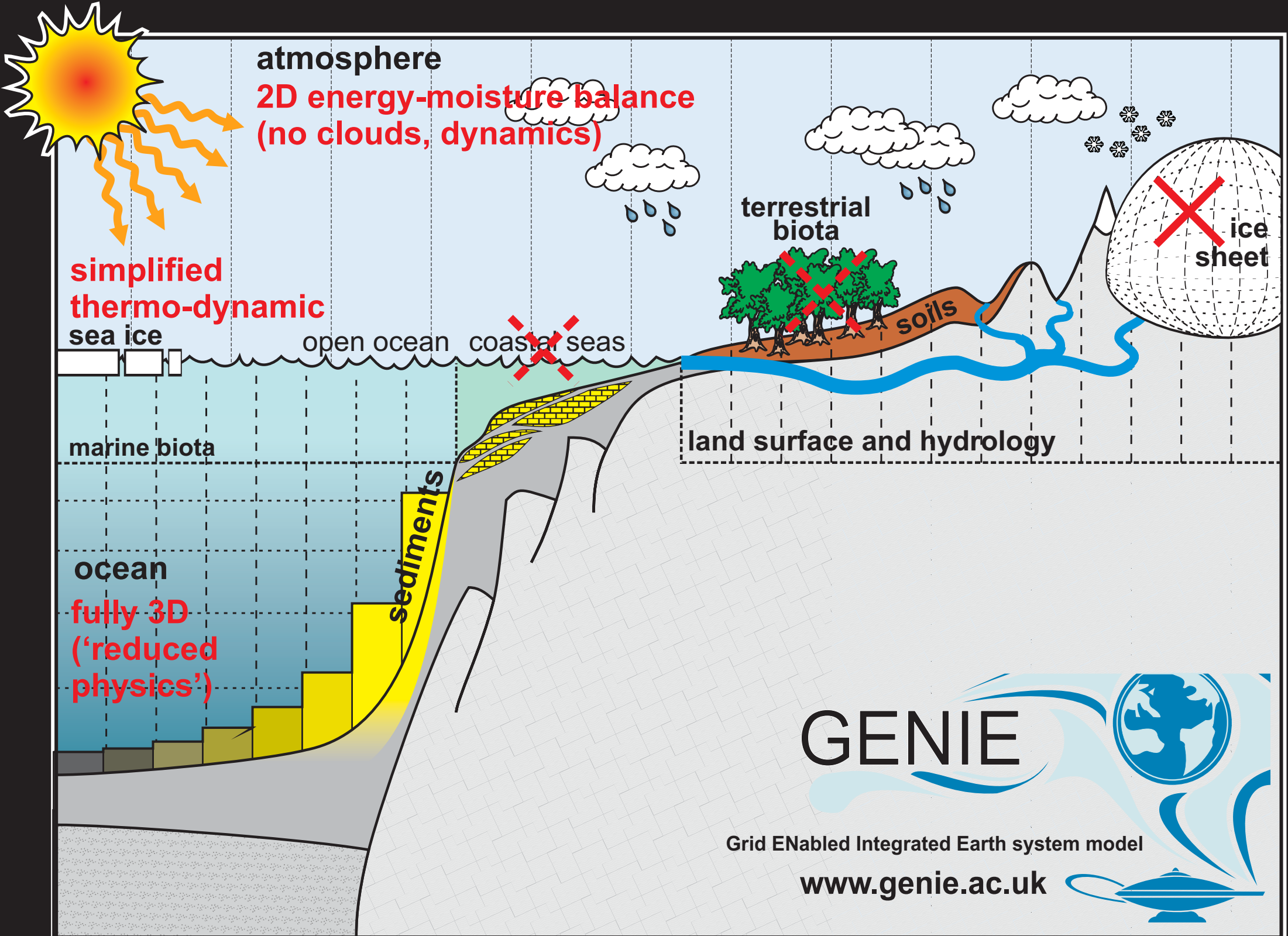
- Communication via argument passing
- Science in the models, coupling logic in genie-main
- Run-time settings read from model specific namelists



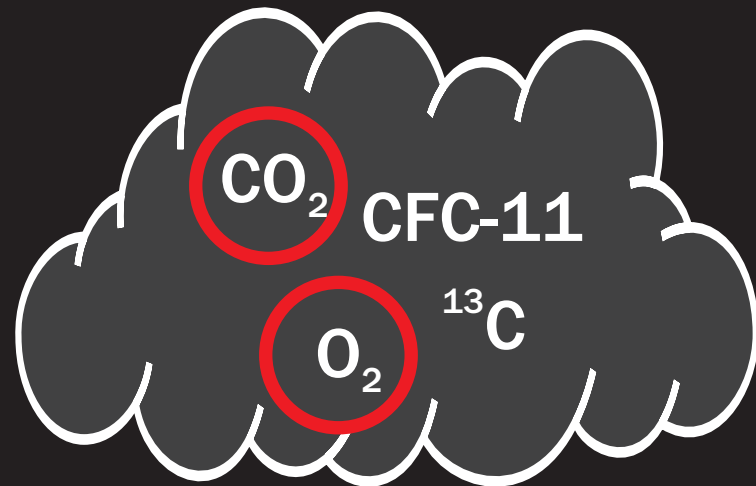
GENIE configuration

Model		Longitude cells res.		Longitude cells res.		Vertical levels
Ocean GOLDSTEIN	⊗	36	10°	36	$\sin(\pi/36)$	8
		72	5°	72	$\sin(\pi/72)$	16
		64	5.625°	32	5.625°	8
		72	10°	60	3°	8
Atmosphere 2-D EMBM	⊗	36	10°	36	$\sin(\pi/36)$	1
		72	5°	72	$\sin(\pi/72)$	1
		64	5.625°	32	5.625°	1
		72	10°	60	3°	1
Atmosphere 3-D IGCM	⊗	64	5.625°	32	5.625°	7

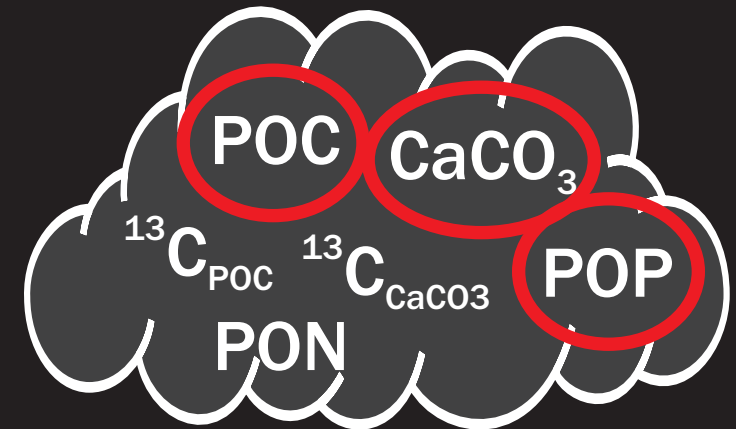




atmospheric tracers (gases)



biogeochemistry
solid tracers (particulates)



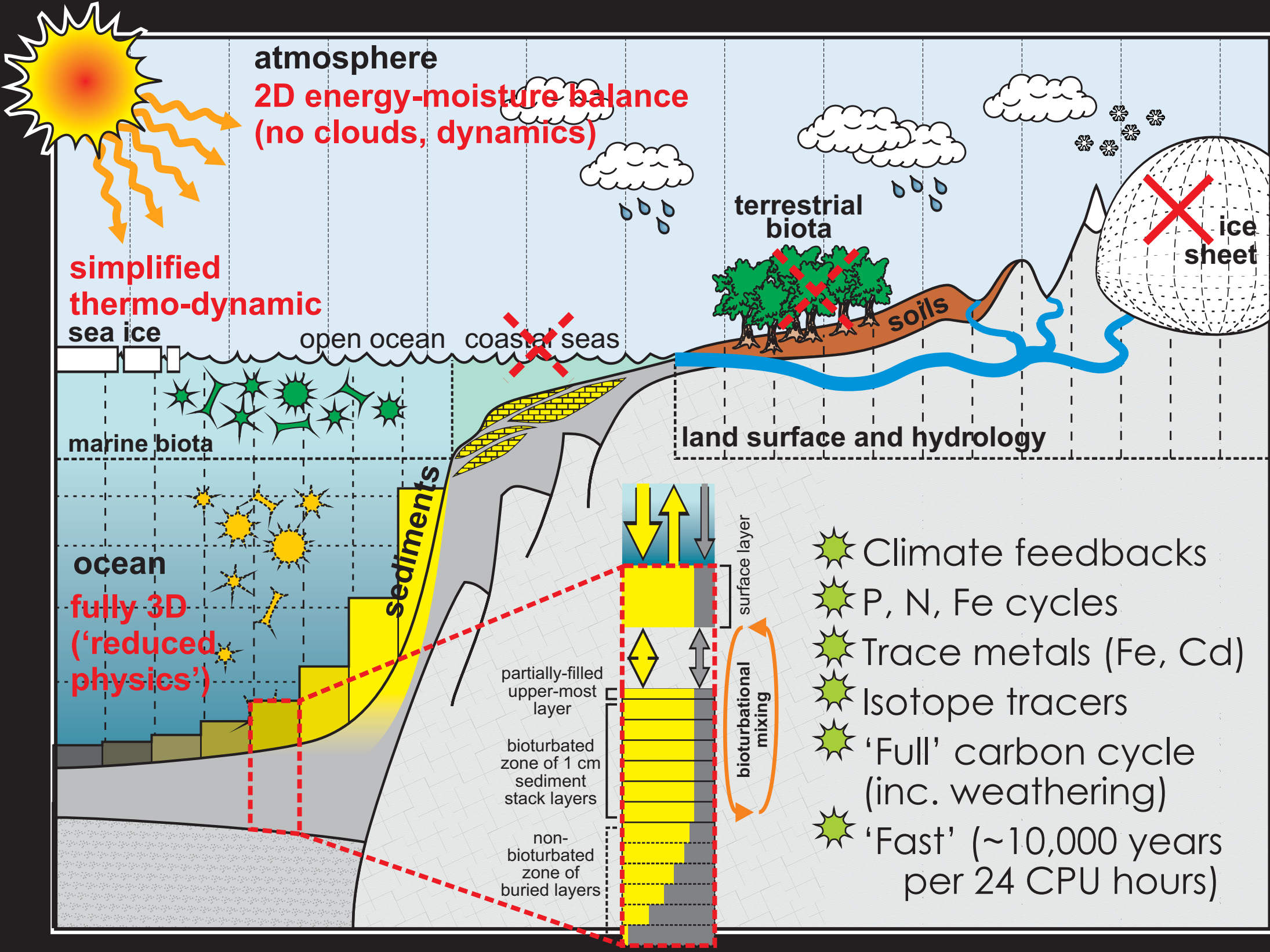
solubility coefficient
Schmidt number

**PRE-DEFINED
RELATIONSHIPS**

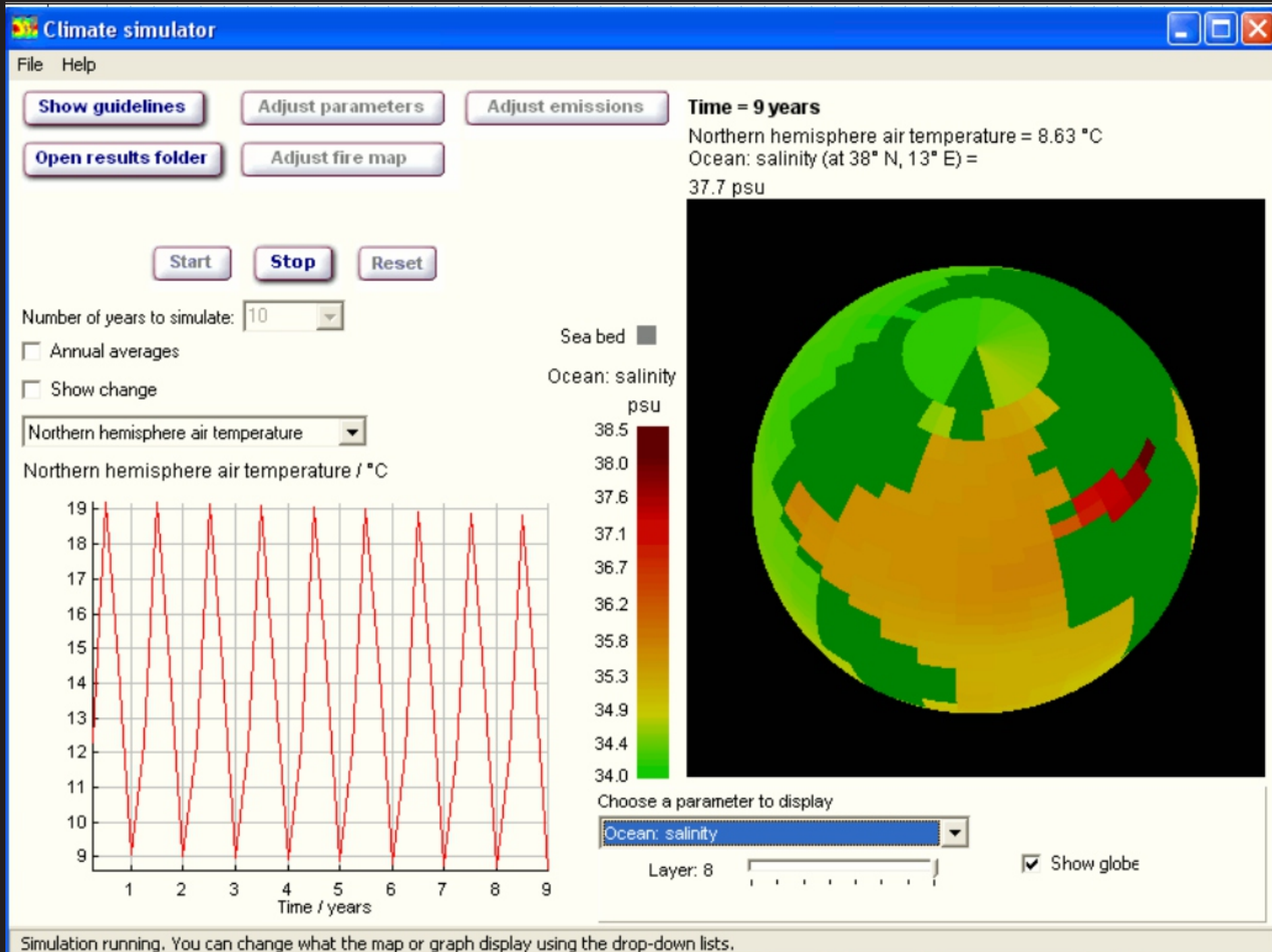
e.g., Redfield ratios



dissolved tracers



cGENIE



cGENIE

! running GENIE

```
./old_rungenie.sh #1 #2 #3 #4 (#5)
```

parameter #1: '*base config*' (e.g., cgenie_eb_go_gs_ac_bg)

parameter #2: '*user config*' directory (e.g., LABS)

parameter #3: '*user config*' file (e.g., exp1_modern)

parameter #4: experiment duration (e.g., 11)

parameter #5: restart experiment name and path (e.g.,
~/genie_output/exp0_spinup)

cGENIE

! directory issues

cGENIE via `runcgenie.sh` **and** `make cleanall` **are run from**
`~/genie/genie-main`

You can change to `~/genie/genie-main` **from** `~`, **either**
incrementally:

```
cd genie  
cd genie-main
```

or directly:

```
cd genie/genie-main  
(or cd ~/genie/genie-main)
```

Return with `cd` **on its own.**

! directory viewing

Don't forget – the RH panel (the remote file system) in the SSH File Transfer Window does not automatically refresh the listing (and hence new experiment directories will be invisible until you refresh).

cGENIE

! make cleanall

This needs to be run only when the continental configuration, resolution of the ocean model, or number of 'tracers' in the ocean have been changed. (You will be advised when this is essential.)

BUT NOTE: If you have carried out a `make cleanall`, BEFORE you can submit an experiment to the cluster the model must be re-compiled – i.e., simply run the model interactively for a few years. Note that it is 'good practice' that when creating a completely new sort of model experiment (i.e., not just simply changing again a single parameter value), that you try running it for a few years interactively, as this will tell you immediately if there is something incorrectly set up in the experiment.

cGENIE

! experiment run length and results saving

By default: cGENIE saves time-slice (netCDF format) results at times centred on years:

0.5 1.5 4.5 9.5 19.5 49.5 99.5 199.5 ...

(a similar pseudo-log sequence is used for time-series saving)

Hence, to capture the final state of the model at the end of an experiment, the experiment length has to be one of:

1 2 5 10 20 50 100 200 ...

as the time-slices are annual averages by default (and saved at the mid-point of the average).

The default time-points for time-slice saving can be changed (via a simple text file), found in `~/cgenie/genie-biogem/data/input` and called: `save_timeslice.dat`

(for time-series saving, the file is called: `save_timeseries.dat`)

cGENIE

! editing experiments

Simply: edit the *user config* text file, and save!

! creating new experiments

Is as simple as copying a pre-existing (and presumably similar) *user config file* and giving it a different name.

Either:

```
cp exp1file exp2file
```

```
cp snowball_x10co2 snowball_x20co2
```

!(then edit it) or, all within Windoz:

Using the file transfer client:

(1) transfer a *user config* file to your local PC (or remote UoB file-space),

(2) rename it

(3) transfer it back

(then edit it)