

# A Hitchhikers Guide to the Black Arts (of Earth system modelling)

## **PART #0000: modeling basics & experiments in climate hysteresis**

Stuff to keep in mind:

- cGENIE is a model. Models ARE NOT the 'real World'. (Don't get confused!)
- The very low (for a 3-D ocean circulation model) resolution of cGENIE limits its applicability to very short time-scales, and because the simplified atmospheric component cannot calculate winds, there is no atmospheric dynamics or inter-annual variability.
- cGENIE is best thought of as a 'discovery and exploring' tool for learning how the Earth system works rather than a detailed 'simulation' tool.
- Have fun (or at least try) ☺

Relevant reading:

(1) Primary model description + evaluation/discussion papers:

Edwards and Marsh [2005] (*Climate Dynamics* 24, 415-433)

→ description and calibration of the climate model component of (c)GENIE

Hargreaves *et al.* [2004] (*Climate Dynamics* 23, 745-760)

→ description of data assimilation methodology and calibrated climatology of the climate model

Ridgwell *et al.* [2007a] (*Biogeosciences* 4, 87-104)

→ description of basic ocean carbon cycle and its calibration against observations

Ridgwell *et al.* [2007b] (*Biogeosciences* 4, 481-492)

→ description of the calibration and application of the pH-responsive pelagic calcification

Ridgwell and Hargreaves [2007] (*Global Biogeochemical Cycles* 21, doi:10.1029/2006GB002764)

→ description and calibration of the sediment model component and response to fossil CO<sub>2</sub> release

(2) Some potted model applications (mostly paleo):

Chikamoto *et al.* [2008] (*JGR* 113, doi:10.1029/2007JG000666)

→ deep-sea CaCO<sub>3</sub> sediment and atmospheric CO<sub>2</sub> response to AMOC shutdown

Panchuk *et al.* [2008] (*Geology* 36, 315-318)

→ configuration of (c)GENIE for Palaeogene marine carbon cycling; assessing PETM CO<sub>2</sub> release

Ridgwell [2007] (*Paleoceanography* 22, doi:10.1029/2006PA001372)

→ description of sediment core modelling; application to the interpretation of PETM CCD changes

Singaraye *et al.* [2008] (*GRL* 35, doi:10.1029/2008GL034074)

→ analysis of ocean circulation and atmospheric radiocarbon variability during the Younger Dryas

(3) Snowball Earth and ice-albedo feedback & hysteresis

Hoffman and Schrag [2002] (*Terra Nova* 14, 129-155)

→ Snowball review.

Hyde *et al.* [2000] (*Nature* 405, 425-429)

→ Model analysis of the inception of a snowball Earth and ice-albedo thresholds.

**This document, plus the details of subsequent workshop exercises/activities can be downloaded from:**

<http://www.seao2.info/mycgenie.html>

under 'cGENIE resources: TEACHING LABS [CURRENT]'

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## 0. Before anything else ...

- 0.0 For some of you, the mechanics of running the model will be about as much fun as sticking your tongue in an electrical outlet (a popular hobby in England). (*However, if you are an experienced linux/unix/tounge-in-electrical-socket user, you can skip on to **Section 0.1.***)

cGENIE has traditionally been configured and accessed at the 'command line' of the linux (or Mac equivalent) operating system. The command line is a place where you type text and when you press Return, something (hopefully, good!) happens. Typically the stuff you type started with a 'Command' word, and often followed by one or more options and parameters. The Command word and any options / parameters MUST be separated by SPACES.

The command line is indicated with something like: \$. The \$ is called the 'prompt' and is 'prompting' you to type some input (Commands, swear words, etc.). See – the computer is just sat there waiting for you to command it to go do something (stupid?!). Often, you will also be informed (reminded) of the username and computer name and current directory at the prompt, e.g.:

```
[username@marble ~]$
```

Which in this example is user 'username' (yours will be different) on computer 'marble' and the current directory is the 'home' directory (~).

If you are not or not very familiar with the linux/unix command line – Appendix 1 contains a quick summary of some of the more important/useful Commands you can use at the command line.

NOTE: In the following practical class instructions, example lines to be typed at the command line are highlighted in yellow (or grey when photocopied ...). Be VERY CAREFUL that spaces are not missed out. Also be careful not to confuse the number one (1) for the letter el (l). Misspelling/typing will probably be the primary reason for any wailing and gnashing of teeth ...

NOTE-the-second: Text highlighted in grey represents instructions specific to using Windoz PCs, and hence may or will differ on different computers and/or under operating systems, e.g. if you have a Macbook. Other software choices for editing files or viewing results are possible as are other ways of configuring software and file editing/transferring methodologies.

**Do what suits you best -- the instructions simply represent an example methodology.**

- 0.1 Some warnings and reminders are repeated over and over and over and ... over again. Some warnings and reminders are repeated over and over and over and ... over again. This is because you will forget immediately each time! ;)
- 0.2 Additional documentation (of varying degrees of up-to-date-ness) lives in the `cgenie.muffin/genie-docs` directory, as well as on the interweb (<http://www.seao2.info/mycgenie.html>) and under: 'cGENIE resources: DOCUMENTATION', and 'Pre-release 'muffin' version of cGENIE'. The documents are:
- (i) The *cGENIE User Manual* (the least up-to-date of all!) [`cGENIE.muffin.User_manual.pdf`]
  - (ii) A set of *Examples* [`cGENIE.muffin.Examples.pdf`]
  - (iii) A *HOW-TO* (potted explanations of how to get useful stuff done) [`cGENIE.muffin.HOWTO.pdf`]
  - (iv) A table of model parameters [`cGENIE.muffin.Parameter_reference_guide.pdf`]
  - (v) A Guide to installing cGENIE [`cGENIE.muffin.QuickStartGuide.pdf`]
  - (vi) A README that will inevitably remain un-read ... [`cGENIE.muffin.README.pdf`]
- 0.3 **Note that you will be using the development branch of the model and a 'pre-release' version, code-named 'muffin' (if Apple can have 'Leopard', 'Lion' etc., I can have baked goods, right?). The documentation may not be fully consistent in this respect ... and you may need to translate occurrences of e.g. a directory named 'cgenie' to 'cgenie.muffin'. Also note that the instructions in general may not be bug-free – use your judgment,**
- 0.4 **OK – now we are ready to start ...**

## 1. Starting (dozing?) off ...

1.0 You are going to be installing the model from scratch – why? Why not? Hell, it saves me installing it a dozen times. Actually, it will be a happy character-building experience for you – trust me.

1.1 Having logged into the PC terminal, log in to the account that has been created for you on the `marble` computing cluster. To do this – first start the SSH Secure Shell program (you can find this via the All Programs menu tree from the Start icon in Windoz). Run the Secure Shell Client (rather than the Secure File Transfer Client) to start off.

Click on the Quick Connect icon in the main Secure Shell Client window. A 'Connect to Remote Host' dialogue box will appear. In the first box, 'Host Name', enter:

```
marble.ggy.bris.ac.uk
```

and your computing cluster user-name on the line below this ('User Name').

When (and only when) you click on the Connect button will you be asked for your password in a new dialogue window that will appear.

You should now have a dull, blank-look window with the command prompt (\$) (see previous page).

For displaying directory contents and transferring model results files we are going to be using the SSH file transfer program. One of the icons towards the middle of the icon bar in the SSH terminal window you have opened is called 'New File Transfer Window' (it should be the 2<sup>nd</sup> icon to the right of the search (binoculars) icon). Click on this to open a file transfer window.

Or: Again from the All Programs menu tree of Windoz Start, select Secure File Transfer Client ('SSH').

You should now have TWO windows open – a 'shell' window (lines of text on an otherwise blank screen) and a file manager (transfer) window. Ensure that you have both these before moving on. It is recommended that you maximize both these windows to full screen. (But no-one will die horribly for not doing so. Probably ...).

1.2 The next step is to download a copy of the source code for the cGENIE model as follows (all this is done in the shell window of your `marble` computer account):

(i) To get a copy of cGENIE: from your home directory type:

```
$ svn co  
https://svn.ggy.bris.ac.uk/subversion/genie/branches/cgenie.GEOGM1xxx.2013  
--username=genie-user cgenie.muffin
```

All this must be on a continuous line, with a S P A C E before '--username', and before `cgenie.muffin`.

(If you get asked about a 'certificate' – enter 'p' to accept 'permanently'.)

Depending on the weather and phase of the moon, you may (or may not!) be asked for a password. If so – it is: `g3n1e-user`. Again – don't mix up the ONE ('1') with an 'el' ('l'). (The mystery character in question is a 'one' if you must know ...)

Some of the files that are installed are quite large, and at times, it may appear like it is 'stuck'. Be patient! Installation should be complete within about 2-3 minutes (longer if everyone else is trying to do this at exactly the same time ...)

(ii) Change directory (see: Appendix I and also Figure 1.1) to `cgenie.muffin/genie-main` – if you are not 'linux-friendly' – maybe at first do this in steps – list the contents of the directory (`ls`) to check where you are, then change to `cgenie.muffin` (`cd cgenie.muffin`), then list again (`ls`), then change to `genie-main` (`cd genie-main`), and then type:

```
$ make testbiogem
```

This compiles a carbon cycle enabled configuration of cGENIE and runs a short test, comparing the results against those of a pre-run experiment (also downloaded alongside the model source code). It serves to check that you have the software environment correctly configured.

There may be some 'Warnings' reported (== someone's sloppy programming) but these are not detrimental to the ultimate science results (we hope!). 'Success' of this test is indicated by:

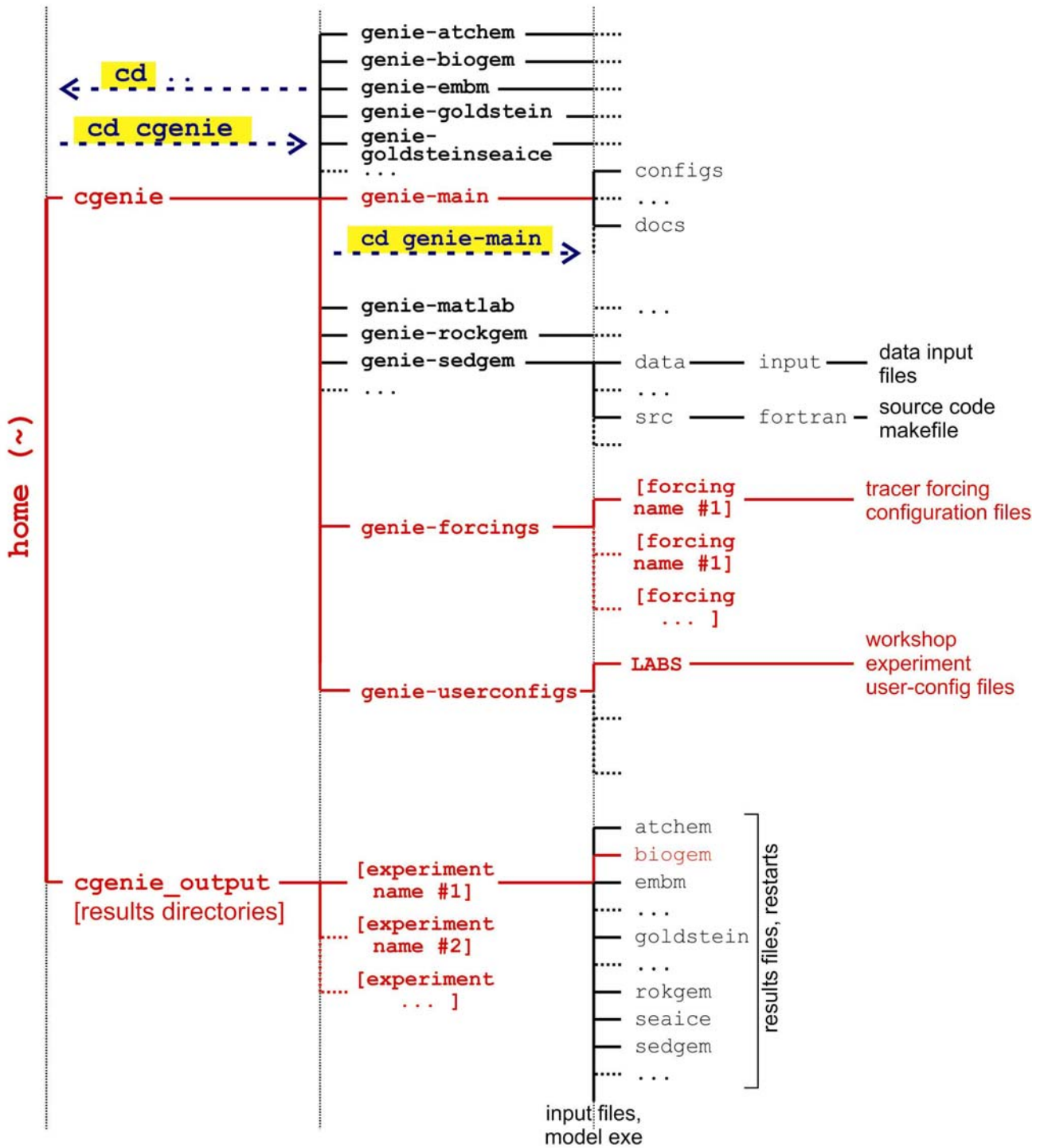
```
**TEST OK**
```

You can then be certain that the model you have installed is producing identical (within tolerance) results to everyone else in the World who has ever installed cGENIE. Note that the model will pause for a long time at the line: `./genie.job -t -k -f configs/eb_go_gs_ac_bg_test.xml -o /home/genie00/cgenie_output -c /home/genie00/cgenie -g ../../cgenie -m "" > testbiogem.out`; – this is quite 'normal' – the model is thinking!

**Ignore the compiler warnings ...** (reflecting my lack of adequate software engineering skills)

(iii) That is it as far basic installation goes.

- 1.3 Later on you will be editing some configuration files. So now might be a good time to check that you can use the editor! (You will also be using the same editor to view some of the model output.) You have two alternative options for editing and viewing text files, depending on whether you are a UNIX nerd with no life, or prefer anything to do with computers to be wrapped in cotton wool and covered with dollops of treacle.
- EITHER: Use the linux `vi` application (or similar) if you are familiar with it. I think that this pretty much sucks as a text editor and life is far too short and brutal ... so I will not \*make\* you ;)
- OR ... Use a suitable linux-friendly text editor (NOT Micro\$oft Notepad) in conjunction with the Secure File Transfer Client. For example: 'SciTE' <http://www.scintilla.org/SciTE.html> is suitable.
- To set SciTE to automatically open the model configuration files: in the Secure File Transfer Client – go to Edit, then Settings... and from the SECOND File Transfer section of the list in the left-hand panel (there are TWO File Transfer section entries and you are after the one near the bottom of the list), click on the button for If a file association is missing, use this application to open the file. Then from Program Files on the C drive of the Windoz machine, find the SciTE editor directory (called: Scintilla Text Editor) and its program executable inside (`SciTE.exe`). Click on OK to close the Settings dialogue box. Then under File in the main menu: Save Settings.
- It should now be possible to double-click on a file in the Secure File Transfer Client and it will open like magic (almost)! Try opening `runmuffin.sh` (directory: `cgenie/genie-main`) in this way. If you edit and save the file, you will be asked whether you want to transfer it back to the remote machine and also whether you want to over-write the original file. Simply click Yes to both.
- Note that Windoz Vista (and maybe subsequent operating system versions) may have alternative ideas and may ask that the `.res` filetype is associated in Windoz too. (Don't fight it – do what it says!)
- 1.4 Next, we are going to be going through how to run and analyze the results of the model, playing around with the 'snowball Earth' hypothesis and assessing the critical ice-albedo feedback in the climate system as an example.



**Figure 1.1 cGENIE model directory structure**

Directory structure of the cGENIE model. Highlighted in red are directories and sub-directories that you will need to access at some point. Note that the main 'cgenie' directory should read `cgenie.muffin ...`

## 2. Running the model ('interactively', in a shell window)

2.1 At the command-line (\$) in the `genie-main` directory (not your home directory), you will be entering in a command (`./runmuffin.sh`) together with a list of parameters that will be passed to the model, and as if by magic the model will run (or sometimes not):

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

You must list at least 4 parameters after `./runmuffin.sh`, separated by S P A C E S and on a single continuous line (even if it 'wraps' around across 2 lines of the screen).

These parameters are:

**#1** ... is the name of the required base (or 'basic') configuration ('*base-config*') of the model.

**#2** ... is the name of the subdirectory (if any) containing the user configuration ('*user-config*') file (i.e., the file containing the specification of a particular experiment).

**#3** ... is the name of the experiment itself. There must exist a file in the directory specified by parameter #2 (LABS) with exactly the same name as you enter here for parameter #3 (i.e. parameter #3 points to a file in the directory given by parameter #2).

**#4** ... is the run length of the experiment in years – this must be entered as an integer.

There is also one optional (5<sup>th</sup>) parameter.

2.2 As an example of running the cGENIE Earth system model:

parameter #1: The base config is: `cgenie.eb_go_gs_ac_bg.p0650e.NONE`

parameter #2: The user config directory is: `LABS`

parameter #3: The user config file (the experiment name) is: `LAB.0000.snowball`

parameter #4: Run the experiment for ten years: `10`

parameter #5: (There is no *restart* file, and so no 5<sup>th</sup> parameter needs to be passed ...)

The full command, which you are going to issue from the `~/cgenie.muffin/genie-main` directory, looks like:

```
$ ./runmuffin.sh cgenie.eb_go_gs_ac_bg.p0650e.NONE LABS LAB.0000.snowball 10
```

REMEMBER: This must be entered on a single CONTINUOUS LINE. The (single) S P A C E S are vital. Take care not to confuse an el ('l') with a one ('1') when typing this in ... (it is a 'one' here).

2.3 What should happen is: First, you will end up twiddling your thumbs a while, as all the components of cGENIE are compiled from the raw source code (FORTRAN). When it has finished doing this, the model will initialize and carry out some brief self-checking. Only then will it start actually 'running' and doing something, starting with a header describing the columns of numbers that follow:

model year – (Guess!)

ice(%) – global sea-ice fraction (%)

<SST> – global sea surface temperature 'SST' (°C)

<SSS> – global sea surface salinity 'SSS' (‰)

The choice of what information to display on screen as the model is running is rather arbitrary, but the chosen metrics do tend to summarize some of the main properties of the climate system and carbon cycle – for my own personal convenience rather than reflecting any fundamental scientific truth ... In later experiments involving the carbon cycle, you will also see columns of information for:

pCO2 (uatm) – mean atmospheric CO<sub>2</sub> concentration (in units of μatm)

d13CO2 – mean δ<sup>13</sup>C value of atmospheric CO<sub>2</sub> (‰) (NOTE: only valid if <sup>13</sup>C tracer is selected)

<DIC> – global mean ocean dissolved inorganic carbon (DIC) concentration (μmol kg<sup>-1</sup>)

<ALK> – global mean ocean alkalinity (ALK) concentration (μeq kg<sup>-1</sup>) and in experiments with a modern continental configuration, also:

AMO (Sv) – Atlantic meridional overturning circulation (Sv)

This information is reported at the same intervals as time-series data (see later and/or refer to the *User Manual*) is saved and is indicated by:

>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :

Interleaved with these lines are lines reporting the saving of time-slice data (the 2- and 3-D model states – more of which later as well as in the *User Manual*). These appear as:

>>> SAVING BIOGEM TIME-SLICE AVERAGE CENTERED @ year:

You can stop the model at any point (all data up to that time will have been saved) by hitting: <Ctrl-C> (CONTROL key + 'C' key).

Just from examining the screen output: how close to steady state does the system appear to have come after this time? i.e., do are SST and/or sea-ice extents appear to be converging towards stable (constant) values? This will be an important question to think about later on: 'has the model reached steady-state (and does it matter)?'

The output should look something like the following:

```
*****
*** Initialisation complete: simulation starting ...
*****

      model year * ice(%) <SST> <SSS>

***          0.00      0.000 -0.000 34.900
>>> SAVING BIOGEM TIME-SLICE AVERAGE CENTERED @ year :      0.500
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      0.500
***          1.00      0.000  2.060 34.902
>>> SAVING BIOGEM TIME-SLICE AVERAGE CENTERED @ year :      1.500
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      1.500
***          2.00      0.000  3.515 34.902
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      2.500
***          3.00      0.000  4.650 34.903
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      3.500
***          4.00      0.000  5.572 34.904
>>> SAVING BIOGEM TIME-SLICE AVERAGE CENTERED @ year :      4.500
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      4.500
***          5.00      0.000  6.335 34.906
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      5.500
***          6.00      0.000  6.971 34.908
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      6.500
***          7.00      0.000  7.505 34.910
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      7.500
***          8.00      0.000  7.974 34.912
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      8.500
***          9.00      0.000  8.408 34.913
>>> SAVING BIOGEM TIME-SLICE AVERAGE CENTERED @ year :      9.500
>>> SAVING BIOGEM TIME-SERIES AVERAGE CENTERED @ year :      9.500
***         10.00      0.000  8.789 34.914
>>> SAVING BIOGEM RESTART <<<
>>> SAVING ATCHEM RESTART <<<

*****
*** Simulation complete: shutdown starting ...
*****
```

### 3. Model output

- 3.1 The first thing to note about output (i.e., saved results files) from cGENIE is that every science module saves its own results in its own sub-directory (and sometimes in very different and difficult-to-fathom ways ...) – see Figure 1.1. All the sub-directories of results, plus copies of input parameters and the model executable, are gathered together in a directory that is assigned the same name as the experiment (= *user-config* file name). The experiment results directories live in:

```
~/cgenie_output
```

and will be assigned a directory name something like:

```
LAB.0000.snowball
```

Within this are each module's results sub-directories.

We will consider primarily only results saved by the ocean biogeochemical module 'BIOGEM' (subdirectory: *biogem*). The results files will thus be found in:

```
~/cgenie_output/LAB.0000.snowball/biogem
```

BIOGEM has a flexible and powerful facility of saving results by means of spatially explicit '*time-slices*', and as a semi-continuous '*time-series*' of a single global (or otherwise representative mean) variable. In contrast, ATCHEM does not save its own results (BIOGEM can save information about atmospheric composition and air-sea gas exchange) while SEDGEM essentially saves results only at the very end of a model experiment (BIOGEM can also save the spatial distribution of sediment composition as time-slices as well as mean composition as a time-series). Furthermore, in order to attain a common format for both ocean physical properties and biogeochemistry, BIOGEM can save a range of ocean results in addition to temperature and salinity, such as: velocities, sea-ice extent, mixed layer depth, convective frequency, etc

#### **Time-slices**

One of the most informative data sets that can be saved is that of the spatial distribution of properties (such as tracers or physical ocean attributes). However, saving full spatial distributions (e.g. a 36×36×86 array) for any or all of the tracers each and every time-step is clearly not practical; not only in terms of data storage but also because of the detrimental effect that repeated file access has on model run-time.

Instead, BIOGEM will save the full spatial distribution of tracer properties only at one or more predefined time points (in units of years). These are termed *time-slices*. At the specified time points, a set of spatially-explicit data fields are saved for all the key tracer, flux, and physical characteristics of the system. However, rather than taking an instantaneous snapshot, the *time-slice* is constructed as an average over a specified integration interval (the default is set to 1.0 years, i.e. an annual average).

#### **Time-series**

The second data format for model output is much more closely spaced in time. Model characteristics must then be reducible to a single meaningful variable for this to be practical (i.e., saving the time-varying nature of 3-D ocean tracer distributions is not). Suitable reduced indicators would be the total inventories in the ocean and/or atmosphere of various tracers (or equivalently, the mean global concentrations / partial pressures, respectively). Like the *time-slices*, the data values saved in the *time-series* files represent averages over a specified integration interval (the default is set to 1.0 years (annual average)).

- 3.2 The results directory will contain files with names of the form:

- (i) *\_restart.nc* (is the re-start file created from the run you have just complete, and can be ignored).
- (ii) *biogem\_series\_\*.res* – these are the time-series files (in ASCII / plain text format).
- (iii) *biogem\_year\_\*\_diag\_GLOBAL.res* – these contain (global diagnostics) summary information and are saved at the same frequency as the time-slices (also as ASCII / plain text).
- (iv) *fields\_biogem\_2d.nc* – 2-D fields of ocean and atmosphere properties, as NetCDF.
- (v) *fields\_biogem\_3d.nc* – 3-D fields of ocean properties, as NetCDF.



## 4. Viewing time-series output

- 4.1 A descriptive summary of all the time-series (biogem\_series\_\*.res) data files is given in the cGENIE *User Manual* if you are really that bored. The files of most immediate use/relevance are:

```
biogem_series_atm_humidity.res - mean atmospheric (surface) humidity
biogem_series_atm_temp.res     - mean atmospheric (surface) air temperature
biogem_series_misc_seaice.res  - mean ocean sea-ice cover and thickness
biogem_series_ocn_sal.res      - mean ocean surface and whole ocean salinity
biogem_series_ocn_temp.res     - mean ocean surface and whole ocean temperature
```

- 4.2 The contents of the files can be viewed by changing directory into the results directory, i.e.,:

```
$ cd ~/cgenie_output/LAB.0000.snowball/biogem
```

and opening a file in the vi editor. But then I promised that I would not suggest anything quite so unpleasant ...

Instead – change to the experiment results directory and then to the BIOGEM sub-directory in the Secure File Transfer Client, and try double-clicking on one of the .res files (listed above). For biogem\_series\_ocn\_temp.res, you should see 2 columns – time and mean (whole) ocean temperature (°C). (However, in subsequent exercises a fuller output will be created with additional columns, with one for mean surface ocean temperature ‘SST’ (°C) as well as mean benthic (bottom water) temperature (°C)). Other results files may differ in the numbers of columns but all should be identifiable from the header information.

Note: The Secure File Transfer Client **does not** automatically refresh the directory listing. If you cannot see the results sub-directory with the experiment name you have just run 99 times out of 100, it is because the display of the Secure File Transfer Client needs to be refreshed – there is an icon at the top of the program window or hit the ‘F5’ key.

- 4.3 For your information and edification (only): Excel, or MUTLAB if you prefer, can be used to graph the time-series results. Either way you will have to deal with the header line(s) that are present at the top of the file (and preceding the rows of data).

In Excel: Chose File then Open. You will want to select Files of Type ‘All Files (\*.\*)’. In the Text Import Wizard window you can request that Excel skips the first few lines to start the import on the 2<sup>nd</sup> or 3<sup>rd</sup> line of the text file. Alternatively, set appropriate column widths manually in Excel to ensure that the columns of data are correctly imported.

MUTLAB will ignore lines starting with a %, which the time-series starts with. However, it may be that the header line wraps-around and there is in effect a 2nd header line but without a %. In this case, extra care (or a quick edit of the header in the ASCII file) will be required to load the data into MUTLAB.

## 5. Viewing time-slice output of 2-D and 3-D environmental property fields

- 5.0 For the time-slice NetCDF (\* .nc) files you will be using a program called 'Panoply'. If you want your own (FREE!) copy of this utility, you can get it here (and is available for: Windoz, Mac, and linux operating systems): <http://www.giss.nasa.gov/tools/panoply/>.
- 5.1 The first time that you try and view a NetCDF file you will need to 'associate' the file format (the .nc file format extension) with the Panoply program. To do this: (1) copy across to a local directory either the 2-D or 3-D NetCDF results file from the BIOGEM results sub-directory, (2) right-mouse-button click over the file, and chose Open With..., (3) Browse ... and find the Panoply program executable. Select and tick: Always use the selected program to open this kind of file. Hopefully ... all you have to do now is to double-click on the .nc file icon in the File Transfer window and the time-slice will be displayed like ... something that is "*indistinguishable form magic in a sufficiently retarded civilization*" (mis-adapted from A. C. Clarke).
- 5.2 When you open the NetCDF file, you will be presented with a 'Datasets and Variables' window (on the left hand side of the application window). This contains a list of all the parameters available that you can display. You will find that the 'Long Name' description of the variable will be the most helpful to identify the one you want. Simply double-click on a variable to display. For the 3-D fields you will be asked first whether you want a 'Lon-Lat' or 'Lat-Vert' plot (for the 2-D fields, the plot display will immediately open).
- For the 'Lon-Lat' plots – there are multiple levels (depth layers) in the ocean of data that can be plotted, form the surface to the abyssal ocean.
- For the 'Lat-Vert' plots – there are multiple possible longitudes at which to plot slices. The default is the global mean meridional distribution.
- There is also an option for 'Lon-Vert' plots (which we will not use).
- For all three: there may be multiple time-slices (i.e., you can plot data saved from different years). You can interpolate the data or not (often you may find that it is clearer not to interpolate the data but to leave it as 'blocky' colors corresponding to the resolution of the model), change the scale and colors, overlay continental outline, change the projection, etc etc. Grey cells represent 'dry' grid points, i.e., continental or oceanic crust.
- NOTE: The default settings in Panoply can mislead:
- (1) the 1st time-slice (often year mid-point 0.5) rather than the experiment end,
  - (2) auto-scaling of the color scale,
  - (3) global zonal averaging of lat-depth plots.
- Be careful when opening a new plot that you are looking at what you \*think\* you are looking at ...
- 5.3 Explore different data fields and play with different ways of displaying them. Aim for a set of display properties that show the information you are interested in / want to present in the clearest possible manner. Try different years (time-slice number), depth level (for a lat-long plot), or longitude (for a vertical section). Note that gray cells represent 'dry' grid points, i.e., continental or oceanic crust.
- For example -- go to the results directory of the experiment and open up the 2-D NetCDF file (from the biogem directory). View the topography (ocean depth) field (grid\_topo) – land is shown in grey by default. Also by default, Panoply will try and plot on the modern continental outline – turn this off by selecting <none> for Overlay in the Map tab. The model has been configured for an idealized super-continent, positioned symmetrically about the Equator, so be shocked (and have expected the modern continental configuration, which you will see in subsequent experiments).
- 5.4 To save plots in Panoply:
- File
  - Save Image As ...
- Then select the location, filename, and graphics format.

## 6. Submitting experiment 'jobs' to a cluster

6.0 This bit is no particular fun at all, but it is a very handy 'trick' for running the model in the background, and maximizes drinking time in the pub vs. sat bored watching a computer screen ☺

6.1 Running jobs interactively is all very well, but there are three important limitations:

(1) The connection between your terminal and the server computer running the model must remain unbroken. Anything more than a fleeting loss of internet connectivity may result in the experiment terminating.

(2) You can only run one experiment at a time ... unless you want to have thousands of separate X-Windows open ...? I thought not ...

(3) Any cluster or computer you are likely to be accessing using a shell will not have many computing cores, either because it is a single machine with only one or two processors, or if a cluster, by using an X-Window you are running on the 'head node', which will have similar computing core limitations to running on a single machine. The more experiments you run simultaneously, the slower they will all run ...

6.2 The alternative is to submit your experiment as a 'job' to a queuing system which then manages what compute resources are used to run the model. Once you have submitted the experiment, that is it – you can go straight to the pub :)

Unless you want to read the *cGENIE User Manual*, for now, take the following suggested way of submitting jobs on trust: to run a similar experiment to before (`LAB.0000.snowball`) for maybe 100 years (or even longer if you wish – I am just pulling factors of 10 out of thin air here) by submitting the experiment as a job to the cluster queue, type:

```
$ qsub -j y -o cgenie_output -V -S /bin/bash runmuffin.sh  
cgenie.eb go gs ac bg.p0650e.NONE LABS LAB.0000.snowball 100
```

(Again: SINGLE, CONTINUOUS LINE.)

Note that now you should omit the `./` bit before `runmuffin.sh`.

(If you are interested (I know that you are not): the options following `qsub` and before `runmuffin.sh` do things like re-directing screen output and error messaging to a file and specify which linux 'shell' to assume. It is even possible to receive an email when the job is done ☺)

The status of the cluster queue and how your experiment job is getting on (e.g., "Is it finished yet?") can be checked by typing:

```
$ qstat -f
```

(`qstat -f -u "*" will show all jobs on the cluster.`)

After submitting an experiment, you receive a job number. This number appears in the first column in the queue status information when you issue a `qstat -f` command. You should see your job appear on one of 4 compute nodes, numbered 0-0 to 0-3), although it might briefly reside as a 'PENDING JOB'. For each node, there are 4 processing cores, meaning that up to 4 instances of *cGENIE* can run simultaneously on each node (i.e., a total of 16 across the entire cluster). For an 8-level ocean based configuration of *cGENIE*, being run for 100 years, the job should remain there in the queue for a few good tens of seconds before 'disappearing' (your clue that it has finished, or died ...). If you periodically re-issue a `qstat -f` command you can follow your job's progress.

A rough rule of thumb is that 8-level ocean *cGENIE* @ a horizontal grid resolution of 36×36 will simulate about 1000 years per CPU hour. The 16-level version (which you will use later), about 300-400 years per CPU hour.

In the special case of this low resolution model with no carbon cycle, it is more like 10000 years per CPU hour.

**NOTE:** If your experiment appears on the queue but vanishes after a few seconds, it has most likely died ☹

## 7. 'Restarts'

7.0 Not much fun here either ... but again – an important and time-saving (== increased drinking time!) modelling technique to learn to use.

7.1 By default, model experiments start from 'cold', i.e., the ocean is at rest and uniform in temperature and salinity while the atmosphere is uniform in temperature and humidity. All biogeochemical tracers in the ocean have uniform concentrations and/or are zero and there are no biogenic materials in deep-sea sediments. From this state it will take several thousand years (kyr) for the climate system to reach steady-state, and closer to 5 kyr (or more) for ocean biogeochemical cycles and atmosphere CO<sub>2</sub> to reach steady-state, and exceeding 100 kyr for sediment composition to re-balance weathering ... Reaching this the equilibrium state is called the 'spin-up' phase of the model.

There is evidently little point in repeating the spin-up for each and every model experiment that are similar except in a single detail (e.g., testing a variety of different CO<sub>2</sub> emissions scenarios all starting from current year 2012 conditions). A facility is thus provided for requesting that a 'restart' is used – starting a new experiment from the end of a previous one, usually a 'spin-up' that has been run explicitly for the purpose of generating a starting point (*restart*) of the system at steady-state (equilibrium) for subsequent experiments to continue on from.

7.1 You will also need to download a *restart* file that has been created (a pre-run 10,000 year spin-up).

To fetch this: Change to the `cgenie_output` directory (perhaps by going 'home' first (`cd <RETURN>`), and then changing to `cgenie_output` – refer to `linux` commands crib sheet and Figure 1.1), and type:

```
$ wget http://www.seao2.info/cgenie/labs/UoB.2013/130328.p0650e.LiCa.OHM10.SPINO.tar.gz
```

This downloads an archived/compressed copy of the *restart* (`130328.p0650e.LiCa.OHM10.SPINO.tar.gz`) from a location on the interweb. Extract the contents of this archive by typing:

```
$ tar xfvz 130328.p0650e.LiCa.OHM10.SPINO.tar.gz
```

Finally, change directory back to `cgenie.muffin` and then `genie-main` so that you are ready to run the model (the model is \*always\* run from `cgenie.muffin/genie-main`).

7.3 A *restart* can be requested by setting the 5<sup>th</sup> (optional) parameter when entering in the `runmuffin.sh` command. A spin-up of a pre-snowball sort of climate state is provided: `130328.p0650e.LiCa.OHM10.SPINO` which you have just unpacked to the `cgenie_output` results output directory.

Create a new (*user config*) experiment configuration file, perhaps named `LAB.0000.snowball2`, by using the given file `LAB.0000.snowball` as a template (no changes to the content need to be made at this stage). You can make copies (`cp` command) of the experiment configuration files (e.g. `LAB.0000.snowball`) and assign them different names, e.g., `twilight`, `rarity`, `applejack` ... Or ... if you and the `linux` command lines are simply not the best of friends, you can drag the *user-config* file (`LAB.0000.snowball`) you want to use as a template to your local PC in the file transfer window, rename it either in the file transfer program or via Windoz file-manager (`LAB.0000.snowball2`), and drag it back again.

Specify the use of the *restart* state by adding the appropriate 5<sup>th</sup> parameter at the command line, e.g.:

```
$ ./runmuffin.sh cgenie.eb_go_gs_ac_bg.p0650e.NONE LABS LAB.0000.snowball2 100  
130328.p0650e.LiCa.OHM10.SPINO
```

The run-time output should now look noticeably different. There should be no (or perhaps just very little) drift in any of the various variable values outputted to the screen – this is because you have (re-)started from the end of a run that had already ready an equilibrium, steady-state.

## 8. Brrrrrrrrrrrr – it's chilly on ... snowball Earth!

8.0 To illustrate how 'easy' it can be to configure an Earth system model such as cGENIE and explore the behavior of the Earth system and its response to perturbation – you are going to induce an extreme cooling of climate and see what happens. Solar output was weaker during the late Neoproterozoic, a time when the Earth experienced a series (2 ish) of extreme glaciations. Thus, having a mild climate state to start with must have been dependent on sufficient CO<sub>2</sub> and/or CH<sub>4</sub> in the atmosphere and hence presumably highly elevated compared to the modern World, so sort of the opposite of the problem we have today ...

8.1 You are going to be running experiments similar to before and using the *restart*.

```
$ ./runmuffin.sh cgenie.eb_go_gs_ac_bg.p0650e.NONE LABS LAB.0000.snowball13 100  
130328.p0650e.LiCa.OHM10.SPINO
```

where LAB.0000.snowball13 is a new experiment configuration file that you are going to derive from LAB.0000.snowball (i.e. you are going to have to make it!). You could alternatively keep using the same experiment (*user-config* file) name, but the results will be over-written each time. You would also have to be especially careful not to have 2 (or more) experiments running simultaneously with exactly the same name.

Your task will be to determine the radiative forcing (or pCO<sub>2</sub> equivalent) threshold required to drive the climate system into a full ice-covered ocean (snowball Earth) state. (Read the *Hyde et al.* [2000] paper.)

Useful 2-D (netCDF—Panoply) variables to view are surface air temperature and sea-ice extent (and/or thickness). Ocean surface temperature and salinity can be viewed in the 3-D NetCDF results file (apologies for ocean temperature being in units of K ...). Time-series (ASCII .res files) are useful for providing simple mean indicators of global climate such as global ocean fractional sea-ice covered.

Note that the model configuration of an idealized super-continent, positioned symmetrically about the Equator, is pretty unrealistic. But the further you go back in time, the more uncertain it becomes as to exactly where and in what orientation the continents were. Sometimes modelers have to resort to somewhat idealized experiments if the uncertainties are too great. In addition, one can conduct sensitivity experiments to test whether the continental configuration is important to the results – in this case, we might have had a second alternative configuration with a super continent positioned over a pole. And/or we could have had a set of very fragmented continents. For instance, *Hoffman and Schrag* [2002] discuss the potential importance of continental configuration, while the entire hypothesis of *Donnadieu et al.* [2004] rests on specific details of the continental configuration being realistic.

Other questions to think about with regards to numerical modeling (and this experiment) are:

- *(Is the model configuration and experimental design 'realistic' ... ?)*
- *What is 'missing' in the model and what might the implications for your predictions and conclusions be? For example, there is no land-surface scheme (and hence no concept of 'snow') in this particular configuration.*
- *Are the simulations being run for sufficiently long? Why not if not (i.e., justify your choices of parameter values and experimental assumptions)? How might the results and conclusions be biased (if at all)?*
- *How would you test model predictions and your overall conclusions?*
- *How could the experimental design be improved?*
- *Etc.*

- 8.2 To search for the atmospheric CO<sub>2</sub> concentration (or rather, radiative forcing equivalent) that would lead to a 'snowball Earth' state in the Neoproterozoic and answer the question:

**'How low does CO<sub>2</sub> have to be to trigger a 'snowball'?'**

you are going to edit the file that controls the specific details of the experiment. This is the *user-config* file. From the `genie-userconfigs/LABS` directory, open one of the snowball experiments in the SciTE text editor. At the top you should see:

```
#
#
# --- CLIMATE -----
#
# scaling for atmospheric CO2 radiative forcing, relative to 278 ppm
ea_radfor_scl_co2=20.0
```

Each line that is not commented out (i.e., no #) contains a parameter of the format:

*PARAMETER=VALUE*

The value of each parameter can be edited to form a new experiment. (Additional parameter value specifications can also be added, or existing ones deleted.) In this example, the line:

```
ea_radfor_scl_co2=20.0
```

specifies a radiative forcing of climate by CO<sub>2</sub> equivalent to ×20 modern (20×278 = 2560 ppm).

*Note that CO<sub>2</sub> is not being explicitly modeled in this experiment, but the long-wave radiative forcing associated with a specified concentration of CO<sub>2</sub> (as a ratio to modern concentrations) is being set instead.*

Edit the value of `ea_radfor_scl_co2` (lower or higher) and save the file. Re-run the experiment to see whether sea-ice extent is approaching a new steady state. You may want to try even longer simulations if it becomes clear that the model is still far from steady-state. You can judge how close to equilibrium things have got by following (and/or plotting) the evolution of e.g., global surface air temperature or sea-ice extent (both time-series files). Note that you *might* want to run the experiment longer than 100 years ...

**HINT:** By submitting the experiments to the cluster will allow you to run all these experiments simultaneously.

- 8.3 For each experiment you want to be assessing how far towards the Equator the sea-ice limit encroaches through some of the time-series and time-slice files or even the on-screen summary lines (assuming running interactively rather than via a job submission to the cluster queue). Informative time-series variables include (but not necessarily be limited to: atmospheric temperature and sea-ice cover. (Sea-ice thickness, on account of the simple physics in the model, low resolution and long time-step, can fluctuate a little in area and volume at times.)

For the time-slice data: atmospheric and ocean surface temperature and sea-ice extent (2-D biogem NetCDF file) may be informative.

**HINT:** Be careful with the default 'auto-scaling' feature in Panoply. At near complete sea-ice cover, you may find Panoply scaling min and max sea-ice between 99.1 and 99.9% or something – it always tries to maximize color contrasts by default and will be at all helpful in this case.

In answering the question think about what an appropriate degree of accuracy might be for your experiments. Just because computer models generally calculate to around 16 significant places of precision, does not mean you have 16 significant figures of accuracy (or realism). For instance – how many significant figures is the solar constant quoted to and what do you think is the uncertainty in this? Harder to judge is how the assumed (incorrect) continental configuration creates additional uncertainty, or the physics assumed in the ocean or sea-ice, or lack of snow on land ...

8.4 Once you are happy about the controls on the snowball threshold try and answer:

**How high does the (CO<sub>2</sub>) radiative forcing have to be in order to escape from a snowball?**

If you run the model with an appropriate radiative forcing to create a snowball, you can use that experiment as a *restart* and be able to carry out a series of experiments with increasing radiative forcing, all starting from the snowball state you have created. Defining the radiative forcing / climate path going out of a snowball would complete the hysteresis loop that *Hyde et al.* [2000] could only generate for going into a snowball, but still got a Nature paper out of ;)

8.5 Finally, cGENIE will fairly happily build up sea-ice, apparently without limit (with the remaining wet ocean becoming progressively colder and more saline). In the real world, one might expect some sort of limit to the maximum thickness achieved as the heat diffusion across a progressively greater thickness of sea-ice approaches the heat input at the bottom of the ocean from geothermal energy. Different modes of ocean circulation are also possible if one considers heating from the bottom as well as cooling (and brine rejection) from the top and which might affect the entry into or exit from a snowball state.

In the experimental setup you have been given, geothermal heat input is specified in the ocean circulation module via the following parameters

```
bg_ctrl_force_GOLDSTEInTS=.TRUE.  
bg_par_Fgeothermal=100.0E-3
```

The first enables the temperature and/or salinity of the ocean to be modified by processes other than redistribution via ocean circulation and exchange with sea-ice and atmosphere (i.e. to impose external forcings). The second sets the geothermal flux in units of W m<sup>-2</sup>. (Note that in the Neoproterozoic, the geothermal heat flux could have been somewhat higher than modern. How much? A question for Google...)

An appropriate research question might be to determine in radiative forcing vs. geothermal space (and requiring a 2D grid of parameter combinations to be created and submitted to the cluster): the equilibrium sea-ice thickness and region in which a snowball solution is not possible. However, more simply and suitable to a short workshop: **How much of a difference to the estimated entry and exit thresholds of radiative forcing, does the inclusion of a geothermal input make?** E.g what happens if you set it to zero? What about 10 times modern (or more, although \*extreme\* seafloor heating can cause numerical instability)?

## Appendix 1 – linux 101

### *Viewing directories; moving around the file system*

When logging in, you always start from your ‘home’ directory. This is represented by a ‘~’ before the command prompt (\$).

At the command line prompt (\$) in linux, you can view the current directory contents:

```
$ ls
```

or for a more complete output:

```
$ ls -la
```

To go down a directory (e.g. `cgenie_output`) relative to where you already are:

```
$ cd cgenie_output
```

and to go back up one is:

```
$ cd ..
```

It is often safer/easier at first, if you need to change more than one directory level to do this in stages. e.g. to change to `cgenie_output/exp0_modern_SPINUP`, change to `cgenie_output` (`cd cgenie_output`) but then check that you are in the place you think you are and/or remind yourself of the spelling of the next directory you need to change to by typing `ls`. Then move on, e.g. `cd exp0_modern_SPINUP`. Note that to go straight from your home directory in one jump, type: `cd cgenie_output/exp0_modern_SPINUP`. If you start from somewhere other than your home directory, give the full path: `cd $HOME/cgenie_output/exp0_modern_SPINUP`.

You can always return to your home directory (~) by typing:

```
$ cd
```

or:

```
$ cd $HOME
```

(or `cd ~`)

### *Copying and moving files*

To copy a file `myconfig` to `myconfig_new`, assuming you are in the same directory where both the old file is and the new file will be:

```
$ cp myconfig myconfig_new
```

To move `myconfig` to the cGENIE *user-config* directory, assuming you are in the directory where the old file is but with the new file in a different directory, give the full path of the new directory:

```
$ mv myconfig ~/cgenie.muffin/genie-userconfigs/LABS/myconfig
```

To rename `myconfig` to `useless_config`:

```
$ mv myconfig useless_config
```

### *Creating directories*

To create a directory `mydirectory`:

```
$ mkdir mydirectory
```

### *Repeating command lines*

You do not have to re-enter lines of commands and options in their entirety each time – by pressing the UP cursor key you get the last command you issued. If you keep pressing the UP cursor key you can recover progressively older commands you have previously entered. When you have recovered a helpful line you can simply just edit it, navigating along with the LEFT and RIGHT cursor keys (press RETURN when you are done).