cGENIE Quick-start Guide

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1. To get a (read-only) copy of the current (development) branch of cGENIE source code:

   From your home directory (or elsewhere, but several path variables will have to be edited – see below), type:
   
   ```
   svn co https://svn.ggy.bris.ac.uk/subversion/genie/tags/cgenie.muffin-rel.0.4 --username=genie-user cgenie.muffin
   ```
   
   NOTE: All this must be typed continuously on ONE LINE, with a SPACE before ‘--username’, and before ‘cgenie’. You will be asked for a password – it is g3n1e-user.

2. If you are installing on your own machine (i.e. not a Bristol (c)genie friendly cluster) you are likely to have to set a couple of environment variables. The compiler name, netCDF library name, and netCDF path, are specified in the file `user.mak` (genie-main directory). If the cgenie code tree (cgenie.muffin) and output directory (cgenie_output) are installed anywhere other than in your account HOME directory, paths specifying this will have to be edited in: `user.mak` and `user.sh` (genie-main directory).

3. Change directory to `cgenie.muffin/genie-main` and 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. If you are unsuccessful here ... double-check the software and directory environment settings in `user.mak` or `user.sh`.

4. At this point, the science modules are currently compiled in a grid and/or number of tracers configuration that is unlikely to be what you want for running experiments. Clean up all the compiled cGENIE modules, ready for re-compiling from the source code, by:

   ```
   make cleanall
   ```

   That is it as far as basic installation goes. Except to read the cGENIE User manual ;)

   (Also see: cGENIE README and cGENIE HOWTO documents.)