

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 S P A C E 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.)