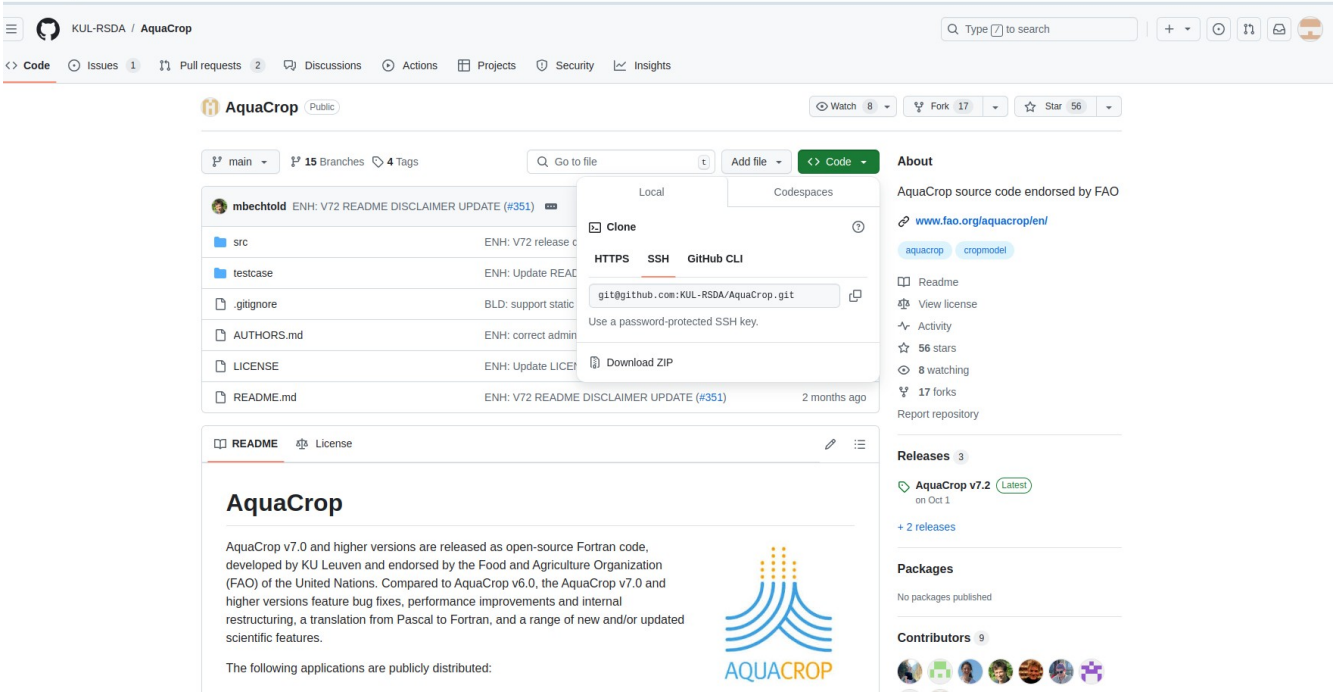
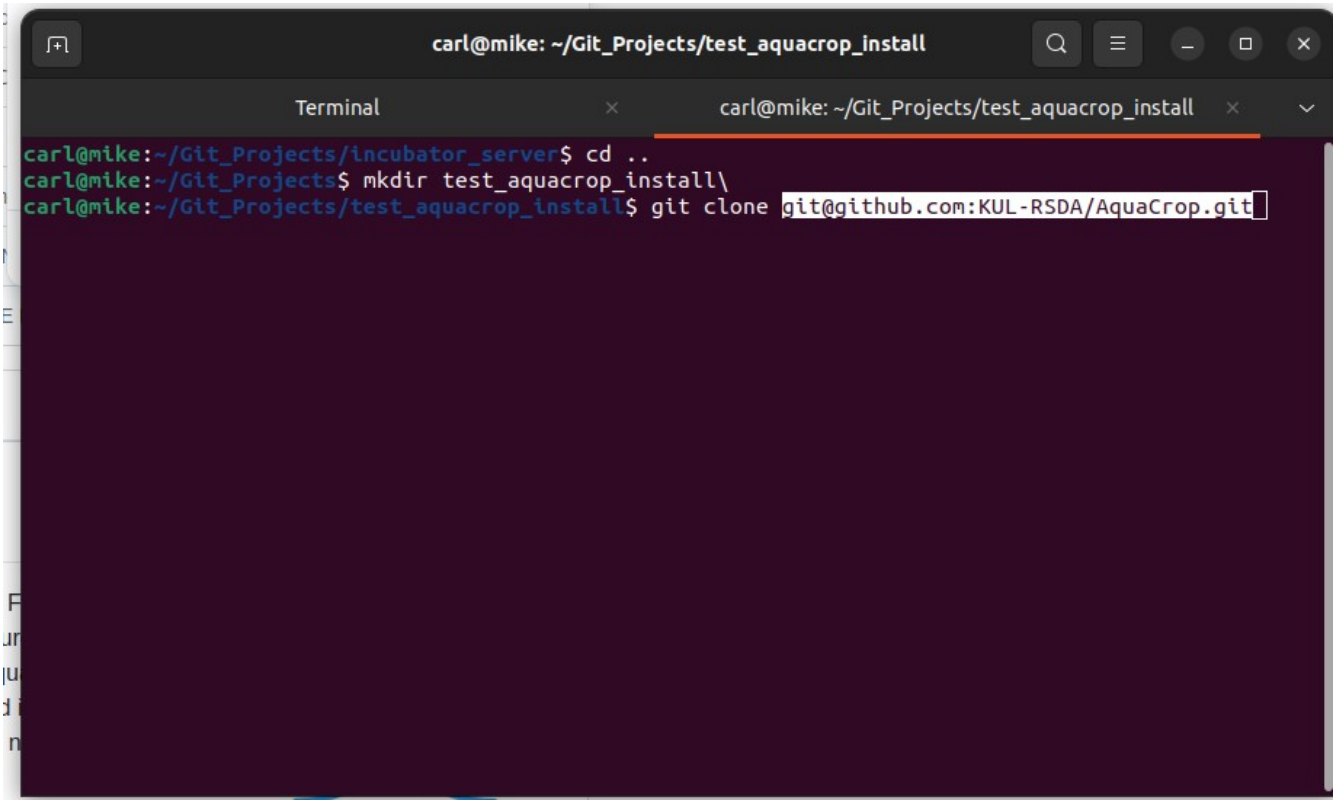
Use git to clone AquaCrop from github.



Make a new directory for Aquacrop



```
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop
Terminal | carl@mike: ~/Git_Projects/test_aquacrop_install/Aq...

carl@mike:~/Git_Projects/incubator_server$ cd ..
carl@mike:~/Git_Projects$ mkdir test_aquacrop_install\
carl@mike:~/Git_Projects/test_aquacrop_install$ git clone git@github.com:KUL-RSDA/AquaCrop.git
Cloning into 'AquaCrop'...
remote: Enumerating objects: 7652, done.
remote: Counting objects: 100% (3751/3751), done.
remote: Compressing objects: 100% (873/873), done.
remote: Total 7652 (delta 3037), reused 3315 (delta 2871), pack-reused 3901 (from 1)
Receiving objects: 100% (7652/7652), 3.26 MiB | 806.00 KiB/s, done.
Resolving deltas: 100% (5919/5919), done.
carl@mike:~/Git_Projects/test_aquacrop_install$ cd AquaCrop/
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$ ls
AUTHORS.md  LICENSE  README.md  src  testcase
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
```

Go to the src directory.

```
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop/src
Terminal | carl@mike: ~/Git_Projects/test_aquacrop_install/Aq...

carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
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carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$ ls\
>
AUTHORS.md  LICENSE  README.md  src  testcase
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$ cd src
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop/src$ ls
aquacrop.F90          inforesults.f90      preparefertilitysalinity.f90  simul.f90
climprocessing.f90    initialsettings.f90  project_input.f90             startunit.F90
defaultcropsoil.f90   kinds.f90            rootunit.f90                  tempprocessing.f90
global.f90            Makefile             run.f90                       utils.f90
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop/src$
```
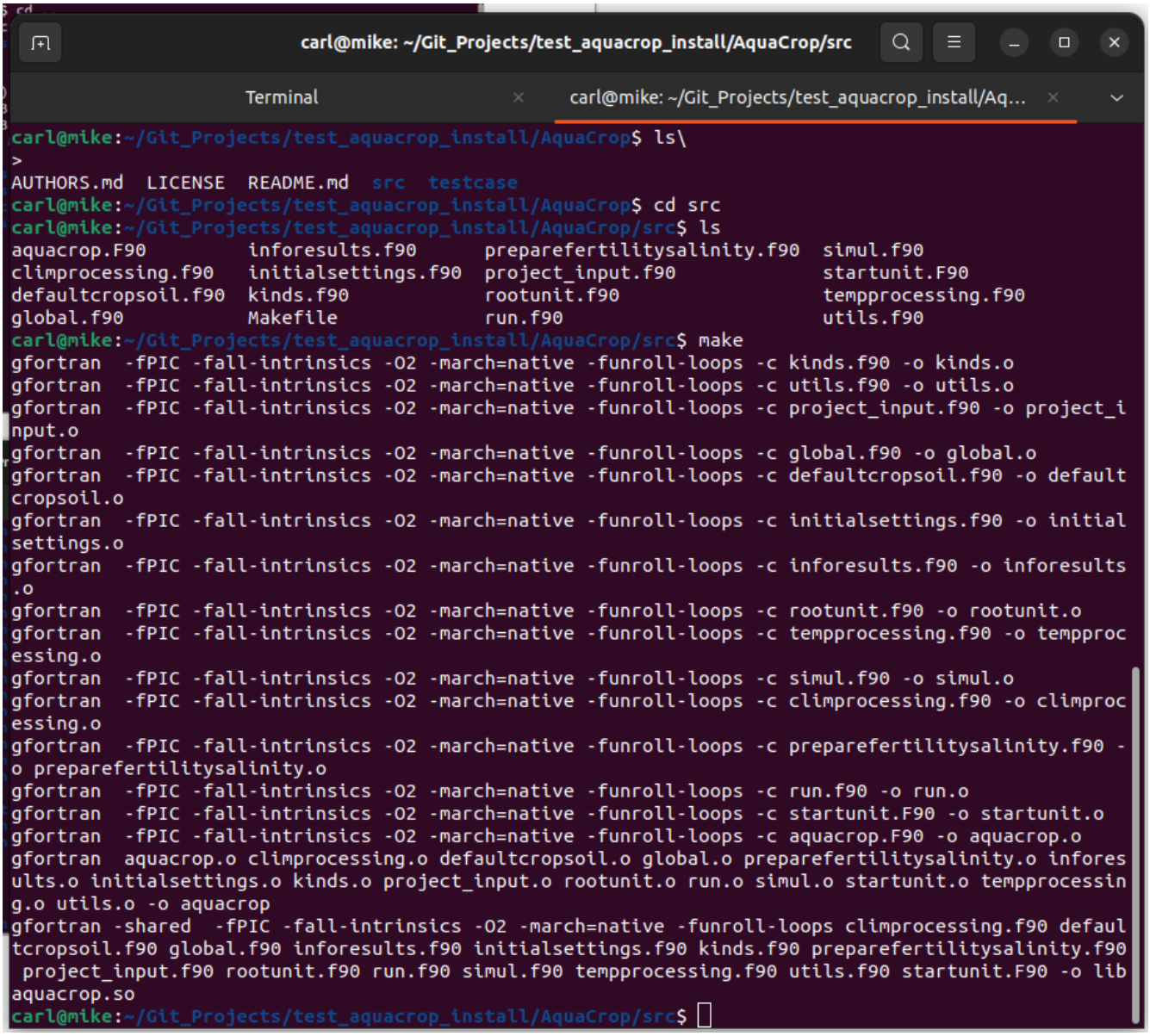
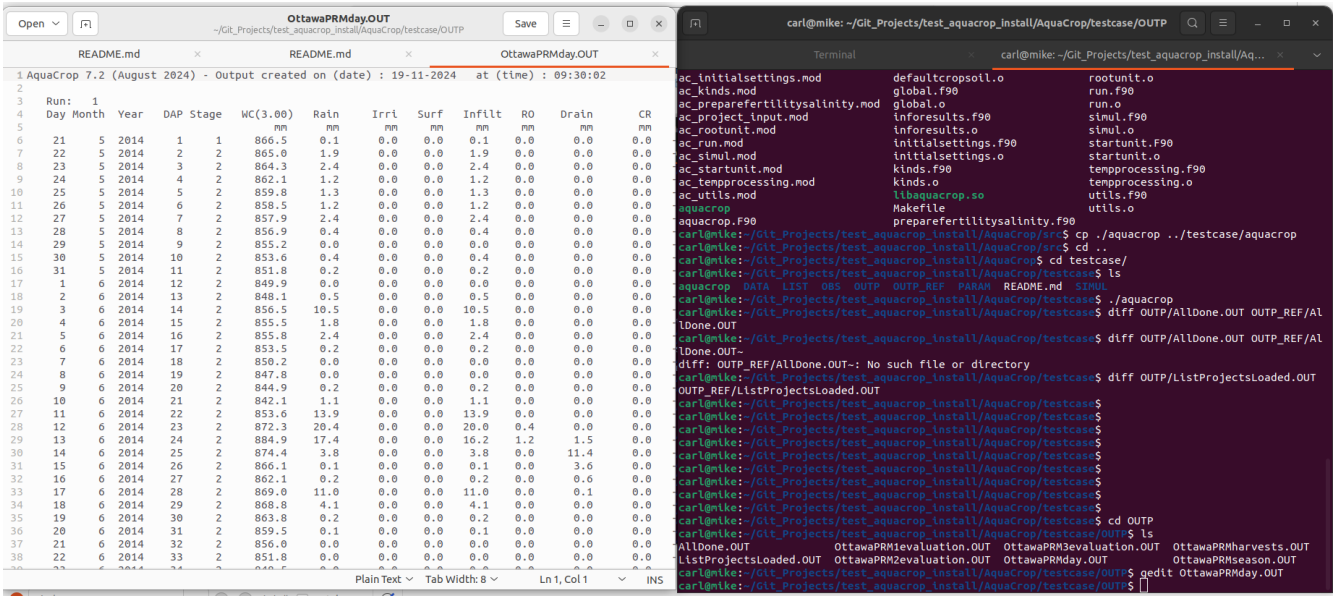

Use make to compile the fortran code. You may need to get a fortran90 compiler, I used on ubuntu: sudo apt-get install gfortran



Copy the executable aquacrop file that you just compiled into the testcase directory.
Now you run the test case: (note that there is no output in the terminal, it's all in the OUTP directory)



Copy the aquacrop executable into the AquaCropOptimise/field_crop_planting_optimization directory
Test with:
python run_many_simulations.py