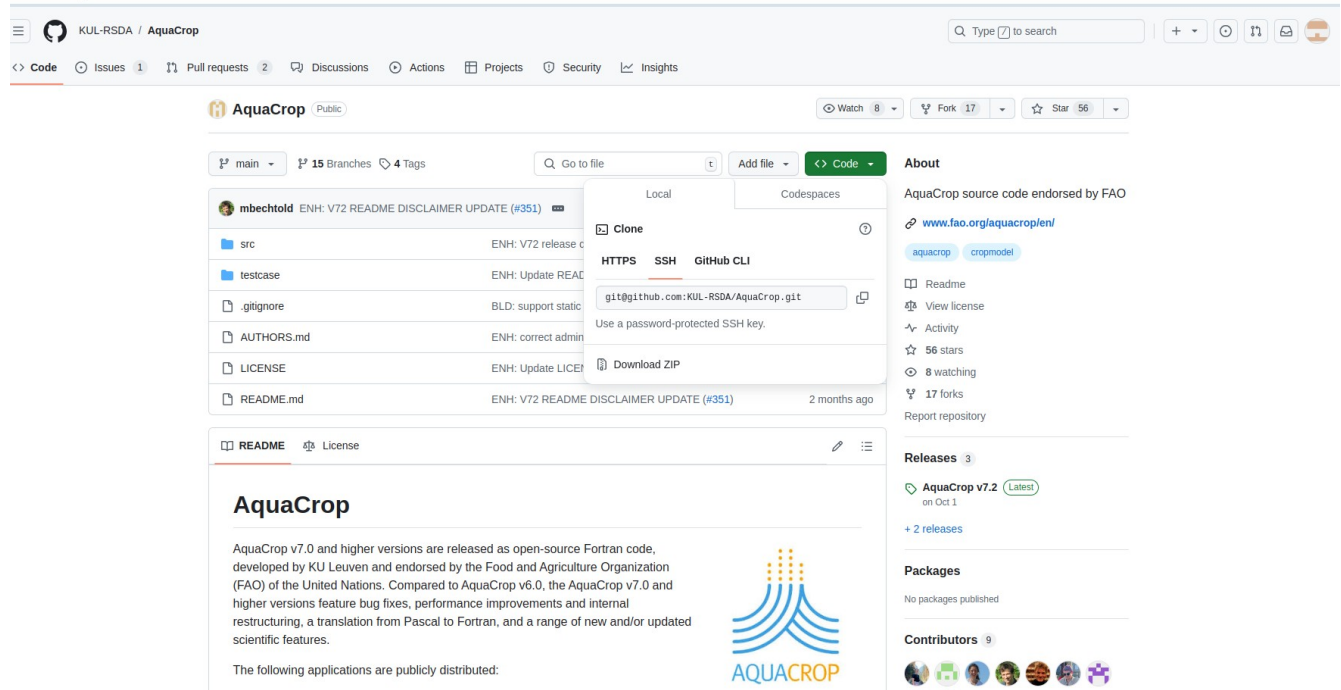


Use git to clone AquaCrop from github.

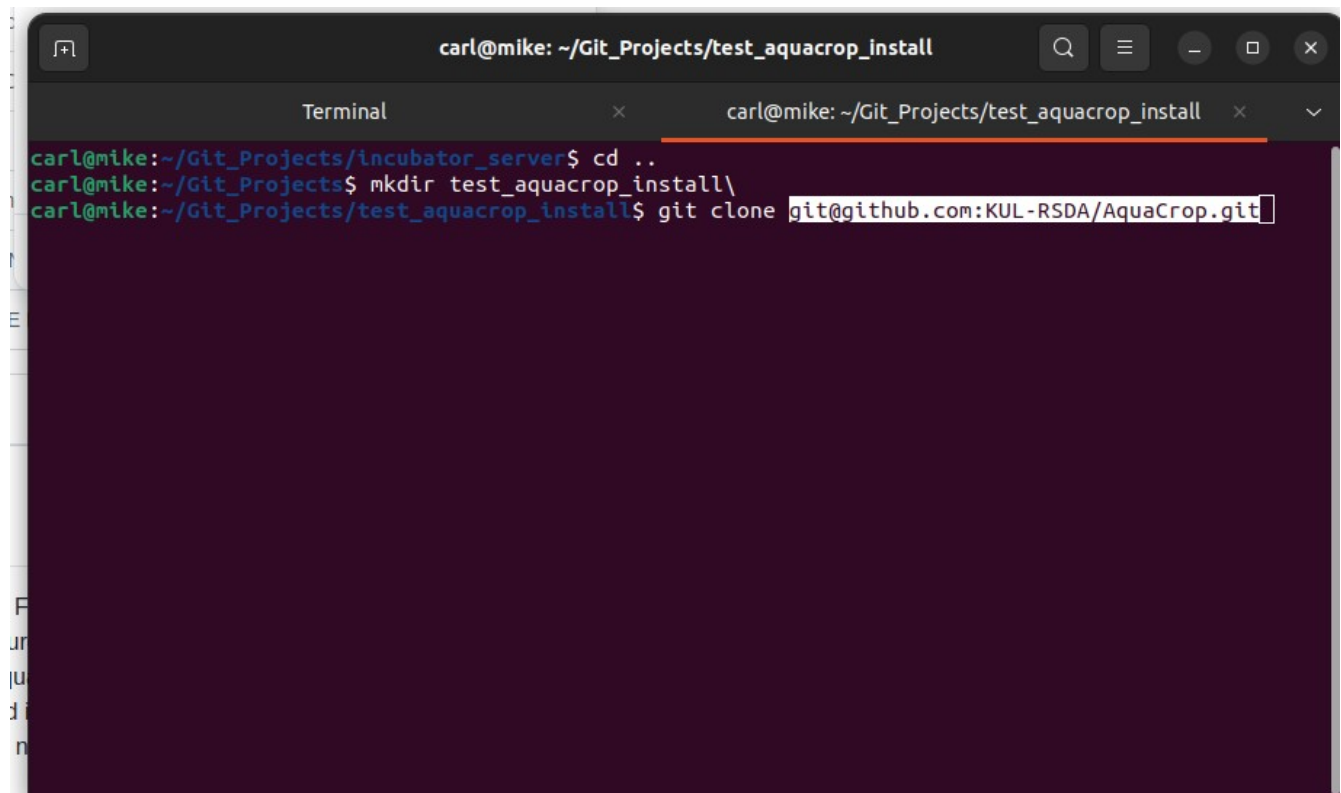


The screenshot shows the GitHub repository page for AquaCrop. The repository is owned by KUL-RSDA and is public. It has 8 watchers, 17 forks, and 56 stars. The repository is currently on the main branch, which has 15 branches and 4 tags. A file explorer shows the repository structure, including a src directory, a testcase directory, and files like .gitignore, AUTHORS.md, LICENSE, and README.md. A 'Clone' button is visible, with options for Local, Codespaces, and HTTPS. The README file is selected, showing the AquaCrop logo and a description of the software. The README states that AquaCrop v7.0 and higher versions are released as open-source Fortran code, developed by KU Leuven and endorsed by the Food and Agriculture Organization (FAO) of the United Nations. It also mentions that higher versions feature bug fixes, performance improvements, and internal restructuring, a translation from Pascal to Fortran, and a range of new and/or updated scientific features. The following applications are publicly distributed:

- src
- testcase
- .gitignore
- AUTHORS.md
- LICENSE
- README.md

The AquaCrop logo is displayed, featuring a stylized blue and yellow design with the text 'AQUACROP' below it.

Make a new directory for Aquacrop



```
carl@mike: ~/Git_Projects/test_aquacrop_install
Terminal
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
```

```
carl@mike: ~/Git_Projects/test_aquacrop_install/AquaCrop
Terminal x carl@mike: ~/Git_Projects/test_aquacrop_install/Aq... x v
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 x carl@mike: ~/Git_Projects/test_aquacrop_install/Aq... x v
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$
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$
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$
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop$
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

```
cd
carl@mike: ~/Git_Projects/test_aquacrop_install/AquaCrop/src
Terminal x carl@mike: ~/Git_Projects/test_aquacrop_install/Aq... x v
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$ make
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c kinds.f90 -o kinds.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c utils.f90 -o utils.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c project_input.f90 -o project_input.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c global.f90 -o global.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c defaultcropsoil.f90 -o defaultcropsoil.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c initialsettings.f90 -o initialsettings.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c inforesults.f90 -o inforesults.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c rootunit.f90 -o rootunit.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c tempprocessing.f90 -o tempprocessing.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c simul.f90 -o simul.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c climprocessing.f90 -o climprocessing.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c preparefertilitysalinity.f90 -o preparefertilitysalinity.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c run.f90 -o run.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c startunit.F90 -o startunit.o
gfortran -fPIC -fall-intrinsics -O2 -march=native -funroll-loops -c aquacrop.F90 -o aquacrop.o
gfortran aquacrop.o climprocessing.o defaultcropsoil.o global.o preparefertilitysalinity.o inforesults.o initialsettings.o kinds.o project_input.o rootunit.o run.o simul.o startunit.o tempprocessing.o utils.o -o aquacrop
gfortran -shared -fPIC -fall-intrinsics -O2 -march=native -funroll-loops climprocessing.f90 defaultcropsoil.f90 global.f90 inforesults.f90 initialsettings.f90 kinds.f90 preparefertilitysalinity.f90 project_input.f90 rootunit.f90 run.f90 simul.f90 tempprocessing.f90 utils.f90 startunit.F90 -o libaquacrop.so
carl@mike:~/Git_Projects/test_aquacrop_install/AquaCrop/src$
```

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)

The screenshot displays a development environment with two main windows. The left window, titled 'OttawaPRMday.OUT', shows a spreadsheet of simulation results for AquaCrop 7.2 (August 2024). The spreadsheet has columns for Run, Day, Month, Year, DAP, Stage, WC(3.00), Rain, Irrig, Surf, Infiltr, RO, Drain, and CR. The data spans from Run 1 to Run 38, covering the year 2014. The right window is a terminal titled 'carl@mike: ~/Git_Projects/test_aquacrop_install/AquaCrop/testcase/OUTP'. It shows the compilation of the aquacrop executable and the execution of a test case. The test case output is listed in the terminal, showing various files and directories created, including 'OUTP_REF', 'OUTP', and 'OUTP_REF/ListProjectsLoaded.OUT'.

Run	Day	Month	Year	DAP	Stage	WC(3.00)	Rain	Irrig	Surf	Infiltr	RO	Drain	CR
1	21	5	2014	1	1	866.5	0.1	0.0	0.0	0.1	0.0	0.0	0.0
2	22	5	2014	2	2	865.0	1.9	0.0	0.0	1.9	0.0	0.0	0.0
3	23	5	2014	3	2	864.3	2.4	0.0	0.0	2.4	0.0	0.0	0.0
4	24	5	2014	4	2	862.1	1.2	0.0	0.0	1.2	0.0	0.0	0.0
5	25	5	2014	5	2	859.8	1.3	0.0	0.0	1.3	0.0	0.0	0.0
6	26	5	2014	6	2	858.5	1.2	0.0	0.0	1.2	0.0	0.0	0.0
7	27	5	2014	7	2	857.9	2.4	0.0	0.0	2.4	0.0	0.0	0.0
8	28	5	2014	8	2	856.9	0.4	0.0	0.0	0.4	0.0	0.0	0.0
9	29	5	2014	9	2	855.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
10	30	5	2014	10	2	853.6	0.4	0.0	0.0	0.4	0.0	0.0	0.0
11	31	5	2014	11	2	851.8	0.2	0.0	0.0	0.2	0.0	0.0	0.0
12	1	6	2014	12	2	849.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0
13	2	6	2014	13	2	848.1	0.5	0.0	0.0	0.5	0.0	0.0	0.0
14	3	6	2014	14	2	856.5	10.5	0.0	0.0	10.5	0.0	0.0	0.0
15	4	6	2014	15	2	855.5	1.8	0.0	0.0	1.8	0.0	0.0	0.0
16	5	6	2014	16	2	855.8	2.4	0.0	0.0	2.4	0.0	0.0	0.0
17	6	6	2014	17	2	853.5	0.2	0.0	0.0	0.2	0.0	0.0	0.0
18	7	6	2014	18	2	850.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
19	8	6	2014	19	2	847.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
20	9	6	2014	20	2	844.9	0.2	0.0	0.0	0.2	0.0	0.0	0.0
21	10	6	2014	21	2	842.1	1.1	0.0	0.0	1.1	0.0	0.0	0.0
22	11	6	2014	22	2	853.6	13.9	0.0	0.0	13.9	0.0	0.0	0.0
23	12	6	2014	23	2	872.3	20.4	0.0	0.0	20.0	0.4	0.0	0.0
24	13	6	2014	24	2	884.9	17.4	0.0	0.0	16.2	1.2	1.5	0.0
25	14	6	2014	25	2	874.4	3.8	0.0	0.0	3.8	0.0	11.4	0.0
26	15	6	2014	26	2	866.1	0.1	0.0	0.0	0.1	0.0	3.6	0.0
27	16	6	2014	27	2	862.1	0.2	0.0	0.0	0.2	0.0	0.6	0.0
28	17	6	2014	28	2	869.0	11.0	0.0	0.0	11.0	0.0	0.1	0.0
29	18	6	2014	29	2	868.8	4.1	0.0	0.0	4.1	0.0	0.0	0.0
30	19	6	2014	30	2	863.8	0.2	0.0	0.0	0.2	0.0	0.0	0.0
31	20	6	2014	31	2	859.5	0.1	0.0	0.0	0.1	0.0	0.0	0.0
32	21	6	2014	32	2	856.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
33	22	6	2014	33	2	851.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0

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

```
carl@mike: ~/Git_Projects/AquaCropOptimise/field_crop_planting_optimization
Terminal
carl@mike:~/Git_Projects/AquaCropOptimise/field_crop_planting_optimization$ ls
aquacrop      load_climate_data.py  PARAM      run_many_simulations.py
climate.csv   multi_year_growing_season.csv  plotting.py  setup_aquacrop_input_files.py
DATA          multi_year_yield.csv    plots.py    SIMUL
IMPORT        OBS                      __pycache__ temp2.csv
LIST          OUTP                     readme.md
carl@mike:~/Git_Projects/AquaCropOptimise/field_crop_planting_optimization$ python run_many_simulat
ions.py
yarA0.csv
yarA1.csv
yarA2.csv
yarA3.csv
yarA4.csv
2007
4
26
getting sim files ready for year = 2007-04-26 00:00:00
42.196 2007 8 14 9.5 2.6 111
2007
4
27
getting sim files ready for year = 2007-04-27 00:00:00
42.317 2007 8 14 9.8 5.3 110
2007
4
28
getting sim files ready for year = 2007-04-28 00:00:00
42.298 2007 8 15 7.6 4.2 110
2007
4
29
getting sim files ready for year = 2007-04-29 00:00:00
42.311 2007 8 15 6.4 3.0 109
2007
4
30
getting sim files ready for year = 2007-04-30 00:00:00
42.368 2007 8 15 8.2 2.8 108
```