**Run PCR-GLOBWB**

**at the global extent – 30arcmin**

**Exercises (cooking recipes)**

1. **Clone/download PCR-GLOBWB\_model**
2. **Adjusting PCR-GLOBWB configuration (.ini) files and starting PCR-GLOBWB runs**
3. **Clone/download PCR-GLOBWB\_model**

On your computational machine, clone/download the PCR-GLOBWB\_model from the github website/url: <https://github.com/UU-Hydro/PCR-GLOBWB_model.git> and switch to the branch **“feature/exercise”**. For an illustration/example, see the following commands for an example.

# for example, I want to download it on my home directory

$ cd

$ pwd

/home/edwin

# clone/download from the github repo

$ git clone https://github.com/UU-Hydro/PCR-GLOBWB\_model.git

Cloning into 'PCR-GLOBWB\_model'...

remote: Enumerating objects: 32729, done.

remote: Counting objects: 100% (11376/11376), done.

remote: Compressing objects: 100% (3007/3007), done.

remote: Total 32729 (delta 8380), reused 11222 (delta 8249), pack-reused 21353

Receiving objects: 100% (32729/32729), 83.32 MiB | 29.79 MiB/s, done.

Resolving deltas: 100% (24127/24127), done.

# go to the directory PCR-GLOBWB\_model

$ cd PCR-GLOBWB\_model

$ pwd

/home/edwin/PCR-GLOBWB\_model

# list all git branches, we will use the branch “**feature/exercise**”

$ git branch -a

\* master

remotes/origin/HEAD -> origin/master

remotes/origin/aqueduct\_2021

remotes/origin/feature/arise\_30sec\_aqueduct\_2022-04-14

remotes/origin/feature/efr

**remotes/origin/****feature/exercise**

remotes/origin/master

# checkout to the branch “**feature/exercise**”

$ git checkout -b **feature/exercise** origin/feature/exercise

Branch 'feature/exercise' set up to track remote branch 'feature/exercise' from 'origin'.

Switched to a new branch 'feature/exercise'

# do git pull, to make sure that you will use the latest version

$ git pull

Already up to date.

# list all files in PCR-GLOBWB\_model

$ ls

LICENSE README.md README.txt clone\_landmask\_maps conda\_env config exercise known\_issues.txt misc model modflow various\_tools

You may want to use “mc” (midnight commander) to explore the content of “PCR-GLOBWB\_model”. The two important folders that will be used are “model” and “config”. The folder “model” contains the model codes (python scripts) of PCR-GLOBWB, while the folder “config” contains the configuration (.ini) files to setup PCR-GLOBWB model runs.

1. **Adjusting .ini (configuration) files for your own case and starting PCR-GLOBWB runs**

**30min global runs at the global extent**

If you explore the folder “config” on the folder “PCRGLOBWB\_model”, you will find a setup/configuration file (.ini) called “**setup\_30min.ini**”. This configuration file is basically using the model parameters and forcing input files as used in the GMD paper run of PCR-GLOBWB 2 (Sutanudjaja et al., 2018, <https://gmd.copernicus.org/articles/11/2429/2018/>).

Please open (and later edit) this file “**setup\_30min.ini**” (e.g. using “geany”).

Please edit and make sure that the field **“inputDir” (input directory)** under the “[globalOptions]” is consistent to the one on your computational machine.

* On velocity, the input files used in Sutanudjaja et al., 2018 are stored on /data/hydroworld/pcrglobwb2\_input\_release/version\_2019\_11\_beta/pcrglobwb2\_input

Please also adopt the location for the cloneMap.

* On velocity, the cloneMap for a global 30min file is on /data/hydroworld/pcrglobwb2\_input\_release/version\_2019\_11\_beta/pcrglobwb2\_input/global\_30min/cloneMaps/clone\_global\_30min.map

Please also adopt the location for the “outputDir” (output directory). You don’t have to create this output directory, but please make sure that you have an access to it

* On velocity, please write your PCR-GLOBWB run output files on /scratch/<your\_username>. An example (for the user name “sutan101”): outputDir = /scratch/sutan101/pcrglobwb2\_output/30min\_global/

Then, you can run PCR-GLOBWB using the following command line. Note that you may want to put this run under a screen session

# python <folder\_where\_ pcrglobwb\_model\_is>/deterministic\_runner.py <your\_ini\_file> debug

# an example:

$ python /home/edwinhs/github/UU-Hydro/PCR-GLOBWB\_model/model/deterministic\_runner.py /home/edwinhs/github/UU-Hydro/PCR-GLOBWB\_model/config/setup\_30min.ini debug

PS: The argument “debug” is optional. If you use it, you will get more information printed on your screen while your model is running.

Your model should run. If not, please check the aforementioned steps or shout to the instructor.

PS: Before running the model, please make sure that you have loaded the software required for running PCR-GLOBWB (e.g. activating the PCR-GLOBWB conda environment, see e.g. <https://github.com/UU-Hydro/PCR-GLOBWB_model#how-to-install>)

While your model is still running, you may already want to explore the files/folders that are written to the output directory “outputDir”.

$ cd /scratch/sutan101/pcrglobwb2\_output/30min\_global/

$ ls

log maps netcdf scripts states tmp

Explore to all sub-folders and try to get some ideas about the files that are written in each sub-folder (also one of the slides from the presentation in the morning):

- log : logger, backup/copy of ini file that you used

- maps : usually empty (mainly used during debugging process)

- netcdf : netcdf output files are stored here

- scripts : backup of the python script files that you used

- states : model states at the end of the each simulation year (\*12-31.map)

- tmp: : used during resampling/cropping processes

You may want to visualize your netcdf output files

$ cd /scratch/sutan101/pcrglobwb2\_output/30min\_global/netcdf/

$ ncview discharge\_dailyTot\_output.nc

**Some extra exercises:**

* Try make some other runs with different settings in your .ini file, i.e. writing to different output folders, different spin-up options, more output variables that will be reported in netcdf files.
  + For variable names that you can report, please check <https://github.com/UU-Hydro/PCR-GLOBWB_model/blob/master/model/variable_list.py>
* An extra challenge: Make a new run using a set of initial conditions that you have generated from one of your previous runs.
* For an example of configuration file for a 5 arcmin run, please refer to the file <https://github.com/UU-Hydro/PCR-GLOBWB_model/blob/master/config/setup_05min.ini>
  + For 5 arcmin run, please do not make a global run on velocity, as this run is quite computationally demanding.
  + Yet, you can test it for a limited/small region, says for an area smaller than 250,000 km2, e.g. the Rhine-Meuse basin.
  + We will do this on the next exercise.