



# HGS-PDAF v1.0 (III)

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# HGS-PDAF: preparation with an example model

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# Where to find the example models

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- If you use git:
  - Github repository for users: [https://github.com/qiqi1023t/HGS-PDAF\\_v1.0\\_GMD](https://github.com/qiqi1023t/HGS-PDAF_v1.0_GMD)
  - Use git clone or svn checkout to download the repository to your local machine
  - The example folder is included together with the source code
- Or download the current version on Zenodo:
  - <https://doi.org/10.5281/zenodo.10000887>
  - Filename: examples.zip
- Follow the Readme file in the source code to get the necessary input files for the model



# What are we going to prepare?

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- Open the runscript:

```
# Define run directory
export BASE_DIR= # root path to the hgs-pdaf directory
export HGS_DIR= # root path to HGS binary
export MODEL_DIR= # root path to the HGS model directory
export WORK_DIR= # root path to the output directory
export ENS_DIR= # root to the output ensemble directory

export BASE_DIR=/p/home/jusers/tang1/jusuf/HGS-PDAF_V1.0/hgs-pdaf
export HGS_DIR=/p/home/jusers/tang1/jusuf/HydroGeoSphere-2529-
Linux/HydroGeoSphere-2529-Linux/
export MODEL_DIR=/p/project/icei-prace-2023-0004/tang1/input_HGS-
PDAF/hgsmodel/synthetic_hete/
export WORK_DIR=/p/scratch/icei-prace-2023-0004/tang1/output/hgs-pdaf
export ENS_DIR=${WORK_DIR}/n2_hete/
```



# **Step 1: prepare the HGS model**

- 
- Adapt the transient HGS model to multiple 1-step models
  - This has already been done for our example case
  - If the user starts with his/her own model, this needs to be done before the DA run!
  - The following slides show how to do this

# Adapt the HGS model to run hgs-pdaf

- Main idea:
  - The transient model is split into multiple short-period model. The length of this short period is equal to the interval between two assimilation steps;
  - After each time step, the initial conditions for the next time step will be replaced by the out put from the current time step;
  - Boundary conditions at each time step is replaced with the real value.

# Example of bash scripts to prepare the HGS model

```
#!/bin/bash

python EXECPROC/Preproc.py
python EXECPROC/Preproc_pdaf.py

cp HGS/Grokfiles/wells/wells_flow_1.inc HGS/Grokfiles/wells_flow.inc
python EXECPROC/Spinup.py

for i in $(seq 1 1 95)
do
    cp HGS/Grokfiles/wells/wells_flow_${i}.inc HGS/Grokfiles/wells_flow.inc

    python EXECPROC/Execproc.py
    python EXECPROC/obshgs2obspesst_Sequential.py

    preplot HGS/Flowo.pm

    cp HGS/Flowo.head_pm.0001 HGS/IC/Ini_pm_SS
    cp HGS/Flowo.head_olf.0001 HGS/IC/Ini_olf_SS

done
#SLEEP 3
#)
```



# Step 2: prepare the observation file

- 
- Generate the head observation
  - The observation file for this test case is already prepared and included in the model folder.
  - If the user starts with his/her own model, this needs to be done before the DA run!
  - The following slides show how to do this

# Find the observation location file

Prepare the file

'*ObservationPoints\_selection.dat*' in the preprocessing folder. The location (x,y,z coordinates) is defined in this file.

55,50,85  
255,50,85  
95,150,85  
35,200,85  
255,250,85  
55,300,85  
235,350,85  
55,450,85

# Find the observation value file

The observation values are stored in separated files. In this example we have 8 obervation points, i.e. 8 files.

Observation 1:

```
365,94.18771457,0.05  
366,94.2420817,0.05  
367,94.13884553,0.05  
368,94.14725778,0.05  
369,94.09936834,0.05  
370,94.09046822,0.05  
371,94.06449754,0.05  
372,94.09066345,0.05  
373,94.1509718,0.05  
374,94.17967425,0.05  
375,94.11391162,0.05  
376,94.16649582,0.05  
377,94.14672236,0.05  
378,94.14981592,0.05
```

# Example of the generated observation file

Copy the HGS generated coordinate file  
*'Flowo.coordinates\_pm'* to the  
preprocessing folder

Run *gen\_obs\_head*

You will get the observation file  
*obs\_HEAD.nc*

```
netcdf obs_HEAD {  
dimensions:  
    n_obs = 8 ;  
    time = 95 ;  
variables:  
    float x(n_obs) ;  
    float y(n_obs) ;  
    float z(n_obs) ;  
    int obs_id(n_obs) ;  
    float time(time, n_obs) ;  
    float Head(time, n_obs) ;  
    float std(time, n_obs) ;  
  
// global attributes:  
    :title = "HEAD observations" ;  
    :_FillValue = 1.e+07f ;
```



# Step 3: Modify the configuration files for the parameters

- Modify the two *namelist* files to specify the parameters for HGS and PDAF

# Step 3: modify the namelist files for HGS

---

- Modify *namelist.hgs*

```
! Namelist for HGS model configuration
&hgs

! Settings for model initialisation
prefix = 'Flow'
trace_name = ''
insuffix = '0001' ! last state output No., e.g., '.0024'
outsuffix = '0001' ! new ini state No., e.g., '.0000'
isolf = .true. ! true if overland flow, false if only pm flow
isconc = .false. ! true with transport, false without
hgs_version = 2 ! 1 for old HGS version, 2 for HGS 2013+
```

/



# Step 3: modify the namelist files for PDAF

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- Modify *namelist.pdaf*

```
! Namelist for PDAF configuration
&pdaf
  ! General control
  str_daspec='da'          Prefix for the data assimilation output file
  filtertype=2              Assimilation method
  printconfig=.true.
  locweight=3               For localised filter, currently not available
  loctype=0
  forget=1.0                For inflation
  varscale=1.0
  type_trans=0
  type_forget=0
  use_global_obs = .true.
  istep=<pdafstep>
```



# Step 3: modify the namelist files for PDAF

---

```
! Settings for initialization
path_init=''
file_init=''
read_inistate=.false.
file_inistate='state_ini_'
```

```
! Output control
write_da = .true.
write_ens = .true.
```

```
/
```

Write the DA output file  
Write the result for each ensemble member

```
! Namelist for parallel configuration for ensemble DA
&pdaf_parallel
dim_ens=<ens_size>
```

```
/
```

# Step 3: modify the namelist files for PDAF

---

```
! Settings for assimilating HEAD observations
&pdaf_hgs
state_type = 6      Which variables will be included into the state vector
assim_o_head=.true.
rms_obs_head=0.05    Observation error
lradius_head=3.0e5
sradius_head=3.0e5
head_fixed_rmse=.true.
head_exclude_diff=1.6
path_obs_head='/p/project/icei-prace-2023-0004
file_head_prefix='obs_HEAD'                                Full name of the observation file
file_head_suffix ='.nc'
```



# Step 3: modify the namelist files for PDAF

---

```
! Settings for assimilating SATURATION observations
assim_o_sat=.false.
rms_obs_sat=0.01e8
lradius_sat=3.0e5
sradius_sat=3.0e5
sat_fixed_rmse=.true.
sat_exclude_diff=1.6
path_obs_sat='/p/project/icei-prace-2023-0004/tang1/i
file_sat_prefix='obs_SAT'
file_sat_suffix ='.nc'
```

ResultPath=<path>

/



# **Step 4: complete the run script**

- 
- Modify the run script
  - The following slides show an example of the run script used for the slurm system

# Step 4: Complete the run script

---

```
#!/bin/bash -x
#SBATCH --account= Your account
#SBATCH --nodes= Number of nodes
#SBATCH --ntasks= Number of tasks
#SBATCH --ntasks-per-node= Number of tasks per node
#SBATCH --output= Name of the job output file
#SBATCH --error= Name of the job error output file
#SBATCH --time= Required run time
#SBATCH --partition=batch
#SBATCH --mail-user= You email address
#SBATCH --mail-type=ALL
```



# Step 4: Complete the run script

```
# *** start of job script ***
ulimit -s unlimited
set -vx
export NOPP=1

echo $NCPUS
# system dependent command lines
#module load Stages/2019a
module load Intel
module load ParaStationMPI
module load imkl netCDF netCDF-Fortran
export NETCDF_Fortran_INCLUDE_DIRECTORIES=${EBROOTNETCDFMINFORTRAN}/include/
export NETCDF_C_INCLUDE_DIRECTORIES=${EBROOTNETCDF}/include/
export NETCDF_CXX_INCLUDE_DIRECTORIES=${EBROOTNETCDFMINCPLUSPLUS4}/include/

module load Python
module load SciPy-Stack

# end

export OMP_WAIT_POLICY=PASSIVE
export CRAY_OMP_CHECK_AFFINITY=TRUE
export OMP_NUM_THREADS=1
```

You may need to  
change these lines  
according to your  
system  
configuration



# Step 4: Complete the run script

---

```
# Ensemble size
export NENS=2

# Total time steps
export TSTEPS=2

# Define run directory
export BASE_DIR= # root path to the hgs-pdaf directory
export HGS_DIR= # root path to HGS binary
export MODEL_DIR= # root path to the HGS model directory
export WORK_DIR= # root path to the output directory
export ENS_DIR= # root to the output ensemble directory

# Define if serial model run or DA run
# A serial run should be done before the ensemble run
export firstrun=T If this is set to F(False), spin-up run will be skipped.
Always keep this as T if parameters are updated.
```



# Step 5: Run the experiment

- Submit the run script by typing:

```
sbatch name_of_the_runscript.sh
```

- You will find the output files in the `$WORK_DIR` directory

A screenshot of a web browser showing the GitHub Discussions page for the repository "HGS-PDAF\_v1.0\_GMD". The browser's address bar shows "github.com". The navigation bar includes links for Code, Issues, Pull requests, Discussions (which is underlined in red), Actions, Projects, Wiki, Security, Insights, and Settings. A search bar at the top right contains the placeholder "Type ⌘ to search" and a "New discussion" button. Below the search bar are filters for "Sort by: Latest activity", "Label", "Filter: Open", and "New discussion". A sidebar on the left titled "Categories" lists "View all discussions" (selected), Announcements, General, Ideas, Polls, Q&A, and Show and tell. A central section titled "Welcome to discussions!" explains the purpose of discussions and provides a "new discussion" link. A callout box titled "Most helpful" encourages marking answers. At the bottom, links lead to "Community guidelines" and "Community insights".

# Discussion on GitHub

If you want to discuss more with other users/developers:

# For advanced user:

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- If you need
  - Assimilate a new observation type
  - Adding a new variable into the state vector
  - Using different types of filters
  - Use localisation
  - Use heterogeneous observation errors
  - Other requirements regarding to the specific assimilation approach

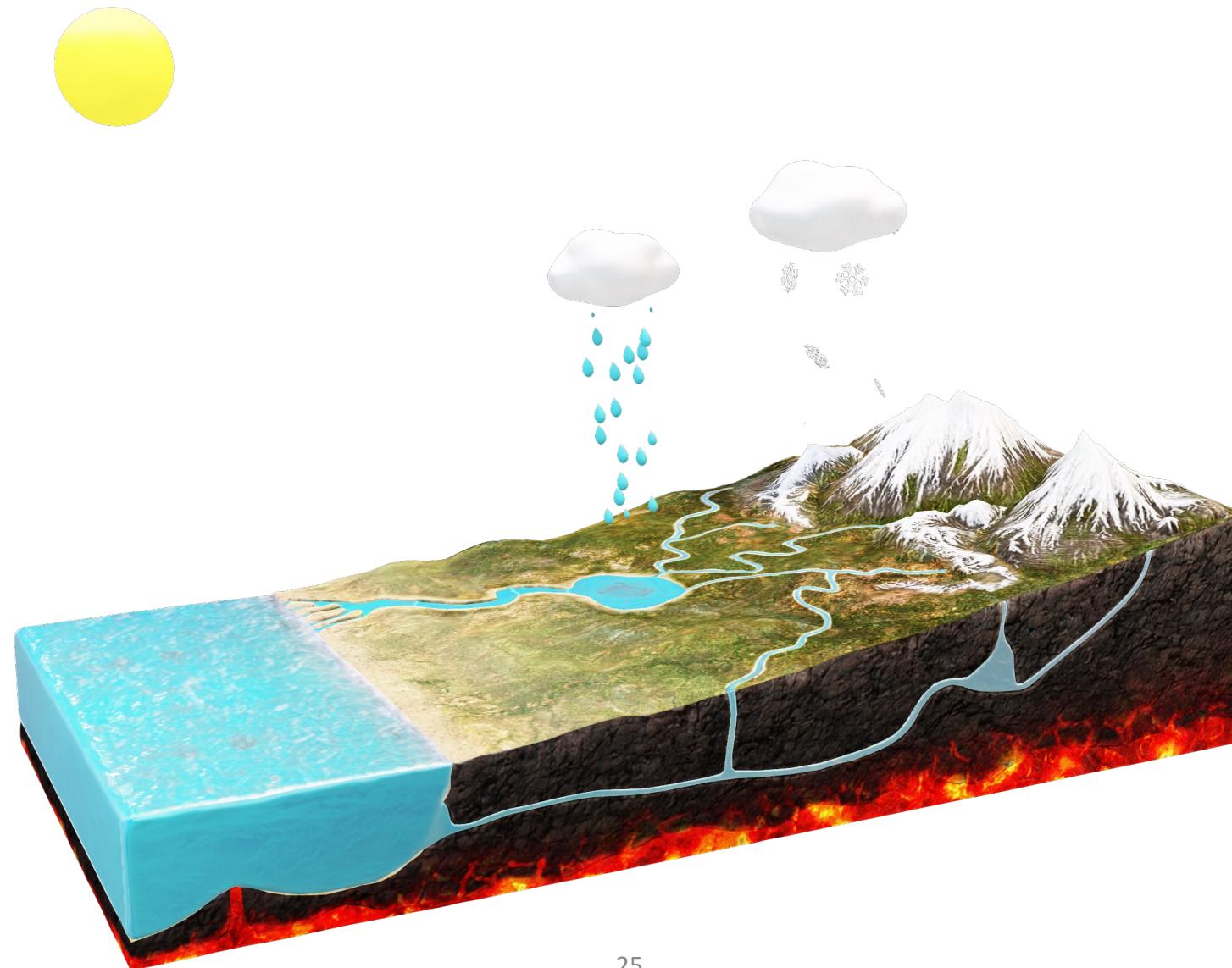
*Please let me know and I'm more than happy to help!*

*Contact: [qi.tang@unine.ch](mailto:qi.tang@unine.ch)*

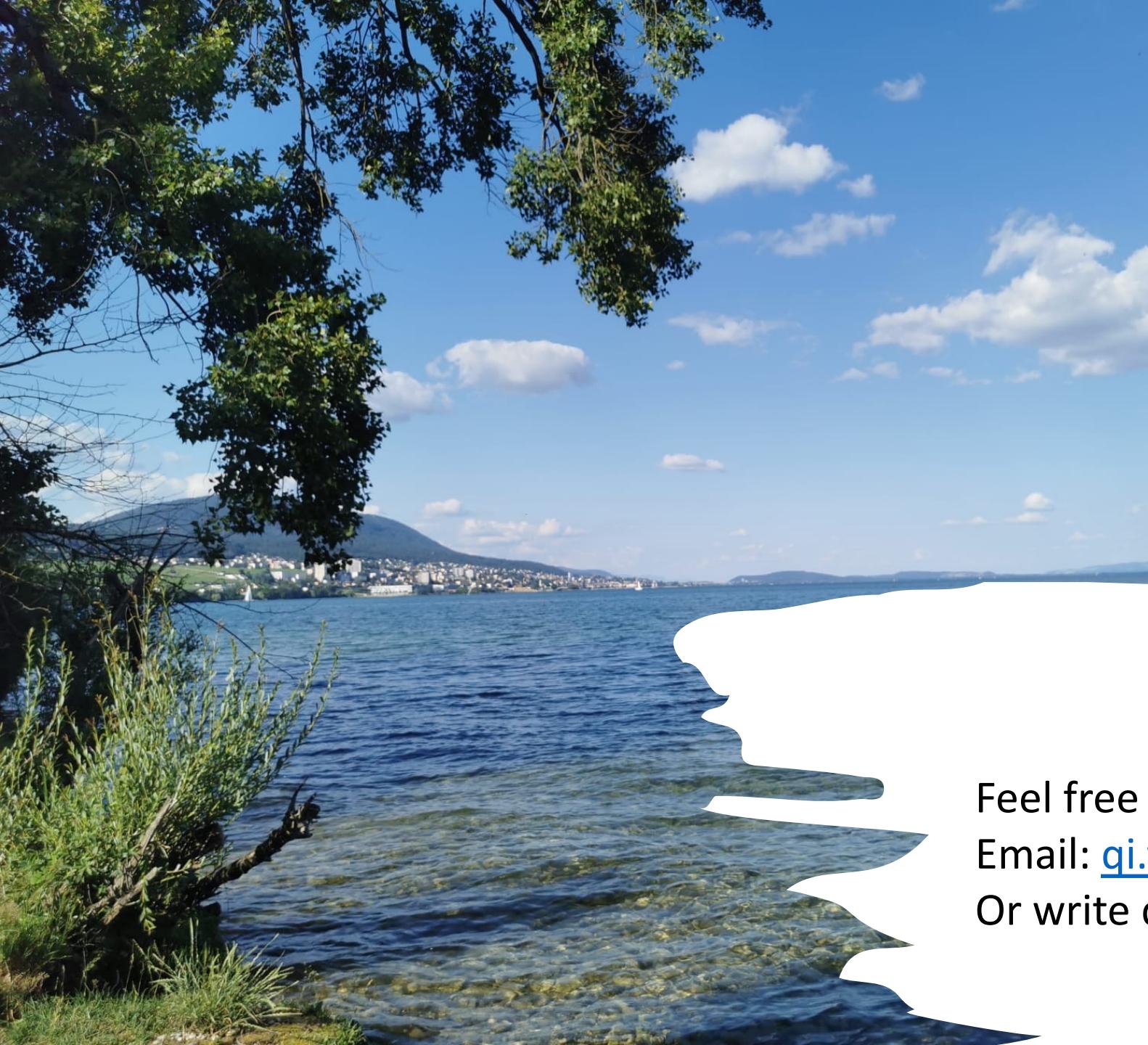


# Next step: Start your own data assimilation experiments

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***Enjoy it!***

Feel free to contact us if you need any help:  
Email: [qi.tang@unine.ch](mailto:qi.tang@unine.ch)  
Or write directly on GitHub!