

Assignment Guidance

Introduction to Bioinformatics
2023-Spring

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☎ If you have any question, ask question in Q&A board or send email

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1. Start with GitHub

Assignment will be provided through GitHub Classroom.

Please make a GitHub account before starting assignment.

<https://github.com>

Issue GitHub Token

- Since August 13, 2021, git no longer supports password authentication. You must use **personal access token** for authentication.
- To issue a token, please follow as the link below.
<https://docs.github.com/en/authentication/keeping-your-account-and-data-secure/creating-a-personal-access-token#creating-a-personal-access-token-classic>
- Please make sure to save token somewhere.

Start assignment with GitHub Classroom

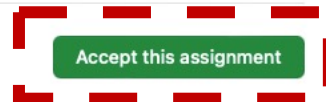
1. Click the invitation link to the assignment and Accept the assignment.

icb-2023-1-classroom

Accept the assignment —

beta-assignment

Once you accept this assignment, you will be granted access to the `beta-assignment-ta-profile` repository in the `icb-2023-1` organization on GitHub.



You accepted the assignment, **beta-assignment**. We're configuring your repository now. This may take a few minutes to complete. Refresh this page to see updates.

Note: You may receive an email invitation to join `icb-2023-1` on your behalf. No further action is necessary.



You're ready to go!

You accepted the assignment, **beta-assignment**.

Your assignment repository has been created:

<https://github.com/icb-2023-1/beta-assignment-ta-profile>

We've configured the repository associated with this assignment.



You can open assignment directly in VS Code if you use that.

Go directly to your repository

2. Set up

Option1. Use your local environment (bash environment available)

- You must pre-install [docker](#) and be available for setting dependencies

Option2. [Google cloud shell](#) editor (bash environment not available)

- If you need guidance for Google cloud shell, [link](#).

Clone your repository

- Open the terminal and clone your repository

```
git clone <GitHub_repository_link>
cd ./<GitHub_repository_name>
```

```
eunbelivable@cloudshell:~$ ls
README-cloudshell.txt
eunbelivable@cloudshell:~$ git clone https://github.com/icb-2023-1/beta-assignment-
ta-profile.git
Cloning into 'beta-assignment-ta-profile'...
Username for 'https://github.com': ta-profile
Password for 'https://ta-profile@github.com': 
-----
remote: Enumerating objects: 16, done.
remote: Counting objects: 100% (16/16), done.
remote: Compressing objects: 100% (11/11), done.
remote: Total 16 (delta 2), reused 10 (delta 0), pack-reused 0
Receiving objects: 100% (16/16), 537.04 KiB | 2.77 MiB/s, done.
Resolving deltas: 100% (2/2), done.
eunbelivable@cloudshell:~$
eunbelivable@cloudshell:~$ ls
beta-assignment-ta-profile  README-cloudshell.txt
eunbelivable@cloudshell:~$ cd beta-assignment-ta-profile/
eunbelivable@cloudshell:~/beta-assignment-ta-profile$
```

Clone your repository

Enter username and password(token)
! For password, you should enter "token"
! It is normal for token not to appear in the interface

Change directory to your cloned repository

Brief introduction of directory

```
eunbelivable@cloudshell:~/beta-assignment-ta-profile$ ls  
command  data  img  main.sh  README.md  restart.sh  result  setup.sh
```

- **command**: directory to store commandXX.sh files.
In commandXX.sh files, you should write your commands
- **data**: directory to store data files used for assignment.
- **result**: result directory to save the result files of your command files.
- **main.sh**: execute all your command files in command directory in once.
- **restart.sh**: restart docker
- **setup.sh**: set up docker to solve assignment
! Please make sure to run docker solving assignment.
- etc (you don't have to touch or execute the contents below)
 - README.md: contain guidance for assignment
 - img: contain images

Workflow

```
eunbelivable@cloudshell:~/beta-assignment-ta-profile$ ls  
command data img main.sh README.md restart.sh result setup.sh
```

- While you solve the assignment, you may change **command**, **data** and **result** directory.
- Workflow
 1. Set up docker before you start.
./setup.sh
 2. After you set up, you can see you user account changed.
Path of copied directory is **/home/exercise03/exercise03**.
Please work in this directory
 3. Write command lines(**command**)
(./command/commandXX.sh)
 4. Save outcome of command file to **result** directory
(./result/resultXX_X.txt or ./result/resultXX_X.csv)
- Execution
 - Run commandXX.sh independently
bash ./command/commandXX.sh
 - Run all commandXX.sh files
bash ./main.sh

```
eunbelivable@cloudshell:~/beta-assignment-ta-profile$ ./setup.sh  
Unable to find image 'khh7840/introbioinfo-exercise03:latest' locally  
latest: Pulling from khb7840/introbioinfo-exercise03  
e79bb959ec00: Pull complete  
7dc808d5d247: Pull complete  
7a8d7e31e945: Pull complete  
39387c6ab5c0: Pull complete  
fa8c9cb53acf: Pull complete  
dealecf9c32: Pull complete  
Digest: sha256:60fc7d81d307cbb758a433194c25c895539ea83abadc436e784  
Status: Downloaded newer image for khb7840/introbioinfo-exercise03  
exercise03@539066f8c6c9:~$ ls  
README exercise03  
exercise03@539066f8c6c9:~$ cd exercise03/  
exercise03@539066f8c6c9:~/exercise03$
```


FAQ

- If you want to use "relative path" to redirect your result, assume your current directory is **/home/exercise03/exercise03**.
- Your assignment will be **graded with automated scripts**.
We will reproduce your result file with main.sh file and grade based on reproduced file.
Please make sure your command files to be executed and be careful with typo, path and error.
- **!** Tools needed for the assignment is pre-installed in docker. Do not install any additional tools.
- **!** If you can't execute a shell file due to "Permission denied error", please try this command and re-execute.
`chmod +x ./<SOME_SHELL_FILENAME>.sh`
- **!** When you exit from the docker and you want to rerun the docker,
`./restart.sh`
- **!** If docker is not set up, please check if you are already running docker.
- You can refer to the [slide](#) to see an example.

3. Submit

Option1. Push the cloned repository

Option2. Use the GitHub interface

Guidance

- You can submit multiple times and your last submission will be graded.
- If you didn't make commit on time, your solution will not be graded.
- Only push files in command and result directory. Do not push files in other directories. (e.g. data directory)

Option1. Push the cloned repository

- At initial stage, you should tell git about your profile.

```
git config --global user.email "you@example.com"
git config --global user.name "Your Name"
```

1. Add edited files to git
2. Commit with commit message
3. Submit your answers by pushing the cloned repository
You may need your github ID and password(token) in this step

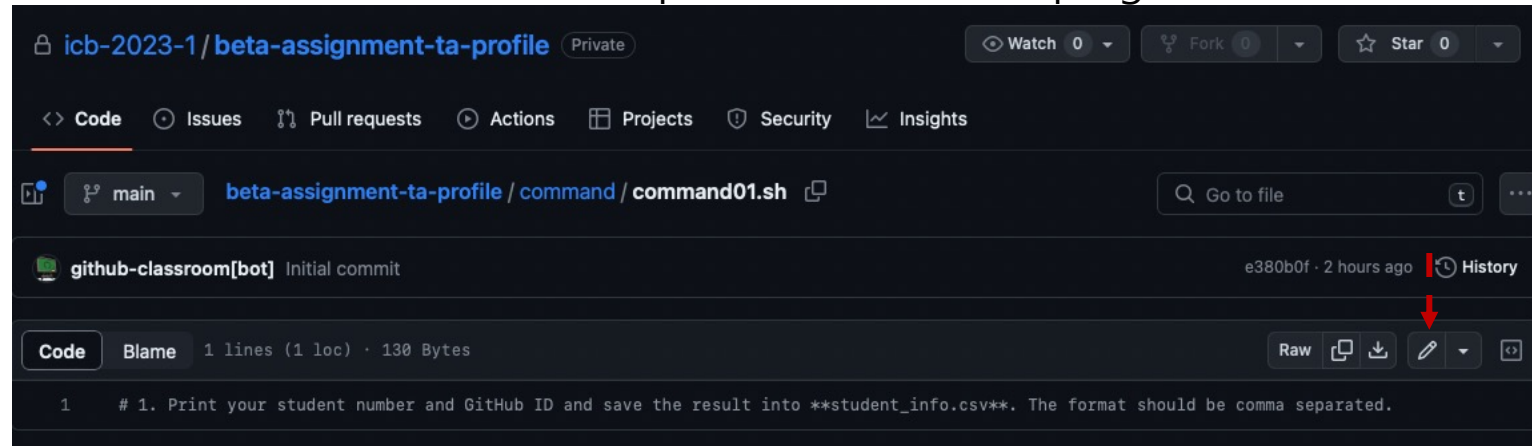
```
git add .
git commit -m "Initial commit" # You can change message as you want
git push origin main
```

```
exercise03@539066f8c6c9:~/exercise03$ git add .
exercise03@539066f8c6c9:~/exercise03$ git commit -m "finished assignment"
[main 1cb51be] finished assignment
 2 files changed, 2 insertions(+), 2 deletions(-)
exercise03@539066f8c6c9:~/exercise03$ git push origin main
Username for 'https://github.com': ta-profile
Password for 'https://ta-profile@github.com':
Counting objects: 8, done.
Delta compression using up to 2 threads.
Compressing objects: 100% (6/6), done.
Writing objects: 100% (8/8), 816 bytes | 0 bytes/s, done.
Total 8 (delta 3), reused 0 (delta 0)
remote: Resolving deltas: 100% (3/3), completed with 2 local objects.
To https://github.com/icb-2023-1/beta-assignment-ta-profile.git
 6780dfe..1cb51be  main -> main
```

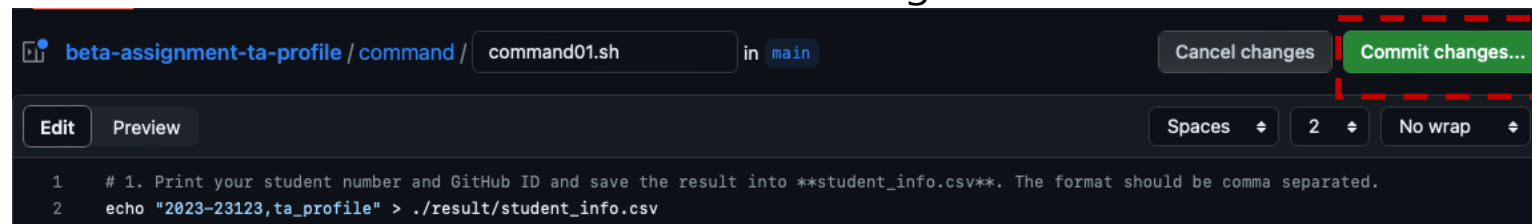
Option2. Use GitHub interface

If you are not familiar with git, you can use the interface as an alternative.

1. Go to a file to edit and click the pencil icon at the top right corner.



2. Edit the file with the text editor and click the green button



! Conflict can be occurred if you change files in the interface.

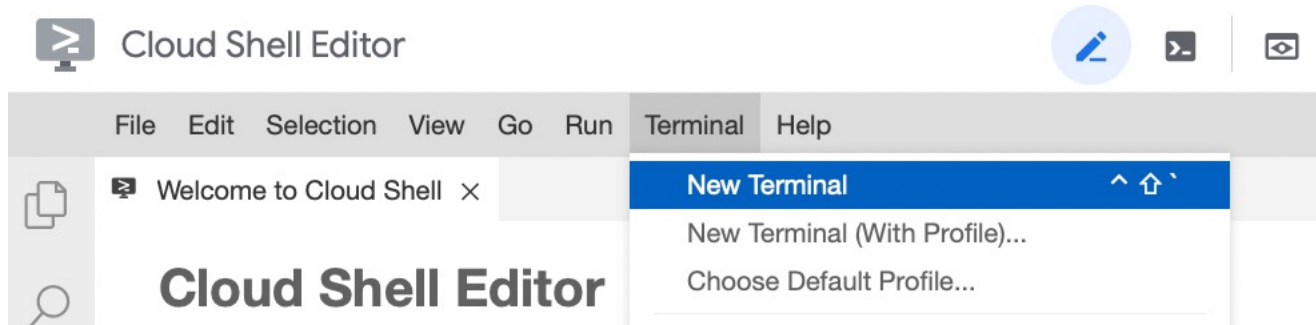
If you want to reflect changes in the interface, pull your remote to local `git pull`

Introduction to Bioinformatics

4. Supporting Information

Introduce CloudShellEditor

1. Open the link <https://ide.cloud.google.com>
2. Open a terminal from the cloud shell editor.



- As a free service, it has some limitations
 - It takes some time when initiating.
 - 5GB storage limit
 - Cannot be opened with secret mode of browser
 - If the session is inactive for 20 minutes, the instance is terminated and any modification outside \$HOME will be deleted
 - Weekly usage limitation: ~50hrs
 - If you don't access cloud shell for 120 days, the \$HOME will be deleted.
- You can see details in <https://cloud.google.com/shell/docs/editor-overview?hl=ko>

Assignment Example

! Note that this example used pseudo assignment

Organization Course Semester Professor T.A.

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Beta Assignment

The goal of this assignment is to guide the procedure solving assignment.

command01.sh

1. Print your student number and GitHub ID and save the result into `student_info.csv`. The format should be comma separated.

e.g.
2023-12345, ta_profile

1. Set up docker
2. Write command line to `./command/command01.sh`

```
exercise03@539066f8c6c9: ~/exercise03 x + - 편집자
# 1. Print your student number and GitHub ID and save the result into **student_info.csv**. The format should be comma separated.
echo "2023-23123, ta_profile" > ./result/student_info.csv
~
~
~
```

3. Run all the command files

```
exercise03@539066f8c6c9:~/exercise03$ vim command/command01.sh
exercise03@539066f8c6c9:~/exercise03$ ls result
exercise03@539066f8c6c9:~/exercise03$ ./main.sh
-----
exercise03@539066f8c6c9:~/exercise03$ ls result
student_info.csv
exercise03@539066f8c6c9:~/exercise03$ cat result/student_info.csv
2023-23123, ta_profile
```

1. Write commands.
2. As you can see here, there's no result file yet.
3. Execute `main.sh` to run all the command files.
4. Result file (`student_info.csv`) generated