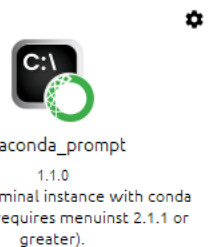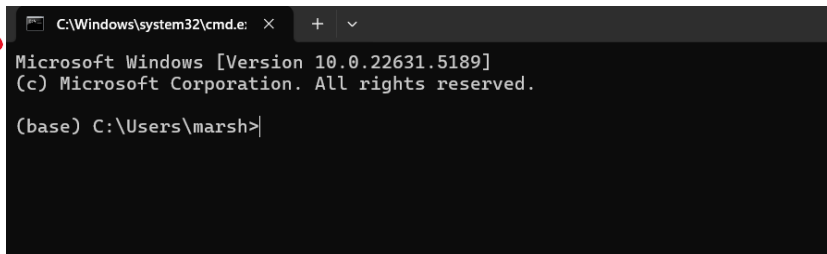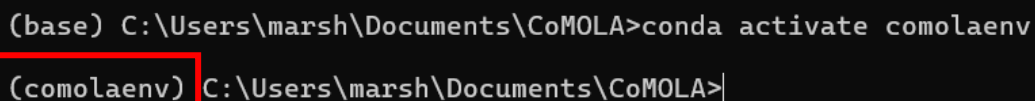Starting CoMOLA on your personal Desktop:

1. Clone the repository from GitHub on the local desktop (or, if provided, directly download the CoMOLA files on your desktop)
2. Download Anaconda on your desktop and sign up with a free account
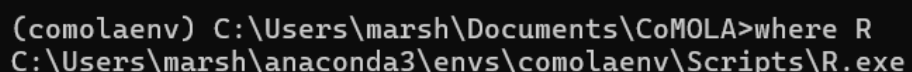3. Launch anaconda_prompt.
   This is what you'll see:

4. Now, we change the working directory to where our CoMOLA folder is. We write: cd <path to the CoMOLA folder>
   Note: If the CoMOLA folder is in a different drive, you might have to change the drive first before changing the working directory. You can simply do if by writing D: or E: or F: and pressing enter.
5. Now, we'll create a conda environment with python 3.11
   conda create -n <suitable name for your environment> python=3.11
   example: conda create -n comolaenv python=3.11
   Proceed by pressing y and enter when prompted.
6. Lets activate our environment: conda activate comolaenv

7. Once the environment is activated, we'll install R:
   7.1 conda install -c conda-forge r-base
       Proceed by pressing y and enter when prompted.
   7.2 *(Optional but recommended)*: Install R essentials (which includes r-essentials, r-devtools, tidyverse, etc.):
       conda install -c conda-forge r-essentials
       Proceed by pressing y and enter when prompted.
   7.3 Check for successful installation of R with: where R

       Note: If you don't see a R path, restart anaconda and simply activate the already created environment and check for R path

8. We also need matplotlib: conda install -c conda-forge matplotlib
   Proceed by pressing y and enter when prompted.
9. At last we need numpy: conda install -c conda-forge numpy=1.26.4
   Proceed by pressing y and enter when prompted.
10. Finally lets check python and R paths within the environment, we need them in or config.ini files.
    where R

```
(comolaenv) C:\Users\marsh\Documents\CoMOLA>where R
C:\Users\marsh\anaconda3\envs\comolaenv\Scripts\R.exe
```

    where python

```
(comolaenv) C:\Users\marsh\Documents\CoMOLA>where python
C:\Users\marsh\anaconda3\envs\comolaenv\python.exe
```

11. Open config.ini files via: notepad config.ini
12. Change the R and python paths in the config.ini file to your comola environment paths and save the file:

```
[config_model]

file_path_R = C:\Users\marsh\anaconda3\envs\comolaenv\Scripts\R.exe
file_path_Python = C:\Users\marsh\anaconda3\envs\comolaenv\python.exe
```

13. You can adjust population size, maximum number of generations in the config.ini file.
    Note: when starting for the first time make sure start_from_previous_gen is False

```
[config_optimization_algorithm]

pop_size = 5
max_generations = 10
mutation_rate = 0.01
crossover_rate = 0.9
priority = True
maximize = True
extreme_seeds = False
max_repair_trials = 10000
start_from_previous_gen = False
```

14. Now, lets run our optimization: python __init__.py

```
(comolaenv) C:\Users\marsh\Documents\CoMOLA>python __init__.py
```

15. Hooray! Now we have a running CoMOLA optimization.