Starting CoMOLA on your personal Desktop:

1. Download Anaconda (https://www.anaconda.com/download) on your desktop and sign up with a free account.
2. We also need Git: while installing please **choose** the option Add Git to PATH - install Git via https://git-scm.com/install/windows
3. Launch anaconda_prompt within Anaconda

CoMOLA Installation to be done once:

4. Now, we change the working directory to where our desired location is. We write: cd <path to the desired location> For example: cd Downloads or cd Documents Note: If the folder is in a different drive, you might have to change the drive first before changing the working directory. You can simply do it by writing D: or E: or F: and pressing enter and then the folder path.
5. Clone the github repository in this location by: git clone --branch Aditi --single-branch https://github.com/Helmholtz-UFZ/CoMOLA.git You will now see a CoMOLA folder at this location.

Creating this conda environment to run CoMOLA within (to be done once):

6. Navigate within the CoMOLA folder using: cd CoMOLA
7. 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+enter when prompted.
8. Lets activate our environment: conda activate comolaenv

```
(base) C:\Users\marsh\Documents\CoMOLA>conda activate comolaenv

(comolaenv) C:\Users\marsh\Documents\CoMOLA>
```

9. Once the environment is activated, we'll install R:
   9.1. conda install -c conda-forge r-base Proceed by pressing y+enter when prompted.
   9.2. (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+enter when prompted.
   9.3. Check for successful installation of R with: where R

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

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

10. We also need matplotlib: conda install -c conda-forge matplotlib
     Proceed by pressing y+enter when prompted.

11. At last we need numpy: conda install -c conda-forge numpy=1.26.4
     Proceed by pressing y+enter when prompted.

Setting up the config.ini file for our optimization run:

12. Finally lets check python and R paths within the environment, we need them in 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
```

13. Open config.ini files via: notepad config.ini

14. 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
```

15. You can adjust population size, maximum number of generations in the config.ini file and save the changes.

```
[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
```

> Note: when starting for the first time make sure start_from_previous_gen is False.

16. Now, lets run our optimization: python __init__.py
17. Hooray! Now we have a running CoMOLA optimization. You will find the results in the output folder.
    Note: When Running the CoMOLA again, you just need to activate the environment, navigate to the CoMOLA folder and run the python script.