Tutorial: CLASS and MONTEPYTHON Installation

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1 Overview

¹CLASS (Cosmic Linear Anisotropy Solving System) is a numerical tool for solving the evolution of linear cosmological perturbations and for computing the cosmological observables for a given input model. CLASS is a flexible and userfriendly code that can be easily generalized to non-minimal cosmological models. CLASS was written by Julien Lesgourgues & Thomas Tram, and first released in 2011.

 $\tt CLASS$ is written in $\tt C$ language for each module. It comes with C++ and Python wrapper.

For more information about CLASS can be found on the website: http: //class-code.net. The CLASS papers can be found below

- CLASS I: Overview, by J. Lesgourgues, arXiv:1104.2932 [astro-ph.IM]
- CLASS II: Approximation schemes, by D. Blas, J. Lesgourgues, T. Tram, arXiv:1104.2933 [astro-ph.CO], JCAP 1107 (2011) 034

2 Pre-requistes

Mac users

Mac users may have to install the Command Line Tools for Xcode in order to use the commands like gcc, git or make or package management tools like Homebrew. You can check if the Command Line Tools have already installed to your system or not by open the terminal and run

\$ xcode-select -p

If they are already installed, it should return a path like /Library/Developer/CommandLineTools. If not, you can install them manually by running the following command

¹Adapted from Deanna C. Hooper

\$ xcode-select --install

Alternatively you can download the Command Line Tools by going to the site: https://developer.apple.com/download/all/ (sign in is required), click download Command Line Tools for XCode (see Figure 1)



Figure 1:

Next step, you need to install Homebrew in the system. Homebrew can be downloaded it by typing this command on the terminal²

After that, you will need to install a C-language compiler such as GCC (Gnu Compiler Collection), which is commonly used as a compiler with support for C, C++, Fortran, etc. GCC can be installed by compiling

```
$ brew install gcc
```

To make sure that CGG works properly, run

\$ gcc --version

Next step, check for the python version with

²You can find installation instructions from https://docs.brew.sh/Installation

\$ python --version

Python wrapper for class may not yet be compatible with Python version \gtrsim 3.11, so we have to specify version of Python in order to set up the wrapper. In this note we will use Python v.3.11. Next step, we need to install Cython. This allows Python code to directly call the C functions in CLASS. To install Cython that associate with the Python v.3.11, use the command below

```
$ python3.11 -m pip install Cython
```

Linux users

You need to have gcc compiler Python, and Cython. To install gcc use the following commands,

```
$ sudo apt update
$ sudo apt upgrade
$ sudo apt install gcc
```

Almost every Linux distribution comes with a version of Python included in the default system packages. Check your Python version by using the following command;

\$ python3 --version

 or

```
$ python --version
```

In case you want a better handling of the Python packages download and install Miniconda or Anaconda from the following links;

Miniconda https://docs.conda.io/projects/miniconda/en/latest/ Anaconda https://www.anaconda.com/download

Next to install cython;

\$ pip install Cython

 \mathbf{or}

\$ conda install Cython

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Figure 2: Screen short of CLASS homepage on github

3 CLASS part

3.1 Downloading CLASS

Before getting CLASS, you may create a project directory using

```
$ mkdir <dirname> && cd $_
```

Replace <dirname> with the name you prefer. After entering the <dirname> directory, download the latest version of CLASS by downloading via git using the command

```
$ git clone https://github.com/lesgourg/class_public.git
```

Or we can also download CLASS directly from github homepage (see Figure 2).

3.2 Installing CLASS

Enter CLASS directory. Compile C code and Python wrapper using the command

```
$ PYTHON=python3.11 make all
```

Or using just

\$ make -j

if you have no multiple versions of Python. Execute the command

```
$ ./class explanatory.ini
```

to test if the $\tt C$ code installed successfully. To test if the Python wrapper setup successfully, compile

```
$ python3.11 -c "import classy; print(classy.__version__)"
```

3.3 Python wrapper in a virtual environment

Create a virtual environment (venv) using

```
$ python3.11 -m venv <myenv>
```

You can replace <myenv> with any name you want. Then activate the virtual environment with

```
$ source <myenv>/bin/activate
```

To make sure that whenever the command python is compiled it point to the correct version of Python as you included in the virtual environment, you can place the function below in .bashrc or .zshrc for z-shell (if you don't have .bashrc or .zshrc, just create one)

```
function venv() {
  source "$1/bin/activate"
  alias python="$1/bin/python"
  alias pip="$1/bin/pip"
}
```

Then restart the terminal. Activate the virtual environment again. Now you can test if the command python points to the same version of Python using in the virtual environment by compiling

```
$ which python; which pip
```

Or, check for the version of Python

```
$ python --version; pip --version
```

After that, install necessary modules to the environment, type

\$ pip install numpy scipy cython matplotlib

In the CLASS directory, go to the 'python' directory and execute the command:

```
$ python setup.py build
$ python setup.py install
```

Checking if the steps above worked properly by compiling

```
$ python -c "import classy; print(classy.__version__)"
```

4 Using CLASS on Jupyter Notebook

Firstly you have to install Jupyter Notebook.

```
$ pip install notebook
```

To make sure that the path of Jupyter Notebook is in the created venv, type

\$ which jupyter

If the Notebook is not in the right path, you may have follow this way:

\$ pip install ipython ipykernel

After installing ipython and ipykernel, run

\$ ipython kernel install --user --name=<myvenv>

and

\$ python -m ipykernel install --user --name=<myvenv>

Now the Jupyter Notebook should be in the right path. You can test it by typing (you probably have to restart the shell, and activate the venv again).

\$ which jupyter

If all thing going fine, to use the Jupyter Notebook, run

\$ jupyter notebook

Creating the alias for the virtual environment (optional)

You can create a command to activate the venv any directory by putting the following command in the file .bashrc or .zshrc. Firstly, open the .bashrc or .zshrc file by typing

\$ vim ~/.bashrc

or

\$ vim ~/.zshrc

(or you can use the text editor, nano, if you prefer). Then, put the command:

\$ alias <your_prefer_name>="source \$HOME/<path/to/myvenv>/bin/activate"

Then, overwrite the file with :wq (in vim command mode), or Ctr+O (for nano).

5 Monte Python part

5.1 Getting Monte Python

MontePython can be downloaded by

\$ git clone https://github.com/brinckmann/montepython_public.git

³You need the Python program version $2.7.x^{**}$ or version $3.x^{**}$. Your Python must have 'numpy' (version >= 1.4.1) and 'Cython'. The last one is used to wrap CLASS in Python.

Optional: If you want to use the plotting capabilities of Monte Python fully, you also need the 'scipy', with interpolate, and 'matplotlib' modules.

After installation, go to the directory:

\$ cd montepython_public

Make a copy of the file default.conf.template and rename it to default.conf (or any name you prefer)

\$ cp default.conf.template default.conf

At minimum, the file default.cof needs one line:

path['cosmo'] = path/to/your/class_public

Make sure that your CLASS directory has the same name as in the path.

Now the code is installed. There are two main (optional) commands in MontePython: the first one is run, for running MCMC to generate chains, another one is info, for analysing chains. More information can be viewed by executing

³Adapted from Benjamin Audren

```
$ python montepython/MontePython.py --help
$ python montepython/MontePython.py run --help
$ python montepython/MontePython.py info --help
```

To test a small running, executing:

path['cosmo'] = path/to/your/class_public

To get running, type:

\$ python montepython/MontePython.py run -o test -p example.param

If the directory 'test/' doesn't exist, it will be created, and a run with the number of steps described in 'example.param' will be started. To run a chain with more steps, one can type:

```
$ python montepython/MontePython.py run -o test -p _{\hookrightarrow} example.param -N 100
```

To analyse the chains, type

```
$ python montepython/MontePython.py info test/
```

For more information, see https://baudren.github.io/montepython.html. The documentation can be found in this link.

The MontePython papers can be found as

- Brinckmann, T. and Lesgourgues, J., "MontePython 3: Boosted MCMC sampler and other features", Physics of the Dark Universe, vol. 24, 2019. doi:10.1016/j.dark.2018.100260.
- Audren, B., Lesgourgues, J., Benabed, K., and Prunet, S., "Conservative constraints on early cosmology with MONTE PYTHON", Journal of Cosmology and Astroparticle Physics, vol. 2013, no. 2, 2013. doi:10.1088/1475-7516/2013/02/001.

6 Setting up Planck likelihoods

⁴The Planck 2018 data can be found on the 'Planck Legacy Archive http: //pla.esac.esa.int/pla/#home. The Planck Likelihood Code (plc) is based on a library called 'clik'. It will be extracted, alongside several '.clik' folders that contain the likelihoods. The code uses an auto installer device, called 'waf'. Here is the detail of the full installation.

Next, create a directory which you want to store Planck data, and go into that directory

⁴Adapted from Deanna C. Hooper

```
$ mkdir -p path/to/planck && cd $_
```

Download the code and baseline data (will need 300 Mb of space)

Uncompress the code and the likelihood, and do some clean-up

```
$ tar -xvzf COM_Likelihood_Code-v3.0_R3.01.tar.gz
$ tar -xvzf COM_Likelihood_Data-baseline_R3.00.tar.gz
$ rm COM_Likelihood_*tar.gz
```

Move into the code directory

\$ cd code/plc_3.0/plc-3.01

Configure the code. Note that you are **strongly advised** to configure clik with the Intel mkl library, and not with lapack. There is a massive gain in execution time: without it, the code is dominated by the execution of the low-l polarisation data. Before the next step, ensure you do NOT have any old Planck likelihoods sourced!

```
$ ./waf configure --lapack_mkl=${MKLROOT} --install_all_deps
```

If everything goes well, you will be ready to install the code

\$./waf install

Next, source the likelihood. If you are running on a shell, type the command

\$ source bin/clik_profile.sh

Running on a z-shell, you will first need to create a .zsh version of the above file. This can be done in many ways, for example

```
$ cp bin/clik_profile.sh bin/clik_profile.zsh
$ sed -i 's/addvar PATH /PATH=$PATH:/g' bin/clik_profile.zsh
$ sed -i 's/addvar PYTHONPATH /PYTHONPATH=$PYTHONPATH:/g'
$ bin/clik_profile.zsh
$ op bi
```

You need to add

\$ source

→ /path/to/planck/code/plc_3.0/plc-3.01/bin/clik_profile.sh

to your .shellrc (or the .zsh to your .zshrc on a z-shell), and you should put it in your scripts for cluster computing.

After successfully installing Planck likelihoods, in MontePython configuration file, you will need to add

```
path['clik'] = '/path/to/planck/code/plc_3.0/plc-3.01'
```

There are nine Planck 2018 likelihoods defined in *Monte Python*: 'Planck_highl_TT', 'Planck_highl_TT_lite', 'Planck_highl_TTTEEE', 'Planck_highl_TTTEEE_lite', 'Planck_lensing', 'Planck_lowl_TT', 'Planck_lowl_EE', 'Planck_lowl_EEBB', 'Planck_lowl_BB', as well as five sets of parameter files, bestfit files, and cov-mats.