CLASS, hi_class and Monte Python basics IFT School on Cosmology Tools

Miguel Zumalacarregui^{1,2}

¹Nordic Institute for Theoretical Physics ²Berkeley Center for Cosmological Physics

March 11, 2017

Abstract

The present document summarizes the basics for the installation and execution of the CLASS, hi_class and Monte Python codes. It is not meant as a comprehensive guide, but rather a basic guide to get the codes up and running and a complement to the school exercises. Resources for further learning, including the official websites, documentation and links to courses are also provided.

Contents

1	Resources	2
2	Download	2
3	Using CLASS & hi_class 3.1 Compile CLASS	3 3 3
4	Using Montepython 4.1 Configuration file (.conf)	4
	4.4 Analyze chains	

1 Resources

Websites:

- CLASS: https://class-code.net https://github.com/lesgourg/class_public
- hi_class: https://hiclass-code.net
 https://github.com/miguelzuma/hi_class_public
- Monte Python: http://baudren.github.io/montepython.html https://github.com/baudren/montepython_public

Documentation

- <u>The codes themselves</u>: nearly as many comment as code lines.
- CLASS: http://lesgourg.github.io/class_public/class_public-2.5.0/doc/manual/html/index.html
- Montepython: http://monte-python.readthedocs.io/en/latest/

Courses:

- CLASS & MP course by Audren, Lesgourgues and Tram ($\sim 13h$) https://lesgourg.github.io/class-tour-Tokyo.html
- CLASS lecture by Julien Lesgourgues ($\sim 4h$) https://lesgourg.github.io/class-tour/Narbonne.pdf
- Montepython's brief presentation by S. Clesse (
 (
 1h)
 https://lesgourg.github.io/class-tour/16.06.02_Lisbon_intro.pdf
- CLASS video tutorial (~ 25') https://www.youtube.com/watch?v=R22XhKUwzX4 (beta version, suggestions welcome!)

Troubleshooting: forums to 1) find answers and 2) ask questions (in that order)

- CLASS: https://github.com/lesgourg/class_public/issues
- hi_class: https://github.com/miguelzuma/hi_class_public/issues https://groups.google.com/d/forum/hi_class
- Montepython: https://github.com/baudren/montepython_public/issues

Few git resources (version control):

- git online book: https://git-scm.com/book/en/Getting-Started-Git-Basics
- git the simple guide: rogerdudler.github.io/git-guide/
- Interactive git in 15': https://try.github.io/

2 Download

In the terminal type

```
git clone https://github.com/lesgourg/class_public.git
git clone https://github.com/miguelzuma/hi_class_public.git
git clone https://github.com/baudren/montepython_public.git
```

This requires git but gives you access to all the previous versions (you should try git, your life won't be the same). If you don't have git click 'Clone or download', 'Download ZIP' in the above address (and seriously, you should try git).

3 Using CLASS & hi_class

3.1 Compile CLASS

In a terminal go to the class_public or hi_class_public directory and enter

make

to compile the executable and *classy*, the python wrapper (this should install the python wrapper locally). Enter make class to build *only* the executable. Remember to enter make clean before to recompile the python wrapper or if you have modified a header file (extension .h). For details on *classy* see https://github.com/lesgourg/class_public/wiki/Python-wrapper.

3.2 Input parameters

The code can be run on the terminal or through classy, the Python wrapper. The following parameters give a Planck Λ CDM model

Terminal: write your_parameter_file.ini

```
h = 0.6774
omega_b = 0.02230
Omega_cdm = 0.2603
Omega_fld = 0
Omega_smg = 0 #GR in hi_class
background_verbose = 1 #info
output = tCl,mPk #what to compute
write background = y
root = output/your_model_ #future files
```

Python: write a dictionary

```
params = {
    "h": 0.6774,
    "omega_b": 0.02230,
    "Omega_cdm": 0.2603,
    "Omega_fld" : 0,
    "Omega_smg" : 0, #GR in hi_class
    "background_verbose" : 1, #info
    "output" : "tCl,mPk" #observables
}
```

- For modified gravity in hi_class you need to set Omega_Lambda = 0 (no CC) and Omega_smg = -1 (determine DE density automatically) and specify a gravity_model_smg, expansion_model_smg.
- The parameter file can be as short as you need, with unspecified parameters set to default values.
- Only lines with an equal sign (=) will be interpreted. Hashtag (#) comments a line.
- Unused or misspelled parameters will be written to an unused_parameters file (using the option write parameters = y). Setting write warnings = y makes CLASS complain in those cases.
- The root directory has to exist.
- All the model and output parameters are described in explanatory.ini (this is the first place to look for information). The hi_class parameters are described in hi_class.ini. Keep those files for reference.

3.3 Run CLASS

To run the code on terminal or *classy*:

```
Terminal:
```

From the to the base directory run

./class your_parameter_file.ini

(plus an optional .pre precision file)

Your output will be ready in the root address.

Python:

```
from classy import Class
cosmos = Class() #create universe
cosmos.set(params) #feed params to cosmos
cosmos.compute() #duh...
... #play with the output
cosmo.struct_cleanup() #free memory
cosmo.empty() #start over
```

See Exercise 1 in the CLASS sheet to familiarize yourself with the output options available to CLASS.

4 Using Montepython

Python is an interpreted language: you don't need to compile MP, but you need to configure it.

Montepython has two execution modes (see below). For help type in the MP directory

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

A very useful example of a complete work session with Montepython is explained in

http://monte-python.readthedocs.io/en/latest/example.html

4.1 Configuration file (.conf)

You need a .conf file to inform MP of the CLASS/hi_class (mandatory) and Planck likelihood (optional). Read the default.conf.template file for details and instructions. Unless other file is specified MP will read from default.conf (but you need to create this first). This is important if you use different CLASS versions (eg. class_public and hi_class_public).

4.2 Parameter file (.param)

Montepython runs with a .param file that specifies the model to be analyzed, data to use and other specifications. This can be kept rather minimal (with unspecified parameters set to defaults).

```
#what expermiennts to include in tha analysis
data.experiments=['bao_boss','bao_boss_aniso']
# parameters: data.parameters[class name] = [mean, min, max, 1-sigma, scale, role]
#cosmological paramters to vary (role = 'cosmo' and 1-sigma not 0)
data.parameters['omega_cdm'] = [0.1120, None, None, 0.0016, 1, 'cosmo']
                            = [0.703, None, None, 0.0065, 1, 'cosmo']
data.parameters['h']
#fixed cosmologial arguments (also if you fix sigma=0)
data.cosmo_arguments['omega_b'] = 0.0222
#Nuisance parameters if your likelihood needs them
#derived parameters (role = 'derived')
data.parameters['z_reio']
                           = [0,
                                       None, None, 0,1, 'derived']
data.parameters['Omega_Lambda'] = [0, None, None, 0,1, 'derived']
#Montepython execution options
data.N=10
data.write_step=5
```

- Please <u>read base.param</u> for further details. Other .param files can be useful too.

 <u>Do not comment in the same line: data.parameters['...'] = [...] #mycomment here will not be read!</u>
- Each experiment is a directory in 1s montepython/likelihoods. More details in each subfolder.
- <u>∧</u> Parameter vectors: For parameters that enter class as a vector (like m_ncdm if N_cdm > 1 or parameters_smg,expansion_smg in hi_class) you need the following format:

```
data.parameters['m_ncdm__1'] = [0.05, 0, None, 0., 1, 'cosmo']
data.parameters['m_ncdm__2'] = [0.01, 0, None, 0., 1, 'cosmo']
```

with two underscores $_$ after the parameter name to specify the position in the entry (if you specify data.cosmo_arguments['N_ncdm'] = 2, if N_ncdm = 1 you don't need this syntax). The above corresponds to m_ncdm = 0.05,0.01 in an .ini file.

You need to specify all vector parameters, even when some are not varied.

4.3 Run chain(s)

To compute a chain for a given model, type from the terminal

python montepython/MontePython.py run -p model.param -o output_directory

This will start a new chain in the designated output_directory as specified in model.param.

- Each output directory is for a choice of model/parameters and experiments. The first run in output_directory will create a log.param with all the specifications for the run. If this file exists the code will ignore model.param and will instead pick the settings from the log.param. This ensures that all the chains in a given directory are consistent.
- This is a very minimal run, and will only produce 10 points (controlled by -N, good for debug). Add at least -N 10000 (or more) if you run a chain for real. Add --update 300 to control how often you update the covariance matrix.

See all the options and their default values running MP with run --help.

• Note that MP's parallelization is optional: you can run several instances of the code (one per core) by repeating the instructions above. Pro tip: run a short sequence with -N 10 to test the code and create the log.param, then type

(this will run 4 chains in $output_directory$ with 10^5 points). Optional parallelization 1) allows you to run in any old computer and 2) simplifies your life when you "meet" a new cluster (and you may "meet" many in your career!).

• Each chain file name reads

```
yyyy-mm-dd_N__id.txt
```

where yyyy-mm-dd is the date in which the chain was launched, N is the desired number of points and id is the identifier (when the date and N are the same).

- The run will also create some additional files such as a covariance matrix. Additional files are created during the chain analysis, see below.
- To increase the convergence it is recommended to run with a covariance matrix (option -c your_file.covmat), especially for models with many parameters.

4.4 Analyze chains

Once you have several decent-sized chains in a file you can analyze them:

```
python montepython/MontePython.py info output_directory/
```

The above command will analyze all the chains in output_directory, computing the convergence of the chains over different paramters and producing statistical information on the posterior, including confidence intervals and plots.

- Several files named output_directory.* will be produced:
 - .bestfit for the best fit model, .covmat for a covariance matrix. These can be passed for future runs.
 - .log for the information on the chains.
 - h_info, v_info with horizontal/vertical tables of the parameter constraints, .tex for table in latex format
 - ★ a directory plot/ with the 1 and 2D marginalized contours.

• This is a very minimal analysis. You can analyze a subset of the chains, produce more/less output and configure it.

See all the options and their default values running MP with info --help.

• You can analyze several folders at a time

```
python montepython/MontePython.py info experiment_1/ experiment_2/ ...
```

This produces combined plots, which is useful to compare models/experiments.

• A very convenient flag is --extra your_file.plot to pack the options in a file: