

MontePython

Thejs Brinckmann

TOOLS 2020

Code developed and maintained by
Audren, Brinckmann, Hooper, Lesgourgues, Schöneberg
& many others

Seminar, Online/Lyon – Nov 4, 2020



Stony Brook University

Overview

1. Brief introduction of new features in **MontePython 3**
2. Overview of the structure of the code
3. Basic introduction on how to use the code

Not covered in this talk, but the extra slides are included on indico:

4. Advanced usage and details on **MontePython 3** improvements

MontePython 3: new features



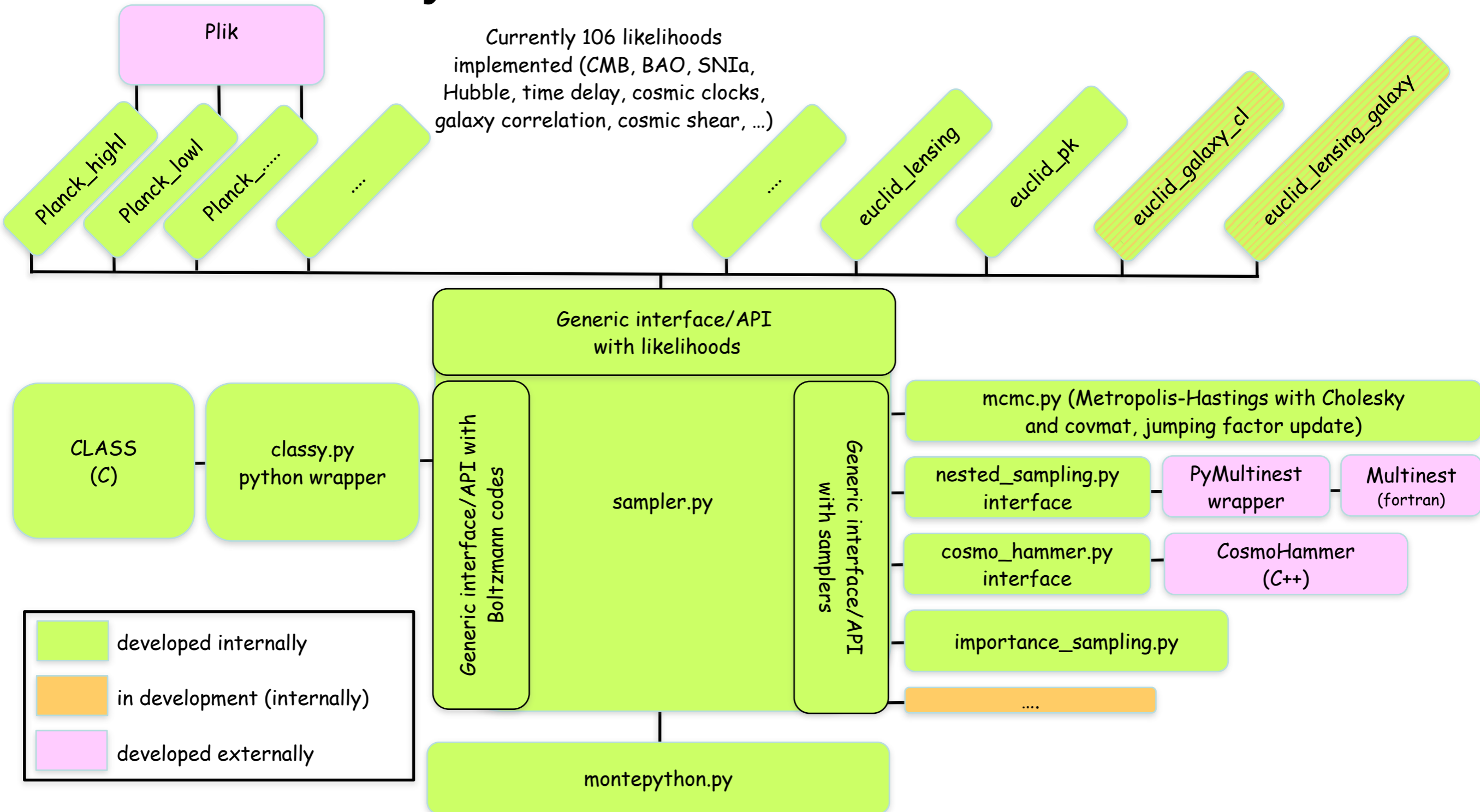
New version 3.3 of **MontePython** earlier this year

► see release paper [Brinckmann & Lesgourgues 1804.07261](#)

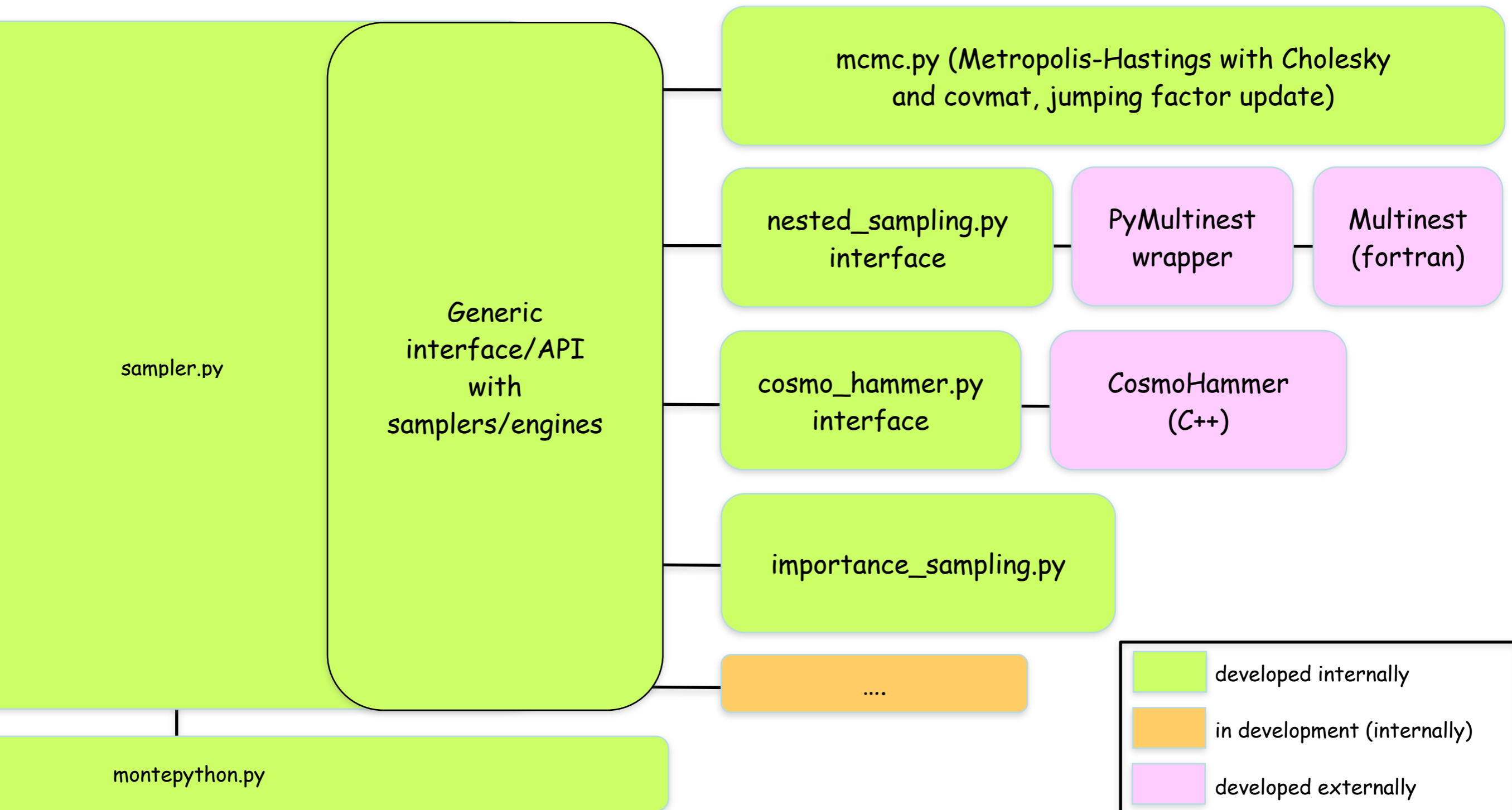
Notable recent features

1. New in v3.3: Python 3 compatibility!
2. In v3.0: Superupdate (speed up & easier to converge)
3. In v3.0: Fisher matrix calculation (speed up & easier to converge)
4. In v3.0: Improved plotting (nice plots, easier to customize)
+ additional significant improvements coming in v3.4.
5. Continuous: New likelihoods (more/new data, mock likelihoods)
+ more with v3.4, e.g. Planck SZ cluster counts, tSZ power spectrum, H0LiCOW, BBN, new BAO, new KiDS, and more!

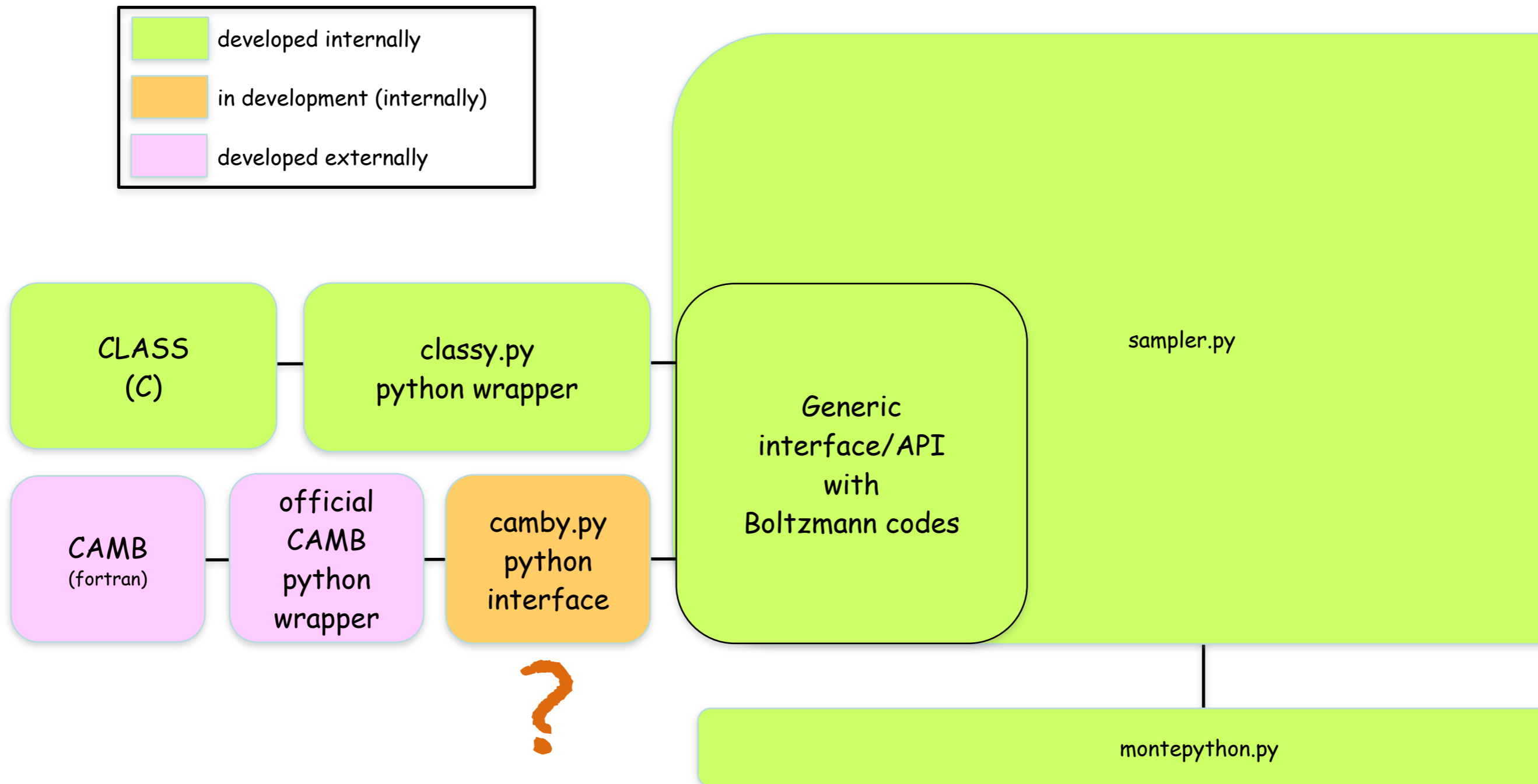
MontePython 3: modular structure



MontePython 3: modular structure

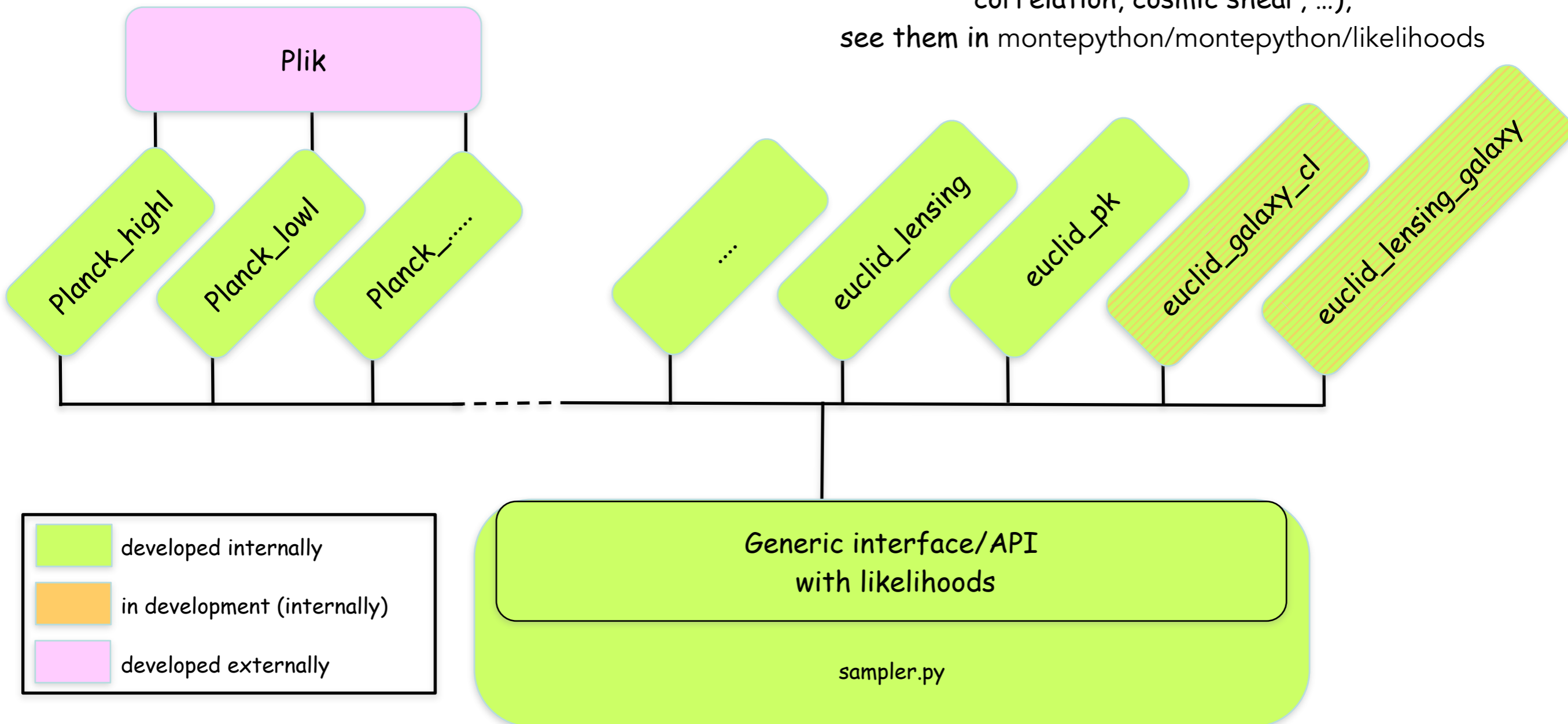


MontePython 3: modular structure



MontePython 3: modular structure

Currently 106 likelihoods implemented (CMB, BAO, SNIa, Hubble, time delay, cosmic clocks, galaxy correlation, cosmic shear, ...), see them in `montepython/montepython/likelihoods`



MontePython 3: param file

Understanding the .param file

```
# Experiments
data.experiments=['Planck_highl_lite','Planck_lowl','Planck_lensing']

# Settings for the over-sampling
data.over_sampling=[1, 4]

# Cosmological parameters list
data.parameters['omega_b'] = [ 2.2253, None, None, 0.028, 0.01, 1, 'cosmo']
data.parameters['omega_cdm'] = [ 0.2747, None, None, 0.028, 0.01, 1, 'cosmo']
data.parameters['100*theta_s'] = [ 1.0418, None, None, 3e-4, 1, 'cosmo']
data.parameters['ln10^{10} A_s'] = [ 0.0753, None, None, 0.0029, 1, 'cosmo']
data.parameters['n_s'] = [ 0.9634, None, None, 0.004, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, 0.04, None, 0.013, 1, 'cosmo']

# Nuisance parameter list, same call, except the name does not have to be a class name
data.parameters['A_planck'] = [100.028, 90, 110, 0.25, 0.01, 'nuisance']

# Derived parameters
data.parameters['z_reio'] = [1, None, None, 0, 1, 'derived']
data.parameters['Omega_Lambda'] = [1, None, None, 0, 1, 'derived']

# Other cosmo parameters (fixed parameters, precision parameters, etc.)
data.cosmo_arguments['sBBN file'] = data.path['cosmo']+'/bbn/sBBN.dat'
data.cosmo_arguments['k_pivot'] = 0.05
```

↑

List of experiments: must match names in likelihood folder

MontePython 3: param file

Understanding the param file Over-sampling of fast nuisance parameters

```

# Experiments
data.experiments = ['Planck_highl_lite', 'Planck_lowl', 'Planck_lensing']

# Settings for the over-sampling
data.over_sampling=[1, 4]

# Cosmological parameters list
data.parameters['omega_b'] = [ 2.2253, None, None, 0.028, 0.01, 'cosmo']
data.parameters['omega_cdm'] = [0.11919, None, None, 0.0027, 1, 'cosmo']
data.parameters['100*theta_s'] = [ 1.0418, None, None, 3e-4, 1, 'cosmo']
data.parameters['ln10(10^{10} h^2 Omega_b h^2)'] = [0.029, 1, 'cosmo']
data.parameters['n_s'] = [0.96229, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio'] = [0.08453, 0.01, 0.013, 1, 'cosmo']

# Nuisance parameter list, same call, except the name does not have to be a class name
data.parameters['A_planck'] = [100.028, 90, 110, 0.25, 0.01, 'nuisance']

# Derived parameters
data.parameters['z_reio'] = [1, None, None, 0, 1, 'derived']
data.parameters['Omega_Lambda'] = [1, None, None, 0, 1, 'derived']

# Other cosmo parameters (fixed parameters, precision parameters, etc.)
data.cosmo_arguments['sBBN file'] = data.path['cosmo']+'/bbn/sBBN.dat'
data.cosmo_arguments['k_pivot'] = 0.05

```

Cosmological parameters

Nuisance parameters are sampled 4x as much

Parameter names must be CLASS compatible, as in explanatory.ini*

Python Lower and upper bound in file

Scaling

Mean

1-sigma

Type

```
# Settings for the over-sampling
data.over_sampling=[1, 4]

# Cosmological parameters list
data.parameters['omega_b'] = [ 2.2253, None, None, 0.028, 0.01, 'cosmo']
data.parameters['omega_cdm'] = [0.11919, None, None, 0.0027, 1, 'cosmo']
data.parameters['100*theta_s'] = [ 1.0418, None, None, 3e-4, 1, 'cosmo']
data.parameters['ln10^{10}A_s'] = [ 3.0753, None, None, 0.0029, 1, 'cosmo']
data.parameters['n_s'] = [0.96229, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, 0.04, None, 0.013, 1, 'cosmo']

# Nuisance parameter list, same call, except the name does not have to be a class name
data.parameters['A_planck'] = [10, 28, 90, 110, 0.25, 0.01, 'nuisance']

# Derived parameters
data.parameters['z_reio'] = [1, None, None, 0, 1, 'derived']
data.parameters['Omega_Lambda'] = [1, None, None, 0, 1, 'derived']

# Other cosmo parameters (e.g. bbn, etc.)
data.cosmo_arguments['sBBN_file'] = data.path['cosmo'] + '/bbn/sBBN.dat'
data.cosmo_arguments['k_pivot'] = 0.05
```

Cosmological parameters

MontePython 3: param file

Understanding the .param file

```
# Experiments
```

```
data.experiments=['Planck_high_lite', 'Planck_lowl', 'Planck_lensing']
```

Nuisance parameters are only used by MontePython, i.e. are not passed to CLASS

```
# Selecting for over-sampling
data.over_sampling=[1, 4]
# Cosmological parameters list
data.parameters['omega_cdm'] = [0.11919, None, None, 0.028, 0.01, 'cosmo']
data.parameters['100*theta_s'] = [1.0418, None, None, 0.0027, 1, 'cosmo']
data.parameters['ln10^{10} h^2 A_s'] = [3.0753, None, None, 0.0029, 1, 'cosmo']
data.parameters['n_s'] = [0.96229, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, 0.04, None, 0.013, 1, 'cosmo']
```

Nuisance type

```
# Nuisance parameter list, same call, except the name does not have to be a class name
data.parameters['A_planck'] = [100.028, 90, 110, 0.25, 0.01, 'nuisance']
```

```
# Derived parameters
```

```
data.parameters['z_reio'] = [1, None, None, 0, 1, 'derived']
```

```
= [1, None, None, 0, 1, 'derived']
```

Nuisance parameters are often faster to vary

Over-sampling speeds up convergence

```
data.cosmo_arguments['k_pivot'] = 0.05
```

MontePython 3: param file

Understanding the .param file

```
# Experiments
data.experiments=['Planck_highl_lite','Planck_lowl','Planck_lensing']

# Settings for the over-sampling
data.over_sampling=[1, 4]
```

Derived parameters do not affect the run and are computed from the other parameters

```
data.parameters['omega_cdm'] = [0.11919, None, None, 0.028, 0.01, 'cosmo']
data.parameters['ln10^{10}A_s'] = [3.0753, None, None, 0.0027, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, None, None, 3e-4, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, None, None, 0.0029, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio'] = [0.09463, None, None, 0.04, None, 'cosmo']
```

Derived type

```
# Nuisance parameter list, same call, except the name does not have to be a class name
data.parameters['A_pt'] = [100.028, 90, 110, 0.25, 0.01, 'nuisance']
```

```
# Derived parameters
data.parameters['z_reio'] = [1, None, None, 0, 1, 'derived']
data.parameters['Omega_Lambda'] = [1, None, None, 0, 1, 'derived']
```

Derived parameters can be added in post-processing

MontePython 3: param file

Understanding the .param file

Arguments control e.g. numerical precision
and fixed cosmological parameters

```
# Experiments
data.experiments=['Planck_high_lite', 'Planck_lowl', 'Planck_lensing']

# Settings for the over-sampling
data.over_sampling=[1, 4]

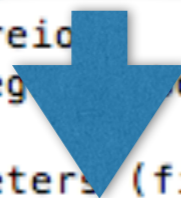
# Cosmological parameters list
data.parameters['omega_b']          = [ 2.2253,  None, None,  0.028, 0.01, 'cosmo']
data.parameters['omega_cdm']       = [0.11919, None, None, 0.0027, 1, 'cosmo']
data.parameters['100+theta_s']     = [ 1.0418, None, None, 3e-4, 1, 'cosmo']
data.parameters['100+theta_A']     = [ 1.0753, None, None, 0.0029, 1, 'cosmo']
data.parameters['100+tau_reio']    = [0.08229, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio']        = [0.09463, 0.04, None, 0.013, 1, 'cosmo']

# Nuisance parameter list, same call, except the name does not have to be a class name
data.parameters['100+tau_reio']    = [100.028, 90, 110, 0.25, 0.01, 'nuisance']

# Derived parameters
data.parameters['z_reio']          = [1, None, None, 0, 1, 'derived']
data.parameters['Omega_b']        = [1, None, None, 0, 1, 'derived']

# Other cosmo parameters (fixed parameters, precision parameters, etc.)
data.cosmo_arguments['sBBN file'] = data.path['cosmo']+'/bbn/sBBN.dat'
data.cosmo_arguments['k_pivot']   = 0.05
```

Cosmological arguments
are fixed parameters
passed to CLASS



MontePython 3: installation

- Download & install CLASS
 - ▶ https://github.com/lesgourg/class_public
 - ▶ compile CLASS with wrapper (i.e. use “make clean;make” not “make class”)
- Need Python 2.7.x or 3.x.x with numpy, scipy, matplotlib and cython
 - ▶ for MPI parallel runs also need mpi4py
- Download or clone MontePython from github
 - ▶ https://github.com/brinckmann/montepython_public
- Set up configuration file
 - ▶ `cp default.conf.template default.conf`
 - ▶ update paths

That's it!

MontePython 3: running the code

Required input

- ▶ `python montepython/MontePython.py run` plus ...
 - p `input/example.param` input parameter file
 - o `chains/planck_run` output directory
 - N `10000` number of proposed steps for each chain

Basic options

- c `covmat/base2015.covmat` use covariance matrix as proposal distribution
- b `bestfit/base2015.bestfit` use a bestfit file as starting point for the run

Possible to launch parallel jobs manually (for Metropolis-Hastings) or using **MPI**

- ▶ `mpirun -np N montepython/MontePython.py run` ...

To use multiple cores per chain first write (**CLASS** is parallelized to 8-32 cores)

- ▶ `OMP_NUM_THREADS=M`

This will create N number **MPI** processes each running on M number of cores

MontePython 3: analyzing output

Plotting received an overhaul in 3.0!

Analyze chains with `info`

▶ `python montepython/MontePython.py info chains/planck_run` plus ...

Additional notable options

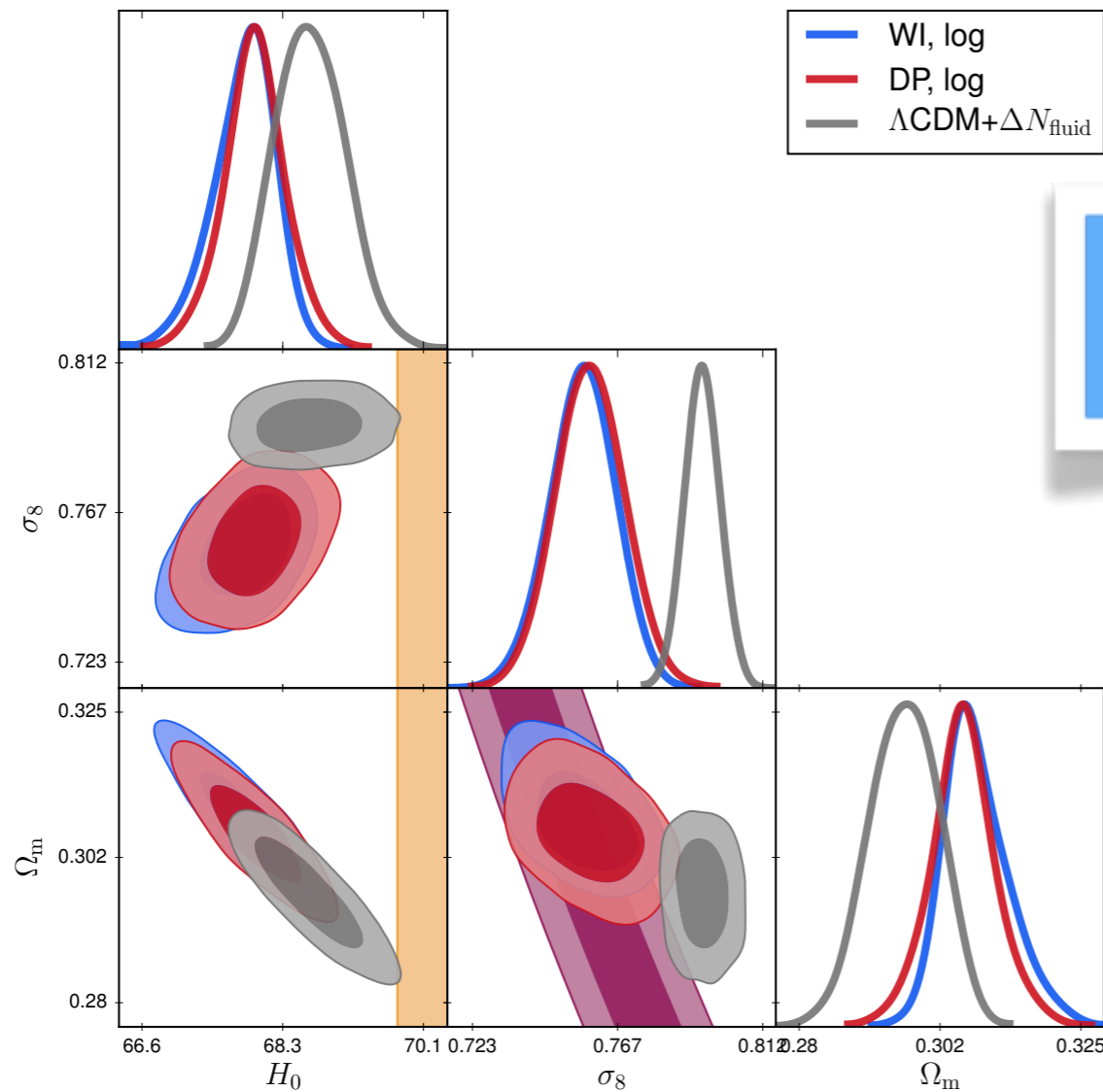
- `--keep-non-markovian` : keep the non-Markovian part of the chains [default: False].
- `--keep-fraction` : pass a decimal fraction, e.g. 0.8 to keep the last 80 % of the part of the chains that remain after the burn-in removal (note: redundant if non-Markovian points are discarded) [default: 1.0]
- `--want-covmat` : compute a covariance matrix based on the chains (note: this will overwrite the one produced by `--update`) [default: False]
- `--minimal` : use this flag to avoid computing posteriors, confidence limits and plots. The code just analyses the chains and outputs the files containing the convergence statistics, the best-fit parameters, and possibly the covariance matrix if `--want-covmat` is on [default: False]

+ many more (see documentation and 3.0 release paper)!

intelligent analysis:
non-Markovian points
removed by default,
no unnecessary
removal of data

Fans of GetDist can also use that, as the chains format is the same and a `.paramnames` file is provided

MontePython 3: plotting



Plotting received an overhaul in 3.0 and more is coming in v3.4!

Improved contours, added control of e.g. colors, axes, legends,

Custom scripts of python code can be added

Created with `MontePython info` using

```

▶ --extra example.plot with two customization scripts passed in example.plot
python montepython/MontePython info dir1 dir2 dir3 --extra plot_files/ex.plot

```

MontePython 3: more information

MontePython 3 paper

► [Brinckmann & Lesgourgues 1804.07261](#)

Official documentation

► <http://monte-python.readthedocs.io/en/latest/>

Help files

► `python montepython/MontePython.py run -h`

(more details: `--help`)

► `python montepython/MontePython.py info -h`

(more details: `--help`)

Github readme

https://github.com/brinckmann/montepython_public

Wiki

https://github.com/audren/montepython_public/wiki

Previous talks and tutorials on Julien Lesgourgues' website

<https://lesgourg.github.io/courses.html>

Problems? Open a ticket on my github page (after trying to find a solution yourself)

https://github.com/brinckmann/montepython_public

See also the rest of the slides that were not covered here, they are included on indico!

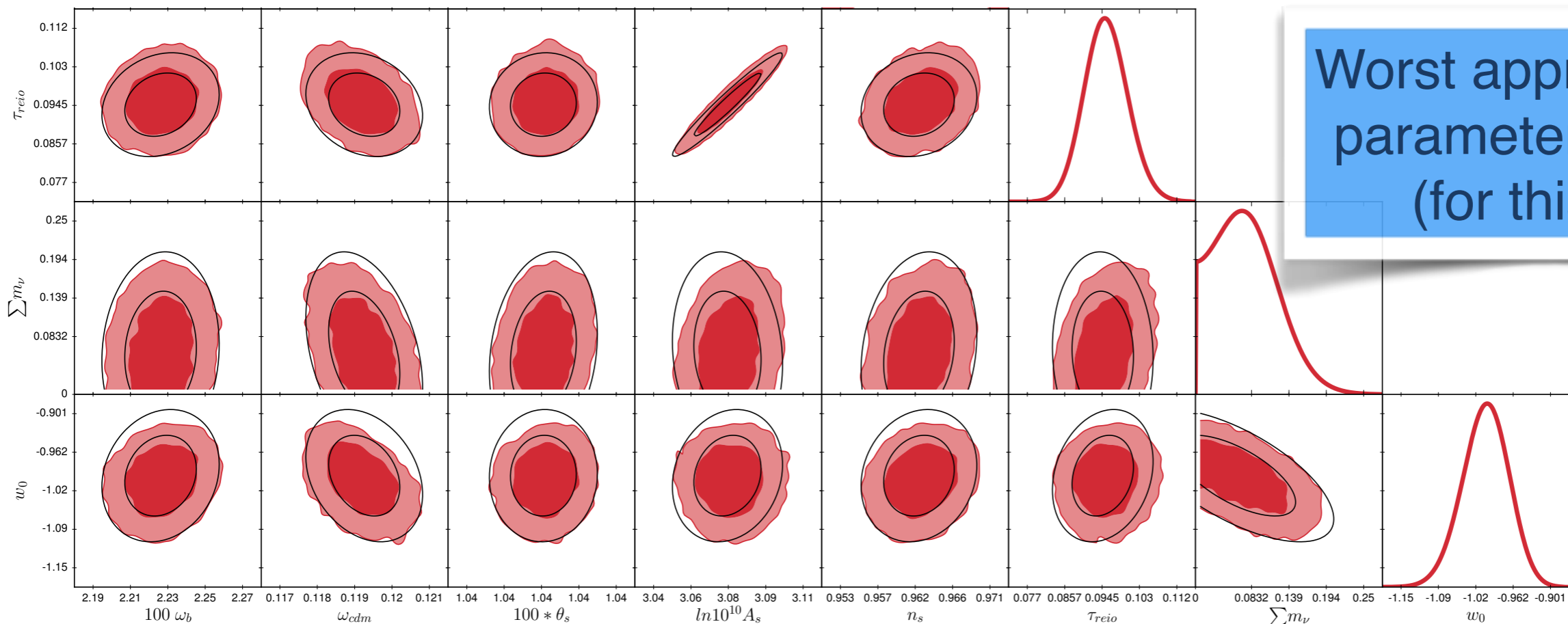
MontePython 3: advanced usage

1. New features and advanced sampling options
2. Sampling new parameters in CLASS
3. Communication with CLASS and adding new parameterizations
4. Adding likelihoods

MontePython 3: Fisher matrix

Compute Fisher matrices by adding

- ▶ `--method Fisher`
- ▶ Can use inverse as input covariance matrix for faster convergence



Worst approximated parameters shown (for this run)

Much better than a poor or no input covariance matrix!

MontePython 3: Fisher matrix

Important

Fisher matrix options

- `--method Fisher` : compute a Fisher matrix [default: MH]
- `--fisher-asymmetric` : allow for asymmetric steps (note: slows down computation) [default: False]
- `--fisher-step-it` : number of step iterations attempted [default: 10]
- `--fisher-delta` : target $\Delta \ln \mathcal{L}$ value for step iteration [default: 0.1]
- `--fisher-tol` : tolerance for $\Delta \ln \mathcal{L}$ (note: decreasing slows down computation) [default: 0.05]
- `--fisher-sym-lkl` : cut-off for switching to symmetric likelihood assumption in units of σ . Relevant when parameter space boundaries are close to the central value [default: 0.1]

Speed up convergence by first computing an inverse Fisher matrix to use as proposal distribution!

MontePython 3: superupdate

Boosting Metropolis-Hastings sampling

Since v2.2 (October 2015)

- `--update U` : update of covariance matrix, \mathbf{C} , every U cycles [default: $U = 50$]

- `--superupdate SU` : additionally, update of jumping factor, j , starting SU cycles after each covariance matrix update [default: $SU = 0$, meaning “deactivated”; recommended: 20]

New in v3.0

`--update` : Periodically updates the covariance matrix

- ▶ changes the shape and size of the proposal distribution
- ▶ particularly important with parameter degeneracies

`--superupdate` : adjusts the jumping factor

- ▶ i.e. re-scales the size of the proposal distribution
- ▶ mitigates ill effects of poor initial knowledge
- ▶ optimizes jumping factor to optimal acceptance rate ($\sim 25\%$)

MontePython 3: superupdate

- `--update U` : update of covariance matrix, C , every U cycles [default: $U = 50$]

- `--superupdate SU` : additionally, update of jumping factor, j , starting SU cycles after each covariance matrix update [default: $SU = 0$, meaning “deactivated”; recommended: 20]

`--superupdate` : adjusts the jumping factor

$$c_k = c_{k-1} + \frac{1}{(k - k_{\text{update}})} (\overline{a.r.} - 0.26) \quad |\overline{a.r.} - 0.26| < 0.01$$

Cosmologists usually aim for an a.r. of 25% since [Dunkley et al. 2005](#)

► achieved by above criteria because in many cases a.r. starts low

The jumping factor is directly related to the covariance matrix

► must update jumping factor after changing the covariance matrix

I.e., we want to keep the volume of the proposal density constant

$$j_{\text{after}} = j_{\text{before}} \left[\frac{\det(C_{\text{before}})}{\det(C_{\text{after}})} \right]^{\frac{1}{2N}}$$

MontePython 3: superupdate

superupdate:
consistent
performance
boost

Planck 2015 (high ℓ TT, low ℓ , lensing) + BAO (MGS, 6dFGS, LOWZ, CMASS)

Running time: 12 hours

model	# param.	$R - 1$: update	$R - 1$: superupdate	$R - 1$: superupdate + Fisher
Λ CDM	6	0.019	0.0098	0.029

2x

Planck 2015 (high ℓ TTTEEE lite, low ℓ , lensing) + BAO (MGS, 6dFGS, LOWZ, CMASS)
+ galaxy clustering (SDSS DR7 LRG), weak lensing (CFHTLenS)

Running time: 12 hours

Λ CDM	6	0.042	0.032	0.018
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Running time: 48 hours

Λ CDM	6	0.0062	0.0047	0.0038
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NB: Fisher method
struggles without
a good bestfit
and/or
with non-Gaussian
parameters

Mock data: fake_planck_realistic, fake_desi_vol

Running time: 12 hours

model	# param.	$R - 1$: update	$R - 1$: superupdate	$R - 1$: superupdate + Fisher
Λ CDM	6	0.030	0.015	0.013
+ $\sum m_\nu + w_0$	8	0.036	0.022	0.018
+ $N_{\text{eff}} + \text{running}$	10	not converged	not converged	0.040
+ Ω_k	11	not converged	not converged	0.048
+ w_a	12	not converged	not converged	0.088

3x

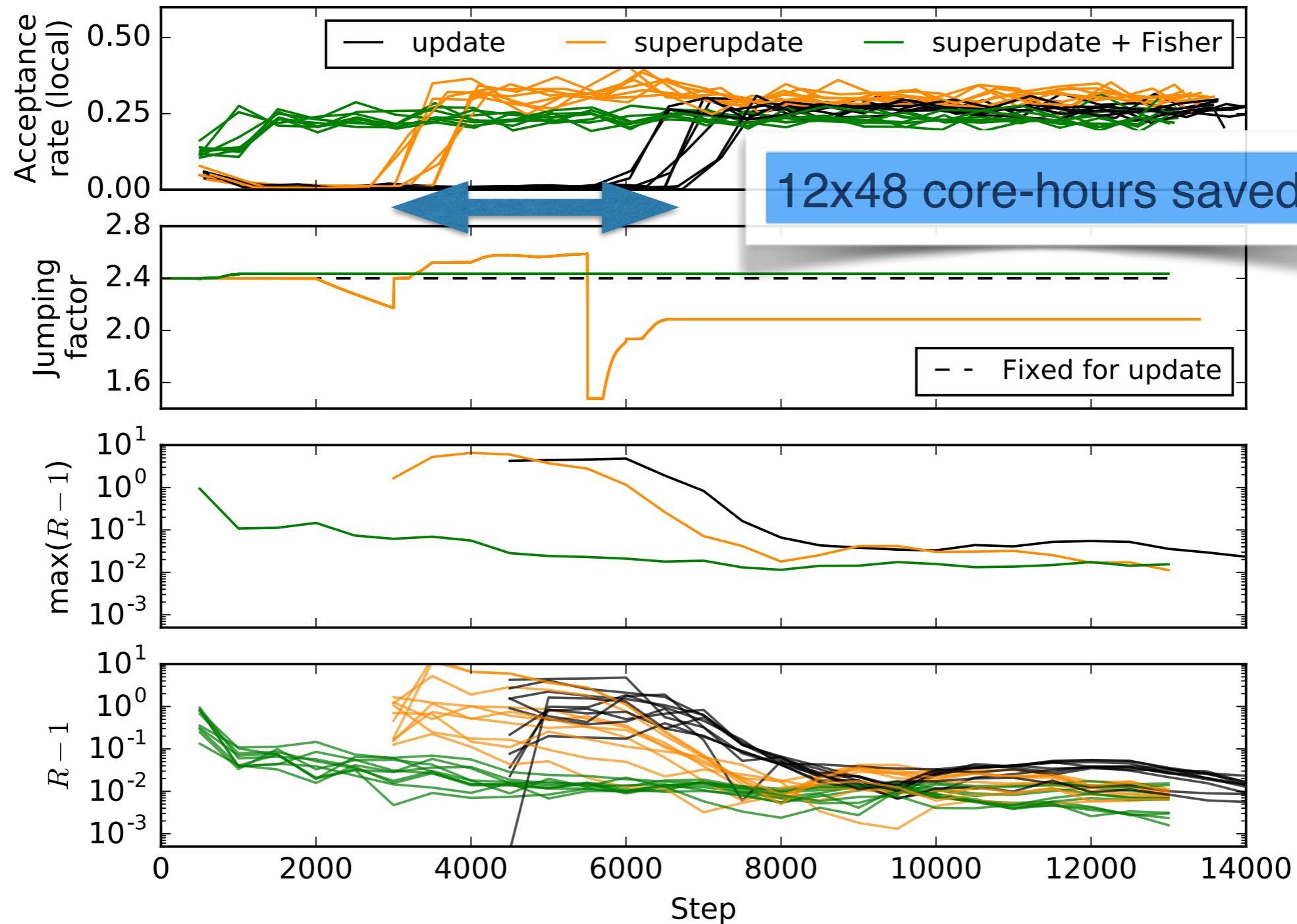
!

Running time: 48 hours

Λ CDM	6	0.0035	0.0029	0.0019
νw_0 CDM + $N_{\text{eff}} + \text{running}$	10	0.014	0.0054	0.0038

3x

MontePython 3: superupdate



MontePython 3: superupdate

Boosting Metropolis-Hastings sampling

Since v2.2 (October 2015)

- `--update U` : update of covariance matrix, \mathbf{C} , every U cycles [default: $U = 50$]
- `--superupdate SU` : additionally, update of jumping factor, j , starting SU cycles after each covariance matrix update [default: $SU = 0$, meaning “deactivated”; recommended: 20]

New in v3.0

Note: `superupdate` always enables `update`

Main advantages

- ▶ faster convergence
- ▶ better at dealing with difficult cases

Always neutral or better

MontePython 3: sampling options

Advanced options

Can also use MultiNest

- `--method` : sampling method (MH, NS, CH, IS, Der, Fisher) [default: MH] which refer respectively to Metropolis-Hastings, Nested Sampling (= MultiNest), Cosmo Hammer (= emcee), Importance Sampling, Derived (= reprocessing the chains to add columns with extra derived parameters requiring a new CLASS run for each model), and Fisher.

Options for Metropolis-Hastings and variants

Important

- `--method MH` : Metropolis-Hastings sampling [default: MH]
- `--update` : proposal distribution update frequency in number of cycles [default: 50]
- `--superupdate` : also adapt jumping factor. Adaptation delay in number of cycles [default: 0] (i.e. deactivated by default. Recommended: 20)
- `--superupdate-ar` : target local acceptance rate [default: 0.26]
- `--superupdate-ar-tol` : tolerance for local acceptance rate [default: 0.01]
- `--adaptive` : running adaptation of covariance matrix and jumping factor (note: only suitable for single chain runs) [default: 0]
- `--adaptive-ts` : starting step for adapting the jumping factor [default: 1000]
- `-f` : jumping factor [default: 2.4]

Speed up convergence of Metropolis-Hastings runs!

MontePython 3: sampling options

Advanced options

Can also use MultiNest

- `--method` : sampling method (MH, NS, CH, IS, Der, Fisher) [default: MH] which refer respectively to Metropolis-Hastings, Nested Sampling (= MultiNest), Cosmo Hammer (= emcee), Importance Sampling, Derived (= reprocessing the chains to add columns with extra derived parameters requiring a new CLASS run for each model), and Fisher.

More options

- `-T` : sample from the probability distribution $P^{1/T}$ instead of P [default: 1.0]
- `--minimize` : attempt to re-evaluate starting point using a χ^2 minimization algorithm [by default uses SLSQP via `numpy.optimize.minimize()`, can be changed in `sampler.py` function `get_minimum()`]
- `--minimize-tol` : tolerance for minimization [default: 10^{-5}]
- `--display-each-chi2` : display the χ^2 contribution of each likelihood in a given point
- `--quiet` : reduce output
- `--silent` : silence all but essential output

E.g. use with bestfit file
`--b <file>` and no jump `-f 0`

Restarting chains

- `-r <file>` : restart chains from previous run. Must pass the lowest index chains file, e.g. 2018-09-12_10000__1.txt . MontePython will then create copies of all chains index 1 through N (number of MPI processes) with new names 2018-09-12_20000__1.txt etc. Once the chains have been copied the old chains can be moved to a backup folder or deleted. Note they will be automatically deleted at the completion of the run.

The old chains should not be included in the analysis

MontePython 3: likelihoods

Likelihoods can be found in the folder:

► `<montepython_directory>/montepython/likelihoods/`

New (18) or updated (3) likelihoods in MontePython 3.0

BK14	<code>__init__.py</code>	core_m5	litebird
BK14priors	acbar	cosmic_clocks_2016	lowlike
CFHTLens	bao	cosmic_clocks_BC03	polarbear
CFHTLens_correlation	bao_angular	cosmic_clocks_BC03_all	quad
ISW	bao_boss	cosmic_clocks_MaStro	sdss_lrgDR4
JLA	bao_boss_aniso	da_rec	sdss_lrgDR7
JLA_simple	bao_boss_aniso_gauss_approx	euclid_lensing	simlow
Planck_SZ	bao_boss_dr12	euclid_pk	sn
Planck_actspt	bao_fs_boss_dr12	fake_desi	spt
Planck_highl	bao_known_rs	fake_desi_euclid_bao	spt_2500
Planck_highl_TTTEEE	bao_smallz_2014	fake_desi_vol	test_gaussian
Planck_highl_TTTEEE_lite	bicep	fake_planck_bluebook	test_nuisance1
Planck_highl_lite	bicep2	fake_planck_realistic	test_nuisance2
Planck_lensing	boomerang	gunn_peterson	timedelay
Planck_lowl	cbi	hst	wmap
WiggleZ	clik_wmap_full	igm_temperature	wmap_9yr
WiggleZ_bao	clik_wmap_lowl	kids450_qe_likelihood_public	

MontePython 3: likelihoods

Easy to do forecasts with MontePython!

Start by creating fiducial spectra (may need to delete existing one first)

► `python montepython/MontePython.py run -p <file> -o <directory> -f 0`

Then run as normal!

No jump

BK14
BK14priors
CFHTLens
CFHTLens_correlation
ISW
JLA
JLA_simple
Planck_SZ
Planck_actspt
Planck_highl
Planck_highl_TTTEEE
Planck_highl_TTTEEE_lite
Planck_highl_lite
Planck_lensing
Planck_lowl
WiggleZ
WiggleZ_bao

More coming soon!

*E.g. CMB-S4, PICO, SKA
updated euclid likelihoods*

__init__.py
act
bao
bao_angular
bao_boss
bao_boss_dr12
bao_boss_dr12_2014
bao_knobs
bicep2
boomerang
cbi
clik_wmap_full
clik_wmap_lowl

core_m5
cosmic_clocks_2016
cosmic_clocks_BC03
cosmic_clocks_BC03_all
cosmic_clocks_MaStro
da_rec
euclid_lensing
euclid_pk
fake_desi
fake_desi_euclid_bao
fake_desi_vol
fake_planck_bluebook
fake_planck_realistic
gunn_peterson
hst
igm_temperature
kids450_qe_likelihood_public

litebird
lowlike
polarbear
quad
sdss_lrgDR4
sdss_lrgDR7
simlow
sn
spt
spt_2500
test_gaussian
test_nuisance1
test_nuisance2
timedelay
wmap
wmap_9yr

MontePython 3: communication with CLASS

MontePython interacts with CLASS through the wrapper and automatically accepts **any** parameter that is implemented in CLASS.

Example: you have implemented a model in CLASS with parameters `my_parameter1` and `my_parameter2`, as well as precision parameters `my_precision1` and `my_precision2`.

These parameters can be directly added to the `.param` file.

```
# Cosmological parameters list

data.parameters['omega_b']      = [ 2.2253,  None, None,  0.028,  0.01, 'cosmo']
data.parameters['omega_cdm']    = [0.11919, None, None, 0.0027,  1, 'cosmo']
data.parameters['100*theta_s']  = [ 1.0418, None, None,  3e-4,  1, 'cosmo']
data.parameters['ln10^{10}A_s'] = [ 3.0753, None, None, 0.0029,  1, 'cosmo']
data.parameters['n_s']          = [0.96229, None, None, 0.0074,  1, 'cosmo']
data.parameters['tau_reio']     = [0.09463, 0.04, None, 0.013,  1, 'cosmo']
data.parameters['my_parameter1'] = [ 0.,    -1.,  1.,  0.1,  1, 'cosmo']
data.parameters['my_parameter2'] = [ 1.,    None, 10., 0.2,  1, 'cosmo']
```

MontePython 3: communication with CLASS

These parameters can be directly added to the `.param` file.

```
# Cosmological parameters list

data.parameters['omega_b']      = [ 2.2253,  None, None,  0.028, 0.01, 'cosmo']
data.parameters['omega_cdm']    = [0.11919, None, None, 0.0027, 1, 'cosmo']
data.parameters['100*theta_s']  = [ 1.0418, None, None, 3e-4, 1, 'cosmo']
data.parameters['ln10^{10}A_s'] = [ 3.0753, None, None, 0.0029, 1, 'cosmo']
data.parameters['n_s']          = [0.96229, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio']     = [0.09463, 0.04, None, 0.013, 1, 'cosmo']
data.parameters['my_parameter1'] = [ 0., -1., 1., 0.1, 1, 'cosmo']
data.parameters['my_parameter2'] = [ 1., None, 10., 0.2, 1, 'cosmo']

# Other cosmo parameters (fixed parameters, precision parameters, etc.)

data.cosmo_arguments['sBBN file'] = data.path['cosmo']+'/bbn/sBBN.dat'
data.cosmo_arguments['k_pivot'] = 0.05
data.cosmo_arguments['my_precision1'] = 0.005
data.cosmo_arguments['my_precision2'] = 0.02
```

That's it!

MontePython 3: communication with CLASS

* We can add a custom parameterization for our new parameters. To do this, we have to modify

► `<montepython_directory>/montepython/data.py`

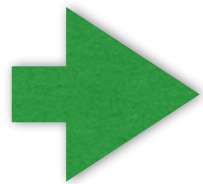
```
def update_cosmo_arguments(self):
    """
    Put in :attr:`cosmo_arguments` the current values of
    :attr:`mcmc_parameters`

    This method is called at every step in the Markov chain, to update the
    dictionary. In the Markov chain, the scale is not remembered, so one
    has to apply it before giving it to the cosmological code.

    .. note::

        When you want to define new parameters in the Markov chain that do
        not have a one to one correspondance to a cosmological name, you
        can redefine its behaviour here. You will find in the source
        several such examples.

    ...
elif elem == 'my_parameterization':
    try:
        self.cosmo_arguments['my_parameter1']
    except:
        warnings.warn('my_parameter1 not defined. This quantity must be define to sample my_parameterization')
        self.cosmo_arguments['my_parameter2'] = self.cosmo_arguments[elem] * self.cosmo_arguments['my_parameter1]**2
```



We have now redefined `my_parameter2` as a function of `my_parameter1` and `my_parameterization`

MontePython 3: communication with CLASS

The new parameterization can be directly added to the `.param` file.

```
# Cosmological parameters list

data.parameters['omega_b']           = [ 2.2253,  None, None,  0.028, 0.01, 'cosmo']
data.parameters['omega_cdm']         = [0.11919, None, None, 0.0027, 1, 'cosmo']
data.parameters['100*theta_s']       = [ 1.0418, None, None, 3e-4, 1, 'cosmo']
data.parameters['ln10^{10}A_s']      = [ 3.0753, None, None, 0.0029, 1, 'cosmo']
data.parameters['n_s']                = [0.96229, None, None, 0.0074, 1, 'cosmo']
data.parameters['tau_reio']           = [0.09463, 0.04, None, 0.013, 1, 'cosmo']
data.parameters['my_parameter1']      = [ 0., -1., 1., 0.1, 1, 'cosmo']
data.parameters['my_parameterization'] = [ 1., None, 10., 0.2, 1, 'cosmo']

# Other cosmo parameters (fixed parameters, precision parameters, etc.)

data.cosmo_arguments['sBBN file'] = data.path['cosmo']+'/bbn/sBBN.dat'
data.cosmo_arguments['k_pivot'] = 0.05
data.cosmo_arguments['my_precision1'] = 0.005
data.cosmo_arguments['my_precision2'] = 0.02
```

That's it!

MontePython 3: communication with CLASS

Can call any function in the wrapper:

```
class my_likelihood(Likelihood_prior):  
  
    # initialisation of the class is done within the parent Likelihood_prior. For  
    # this case, it does not differ, actually, from the __init__ method in  
    # Likelihood class.  
    def loglkl(self, cosmo, data):  
        tau = cosmo.tau_reio()  
        loglkl = -0.5 * (tau - self.tau) ** 2 / (self.sigma ** 2)  
        return loglkl  
  
class my_likelihood(Likelihood_prior):  
  
    # initialisation of the class is done within the parent Likelihood_prior. For  
    # this case, it does not differ, actually, from the __init__ method in  
    # Likelihood class.  
    def loglkl(self, cosmo, data):  
        rs_drag_theo = cosmo.rs_drag()  
        loglkl = -0.5 * (rs_drag_theo - self.rs_drag) ** 2 / (self.sigma ** 2)  
        return loglkl
```

MontePython 3: adding likelihoods

1. Create folder, e.g. starting from a similar likelihood

▶ `cp -r simlow my_likelihoood`

The folder contains two files

▶ `__init__.py simlow.data`

2. Rename .data file to match folder name, i.e. **my_likelihoood**


▶ `__init__.py my_likelihoood.data`

MontePython 3: adding likelihoods

3. Rename class in `__init__.py` to match folder name



```
import os
from montepython.likelihood_class import Likelihood_prior

class simlow(Likelihood_prior):
    # initialization of the class is done within the parent Likelihood_prior. For
    # this case, it does not differ, actually, from the __init__ method in
    # Likelihood class.
    def loglkl(self, cosmo, data):
```



```
import os
from montepython.likelihood_class import Likelihood_prior

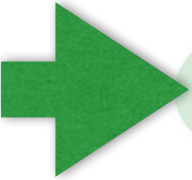
class my_likelihood(Likelihood_prior):
    # initialization of the class is done within the parent Likelihood_prior. For
    # this case, it does not differ, actually, from the __init__ method in
    # Likelihood class.
    def loglkl(self, cosmo, data):
```




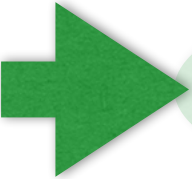
MontePython 3: adding likelihoods

4. Rename class variables in `my_likelihood.data`

```
# Values for tau (following Astro-ph/1605.02985)
# This likelihood is a prior on tau_reio inspired
# by simlow, the low multipole polarization
# likelihood from the Planck 2016 paper
simlow.tau      = 0.055
simlow.sigma    = 0.009
```



```
# Values for tau (following Astro-ph/1605.02985)
# This likelihood is a prior on tau_reio inspired
# by simlow, the low multipole polarization
# likelihood from the Planck 2016 paper
my_likelihood.tau      = 0.055
my_likelihood.sigma    = 0.009
```





MontePython 3: adding likelihoods


Perhaps we want a prior on the sound horizon at drag epoch

5. Modify `my_likelihood.data` as necessary, e.g. in our example

```
# Values for tau (following Astro-ph/1605.02985)
# This likelihood is a prior on tau_reio inspired
# by simlow, the low multipole polarization
# likelihood from the Planck 2016 paper
my_likelihood.tau      = 0.055
my_likelihood.sigma    = 0.009
```




```
# Planck 2015 prior for the sound horizon at drag epoch
my_likelihood.rs_drag = 147.41
my_likelihood.sigma   = 0.30
```




MontePython 3: adding likelihoods

6. Modify `__init__.py` as necessary, e.g. in our example

```
class my_likelihood(Likelihood_prior):  
  
    # initialisation of the class is done within the parent Likelihood_prior. For  
    # this case, it does not differ, actually, from the __init__ method in  
    # Likelihood class.  
    def loglkl(self, cosmo, data):  
        tau = cosmo.tau_reio()  
        loglkl = -0.5 * (tau - self.tau) ** 2 / (self.sigma ** 2)  
        return loglkl
```



```
class my_likelihood(Likelihood_prior):  
  
    # initialisation of the class is done within the parent Likelihood_prior. For  
    # this case, it does not differ, actually, from the __init__ method in  
    # Likelihood class.  
    def loglkl(self, cosmo, data):  
        rs_drag_theo = cosmo.rs_drag()  
        loglkl = -0.5 * (rs_drag_theo - self.rs_drag) ** 2 / (self.sigma ** 2)  
        return loglkl
```



MontePython 3: more information

MontePython 3 paper

▶ [Brinckmann & Lesgourgues 1804.07261](#)

Official documentation

▶ <http://monte-python.readthedocs.io/en/latest/>

Help files

▶ `python montepython/MontePython.py run -h`

(more details: `--help`)

▶ `python montepython/MontePython.py info -h`

(more details: `--help`)

Github readme

https://github.com/brinckmann/montepython_public

Wiki

https://github.com/audren/montepython_public/wiki

Previous talks and tutorials on Julien Lesgourgues' website

<https://lesgourg.github.io/courses.html>

Problems? Open a ticket on my github page (after trying to find a solution yourself)

https://github.com/brinckmann/montepython_public