Quick introduction to MontePython in 10 slides

code: https://github.com/baudren/montepython_public

doc: http://monte-python.readthedocs.io

Main developers: Benjamin Audren, Julien Lesgourgues, + input from many others

Lisbon EUCLID meeting, 2.06.2016

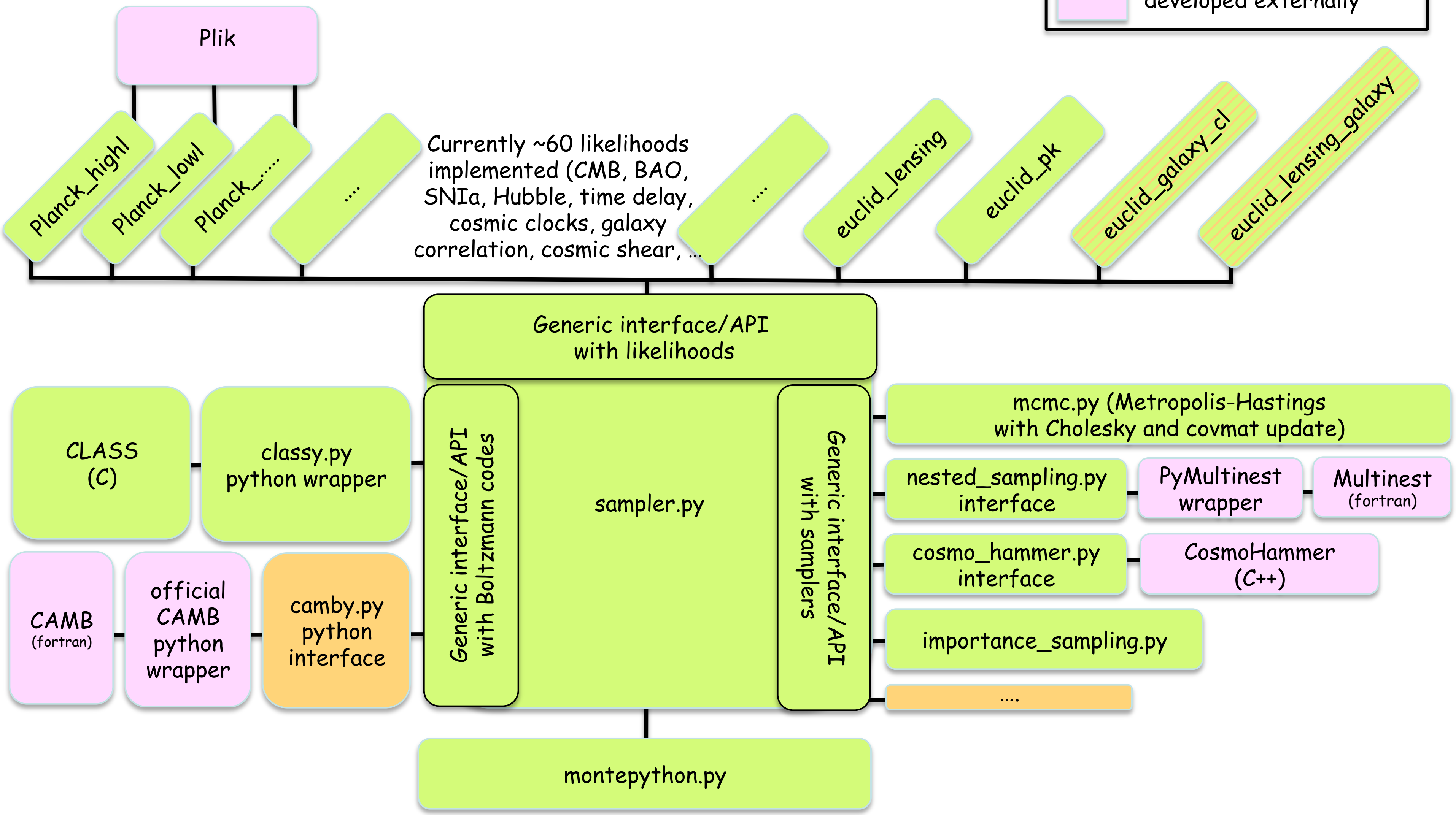
Sébastien Clesse (RWTH Aachen University)

Modularity in MontePython

🟩 developed internally

🟧 in development (internally)

🟪 developed externally



Currently ~60 likelihoods implemented (CMB, BAO, SNIa, Hubble, time delay, cosmic clocks, galaxy correlation, cosmic shear, …

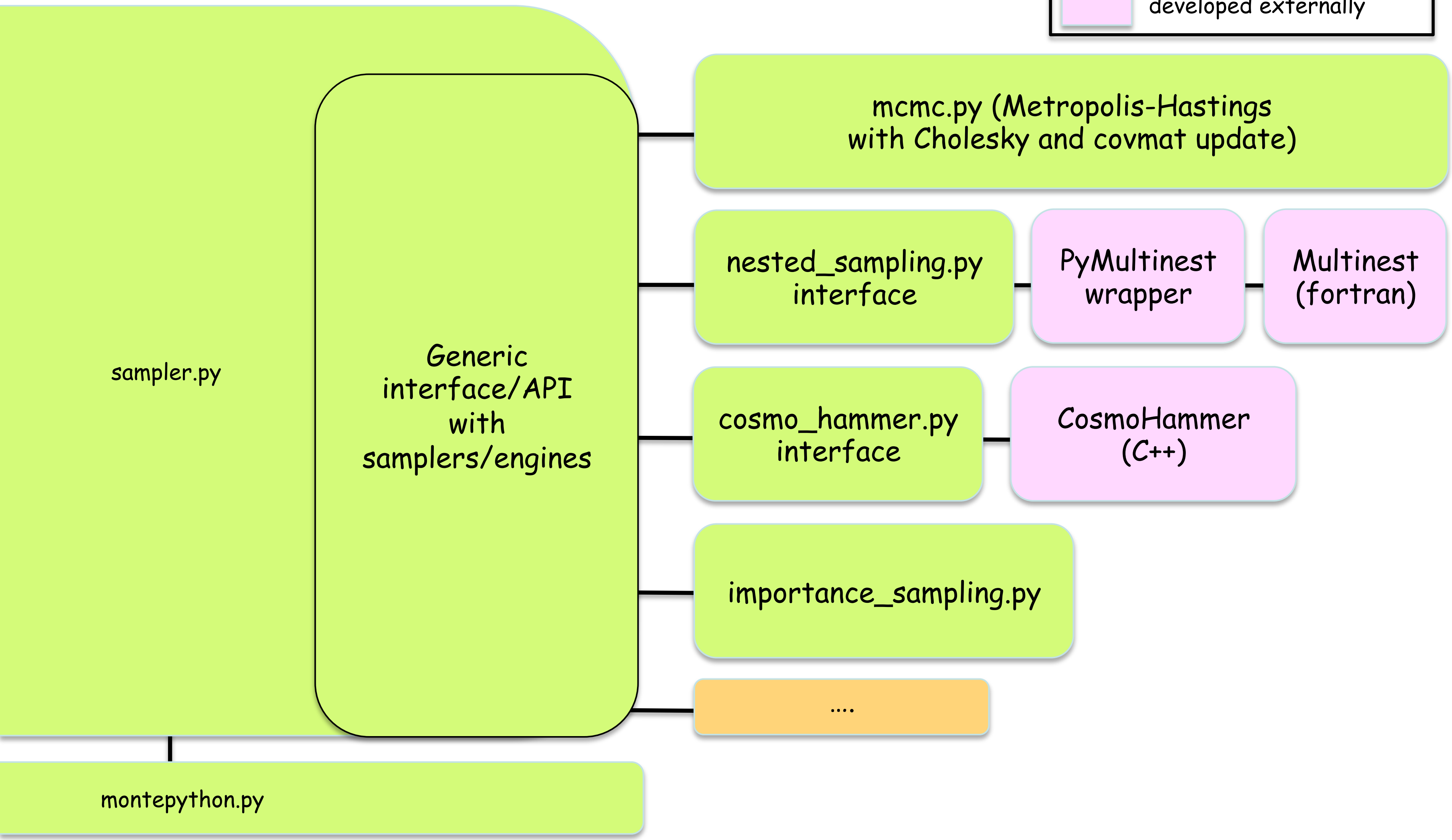
Plik
Planck_highl
Planck_lowl
Planck_.....
...
...
euclid_lensing
euclid_pk
euclid_galaxy_cl
euclid_lensing_galaxy
Generic interface/API with likelihoods
CLASS (C)
classy.py python wrapper
Generic interface/API with Boltzmann codes
sampler.py
Generic interface/API with samplers
mcmc.py (Metropolis-Hastings with Cholesky and covmat update)
nested_sampling.py interface
PyMultinest wrapper
Multinest (fortran)
cosmo_hammer.py interface
CosmoHammer (C++)
importance_sampling.py
....
CAMB (fortran)
official CAMB python wrapper
camby.py python interface
montepython.py

Modularity in MontePython

🟩 developed internally

🟧 in development (internally)

🟪 developed externally



mcmc.py (Metropolis-Hastings with Cholesky and covmat update)

nested_sampling.py interface

PyMultinest wrapper

Multinest (fortran)

sampler.py

Generic interface/API with samplers/engines

cosmo_hammer.py interface

CosmoHammer (C++)

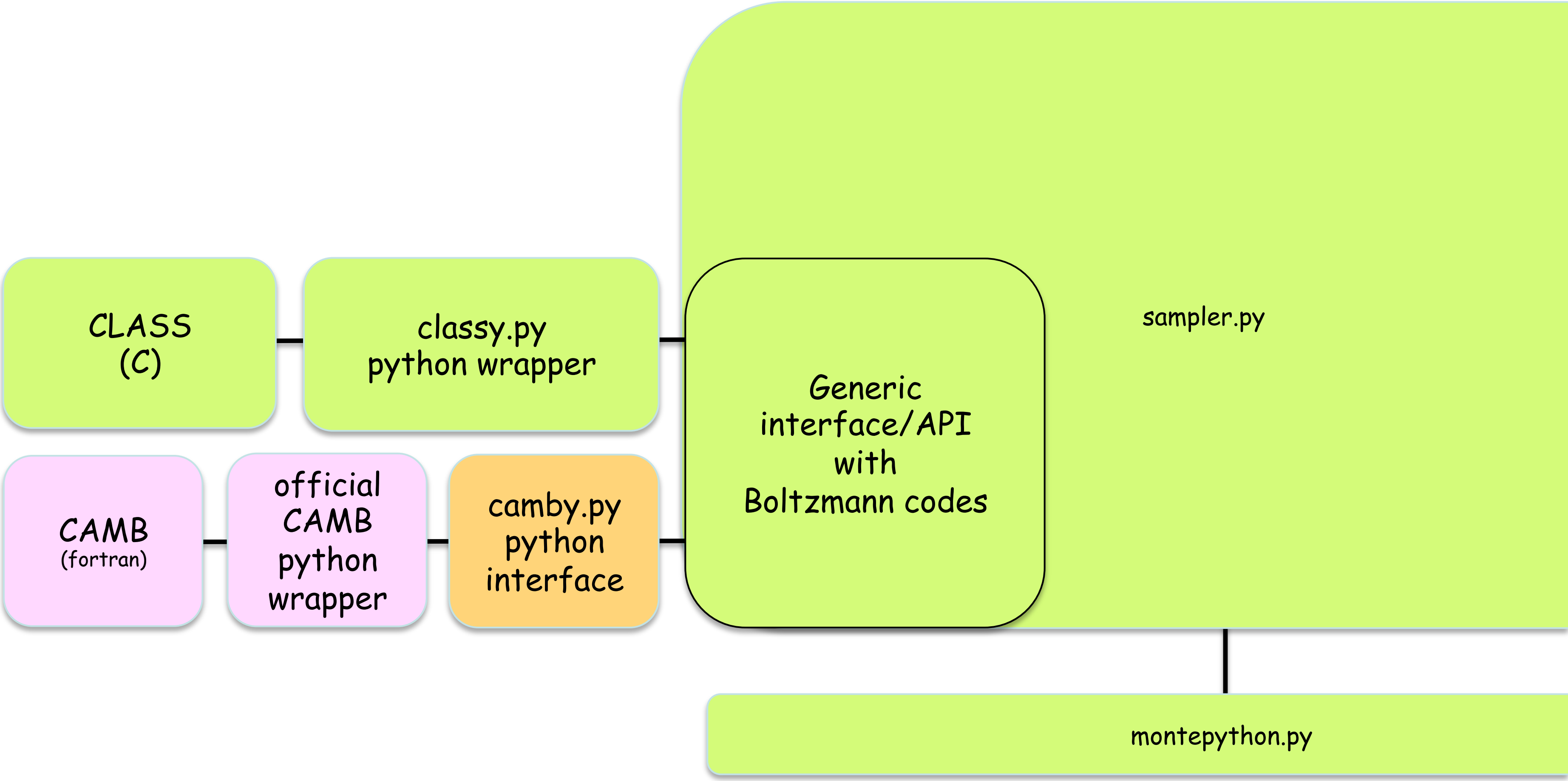
importance_sampling.py

....

montepython.py

Modularity in MontePython

- 🟩 developed internally
- 🟧 in development (internally)
- 🟪 developed externally



CLASS (C)

classy.py python wrapper

CAMB (fortran)

official CAMB python wrapper

camby.py python interface

Generic interface/API with Boltzmann codes

sampler.py

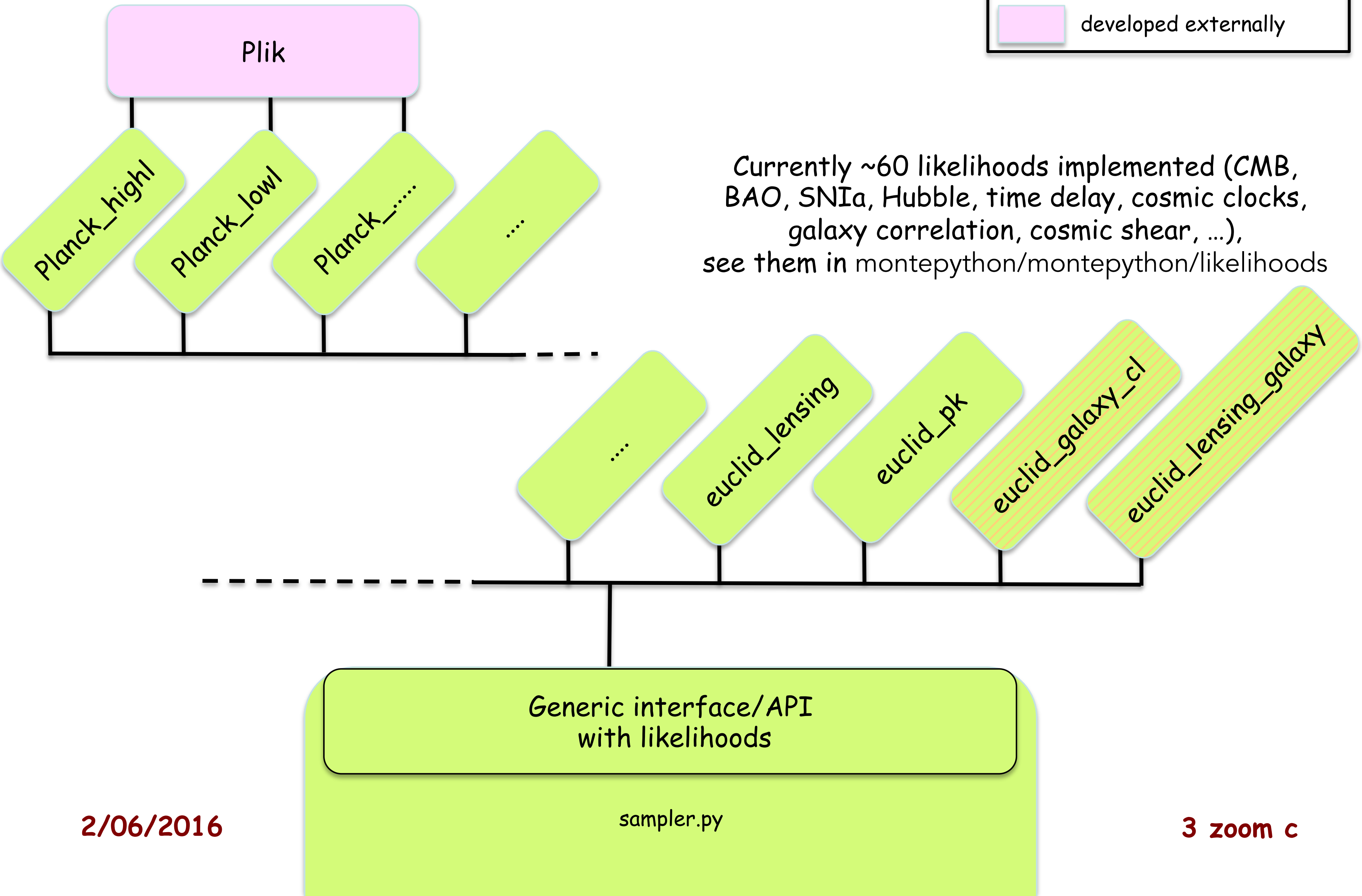
montepython.py

Modularity in MontePython

🟩 developed internally

🟧 in development (internally)

🟪 developed externally



Currently ~60 likelihoods implemented (CMB, BAO, SNIa, Hubble, time delay, cosmic clocks, galaxy correlation, cosmic shear, ...), see them in montepython/montepython/likelihoods

Documentation

- CLASS html documentation:

  http://www.class-code.net →click: online html documentation

- MontePython html documentation:

  http://monte-python.readthedocs.io

Installation

- Install CLASS and classy.py as explained in:

  https://github.com/lesgourg/class_public/wiki/Installation

- Install the other python modules necessary for MontePython as explained in:

  [short version:] https://github.com/baudren/montepython_public/wiki/Installation

  [or more details at:] http://monte-python.readthedocs.io →click: Installation Guide

- Running with MPI requires one extra python module mpi4py, but this is is *optional.*
  - Advantage: run N chains from *single* command instead of N *identical* command lines.
  - But even without MPI, the covariance matrix will be updated using *all* chains (communication through file reading/writing instead of MPI).

Quick start

- Code can be called in two modes (equivalents of CosmoMC and GetDist)

```
python montepython/MontePython.py run <options>
python montepython/MontePython.py info <options>
```

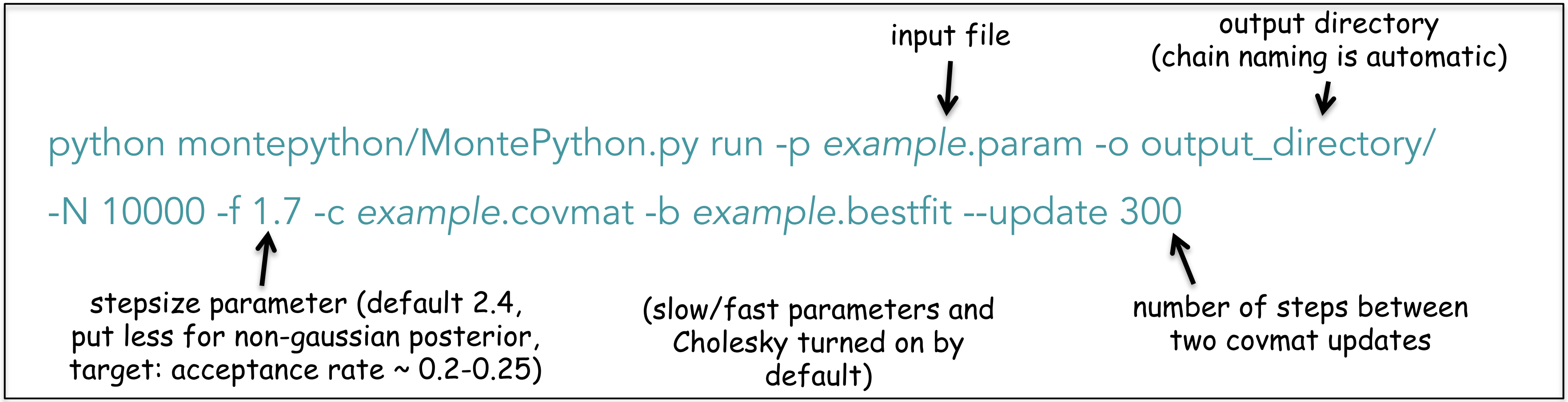
- Get a list of all options available separately for run and info with:

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

- GetDist fans can still use it instead of info (identical format of the chains; *new:* MontePython also writes .paramnames files for improved compatibility with GetDist)

Typical run command

- Code can be called with (example for Metropolis-Hastings without MPI):



```
python montepython/MontePython.py run -p example.param -o output_directory/
-N 10000 -f 1.7 -c example.covmat -b example.bestfit --update 300
```

input file

output directory
(chain naming is automatic)

stepsize parameter (default 2.4,
put less for non-gaussian posterior,
target: acceptance rate ~ 0.2-0.25)

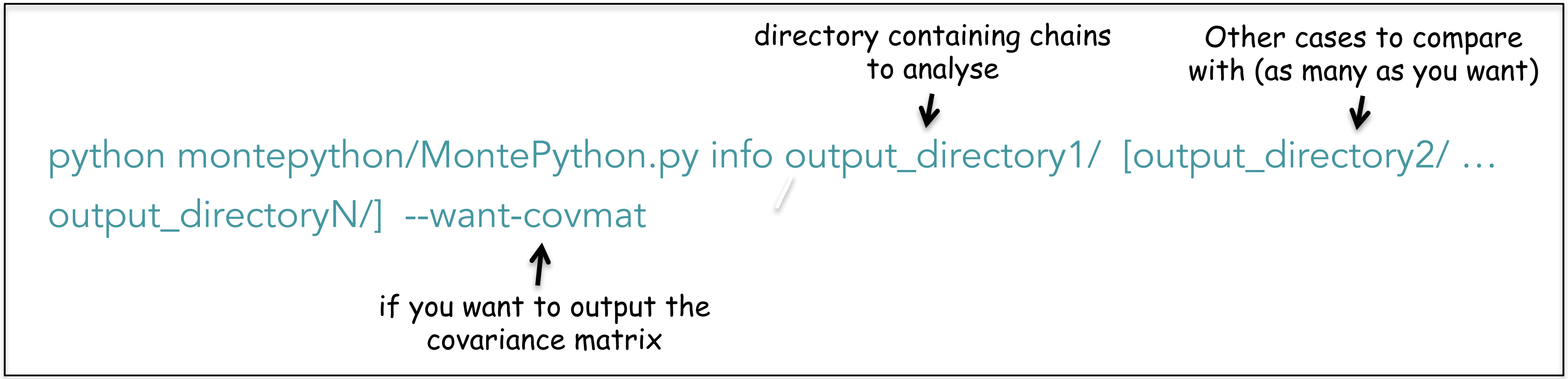
(slow/fast parameters and
Cholesky turned on by
default)

number of steps between
two covmat updates

- First job in given directory will create a file output_directory/log.param
  - log.param stores for records everything you may need to remember on this run (details on dataset, Boltzmann code version, all cosmo/nuisance/derived/fixed parameters, etc.)
  - once it exists, log.param used as input file, with priority over –p xxx.param, to ensure that all chains in given directory correspond precisely to same model and datasets (if Boltzmann code version changed: run stops, forcing you to create a new output directory)

Typical info command

- Chain analysis can be done with :



directory containing chains to analyse

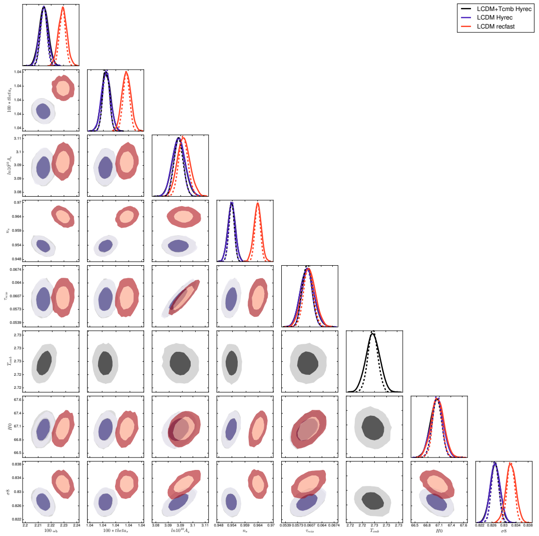
Other cases to compare with (as many as you want)

```
python montepython/MontePython.py info output_directory1/  [output_directory2/ …
output_directoryN/]  --want-covmat
```

if you want to output the covariance matrix

… plus lots of customisation options (see them with --help)

… with --extra *optional_plot_file*, any pyplot command can be passed directly to the code in order to customise the plots



doc: http://monte-python.readthedocs.io

Typical input file

```
#------Experiments to test (separated with commas)-----
data.experiments=[’planck_lite’, 'euclid_pk']

#------ Settings for fast (nuisance) parameters, number of blocks depends on number of likelihoods with nuisance parameters
data.over_sampling=[1, 4]

#------ Parameter list  (format:   data.parameters[name] = [mean, min, max, 1-sigma, scale, role] ) -----------

# 1. Cosmological parameters list (name must be directly understood by Boltzmann code’s parser)
data.parameters['omega_cdm'] = [0.1120, None, None, 0.0016,1,   'cosmo']
data.parameters[’tau_reio']        = [0,  0, None, 0.03, 1,   'cosmo']
data.parameters['A_s']         = [2.42,   -1,-1, 0.038, 1e-9,'cosmo']
…
# 2. Nuisance parameter list, same call; names must not be understood by Boltzmann code, but by at least one likelihood code
data.parameters['P_shot'] = [0, None, 1,1,1,'nuisance']
…
# 3. Derived parameter list list (name must be understood by Boltzmann code’s wrapper: these are output from the Boltzmann code)
data.parameters['Omega_Lambda'] = [0,  None, None, 0, 1,  'derived']
data.parameters['sigma8']              =  [0,  None, None, 0, 1,  'derived']
…
# fixed parameters for the Boltzmann code (physical parameters, precision parameters, etc.)
data.cosmo_arguments['k_pivot'] = 0.05
…
```

doc: http://monte-python.readthedocs.io

Adding likelihoods

doc: http://monte-python.readthedocs.io

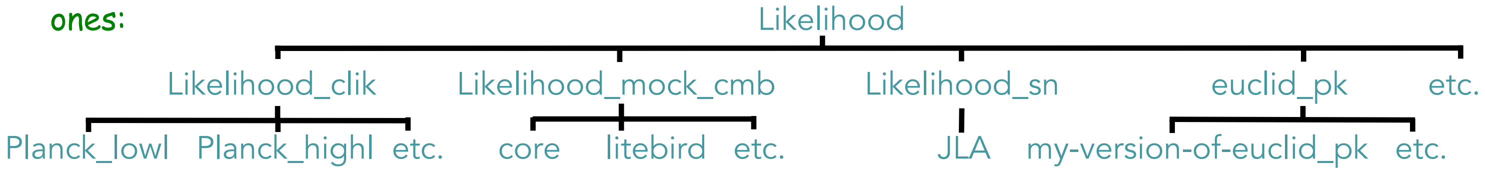
- One likelihood = one python class defined in

  montepython/likelihoods/some-name/__init.py__

  which reads all settings / parameters / data files in

  montepython/likelihoods/some-name/some-name.data

- This class inherits from properties of a mother class. May inherit from most general one, or from specific ones:



- No need to duplicate code when your new likelihood has things in common with its mother… e.g. here is the whole likelihood code in montepython/likelihoods/Planck_highl_TTTEEE/__init.py__ :

```
from montepython.likelihood_class import Likelihood_clik
class Planck_highl_TTTEEE(Likelihood_clik):
    pass
```

while montepython/likelihoods/Planck_highl_TTTEEE/Planck_highl_TTTEEE.dat just contains the path to clik and the definition of nuisance parameters…

Running with mock data

- your likelihood file montepython/likelihoods/some-name/some-name.data contains the path to some fiducial model, e.g. data/some-name_fiducial.dat

- First run: the code finds no file there. Then it automatically computes the fiducial model at the starting point of the MCMC, stores it in this file, and stops with a warning.

- Later runs: the code will use this fiducial model as mock data.

- This logic is in-built, you don't need to think about it anymore when you add a new mock likelihood.

doc: http://monte-python.readthedocs.io