Basic structure of Monte Python

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1. Code Structure
2. Important Modules in (some) detail
3. Usage
4. Practice with Monte Python

Outline

classy - wrapper around CLASS

Cython

- language to **interface** Python with C
- can be used to **speed up** a bottleneck in Python or...
- to wrap an **existing C code** and call it from Python as a normal function

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- classy.pyx **wraps** CLASS modules and some functions (only the ones needed from within Monte Python).
- uses a **dictionary** in place of the **.ini file** to give parameters (file content)
- if no arguments are specified, CLASS **default values** will be used.

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Last word

You (most probably) don't need to know how `classy.pyx` is written. The only important thing is **its interface**.

General structure of the modules

Files

Input Files

- configuration file: **path to codes on machine**
- parameter file: **parameters, prior range, proposal, experiments**

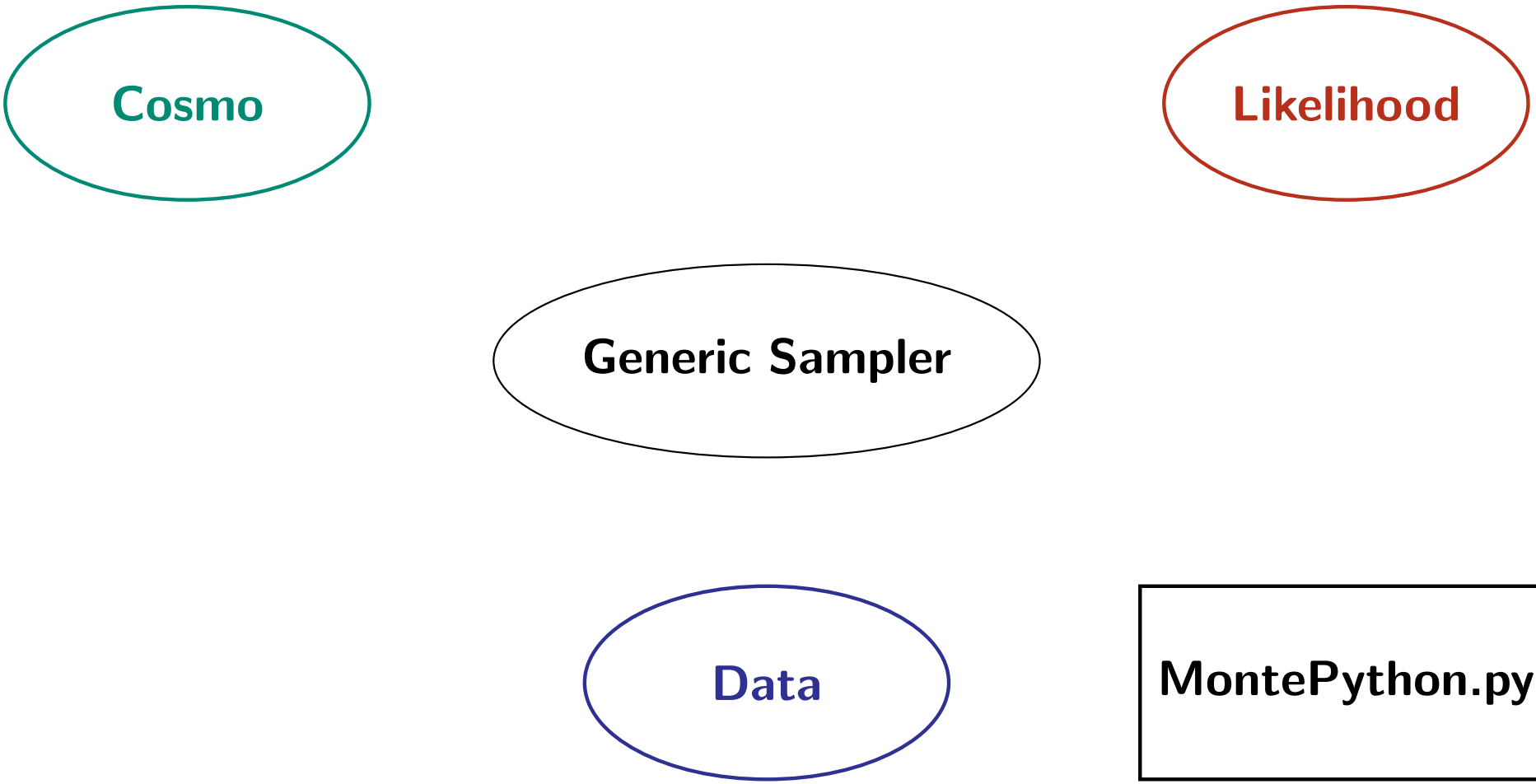
opt covariance matrix, bestfit file

Ouptut

- a folder: **stores every information concerning the run**
- a chain per run: **Markov Chain of a given length**

General structure of the modules

A drawing



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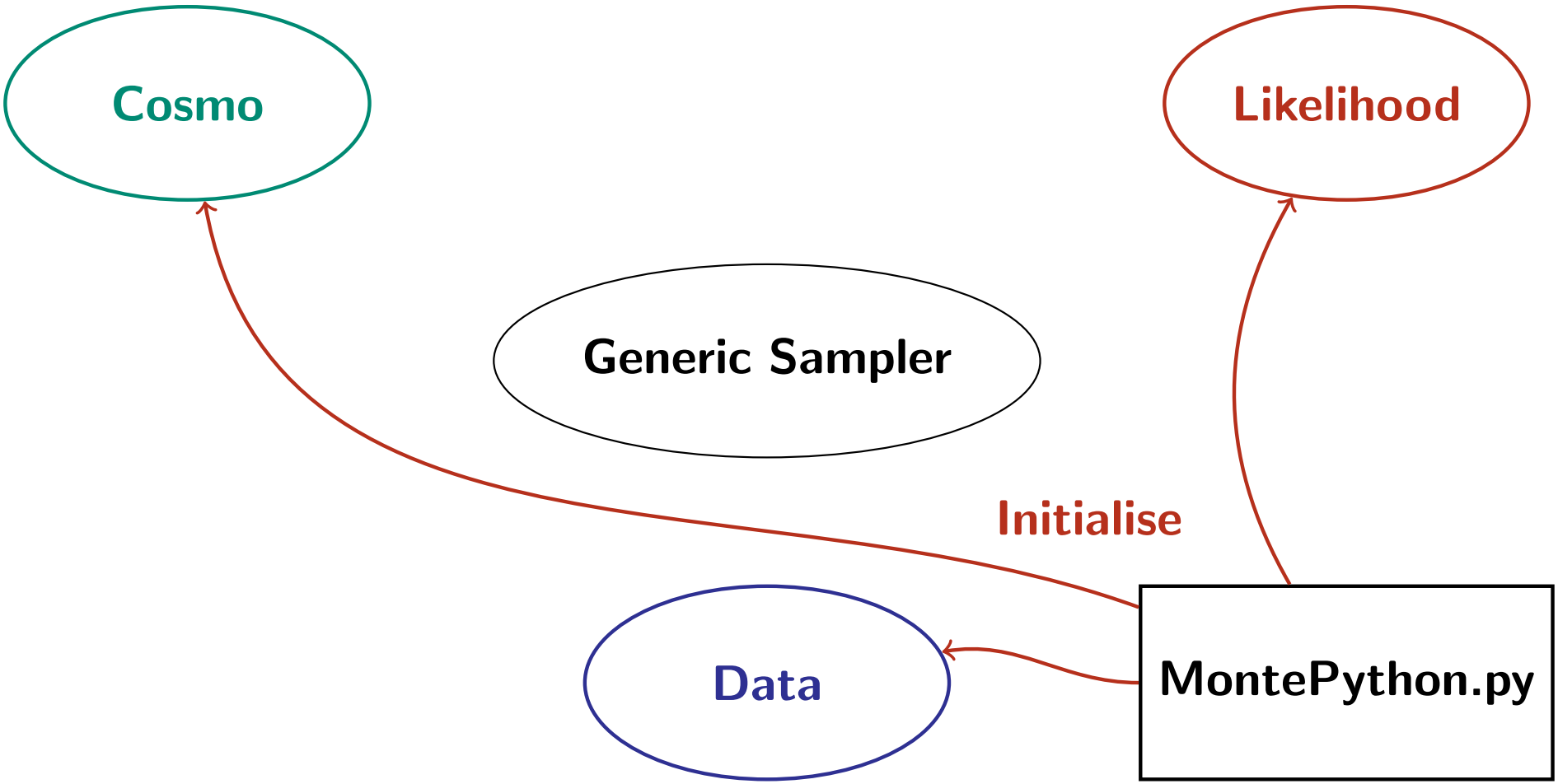

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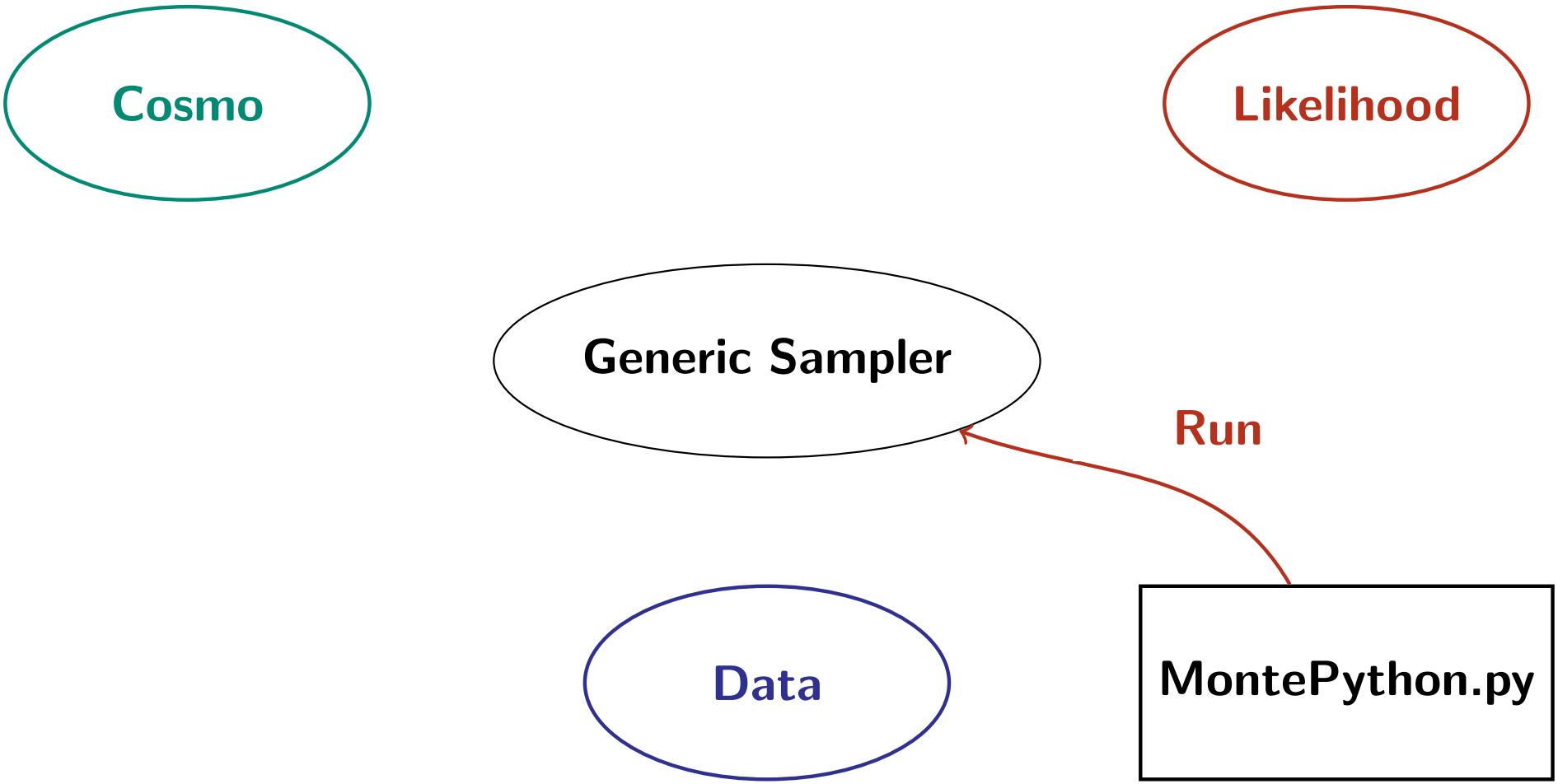

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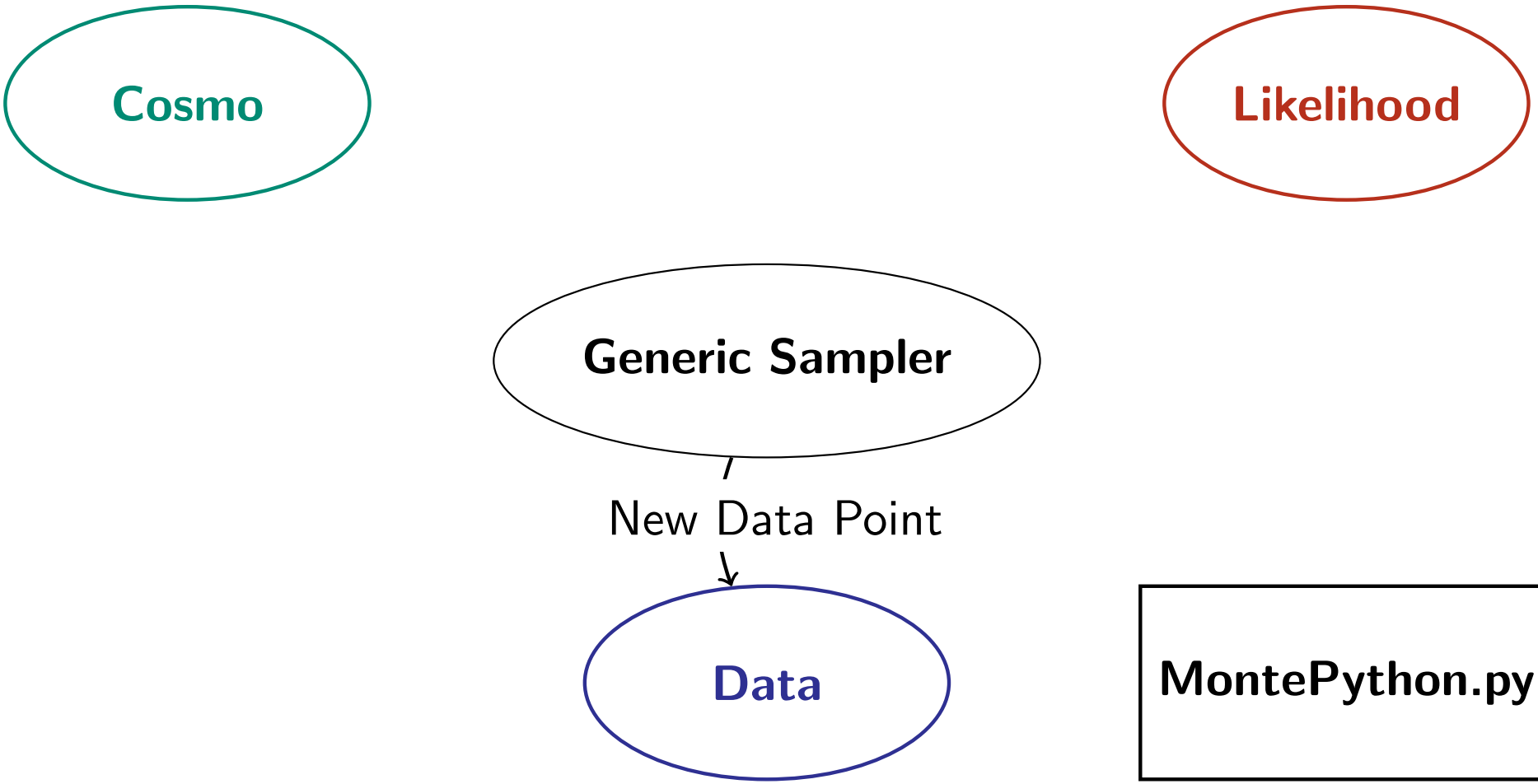

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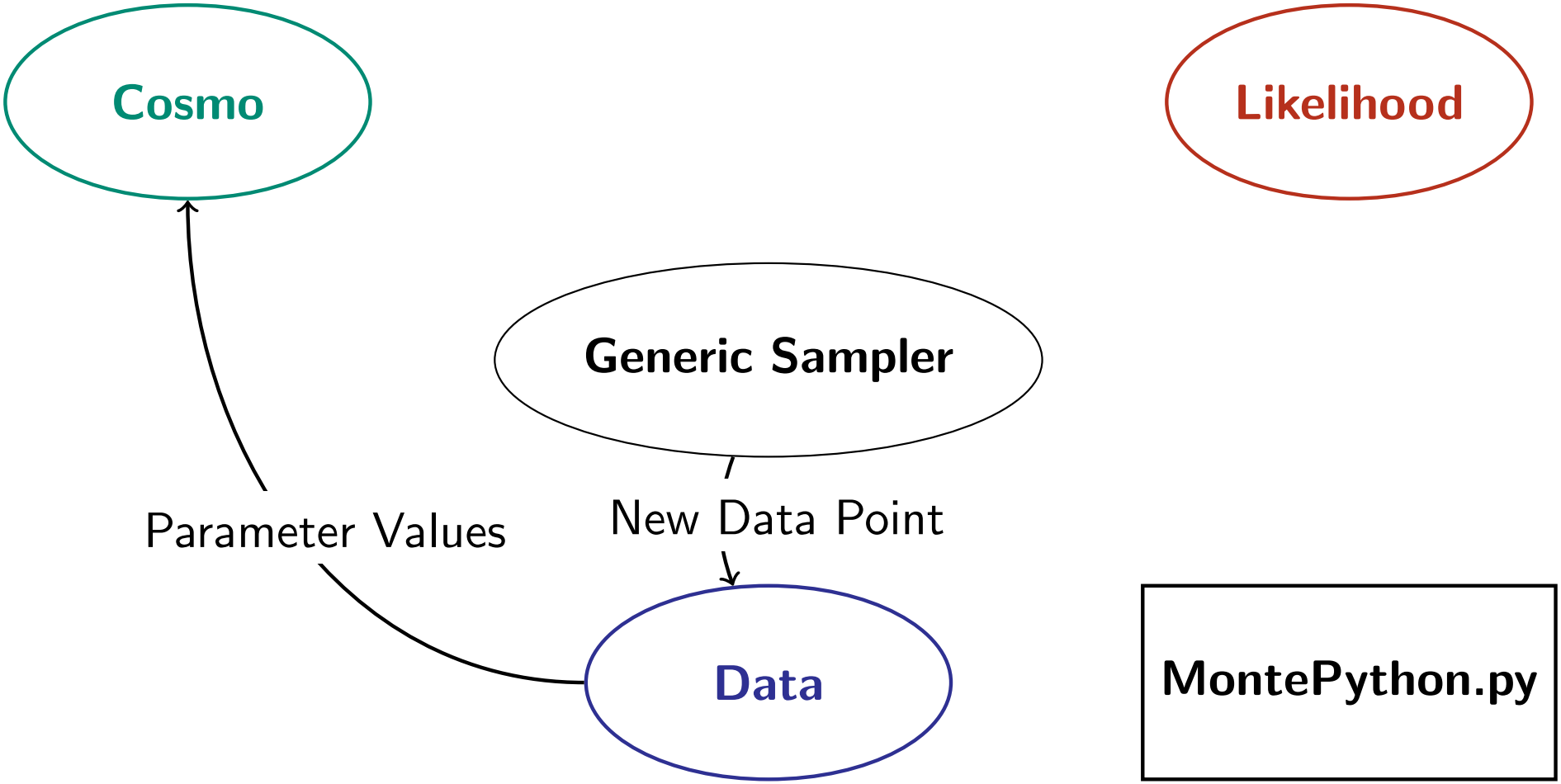

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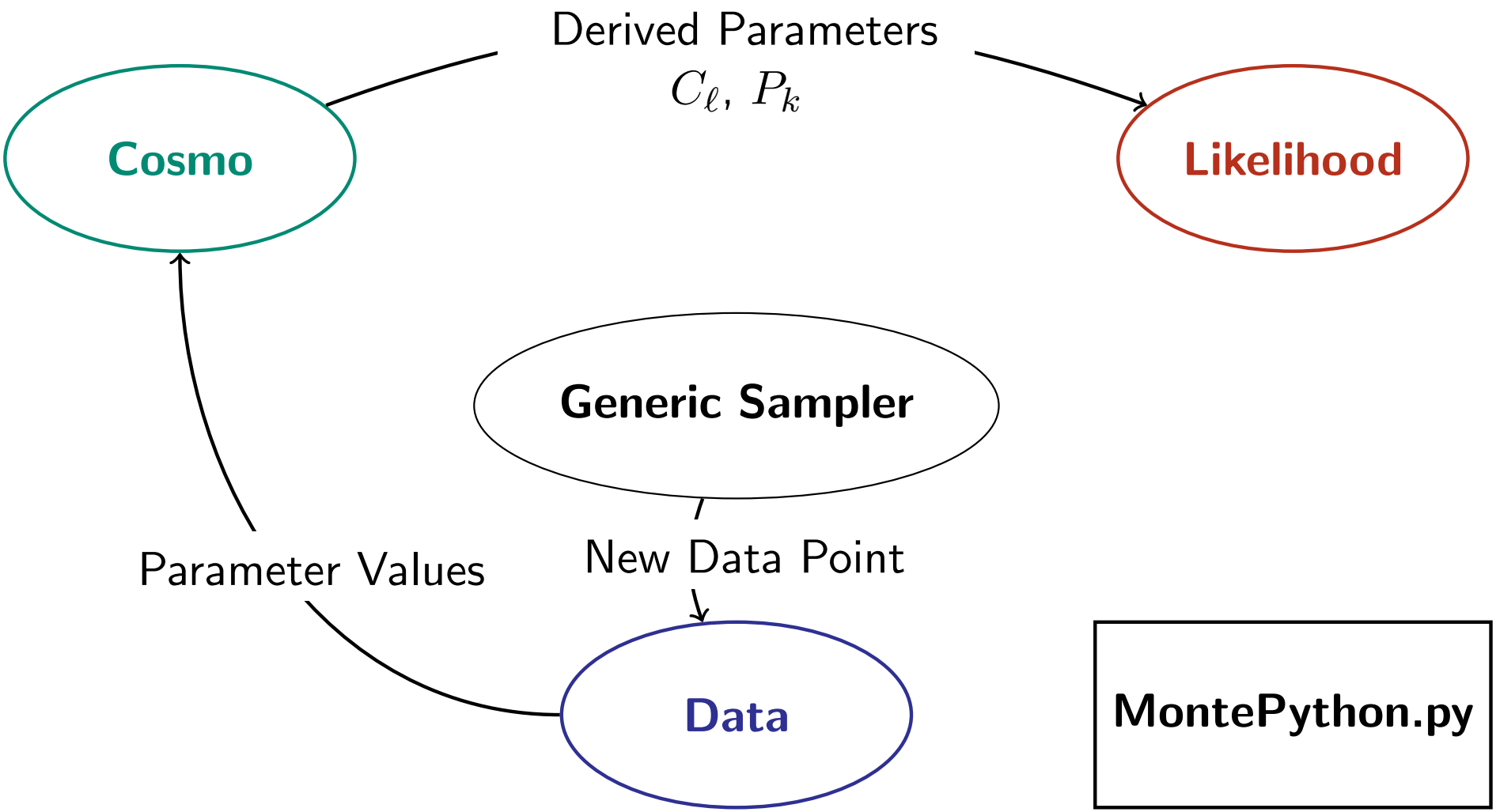

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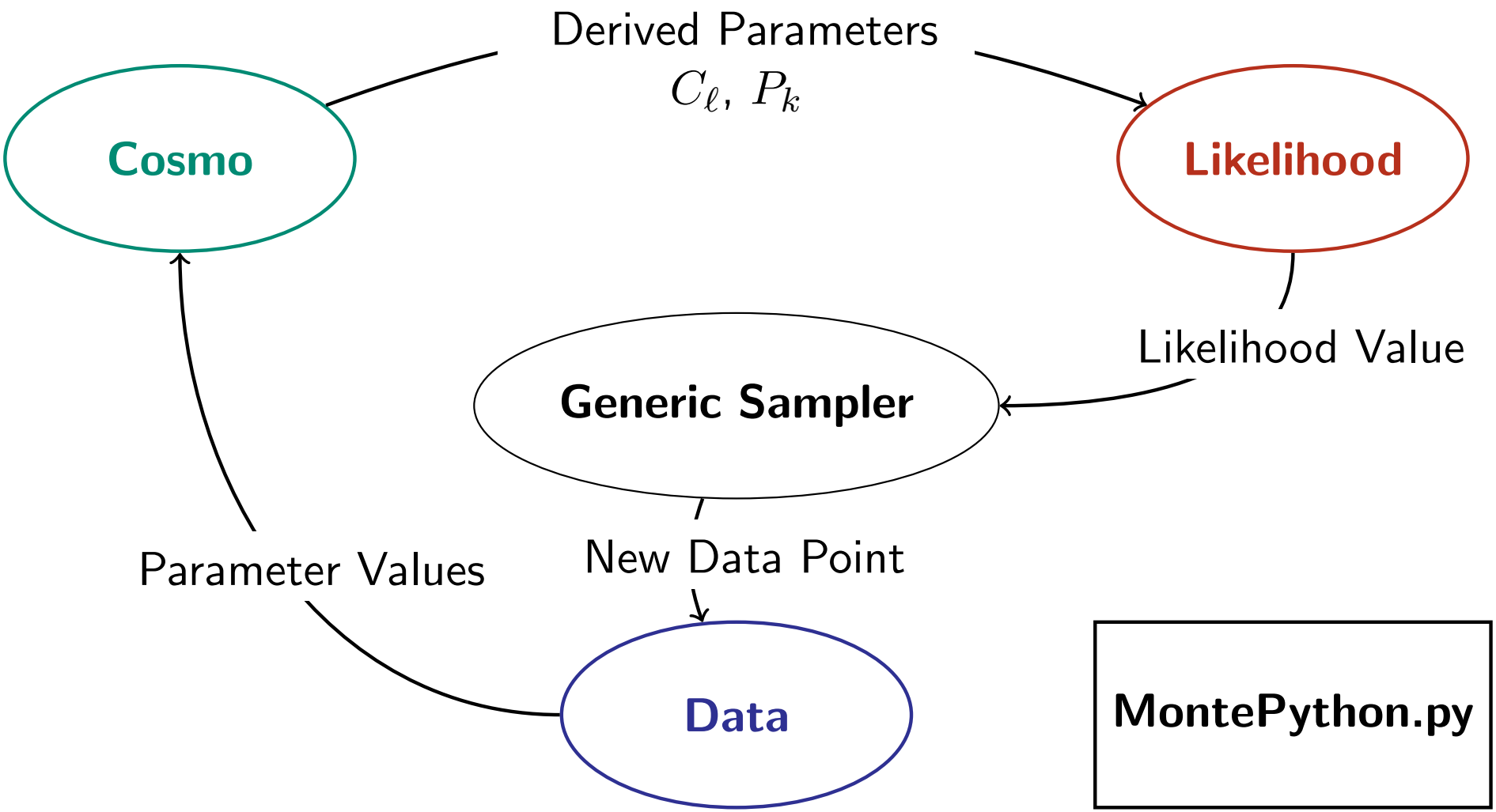

Information containers

Foreword: class definitions in capital letters, instances in small.

Classes

- **Data** defined in `data.py`
- **Class** defined in `classy.pyx`
- **Likelihood** defined in `likelihood_class.py`

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- **Class** defined in `classy.pyx`
- **Likelihood** defined in `likelihood_class.py`

instances

- **data** initialized in `initialise.py`
- **cosmo** initialized in `initialise.py`
- **hst, bicep2, ...** initialized in `initialise.py`

General structure of the modules

Main Modules

- `MontePython` **Simple script launching the code**

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Helper Modules

- `analyze` Computes convergence, posterior from chains
- `io_mp` **Handles I/O, error message**

Outline

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Use it!

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Use the wiki!

https://github.com/baudren/montepython_public/wiki, or https://github.com/lesgourg/class_public/wiki for classy business.

MontePython.py

Role

Convenience script that calls the Monte Python run function.

Initialise I

Main

- **Reads command line, configuration file**

```
29    # Parsing line argument
30    command_line = parser_mp.parse(custom_command)
31
32    # Recovering the local configuration
33    path = recover_local_path(command_line)
```

Initialise I

Main

- Reads command line, configuration file
- **Creates a data instance**

```
56          data = Data(command_line, path)
```

Initialise I

Main

- Reads command line, configuration file
- Creates a data instance
- **Initializes the cosmological module**

```
72    # Loading up the cosmological backbone. For the moment, only
          CLASS has been
73    # wrapped.
74    cosmo = recover_cosmological_module(data)
```

Data I

Defining a data class

- **Initialization**

```
35 class Data(object):
36     """
37     Store all relevant data to communicate between the different
           modules.
38
39     """
40
41     def __init__(self, command_line, path):

136         self.cosmo_arguments = {}

145         self.mcmc_parameters = od()
```

Data I

Defining a data class

- Initialization
- **Fill in parameter information**

```
195         # Read from the parameter file to fill properly the
                mcmc_parameters
196         # dictionary.
197         self.fill_mcmc_parameters()
```

Data I

Defining a data class

- Initialization
- Fill in parameter information
- **Log parameter file if needed**

Data II

Defining a data class

- **Initialization of likelihood (dynamical)**

```
338         for elem in self.experiments:

343             # ... import easily the likelihood.py program
344             exec "from likelihoods.%s import %s" % (
345                 elem, elem)

350             exec "self.lkl['%s'] = %s('%s/%s.data',\
351                 self,command_line)" % (
352                 elem, elem, folder, elem)
```

Data II

Defining a data class

- Initialization of likelihood (dynamical)

Why so complicated

No hard coded likelihood! The code does not know the names: **no need to modify the core code to add a new likelihood**

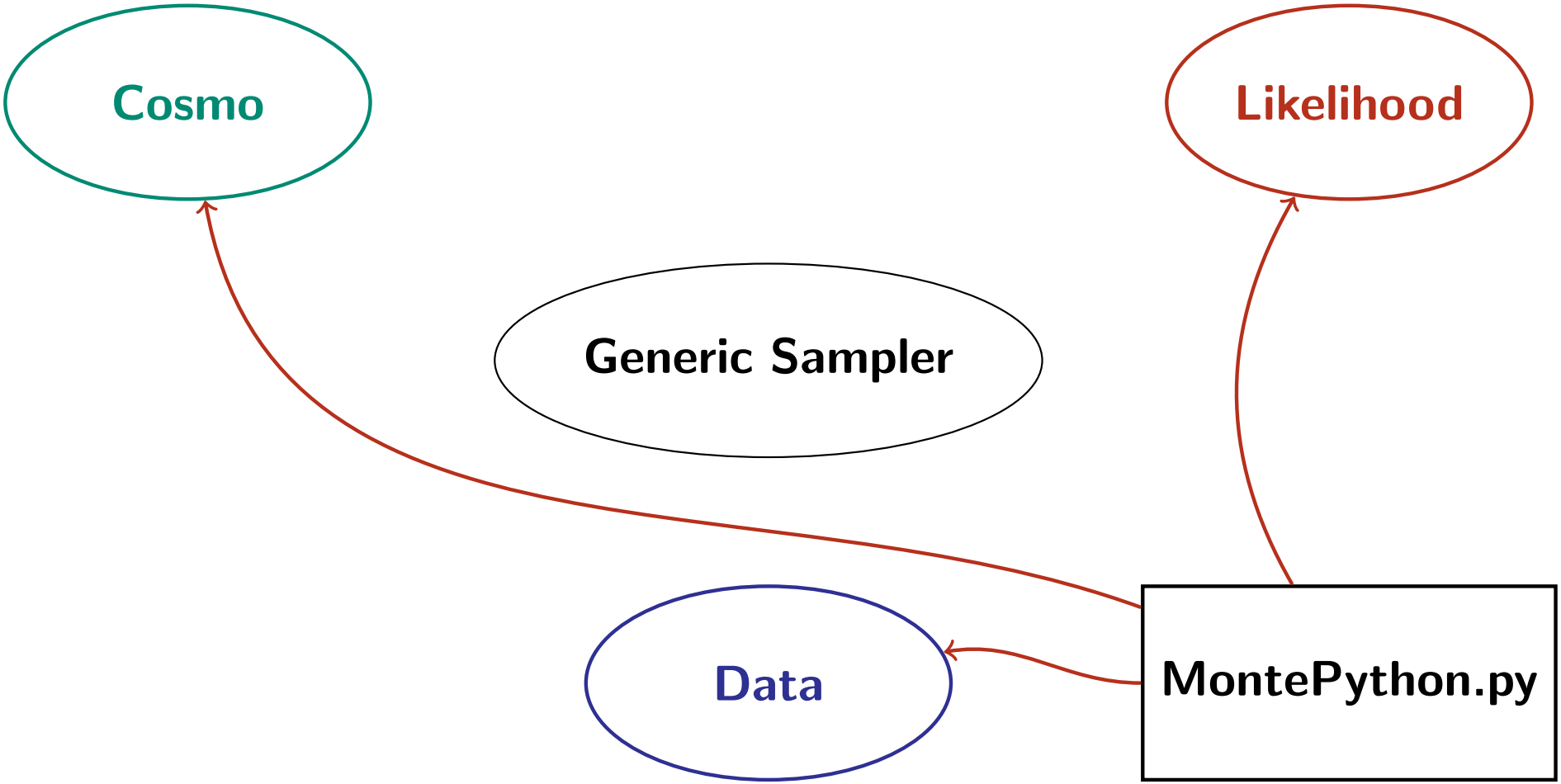
Data III

essential function

`get_mcmc_parameters` returns the list of desired parameters.

- `get_mcmc_parameters(['varying'])`
- `get_mcmc_parameters(['cosmo', 'nuisance'])`
- `get_mcmc_parameters(['cosmo', 'varying'])`

Recap Initialisation



Sampler I

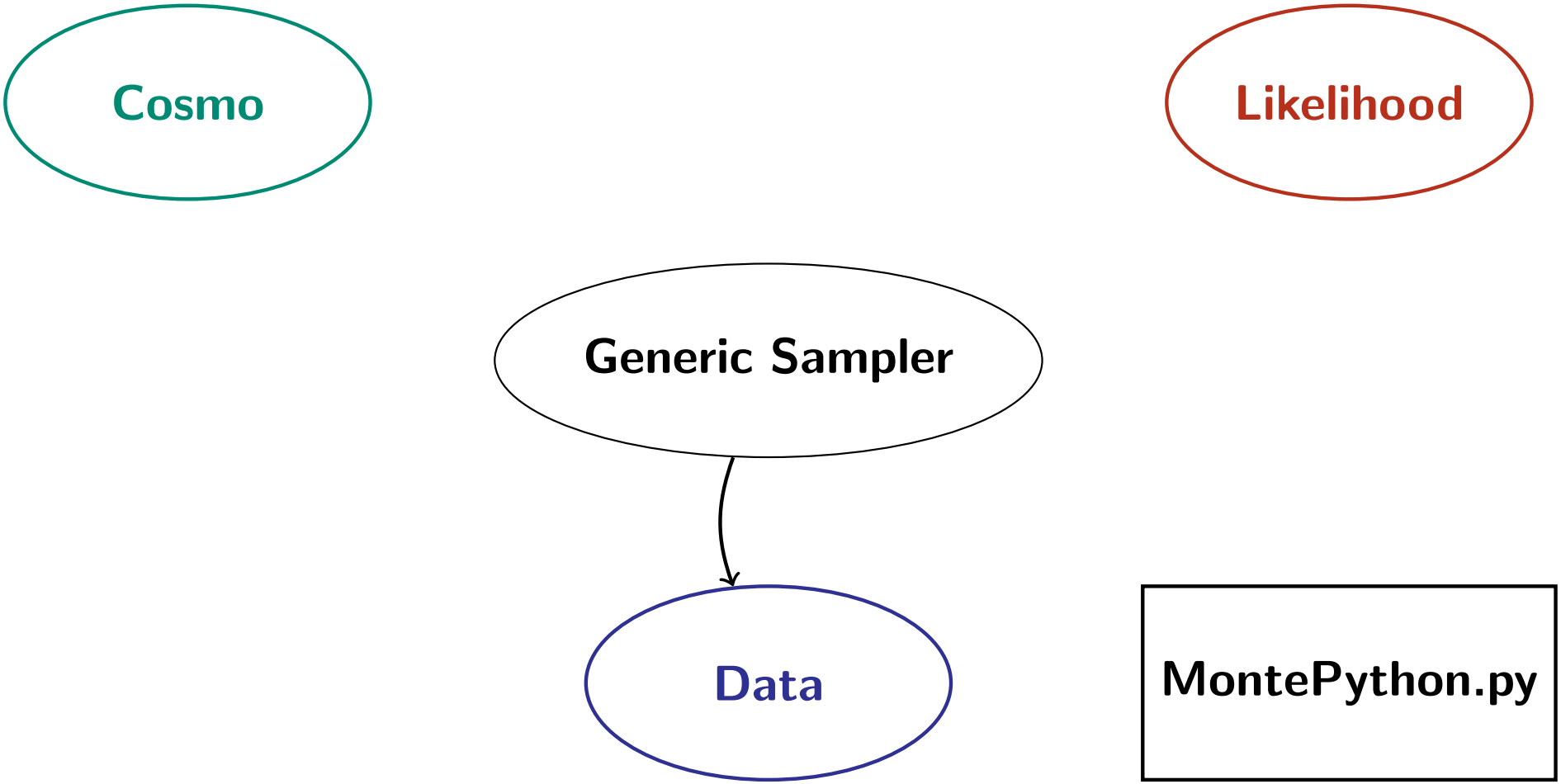
Generic helper functions

- `compute_lkl(cosmo, data)`
- `get_covariance_matrix(data, command_line)`

Role

calling the sampler specified via the **command line**

Choosing a new point



Sampler II

Get new position

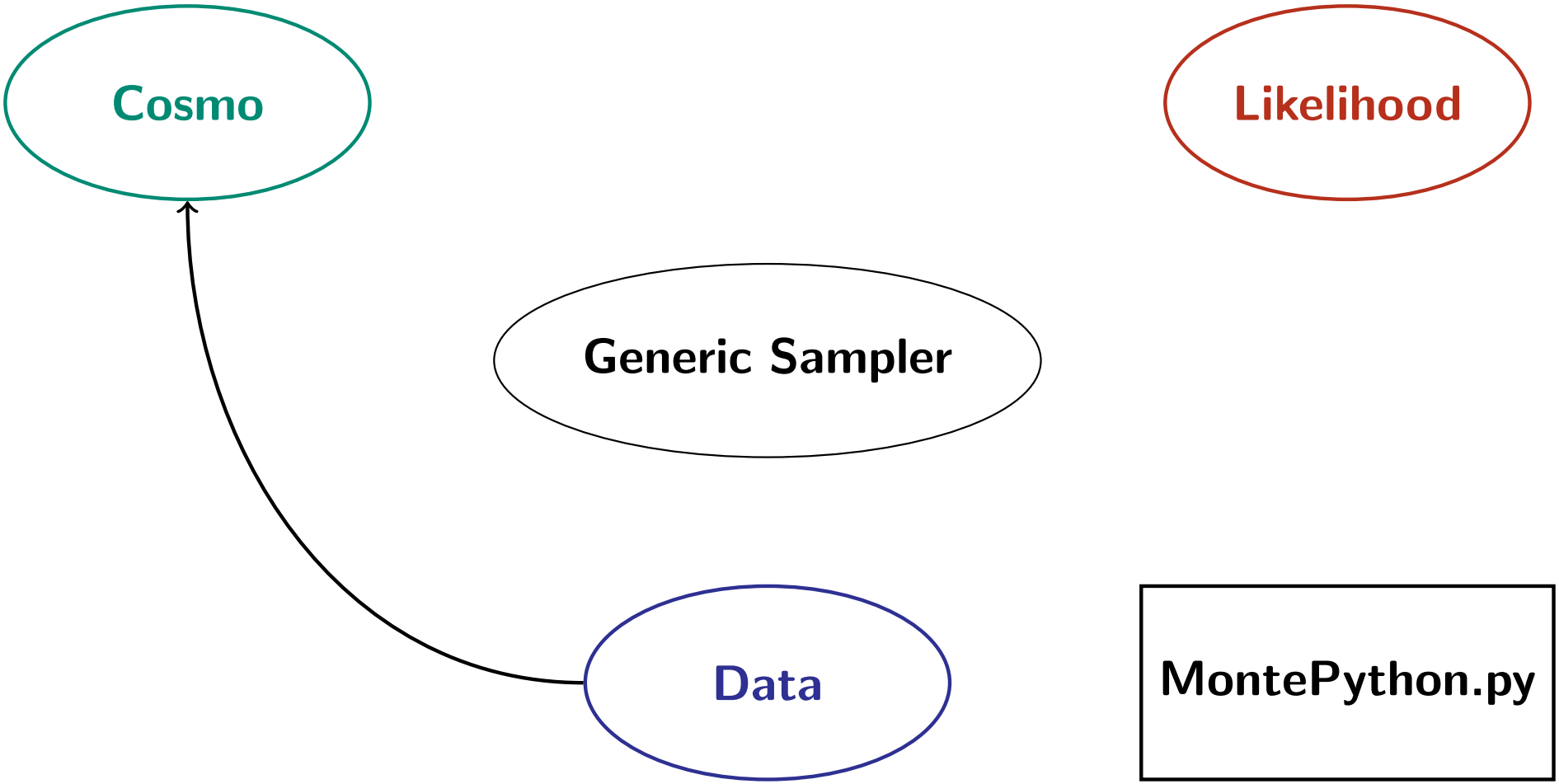
Sampler

How to choose a new point?

- basic eigen-values/vector decomposition
- Cholesky decomposition (Planck) (`-j fast`)
- Nested Sampling with MultiNest (`-m NS`)
- Emcee with Cosmo Hammer (`-m CH`)

Compute Likelihood

Set the cosmo



Sampler III

Compute likelihood

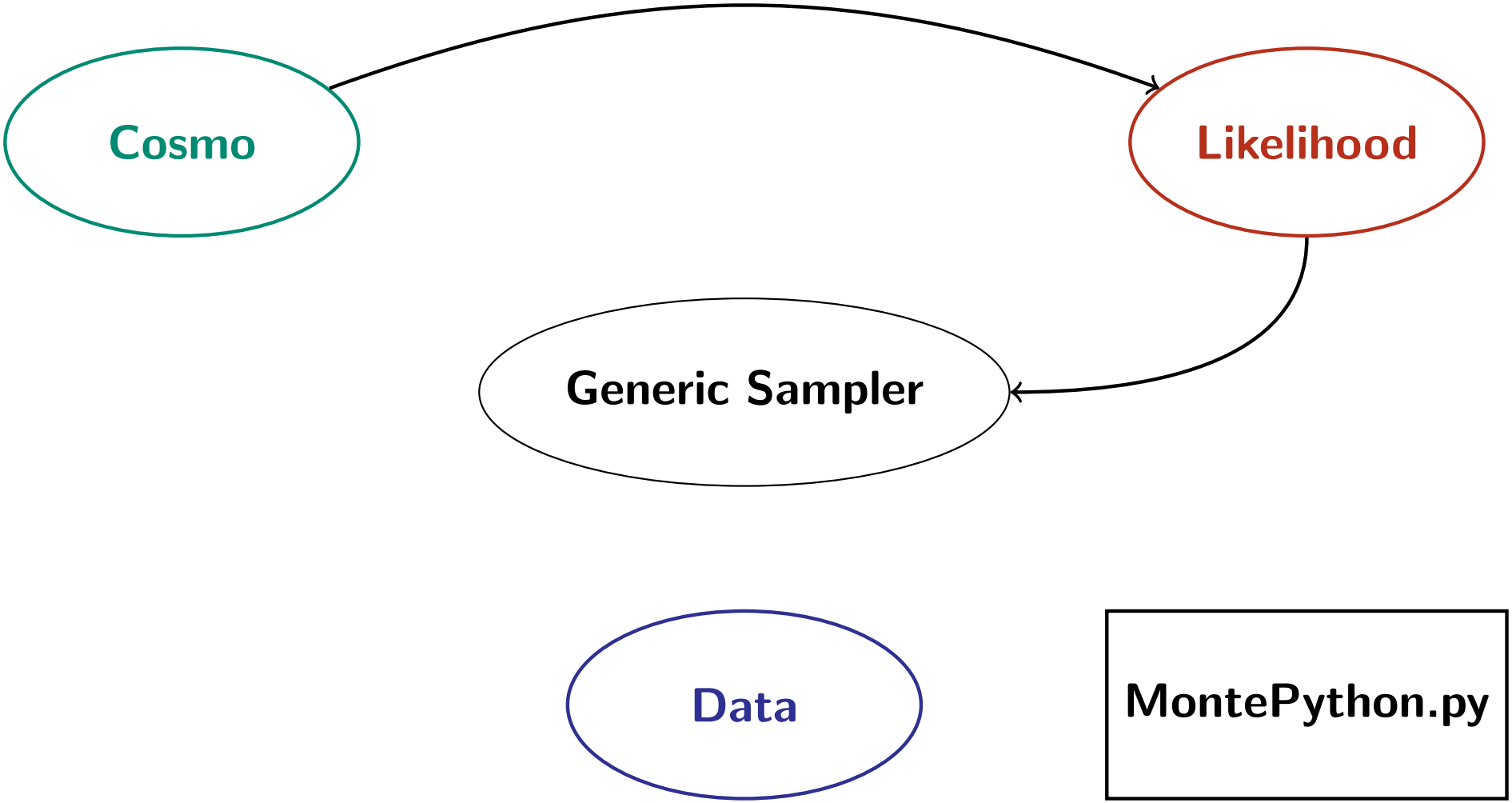
```
334 def compute_lkl(cosmo, data):

370     if ((data.need_cosmo_update) or
371             (not cosmo.state) or
372             (data.jumping_factor == 0)):
373
374         # Prepare the cosmological module with the new set of
                parameters
375         cosmo.set(data.cosmo_arguments)

390         try:
391             cosmo.compute()
392         except CosmoComputationError:
393             return data.boundary_loglike
394         except CosmoSevereError, message:
395             print str(message)
396             raise io_mp.CosmologicalModuleError(
397                 "Something went wrong when calling CLASS")
```

Compute Likelihood

For each likelihood



Sampler III

Compute likelihood

```
404     loglike = 0
```

```
410     for likelihood in data.lkl.itervalues():
411         if likelihood.need_update is True:
412             value = likelihood.loglkl(cosmo, data)
413             # Storing the result
414             likelihood.backup_value = value
415         # Otherwise, take the existing value
416         else:
417             value = likelihood.backup_value
418         loglike += value
```

. . . fiducial . . .

```
446     return loglike
```

Sampler IV

Get the covariance matrix

Main ideas

- **stores values without scale factors for numerical reason**

Sampler IV

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Sampler IV

Get the covariance matrix

Main ideas

- stores values without scale factors for numerical reason
- automatic handling of parameters
- **computes eigen vectors, values, and Cholesky decomposition**

Likelihood class

Heavily object oriented

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- `Likelihood_clik` (Planck, WMAP)
- `Likelihood_mpk` (WiggleZ, Euclid)

Likelihoods

Implementation

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Likelihoods

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in the `likelihoods` folder, always the following structure:

- `likelihoods/something/__init__.py` and
- `likelihoods/something/something.data`
- alway **inherit** at least from: `Likelihood`

Analyze

called with:

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

Analyze

Convergence Computation

Gelman-Rubin Diagnostic:
variance between chains $=$ variance within chains
This gives a number R, that must be < 0.01.
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pdf output (or png): triangle plot and 1-dimensional **marginalized posterior** and **Mean likelihood** (visual indication of convergence)

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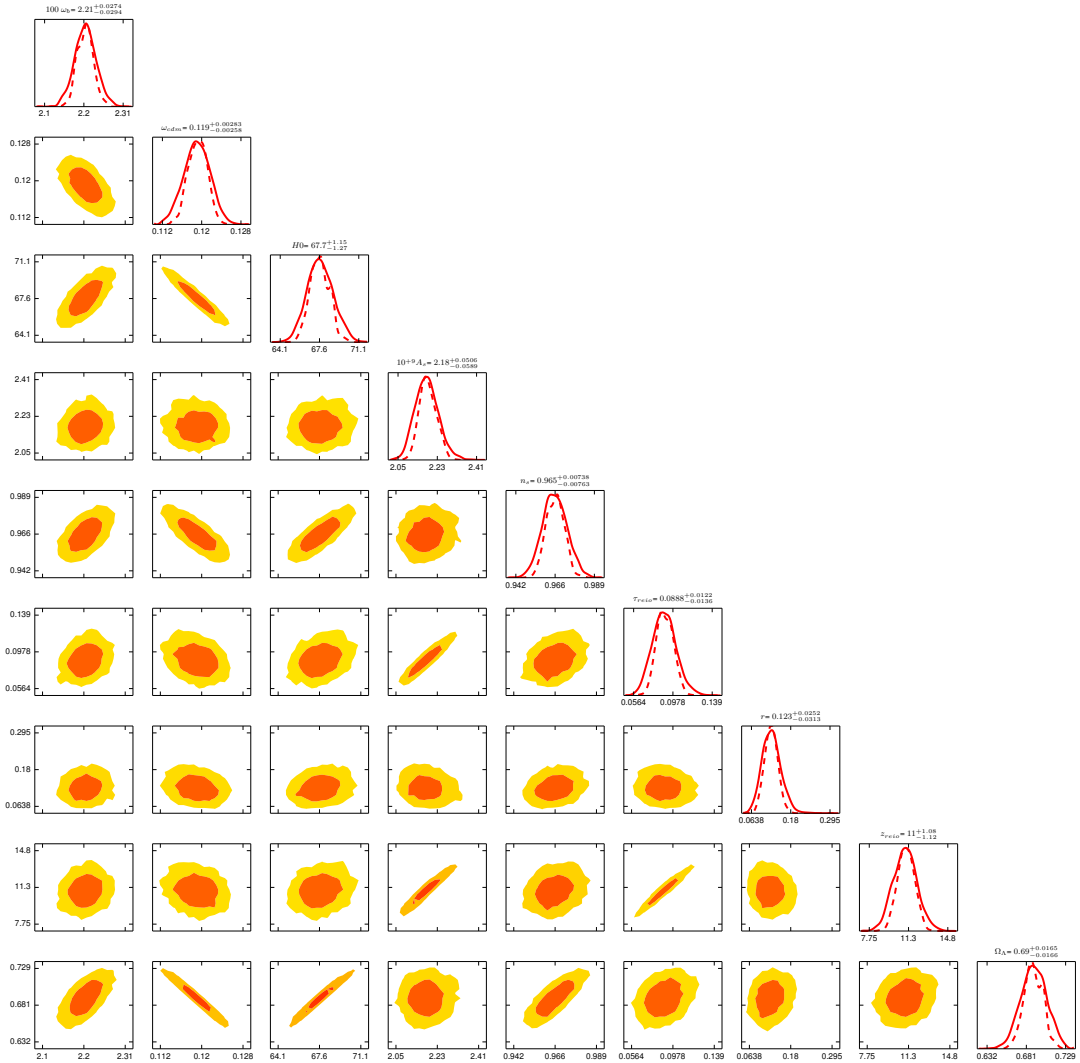
pdf output (or png): triangle plot and 1-dimensional **marginalized posterior** and **Mean likelihood** (visual indication of convergence)

Output Files

`.covmat`, `.v_info`, `h_info`, `.bestfit`, `.log`

Analyze



Analyze

horizontal info

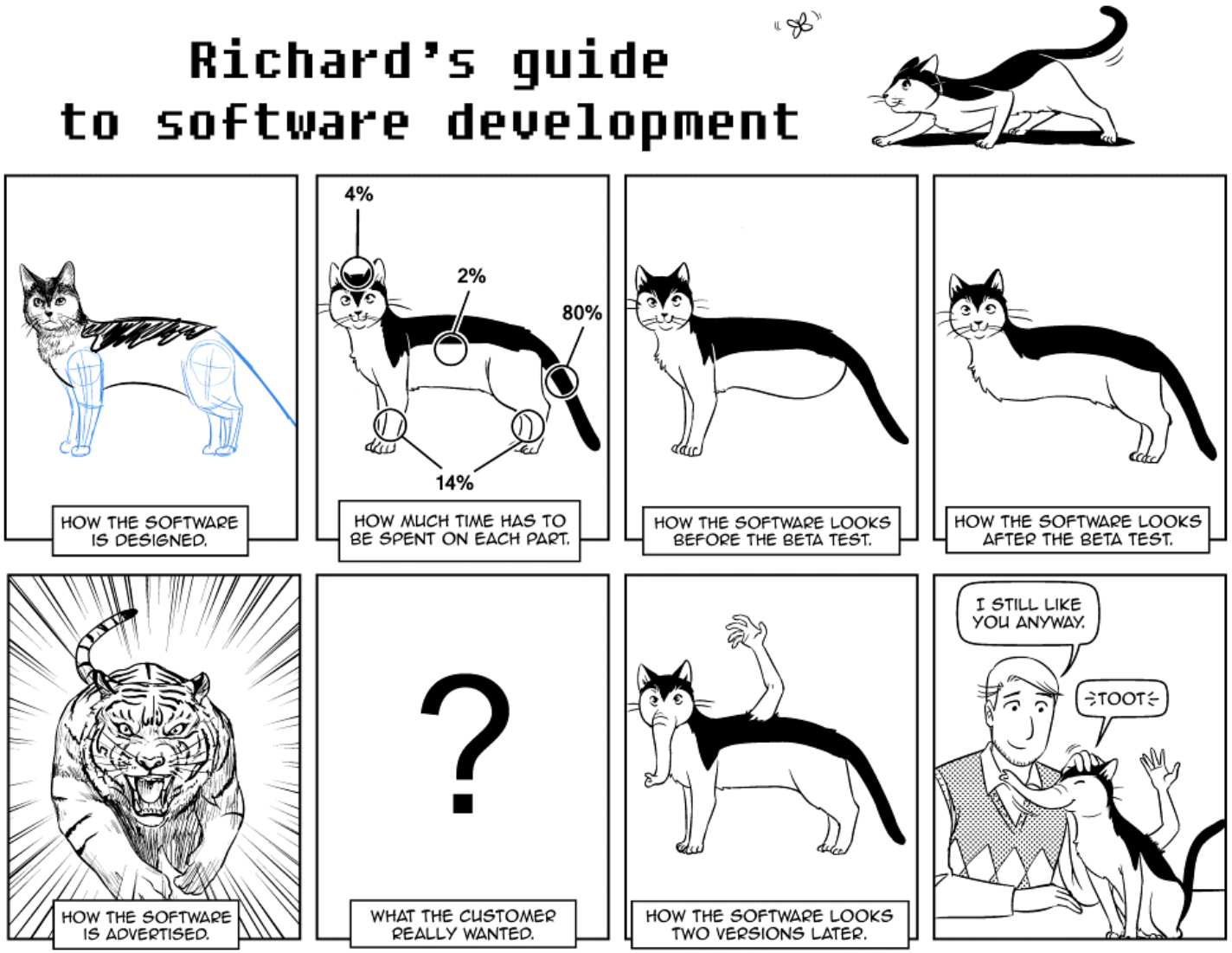
```
param names   :   Omega_L           h
R-1 values :   0.000055   0.000015
Best Fit     :   7.918934e-01   7.339652e-01
mean         :   7.781465e-01   7.308724e-01
sigma        :   6.793778e-02   2.382595e-02

1-sigma -    :  -5.799105e-02  -2.310380e-02
1-sigma +    :   7.788452e-02   2.454811e-02
2-sigma -    :  -1.418414e-01  -4.808685e-02
2-sigma +    :   1.333294e-01   4.764994e-02
3-sigma -    :  -2.379013e-01  -7.257030e-02
3-sigma +    :   1.779086e-01   6.790438e-02

1-sigma >    :   7.201555e-01   7.077686e-01
1-sigma <    :   8.560310e-01   7.554205e-01
2-sigma >    :   6.363051e-01   6.827856e-01
2-sigma <    :   9.114759e-01   7.785224e-01
3-sigma >    :   5.402452e-01   6.583021e-01
3-sigma <    :   9.560552e-01   7.987768e-01
```

Analyze

other files

- run.log
- run.covmat
- run.tex

Conclusion on Design



Outline

Work session example

Test a model with running tilt with Planck data

- **Copy** `base.param` **into** `base_r.param`

```
data.experiments=['Planck_highl','Planck_lowl','lowlike']

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['H0']        = [67.802,  None, None, 1.2,       1,   'cosmo']
data.parameters['A_s']       = [2.2177,    0,  None, 0.055, 1.e-9,   'cosmo']
data.parameters['n_s']       = [0.96229,   0,  None, 0.0074,    1,   'cosmo']
data.parameters['tau_reio']  = [0.09463,   0,  None, 0.013,     1,   'cosmo']
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- Edit `base_r.param`, add r, impose self-consistency condition
- **Launch a short run to see if it works:**

```
python montepython/MontePython.py -o chains/planck_r \
-p base_r.param -N 10
```

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-p base_r.param -N 10
```

- **Launch many chains:**

```
export OMP_NUM_THREADS=2
mpirun -np 24 python montepython/MontePython.py \
-o chains/planck_r -N 10000
```

Analyzing and Plotting

After running longer chains

- do: `python montepython/MontePython.py info chains/planck_r/*10000*`
- use the output covariance matrix as an input (new chains!)

Outline

Exercices

I) Hst, SN, BAO

Make a ΛCDM run with Hubble Space Telescope, Super Novae and BAO data. Look at `montepython/likelihoods` for the names.

II) Have fun with classy

Use the classy wrapper in a Python interpreter (notebook) to redo yesterday's exercices (see `https://github.com/lesgourg/class_public/wiki/Python-wrapper`).

III) Installing Planck likelihood

and trying it with `base.param`

`http://pla.esac.esa.int/pla/aio/planckProducts.html`