

Monte Python likelihoods

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4 rules, for MyLikelihood

- `Mylikelihood` must be a folder in `montepython/likelihoods/`
- `Mylikelihood` must contain two files, `__init__.py` and `Mylikelihood.data`
- `__init__.py` must define a `class` called `Mylikelihood`, inheriting from `Likelihood` (at least)
- `class Mylikelihood` must define a function called `loglk1` that returns the **log likelihood**

- no **hard-coding** of acceptable likelihoods
- no need to touch the **source code** when adding a likelihood
- **object oriented** design (look at the Planck likelihoods)

Available functions

- `self.need_cosmo_arguments(data, {'output': 'mPk'})`
- `data.mcmc_parameters['alpha']['current']`
- `data.get_mcmc_parameters(['cosmo'])`

Practical example: JLA

data file

```
JLA.data_directory = os.path.join(data.path['data'], 'JLA')
JLA.settings       = 'jla.dataset'
JLA.conflicting_experiments = ['JLA_simple']

JLA.use_nuisance = ['alpha', 'beta', 'M', 'Delta_M']
```

Practical example: JLA

source file

```
class JLA(Likelihood_sn):

    def __init__(self, path, data, command_line):

        Likelihood_sn.__init__(self, path, data, command_line)

        # Load matrices from text files, whose names were read in the
        # configuration file
        self.C00 = self.read_matrix(self.mag_covmat_file)
        self.C11 = self.read_matrix(self.stretch_covmat_file)
        self.C22 = self.read_matrix(self.colour_covmat_file)
        self.C01 = self.read_matrix(self.mag_stretch_covmat_file)
        self.C02 = self.read_matrix(self.mag_colour_covmat_file)
        self.C12 = self.read_matrix(self.stretch_colour_covmat_file)

        # Reading light-curve parameters from self.data_file (jla_lparams.txt)
        self.light_curve_params = self.read_light_curve_parameters()
```

Practical example: JLA

source file

```
class JLA(Likelihood_sn):

    def loglkl(self, cosmo, data):
        """
        Compute negative log-likelihood (eq.15 Betoule et al. 2014)
        """

    ...

    redshifts = self.light_curve_params.zcmb
    size = redshifts.size

    moduli = np.empty((size, ))
    for index, row in self.light_curve_params.iterrows():
        z_cmb = row['zcmb']
        moduli[index] = cosmo.luminosity_distance(z_cmb)
    moduli = 5 * np.log10(moduli) + 25
```

Practical example: JLA

source file

```
class JLA(Likelihood_sn):

    def loglkl(self, cosmo, data):
        """
        Compute negative log-likelihood (eq.15 Betoule et al. 2014)
        """

    ...

    # Compute the residuals (estimate of distance moduli - exact moduli)
    residuals = np.empty((size,))
    sn = self.light_curve_params
    # This operation loops over all supernovae!
    # Compute the approximate moduli
    residuals = sn.mb - (
        M - alpha*sn.x1 + beta*sn.color + Delta_M*(
            sn.thirdvar > self.scriptcut))
    # Remove from the approximate moduli the one computed from CLASS
    residuals -= moduli

    # Update the diagonal terms of the covariance matrix with the
    # statistical error
    cov += np.diag(sn.dmb**2 + (alpha*sn.dx1)**2 + (beta*sn.dcolor)**2
                   + 2.*alpha*sn.cov_m_s
                   - 2.*beta*sn.cov_m_c
                   - 2.*alpha*beta*sn.cov_s_c)
```


Practical example: JLA

source file

```
class JLA(Likelihood_sn):
```

```
    def loglkl(self, cosmo, data):  
        """  
        Compute negative log-likelihood (eq.15 Betoule et al. 2014)  
        """
```

```
    ...
```

```
        # Whiten the residuals, in two steps  
        # 1) Compute the Cholesky decomposition of the covariance matrix, in  
        # place. This is a time expensive (0.015 seconds) part  
        cov = la.cholesky(cov, lower=True, overwrite_a=True)  
  
        # 2) Solve the triangular system, also time expensive (0.02 seconds)  
        residuals = la.solve_triangular(cov, residuals, lower=True, check_finite=False)  
  
        # Finally, compute the chi2 as the sum of the squared residuals  
        chi2 = (residuals**2).sum()
```

List of existing likelihoods in Monte Python

ls montepython/likelihoods

- Planck_highl, Planck_lowl
- Planck_actstp, Planck_lensing
- Planck_SZ, lowlike
- clik_wmap_full and lowl
- bicep, bicep2, acbar
- boomerang, cbi, quad
- spt and spt_2500
- WiggleZ, sdss_lrgDR4
- euclid_lensing, euclid_pk
- sn, hst, timedelay
- bao, bao_boss, ...

Exercise: Implementing a new likelihood

Simplest example

1) HST-like likelihood

An experiment called `hubble_2013` measured

$$h = 0.712 \pm 0.012$$

Create this likelihood and use it in a run.

Hints for Exercise I

- create all the needed files/folder first
- define the data associated to the measurement in the `.data` file
- inherit from `Likelihood`
- get inspiration from `hst`