

# Monte Python: all run and analyze options

Benjamin Audren

École Polytechnique Fédérale de Lausanne

29/10/2014

# Outline

1 Running

2 Analysis

# Outline

- 1 Running
- 2 Analysis

# Methods

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

## Choosing the Sampling Method

- **flag:** `-m [MH, NS, CH, IS, Der]`

# Cholesky Decomposition

## Idea

**Cosmological** parameters are slow to update (CLASS), but **nuisance** parameters can be fast.

If **varied together**, this distinction is lost.

But, there are **correlations between them!**

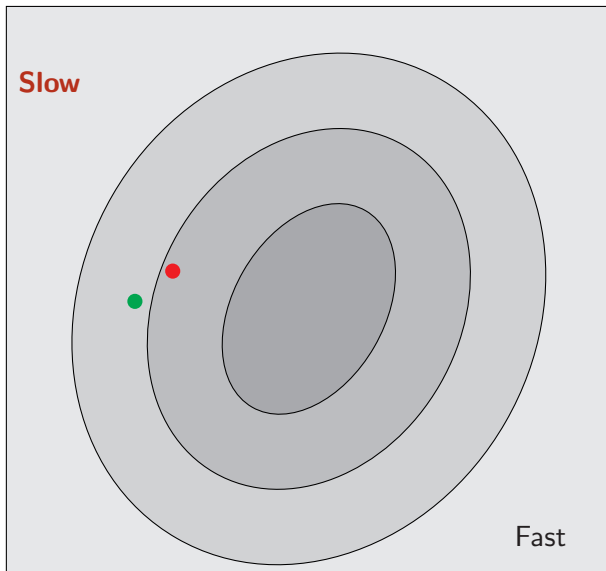
## Proposition

Instead of varying all the parameters at each step, we vary **both fast and slow** some of the time, and **only the fast one** the rest of the time.

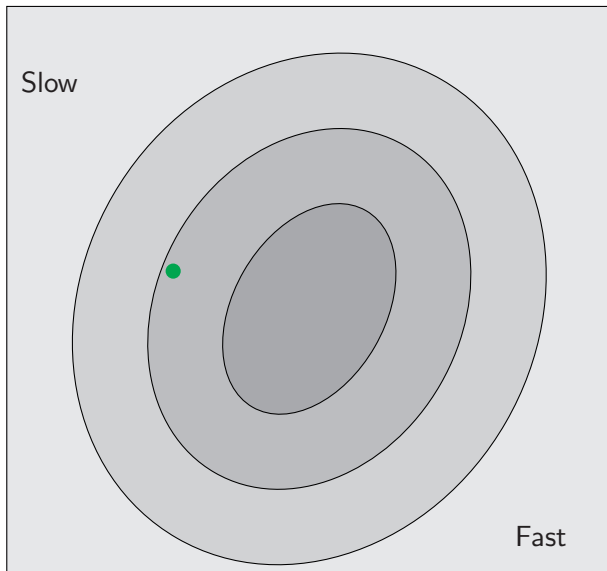
# Cholesky Decomposition and Over-sampling



# Cholesky Decomposition and Over-sampling

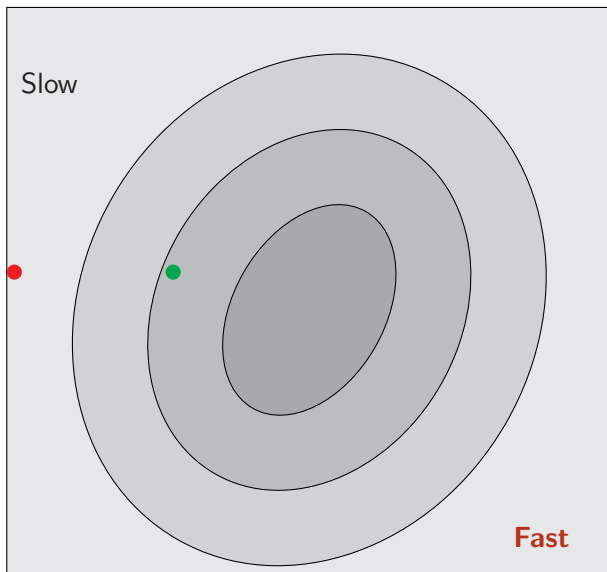


# Cholesky Decomposition and Over-sampling

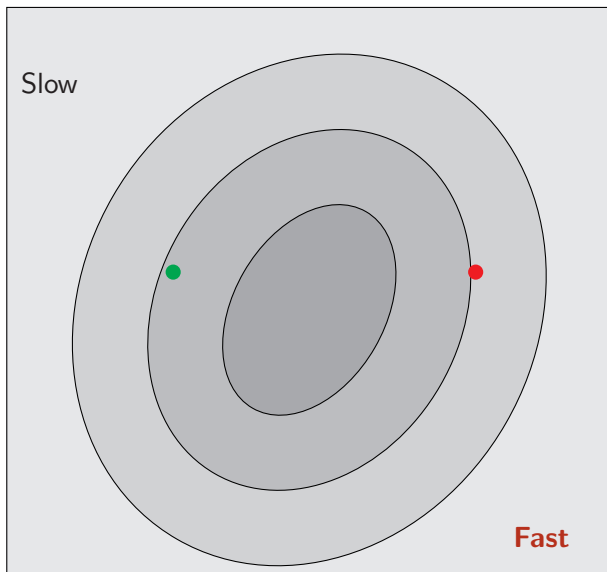




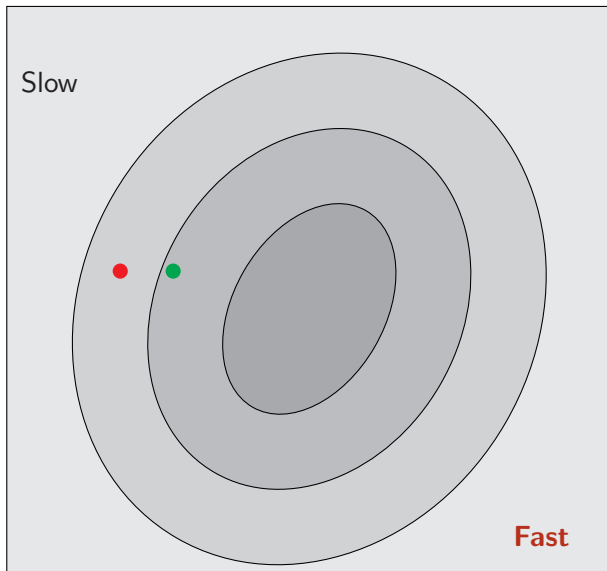
# Cholesky Decomposition and Over-sampling



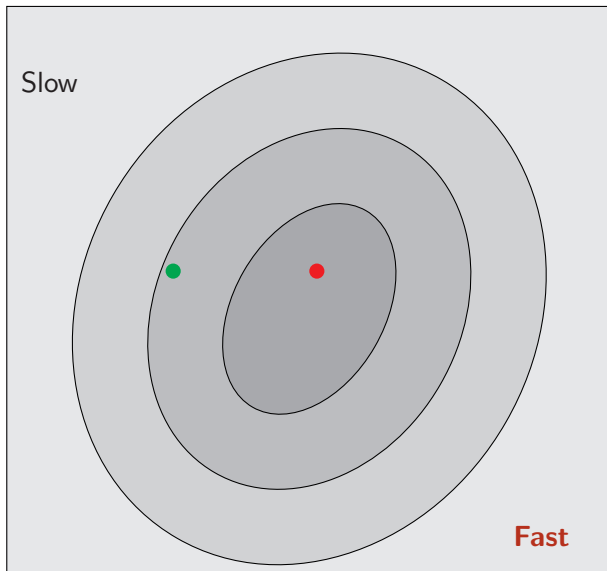
# Cholesky Decomposition and Over-sampling



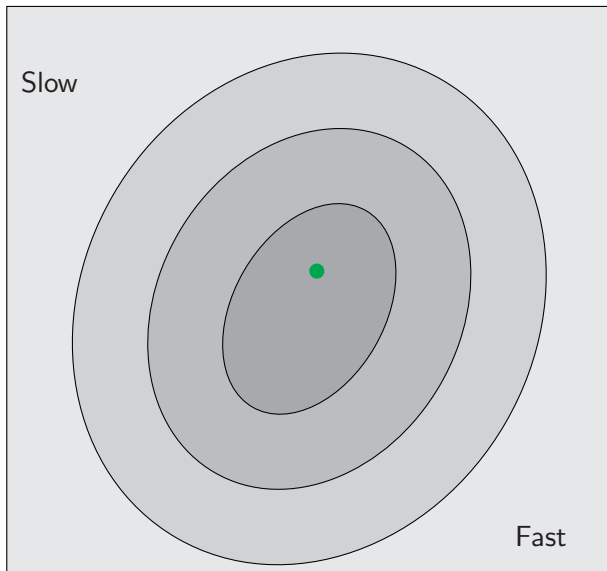
# Cholesky Decomposition and Over-sampling



# Cholesky Decomposition and Over-sampling



# Cholesky Decomposition and Over-sampling



# Metropolis Hastings

## Basic Options

- **Number of steps:** `-N 1000`
- **Jumping factor:** `-f 1.4`
- **Jumping strategy:** `-j [global, sequential, fast]`
- **Best-fit file:** `-b, --bestfit` best-fit point
- **Covmat file:** `-c, --covmat` proposal density
- **Restart:** `-r filename` restart from chain?

# Metropolis Hastings

## Tricks

### Computing the likelihood in one point

```
python montepython/MontePython.py run -o chains/jla -N 1 -f 0
```

### Cholesky decomposition

```
python montepython/MontePython.py run -o chains/jla -j fast
```

# Nested Sampling

Full description at <http://monte-python.readthedocs.org/en/latest/nested.html>

## Principle

- All options from MultiNest can be used
- Simply use `--NS_option_from_MultiNest`
- Most important one: `--NS_n_live_points 100`

## Strategy

- separate subfolder (NS)
- chains are translated with `info chains/folder/NS`

## Warning

- To see the options, either edit `montepython/nested_sampling.py`
- or `pip install pymultinest (--user)` then run `--help`



# Cosmo Hammer

Full description at <http://www.astro.ethz.ch/refregier/research/Software/cosmohammer/>

## Principle

- All options from CosmoHammer can be used
- Simply use `--CH_option_from_CosmoHammer`
- Most important one: `--CH_walkersRatio`

## Strategy

- separate subfolder (CH)
- chains are translated with `info chains/folder/CH`

## Doc

- To see the options, either edit `montepython/cosmo_hammer.py`

# Importance Sampling

## Syntax

```
run -m IS -o chains/new -p new.param \  
    --IS_starting_folder chains/old
```

## Warning

- `new.param` and `old.param` should differ **only through the list of experiments**, and by a mildly constraining likelihood
- Notably, the updated list of experiment can not contain **more nuisance parameters**.

## Adding a derived parameter

### Syntax

```
run -o existing_folder -m Der \  
    --Der-target-folder non_existing_folder \  
    --Der-param-list Omega_Lambda
```

### Warning

You obviously can add only derived parameters known to CLASS

# Outline

1 Running

2 Analysis

# Reminder

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

# Options when analyzing

## Main options

- compare several folders `info folder_1 folder_2`
- Remove the mean-likelihood with `--no-mean`
- Only compute the covmat with `--noplot`
- Output all sub plots with `--all`

# Using an extra file for plotting options

## Alternative to command line

- example in `plot_files/example.plot`
- syntax: `--extra plot_files/example.plot`

# Using an extra file for plotting options

## Alternative to command line

- example in `plot_files/example.plot`
- syntax: `--extra plot_files/example.plot`

## 4 exclusive arguments

- **redefine**: dict for **combining parameters**
- **to change**: dict for **renaming**
- **new scales**: dict for **rescaling**
- **to plot**: list for **plotting new names**



# Renaming parameters

```
info.to_change = {'Omega_cdm': r'$\Omega_{\rm cdm}$', 'alpha': '$\gamma$'}  
info.new_scales = {'$\gamma$': 10}  
info.to_plot = [r'$\Omega_{\rm cdm}$', '$\gamma$', 'beta']
```

# Full example

```

import matplotlib.pyplot as plt

info.redefine = {'log_alpha': 'log_alpha/math.log(10)',
                 'log_sound_speed_sq': 'log_sound_speed_sq/math.log(10)'}
info.to_change = {'log_alpha': r'$\log_{10}(\alpha)$',
                 'log_sound_speed_sq': r'$\log_{10}(c_{\chi^2})$',
                 'Y_dm': 'Y'}

info.to_plot    = [r'$\log_{10}(\alpha)$', r'$\log_{10}(c_{\chi^2})$', 'Y']

info.fontsize = 24
info.ticksize = 12
info.ticknumber = 5
info.decimal = 2
info.legend-style = 'top'

info.bins = 16

info.cm = [(0.99843, 0.25392, 0.14765, 1.),]
info.cmaps = [plt.cm.Red]

```

# Beware of non-raw strings

Python is picky about that