GetDist Documentation

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Contents

GetDist is a Python package for analysing and plotting Monte Carlo (or other) samples.

CHAPTER 1

GetDist

GetDist MCMC sample analysis, plotting and GUI

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Homepage https://getdist.readthedocs.io

Source https://github.com/cmbant/getdist

Reference https://arxiv.org/abs/1910.13970

1.1 Description

GetDist is a Python package for analysing Monte Carlo samples, including correlated samples from Markov Chain Monte Carlo (MCMC).

- **Point and click GUI** - select chain files, view plots, marginalized constraints, LaTeX tables and more
- **Plotting library** - make custom publication-ready 1D, 2D, 3D-scatter, triangle and other plots
- **Named parameters** - simple handling of many parameters using parameter names, including LaTeX labels and prior bounds
- **Optimized Kernel Density Estimation** - automated optimal bandwidth choice for 1D and 2D densities (Botev et al. Improved Sheather-Jones method), with boundary and bias correction
- **Convergence diagnostics** - including correlation length and diagonalized Gelman-Rubin statistics
- **LaTeX tables** for marginalized 1D constraints

See the Plot Gallery and tutorial (run online) and GetDist Documentation.

1.2 Getting Started

Install getdist using pip:

```
$ pip install getdist
```

or from source files using:

```
$ python setup.py install
```

You can test if things are working using the unit test by running:

```
$ python setup.py test
```

Check the dependencies listed in the next section are installed. You can then use the getdist module from your scripts, or use the GetDist GUI (*getdist-gui* command).

Once installed, the best way to get up to speed is probably to read through the Plot Gallery and tutorial.

1.3 Dependencies

- Python 3.6+
- matplotlib 2.2+ (3.1+ recommended)
- scipy
- PySide2 - optional, only needed for GUI
- Working LaTeX installation (not essential, only for some plotting/table functions)

Python distributions like Anaconda have most of what you need (except for LaTeX).

To use the GUI you need PySide2. See the GUI docs for suggestions on how to install.

1.4 Algorithm details

Details of kernel density estimation (KDE) algorithms and references are give in the GetDist notes arXiv:1910.13970.

1.5 Samples file format

The GetDist GUI (and getdist.loadMCSamples function) read parameter sample/chain files in plain text format. In general there are a set of plain text files of the form:

```
xxx_1.txt
xxx_2.txt
...
xxx.paramnames
xxx.ranges
```

where "xxx" is some root file name.

The .txt files are separate chain files (there can also be just one xxx.txt file). Each row of each sample .txt file is in the format

weight like param1 param2 param3 ...

The *weight* gives the number of samples (or importance weight) with these parameters. *like* gives -log(likelihood), and *param1, param2...* are the values of the parameters at the sample point. The first two columns can be 1 and 0 if they are not known or used.

The .paramnames file lists the names of the parameters, one per line, optionally followed by a LaTeX label. Names cannot include spaces, and if they end in "*" they are interpreted as derived (rather than MCMC) parameters, e.g.:

```
x1    x_1
y1    y_1
x2    x_2
xy*   x_1+y_1
```

The .ranges file gives hard bounds for the parameters, e.g.:

```
x1  -5 5
x2   0 N
```

Note that not all parameters need to be specified, and "N" can be used to denote that a particular upper or lower limit is unbounded. The ranges are used to determine densities and plot bounds if there are samples near the boundary; if there are no samples anywhere near the boundary the ranges have no affect on plot bounds, which are chosen appropriately for the range of the samples.

There can also optionally be a .properties.ini file, which can specify *burn_removed=T* to ensure no burn in is removed, or *ignore_rows=x* to ignore the first fraction *x* of the file rows (or if *x > 1*, the specified number of rows).

1.6 Loading samples

To load an MCSamples object from text files do:

```
from getdist import loadMCSamples
samples = loadMCSamples('/path/to/xxx', settings={'ignore_rows':0.3})
```

Here *settings* gives optional parameter settings for the analysis. *ignore_rows* is useful for MCMC chains where you want to discard some fraction from the start of each chain as burn in (use a number >1 to discard a fixed number of sample lines rather than a fraction). The MCSamples object can be passed to plot functions, or used to get many results. For example, to plot marginalized parameter densities for parameter names *x1* and *x2*:

```
from getdist import plots
g = plots.get_single_plotter()
g.plot_2d(samples, ['x1', 'x2'])
```

When you have many different chain files in the same directory, plotting can work directly with the root file names. For example to compare *x* and *y* constraints from two chains with root names *xxx* and *yyy*:

```
from getdist import plots
g = plots.get_single_plotter(chain_dir='/path/to/', analysis_settings={'ignore_rows
↪':0.3})
g.plot_2d(['xxx','yyy'], ['x', 'y'])
```

MCSamples objects can also be constructed directly from numpy arrays in memory, see the example in the Plot Gallery.

1.7 GetDist script

If you have chain files on on disk, you can also quickly calculate convergence and marginalized statistics using the *getdist* script:

usage: getdist [-h] [–ignore_rows IGNORE_ROWS] [-V] [ini_file] [chain_root]

GetDist sample analyser

positional arguments: *ini_file* .ini file with analysis settings (optional, if omitted uses defaults

chain_root Root name of chain to analyse (e.g. chains/test), required unless file_root specified in ini_file

optional arguments:

-h, --help show this help message and exit

--ignore_rows IGNORE_ROWS set initial fraction of chains to cut as burn in (fraction of total rows, or >1 number of rows); overrides any value in ini_file if set

--make_param_file MAKE_PARAM_FILE Produce a sample distparams.ini file that you can edit and use when running GetDist

-V, --version show program's version number and exit

where *ini_file* is optionally a .ini file listing *key*=*value* parameter option values, and chain_root is the root file name of the chains. For example:

```
getdist distparams.ini chains/test_chain
```

This produces a set of files containing parameter means and limits (.margestats), N-D likelihood contour boundaries and best-fit sample (.likestats), convergence diagnostics (.converge), parameter covariance and correlation (.covmat and .corr), and optionally various simple plotting scripts. If no *ini_file* is given, default settings are used. The *ignore_rows* option allows some of the start of each chain file to be removed as burn in.

To customize settings you can run:

```
getdist --make_param_file distparams.ini
```

to produce the setting file distparams.ini, edit it, then run with your custom settings.

1.8 GetDist GUI

Run *getdist-gui* to run the graphical user interface. This requires PySide2, but will run on Windows, Linux and Mac. It allows you to open a folder of chain files, then easily select, open, plot and compare, as well as viewing standard GetDist outputs and tables. See the GUI Readme.

1.9 Using with CosmoMC and Cobaya

This GetDist package is general, but is mainly developed for analysing chains from the CosmoMC and Cobaya sampling programs. No need to install this package separately if you have a full CosmoMC installation; the Cobaya installation will also install GetDist as a dependency. Detailed help is available for plotting Planck chains and using CosmoMC parameter grids in the Readme.

1.10 Citation

You can refer to the notes:

```
@article{Lewis:2019xzd,
 author          = "Lewis, Antony",
 title           = "{GetDist: a Python package for analysing Monte Carlo
                    samples}",
 year            = "2019",
 eprint          = "1910.13970",
 archivePrefix   = "arXiv",
 primaryClass    = "astro-ph.IM",
 SLACcitation    = "%%CITATION = ARXIV:1910.13970;%%",
 url             = "https://getdist.readthedocs.io"
}
```

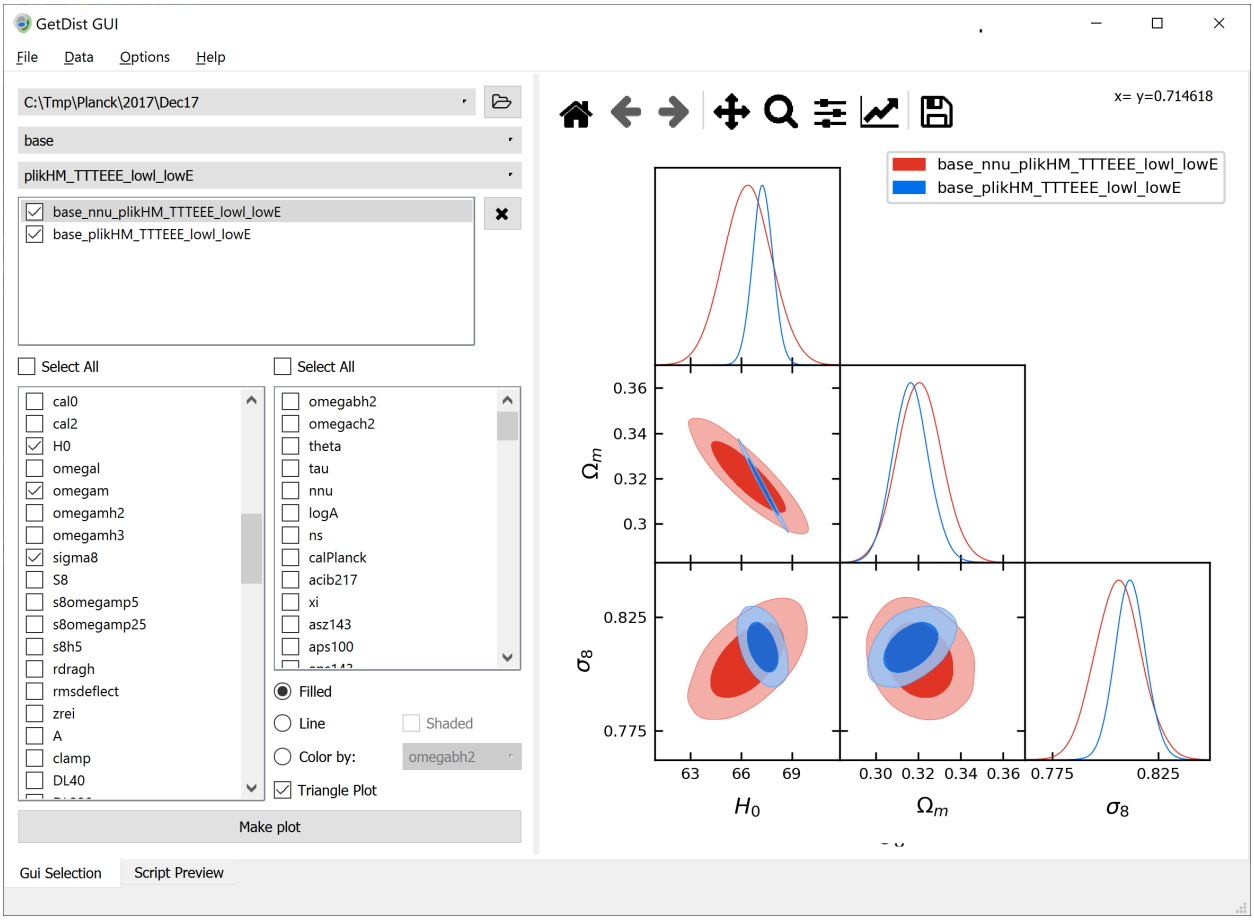
and references therein as appropriate.

CHAPTER 2

GetDist GUI

Run the *getdist-gui* script to run the graphical user interface. This requires PySide2 <https://wiki.qt.io/Qt_for_Python>‘_ to be installed, but will run on Windows, Linux and Mac.

It allows you to open a folder of chain files, then easily select, open, plot and compare, as well as viewing standard GetDist outputs and tables.



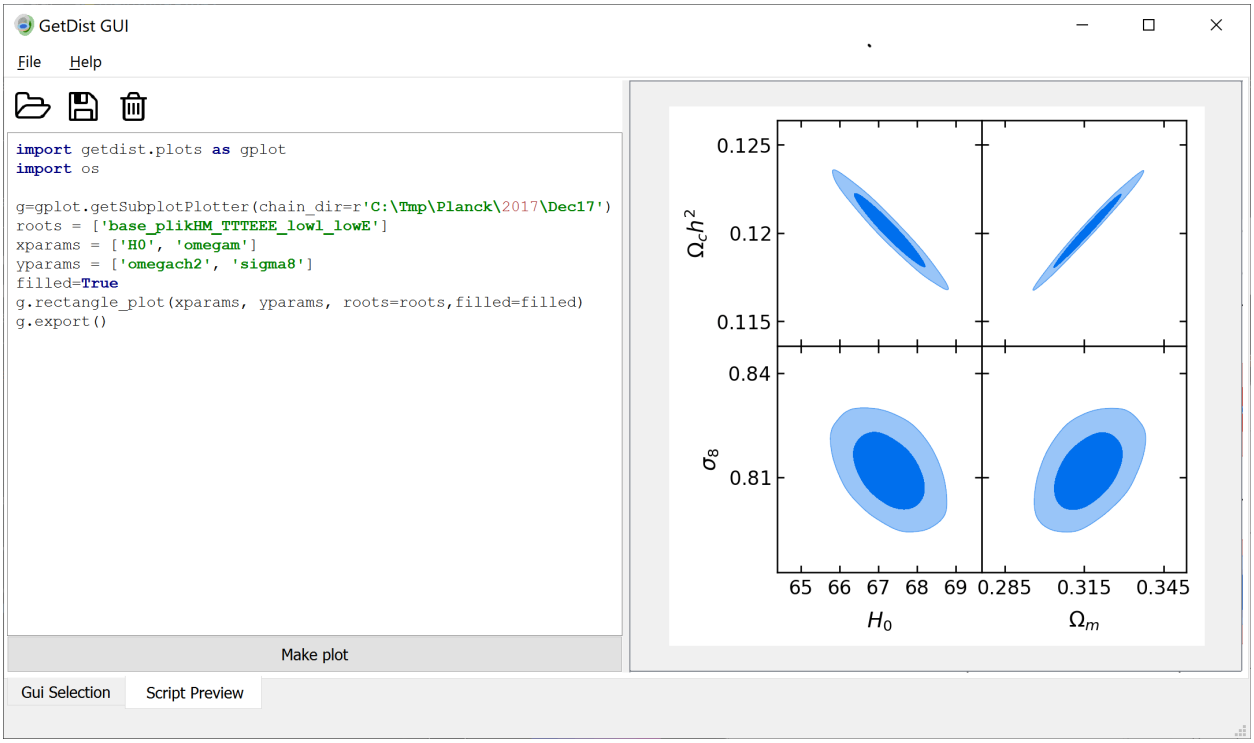
It can open chain files under a selected directry structure (and also paramgrid directories as show above). See the intro for a description of chain file formats. A grid of sample chains files can be downloaded here, after downloading a file just unzip and open the main directory in the GUI.

After opening a directory, you can select each chain root name you want to plot. It is then added to the list box below. The selected chains can be dragged and dropped to change the order if needed. Then select the parameter names to plot in the checkboxes below that, and correspond to the names available in the first selected chain.

The Gui supports 1D, 2D (line and filled), 3D (select two parameters and "color by"), and triangle and rectangle plots.

2.1 Script preview

Use the option on the File menu to export a plot as-is to PDF or other image file. For better quality (i.e. not formatted for the current window shape) and fine control (e.g. add custom legend text, etc), export the script, edit and then run it separately. The Script Preview tab also gives a convenient way to view the script for the current plot, and preview exactly what it will produce when run:



You can also edit and customize the script, or open and play with existing plot scripts.

2.2 Statistics and tables

The Data menu has an option to let you view the parameter statistics (.margestats) and latex tables, convergence stats, and view PCA constraints for selected parameters. Note that you need a working latex installation to view rendered parameter tables.

2.3 Settings

The Options menu allows you to change a settings defining how limits, lines and contours are calculated, and customize plot options. The "Plot module config" option lets you use a different module to define the plotting functions (the default is getdist.plots).

2.4 Installation

To run the GUI you need PySide2. This is not included in default dependencies because it is only needed for the GUI and on some systems installation from pip may not work easily.

Install PySide2 from pip using:

```
pip install PySide2
```

You can also use Anaconda, making a consistent new environment from conda-forge (which includes PySide2) using:

```
conda create -n py37forge -c conda-forge python=3.7 scipy pandas matplotlib PySide2
```

(note that PySide2 is currently not included in the default Anaconda packages).

Once PySide2 is set up, (re)install getdist and you should then be able to use the getdist-gui script on your path. On a Mac the installation will also make a GetDist GUI Mac app, which you can find using Spotlight.

If you don't want to install dependencies locally, you can also use a pre-configured virtual environment.

Example usage notebooks:

High-level modules for analysing samples and plotting:

CHAPTER 3

getdist.mcsamples

getdist.mcsamples.**loadMCSamples**(*file_root*, *ini=None*, *jobItem=None*, *no_cache=False*, *settings=None*)

Loads a set of samples from a file or files.

Sample files are plain text (*file_root.txt*) or a set of files (*file_root_1.txt*, *file_root_2.txt*, etc.).

Auxiliary files **file_root.paramnames** gives the parameter names and (optionally) **file_root.ranges** gives hard prior parameter ranges.

For a description of the various analysis settings and default values see analysis_defaults.ini.

Parameters

- **file_root** – The root name of the files to read (no extension)
- **ini** – The name of a .ini file with analysis settings to use
- **jobItem** – an optional grid jobItem instance for a CosmoMC grid output
- **no_cache** – Indicates whether or not we should cache loaded samples in a pickle
- **settings** – dictionary of analysis settings to override defaults

Returns The *MCSamples* instance

class getdist.mcsamples.**MCSamples**(*root=None*, *jobItem=None*, *ini=None*, *settings=None*, *ranges=None*, *samples=None*, *weights=None*, *loglikes=None*, ***kwargs*)

The main high-level class for a collection of parameter samples.

Derives from *chains.Chains*, adding high-level functions including Kernel Density estimates, parameter ranges and custom settings.

For a description of the various analysis settings and default values see analysis_defaults.ini.

Parameters

- **root** – A root file name when loading from file

- **jobItem** – optional jobItem for parameter grid item. Should have jobItem.chainRoot and jobItem.batchPath
- **ini** – a .ini file to use for custom analysis settings
- **settings** – a dictionary of custom analysis settings
- **ranges** – a dictionary giving any additional hard prior bounds for parameters, eg. {'x':[0, 1], 'y':[None,2]}
- **samples** – if not loading from file, array of parameter values for each sample, passed to *setSamples()*, or list of arrays if more than one chain
- **weights** – array of weights for samples, or list of arrays if more than one chain
- **loglikes** – array of -log(Likelihood) for samples, or list of arrays if more than one chain
- **kwargs** –

  keyword arguments passed to inherited classes, e.g. to manually make a samples object from sample arrays in memory:

  - **paramNamesFile**: optional name of .paramnames file with parameter names
  - **names**: list of names for the parameters, or list of arrays if more than one chain
  - **labels**: list of latex labels for the parameters
  - **renames**: dictionary of parameter aliases
  - **ignore_rows**:
    - if int >=1: The number of rows to skip at the file in the beginning of the file
    - if float <1: The fraction of rows to skip at the beginning of the file
  - **label**: a latex label for the samples
  - **name_tag**: a name tag for this instance
  - **sampler**: string describing the type of samples; if "nested" or "uncorrelated" the effective number of samples is calculated using uncorrelated approximation. If not specified will be read from the root.properties.ini file if it exists and otherwise default to "mcmc".

PCA(*params*, *param_map=None*, *normparam=None*, *writeDataToFile=False*, *filename=None*, *conditional_params=()*, *n_best_only=None*)

Perform principle component analysis (PCA). In other words, get eigenvectors and eigenvalues for normalized variables with optional (log modulus) mapping to find power law fits.

Parameters

- **params** – List of names of the parameters to use
- **param_map** – A transformation to apply to parameter values; A list or string containing either N (no transformation) or L (for log transform) for each parameter. By default uses log if no parameter values cross zero
- **normparam** – optional name of parameter to normalize result (i.e. this parameter will have unit power)
- **writeDataToFile** – True if should write the output to file.
- **filename** – The filename to write, by default root_name.PCA.
- **conditional_params** – optional list of parameters to treat as fixed, i.e. for PCA conditional on fixed values of these parameters

- **n_best_only** – return just the short summary constraint for the tightest n_best_only constraints

Returns a string description of the output of the PCA

addDerived(*paramVec*, *name*, *label=''*, *comment=''*, *range=None*)
Adds a new derived parameter

Parameters

- **paramVec** – The vector of parameter values to add. For example a combination of parameter arrays from MCSamples.getParams()
- **name** – The name for the new parameter
- **label** – optional latex label for the parameter
- **comment** – optional comment describing the parameter
- **range** – if specified, a tuple of min, max values for the new parameter hard prior bounds (either can be None for one-side bound)

Returns The added parameter's *ParamInfo* object

changeSamples(*samples*)
Sets the samples without changing weights and loglikes.

Parameters **samples** – The samples to set

confidence(*paramVec*, *limfrac*, *upper=False*, *start=0*, *end=None*, *weights=None*)
Calculate sample confidence limits, not using kernel densities just counting samples in the tails

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **limfrac** – fraction of samples in the tail, e.g. 0.05 for a 95% one-tail limit, or 0.025 for a 95% two-tail limit
- **upper** – True to get upper limit, False for lower limit
- **start** – Start index for the vector to use
- **end** – The end index, use None to go all the way to the end of the vector.
- **weights** – numpy array of weights for each sample, by default self.weights

Returns confidence limit (parameter value when limfac of samples are further in the tail)

cool(*cool*)
Cools the samples, i.e. multiples log likelihoods by cool factor and re-weights accordingly

Parameters **cool** – cool factor

copy(*label=None*, *settings=None*)
Create a copy of this sample object

Parameters

- **label** – optional lable for the new copy
- **settings** – optional modified settings for the new copy

Returns copyied *MCSamples* instance

corr(*pars=None*)
Get the correlation matrix

Parameters **pars** – If specified, list of parameter vectors or int indices to use

Returns The correlation matrix.

cov(*pars=None*, *where=None*)
Get parameter covariance

Parameters

- **pars** – if specified, a list of parameter vectors or int indices to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns The covariance matrix

deleteFixedParams()
Delete parameters that are fixed (the same value in all samples)

deleteZeros()
Removes samples with zero weight

filter(*where*)
Filter the stored samples to keep only samples matching filter

Parameters **where** – list of sample indices to keep, or boolean array filter (e.g. x>5 to keep only samples where x>5)

get1DDensity(*name*, ***kwargs*)
Returns a *Density1D* instance for parameter with given name. Result is cached.

Parameters

- **name** – name of the parameter
- **kwargs** – arguments for *get1DDensityGridData()*

Returns A *Density1D* instance for parameter with given name

get1DDensityGridData(*j*, *paramConfid=None*, *meanlikes=False*, ***kwargs*)
Low-level function to get a *Density1D* instance for the marginalized 1D density of a parameter. Result is not cached.

Parameters

- **j** – a name or index of the parameter
- **paramConfid** – optional cached *ParamConfidenceData* instance
- **meanlikes** – include mean likelihoods
- **kwargs** – optional settings to override instance settings of the same name (see *analysis_settings*):
  - **smooth_scale_1D**
  - **boundary_correction_order**
  - **mult_bias_correction_order**
  - **fine_bins**
  - **num_bins**

Returns A *Density1D* instance

get2DDensity(*x*, *y*, *normalized=False*, ***kwargs*)
Returns a *Density2D* instance with marginalized 2D density.

Parameters

- **x** – index or name of x parameter
- **y** – index or name of y parameter
- **normalized** – if False, is normalized so the maximum is 1, if True, density is normalized
- **kwargs** – keyword arguments for the *get2DDensityGridData()* function

Returns *Density2D* instance

get2DDensityGridData(*j*, *j2*, *num_plot_contours=None*, *get_density=False*, *meanlikes=False*, ***kwargs*)

Low-level function to get 2D plot marginalized density and optional additional plot data.

Parameters

- **j** – name or index of the x parameter
- **j2** – name or index of the y parameter.
- **num_plot_contours** – number of contours to calculate and return in density.contours
- **get_density** – only get the 2D marginalized density, don't calculate confidence level members
- **meanlikes** – calculate mean likelihoods as well as marginalized density (returned as array in density.likes)
- **kwargs** – optional settings to override instance settings of the same name (see *analysis_settings*):
  - **fine_bins_2D**
  - **boundary_correction_order**
  - **mult_bias_correction_order**
  - **smooth_scale_2D**

Returns a *Density2D* instance

getAutoBandwidth1D(*bins*, *par*, *param*, *mult_bias_correction_order=None*, *kernel_order=1*, *N_eff=None*)

Get optimized kernel density bandwidth (in units of the range of the bins) Based on optimal Improved Sheather-Jones bandwidth for basic Parzen kernel, then scaled if higher-order method being used. For details see the notes at arXiv:1910.13970.

Parameters

- **bins** – numpy array of binned weights for the samples
- **par** – A *ParamInfo* instance for the parameter to analyse
- **param** – index of the parameter to use
- **mult_bias_correction_order** – order of multiplicative bias correction (0 is basic Parzen kernel); by default taken from instance settings.
- **kernel_order** – order of the kernel (0 is Parzen, 1 does linear boundary correction, 2 is a higher-order kernel)
- **N_eff** – effective number of samples. If not specified estimated using weights, autocorrelations, and fiducial bandwidth

Returns kernel density bandwidth (in units the range of the bins)

getAutoBandwidth2D(*bins*, *parx*, *pary*, *paramx*, *paramy*, *corr*, *rangex*, *rangey*, *base_fine_bins_2D*, *mult_bias_correction_order=None*, *min_corr=0.2*, *N_eff=None*, *use_2D_Neff=False*)

Get optimized kernel density bandwidth matrix in parameter units, using Improved Sheather Jones method in sheared parameters. The shearing is determined using the covariance, so you know the distribution is multi-modal, potentially giving 'fake' correlation, turn off shearing by setting min_corr=1. For details see the notes arXiv:1910.13970.

Parameters

- **bins** – 2D numpy array of binned weights
- **parx** – A *ParamInfo* instance for the x parameter
- **pary** – A *ParamInfo* instance for the y parameter
- **paramx** – index of the x parameter
- **paramy** – index of the y parameter
- **corr** – correlation of the samples
- **rangex** – scale in the x parameter
- **rangey** – scale in the y parameter
- **base_fine_bins_2D** – number of bins to use for re-binning in rotated parameter space
- **mult_bias_correction_order** – multiplicative bias correction order (0 is Parzen kernel); by default taken from instance settings
- **min_corr** – minimum correlation value at which to bother de-correlating the parameters
- **N_eff** – effective number of samples. If not specified, uses rough estimate that accounts for weights and strongly-correlated nearby samples (see notes)
- **use_2D_Neff** – if N_eff not specified, whether to use 2D estimate of effective number, or approximate from the 1D results (default from use_effective_samples_2D setting)

Returns kernel density bandwidth matrix in parameter units

getAutocorrelation(*paramVec*, *maxOff=None*, *weight_units=True*, *normalized=True*)

Gets auto-correlation of an array of parameter values (e.g. for correlated samples from MCMC)

By default uses weight units (i.e. standard units for separate samples from original chain). If samples are made from multiple chains, neglects edge effects.

Parameters

- **paramVec** – an array of parameter values, or the int index of the parameter in stored samples to use
- **maxOff** – maximum autocorrelation distance to return
- **weight_units** – False to get result in sample point (row) units; weight_units=False gives standard definition for raw chains
- **normalized** – Set to False to get covariance (note even if normalized, corr[0]<>1 in general unless weights are unity).

Returns zero-based array giving auto-correlations

getBestFit(*max_posterior=True*)

Returns a *BestFit* object with best-fit point stored in .minimum or .bestfit file

Parameters **max_posterior** – whether to get maximum posterior (from .minimum file) or maximum likelihood (from .bestfit file)

Returns

getBounds()
Returns the bounds in the form of a *ParamBounds* instance, for example for determining plot ranges

Bounds are not the same as self.ranges, as if samples are not near the range boundary, the bound is set to None

Returns a *ParamBounds* instance

getCombinedSamplesWithSamples(*samps2*, *sample_weights=(1, 1)*)
Make a new *MCSamples* instance by appending samples from samps2 for parameters which are in common. By default they are weighted so that the probability mass of each set of samples is the same, independent of tha actual sample sizes. The Weights parameter can be adjusted to change the relative weighting. :param samps2: *MCSamples* instance to merge :param sample_weights: relative weights for combining the samples. Set to None to just directly append samples. :return: a new *MCSamples* instance with the combined samples

getConvergeTests(*test_confidence=0.95*, *writeDataToFile=False*, *what=('MeanVar', 'GelmanRubin', 'SplitTest', 'RafteryLewis', 'CorrLengths')*, *filename=None*, *feedback=False*)
Do convergence tests.

Parameters

- **test_confidence** – confidence limit to test for convergence (two-tail, only applies to some tests)
- **writeDataToFile** – True if should write output to a file
- **what** – The tests to run. Should be a list of any of the following:
  - 'MeanVar': Gelman-Rubin sqrt(var(chain mean)/mean(chain var)) test in individual parameters (multiple chains only)
  - 'GelmanRubin': Gelman-Rubin test for the worst orthogonalized parameter (multiple chains only)
  - 'SplitTest': Crude test for variation in confidence limits when samples are split up into subsets
  - 'RafteryLewis': Raftery-Lewis test (integer weight samples only)
  - 'CorrLengths': Sample correlation lengths
- **filename** – The filename to write to, default is file_root.converge
- **feedback** – If set to True, Prints the output as well as returning it.

Returns text giving the output of the tests

getCorrelatedVariable2DPlots(*num_plots=12*, *nparam=None*)
Gets a list of most correlated variable pair names.

Parameters

- **num_plots** – The number of plots
- **nparam** – maximum number of pairs to get

Returns list of [x,y] pair names

getCorrelationLength(*j*, *weight_units=True*, *min_corr=0.05*, *corr=None*)
Gets the auto-correlation length for parameter j

Parameters

- **j** – The index of the parameter to use
- **weight_units** – False to get result in sample point (row) units; weight_units=False gives standard definition for raw chains
- **min_corr** – specifies a minimum value of the autocorrelation to use, e.g. where sampling noise is typically as large as the calculation
- **corr** – The auto-correlation array to use, calculated internally by default using *getAutocorrelation()*

Returns the auto-correlation length

getCorrelationMatrix()
Get the correlation matrix of all parameters

Returns The correlation matrix

getCov(*nparam=None*, *pars=None*)
Get covariance matrix of the parameters. By default uses all parameters, or can limit to max number or list.

Parameters

- **nparam** – if specified, only use the first nparam parameters
- **pars** – if specified, a list of parameter indices (0,1,2..) to include

Returns covariance matrix.

getCovMat()
Gets the CovMat instance containing covariance matrix for all the non-derived parameters (for example useful for subsequent MCMC runs to orthogonalize the parameters)

Returns A *CovMat* object holding the covariance

getEffectiveSamples(*j=0*, *min_corr=0.05*)
Gets effective number of samples N_eff so that the error on mean of parameter j is sigma_j/N_eff

Parameters

- **j** – The index of the param to use.
- **min_corr** – the minimum value of the auto-correlation to use when estimating the correlation length

getEffectiveSamplesGaussianKDE(*paramVec*, *h=0.2*, *scale=None*, *maxoff=None*, *min_corr=0.05*)
Roughly estimate an effective sample number for use in the leading term for the MISE (mean integrated squared error) of a Gaussian-kernel KDE (Kernel Density Estimate). This is used for optimizing the kernel bandwidth, and though approximate should be better than entirely ignoring sample correlations, or only counting distinct samples.

Uses fiducial assumed kernel scale h; result does depend on this (typically by factors O(2))

For bias-corrected KDE only need very rough estimate to use in rule of thumb for bandwidth.

In the limit h-> 0 (but still >0) answer should be correct (then just includes MCMC rejection duplicates). In reality correct result for practical h should depends on shape of the correlation function.

If self.sampler is 'nested' or 'uncorrelated' return result for uncorrelated samples.

Parameters

- **paramVec** – parameter array, or int index of parameter to use
- **h** – fiducial assumed kernel scale.

- **scale** – a scale parameter to determine fiducial kernel width, by default the parameter standard deviation
- **maxoff** – maximum value of auto-correlation length to use
- **min_corr** – ignore correlations smaller than this auto-correlation

Returns A very rough effective sample number for leading term for the MISE of a Gaussian KDE.

getEffectiveSamplesGaussianKDE_2d(*i*, *j*, *h=0.3*, *maxoff=None*, *min_corr=0.05*)

Roughly estimate an effective sample number for use in the leading term for the 2D MISE. If self.sampler is 'nested' or 'uncorrelated' return result for uncorrelated samples.

Parameters

- **i** – parameter array, or int index of first parameter to use
- **j** – parameter array, or int index of second parameter to use
- **h** – fiducial assumed kernel scale.
- **maxoff** – maximum value of auto-correlation length to use
- **min_corr** – ignore correlations smaller than this auto-correlation

Returns A very rough effective sample number for leading term for the MISE of a Gaussian KDE.

getFractionIndices(*weights*, *n*)

Calculates the indices of weights that split the weights into sets of equal 1/n fraction of the total weight

Parameters

- **weights** – array of weights
- **n** – number of groups to split in to

Returns array of indices of the boundary rows in the weights array

getGelmanRubin(*nparam=None*, *chainlist=None*)

Assess the convergence using the maximum var(mean)/mean(var) of orthogonalized parameters c.f. Brooks and Gelman 1997.

Parameters

- **nparam** – The number of parameters, by default uses all
- **chainlist** – list of *WeightedSamples*, the samples to use. Defaults to all the separate chains in this instance.

Returns The worst var(mean)/mean(var) for orthogonalized parameters. Should be <<1 for good convergence.

getGelmanRubinEigenvalues(*nparam=None*, *chainlist=None*)

Assess convergence using var(mean)/mean(var) in the orthogonalized parameters c.f. Brooks and Gelman 1997.

Parameters

- **nparam** – The number of parameters (starting at first), by default uses all of them
- **chainlist** – list of *WeightedSamples*, the samples to use. Defaults to all the separate chains in this instance.

Returns array of var(mean)/mean(var) for orthogonalized parameters

getInlineLatex(*param*, *limit=1*, *err_sig_figs=None*)
Get snippet like: A=x\pm y. Will adjust appropriately for one and two tail limits.

Parameters

- **param** – The name of the parameter
- **limit** – which limit to get, 1 is the first (default 68%), 2 is the second (limits array specified by self.contours)
- **err_sig_figs** – significant figures in the error

Returns The tex snippet.

getLabel()
Return the latex label for the samples

Returns the label

getLatex(*params=None*, *limit=1*, *err_sig_figs=None*)
Get tex snippet for constraints on a list of parameters

Parameters

- **params** – list of parameter names, or a single parameter name
- **limit** – which limit to get, 1 is the first (default 68%), 2 is the second (limits array specified by self.contours)
- **err_sig_figs** – significant figures in the error

Returns labels, texs: a list of parameter labels, and a list of tex snippets, or for a single parameter, the latex snippet.

getLikeStats()
Get best fit sample and n-D confidence limits, and various likelihood based statistics

Returns a *LikeStats* instance storing N-D limits for parameter i in result.names[i].ND_limit_top, result.names[i].ND_limit_bot, and best-fit sample value in result.names[i].bestfit_sample

getLower(*name*)
Return the lower limit of the parameter with the given name.

Parameters **name** – parameter name

Returns The lower limit if name exists, None otherwise.

getMargeStats(*include_bestfit=False*)
Returns a *MargeStats* object with marginalized 1D parameter constraints

Parameters **include_bestfit** – if True, set best fit values by loading from root_name.minimum file (assuming it exists)

Returns A *MargeStats* instance

getMeans(*pars=None*)
Gets the parameter means, from saved array if previously calculated.

Parameters **pars** – optional list of parameter indices to return means for

Returns numpy array of parameter means

getName()
Returns the name tag of these samples.

Returns The name tag

getNumSampleSummaryText()
Returns a summary text describing numbers of parameters and samples, and various measures of the effective numbers of samples.

Returns The summary text as a string.

getParamBestFitDict(*best_sample=False*, *want_derived=True*, *want_fixed=True*, *max_posterior=True*)
Gets an ordered dictionary of parameter values for the best fit point, assuming calculated results from mimimization runs in .minimum (max posterior) .bestfit (max likelihood) files exists.

Can also get the best-fit (max posterior) sample, which typically has a likelihood that differs significantly from the true best fit in high dimensions.

Parameters

- **best_sample** – load from global minimum files (False, default) or using maximum posterior sample (True)
- **want_derived** – include derived parameters
- **want_fixed** – also include values of any fixed parameters
- **max_posterior** – whether to get maximum posterior (from .minimum file) or maximum likelihood (from .bestfit file)

Returns ordered dictionary of parameter values

getParamNames()
Get *ParamNames* object with names for the parameters

Returns *ParamNames* object giving parameter names and labels

getParamSampleDict(*ix*, *want_derived=True*, *want_fixed=True*)
Gets a dictionary of parameter values for sample number ix

Parameters

- **ix** – index of the sample to return (zero based)
- **want_derived** – include derived parameters
- **want_fixed** – also include values of any fixed parameters

Returns ordered dictionary of parameter values

getParams()
Creates a *ParSamples* object, with variables giving vectors for all the parameters, for example samples.getParams().name1 would be the vector of samples with name 'name1'

Returns A *ParSamples* object containing all the parameter vectors, with attributes given by the parameter names

getRenames()
Gets dictionary of renames known to each parameter.

getSeparateChains()
Gets a list of samples for separate chains. If the chains have already been combined, uses the stored sample offsets to reconstruct the array (generally no array copying)

Returns The list of *WeightedSamples* for each chain.

getSignalToNoise(*params*, *noise=None*, *R=None*, *eigs_only=False*)
Returns w, M, where w is the eigenvalues of the signal to noise (small y better constrained)

Parameters

- **params** – list of parameters indices to use
- **noise** – noise matrix
- **R** – rotation matrix, defaults to inverse of Cholesky root of the noise matrix
- **eigs_only** – only return eigenvalues

Returns w, M, where w is the eigenvalues of the signal to noise (small y better constrained)

getTable(*columns=1*, *include_bestfit=False*, ***kwargs*)
Creates and returns a *ResultTable* instance. See also *getInlineLatex()*.

Parameters

- **columns** – number of columns in the table
- **include_bestfit** – True if should include the bestfit parameter values (assuming set)
- **kwargs** – arguments for *ResultTable* constructor.

Returns A *ResultTable* instance

getUpper(*name*)
Return the upper limit of the parameter with the given name.

Parameters **name** – parameter name

Returns The upper limit if name exists, None otherwise.

getVars()
Get the parameter variances

Returns A numpy array of variances.

get_norm(*where=None*)
gets the normalization, the sum of the sample weights: sum_i w_i

Parameters **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns normalization

initParamConfidenceData(*paramVec*, *start=0*, *end=None*, *weights=None*)
Initialize cache of data for calculating confidence intervals

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **start** – The sample start index to use
- **end** – The sample end index to use, use None to go all the way to the end of the vector
- **weights** – A numpy array of weights for each sample, defaults to self.weights

Returns *ParamConfidenceData* instance

initParameters(*ini*)
Initializes settings. Gets parameters from *IniFile*.

Parameters **ini** – The *IniFile* to be used

loadChains(*root*, *files_or_samples: Sequence[T_co]*, *weights=None*, *loglikes=None*, *ignore_lines=None*)
Loads chains from files.

Parameters

- **root** – Root name
- **files_or_samples** – list of file names or list of arrays of samples, or single array of samples
- **weights** – if loading from arrays of samples, corresponding list of arrays of weights
- **loglikes** – if loading from arrays of samples, corresponding list of arrays of -2 log(likelihood)
- **ignore_lines** – Amount of lines at the start of the file to ignore, None if should not ignore

Returns True if loaded successfully, False if none loaded

makeSingle()
Combines separate chains into one samples array, so self.samples has all the samples and this instance can then be used as a general *WeightedSamples* instance.

Returns self

makeSingleSamples(*filename=''*, *single_thin=None*)
Make file of unit weight samples by choosing samples with probability proportional to their weight.

Parameters

- **filename** – The filename to write to, leave empty if no output file is needed
- **single_thin** – factor to thin by; if not set generates as many samples as it can up to self.max_scatter_points

Returns numpy array of selected weight-1 samples if no filename

mean(*paramVec*, *where=None*)
Get the mean of the given parameter vector.

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns parameter mean

mean_diff(*paramVec*, *where=None*)
Calculates an array of differences between a parameter vector and the mean parameter value

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns array of p_i - mean(p_i)

mean_diffs(*pars: Union[None*, *int*, *Sequence[T_co]] = None*, *where=None*) → Sequence[T_co]
Calculates a list of parameter vectors giving distances from parameter means

Parameters

- **pars** – if specified, list of parameter vectors or int parameter indices to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns list of arrays p_i-mean(p-i) for each parameter

parLabel(*i*)
Gets the latex label of the parameter

Parameters **i** – The index or name of a parameter.

Returns The parameter's label.

parName(*i*, *starDerived=False*)
Gets the name of i'th parameter

Parameters

- **i** – The index of the parameter
- **starDerived** – add a star at the end of the name if the parameter is derived

Returns The name of the parameter (string)

random_single_samples_indices()
Returns an array of sample indices that give a list of weight-one samples, by randomly selecting samples depending on the sample weights

Returns array of sample indices

readChains(*files_or_samples*, *weights=None*, *loglikes=None*)
Loads samples from a list of files or array(s), removing burn in, deleting fixed parameters, and combining into one self.samples array

Parameters

- **files_or_samples** – The list of file names to read, samples or list of samples
- **weights** – array of weights if setting from arrays
- **loglikes** – array of -2 log(likelihood) if setting from arrays

Returns self.

removeBurn(*remove=0.3*)
removes burn in from the start of the samples

Parameters **remove** – fraction of samples to remove, or if int >1, the number of sample rows to remove

removeBurnFraction(*ignore_frac*)
Remove a fraction of the samples as burn in

Parameters **ignore_frac** – fraction of sample points to remove from the start of the samples, or each chain if not combined

reweightAddingLogLikes(*logLikes*)
Importance sample the samples, by adding logLike (array of -log(likelihood values) to the currently stored likelihoods, and re-weighting accordingly, e.g. for adding a new data constraint

Parameters **logLikes** – array of -log(likelihood) for each sample to adjust

saveAsText(*root*, *chain_index=None*, *make_dirs=False*)
Saves the samples as text files, including parameter names as .paramnames file.

Parameters

- **root** – The root name to use
- **chain_index** – Optional index to be used for the filename, zero based, e.g. for saving one of multiple chains

- **make_dirs** – True if this should (recursively) create the directory if it doesn't exist

savePickle(*filename*)
Save the current object to a file in pickle format

Parameters **filename** – The file to write to

saveTextMetadata(*root*, *properties=None*)
Saves metadata about the sames to text files with given file root

Parameters

- **root** – root file name
- **properties** – optional dictiory of values to save in root.properties.ini

setColData(*coldata*, *are_chains=True*)
Set the samples given an array loaded from file

Parameters

- **coldata** – The array with columns of [weights, -log(Likelihoods)] and sample parameter values
- **are_chains** – True if coldata starts with two columns giving weight and -log(Likelihood)

setDiffs()
saves self.diffs array of parameter differences from the y, e.g. to later calculate variances etc.

Returns array of differences

setMeans()
Calculates and saves the means of the samples

Returns numpy array of parameter means

setMinWeightRatio(*min_weight_ratio=1e-30*)
Removes samples with weight less than min_weight_ratio times the maximum weight

Parameters **min_weight_ratio** – minimum ratio to max to exclude

setParamNames(*names=None*)
Sets the names of the params.

Parameters **names** – Either a *ParamNames* object, the name of a .paramnames file to load, a list of name strings, otherwise use default names (param1, param2...).

setParams(*obj*)
Adds array variables obj.name1, obj.name2 etc, where obj.name1 is the vector of samples with name 'name1'

if a parameter name is of the form aa.bb.cc, it makes subobjects so you can reference obj.aa.bb.cc

Parameters **obj** – The object instance to add the parameter vectors variables

Returns The obj after alterations.

setRanges(*ranges*)
Sets the ranges parameters, e.g. hard priors on positivity etc. If a min or max value is None, then it is assumed to be unbounded.

Parameters **ranges** – A list or a tuple of [min,max] values for each parameter, or a dictionary giving [min,max] values for specific parameter names

setSamples(*samples*, *weights=None*, *loglikes=None*, *min_weight_ratio=None*)
Sets the samples from numpy arrays

Parameters

- **samples** – The samples values, n_samples x n_parameters numpy array, or can be a list of parameter vectors
- **weights** – Array of weights for each sample. Defaults to 1 for all samples if unspecified.
- **loglikes** – Array of -log(Likelihood) values for each sample
- **min_weight_ratio** – remove samples with weight less than min_weight_ratio of the maximum

std(*paramVec*, *where=None*)
Get the standard deviation of the given parameter vector.

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns parameter standard deviation.

thin(*factor*)
Thin the samples by the given factor, giving set of samples with unit weight

Parameters **factor** – The factor to thin by

thin_indices(*factor*, *weights=None*)
Indices to make single weight 1 samples. Assumes integer weights.

Parameters

- **factor** – The factor to thin by, should be int.
- **weights** – The weights to thin, None if this should use the weights stored in the object.

Returns array of indices of samples to keep

twoTailLimits(*paramVec*, *confidence*)
Calculates two-tail equal-area confidence limit by counting samples in the tails

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **confidence** – confidence limit to calculate, e.g. 0.95 for 95% confidence

Returns min, max values for the confidence interval

updateBaseStatistics()
Updates basic computed statistics (y, covariance etc), e.g. after a change in samples or weights

Returns self

updateRenames(*renames*)
Updates the renames known to each parameter with the given dictionary of renames.

updateSettings(*settings=None*, *ini=None*, *doUpdate=True*)
Updates settings from a .ini file or dictionary

Parameters

- **settings** – The a dict containing settings to set, taking preference over any values in ini

- **ini** – The name of .ini file to get settings from, or an *IniFile* instance; by default uses current settings
- **doUpdate** – True if should update internal computed values, False otherwise (e.g. if want to make other changes first)

var(*paramVec*, *where=None*)
Get the variance of the given parameter vector.

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns parameter variance

weighted_sum(*paramVec*, *where=None*)
Calculates the weighted sum of a parameter vector, sum_i w_i p_i

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns weighted sum

weighted_thin(*factor*)
Thin the samples by the given factor, preserving the weights. This function also preserves separate chains.

Parameters **factor** – The (integer) factor to thin by

writeCorrelationMatrix(*filename=None*)
Write the correlation matrix to a file

Parameters **filename** – The file to write to, If none writes to file_root.corr

writeCovMatrix(*filename=None*)
Writes the covrariance matrix of non-derived parameters to a file.

Parameters **filename** – The filename to write to; default is file_root.covmat

writeThinData(*fname*, *thin_ix*, *cool=1*)
Writes samples at thin_ix to file

Parameters

- **fname** – The filename to write to.
- **thin_ix** – Indices of the samples to write
- **cool** – if not 1, cools the samples by this factor

exception getdist.mcsamples.**MCSamplesError**
An Exception that is raised when there is an error inside the MCSamples class.

exception getdist.mcsamples.**ParamError**
An Exception that indicates a bad parameter.

exception getdist.mcsamples.**SettingError**
An Exception that indicates bad settings.

CHAPTER 4

getdist.plots

This module is used for making plots from samples. The *get_single_plotter()* and *get_subplot_plotter()* functions are used to make a plotter instance, which is then used to make and export plots.

Many plotter functions take a **roots** argument, which is either a root name for some chain files, or an in-memory *MCSamples* instance. You can also make comparison plots by giving a list of either of these.

Parameter are referenced simply by name (as specified in the .paramnames file when loading from file, or set in the *MCSamples* instance). For functions that takes lists of parameters, these can be just lists of names. You can also use glob patterns to match specific subsets of parameters (e.g. *x** to match all parameters with names starting with *x*).

get_single_plotter	Get a *GetDistPlotter* for making a single plot of fixed width.
get_subplot_plotter	Get a *GetDistPlotter* for making an array of sub-plots.
GetDistPlotter	Main class for making plots from one or more sets of samples.
GetDistPlotSettings	Settings class (colors, sizes, font, styles etc.)

4.1 getdist.plots.get_single_plotter

getdist.plots.**get_single_plotter**(*ratio=None*, *width_inch=None*, *scaling=None*, *rc_sizes=False*, *style=None*, ***kwargs*)

Get a *GetDistPlotter* for making a single plot of fixed width.

For a half-column plot for a paper use width_inch=3.464.

Use this or *get_subplot_plotter()* to make a *GetDistPlotter* instance for making plots. This function will use the active style by default, which will determine defaults for the various optional parameters (see *set_active_style()*).

Parameters

- **ratio** – The ratio between height and width.
- **width_inch** – The width of the plot in inches
- **scaling** – whether to scale down fonts and line widths for small subplot axis sizes (relative to reference sizes, 3.5 inch)
- **rc_sizes** – set default font sizes from matplotlib's current rcParams if no explicit settings passed in kwargs
- **style** – name of a plotter style (associated with custom plotter class/settings), otherwise uses active
- **kwargs** – arguments for *GetDistPlotter*

Returns The *GetDistPlotter* instance

4.2 getdist.plots.get_subplot_plotter

getdist.plots.**get_subplot_plotter**(*subplot_size=None*, *width_inch=None*, *scaling=None*, *rc_sizes=False*, *subplot_size_ratio=None*, *style=None*, ***kwargs*)

Get a *GetDistPlotter* for making an array of subplots.

If width_inch is None, just makes plot as big as needed for given subplot_size, otherwise fixes total width and sets default font sizes etc. from matplotlib's default rcParams.

Use this or *get_single_plotter()* to make a *GetDistPlotter* instance for making plots. This function will use the active style by default, which will determine defaults for the various optional parameters (see *set_active_style()*).

Parameters

- **subplot_size** – The size of each subplot in inches
- **width_inch** – Optional total width in inches
- **scaling** – whether to scale down fonts and line widths for small sizes (relative to reference sizes, 3.5 inch)
- **rc_sizes** – set default font sizes from matplotlib's current rcParams if no explicit settings passed in kwargs
- **subplot_size_ratio** – ratio of height to width for subplots
- **style** – name of a plotter style (associated with custom plotter class/settings), otherwise uses active
- **kwargs** – arguments for *GetDistPlotter*

Returns The *GetDistPlotter* instance

4.3 getdist.plots.GetDistPlotter

class getdist.plots.**GetDistPlotter**(*chain_dir=None*, *settings=None*, *analysis_settings=None*, *auto_close=False*)

Main class for making plots from one or more sets of samples.

Variables

- **settings** – a *GetDistPlotSettings* instance with settings
- **subplots** – a 2D array of Axes for subplots
- **sample_analyser** – a *MCSampleAnalysis* instance for getting *MCSamples* and derived data from a given root name tag (e.g. sample_analyser.samples_for_root('rootname'))

Parameters

- **chain_dir** – Set this to a directory or grid directory hierarchy to search for chains (can also be a list of such, searched in order)
- **analysis_settings** – The settings to be used by *MCSampleAnalysis* when analysing samples
- **auto_close** – whether to automatically close the figure whenever a new plot made or this instance released

__init__(*chain_dir=None*, *settings=None*, *analysis_settings=None*, *auto_close=False*)

Parameters

- **chain_dir** – Set this to a directory or grid directory hierarchy to search for chains (can also be a list of such, searched in order)
- **analysis_settings** – The settings to be used by *MCSampleAnalysis* when analysing samples
- **auto_close** – whether to automatically close the figure whenever a new plot made or this instance released

Methods

__init__([chain_dir, settings, ...])	**param chain_dir** Set this to a directory or grid directory hierarchy to search for chains
add_1d(root, param[, plotno, normalized, ...])	Low-level function to add a 1D marginalized density line to a plot
add_2d_contours(root[, param1, param2, ...])	Low-level function to add 2D contours to plot for samples with given root name and parameters
add_2d_covariance(means, cov[, xvals, ...])	Plot 2D Gaussian ellipse.
add_2d_density_contours(density, **kwargs)	Low-level function to add 2D contours to a plot using provided density
add_2d_mixture_projection(mixture, param1, ...)	
add_2d_scatter(root, x, y[, color, alpha, ...])	Low-level function to adds a 2D sample scatter plot to the current axes (or ax if specified).
add_2d_shading(root, param1, param2[, ...])	Low-level function to add 2D density shading to the given plot.
add_3d_scatter(root, params[, color_bar, ...])	Low-level function to add a 3D scatter plot to the current axes (or ax if specified).
add_bands(x, y, errors[, color, nbands, ...])	Add a constraint band as a function of x showing e.g.
add_colorbar(param[, orientation, mappable, ax])	Adds a color bar to the given plot.

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add_colorbar_label(cb, param[, label_rotation])	Adds a color bar label.
add_legend(legend_labels[, legend_loc, ...])	Add a legend to the axes or figure.
add_line(xdata, ydata[, zorder, color, ls, ax])	Adds a line to the given axes, using Line2D
add_text(text_label[, x, y, ax])	Add text to given axis.
add_text_left(text_label[, x, y, ax])	Add text to the left, Wraps add_text.
add_x_bands(x, sigma[, color, ax, alpha1, ...])	Adds vertical shaded bands showing one and two sigma ranges.
add_x_marker(marker[, color, ls, lw, ax])	Adds a vertical line marking some x value.
add_y_bands(y, sigma[, color, ax, alpha1, ...])	Adds horizontal shaded bands showing one and two sigma ranges.
add_y_marker(marker[, color, ls, lw, ax])	Adds a horizontal line marking some y value.
default_col_row([nplot, nx, ny])	Get default subplot columns and rows depending on number of subplots.
export([fname, adir, watermark, tag])	Exports given figure to a file.
finish_plot([legend_labels, legend_loc, ...])	Finish the current plot, adjusting subplot spacing and adding legend if required.
get_axes([ax, pars])	Get the axes instance corresponding to the given subplot (y,x) coordinates, parameter list, or otherwise if ax is None get the last subplot axes used, or generate the first (possibly only) subplot if none.
get_axes_for_params(*pars, **kwargs)	Get axes corresponding to given parameters
get_param_array(root, params, str, ...)	Gets an array of ParamInfo for named params in the given *root*.
get_single_plotter([scaling, rc_sizes])	
get_subplot_plotter([subplot_size, ...])	
make_figure([nplot, nx, ny, xstretch, ...])	Makes a new figure with one or more subplots.
new_plot([close_existing])	Resets the given plotter to make a new empty plot.
param_bounds_for_root(root)	Get any hard prior bounds for the parameters with root file name
param_latex_label(root, name[, label_params])	Returns the latex label for given parameter.
param_names_for_root(root)	Get the parameter names and labels ParamNames instance for the given root name
plot_1d(roots, param[, marker, ...])	Make a single 1D plot with marginalized density lines.
plot_2d(roots[, param1, param2, param_pair, ...])	Create a single 2D line, contour or filled plot.
plot_2d_scatter(roots, param1, param2[, ...])	Make a 2D sample scatter plot.
plot_3d(roots[, params, params_for_plots, ...])	Make a 2D scatter plot colored by the value of a third parameter (a 3D plot).
plots_1d(roots[, params, legend_labels, ...])	Make an array of 1D marginalized density subplots
plots_2d(roots[, param1, params2, ...])	Make an array of 2D line, filled or contour plots.
plots_2d_triplets(root_params_triplets[, ...])	Creates an array of 2D plots, where each plot uses different samples, x and y parameters
plots_3d(roots, param_sets[, nx, legend_labels])	Create multiple 3D subplots
plots_3d_z(roots, param_x, param_y[, ...])	Make set of sample scatter subplots of param_x against param_y, each coloured by values of parameters in param_z (all if None).
rectangle_plot(xparams, yparams[, yroots, ...])	Make a grid of 2D plots.

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rotate_xticklabels([ax, rotation, labelsize])	Rotates the x-tick labels by given rotation (degrees)
rotate_yticklabels([ax, rotation, labelsize])	Rotates the y-tick labels by given rotation (degrees)
samples_for_root(root[, file_root, cache, ...])	Gets *MCSamples* from root name (or just return root if it is already an MCSamples instance).
set_axes([params, lims, do_xlabel, ...])	Set the axis labels and ticks, and various styles.
set_default_settings()	
set_xlabel(param[, ax])	Sets the label for the x axis.
set_ylabel(param[, ax])	Sets the label for the y axis.
show_all_settings()	Prints settings and library versions
triangle_plot(roots[, params, ...])	Make a trianglular array of 1D and 2D plots.

4.4 getdist.plots.GetDistPlotSettings

class getdist.plots.**GetDistPlotSettings**(*subplot_size_inch=2*, *fig_width_inch=None*)

Settings class (colors, sizes, font, styles etc.)

Variables

- **alpha_factor_contour_lines** – alpha factor for adding contour lines between filled contours
- **alpha_filled_add** – alpha for adding filled contours to a plot
- **axes_fontsize** – Size for axis font at reference axis size
- **axes_labelsize** – Size for axis label font at reference axis size
- **axis_marker_color** – The color for a marker
- **axis_marker_ls** – The line style for a marker
- **axis_marker_lw** – The line width for a marker
- **axis_tick_powerlimits** – exponents at which to use scientific notation for axis tick labels
- **axis_tick_max_labels** – maximum number of tick labels per axis
- **axis_tick_step_groups** – steps to try for axis ticks, in grouped in order of preference
- **axis_tick_x_rotation** – The rotation for the x tick label in degrees
- **axis_tick_y_rotation** – The rotation for the y tick label in degrees
- **colorbar_axes_fontsize** – size for tick labels on colorbar (None for default to match axes font size)
- **colorbar_label_pad** – padding for the colorbar label
- **colorbar_label_rotation** – angle to rotate colorbar label (set to zero if -90 default gives layout problem)
- **colorbar_tick_rotation** – angle to rotate colorbar tick labels
- **colormap** – a Matplotlib color map for shading
- **colormap_scatter** – a Matplotlib color map for 3D scatter plots
- **constrained_layout** – use matplotlib's constrained-layout to fit plots within the figure and avoid overlaps
- **fig_width_inch** – The width of the figure in inches

- **figure_legend_frame** – draw box around figure legend
- **figure_legend_loc** – The location for the figure legend
- **figure_legend_ncol** – number of columns for figure legend (set to zero to use defaults)
- **fontsize** – font size for text (and ultimate fallback when others not set)
- **legend_colored_text** – use colored text for legend labels rather than separate color blocks
- **legend_fontsize** – The font size for the legend (defaults to fontsize)
- **legend_frac_subplot_margin** – fraction of subplot size to use for spacing figure legend above plots
- **legend_frame** – draw box around legend
- **legend_loc** – The location for the legend
- **legend_rect_border** – whether to have black border around solid color boxes in legends
- **line_dash_styles** – dict mapping line styles to detailed dash styles, default: {'–': (3, 2), '-.': (4, 1, 1, 1)}
- **line_labels** – True if you want to automatically add legends when adding more than one line to subplots
- **line_styles** – list of default line styles/colors (['-k', '-r', '–C0', ...]) or name of a standard colormap (e.g. tab10), or a list of tuples of line styles and colors for each line
- **linewidth** – relative linewidth (at reference size)
- **linewidth_contour** – linewidth for lines in filled contours
- **linewidth_meanlikes** – linewidth for mean likelihood lines
- **no_triangle_axis_labels** – whether subplots in triangle plots should show axis labels if not at the edge
- **norm_1d_density** – whether to normolize 1D densities (otherwise normalized to unit peak value)
- **norm_prob_label** – label for the y axis in normalized 1D density plots
- **num_plot_contours** – number of contours to plot in 2D plots (up to number of contours in analysis settings)
- **num_shades** – number of distinct colors to use for shading shaded 2D plots
- **param_names_for_labels** – file name of .paramnames file to use for overriding parameter labels for plotting
- **plot_args** – dict, or list of dicts, giving settings like color, ls, alpha, etc. to apply for a plot or each line added
- **plot_meanlikes** – include mean likelihood lines in 1D plots
- **prob_label** – label for the y axis in unnormalized 1D density plots
- **prob_y_ticks** – show ticks on y axis for 1D density plots
- **progress** – write out some status
- **scaling** – True to scale down fonts and lines for smaller subplots; False to use fixed sizes.

- **scaling_max_axis_size** – font sizes will only be scaled for subplot widths (in inches) smaller than this.
- **scaling_factor** – factor by which to multiply the different of the axis size to the reference size when scaling font sizes
- **scaling_reference_size** – axis width (in inches) at which font sizes are specified.
- **scatter_size** – size of points in "3D" scatter plots
- **shade_level_scale** – shading contour colors are put at [0:1:spacing]**shade_level_scale
- **shade_meanlikes** – 2D shading uses mean likelihoods rather than marginalized density
- **solid_colors** – List of default colors for filled 2D plots or the name of a colormap (e.g. tab10). If a list, each element is either a color, or a tuple of values for different contour levels.
- **solid_contour_palefactor** – factor by which to make 2D outer filled contours paler when only specifying one contour color
- **subplot_size_ratio** – ratio of width and height of subplots
- **tight_layout** – use tight_layout to layout, avoid overlaps and remove white space; if it doesn't work try constrained_layout. If true it is applied when calling *finish_plot()* (which is called automatically by plots_xd(), triangle_plot and rectangle_plot).
- **title_limit** – show parameter limits over 1D plots, 1 for first limit (68% default), 2 second, etc.
- **title_limit_labels** – whether or not to include parameter label when adding limits above 1D plots
- **title_limit_fontsize** – font size to use for limits in plot titles (defaults to axes_labelsize)

If fig_width_inch set, fixed setting for fixed total figure size in inches. Otherwise use subplot_size_inch to determine default font sizes etc., and figure will then be as wide as necessary to show all subplots at specified size.

Parameters

- **subplot_size_inch** – Determines the size of subplots, and hence default font sizes
- **fig_width_inch** – The width of the figure in inches, If set, forces fixed total size.

__init__(*subplot_size_inch=2*, *fig_width_inch=None*)

If fig_width_inch set, fixed setting for fixed total figure size in inches. Otherwise use subplot_size_inch to determine default font sizes etc., and figure will then be as wide as necessary to show all subplots at specified size.

Parameters

- **subplot_size_inch** – Determines the size of subplots, and hence default font sizes
- **fig_width_inch** – The width of the figure in inches, If set, forces fixed total size.

Methods

__init__([subplot_size_inch, fig_width_inch])	If fig_width_inch set, fixed setting for fixed total figure size in inches.
rc_sizes([axes_fontsize, lab_fontsize, ...])	Sets the font sizes by default from matplotlib.rcParams defaults
scaled_fontsize(ax_size, var[, default])	
scaled_linewidth(ax_size, linewidth)	
set_with_subplot_size([size_inch, size_mm, ...])	Sets the subplot's size, either in inches or in millimeters.

exception getdist.plots.**GetDistPlotError**
An exception that is raised when there is an error plotting

class getdist.plots.**GetDistPlotSettings**(*subplot_size_inch=2*, *fig_width_inch=None*)
Settings class (colors, sizes, font, styles etc.)

Variables

- **alpha_factor_contour_lines** – alpha factor for adding contour lines between filled contours
- **alpha_filled_add** – alpha for adding filled contours to a plot
- **axes_fontsize** – Size for axis font at reference axis size
- **axes_labelsize** – Size for axis label font at reference axis size
- **axis_marker_color** – The color for a marker
- **axis_marker_ls** – The line style for a marker
- **axis_marker_lw** – The line width for a marker
- **axis_tick_powerlimits** – exponents at which to use scientific notation for axis tick labels
- **axis_tick_max_labels** – maximum number of tick labels per axis
- **axis_tick_step_groups** – steps to try for axis ticks, in grouped in order of preference
- **axis_tick_x_rotation** – The rotation for the x tick label in degrees
- **axis_tick_y_rotation** – The rotation for the y tick label in degrees
- **colorbar_axes_fontsize** – size for tick labels on colorbar (None for default to match axes font size)
- **colorbar_label_pad** – padding for the colorbar label
- **colorbar_label_rotation** – angle to rotate colorbar label (set to zero if -90 default gives layout problem)
- **colorbar_tick_rotation** – angle to rotate colorbar tick labels
- **colormap** – a Matplotlib color map for shading
- **colormap_scatter** – a Matplotlib color map for 3D scatter plots
- **constrained_layout** – use matplotlib's constrained-layout to fit plots within the figure and avoid overlaps
- **fig_width_inch** – The width of the figure in inches
- **figure_legend_frame** – draw box around figure legend
- **figure_legend_loc** – The location for the figure legend

- **figure_legend_ncol** – number of columns for figure legend (set to zero to use defaults)
- **fontsize** – font size for text (and ultimate fallback when others not set)
- **legend_colored_text** – use colored text for legend labels rather than separate color blocks
- **legend_fontsize** – The font size for the legend (defaults to fontsize)
- **legend_frac_subplot_margin** – fraction of subplot size to use for spacing figure legend above plots
- **legend_frame** – draw box around legend
- **legend_loc** – The location for the legend
- **legend_rect_border** – whether to have black border around solid color boxes in legends
- **line_dash_styles** – dict mapping line styles to detailed dash styles, default: {'–': (3, 2), '-.': (4, 1, 1, 1)}
- **line_labels** – True if you want to automatically add legends when adding more than one line to subplots
- **line_styles** – list of default line styles/colors (['-k', '-r', '–C0', ...]) or name of a standard colormap (e.g. tab10), or a list of tuples of line styles and colors for each line
- **linewidth** – relative linewidth (at reference size)
- **linewidth_contour** – linewidth for lines in filled contours
- **linewidth_meanlikes** – linewidth for mean likelihood lines
- **no_triangle_axis_labels** – whether subplots in triangle plots should show axis labels if not at the edge
- **norm_1d_density** – whether to normolize 1D densities (otherwise normalized to unit peak value)
- **norm_prob_label** – label for the y axis in normalized 1D density plots
- **num_plot_contours** – number of contours to plot in 2D plots (up to number of contours in analysis settings)
- **num_shades** – number of distinct colors to use for shading shaded 2D plots
- **param_names_for_labels** – file name of .paramnames file to use for overriding parameter labels for plotting
- **plot_args** – dict, or list of dicts, giving settings like color, ls, alpha, etc. to apply for a plot or each line added
- **plot_meanlikes** – include mean likelihood lines in 1D plots
- **prob_label** – label for the y axis in unnormalized 1D density plots
- **prob_y_ticks** – show ticks on y axis for 1D density plots
- **progress** – write out some status
- **scaling** – True to scale down fonts and lines for smaller subplots; False to use fixed sizes.
- **scaling_max_axis_size** – font sizes will only be scaled for subplot widths (in inches) smaller than this.

- **scaling_factor** – factor by which to multiply the different of the axis size to the reference size when scaling font sizes
- **scaling_reference_size** – axis width (in inches) at which font sizes are specified.
- **scatter_size** – size of points in "3D" scatter plots
- **shade_level_scale** – shading contour colors are put at [0:1:spacing]**shade_level_scale
- **shade_meanlikes** – 2D shading uses mean likelihoods rather than marginalized density
- **solid_colors** – List of default colors for filled 2D plots or the name of a colormap (e.g. tab10). If a list, each element is either a color, or a tuple of values for different contour levels.
- **solid_contour_palefactor** – factor by which to make 2D outer filled contours paler when only specifying one contour color
- **subplot_size_ratio** – ratio of width and height of subplots
- **tight_layout** – use tight_layout to layout, avoid overlaps and remove white space; if it doesn't work try constrained_layout. If true it is applied when calling *finish_plot()* (which is called automatically by plots_xd(), triangle_plot and rectangle_plot).
- **title_limit** – show parameter limits over 1D plots, 1 for first limit (68% default), 2 second, etc.
- **title_limit_labels** – whether or not to include parameter label when adding limits above 1D plots
- **title_limit_fontsize** – font size to use for limits in plot titles (defaults to axes_labelsize)

If fig_width_inch set, fixed setting for fixed total figure size in inches. Otherwise use subplot_size_inch to determine default font sizes etc., and figure will then be as wide as necessary to show all subplots at specified size.

Parameters

- **subplot_size_inch** – Determines the size of subplots, and hence default font sizes
- **fig_width_inch** – The width of the figure in inches, If set, forces fixed total size.

rc_sizes(*axes_fontsize=None*, *lab_fontsize=None*, *legend_fontsize=None*)

Sets the font sizes by default from matplotlib.rcParams defaults

Parameters

- **axes_fontsize** – The font size for the plot axes tick labels (default: xtick.labelsize).
- **lab_fontsize** – The font size for the plot's axis labels (default: axes.labelsize)
- **legend_fontsize** – The font size for the plot's legend (default: legend.fontsize)

set_with_subplot_size(*size_inch=3.5*, *size_mm=None*, *size_ratio=None*)

Sets the subplot's size, either in inches or in millimeters. If both are set, uses millimeters.

Parameters

- **size_inch** – The size to set in inches; is ignored if size_mm is set.
- **size_mm** – None if not used, otherwise the size in millimeters we want to set for the subplot.
- **size_ratio** – ratio of height to width of subplots

class getdist.plots.**GetDistPlotter**(*chain_dir=None*, *settings=None*, *analysis_settings=None*, *auto_close=False*)

Main class for making plots from one or more sets of samples.

Variables

- **settings** – a *GetDistPlotSettings* instance with settings
- **subplots** – a 2D array of Axes for subplots
- **sample_analyser** – a *MCSampleAnalysis* instance for getting *MCSamples* and derived data from a given root name tag (e.g. sample_analyser.samples_for_root('rootname'))

Parameters

- **chain_dir** – Set this to a directory or grid directory hierarchy to search for chains (can also be a list of such, searched in order)
- **analysis_settings** – The settings to be used by *MCSampleAnalysis* when analysing samples
- **auto_close** – whether to automatically close the figure whenever a new plot made or this instance released

add_1d(*root*, *param*, *plotno=0*, *normalized=None*, *ax=None*, *title_limit=None*, ***kwargs*)

Low-level function to add a 1D marginalized density line to a plot

Parameters

- **root** – The root name of the samples
- **param** – The parameter name
- **plotno** – The index of the line being added to the plot
- **normalized** – True if areas under lines should match, False if normalized to unit maximum. Default from settings.norm_1d_density.
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **title_limit** – if not None, a maginalized limit (1,2..) to print as the title of the plot
- **kwargs** – arguments for plot()

Returns min, max for the plotted density

add_2d_contours(*root*, *param1=None*, *param2=None*, *plotno=0*, *of=None*, *cols=None*, *contour_levels=None*, *add_legend_proxy=True*, *param_pair=None*, *density=None*, *alpha=None*, *ax=None*, ***kwargs*)

Low-level function to add 2D contours to plot for samples with given root name and parameters

Parameters

- **root** – The root name of samples to use or a MixtureND gaussian mixture
- **param1** – x parameter
- **param2** – y parameter
- **plotno** – The index of the contour lines being added
- **of** – the total number of contours being added (this is line plotno of of)
- **cols** – optional list of colors to use for contours, by default uses default for this plotno

- **contour_levels** – levels at which to plot the contours, by default given by contours array in the analysis settings
- **add_legend_proxy** – True if should add a proxy to the legend of this plot.
- **param_pair** – an [x,y] parameter name pair if you prefer to provide this rather than param1 and param2
- **density** – optional *Density2D* to plot rather than that computed automatically from the samples
- **alpha** – alpha for the contours added
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – optional keyword arguments:
  - **filled**: True to make filled contours
  - **color**: top color to automatically make paling contour colours for a filled plot
  - kwargs for contour() and contourf()

Returns bounds (from *bounds()*) for the 2D density plotted

add_2d_covariance(*means*, *cov*, *xvals=None*, *yvals=None*, *def_width=4.0*, *samples_per_std=50.0*, ***kwargs*)

Plot 2D Gaussian ellipse. By default plots contours for 1 and 2 sigma. Specify contour_levels argument to plot other contours (for density normalized to peak at unity).

Parameters

- **means** – array of y
- **cov** – the 2x2 covariance
- **xvals** – optional array of x values to evaluate at
- **yvals** – optional array of y values to evaluate at
- **def_width** – if evaluation array not specified, width to use in units of standard deviation
- **samples_per_std** – if evaluation array not specified, number of grid points per standard deviation
- **kwargs** – keyword arguments for add_2D_contours()

add_2d_density_contours(*density*, ***kwargs*)

Low-level function to add 2D contours to a plot using provided density

Parameters

- **density** – a *densities.Density2D* instance
- **kwargs** – arguments for *add_2d_contours()*

Returns bounds (from bounds()) of density

add_2d_scatter(*root*, *x*, *y*, *color='k'*, *alpha=1*, *extra_thin=1*, *scatter_size=None*, *ax=None*)

Low-level function to adds a 2D sample scatter plot to the current axes (or ax if specified).

Parameters

- **root** – The root name of the samples to use
- **x** – name of x parameter
- **y** – name of y parameter

- **color** – color to plot the samples
- **alpha** – The alpha to use.
- **extra_thin** – thin the weight one samples by this additional factor before plotting
- **scatter_size** – point size (default: settings.scatter_size)
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)

Returns (xmin, xmax), (ymin, ymax) bounds for the axes.

add_2d_shading(*root*, *param1*, *param2*, *colormap=None*, *density=None*, *ax=None*, ***kwargs*)
Low-level function to add 2D density shading to the given plot.

Parameters

- **root** – The root name of samples to use
- **param1** – x parameter
- **param2** – y parameter
- **colormap** – color map, default to settings.colormap (see *GetDistPlotSettings*)
- **density** –

  optional user-provided *Density2D* to plot rather than the auto-generated density from the samples

  param ax optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)

- **kwargs** – keyword arguments for contourf()

add_3d_scatter(*root*, *params*, *color_bar=True*, *alpha=1*, *extra_thin=1*, *scatter_size=None*, *ax=None*, *alpha_samples=False*, ***kwargs*)
Low-level function to add a 3D scatter plot to the current axes (or ax if specified).

Parameters

- **root** – The root name of the samples to use
- **params** – list of parameters to plot
- **color_bar** – True to add a colorbar for the plotted scatter color
- **alpha** – The alpha to use.
- **extra_thin** – thin the weight one samples by this additional factor before plotting
- **scatter_size** – point size (default: settings.scatter_size)
- **alpha_samples** – use all samples, giving each point alpha corresponding to relative weight
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – arguments for *add_colorbar()*

Returns (xmin, xmax), (ymin, ymax) bounds for the axes.

add_bands(*x*, *y*, *errors*, *color='gray'*, *nbands=2*, *alphas=(0.25*, *0.15*, *0.1)*, *lw=0.2*, *lw_center=None*, *linecolor='k'*, *ax=None*)
Add a constraint band as a function of x showing e.g. a 1 and 2 sigma range.

Parameters

- **x** – array of x values
- **y** – array of central values for the band as function of x
- **errors** – array of errors as a function of x
- **color** – a fill color
- **nbands** – number of bands to plot. If errors are 1 sigma, using nbands=2 will plot 1 and 2 sigma.
- **alphas** – tuple of alpha factors to use for each error band
- **lw** – linewidth for the edges of the bands
- **lw_center** – linewidth for the central mean line (zero or None not to have one, the default)
- **linecolor** – a line color for central line
- **ax** – optional `Axes` instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)

add_colorbar(*param*, *orientation='vertical'*, *mappable=None*, *ax=None*, ***ax_args*)
Adds a color bar to the given plot.

Parameters

- **param** – a *ParamInfo* with label for the parameter the color bar is describing
- **orientation** – The orientation of the color bar (default: 'vertical')
- **mappable** – the thing to color, defaults to current scatter
- **ax** – optional `Axes` instance to add to (defaults to current plot)
- **ax_args** – extra arguments -

  color_label_in_axes - if True, label is not added (insert as text label in plot instead)

Returns The new `Colorbar` instance

add_colorbar_label(*cb*, *param*, *label_rotation=None*)
Adds a color bar label.

Parameters

- **cb** – a `Colorbar` instance
- **param** – a *ParamInfo* with label for the plotted parameter
- **label_rotation** – If set rotates the label (degrees)

add_legend(*legend_labels*, *legend_loc=None*, *line_offset=0*, *legend_ncol=None*, *colored_text=None*, *figure=False*, *ax=None*, *label_order=None*, *align_right=False*, *fontsize=None*, *figure_legend_outside=True*, ***kwargs*)
Add a legend to the axes or figure.

Parameters

- **legend_labels** – The labels
- **legend_loc** – The legend location, default from settings
- **line_offset** – The offset of plotted lines to label (e.g. 1 to not label first line)
- **legend_ncol** – The number of columns in the legend, defaults to 1

- **colored_text** –
  - True: legend labels are colored to match the lines/contours
  - False: colored lines/boxes are drawn before black labels
- **figure** – True if legend is for the figure rather than the selected axes
- **ax** – if figure == False, the Axes instance to use; defaults to current axes.
- **label_order** – minus one to show legends in reverse order that lines were added, or a list giving specific order of line indices
- **align_right** – True to align legend text at the right
- **fontsize** – The size of the font, default from settings
- **figure_legend_outside** – whether figure legend is outside or inside the sub-plots box
- **kwargs** – optional extra arguments for legend function

Returns a matplotlib.legend.Legend instance

add_line(*xdata*, *ydata*, *zorder=0*, *color=None*, *ls=None*, *ax=None*, ***kwargs*)
Adds a line to the given axes, using Line2D

Parameters

- **xdata** – pair of x coordinates
- **ydata** – pair of y coordinates
- **zorder** – Z-order for Line2D
- **color** – The color of the line, uses settings.axis_marker_color by default
- **ls** – The line style to be used, uses settings.axis_marker_ls by default
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – Additional arguments for Line2D

add_text(*text_label*, *x=0.95*, *y=0.06*, *ax=None*, ***kwargs*)
Add text to given axis.

Parameters

- **text_label** – The label to add.
- **x** – The x coordinate of where to add the label
- **y** – The y coordinate of where to add the label.
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – keyword arguments for text()

add_text_left(*text_label*, *x=0.05*, *y=0.06*, *ax=None*, ***kwargs*)
Add text to the left, Wraps add_text.

Parameters

- **text_label** – The label to add.
- **x** – The x coordinate of where to add the label

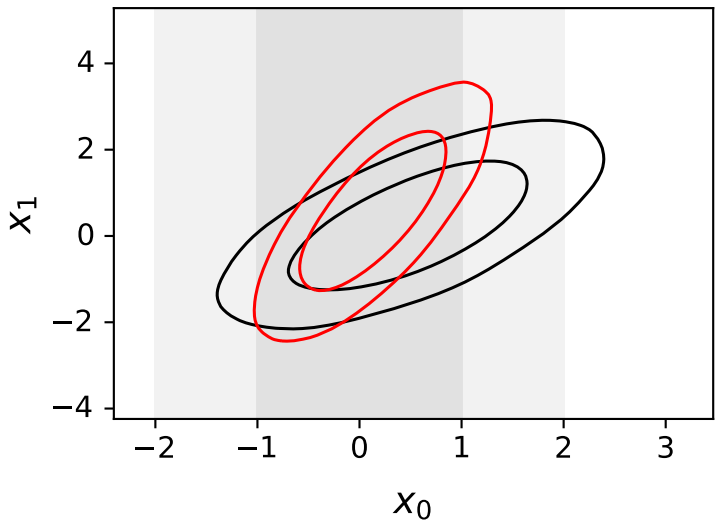
- **y** – The y coordinate of where to add the label.
- **ax** – optional `Axes` instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – keyword arguments for `text()`

add_x_bands(*x*, *sigma*, *color='gray'*, *ax=None*, *alpha1=0.15*, *alpha2=0.1*, ***kwargs*)
Adds vertical shaded bands showing one and two sigma ranges.

Parameters

- **x** – central x value for bands
- **sigma** – 1 sigma error on x
- **color** – The base color to use
- **ax** – optional `Axes` instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **alpha1** – alpha for the 1 sigma band; note this is drawn on top of the 2 sigma band. Set to zero if you only want 2 sigma band
- **alpha2** – alpha for the 2 sigma band. Set to zero if you only want 1 sigma band
- **kwargs** – optional keyword arguments for `axvspan()`

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=2,␣
↪nMCSamples=2)
g = plots.get_single_plotter(width_inch=4)
g.plot_2d([samples1, samples2], ['x0','x1'], filled=False);
g.add_x_bands(0, 1)
```



add_x_marker(*marker*, *color=None*, *ls=None*, *lw=None*, *ax=None*, ***kwargs*)
Adds a vertical line marking some x value. Optional arguments can override default settings.

Parameters

- **marker** – The x coordinate of the location the marker line

- **color** – optional color of the marker
- **ls** – optional line style of the marker
- **lw** – optional line width
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – additional arguments to pass to axvline()

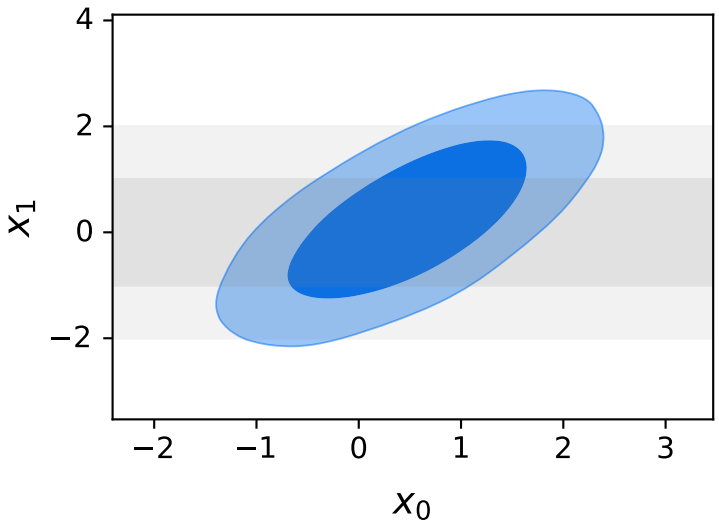
add_y_bands(*y*, *sigma*, *color='gray'*, *ax=None*, *alpha1=0.15*, *alpha2=0.1*, ***kwargs*)

Adds horizontal shaded bands showing one and two sigma ranges.

Parameters

- **y** – central y value for bands
- **sigma** – 1 sigma error on y
- **color** – The base color to use
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **alpha1** – alpha for the 1 sigma band; note this is drawn on top of the 2 sigma band. Set to zero if you only want 2 sigma band
- **alpha2** – alpha for the 2 sigma band. Set to zero if you only want 1 sigma band
- **kwargs** – optional keyword arguments for axhspan()

```
from getdist import plots, gaussian_mixtures
samples= gaussian_mixtures.randomTestMCSamples(ndim=2, nMCSamples=1)
g = plots.get_single_plotter(width_inch=4)
g.plot_2d(samples, ['x0','x1'], filled=True);
g.add_y_bands(0, 1)
```



add_y_marker(*marker*, *color=None*, *ls=None*, *lw=None*, *ax=None*, ***kwargs*)

Adds a horizontal line marking some y value. Optional arguments can override default settings.

Parameters

- **marker** – The y coordinate of the location the marker line
- **color** – optional color of the marker
- **ls** – optional line style of the marker
- **lw** – optional line width.
- **ax** – optional `Axes` instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – additional arguments to pass to `axhline()`

default_col_row(*nplot=1*, *nx=None*, *ny=None*)

Get default subplot columns and rows depending on number of subplots.

Parameters

- **nplot** – total number of subplots
- **nx** – optional specified number of columns
- **ny** – optional specified number of rows

Returns n_cols, n_rows

export(*fname=None*, *adir=None*, *watermark=None*, *tag=None*)

Exports given figure to a file. If the filename is not specified, saves to a file with the same name as the calling script (useful for plot scripts where the script name matches the output figure).

Parameters

- **fname** – The filename to export to. The extension (.pdf, .png, etc) determines the file type
- **adir** – The directory to save to
- **watermark** – a watermark text, e.g. to make the plot with some pre-final version number
- **tag** – A suffix to add to the filename.

finish_plot(*legend_labels=None*, *legend_loc=None*, *line_offset=0*, *legend_ncol=None*, *label_order=None*, *no_extra_legend_space=False*, *no_tight=False*, ***legend_args*)

Finish the current plot, adjusting subplot spacing and adding legend if required.

Parameters

- **legend_labels** – The labels for a figure legend
- **legend_loc** – The legend location, default from settings (figure_legend_loc)
- **line_offset** – The offset of plotted lines to label (e.g. 1 to not label first line)
- **legend_ncol** – The number of columns in the legend, defaults to 1
- **label_order** – minus one to show legends in reverse order that lines were added, or a list giving specific order of line indices
- **no_extra_legend_space** – True to put figure legend inside the figure box
- **no_tight** – don't use `tight_layout()` to adjust subplot positions
- **legend_args** – optional parameters for the legend

get_axes(*ax=None*, *pars=None*)

Get the axes instance corresponding to the given subplot (y,x) coordinates, parameter list, or otherwise if ax is None get the last subplot axes used, or generate the first (possibly only) subplot if none.

Parameters

- **ax** – optional Axes, (y,x) subplot coordinate, tuple of parameter names, or None to get last axes used or otherwise default to first subplot
- **pars** – optional list of parameters to associate with the axes

Returns an Axes instance, or None if the specified axes don't exist

get_axes_for_params(**pars*, ***kwargs*)
Get axes corresponding to given parameters

Parameters

- **pars** – x or x,y or x,y,color parameters
- **kwargs** – set ordered=False to match y,x as well as x,y

Returns axes instance or None if not found

get_param_array(*root*, *params: Union[None, str, Sequence[T_co]] = None*, *renames: Mapping[KT, VT_co] = None*)
Gets an array of ParamInfo for named params in the given *root*.

If a parameter is not found in *root*, returns the original ParamInfo if ParamInfo was passed, or fails otherwise.

Parameters

- **root** – The root name of the samples to use
- **params** – the parameter names (if not specified, get all)
- **renames** – optional dictionary mapping input names and equivalent names used by the samples

Returns list of ParamInfo instances for the parameters

make_figure(*nplot=1*, *nx=None*, *ny=None*, *xstretch=1.0*, *ystretch=1.0*, *sharex=False*, *sharey=False*)
Makes a new figure with one or more subplots.

Parameters

- **nplot** – number of subplots
- **nx** – number of subplots in each row
- **ny** – number of subplots in each column
- **xstretch** – The parameter of how much to stretch the width, 1 is default
- **ystretch** – The parameter of how much to stretch the height, 1 is default. Note this multiplies settings.subplot_size_ratio before determining actual stretch.
- **sharex** – no vertical space between subplots
- **sharey** – no horizontal space between subplots

Returns The plot_col, plot_row numbers of subplots for the figure

new_plot(*close_existing=None*)
Resets the given plotter to make a new empty plot.

Parameters **close_existing** – True to close any current figure

param_bounds_for_root(*root*)
Get any hard prior bounds for the parameters with root file name

Parameters **root** – The root name to be used

Returns object with get_upper() or getUpper() and get_lower() or getLower() bounds functions

param_latex_label(*root*, *name*, *label_params=None*)
Returns the latex label for given parameter.

Parameters

- **root** – root name of the samples having the parameter (or *MCSamples* instance)
- **name** – The param name
- **label_params** – optional name of .paramnames file to override parameter name labels

Returns The latex label

param_names_for_root(*root*)
Get the parameter names and labels *ParamNames* instance for the given root name

Parameters **root** – The root name of the samples.

Returns *ParamNames* instance

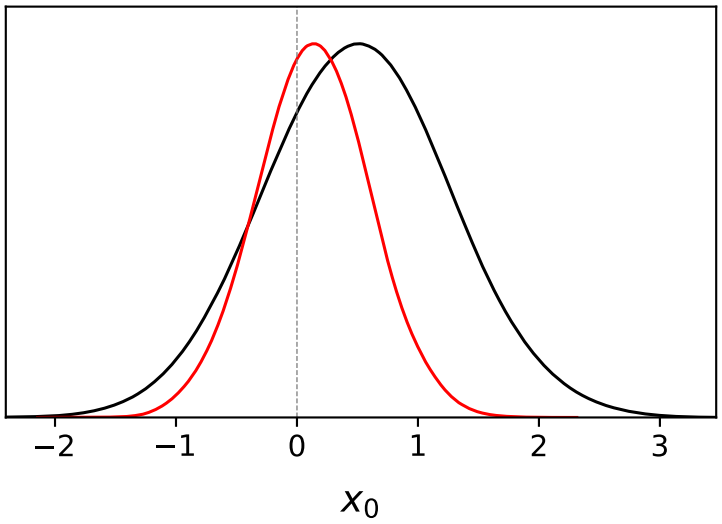
plot_1d(*roots*, *param*, *marker=None*, *marker_color=None*, *label_right=False*, *title_limit=None*, *no_ylabel=False*, *no_ytick=False*, *no_zero=False*, *normalized=False*, *param_renames=None*, *ax=None*, ***kwargs*)
Make a single 1D plot with marginalized density lines.

Parameters

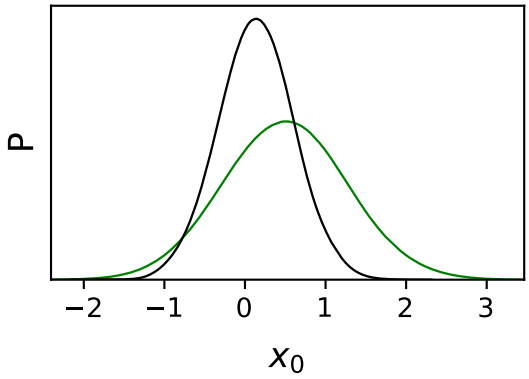
- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **param** – the parameter name to plot
- **marker** – If set, places a marker at given coordinate.
- **marker_color** – If set, sets the marker color.
- **label_right** – If True, label the y axis on the right rather than the left
- **title_limit** – If not None, a maginalized limit (1,2..) of the first root to print as the title of the plot
- **no_ylabel** – If True excludes the label on the y axis
- **no_ytick** – If True show no y ticks
- **no_zero** – If true does not show tick label at zero on y axis
- **normalized** – plot normalized densities (if False, densities normalized to peak at 1)
- **param_renames** – optional dictionary mapping input parameter names to equivalent names used by the samples
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – additional optional keyword arguments:
  - **lims**: optional limits for x range of the plot [xmin, xmax]
  - **ls** : list of line styles for the different lines plotted

- **colors**: list of colors for the different lines plotted
- **lws**: list of line widths for the different lines plotted
- **alphas**: list of alphas for the different lines plotted
- **line_args**: a list of dictionaries with settings for each set of lines
- arguments for *set_axes()*

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=2,␣
↪nMCSamples=2)
g = plots.get_single_plotter(width_inch=4)
g.plot_1d([samples1, samples2], 'x0', marker=0)
```




```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=2,␣
↪nMCSamples=2)
g = plots.get_single_plotter(width_inch=3)
g.plot_1d([samples1, samples2], 'x0', normalized=True, colors=['green','black
↪'])
```



plot_2d(*roots*, *param1=None*, *param2=None*, *param_pair=None*, *shaded=False*, *add_legend_proxy=True*, *line_offset=0*, *proxy_root_exclude=()*, *ax=None*, ***kwargs*)

Create a single 2D line, contour or filled plot.

Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **param1** – x parameter name
- **param2** – y parameter name
- **param_pair** – An [x,y] pair of params; can be set instead of param1 and param2
- **shaded** – True if plot should be a shaded density plot (for the first samples plotted)
- **add_legend_proxy** – True if should add to the legend proxy
- **line_offset** – line_offset if not adding first contours to plot
- **proxy_root_exclude** – any root names not to include when adding to the legend proxy
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – additional optional arguments:
  - **filled**: True for filled contours
  - **lims**: list of limits for the plot [xmin, xmax, ymin, ymax]
  - **ls** : list of line styles for the different sample contours plotted
  - **colors**: list of colors for the different sample contours plotted
  - **lws**: list of line widths for the different sample contours plotted
  - **alphas**: list of alphas for the different sample contours plotted
  - **line_args**: a list of dictionaries with settings for each set of contours
  - arguments for *set_axes()*

Returns The xbounds, ybounds of the plot.

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=4,␣
↪nMCSamples=2)
g = plots.get_single_plotter(width_inch = 4)
g.plot_2d([samples1,samples2], 'x1', 'x2', filled=True);
```

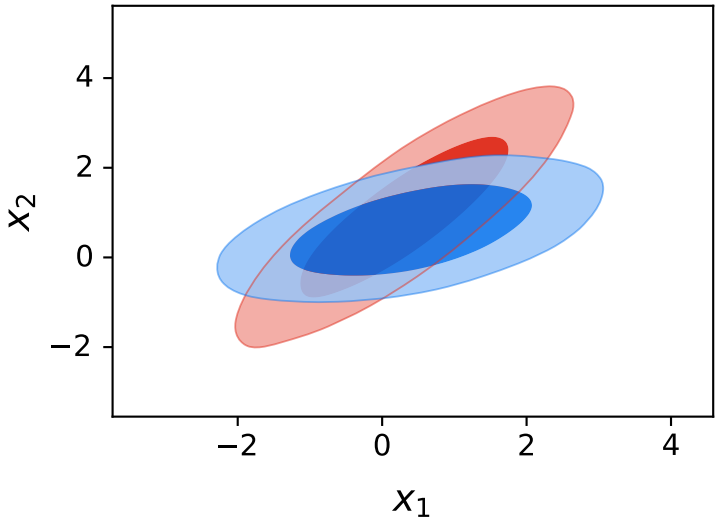
plot_2d_scatter(*roots*, *param1*, *param2*, *color='k'*, *line_offset=0*, *add_legend_proxy=True*, ***kwargs*)

Make a 2D sample scatter plot.

If roots is a list of more than one, additional densities are plotted as contour lines.

Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **param1** – name of x parameter
- **param2** – name of y parameter



- **color** – color to plot the samples
- **line_offset** – The line index offset for added contours
- **add_legend_proxy** – True if should add a legend proxy
- **kwargs** – additional optional arguments:
  - **filled**: True for filled contours for second and later items in roots
  - **lims**: limits for the plot [xmin, xmax, ymin, ymax]
  - **ls** : list of line styles for the different sample contours plotted
  - **colors**: list of colors for the different sample contours plotted
  - **lws**: list of linewidths for the different sample contours plotted
  - **alphas**: list of alphas for the different sample contours plotted
  - **line_args**: a list of dict with settings for contours from each root

plot_3d(*roots*, *params=None*, *params_for_plots=None*, *color_bar=True*, *line_offset=0*, *add_legend_proxy=True*, *alpha_samples=False*, *ax=None*, ***kwargs*)

Make a 2D scatter plot colored by the value of a third parameter (a 3D plot).

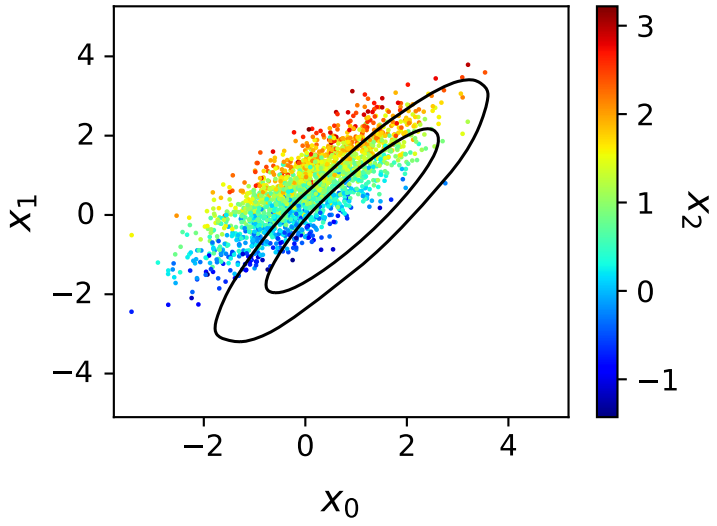
If roots is a list of more than one, additional densities are plotted as contour lines.

Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **params** – list with the three parameter names to plot (x, y, color)
- **params_for_plots** – list of parameter triplets to plot for each root plotted; more general alternative to params
- **color_bar** – True if should include a color bar
- **line_offset** – The line index offset for added contours
- **add_legend_proxy** – True if should add a legend proxy

- **alpha_samples** – if True, use alternative scatter style where all samples are plotted alphaed by their weights
- **ax** – optional `Axes` instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – additional optional arguments:
  - **filled**: True for filled contours for second and later items in roots
  - **lims**: limits for the plot [xmin, xmax, ymin, ymax]
  - **ls** : list of line styles for the different sample contours plotted
  - **colors**: list of colors for the different sample contours plotted
  - **lws**: list of linewidths for the different sample contours plotted
  - **alphas**: list of alphas for the different sample contours plotted
  - **line_args**: a list of dict with settings for contours from each root
  - arguments for *add_colorbar()*

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=3,␣
↪nMCSamples=2)
g = plots.get_single_plotter(width_inch=4)
g.plot_3d([samples1, samples2], ['x0','x1','x2']);
```



plots_1d(*roots*, *params=None*, *legend_labels=None*, *legend_ncol=None*, *label_order=None*, *nx=None*, *param_list=None*, *roots_per_param=False*, *share_y=None*, *markers=None*, *title_limit=None*, *xlims=None*, *param_renames=None*, ***kwargs*)

Make an array of 1D marginalized density subplots

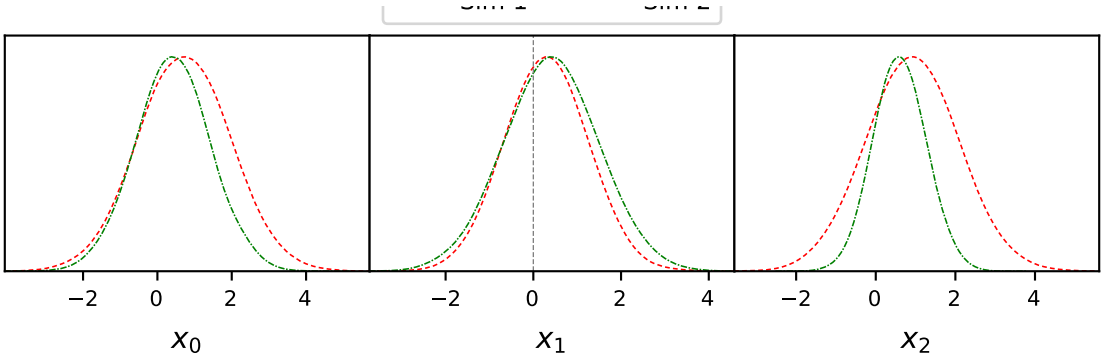
Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **params** – list of names of parameters to plot

- **legend_labels** – list of legend labels
- **legend_ncol** – Number of columns for the legend.
- **label_order** – minus one to show legends in reverse order that lines were added, or a list giving specific order of line indices
- **nx** – number of subplots per row
- **param_list** – name of .paramnames file listing specific subset of parameters to plot
- **roots_per_param** – True to use a different set of samples for each parameter: plots param[i] using roots[i] (where roots[i] is the list of sample root names to use for plotting parameter i). This is useful for example for plotting one-parameter extensions of a baseline model, each with various data combinations.
- **share_y** – True for subplots to share a common y axis with no horizontal space between subplots
- **markers** – optional dict giving vertical marker values indexed by parameter, or a list of marker values for each parameter plotted
- **title_limit** – if not None, a maginalized limit (1,2..) of the first root to print as the title of each of the plots
- **xlims** – list of [min,max] limits for the range of each parameter plot
- **param_renames** – optional dictionary holding mapping between input names and equivalent names used in the samples.
- **kwargs** – optional keyword arguments for *plot_1d()*

Returns The plot_col, plot_row subplot dimensions of the new figure

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=4,␣
↪nMCSamples=2)
g = plots.get_subplot_plotter()
g.plots_1d([samples1, samples2], ['x0', 'x1', 'x2'], nx=3, share_y=True,␣
↪legend_ncol =2,
             markers={'x1':0}, colors=['red', 'green'], ls=['--', '-.'])
```



plots_2d(*roots*, *param1=None*, *params2=None*, *param_pairs=None*, *nx=None*, *legend_labels=None*, *legend_ncol=None*, *label_order=None*, *filled=False*, *shaded=False*, ***kwargs*)

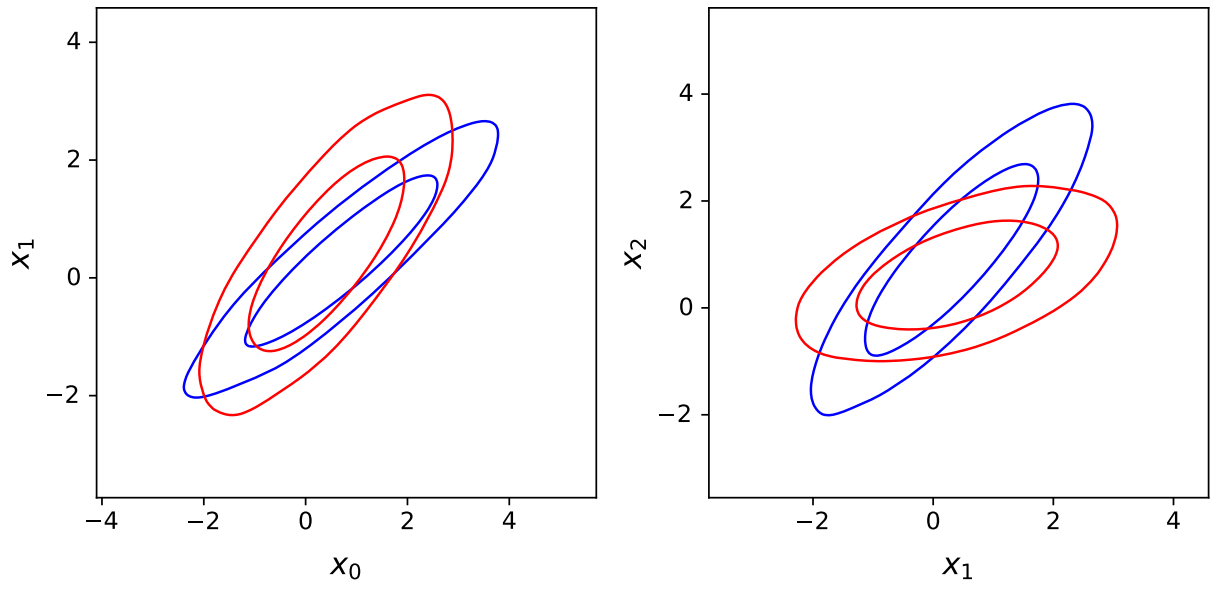
Make an array of 2D line, filled or contour plots.

Parameters

- **roots** – root name or *MCSamples* instance (or list of either of these) for the samples to plot
- **param1** – x parameter to plot
- **params2** – list of y parameters to plot against x
- **param_pairs** – list of [x,y] parameter pairs to plot; either specify param1, param2, or param_pairs
- **nx** – number of subplots per row
- **legend_labels** – The labels used for the legend.
- **legend_ncol** – The amount of columns in the legend.
- **label_order** – minus one to show legends in reverse order that lines were added, or a list giving specific order of line indices
- **filled** – True to plot filled contours
- **shaded** – True to shade by the density for the first root plotted
- **kwargs** – optional keyword arguments for *plot_2d()*

Returns The plot_col, plot_row subplot dimensions of the new figure

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=4,␣
↪nMCSamples=2)
g = plots.get_subplot_plotter(subplot_size=4)
g.settings.legend_frac_subplot_margin = 0.05
g.plots_2d([samples1, samples2], param_pairs=[['x0', 'x1'], ['x1', 'x2']],
                         nx=2, legend_ncol=2, colors=['blue', 'red'])
```



plots_2d_triplets(*root_params_triplets*, *nx=None*, *filled=False*, *x_lim=None*)

Creates an array of 2D plots, where each plot uses different samples, x and y parameters

Parameters

- **root_params_triplets** – a list of (root, x, y) giving sample root names, and x and y parameter names to plot in each subplot
- **nx** – number of subplots per row
- **filled** – True for filled contours
- **x_lim** – limits for all the x axes.

Returns The plot_col, plot_row subplot dimensions of the new figure

plots_3d(*roots*, *param_sets*, *nx=None*, *legend_labels=None*, ***kwargs*)

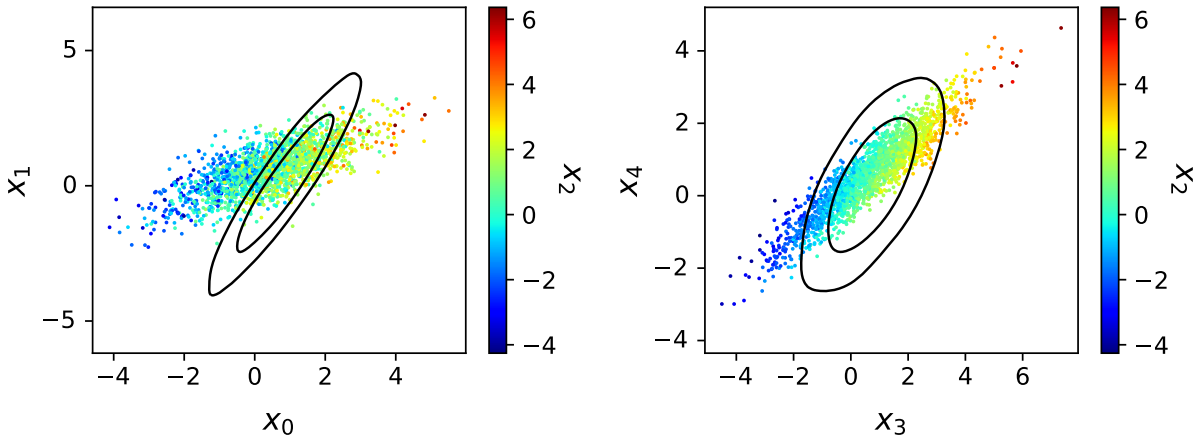
Create multiple 3D subplots

Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **param_sets** – A list of triplets of parameter names to plot [(x,y, color), (x2,y2,color2)..]
- **nx** – number of subplots per row
- **legend_labels** – list of legend labels
- **kwargs** – keyword arguments for *plot_3d()*

Returns The plot_col, plot_row subplot dimensions of the new figure

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=5,␣
↪nMCSamples=2)
g = plots.get_subplot_plotter(subplot_size=4)
g.plots_3d([samples1, samples2], [['x0', 'x1', 'x2'], ['x3', 'x4', 'x2']],␣
↪nx=2);
```



plots_3d_z(*roots*, *param_x*, *param_y*, *param_z=None*, *max_z=None*, ***kwargs*)

Make set of sample scatter subplots of param_x against param_y, each coloured by values of parameters in param_z (all if None). Any second or more samples in root are shown as contours.

Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **param_x** – x parameter name
- **param_y** – y parameter name
- **param_z** – list of parameter to names to color samples in each subplot (default: all)
- **max_z** – The maximum number of z parameters we should use.
- **kwargs** – keyword arguments for *plot_3d()*

Returns The plot_col, plot_row subplot dimensions of the new figure

rectangle_plot(*xparams*, *yparams*, *yroots=None*, *roots=None*, *plot_roots=None*, *plot_texts=None*, *xmarkers=None*, *ymarkers=None*, *marker_args=mappingproxy({})*, *param_limits=mappingproxy({})*, *legend_labels=None*, *legend_ncol=None*, *label_order=None*, ***kwargs*)

Make a grid of 2D plots.

A rectangle plot shows all x parameters plotted againts all y parameters in a grid of subplots with no spacing.

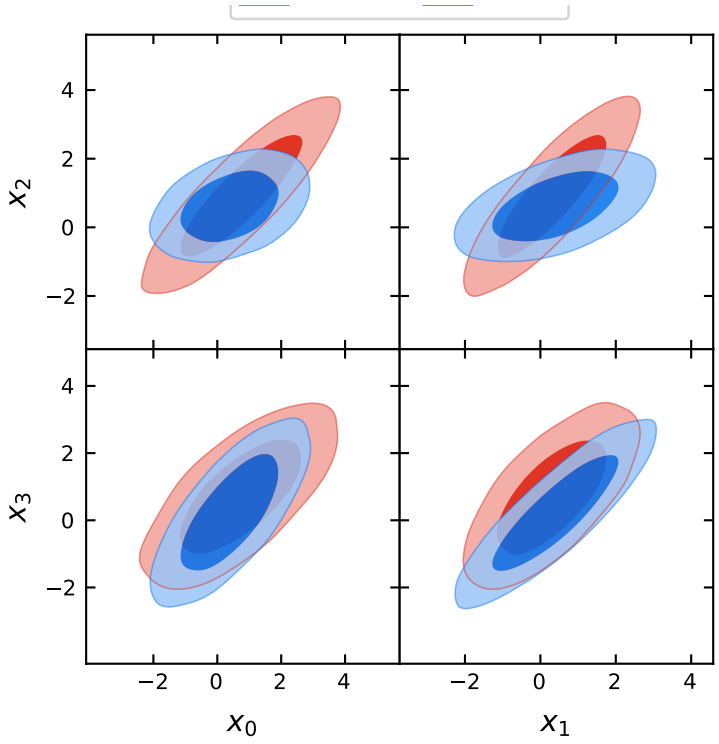
Set roots to use the same set of roots for every plot in the rectangle, or set yroots (list of list of roots) to use different set of roots for each row of the plot; alternatively plot_roots allows you to specify explicitly (via list of list of list of roots) the set of roots for each individual subplot.

Parameters

- **xparams** – list of parameters for the x axes
- **yparams** – list of parameters for the y axes
- **yroots** – (list of list of roots) allows use of different set of root names for each row of the plot; set either roots or yroots
- **roots** – list of root names or *MCSamples* instances. Uses the same set of roots for every plot in the rectangle; set either roots or yroots.
- **plot_roots** – Allows you to specify (via list of list of list of roots) the set of roots for each individual subplot
- **plot_texts** – a 2D array (or list of lists) of a text label to put in each subplot (use a None entry to skip one)
- **xmarkers** – optional dict giving vertical marker values indexed by parameter, or a list of marker values for each x parameter plotted
- **ymarkers** – optional dict giving horizontal marker values indexed by parameter, or a list of marker values for each y parameter plotted
- **marker_args** – arguments for *add_x_marker()* and *add_y_marker()*
- **param_limits** – a dictionary holding a mapping from parameter names to axis limits for that parameter
- **legend_labels** – list of labels for the legend
- **legend_ncol** – The number of columns for the legend
- **label_order** – minus one to show legends in reverse order that lines were added, or a list giving specific order of line indices
- **kwargs** – arguments for *plot_2d()*.

Returns the 2D list of Axes created

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=4,␣
↪nMCSamples=2)
g = plots.get_subplot_plotter()
g.rectangle_plot(['x0','x1'], ['x2','x3'], roots = [samples1, samples2],␣
↪filled=True)
```



rotate_xticklabels(*ax=None*, *rotation=90*, *labelsize=None*)
Rotates the x-tick labels by given rotation (degrees)

Parameters

- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **rotation** – How much to rotate in degrees.
- **labelsize** – size for tick labels (default from settings.axes_fontsize)

rotate_yticklabels(*ax=None*, *rotation=90*, *labelsize=None*)
Rotates the y-tick labels by given rotation (degrees)

Parameters

- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **rotation** – How much to rotate in degrees.
- **labelsize** – size for tick labels (default from settings.axes_fontsize)

samples_for_root(*root*, *file_root=None*, *cache=True*, *settings=None*)
Gets *MCSamples* from root name (or just return root if it is already an MCSamples instance).

Parameters

- **root** – The root name (without path, e.g. my_chains)
- **file_root** – optional full root path, by default searches in self.chain_dirs
- **cache** – if True, return cached object if already loaded
- **settings** – optional dictionary of settings to use

Returns *MCSamples* for the given root name

set_axes(*params=()*, *lims=None*, *do_xlabel=True*, *do_ylabel=True*, *no_label_no_numbers=False*, *pos=None*, *color_label_in_axes=False*, *ax=None*, ***other_args*)
Set the axis labels and ticks, and various styles. Do not usually need to call this directly.

Parameters

- **params** – [x,y] list of the *ParamInfo* for the x and y parameters to use for labels
- **lims** – optional [xmin, xmax, ymin, ymax] to fix specific limits for the axes
- **do_xlabel** – True if should include label for x axis.
- **do_ylabel** – True if should include label for y axis.
- **no_label_no_numbers** – True to hide tick labels
- **pos** – optional position of the axes [‘left’ | ‘bottom’ | ‘width’ | ‘height’]
- **color_label_in_axes** – If True, and params has at last three entries, puts text in the axis to label the third parameter
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **other_args** – Not used, just quietly ignore so that set_axes can be passed general kwargs

Returns an Axes instance

set_xlabel(*param*, *ax=None*)
Sets the label for the x axis.

Parameters

- **param** – the *ParamInfo* for the x axis parameter
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)

set_ylabel(*param*, *ax=None*, ***kwargs*)
Sets the label for the y axis.

Parameters

- **param** – the *ParamInfo* for the y axis parameter
- **ax** – optional Axes instance (or y,x subplot coordinate) to add to (defaults to current plot or the first/main plot if none)
- **kwargs** – opional extra arguments for Axes set_ylabel

show_all_settings()
Prints settings and library versions

triangle_plot(*roots*, *params=None*, *legend_labels=None*, *plot_3d_with_param=None*, *filled=False*, *shaded=False*, *contour_args=None*, *contour_colors=None*, *contour_ls=None*, *contour_lws=None*, *line_args=None*, *label_order=None*, *legend_ncol=None*, *legend_loc=None*, *title_limit=None*, *upper_roots=None*, *upper_kwargs=mappingproxy({})*, *upper_label_right=False*, *diag1d_kwargs=mappingproxy({})*, *markers=None*, *marker_args=mappingproxy({})*, *param_limits=mappingproxy({})*, ***kwargs*)

Make a trianglular array of 1D and 2D plots.

A triangle plot is an array of subplots with 1D plots along the diagonal, and 2D plots in the lower corner. The upper triangle can also be used by setting upper_roots.

Parameters

- **roots** – root name or *MCSamples* instance (or list of any of either of these) for the samples to plot
- **params** – list of parameters to plot (default: all, can also use glob patterns to match groups of parameters)
- **legend_labels** – list of legend labels
- **plot_3d_with_param** – for the 2D plots, make sample scatter plot, with samples colored by this parameter name (to make a '3D' plot)
- **filled** – True for filled contours
- **shaded** – plot shaded density for first root (cannot be used with filled)
- **contour_args** – optional dict (or list of dict) with arguments for each 2D plot (e.g. specifying color, alpha, etc)
- **contour_colors** – list of colors for plotting contours (for each root)
- **contour_ls** – list of Line styles for contours (for each root)
- **contour_lws** – list of Line widths for contours (for each root)
- **line_args** – dict (or list of dict) with arguments for each 2D plot (e.g. specifying ls, lw, color, etc)
- **label_order** – minus one to show legends in reverse order that lines were added, or a list giving specific order of line indices
- **legend_ncol** – The number of columns for the legend
- **legend_loc** – The location for the legend
- **title_limit** – if not None, a maginalized limit (1,2..) to print as the title of the first root on the diagonal 1D plots
- **upper_roots** – set to fill the upper triangle with subplots using this list of sample root names
- **upper_kwargs** – dict for same-named arguments for use when making upper-triangle 2D plots (contour_colors, etc). Set show_1d=False to not add to the diagonal.
- **upper_label_right** – when using upper_roots whether to label the y axis on the top-right axes (splits labels between left and right, but avoids labelling 1D y axes top left)
- **diag1d_kwargs** – list of dict for arguments when making 1D plots on grid diagonal

- **markers** – optional dict giving marker values indexed by parameter, or a list of marker values for each parameter plotted
- **marker_args** – dictionary of optional arguments for adding markers (passed to axvline and/or axhline)
- **param_limits** – a dictionary holding a mapping from parameter names to axis limits for that parameter
- **kwargs** – optional keyword arguments for *plot_2d()* or *plot_3d()* (lower triangle only)

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=4,␣
↪nMCSamples=2)
g = plots.get_subplot_plotter()
g.triangle_plot([samples1, samples2], filled=True, legend_labels = ['Contour␣
↪1', 'Contour 2'])
```

```
from getdist import plots, gaussian_mixtures
samples1, samples2 = gaussian_mixtures.randomTestMCSamples(ndim=4,␣
↪nMCSamples=2)
g = plots.get_subplot_plotter()
g.triangle_plot([samples1, samples2], ['x0','x1','x2'], plot_3d_with_param=
↪'x3')
```

class getdist.plots.**MCSampleAnalysis**(*chain_locations*, *settings=None*)

A class that loads and analyses samples, mapping root names to *MCSamples* objects with caching. Typically accessed as the instance stored in plotter.sample_analyser, for example to get an *MCSamples* instance from a root name being used by a plotter, use plotter.sample_analyser.samples_for_root(name).

Parameters

- **chain_locations** – either a directory or the path of a grid of runs; it can also be a list of such, which is searched in order
- **settings** – Either an *IniFile* instance, the name of an .ini file, or a dict holding sample analysis settings.

add_chain_dir(*chain_dir*)

Adds a new chain directory or grid path for searching for samples

Parameters **chain_dir** – The root directory to add

add_root(*file_root*)

Add a root file for some new samples

Parameters **file_root** – Either a file root name including path or a `RootInfo` instance

Returns *MCSamples* instance for given root file.

add_roots(*roots*)

A wrapper for add_root that adds multiple file roots

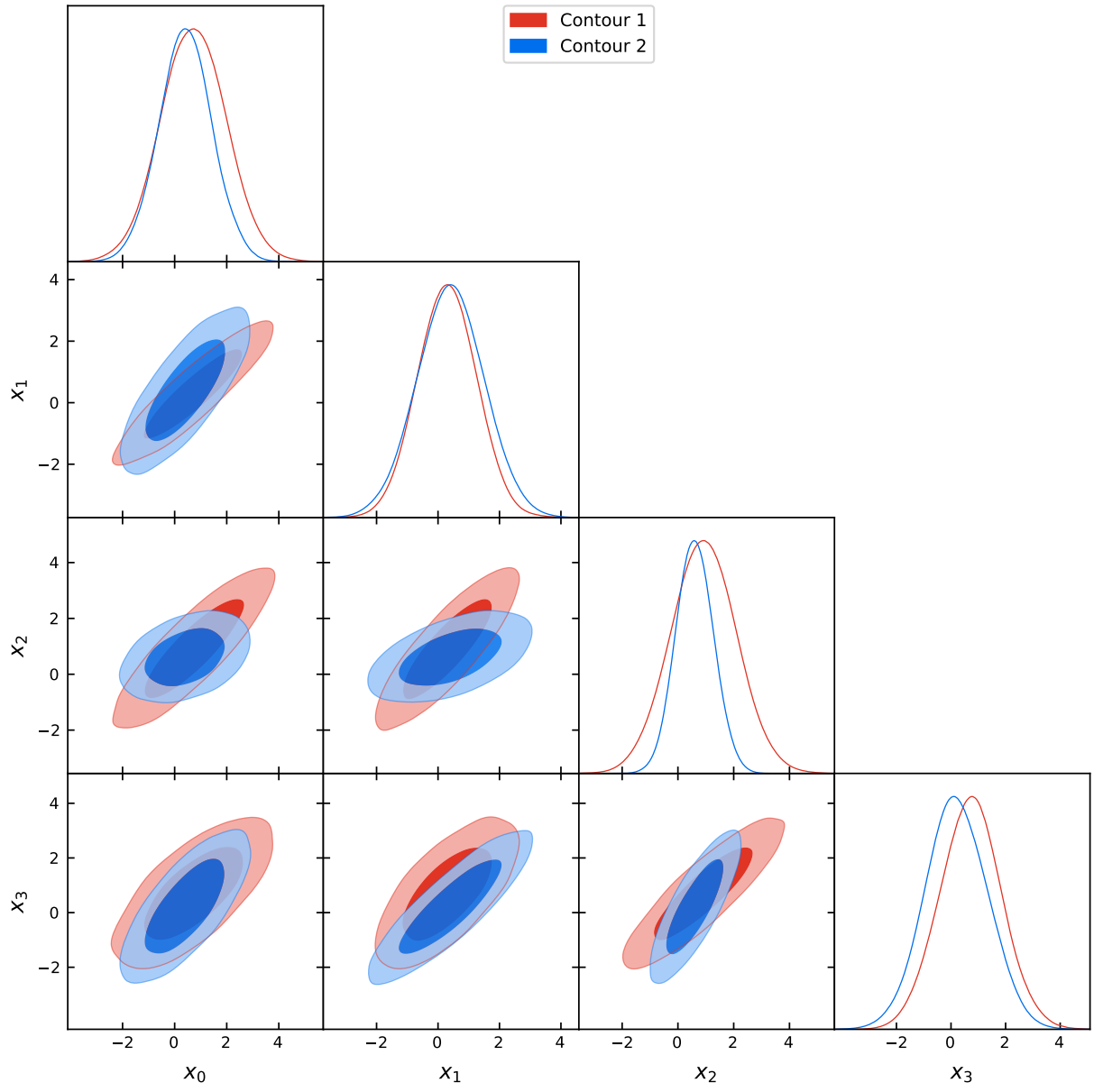
Parameters **roots** – An iterable containing filenames or `RootInfo` objects to add

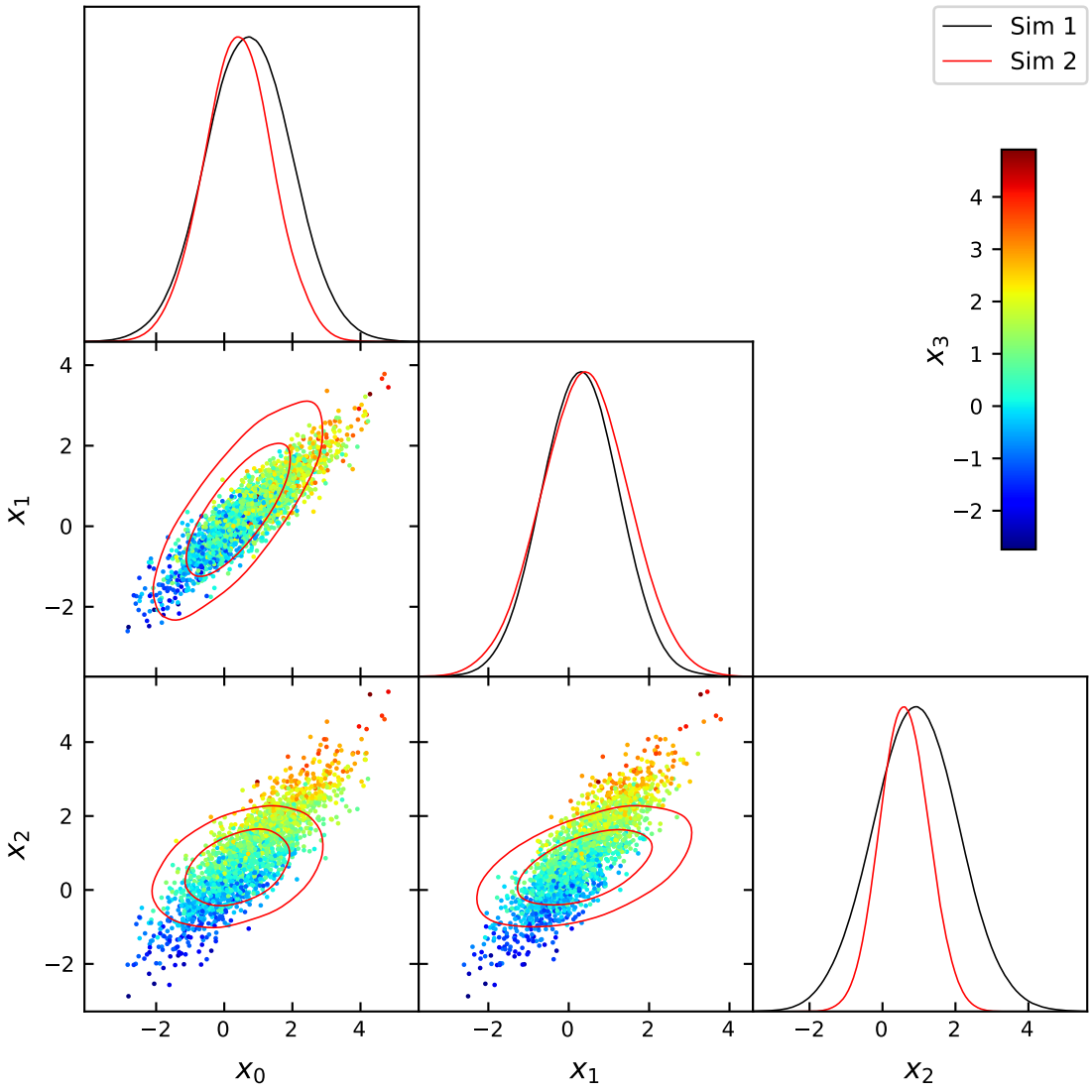
bounds_for_root(*root*)

Returns an object with get_upper/getUpper and get_lower/getLower to get hard prior bounds for given root name

Parameters **root** – The root name to use.

Returns object with get_upper() or getUpper() and get_lower() or getLower() functions


Contour 1
Contour 2
x_0
x_1
x_2
x_3


Sim 1
Sim 2
x_3
4
3
2
1
0
−1
−2
x_0
x_1
x_2
−2
0
2
4

get_density(*root*, *param*, *likes=False*)
Get *Density1D* for given root name and parameter

Parameters

- **root** – The root name of the samples to use
- **param** – name of the parameter
- **likes** – whether to include mean likelihood in density.likes

Returns *Density1D* instance with 1D marginalized density

get_density_grid(*root*, *param1*, *param2*, *conts=2*, *likes=False*)
Get 2D marginalized density for given root name and parameters

Parameters

- **root** – The root name for samples to use.
- **param1** – x parameter
- **param2** – y parameter
- **conts** – number of contour levels (up to maximum calculated using contours in analysis settings)
- **likes** – whether to include mean likelihoods

Returns *Density2D* instance with marginalized density

load_single_samples(*root*)
Gets a set of unit weight samples for given root name, e.g. for making sample scatter plot

Parameters **root** – The root name to use.

Returns array of unit weight samples

params_for_root(*root*, *label_params=None*)
Returns a *ParamNames* with names and labels for parameters used by samples with a given root name.

Parameters

- **root** – The root name of the samples to use.
- **label_params** – optional name of .paramnames file containing labels to use for plots, overriding default

Returns *ParamNames* instance

remove_root(*root*)
Remove a given root file (does not delete it)

Parameters **root** – The root name to remove

reset(*settings=None*, *chain_settings_have_priority=True*)
Resets the caches, starting afresh optionally with new analysis settings

Parameters

- **settings** – Either an *IniFile* instance, the name of an .ini file, or a dict holding sample analysis settings.
- **chain_settings_have_priority** – whether to prioritize settings saved with the chain

samples_for_root(*root*, *file_root=None*, *cache=True*, *settings=None*)
Gets *MCSamples* from root name (or just return root if it is already an MCSamples instance).

Parameters

- **root** – The root name (without path, e.g. my_chains)
- **file_root** – optional full root path, by default searches in self.chain_dirs
- **cache** – if True, return cached object if already loaded
- **settings** – optional dictionary of settings to use

Returns *MCSamples* for the given root name

getdist.plots.**add_plotter_style**(*name*, *cls*, *activate=False*)

Add a plotting style, consistenting of style name and a class type to use when making plotter instances.

Parameters

- **name** – name for the style
- **cls** – a class inherited from *GetDistPlotter*
- **activate** – whether to make it the active style

getdist.plots.**get_plotter**(*style=None*, ***kwargs*)

Creates a new plotter and returns it

Parameters

- **style** – name of a plotter style (associated with custom plotter class/settings), otherwise uses active
- **kwargs** – arguments for the style's *GetDistPlotter*

Returns The *GetDistPlotter* instance

getdist.plots.**get_single_plotter**(*ratio=None*, *width_inch=None*, *scaling=None*, *rc_sizes=False*, *style=None*, ***kwargs*)

Get a *GetDistPlotter* for making a single plot of fixed width.

For a half-column plot for a paper use width_inch=3.464.

Use this or *get_subplot_plotter()* to make a *GetDistPlotter* instance for making plots. This function will use the active style by default, which will determine defaults for the various optional parameters (see *set_active_style()*).

Parameters

- **ratio** – The ratio between height and width.
- **width_inch** – The width of the plot in inches
- **scaling** – whether to scale down fonts and line widths for small subplot axis sizes (relative to reference sizes, 3.5 inch)
- **rc_sizes** – set default font sizes from matplotlib's current rcParams if no explicit settings passed in kwargs
- **style** – name of a plotter style (associated with custom plotter class/settings), otherwise uses active
- **kwargs** – arguments for *GetDistPlotter*

Returns The *GetDistPlotter* instance

getdist.plots.**get_subplot_plotter**(*subplot_size=None*, *width_inch=None*, *scaling=None*, *rc_sizes=False*, *subplot_size_ratio=None*, *style=None*, ***kwargs*)

Get a *GetDistPlotter* for making an array of subplots.

If width_inch is None, just makes plot as big as needed for given subplot_size, otherwise fixes total width and sets default font sizes etc. from matplotlib's default rcParams.

Use this or *get_single_plotter()* to make a *GetDistPlotter* instance for making plots. This function will use the active style by default, which will determine defaults for the various optional parameters (see *set_active_style()*).

Parameters

- **subplot_size** – The size of each subplot in inches
- **width_inch** – Optional total width in inches
- **scaling** – whether to scale down fonts and line widths for small sizes (relative to reference sizes, 3.5 inch)
- **rc_sizes** – set default font sizes from matplotlib's current rcParams if no explicit settings passed in kwargs
- **subplot_size_ratio** – ratio of height to width for subplots
- **style** – name of a plotter style (associated with custom plotter class/settings), otherwise uses active
- **kwargs** – arguments for *GetDistPlotter*

Returns The *GetDistPlotter* instance

getdist.plots.**set_active_style**(*name=None*)

Set an active style name. Each style name is associated with a *GetDistPlotter* class used to generate plots, with optional custom plot settings and rcParams. The corresponding style module must have been loaded before using this.

Note that because style modules can change rcParams, which is a global parameter, in general style settings are changed globally until changed back. But if your style does not change rcParams then you can also just pass a style name parameter when you make a plot instance.

The supplied example styles are 'default', 'tab10' (default matplotlib color scheme) and 'planck' (more compilcated example using latex and various customized settings). Use *add_plotter_style()* to add your own style class.

Parameters **name** – name of the style, or none to revert to default

Returns the previously active style name

See also:

CHAPTER 5

Analysis settings

Samples are analysed using various analysis settings. These can be specified from a .ini file or overridden using a dictionary.

Default settings from analysis_defaults.ini:

```
#For disgarding burn-in if using raw chains
#if < 1 interpreted as a fraction of the total number of rows (0.3 ignores first 30%␣
↪of lines)
#(ignored when parameter grid or chain .properties.ini settings are explicitly set)
ignore_rows = 0

#Minimum-weight sample to keep, as ratio to the maximum weight sample.
#This avoids very wide ranges of parameters (much wider than the posterior), e.g.␣
↪when using nested sampling
min_weight_ratio =  1e-30

#Confidence limits for marginalized constraints.
#Also used for 2D plots, but only number set by plot settings actually shown
contours = 0.68 0.95 0.99

#If the distribution is skewed, so two probability of tails differs by more
#than credible_interval_threshold of the peak value, use equal-probability limits
#rather than integrating inwards equally at both tails.
#Note credible interval depends on density estimation parameters
credible_interval_threshold = 0.05

#Determine bounds from projected ND confidence range for contours[ND_contour_range]
#If -1 use bounds determined entirely from 1D marginalized densities
#Use 0 or 1 if 2D plot contours are hitting edges
range_ND_contour = -1

#1D marginalized confidence limit to use to determine parameter ranges
range_confidence = 0.001

#Confidence limit to use for convergence tests (splits and Raftery Lewis)
```

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```
converge_test_limit = 0.95

#Sample binning for 1D plots
fine_bins = 1024

#if -1: set optimized smoothing bandwidth automatically for each parameter
#if >= 1: smooth by smooth_scale_1D bin widths
#if > 0  and <1: smooth by Gaussian of smooth_scale_1D standard deviations in each␣
↪parameter
#                (around 0.2-0.5 is often good)
#if < 0: automatic, with the overall smoothing length scaled by abs(smooth_scale_1D)␣
↪from default
smooth_scale_1D =-1

#0 is basic normalization correction
#1 is linear boundary kernel (should get gradient correct)
#2 is a higher order kernel, that also affects estimates way from the boundary (1D␣
↪only)
boundary_correction_order=1

#Correct for (over-smoothing) biases using multiplicative bias correction
#i.e. by interating estimates using the re-weighted 'flattened' bins
#Note that automatic bandwidth accounts for this by increasing the smoothing scale
#as mult_bias_correction_order increases (may not converge for large values).
mult_bias_correction_order = 1

#if -1: automatic optimized bandwidth matrix selection
#if >= 1: smooth by smooth_scale_2D bin widths
#if > 0  and <1: smooth by Gaussian of smooth_scale_2D standard deviations in each␣
↪parameter
#                (around 0.3-0.7 is often good)
#if < 0: automatic, with the overall smoothing length scaled by abs(smooth_scale_2D)␣
↪from default
smooth_scale_2D = -1

#maximum correlation ellipticity to allow for 2D kernels. Set to 0 to force non-
↪elliptical.
max_corr_2D = 0.99

#sample binning in each direction for 2D plotting
fine_bins_2D = 256

#Whether to use 2D-specific rough estimate of the effective number of samples when␣
↪estimating
#2D densities
use_effective_samples_2D = F

#maximum number of points for 3D plots
max_scatter_points = 2000

#output bins for 1D plotting (only for getdist output to files, or scale if smooth_
↪scale_2D>1)
num_bins = 100

#output bins for 2D plotting (not used, just scale if smooth_scale_2D>1)
num_bins_2D=40
```

You can also change the default analysis settings file by setting the GETDIST_CONFIG environment variable to the location of a config.ini file, where config.ini contains a default_getdist_settings parameter set to the name of the ini file you want to use instead.

Other main modules:

CHAPTER 6

getdist.chains

class getdist.chains.**Chains**(*root=None*, *jobItem=None*, *paramNamesFile=None*, *names=None*, *labels=None*, *renames=None*, *sampler=None*, ***kwargs*)

Holds one or more sets of weighted samples, for example a set of MCMC chains. Inherits from *WeightedSamples*, also adding parameter names and labels

Variables **paramNames** – a *ParamNames* instance holding the parameter names and labels

Parameters

- **root** – optional root name for files
- **jobItem** – optional jobItem for parameter grid item. Should have jobItem.chainRoot and jobItem.batchPath
- **paramNamesFile** – optional filename of a .paramnames files that holds parameter names
- **names** – optional list of names for the parameters
- **labels** – optional list of latex labels for the parameters
- **renames** – optional dictionary of parameter aliases
- **sampler** – string describing the type of samples (default :mcmc); if "nested" or "uncorrelated" the effective number of samples is calculated using uncorrelated approximation
- **kwargs** – extra options for *WeightedSamples*'s constructor

addDerived(*paramVec*, *name*, ***kwargs*)

Adds a new parameter

Parameters

- **paramVec** – The vector of parameter values to add.
- **name** – The name for the new parameter
- **kwargs** – arguments for paramnames' `paramnames.ParamList.addDerived()`

Returns The added parameter's *ParamInfo* object

deleteFixedParams()
Delete parameters that are fixed (the same value in all samples)

filter(*where*)
Filter the stored samples to keep only samples matching filter

Parameters **where** – list of sample indices to keep, or boolean array filter (e.g. x>5 to keep only samples where x>5)

getGelmanRubin(*nparam=None*, *chainlist=None*)
Assess the convergence using the maximum var(mean)/mean(var) of orthogonalized parameters c.f. Brooks and Gelman 1997.

Parameters

- **nparam** – The number of parameters, by default uses all
- **chainlist** – list of *WeightedSamples*, the samples to use. Defaults to all the separate chains in this instance.

Returns The worst var(mean)/mean(var) for orthogonalized parameters. Should be <<1 for good convergence.

getGelmanRubinEigenvalues(*nparam=None*, *chainlist=None*)
Assess convergence using var(mean)/mean(var) in the orthogonalized parameters c.f. Brooks and Gelman 1997.

Parameters

- **nparam** – The number of parameters (starting at first), by default uses all of them
- **chainlist** – list of *WeightedSamples*, the samples to use. Defaults to all the separate chains in this instance.

Returns array of var(mean)/mean(var) for orthogonalized parameters

getParamNames()
Get *ParamNames* object with names for the parameters

Returns *ParamNames* object giving parameter names and labels

getParamSampleDict(*ix*, *want_derived=True*)
Returns a dictionary of parameter values for sample number ix

Parameters

- **ix** – sample index
- **want_derived** – include derived parameters

Returns ordered dictionary of parameter values

getParams()
Creates a *ParSamples* object, with variables giving vectors for all the parameters, for example samples.getParams().name1 would be the vector of samples with name 'name1'

Returns A *ParSamples* object containing all the parameter vectors, with attributes given by the parameter names

getRenames()
Gets dictionary of renames known to each parameter.

getSeparateChains()
Gets a list of samples for separate chains. If the chains have already been combined, uses the stored sample offsets to reconstruct the array (generally no array copying)

Returns The list of *WeightedSamples* for each chain.

loadChains(*root, files_or_samples: Sequence[T_co], weights=None, loglikes=None, ignore_lines=None*)
Loads chains from files.

Parameters

- **root** – Root name
- **files_or_samples** – list of file names or list of arrays of samples, or single array of samples
- **weights** – if loading from arrays of samples, corresponding list of arrays of weights
- **loglikes** – if loading from arrays of samples, corresponding list of arrays of -2 log(likelihood)
- **ignore_lines** – Amount of lines at the start of the file to ignore, None if should not ignore

Returns True if loaded successfully, False if none loaded

makeSingle()
Combines separate chains into one samples array, so self.samples has all the samples and this instance can then be used as a general *WeightedSamples* instance.

Returns self

removeBurnFraction(*ignore_frac*)
Remove a fraction of the samples as burn in

Parameters **ignore_frac** – fraction of sample points to remove from the start of the samples, or each chain if not combined

saveAsText(*root*, *chain_index=None*, *make_dirs=False*)
Saves the samples as text files, including parameter names as .paramnames file.

Parameters

- **root** – The root name to use
- **chain_index** – Optional index to be used for the filename, zero based, e.g. for saving one of multiple chains
- **make_dirs** – True if this should (recursively) create the directory if it doesn't exist

savePickle(*filename*)
Save the current object to a file in pickle format

Parameters **filename** – The file to write to

saveTextMetadata(*root*)
Saves metadata about the sames to text files with given file root

Parameters **root** – root file name

setParamNames(*names=None*)
Sets the names of the params.

Parameters **names** – Either a *ParamNames* object, the name of a .paramnames file to load, a list of name strings, otherwise use default names (param1, param2...).

setParams(*obj*)
Adds array variables obj.name1, obj.name2 etc, where obj.name1 is the vector of samples with name 'name1'

if a parameter name is of the form aa.bb.cc, it makes subobjects so you can reference obj.aa.bb.cc

Parameters **obj** – The object instance to add the parameter vectors variables

Returns The obj after alterations.

updateBaseStatistics()
Updates basic computed statistics for this chain, e.g. after any changes to the samples or weights

Returns self after updating statistics.

updateRenames(*renames*)
Updates the renames known to each parameter with the given dictionary of renames.

class getdist.chains.**ParSamples**
An object used as a container for named parameter sample arrays

class getdist.chains.**ParamConfidenceData**(*paramVec*, *norm*, *indexes*, *cumsum*)
Create new instance of ParamConfidenceData(paramVec, norm, indexes, cumsum)

cumsum
Alias for field number 3

indexes
Alias for field number 2

norm
Alias for field number 1

paramVec
Alias for field number 0

exception getdist.chains.**ParamError**
An Exception that indicates a bad parameter.

exception getdist.chains.**WeightedSampleError**
An exception that is raised when a WeightedSamples error occurs

class getdist.chains.**WeightedSamples**(*filename=None*, *ignore_rows=0*, *samples=None*, *weights=None*, *loglikes=None*, *name_tag=None*, *label=None*, *files_are_chains=True*, *min_weight_ratio=1e-30*)
WeightedSamples is the base class for a set of weighted parameter samples

Variables

- **weights** – array of weights for each sample (default: array of 1)
- **loglikes** – array of -log(Likelihoods) for each sample (default: array of 0)
- **samples** – n_samples x n_parameters numpy array of parameter values
- **n** – number of parameters
- **numrows** – number of samples positions (rows in the samples array)
- **name_tag** – name tag for the samples

Parameters

- **filename** – A filename of a plain text file to load from
- **ignore_rows** –

  - if int >=1: The number of rows to skip at the file in the beginning of the file
  - if float <1: The fraction of rows to skip at the beginning of the file
- **samples** – array of parameter values for each sample, passed to *setSamples()*
- **weights** – array of weights
- **loglikes** – array of -log(Likelihood)
- **name_tag** – The name of this instance.
- **label** – latex label for these samples
- **files_are_chains** – use False if the samples file (filename) does not start with two columns giving weights and -log(Likelihoods)
- **min_weight_ratio** – remove samples with weight less than min_weight_ratio times the maximum weight

changeSamples(*samples*)
Sets the samples without changing weights and loglikes.

Parameters **samples** – The samples to set

confidence(*paramVec*, *limfrac*, *upper=False*, *start=0*, *end=None*, *weights=None*)
Calculate sample confidence limits, not using kernel densities just counting samples in the tails

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **limfrac** – fraction of samples in the tail, e.g. 0.05 for a 95% one-tail limit, or 0.025 for a 95% two-tail limit
- **upper** – True to get upper limit, False for lower limit
- **start** – Start index for the vector to use
- **end** – The end index, use None to go all the way to the end of the vector.
- **weights** – numpy array of weights for each sample, by default self.weights

Returns confidence limit (parameter value when limfac of samples are further in the tail)

cool(*cool*)
Cools the samples, i.e. multiples log likelihoods by cool factor and re-weights accordingly

Parameters **cool** – cool factor

corr(*pars=None*)
Get the correlation matrix

Parameters **pars** – If specified, list of parameter vectors or int indices to use

Returns The correlation matrix.

cov(*pars=None*, *where=None*)
Get parameter covariance

Parameters

- **pars** – if specified, a list of parameter vectors or int indices to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns The covariance matrix

deleteFixedParams()
Removes parameters that do not vary (are the same in all samples)

Returns tuple (list of fixed parameter indices that were removed, fixed values)

deleteZeros()
Removes samples with zero weight

filter(*where*)
Filter the stored samples to keep only samples matching filter

Parameters **where** – list of sample indices to keep, or boolean array filter (e.g. x>5 to keep only samples where x>5)

getAutocorrelation(*paramVec*, *maxOff=None*, *weight_units=True*, *normalized=True*)
Gets auto-correlation of an array of parameter values (e.g. for correlated samples from MCMC)

By default uses weight units (i.e. standard units for separate samples from original chain). If samples are made from multiple chains, neglects edge effects.

Parameters

- **paramVec** – an array of parameter values, or the int index of the parameter in stored samples to use
- **maxOff** – maximum autocorrelation distance to return
- **weight_units** – False to get result in sample point (row) units; weight_units=False gives standard definition for raw chains
- **normalized** – Set to False to get covariance (note even if normalized, corr[0]<>1 in general unless weights are unity).

Returns zero-based array giving auto-correlations

getCorrelationLength(*j*, *weight_units=True*, *min_corr=0.05*, *corr=None*)
Gets the auto-correlation length for parameter j

Parameters

- **j** – The index of the parameter to use
- **weight_units** – False to get result in sample point (row) units; weight_units=False gives standard definition for raw chains
- **min_corr** – specifies a minimum value of the autocorrelation to use, e.g. where sampling noise is typically as large as the calculation
- **corr** – The auto-correlation array to use, calculated internally by default using *getAutocorrelation()*

Returns the auto-correlation length

getCorrelationMatrix()
Get the correlation matrix of all parameters

Returns The correlation matrix

getCov(*nparam=None*, *pars=None*)
Get covariance matrix of the parameters. By default uses all parameters, or can limit to max number or list.

Parameters

- **nparam** – if specified, only use the first nparam parameters

- **pars** – if specified, a list of parameter indices (0,1,2..) to include

Returns covariance matrix.

getEffectiveSamples(*j=0*, *min_corr=0.05*)

Gets effective number of samples N_eff so that the error on mean of parameter j is sigma_j/N_eff

Parameters

- **j** – The index of the param to use.
- **min_corr** – the minimum value of the auto-correlation to use when estimating the correlation length

getEffectiveSamplesGaussianKDE(*paramVec*, *h=0.2*, *scale=None*, *maxoff=None*, *min_corr=0.05*)

Roughly estimate an effective sample number for use in the leading term for the MISE (mean integrated squared error) of a Gaussian-kernel KDE (Kernel Density Estimate). This is used for optimizing the kernel bandwidth, and though approximate should be better than entirely ignoring sample correlations, or only counting distinct samples.

Uses fiducial assumed kernel scale h; result does depend on this (typically by factors O(2))

For bias-corrected KDE only need very rough estimate to use in rule of thumb for bandwidth.

In the limit h-> 0 (but still >0) answer should be correct (then just includes MCMC rejection duplicates). In reality correct result for practical h should depends on shape of the correlation function.

If self.sampler is 'nested' or 'uncorrelated' return result for uncorrelated samples.

Parameters

- **paramVec** – parameter array, or int index of parameter to use
- **h** – fiducial assumed kernel scale.
- **scale** – a scale parameter to determine fiducial kernel width, by default the parameter standard deviation
- **maxoff** – maximum value of auto-correlation length to use
- **min_corr** – ignore correlations smaller than this auto-correlation

Returns A very rough effective sample number for leading term for the MISE of a Gaussian KDE.

getEffectiveSamplesGaussianKDE_2d(*i*, *j*, *h=0.3*, *maxoff=None*, *min_corr=0.05*)

Roughly estimate an effective sample number for use in the leading term for the 2D MISE. If self.sampler is 'nested' or 'uncorrelated' return result for uncorrelated samples.

Parameters

- **i** – parameter array, or int index of first parameter to use
- **j** – parameter array, or int index of second parameter to use
- **h** – fiducial assumed kernel scale.
- **maxoff** – maximum value of auto-correlation length to use
- **min_corr** – ignore correlations smaller than this auto-correlation

Returns A very rough effective sample number for leading term for the MISE of a Gaussian KDE.

getLabel()

Return the latex label for the samples

Returns the label

getMeans(*pars=None*)
Gets the parameter means, from saved array if previously calculated.

Parameters **pars** – optional list of parameter indices to return means for

Returns numpy array of parameter means

getName()
Returns the name tag of these samples.

Returns The name tag

getSignalToNoise(*params*, *noise=None*, *R=None*, *eigs_only=False*)
Returns w, M, where w is the eigenvalues of the signal to noise (small y better constrained)

Parameters

- **params** – list of parameters indices to use
- **noise** – noise matrix
- **R** – rotation matrix, defaults to inverse of Cholesky root of the noise matrix
- **eigs_only** – only return eigenvalues

Returns w, M, where w is the eigenvalues of the signal to noise (small y better constrained)

getVars()
Get the parameter variances

Returns A numpy array of variances.

get_norm(*where=None*)
gets the normalization, the sum of the sample weights: sum_i w_i

Parameters **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns normalization

initParamConfidenceData(*paramVec*, *start=0*, *end=None*, *weights=None*)
Initialize cache of data for calculating confidence intervals

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **start** – The sample start index to use
- **end** – The sample end index to use, use None to go all the way to the end of the vector
- **weights** – A numpy array of weights for each sample, defaults to self.weights

Returns *ParamConfidenceData* instance

mean(*paramVec*, *where=None*)
Get the mean of the given parameter vector.

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns parameter mean

mean_diff(*paramVec*, *where=None*)
Calculates an array of differences between a parameter vector and the mean parameter value

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns array of p_i - mean(p_i)

mean_diffs(*pars: Union[None*, *int*, *Sequence[T_co]] = None*, *where=None*) → Sequence[T_co]
Calculates a list of parameter vectors giving distances from parameter means

Parameters

- **pars** – if specified, list of parameter vectors or int parameter indices to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns list of arrays p_i-mean(p-i) for each parameter

random_single_samples_indices()
Returns an array of sample indices that give a list of weight-one samples, by randomly selecting samples depending on the sample weights

Returns array of sample indices

removeBurn(*remove=0.3*)
removes burn in from the start of the samples

Parameters **remove** – fraction of samples to remove, or if int >1, the number of sample rows to remove

reweightAddingLogLikes(*logLikes*)
Importance sample the samples, by adding logLike (array of -log(likelihood values) to the currently stored likelihoods, and re-weighting accordingly, e.g. for adding a new data constraint

Parameters **logLikes** – array of -log(likelihood) for each sample to adjust

saveAsText(*root*, *chain_index=None*, *make_dirs=False*)
Saves the samples as text files

Parameters

- **root** – The root name to use
- **chain_index** – Optional index to be used for the samples' filename, zero based, e.g. for saving one of multiple chains
- **make_dirs** – True if this should create the directories if necessary.

setColData(*coldata*, *are_chains=True*)
Set the samples given an array loaded from file

Parameters

- **coldata** – The array with columns of [weights, -log(Likelihoods)] and sample parameter values
- **are_chains** – True if coldata starts with two columns giving weight and -log(Likelihood)

setDiffs()
saves self.diffs array of parameter differences from the y, e.g. to later calculate variances etc.

Returns array of differences

setMeans()
Calculates and saves the means of the samples

Returns numpy array of parameter means

setMinWeightRatio(*min_weight_ratio=1e-30*)
Removes samples with weight less than min_weight_ratio times the maximum weight

Parameters **min_weight_ratio** – minimum ratio to max to exclude

setSamples(*samples*, *weights=None*, *loglikes=None*, *min_weight_ratio=None*)
Sets the samples from numpy arrays

Parameters

- **samples** – The samples values, n_samples x n_parameters numpy array, or can be a list of parameter vectors
- **weights** – Array of weights for each sample. Defaults to 1 for all samples if unspecified.
- **loglikes** – Array of -log(Likelihood) values for each sample
- **min_weight_ratio** – remove samples with weight less than min_weight_ratio of the maximum

std(*paramVec*, *where=None*)
Get the standard deviation of the given parameter vector.

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns parameter standard deviation.

thin(*factor*)
Thin the samples by the given factor, giving set of samples with unit weight

Parameters **factor** – The factor to thin by

thin_indices(*factor*, *weights=None*)
Indices to make single weight 1 samples. Assumes integer weights.

Parameters

- **factor** – The factor to thin by, should be int.
- **weights** – The weights to thin, None if this should use the weights stored in the object.

Returns array of indices of samples to keep

twoTailLimits(*paramVec*, *confidence*)
Calculates two-tail equal-area confidence limit by counting samples in the tails

Parameters

- **paramVec** – array of parameter values or int index of parameter to use

- **confidence** – confidence limit to calculate, e.g. 0.95 for 95% confidence

Returns min, max values for the confidence interval

var(*paramVec*, *where=None*)
Get the variance of the given parameter vector.

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns parameter variance

weighted_sum(*paramVec*, *where=None*)
Calculates the weighted sum of a parameter vector, sum_i w_i p_i

Parameters

- **paramVec** – array of parameter values or int index of parameter to use
- **where** – if specified, a filter for the samples to use (where x>=5 would mean only process samples with x>=5).

Returns weighted sum

weighted_thin(*factor*)
Thin the samples by the given factor, preserving the weights. This function also preserves separate chains.

Parameters **factor** – The (integer) factor to thin by

getdist.chains.**chainFiles**(*root*, *chain_indices=None*, *ext='.txt'*, *separator='_'*, *first_chain=0*, *last_chain=-1*, *chain_exclude=None*)
Creates a list of file names for samples given a root name and optional filters

Parameters

- **root** – Root name for files (no extension)
- **chain_indices** – If True, only indexes inside the list included, If False, includes all indexes.
- **ext** – extension for files
- **separator** – separator character used to indicate chain number (usually _ or .)
- **first_chain** – The first index to include.
- **last_chain** – The last index to include.
- **chain_exclude** – A list of indexes to exclude, None to include all

Returns The list of file names

getdist.chains.**covToCorr**(*cov*, *copy=True*)
Convert covariance matrix to correlation matrix

Parameters

- **cov** – The covariance matrix to work on
- **copy** – True if we shouldn't modify the input matrix, False otherwise.

Returns correlation matrix

getdist.chains.**findChainFileRoot**(*chain_dir*, *root*, *search_subdirectories=True*)
Finds chain files with name root somewhere under chain_dir directory tree. root can also be a relative path relaqtive to chain_dir, or have leading directories as needed to make unique

Parameters

- **chain_dir** – root directory of hierarchy of directories to look in
- **root** – root name for the chain
- **search_subdirectories** – recursively look in subdirectories under chain_dir

Returns full path and root if found, otherwise None

getdist.chains.**getSignalToNoise**(*C*, *noise=None*, *R=None*, *eigs_only=False*)
Returns w, M, where w is the eigenvalues of the signal to noise (small y better constrained)

Parameters

- **C** – covariance matrix
- **noise** – noise matrix
- **R** – rotation matrix, defaults to inverse of Cholesky root of the noise matrix
- **eigs_only** – only return eigenvalues

Returns eigenvalues and matrix

getdist.chains.**last_modified**(*files*)
Returns the the latest "last modified" time for the given list of files. Ignores files that do not exist.

Parameters **files** – An iterable of file names.

Returns The latest "last modified" time

getdist.chains.**loadNumpyTxt**(*fname*, *skiprows=None*)
Utility routine to loads numpy array from file. Uses faster pandas read routine if pandas is installed, or falls back to numpy's loadtxt otherwise

Parameters

- **fname** – The file to load
- **skiprows** – The number of rows to skip at the begging of the file

Returns numpy array of the data values

CHAPTER 7

getdist.chains_tension

CHAPTER 8

getdist.covmat

class getdist.covmat.**CovMat**(*filename=''*, *matrix=None*, *paramNames=None*)

Class holding a covariance matrix for some named parameters

Variables

- **matrix** – the covariance matrix (square numpy array)
- **paramNames** – list of parameter name strings

Parameters **filename** – optionally, a file name to load from

correlation()

Get the correlation matrix

Returns numpy array giving the correlation matrix

plot()

Plot the correlation matrix as grid of colored squares

rescaleParameter(*name*, *scale*)

Used to rescale a covariance if a parameter is renormalized

Parameters

- **name** – parameter name to rescale
- **scale** – value to rescale by

saveToFile(*filename*)

Save the covariance matrix to a text file, with comment header listing the parameter names

Parameters **filename** – name of file to save to (.covmat)

CHAPTER 9

getdist.densities

exception getdist.densities.**DensitiesError**

class getdist.densities.**Density1D**(*x*, *P=None*, *view_ranges=None*)

Class for 1D marginalized densities, inheriting from *GridDensity*. You can call it like a InterpolatedUnivariateSpline obect to get interpolated values, or call Prob.

Parameters

- **x** – array of x values
- **P** – array of densities at x values
- **view_ranges** – optional range for viewing density

Prob(*x*, *derivative=0*)

Calculate density at position x by interpolation in the density grid

Parameters

- **x** – x value
- **derivative** – optional order of derivative to calculate (default: no derivative)

Returns P(x) density value

bounds()

Get min, max bounds (from view_ranges if set)

getLimits(*p*, *interpGrid=None*, *accuracy_factor=None*)

Get parameter equal-density confidence limits (a credible interval). If the density is bounded, may only have a one-tail limit.

Parameters

- **p** – list of limits to calculate, e.g. [0.68, 0.95]
- **interpGrid** – optional pre-computed cache
- **accuracy_factor** – parameter to boost default accuracy for fine sampling

Returns list of (min, max, has_min, has_top) values where has_min and has_top are True or False depending on whether lower and upper limit exists

class getdist.densities.**Density2D**(*x*, *y*, *P=None*, *view_ranges=None*)
Class for 2D marginalized densities, inheriting from *GridDensity*. You can call it like a RectBivariateSpline object to get interpolated values.

Parameters

- **x** – array of x values
- **y** – array of y values
- **P** – 2D array of density values at x, y
- **view_ranges** – optional ranges for viewing density

Prob(*x*, *y*, *grid=False*)
Evaluate density at x,y using interpolation

Parameters

- **x** – x value or array
- **y** – y value or array
- **grid** – whether to make a grid, see RectBivariateSpline. Default False.

class getdist.densities.**DensityND**(*xs*, *P=None*, *view_ranges=None*)
Class for ND marginalized densities, inheriting from *GridDensity* and LinearNDInterpolator.

This is not well tested recently.

Parameters

- **xs** – list of arrays of x values
- **P** – ND array of density values at xs
- **view_ranges** – optional ranges for viewing density

Prob(*xs*)
Evaluate density at x,y,z using interpolation

class getdist.densities.**GridDensity**
Base class for probability density grids (normalized or not)

Variables **P** – array of density values

bounds()
Get bounds in order x, y, z..

Returns list of (min,max) values

getContourLevels(*contours=(0.68*, *0.95)*)
Get contour levels

Parameters **contours** – list of confidence limits to get (default [0.68, 0.95])

Returns list of contour levels

normalize(*by='integral'*, *in_place=False*)
Normalize the density grid

Parameters

- **by** – 'integral' for standard normalization, or 'max', to normalize so the maximum value is unity

- **in_place** – if True, normalize in place, otherwise make copy (in case self.P is used elsewhere)

setP(*P=None*)
Set the density grid values

Parameters **P** – numpy array of density values

getdist.densities.**getContourLevels**(*inbins*, *contours=(0.68*, *0.95)*, *missing_norm=0*, *half_edge=True*)
Get contour levels enclosing "contours" fraction of the probability, for any dimension bins array

Parameters

- **inbins** – binned density.
- **contours** – list or tuple of confidence contours to calculate, default [0.68, 0.95]
- **missing_norm** – accounts of any points not included in inbins (e.g. points in far tails that are not in inbins)
- **half_edge** – If True, edge bins are only half integrated over in each direction.

Returns list of density levels

CHAPTER 10

getdist.gaussian_mixtures

class getdist.gaussian_mixtures.**Gaussian1D**(*mean*, *sigma*, ***kwargs*)
Simple 1D Gaussian

Parameters

- **mean** – mean
- **sigma** – standard deviation
- **kwargs** – arguments passed to *Mixture1D*

class getdist.gaussian_mixtures.**Gaussian2D**(*mean*, *cov*, ***kwargs*)
Simple special case of a 2D Gaussian mixture model with only one Gaussian component

Parameters

- **mean** – 2 element array with mean
- **cov** – 2x2 array of covariance, or list of [sigma_x, sigma_y, correlation] values
- **kwargs** – arguments passed to *Mixture2D*

class getdist.gaussian_mixtures.**GaussianND**(*mean*, *cov*, *is_inv_cov=False*, ***kwargs*)
Simple special case of a Gaussian mixture model with only one Gaussian component

Parameters

- **mean** – array specifying y of parameters
- **cov** – covariance matrix (or filename of text file with covariance matrix)
- **is_inv_cov** – set True if cov is actually an inverse covariance
- **kwargs** – arguments passed to *MixtureND*

class getdist.gaussian_mixtures.**Mixture1D**(*means*, *sigmas*, *weights=None*, *lims=None*, *name='x'*, *xmin=None*, *xmax=None*, ***kwargs*)
Gaussian mixture model in 1D with optional boundaries for fixed ranges

Parameters

- **means** – array of y for each component
- **sigmas** – array of standard deviations for each component
- **weights** – weights for each component (defaults to equal weight)
- **lims** – optional array limits for each component
- **name** – parameter name (default 'x')
- **xmin** – optional lower limit
- **xmax** – optional upper limit
- **kwargs** – arguments passed to *MixtureND*

pdf(*x*)

Calculate the PDF. Note this assumes x is within the boundaries (does not return zero outside) Result is also only normalized if no boundaries.

Parameters **x** – array of parameter values to evaluate at

Returns pdf at x

class getdist.gaussian_mixtures.**Mixture2D**(*means*, *covs*, *weights=None*, *lims=None*, *names=('x', 'y')*, *xmin=None*, *xmax=None*, *ymin=None*, *ymax=None*, ***kwargs*)

Gaussian mixture model in 2D with optional boundaries for fixed x and y ranges

Parameters

- **means** – list of y for each Gaussian in the mixture
- **covs** – list of covariances for the Gaussians in the mixture. Instead of 2x2 arrays, each cov can also be a list of [sigma_x, sigma_y, correlation] parameters
- **weights** – optional weight for each component (defaults to equal weight)
- **lims** – optional list of hard limits for each parameter, [[x1min,x1max], [x2min,x2max]]; use None for no limit
- **names** – list of names (strings) for each parameter. If not set, set to x, y
- **xmin** – optional lower hard bound for x
- **xmax** – optional upper hard bound for x
- **ymin** – optional lower hard bound for y
- **ymax** – optional upper hard bound for y
- **kwargs** – arguments passed to *MixtureND*

pdf(*x*, *y=None*)

Calculate the PDF. Note this assumes x and y are within the boundaries (does not return zero outside) Result is also only normalized if no boundaries

Parameters

- **x** – value of x to evaluate pdf
- **y** – optional value of y to evaluate pdf. If not specified, returns 1D marginalized value for x.

Returns value of pdf at x or x,y

class getdist.gaussian_mixtures.**MixtureND**(*means*, *covs*, *weights=None*, *lims=None*, *names=None*, *label=''*, *labels=None*)

Gaussian mixture model with optional boundary ranges. Includes functions for generating samples and projecting.

Parameters

- **means** – list of y for each Gaussian in the mixture
- **covs** – list of covariances for the Gaussians in the mixture
- **weights** – optional weight for each component (defaults to equal weight)
- **lims** – optional list of hard limits for each parameter, [[x1min,x1max], [x2min,x2max]]; use None for no limit
- **names** – list of names (strings) for each parameter. If not set, set to "param1", "param2"...
- **label** – name for labelling this mixture
- **labels** – list of latex labels for each parameter. If not set, defaults to p_{1}, p_{2}...

MCSamples(*size*, *names=None*, *logLikes=False*, ***kwargs*)

Gets a set of independent samples from the mixture as a *mcsamples.MCSamples* object ready for plotting etc.

Parameters

- **size** – number of samples
- **names** – set to override existing names
- **logLikes** – if True set the sample likelihood values from the pdf, if false, don't store log likelihoods

Returns a new *mcsamples.MCSamples* instance

conditionalMixture(*fixed_params*, *fixed_param_values*, *label=None*)

Returns a reduced conditional mixture model for the distribution when certainly parameters are fixed.

Parameters

- **fixed_params** – list of names or numbers of parameters to fix
- **fixed_param_values** – list of values for the fixed parameters
- **label** – optional label for the new mixture

Returns A new *MixtureND* instance with cov_i = Projection(Cov_i^{-1})^{-1} and shifted conditional y

density1D(*index=0*, *num_points=1024*, *sigma_max=4*, *no_limit_marge=False*)

Get 1D marginalized density. Only works if no hard limits in other parameters.

Parameters

- **index** – parameter name or index
- **num_points** – number of grid points to evaluate PDF
- **sigma_max** – maximum number of standard deviations away from y to include in computed range
- **no_limit_marge** – if true don't raise error if limits on other parameters

Returns *Density1D* instance

density2D(*params=None*, *num_points=1024*, *xmin=None*, *xmax=None*, *ymin=None*, *ymax=None*, *sigma_max=5*)

Get 2D marginalized density for a pair of parameters.

Parameters

- **params** – list of two parameter names or indices to use. If already 2D, can be None.
- **num_points** – number of grid points for evaluation
- **xmin** – optional lower value for first parameter
- **xmax** – optional upper value for first parameter
- **ymin** – optional lower value for second parameter
- **ymax** – optional upper value for second parameter
- **sigma_max** – maximum number of standard deviations away from mean to include in calculated range

Returns *Density2D* instance

marginalizedMixture(*params*, *label=None*, *no_limit_marge=False*)

Calculates a reduced mixture model by marginalization over unwanted parameters

Parameters

- **params** – array of parameter names or indices to retain. If none, will simply return a copy of this mixture.
- **label** – optional label for the marginalized mixture
- **no_limit_marge** – if true don't raise an error if mixture has limits.

Returns a new marginalized *MixtureND* instance

pdf(*x*)

Calculate the PDF. Note this assumes x is within the boundaries (does not return zero outside) Result is also only normalized if no boundaries.

Parameters **x** – array of parameter values to evaluate at

Returns pdf at x

pdf_marged(*index*, *x*, *no_limit_marge=False*)

Calculate the 1D marginalized PDF. Only works if no other parameter limits are marginalized

Parameters

- **index** – index or name of parameter
- **x** – value to evaluate PDF at
- **no_limit_marge** – if true don't raise an error if mixture has limits

Returns marginalized 1D pdf at x

sim(*size*)

Generate an array of independent samples

Parameters **size** – number of samples

Returns 2D array of sample values

class getdist.gaussian_mixtures.**RandomTestMixtureND**(*ndim=4*, *ncomponent=1*, *names=None*, *weights=None*, *seed=0*, *label='RandomMixture'*)

class for randomly generating an N-D gaussian mixture for testing (a mixture with random parameters, not random samples from the mixture).

Parameters

- **ndim** – number of dimensions
- **ncomponent** – number of components
- **names** – names for the parameters
- **weights** – weights for each component
- **seed** – random seed
- **label** – label for the generated mixture

getdist.gaussian_mixtures.**randomTestMCSamples**(*ndim=4*, *ncomponent=1*, *nsamp=10009*, *nMCSamples=1*, *seed=10*, *names=None*, *labels=None*)

get a list of MCSamples instances with random samples from random covariances and y

CHAPTER 11

getdist.inifile

exception getdist.inifile.**IniError**

class getdist.inifile.**IniFile**(*settings=None*, *keep_includes=False*, *expand_environment_variables=True*)

Class for storing option parameter values and reading/saving to file

Unlike standard .ini files, IniFile allows inheritance, in that a .ini file can use INCLUDE(..) and DEFAULT(...) to include or override settings in another file (to avoid duplication)

Variables

- **params** – dictionary of name, values stored
- **comments** – dictionary of optional comments for parameter names

Parameters

- **settings** – a filename of a .ini file to read, or a dictionary of name/values
- **keep_includes** –
  - False: load all INCLUDE and DEFAULT files, making one params dictionary
  - True: only load settings in main file, and store INCLUDE and DEFAULT entries into defaults and includes filename lists.
- **expand_environment_variables** – whether to expand $(var) placeholders in parameter values using environment variables

array_bool(*name*, *index=1*, *default=None*)

Get one boolean value, for entries of the form name(index)

Parameters

- **name** – base parameter name
- **index** – index (in brackets)
- **default** – default value

array_float(*name*, *index=1*, *default=None*)
Get one float value, for entries of the form name(index)

Parameters

- **name** – base parameter name
- **index** – index (in brackets)
- **default** – default value

array_int(*name*, *index=1*, *default=None*)
Get one int value, for entries of the form name(index)

Parameters

- **name** – base parameter name
- **index** – index (in brackets)
- **default** – default value

array_string(*name*, *index=1*, *default=None*)
Get one str value, for entries of the form name(index)

Parameters

- **name** – base parameter name
- **index** – index (in brackets)
- **default** – default value

bool(*name*, *default=False*)
Get boolean value

Parameters

- **name** – parameter name
- **default** – default value if not set

bool_list(*name*, *default=None*)
Get list of boolean values, e.g. from name = T F T

Parameters

- **name** – parameter name
- **default** – default value if not set

expand_placeholders(*s*)
Expand shell variables of the forms $(var), like in Makefiles

float(*name*, *default=None*)
Get float value

Parameters

- **name** – parameter name
- **default** – default value

float_list(*name*, *default=None*)
Get list of float values

Parameters

- **name** – parameter name

- **default** – default value

hasKey(*name*)
Test if key name exists

Parameters **name** – parameter name

Returns True or False test if key name exists

int(*name*, *default=None*)
Get int value

Parameters

- **name** – parameter name
- **default** – default value

int_list(*name*, *default=None*)
Get list of int values

Parameters

- **name** – parameter name
- **default** – default value

isSet(*name*, *allowEmpty=False*)
Tests whether value for name is set or is empty

Parameters

- **name** – name of parameter
- **allowEmpty** – whether to allow empty strings (return True is parameter name exists but is not set, "x = ")

list(*name*, *default=None*, *tp=None*)
Get list (from space-separated values)

Parameters

- **name** – parameter name
- **default** – default value
- **tp** – type for each member of the list

ndarray(*name*, *default=None*, *tp=<class 'numpy.float64'>*)
Get numpy array of values

Parameters

- **name** – parameter name
- **default** – default value
- **tp** – type for array

saveFile(*filename=None*)
Save to a .ini file

Parameters **filename** – name of file to save to

setAttr(*name*, *instance*, *default=None*, *allowEmpty=False*)
Set attribute of an object to value of parameter, using same type as existing value or default

Parameters

- **name** – parameter name
- **instance** – instance of an object, so instance.name is the value to set
- **default** – default value if instance.name does not exist
- **allowEmpty** – whether to allow empty values

split(*name*, *default=None*, *tp=None*)
Gets a list of values, optionally cast to type tp

Parameters

- **name** – parameter name
- **default** – default value
- **tp** – type for each list member

string(*name*, *default=None*, *allowEmpty=True*)
Get string value

Parameters

- **name** – parameter name
- **default** – default value if not set
- **allowEmpty** – whether to return empty string if value is empty (otherwise return default)

CHAPTER 12

getdist.paramnames

class getdist.paramnames.**ParamInfo**(*line=None*, *name=''*, *label=''*, *comment=''*, *derived=False*, *renames=None*, *number=None*)

Parameter information object.

Variables

- **name** – the parameter name tag (no spacing or punctuation)
- **label** – latex label (without enclosing $)
- **comment** – any descriptive comment describing the parameter
- **isDerived** – True if a derived parameter, False otherwise (e.g. for MCMC parameters)

class getdist.paramnames.**ParamList**(*fileName=None*, *setParamNameFile=None*, *default=0*, *names=None*, *labels=None*)

Holds an orders list of *ParamInfo* objects describing a set of parameters.

Variables **names** – list of *ParamInfo* objects

Parameters

- **fileName** – name of .paramnames file to load from
- **setParamNameFile** – override specific parameter names' labels using another file
- **default** – set to int>0 to automatically generate that number of default names and labels (param1, p_{1}, etc.)
- **names** – a list of name strings to use

addDerived(*name*, ***kwargs*)

adds a new parameter

Parameters

- **name** – name tag for the new parameter
- **kwargs** – other arguments for constructing the new *ParamInfo*

getDerivedNames()
Get the names of all derived parameters

getRenames(*keep_empty=False*)
Gets dictionary of renames known to each parameter.

getRunningNames()
Get the names of all running (non-derived) parameters

labels()
Gets a list of parameter labels

list()
Gets a list of parameter name strings

numberOfName(*name*)
Gets the parameter number of the given parameter name

Parameters **name** – parameter name tag

Returns index of the parameter, or -1 if not found

parWithName(*name*, *error=False*, *renames=None*)
Gets the *ParamInfo* object for the parameter with the given name

Parameters

- **name** – name of the parameter
- **error** – if True raise an error if parameter not found, otherwise return None
- **renames** – a dictionary that is used to provide optional name mappings to the stored names

parsWithNames(*names*, *error=False*, *renames=None*)
gets the list of *ParamInfo* instances for given list of name strings. Also expands any names that are globs into list with matching parameter names

Parameters

- **names** – list of name strings
- **error** – if True, raise an error if any name not found, otherwise returns None items. Can be a list of length *len(names)*
- **renames** – optional dictionary giving mappings of parameter names

saveAsText(*filename*)
Saves to a plain text .paramnames file

Parameters **filename** – filename to save to

updateRenames(*renames*)
Updates the renames known to each parameter with the given dictionary of renames.

class getdist.paramnames.**ParamNames**(*fileName=None*, *setParamNameFile=None*, *default=0*, *names=None*, *labels=None*)
Holds an orders list of *ParamInfo* objects describing a set of parameters, inheriting from *ParamList*.

Can be constructed programmatically, and also loaded and saved to a .paramnames files, which is a plain text file giving the names and optional label and comment for each parameter, in order.

Variables

- **names** – list of *ParamInfo* objects describing each parameter
- **filenameLoadedFrom** – if loaded from file, the file name

Parameters

- **fileName** – name of .paramnames file to load from
- **setParamNameFile** – override specific parameter names' labels using another file
- **default** – set to int>0 to automatically generate that number of default names and labels (param1, p_{1}, etc.)
- **names** – a list of name strings to use

loadFromFile(*fileName*)
loads from fileName, a plain text .paramnames file or a "full" yaml file

getdist.paramnames.**makeList**(*roots*)
Checks if the given parameter is a list. If not, Creates a list with the parameter as an item in it.

Parameters **roots** – The parameter to check

Returns A list containing the parameter.

getdist.paramnames.**mergeRenames**(**dicts*, ***kwargs*)
Joins several dicts of renames.

If *keep_names_1st=True* (default: *False*), keeps empty entries when possible in order to preserve the parameter names of the first input dictionary.

Returns a merged dictionary of renames, whose keys are chosen from the left-most input.

CHAPTER 13

getdist.parampriors

class getdist.parampriors.**ParamBounds**(*fileName=None*)

Class for holding list of parameter bounds (e.g. for plotting, or hard priors). A limit is None if not specified, denoted by 'N' if read from a string or file

Variables

- **names** – list of parameter names
- **lower** – dict of lower limits, indexed by parameter name
- **upper** – dict of upper limits, indexed by parameter name

Parameters **fileName** – optional file name to read from

fixedValue(*name*)

Parameters **name** – parameter name

Returns if range has zero width return fixed value else return None

fixedValueDict()

Returns dictionary of fixed parameter values

getLower(*name*)

Parameters **name** – parameter name

Returns lower limit, or None if not specified

getUpper(*name*)

Parameters **name** – parameter name

Returns upper limit, or None if not specified

saveToFile(*fileName*)

Save to a plain text file

Parameters **fileName** – file name to save to

CHAPTER 14

getdist.types

class getdist.types.**BestFit**(*fileName=None*, *setParamNameFile=None*, *want_fixed=False*, *max_posterior=True*)

Class holding the result of a likelihood minimization, inheriting from *ParamResults*. The data is read from a specific formatted text file (.minimum or .bestfit) as output by CosmoMC or Cobaya.

Parameters

- **fileName** – text file to load from, assumed to be in CosmoMC's .minimum format
- **setParamNameFile** – optional name of .paramnames file listing preferred parameter labels for the parameters
- **want_fixed** – whether to include values of parameters that are not allowed to vary
- **max_posterior** – whether the file is a maximum posterior (default) or maximum likelihood

class getdist.types.**ConvergeStats**(*fileName=None*, *setParamNameFile=None*, *default=0*, *names=None*, *labels=None*)

Parameters

- **fileName** – name of .paramnames file to load from
- **setParamNameFile** – override specific parameter names' labels using another file
- **default** – set to int>0 to automatically generate that number of default names and labels (param1, p_{1}, etc.)
- **names** – a list of name strings to use

class getdist.types.**LikeStats**(*fileName=None*, *setParamNameFile=None*, *default=0*, *names=None*, *labels=None*)

Stores likelihood-related statistics, including best-fit sample and extremal values of the N-D confidence region, inheriting from *ParamResults*. TODO: currently only saves to text, does not load full data from file

Parameters

- **fileName** – name of .paramnames file to load from

- **setParamNameFile** – override specific parameter names' labels using another file
- **default** – set to int>0 to automatically generate that number of default names and labels (param1, p_{1}, etc.)
- **names** – a list of name strings to use

class getdist.types.**MargeStats**(*fileName=None*, *setParamNameFile=None*, *default=0*, *names=None*, *labels=None*)

Stores marginalized 1D parameter statistics, including mean, variance and confidence limits, inheriting from *ParamResults*.

Values are stored as attributes of the *ParamInfo* objects stored in self.names. Use *par= margeStats.parWithName('xxx')* to get the *ParamInfo* for parameter *xxx*; Values stored are:

- *par.mean*: parameter mean
- *par.err*: standard deviation
- *limits*: list of *ParamLimit* objects for the stored number of marginalized limits

For example to get the first and second lower limits (default 68% and 95%) for parameter *xxx*:

```
print(margeStats.names.parWithName('xxx').limits[0].lower)
print(margeStats.names.parWithName('xxx').limits[1].lower)
```

See *ParamLimit* for details of limits.

Parameters

- **fileName** – name of .paramnames file to load from
- **setParamNameFile** – override specific parameter names' labels using another file
- **default** – set to int>0 to automatically generate that number of default names and labels (param1, p_{1}, etc.)
- **names** – a list of name strings to use

loadFromFile(*filename*)

Load from a plain text file

Parameters **filename** – file to load from

class getdist.types.**ParamLimit**(*minmax*, *tag='two'*)

Class containing information about a marginalized parameter limit.

Variables

- **lower** – lower limit
- **upper** – upper limit
- **twotail** – True if a two-tail limit, False if one-tail
- **onetail_upper** – True if one-tail upper limit
- **onetail_lower** – True if one-tail lower limit

Parameters

- **minmax** – a [min,max] tuple with lower and upper limits. Entries be None if no limit.
- **tag** – a text tag descibing the limit, one of ['two' | '>' | '<' | 'none']

limitTag()

Returns

Short text tag describing the type of limit (one-tail or two tail):

- *two*: two-tail limit
- >: a one-tail upper limit
- <: a one-tail lower limit
- *none*: no limits (both boundaries have high probability)

limitType()

Returns

a text description of the type of limit. One of:

- *two tail*
- *one tail upper limit*
- *one tail lower limit*
- *none*

class getdist.types.**ParamResults**(*fileName=None*, *setParamNameFile=None*, *default=0*, *names=None*, *labels=None*)

Base class for a set of parameter results, inheriting from `ParamList`, so that self.names is a list of `ParamInfo` instances for each parameter, which have attribute holding results for the different parameters.

Parameters

- **fileName** – name of .paramnames file to load from
- **setParamNameFile** – override specific parameter names' labels using another file
- **default** – set to int>0 to automatically generate that number of default names and labels (param1, p_{1}, etc.)
- **names** – a list of name strings to use

class getdist.types.**ResultTable**(*ncol*, *results*, *limit=2*, *tableParamNames=None*, *titles=None*, *formatter=None*, *numFormatter=None*, *blockEndParams=None*, *paramList=None*, *refResults=None*, *shiftSigma_indep=False*, *shiftSigma_subset=False*)

Class for holding a latex table of parameter statistics

Parameters

- **ncol** – number of columns
- **results** – a `MargeStats` or `BestFit` instance, or a list of them for comparing different results
- **limit** – which limit to include (1 is first limit calculated, usually 68%, 2 the second, usually 95%)
- **tableParamNames** – optional `ParamNames` instance listing particular parameters to include
- **titles** – optional titles describing different results
- **formatter** – a table formatting class
- **numFormatter** – a number formatting class
- **blockEndParams** – mark parameters in blocks, ending on this list of parameter names

- **paramList** – a list of parameter names (strings) to include
- **refResults** – for showing parameter shifts, a reference *MargeStats* instance to show differences to
- **shiftSigma_indep** – show parameter shifts in sigma assuming data are independent
- **shiftSigma_subset** – show parameter shifts in sigma assuming data are a subset of each other

tablePNG(*dpi=None*, *latex_preamble=None*, *filename=None*, *bytesIO=False*)
Get a .png file image of the table. You must have latex installed to use this.

Parameters

- **dpi** – dpi settings for the png
- **latex_preamble** – any latex preamble
- **filename** – filename to save to (defaults to file in the temp directory)
- **bytesIO** – if True, return a BytesIO instance holding the .png data

Returns if bytesIO, the BytesIO instance, otherwise name of the output file

tableTex(*document=False*, *latex_preamble=None*, *packages=('amsmath', 'amssymb', 'bm')*)
Get the latex string for the table

Parameters

- **document** – if True, make a full latex file, if False just the snippet for including in another file
- **latex_preamble** – any preamble to include in the latex file
- **packages** – list of packages to load

write(*fname*, ***kwargs*)
Write the latex for the table to a file

Parameters

- **fname** – filename to write
- **kwargs** – arguments for *tableTex()*

getdist.types.**float_to_decimal**(*f*)
Convert a floating point number to a Decimal with no loss of information

Interface modules:

CHAPTER 15

getdist.cobaya_interface

getdist.cobaya_interface.**MCSamplesFromCobaya**(*info*, *collections*, *name_tag=None*, *ignore_rows=0*, *ini=None*, *settings=None*)

Creates a set of samples from Cobaya's output. Parameter names, ranges and labels are taken from the "info" dictionary (always use the "updated" one generated by *cobaya.run*).

For a description of the various analysis settings and default values see analysis_defaults.ini.

Parameters

- **collections** – collection(s) of samples from Cobaya
- **info** – info dictionary, common to all collections (use the "updated" one, returned by *cobaya.run*)
- **name_tag** – name for this sample to be shown in the plots' legend
- **ignore_rows** – initial samples to skip, number (*int>=1*) or fraction (*float<1*)
- **ini** – The name of a .ini file with analysis settings to use
- **settings** – dictionary of analysis settings to override defaults

Returns The MCSamples instance

getdist.cobaya_interface.**expand_info_param**(*info_param*)

Expands the info of a parameter, from the user friendly, shorter format to a more unambiguous one.

getdist.cobaya_interface.**fixed_value**(*info_param*)

Returns True if the parameter has been fixed to a value or through a function.

getdist.cobaya_interface.**get_info_params**(*info*)

Extracts parameter info from the new yaml format.

getdist.cobaya_interface.**is_derived_param**(*info_param*)

Returns True if the parameter is saved as a derived one.

getdist.cobaya_interface.**is_fixed_param**(*info_param*)

Returns True if the parameter has been fixed to a value or through a function.

getdist.cobaya_interface.**is_sampled_param**(*info_param*)
Returns True if the parameter has a prior.

CHAPTER 16

getdist.cosmosis_interface

File with tools to interface Cosmosis runs with GetDist.

chain = loadMCSamples('./../test_chains/1p2_SN1_zcut0p3_abs') chain_root = './../test_chains/d_1sigD_s8/d_TTlite_1sigD_s8_noisy_poly_chain' chain_root = './../test_chains/d_1sigD_s8' param_label_dict=None

getdist.cosmosis_interface.**MCSamplesFromCosmosis**(*chain_root*, *param_label_dict=None*, *name_tag=None*, *settings=None*)

Function to import Cosmosis chains in GetDist.

Parameters

- **chain_root** – the name and path to the chain or the path to the folder that contains it.
- **param_label_dict** – dictionary with the mapping between parameter names and parameter labels, since Cosmosis does not save the labels in the chain.
- **name_tag** – a string with the name tag for the chain.
- **settings** – dictionary of analysis settings to override defaults

Returns The `MCSamples` instance

getdist.cosmosis_interface.**get_cosmosis_info**(*file*)

Parse a file to get all the information about a Cosmosis run.

Parameters **file** – path and name of the file to parse.

Returns a list of strings with the cosmosis parameters for the run.

getdist.cosmosis_interface.**get_maximum_likelihood**(*chain_root*, *param_label_dict*)

Import the maximum likelihood file for a Cosmosis run, if present.

Parameters

- **chain_root** – name of the chain file or the folder that contains it.
- **param_label_dict** – dictionary with the mapping between the parameter names and the labels.

Returns *BestFit* the best fit object.

getdist.cosmosis_interface.**get_name_tag**(*info*)
Get the name tag for a chain given the a list of strings containing the cosmosis run parameter informations.

Parameters **info** – a list of strings with the cosmosis parameters for the run.

Returns a string with the name tag if any, otherwise returns none.

getdist.cosmosis_interface.**get_param_labels**(*info*, *param_names*, *param_label_dict*)
Get the labels for the parameter names of a Cosmosis run.

Parameters

- **info** – a list of strings with the cosmosis parameters for the run.
- **param_names** – a list of strings with the parameter names.
- **param_label_dict** – a dictionary with the mapping between names and labels.

Returns a list of strings with the parameter labels.

getdist.cosmosis_interface.**get_param_names**(*info*)
Get the parameter names for a Cosmosis run.

Parameters **info** – a list of strings with the cosmosis parameters for the run.

Returns a list of strings with the parameter names.

getdist.cosmosis_interface.**get_ranges**(*info*, *param_names*)
Get the ranges for the parameters from the info file.

Parameters

- **info** – a list of strings with the cosmosis parameters for the run.
- **param_names** – a list with the parameter names.

Returns a dictionary with the parameter ranges.

getdist.cosmosis_interface.**get_sampler_type**(*info*)
Get the sampler type for a chain given the a list of strings containing the cosmosis run parameter informations. To process the sampler type the function defines internally a dictionary with the mapping from sampler name to sampler type.

Parameters **info** – a list of strings with the cosmosis parameters for the run.

Returns a string with the sampler type if any, otherwise returns none.

getdist.cosmosis_interface.**polish_samples**(*chain*)
Remove fixed parameters and samples with some parameter that is Nan from the input chain.

Parameters **chain** – *MCSamples* the input chain.

Returns *MCSamples* the polished chain.

- genindex

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