
BayesPy Documentation

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CONTENTS

1	Introduction	1
1.1	Project information	1
1.2	Similar projects	2
2	User guide	3
2.1	Installation	3
2.2	Quick start guide	5
2.3	Constructing the model	8
2.4	Performing inference	15
2.5	Examining the results	20
3	Examples	27
3.1	Regression	27
3.2	Gaussian mixture model	34
3.3	Bernoulli mixture model	34
3.4	Discrete hidden Markov model	35
3.5	Hidden Markov model	39
3.6	Principal component analysis	39
3.7	Linear state-space model	39
3.8	Latent Dirichlet allocation	43
4	Developer guide	45
4.1	Variational message passing	45
4.2	Implementing nodes	46
5	User API	47
5.1	bayespy.nodes	47
5.2	bayespy.inference	132
5.3	bayespy.plot	140
6	Developer API	147
6.1	Nodes	147
6.2	Moments	158
7	Indices and tables	159
	Bibliography	161
	Python Module Index	163
	Index	165

INTRODUCTION

BayesPy provides tools for Bayesian inference with Python. The user constructs a model as a Bayesian network, observes data and runs posterior inference. The goal is to provide a tool which is efficient, flexible and extendable enough for expert use but also accessible for more casual users.

Currently, only variational Bayesian inference for conjugate-exponential family (variational message passing) has been implemented. Future work includes variational approximations for other types of distributions and possibly other approximate inference methods such as expectation propagation, Laplace approximations, Markov chain Monte Carlo (MCMC) and other methods. Contributions are welcome.

It is recommended to use the latest version from the GitHub master branch. The version in PyPI is quite outdated.

1.1 Project information

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BayesPy including the documentation is licensed under Version 3.0 of the GNU General Public License. See LICENSE file for a text of the license or visit <http://www.gnu.org/copyleft/gpl.html>.

- Documentation:
 - <http://bayespy.org>
 - PDF file
 - RST format in `doc` directory
- Repository: <https://github.com/bayespy/bayespy.git>
- Bug reports: <https://github.com/bayespy/bayespy/issues>
- Mailing list: bayespy@googlegroups.com
- IRC: #bayespy @ freenode
- Author: Jaakko Luttinen jaakko.luttinen@iki.fi
- Latest release:
- Build status:
- Unit test coverage:

1.2 Similar projects

VIBES (<http://vibes.sourceforge.net/>) allows variational inference to be performed automatically on a Bayesian network. It is implemented in Java and released under revised BSD license.

Bayes Blocks (<http://research.ics.aalto.fi/bayes/software/>) is a C++/Python implementation of the variational building block framework. The framework allows easy learning of a wide variety of models using variational Bayesian learning. It is available as free software under the GNU General Public License.

Infer.NET (<http://research.microsoft.com/infernet/>) is a .NET framework for machine learning. It provides message-passing algorithms and statistical routines for performing Bayesian inference. It is partly closed source and licensed for non-commercial use only.

PyMC (<https://github.com/pymc-devs/pymc>) provides MCMC methods in Python. It is released under the Academic Free License.

OpenBUGS (<http://www.openbugs.info>) is a software package for performing Bayesian inference using Gibbs sampling. It is released under the GNU General Public License.

Dimple (<http://dimple.probplog.org/>) provides Gibbs sampling, belief propagation and a few other inference algorithms for Matlab and Java. It is released under the Apache License.

Stan (<http://mc-stan.org/>) provides inference using MCMC with an interface for R and Python. It is released under the New BSD License.

PBNT - Python Bayesian Network Toolbox (<http://pbnt.berlios.de/>) is Bayesian network library in Python supporting static networks with discrete variables. There was no information about the license.

USER GUIDE

2.1 Installation

BayesPy is a Python 3 package and it can be installed from PyPI or the latest development version from GitHub. The instructions below explain how to set up the system by installing required packages, how to install BayesPy and how to compile this documentation yourself. However, if these instructions contain errors or some relevant details are missing, please file a bug report at <https://github.com/bayespy/bayespy/issues>.

2.1.1 Installing requirements

BayesPy requires Python 3.2 (or later) and the following packages:

- NumPy ($\geq 1.8.0$),
- SciPy ($\geq 0.13.0$)
- matplotlib (≥ 1.2)
- h5py

Ideally, a manual installation of these dependencies is not required and you can skip to the next section “Installing BayesPy”. However, there are several reasons why the installation of BayesPy as described in the next section won’t work because of your system. Thus, this section tries to give as detailed and robust a method of setting up your system such that the installation of BayesPy should work.

A proper installation of the dependencies for Python 3 can be a bit tricky and you may refer to <http://www.scipy.org/install.html> for more detailed instructions about the SciPy stack. If your system has an older version of any of the packages (NumPy, SciPy or matplotlib) or it does not provide the packages for Python 3, you may set up a virtual environment and install the latest versions there. To create and activate a new virtual environment, run

```
virtualenv -p python3 --system-site-packages ENV
source ENV/bin/activate
```

If you have relevant system libraries installed (C compiler, Python development files, BLAS/LAPACK etc.), you may be able to install the Python packages from PyPI. For instance, on Ubuntu (≥ 12.10), you may install the required system libraries for each package as:

```
sudo apt-get build-dep python3-numpy
sudo apt-get build-dep python3-scipy
sudo apt-get build-dep python3-matplotlib
sudo apt-get build-dep python-h5py
```

Then installation/upgrade from PyPI should work:

```
pip install distribute --upgrade
pip install numpy --upgrade
pip install scipy --upgrade
pip install matplotlib --upgrade
pip install h5py
```

Note that Matplotlib requires a quite recent version of Distribute ($\geq 0.6.28$). If you have problems installing any of these packages, refer to the manual of that package.

2.1.2 Installing BayesPy

If the system has been properly set up and the virtual environment is activated (optional), latest release of BayesPy can be installed from PyPI simply as

```
pip install bayespy
```

If you want to install the latest development version of BayesPy, use GitHub instead:

```
pip install https://github.com/bayespy/bayespy/archive/master.zip
```

It is recommended to run the unit tests in order to check that BayesPy is working properly. Thus, install Nose and run the unit tests:

```
pip install nose
nosetests bayespy
```

2.1.3 Compiling documentation

This documentation can be found at <http://bayespy.org/>. The documentation source files are readable as such in reStructuredText format in `doc/source/` directory. It is possible to compile the documentation into HTML or PDF yourself. In order to compile the documentation, Sphinx is required and a few extensions for it. Those can be installed as:

```
pip install sphinx sphinxcontrib-tikz sphinxcontrib-bayesnet
```

In addition, the `numpydoc` extension for Sphinx is required. However, the latest stable release (0.4) does not support Python 3, thus one needs to install the development version:

```
pip install https://github.com/numpy/numpydoc/archive/master.zip
```

In order to visualize graphical models in HTML, you need to have `pnmcrop`. On Ubuntu, it can be installed as

```
sudo apt-get install netpbm
```

The documentation can be compiled to HTML and PDF by running the following commands in the `doc` directory:

```
make html
make latexpdf
```

2.1.4 Converting notebooks

The documentation uses IPython notebooks for the examples. This is a convenient format for sharing Python examples with comments. The notebooks can be converted, for instance, to documentation files or Python scripts. BayesPy repository contains those notebook files (`.ipynb`) and their conversions to RST format for the documentation. If you

want to convert the notebooks into RST files, Python scripts or some other format yourself, follow these instructions. First, the following packages are required:

```
pip install ipython pyzmq
```

You need quite a recent IPython. You may also need to install Pandoc. In Ubuntu, this can be done as:

```
sudo aptitude install pandoc
```

Now, the notebooks can be converted to RST for the documentation by running the following command in the `doc` directory:

```
make notebooks
```

Or you can convert the notebooks to RST or Python (or something else) for your own use:

```
ipython nbconvert --to rst doc/source/_notebooks/*.ipynb
ipython nbconvert --to python doc/source/_notebooks/*.ipynb
```

The Python scripts can be used to run the examples as such. There are also more formats available in case you want the examples in HTML, LaTeX, or some other format.

You can also open the notebooks interactively in a web browser by going to the notebooks directory and running the IPython notebook:

```
cd doc/source/_notebooks
ipython notebook
```

This should run a simple server and open a web browser.

You can also run doctest to test code snippets in the documentation:

```
make doctest
```

or in the docstrings:

```
nosetests --with-doctest bayespy
```

2.2 Quick start guide

This short guide shows the key steps in using BayesPy for variational Bayesian inference by applying BayesPy to a simple problem. The key steps in using BayesPy are the following:

- Construct the model
- Observe some of the variables by providing the data in a proper format
- Run variational Bayesian inference
- Examine the resulting posterior approximation

To demonstrate BayesPy, we'll consider a very simple problem: we have a set of observations from a Gaussian distribution with unknown mean and variance, and we want to learn these parameters. In this case, we do not use any real-world data but generate some artificial data. The dataset consists of ten samples from a Gaussian distribution with mean 5 and standard deviation 10. This dataset can be generated with NumPy as follows:

```
>>> import numpy as np
>>> data = np.random.normal(5, 10, size=(10,))
```

2.2.1 Constructing the model

Now, given this data we would like to estimate the mean and the standard deviation as if we didn't know their values. The model can be defined as follows:

$$p(\mathbf{y}|\mu, \tau) = \prod_{n=0}^9 \mathcal{N}(y_n|\mu, \tau)$$

$$p(\mu) = \mathcal{N}(\mu|0, 10^{-6})$$

$$p(\tau) = \mathcal{G}(\tau|10^{-6}, 10^{-6})$$

where \mathcal{N} is the Gaussian distribution parameterized by its mean and precision (i.e., inverse variance), and \mathcal{G} is the gamma distribution parameterized by its shape and rate parameters. Note that we have given quite uninformative priors for the variables μ and τ . This simple model can also be shown as a directed factor graph: This model can be

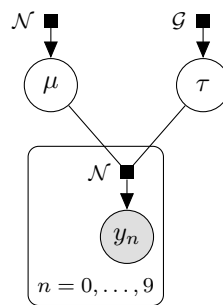


Figure 2.1: Directed factor graph of the example model.

constructed in BayesPy as follows:

```
>>> from bayespy.nodes import GaussianARD, Gamma
>>> mu = GaussianARD(0, 1e-6)
>>> tau = Gamma(1e-6, 1e-6)
>>> y = GaussianARD(mu, tau, plates=(10,))
```

This is quite self-explanatory given the model definitions above. We have used two types of nodes `GaussianARD` and `Gamma` to represent Gaussian and gamma distributions, respectively. There are much more distributions in `bayespy.nodes` so you can construct quite complex conjugate exponential family models. The node `y` uses keyword argument `plates` to define the plates $n = 0, \dots, 9$.

2.2.2 Performing inference

Now that we have created the model, we can provide our data by setting `y` as observed:

```
>>> y.observe(data)
```

Next we want to estimate the posterior distribution. In principle, we could use different inference engines (e.g., MCMC or EP) but currently only variational Bayesian (VB) engine is implemented. The engine is initialized by giving all the nodes of the model:

```
>>> from bayespy.inference import VB
>>> Q = VB(mu, tau, y)
```

The inference algorithm can be run as long as wanted (max. 20 iterations in this case):

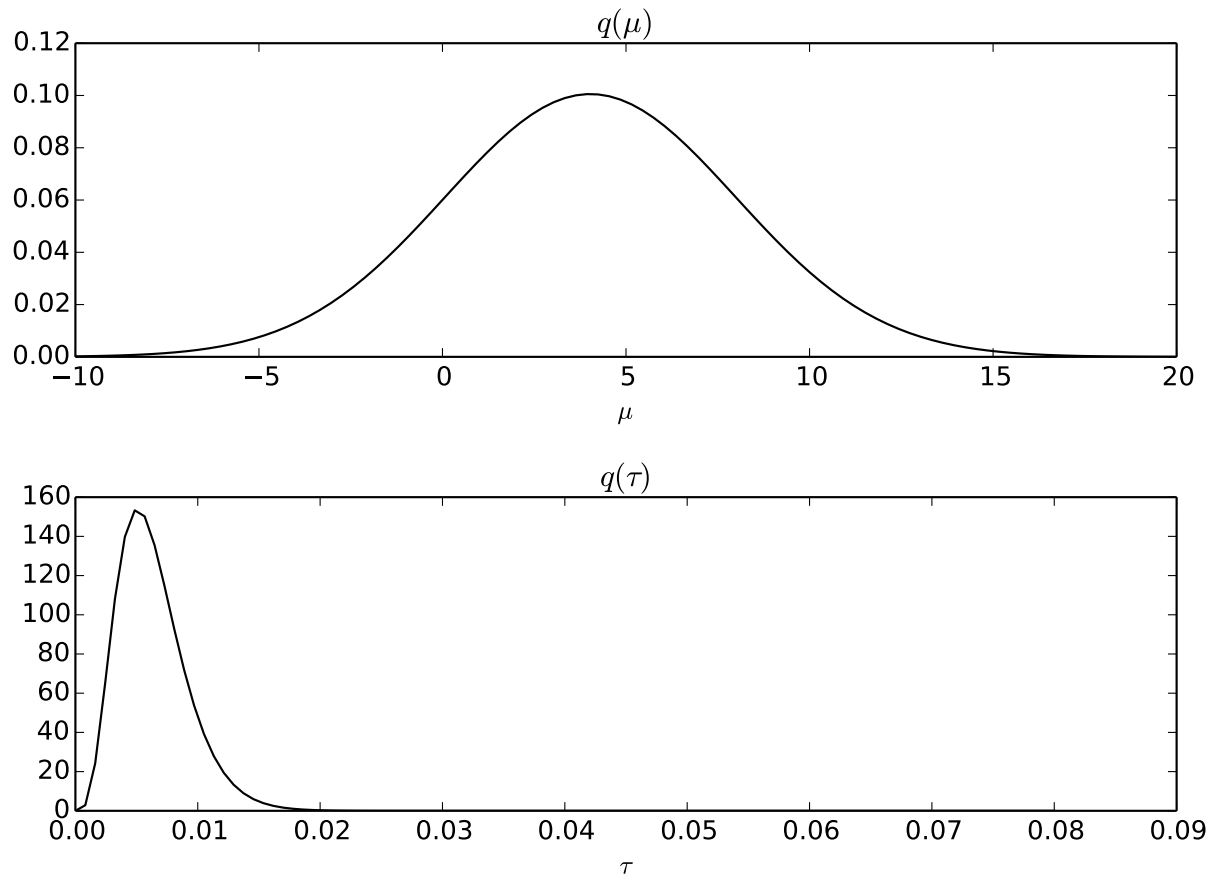
```
>>> Q.update(repeat=20)
Iteration 1: loglike=-6.020956e+01 (... seconds)
Iteration 2: loglike=-5.820527e+01 (... seconds)
Iteration 3: loglike=-5.820290e+01 (... seconds)
Iteration 4: loglike=-5.820288e+01 (... seconds)
Converged at iteration 4.
```

Now the algorithm converged after four iterations, before the requested 20 iterations. VB approximates the true posterior $p(\mu, \tau | y)$ with a distribution which factorizes with respect to the nodes: $q(\mu)q(\tau)$.

2.2.3 Examining posterior approximation

The resulting approximate posterior distributions $q(\mu)$ and $q(\tau)$ can be examined, for instance, by plotting the marginal probability density functions:

```
>>> import bayespy.plot as bpplt
>>> bpplt.pyplot.subplot(2, 1, 1)
<matplotlib.axes.AxesSubplot object at 0x...>
>>> bpplt.pdf(mu, np.linspace(-10, 20, num=100), color='k', name=r'\mu')
[<matplotlib.lines.Line2D object at 0x...>]
>>> bpplt.pyplot.subplot(2, 1, 2)
<matplotlib.axes.AxesSubplot object at 0x...>
>>> bpplt.pdf(tau, np.linspace(1e-6, 0.08, num=100), color='k', name=r'\tau')
[<matplotlib.lines.Line2D object at 0x...>]
>>> bpplt.pyplot.tight_layout()
>>> bpplt.pyplot.show()
```



This example was a very simple introduction to using BayesPy. The model can be much more complex and each phase contains more options to give the user more control over the inference. The following sections give more details about the phases.

2.3 Constructing the model

In BayesPy, the model is constructed by creating nodes which form a directed network. There are two types of nodes: stochastic and deterministic. A stochastic node corresponds to a random variable (or a set of random variables) from a specific probability distribution. A deterministic node corresponds to a deterministic function of its parents. For a list of built-in nodes, see the [User API](#).

2.3.1 Creating nodes

Creating a node is basically like writing the conditional prior distribution of the variable in Python. The node is constructed by giving the parent nodes, that is, the conditioning variables as arguments. The number of parents and their meaning depend on the node. For instance, a `Gaussian` node is created by giving the mean vector and the precision matrix. These parents can be constant numerical arrays if they are known:

```
>>> from bayespy.nodes import Gaussian
>>> X = Gaussian([2, 5], [[1.0, 0.3], [0.3, 1.0]])
```

or other nodes if they are unknown and given prior distributions:

```
>>> from bayespy.nodes import Gaussian, Wishart
>>> mu = Gaussian([0, 0], [[1e-6, 0], [0, 1e-6]])
>>> Lambda = Wishart(2, [[1, 0], [0, 1]])
>>> X = Gaussian(mu, Lambda)
```

Nodes can also be named by providing `name` keyword argument:

```
>>> X = Gaussian(mu, Lambda, name='x')
```

The name may be useful when referring to the node using an inference engine.

For the parent nodes, there are two main restrictions: non-constant parent nodes must be conjugate and the parent nodes must be mutually independent in the posterior approximation.

Conjugacy of the parents

In Bayesian framework in general, one can give quite arbitrary probability distributions for variables. However, one often uses distributions that are easy to handle in practice. Quite often this means that the parents are given conjugate priors. This is also one of the limitations in BayesPy: only conjugate family prior distributions are accepted currently. Thus, although in principle one could give, for instance, gamma prior for the mean parameter `mu`, only Gaussian-family distributions are accepted because of the conjugacy. If the parent is not of a proper type, an error is raised. This conjugacy is checked automatically by BayesPy and `NoConverterError` is raised if a parent cannot be interpreted as being from a conjugate distribution.

Independence of the parents

Another a bit rarely encountered limitation is that the parents must be mutually independent (in the posterior factorization). Thus, a node cannot have the same stochastic node as several parents without intermediate stochastic nodes. For instance, the following leads to an error:

```
>>> from bayespy.nodes import Dot
>>> Y = Dot(X, X)
Traceback (most recent call last):
...
ValueError: Parent nodes are not independent
```

The error is raised because `X` is given as two parents for `Y`, and obviously `X` is not independent of `X` in the posterior approximation. Even if `X` is not given several times directly but there are some intermediate deterministic nodes, an error is raised because the deterministic nodes depend on their parents and thus the parents of `Y` would not be independent. However, it is valid that a node is a parent of another node via several paths if all the paths or all except one path has intermediate stochastic nodes. This is valid because the intermediate stochastic nodes have independent posterior approximations. Thus, for instance, the following construction does not raise errors:

```
>>> from bayespy.nodes import Dot
>>> Z = Gaussian(X, [[1, 0], [0, 1]])
>>> Y = Dot(X, Z)
```

This works because there is now an intermediate stochastic node `Z` on the other path from `X` node to `Y` node.

2.3.2 Effects of the nodes on inference

When constructing the network with nodes, the stochastic nodes actually define three important aspects:

1. the prior probability distribution for the variables,
2. the factorization of the posterior approximation,

3. the functional form of the posterior approximation for the variables.

Prior probability distribution

First, the most intuitive feature of the nodes is that they define the prior distribution. In the previous example, `mu` was a stochastic `GaussianARD` node corresponding to μ from the normal distribution, `tau` was a stochastic `Gamma` node corresponding to τ from the gamma distribution, and `y` was a stochastic `GaussianARD` node corresponding to y from the normal distribution with mean μ and precision τ . If we denote the set of all stochastic nodes by Ω , and by π_X the set of parents of a node X , the model is defined as

$$p(\Omega) = \prod_{X \in \Omega} p(X|\pi_X),$$

where nodes correspond to the terms $p(X|\pi_X)$.

Posterior factorization

Second, the nodes define the structure of the posterior approximation. The variational Bayesian approximation factorizes with respect to nodes, that is, each node corresponds to an independent probability distribution in the posterior approximation. In the previous example, `mu` and `tau` were separate nodes, thus the posterior approximation factorizes with respect to them: $q(\mu)q(\tau)$. Thus, the posterior approximation can be written as:

$$p(\tilde{\Omega}|\hat{\Omega}) \approx \prod_{X \in \tilde{\Omega}} q(X),$$

where $\tilde{\Omega}$ is the set of latent stochastic nodes and $\hat{\Omega}$ is the set of observed stochastic nodes. Sometimes one may want to avoid the factorization between some variables. For this purpose, there are some nodes which model several variables jointly without factorization. For instance, `GaussianGammaISO` is a joint node for μ and τ variables from the normal-gamma distribution and the posterior approximation does not factorize between μ and τ , that is, the posterior approximation is $q(\mu, \tau)$.

Functional form of the posterior

Last, the nodes define the functional form of the posterior approximation. Usually, the posterior approximation has the same or similar functional form as the prior. For instance, `Gamma` uses gamma distribution to also approximate the posterior distribution. Similarly, `GaussianARD` uses Gaussian distribution for the posterior. However, the posterior approximation of `GaussianARD` uses a full covariance matrix although the prior assumes a diagonal covariance matrix. Thus, there can be slight differences in the exact functional form of the posterior approximation but the rule of thumb is that the functional form of the posterior approximation is the same as or more general than the functional form of the prior.

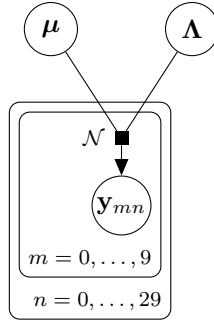
2.3.3 Using plate notation

Defining plates

Stochastic nodes take the optional parameter `plates`, which can be used to define plates of the variable. A plate defines the number of repetitions of a set of variables. For instance, a set of random variables \mathbf{y}_{mn} could be defined as

$$\mathbf{y}_{mn} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Lambda}), \quad m = 0, \dots, 9, \quad n = 0, \dots, 29.$$

This can also be visualized as a graphical model:



The variable has two plates: one for the index m and one for the index n . In BayesPy, this random variable can be constructed as:

```
>>> y = Gaussian(mu, Lambda, plates=(10,30))
```

Note: The plates are always given as a tuple of positive integers.

Plates also define indexing for the nodes, thus you can use simple NumPy-style slice indexing to obtain a subset of the plates:

```
>>> y_0 = y[0]
>>> y_0.plates
(30,)
>>> y_even = y[:,::2]
>>> y_even.plates
(10, 15)
>>> y_complex = y[:,5, 10:20:5]
>>> y_complex.plates
(5, 2)
```

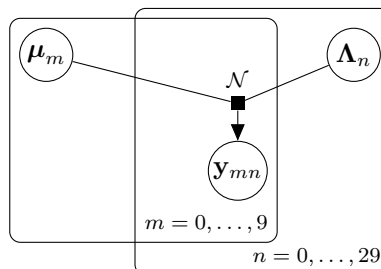
Note that this indexing is for the plates only, not for the random variable dimensions.

Sharing and broadcasting plates

Instead of having a common mean and precision matrix for all y_{mn} , it is also possible to share plates with parents. For instance, the mean could be different for each index m and the precision for each index n :

$$y_{mn} \sim \mathcal{N}(\mu_m, \Lambda_n), \quad m = 0, \dots, 9, \quad n = 0, \dots, 29.$$

which has the following graphical representation:



This can be constructed in BayesPy, for instance, as:

```
>>> from bayespy.nodes import Gaussian, Wishart
>>> mu = Gaussian([0, 0], [[1e-6, 0], [0, 1e-6]], plates=(10,1))
>>> Lambda = Wishart(2, [[1, 0], [0, 1]], plates=(1,30))
>>> X = Gaussian(mu, Lambda)
```

There are a few things to notice here. First, the plates are defined similarly as shapes in NumPy, that is, they use similar broadcasting rules. For instance, the plates $(10, 1)$ and $(1, 30)$ broadcast to $(10, 30)$. In fact, one could use plates $(10, 1)$ and $(30,)$ to get the broadcasted plates $(10, 30)$ because broadcasting compares the plates from right to left starting from the last axis. Second, X is not given `plates` keyword argument because the default plates are the plates broadcasted from the parents and that was what we wanted so it was not necessary to provide the keyword argument. If we wanted, for instance, plates $(20, 10, 30)$ for X , then we would have needed to provide `plates=(20, 10, 30)`.

The validity of the plates between a child and its parents is checked as follows. The plates are compared plate-wise starting from the last axis and working the way forward. A plate of the child is compatible with a plate of the parent if either of the following conditions is met:

1. The two plates have equal size
2. The parent has size 1 (or no plate)

Table below shows an example of compatible plates for a child node and its two parent nodes:

node	plates						
parent1		3	1	1	1	8	10
parent2			1	1	5	1	10
child	5	3	1	7	5	8	10

Plates in deterministic nodes

Note that plates can be defined explicitly only for stochastic nodes. For deterministic nodes, the plates are defined implicitly by the plate broadcasting rules from the parents. Deterministic nodes do not need more plates than this because there is no randomness. The deterministic node would just have the same value over the extra plates, but it is not necessary to do this explicitly because the child nodes of the deterministic node can utilize broadcasting anyway. Thus, there is no point in having extra plates in deterministic nodes, and for this reason, deterministic nodes do not use `plates` keyword argument.

Plates in constants

It is useful to understand how the plates and the shape of a random variable are connected. The shape of an array which contains all the plates of a random variable is the concatenation of the plates and the shape of the variable. For instance, consider a 2-dimensional Gaussian variable with plates $(3,)$. If you want the value of the constant mean vector and constant precision matrix to vary between plates, they are given as $(3, 2)$ -shape and $(3, 2, 2)$ -shape arrays, respectively:

```
>>> import numpy as np
>>> mu = [ [0,0], [1,1], [2,2] ]
>>> Lambda = [ [[1.0, 0.0],
...             [0.0, 1.0]],
...            [[1.0, 0.9],
...             [0.9, 1.0]],
...            [[1.0, -0.3],
...             [-0.3, 1.0]] ]
>>> X = Gaussian(mu, Lambda)
>>> np.shape(mu)
(3, 2)
>>> np.shape(Lambda)
(3, 2, 2)
>>> X.plates
(3,)
```


Thus, the leading axes of an array are the plate axes and the trailing axes are the random variable axes. In the example above, the mean vector has plates $(3,)$ and shape $(2,)$, and the precision matrix has plates $(3,)$ and shape $(2,2)$.

Factorization of plates

It is important to understand the independency structure the plates induce for the model. First, the repetitions defined by a plate are independent a priori given the parents. Second, the repetitions are independent in the posterior approximation, that is, the posterior approximation factorizes with respect to plates. Thus, the plates also have an effect on the independence structure of the posterior approximation, not only prior. If dependencies between a set of variables need to be handled, that set must be handled as a some kind of multi-dimensional variable.

Irregular plates

The handling of plates is not always as simple as described above. There are cases in which the plates of the parents do not map directly to the plates of the child node. The user API should mention such irregularities.

For instance, the parents of a mixture distribution have a plate which contains the different parameters for each cluster, but the variable from the mixture distribution does not have that plate:

```
>>> from bayespy.nodes import Gaussian, Wishart, Categorical, Mixture
>>> mu = Gaussian([[0], [0], [0]], [ [[1]], [[1]], [[1]] ])
>>> Lambda = Wishart(1, [ [[1]], [[1]], [[1]] ])
>>> Z = Categorical([1/3, 1/3, 1/3], plates=(100,))
>>> X = Mixture(Z, Gaussian, mu, Lambda)
>>> mu.plates
(3,)
>>> Lambda.plates
(3,)
>>> Z.plates
(100,)
>>> X.plates
(100,)
```

The plates $(3,)$ and $(100,)$ should not broadcast according to the rules mentioned above. However, when validating the plates, `Mixture` removes the plate which corresponds to the clusters in `mu` and `Lambda`. Thus, `X` has plates which are the result of broadcasting plates $()$ and $(100,)$ which equals $(100,)$.

Also, sometimes the plates of the parents may be mapped to the variable axes. For instance, an automatic relevance determination (ARD) prior for a Gaussian variable is constructed by giving the diagonal elements of the precision matrix (or tensor). The Gaussian variable itself can be a scalar, a vector, a matrix or a tensor. A set of five 4×3 -dimensional Gaussian matrices with ARD prior is constructed as:

```
>>> from bayespy.nodes import GaussianARD, Gamma
>>> tau = Gamma(1, 1, plates=(5,4,3))
>>> X = GaussianARD(0, tau, shape=(4,3))
>>> tau.plates
(5, 4, 3)
>>> X.plates
(5,)
```

Note how the last two plate axes of `tau` are mapped to the variable axes of `X` with shape $(4,3)$ and the plates of `X` are obtained by taking the remaining leading plate axes of `tau`.

2.3.4 Example model: Principal component analysis

Now, we'll construct a bit more complex model which will be used in the following sections. The model is a probabilistic version of principal component analysis (PCA):

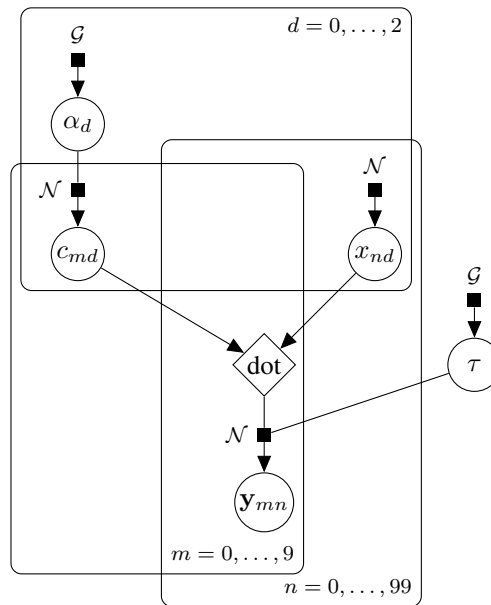
$$\mathbf{Y} = \mathbf{C}\mathbf{X}^T + \text{noise}$$

where \mathbf{Y} is $M \times N$ data matrix, \mathbf{C} is $M \times D$ loading matrix, \mathbf{X} is $N \times D$ state matrix, and noise is isotropic Gaussian. The dimensionality D is usually assumed to be much smaller than M and N .

A probabilistic formulation can be written as:

$$\begin{aligned} p(\mathbf{Y}) &= \prod_{m=0}^{M-1} \prod_{n=0}^{N-1} \mathcal{N}(y_{mn} | \mathbf{c}_m^T \mathbf{x}_n, \tau) \\ p(\mathbf{X}) &= \prod_{n=0}^{N-1} \prod_{d=0}^{D-1} \mathcal{N}(x_{nd} | 0, 1) \\ p(\mathbf{C}) &= \prod_{m=0}^{M-1} \prod_{d=0}^{D-1} \mathcal{N}(c_{md} | 0, \alpha_d) \\ p(\boldsymbol{\alpha}) &= \prod_{d=0}^{D-1} \mathcal{G}(\alpha_d | 10^{-3}, 10^{-3}) \\ p(\tau) &= \mathcal{G}(\tau | 10^{-3}, 10^{-3}) \end{aligned}$$

where we have given automatic relevance determination (ARD) prior for \mathbf{C} . This can be visualized as a graphical model:



Now, let us construct this model in BayesPy. First, we'll define the dimensionality of the latent space in our model:

```
>>> D = 3
```

Then the prior for the latent states \mathbf{X} :

```
>>> X = GaussianARD(0, 1,
...                 shape=(D, ),
...                 plates=(1, 100),
...                 name='X')
```

Note that the shape of X is $(D,)$, although the latent dimensions are marked with a plate in the graphical model and they are conditionally independent in the prior. However, we want to (and need to) model the posterior dependency of the latent dimensions, thus we cannot factorize them, which would happen if we used `plates=(1, 100, D)` and `shape=()`. The first plate axis with size 1 is given just for clarity.

The prior for the ARD parameters α of the loading matrix:

```
>>> alpha = Gamma(1e-3, 1e-3,
...                plates=(D, ),
...                name='alpha')
```

The prior for the loading matrix C :

```
>>> C = GaussianARD(0, alpha,
...                 shape=(D, ),
...                 plates=(10, 1),
...                 name='C')
```

Again, note that the shape is the same as for X for the same reason. Also, the plates of α , $(D,)$, are mapped to the full shape of the node C , $(10, 1, D)$, using standard broadcasting rules.

The dot product is just a deterministic node:

```
>>> F = Dot(C, X)
```

However, note that `Dot` requires that the input Gaussian nodes have the same shape and that this shape has exactly one axis, that is, the variables are vectors. This is the reason why we used shape $(D,)$ for X and C but from a bit different perspective. The node computes the inner product of D -dimensional vectors resulting in plates $(10, 100)$ broadcasted from the plates $(1, 100)$ and $(10, 1)$:

```
>>> F.plates
(10, 100)
```

The prior for the observation noise τ :

```
>>> tau = Gamma(1e-3, 1e-3, name='tau')
```

Finally, the observations are conditionally independent Gaussian scalars:

```
>>> Y = GaussianARD(F, tau, name='Y')
```

Now we have defined our model and the next step is to observe some data and to perform inference.

2.4 Performing inference

Approximation of the posterior distribution can be divided into several steps:

- Observe some nodes
- Choose the inference engine
- Initialize the posterior approximation
- Run the inference algorithm

In order to illustrate these steps, we'll be using the PCA model constructed in the previous section.

2.4.1 Observing nodes

First, let us generate some toy data:

```
>>> c = np.random.randn(10, 2)
>>> x = np.random.randn(2, 100)
>>> data = np.dot(c, x) + 0.1*np.random.randn(10, 100)
```

The data is provided by simply calling `observe` method of a stochastic node:

```
>>> Y.observe(data)
```

It is important that the shape of the `data` array matches the plates and shape of the node `Y`. For instance, if `Y` was `Wishart` node for 3×3 matrices with plates $(5, 1, 10)$, the full shape of `Y` would be $(5, 1, 10, 3, 3)$. The data array should have this shape exactly, that is, no broadcasting rules are applied.

Missing values

It is possible to mark missing values by providing a mask which is a boolean array:

```
>>> Y.observe(data, mask=[[True], [False], [False], [True], [True],
...                        [False], [True], [True], [True], [False]])
```

`True` means that the value is observed and `False` means that the value is missing. The shape of the above mask is $(10, 1)$, which broadcasts to the plates of `Y`, $(10, 100)$. Thus, the above mask means that the second, third, sixth and tenth rows of the 10×100 data matrix are missing.

The mask is applied to the *plates*, not to the data array directly. This means that it is not possible to observe a random variable partially, each repetition defined by the plates is either fully observed or fully missing. Thus, the mask is applied to the plates. It is often possible to circumvent this seemingly tight restriction by adding an observable child node which factorizes more.

The shape of the mask is broadcasted to plates using standard NumPy broadcasting rules. So, if the variable has plates $(5, 1, 10)$, the mask could have a shape $()$, $(1,)$, $(1, 1)$, $(1, 1, 1)$, $(10,)$, $(1, 10)$, $(1, 1, 10)$, $(5, 1, 1)$ or $(5, 1, 10)$. In order to speed up the inference, missing values are automatically integrated out if they are not needed as latent variables to child nodes. This leads to faster convergence and more accurate approximations.

2.4.2 Choosing the inference method

Inference methods can be found in `bayespy.inference` package. Currently, only variational Bayesian approximation is implemented (`bayespy.inference.VB`). The inference engine is constructed by giving the stochastic nodes of the model.

```
>>> from bayespy.inference import VB
>>> Q = VB(Y, C, X, alpha, tau)
```

There is no need to give any deterministic nodes. Currently, the inference engine does not automatically search for stochastic parents and children, thus it is important that all stochastic nodes of the model are given. This should be made more robust in future versions.

A node of the model can be obtained by using the name of the node as a key:

```
>>> Q['X']
<bayespy.inference.vmp.nodes.gaussian.GaussianARD object at 0x...>
```

Note that the returned object is the same as the node object itself:

```
>>> Q['X'] is X
True
```

Thus, one may use the object `X` when it is available. However, if the model and the inference engine are constructed in another function or module, the node object may not be available directly and this feature becomes useful.

2.4.3 Initializing the posterior approximation

The inference engines give some initialization to the stochastic nodes by default. However, the inference algorithms can be sensitive to the initialization, thus it is sometimes necessary to have better control over the initialization. For VB, the following initialization methods are available:

- `initialize_from_prior`: Use the current states of the parent nodes to update the node. This is the default initialization.
- `initialize_from_parameters`: Use the given parameter values for the distribution.
- `initialize_from_value`: Use the given value for the variable.
- `initialize_from_random`: Draw a random value for the variable. The random sample is drawn from the current state of the node's distribution.

Note that `initialize_from_value` and `initialize_from_random` initialize the distribution with a value of the variable instead of parameters of the distribution. Thus, the distribution is actually a delta distribution with a peak on the value after the initialization. This state of the distribution does not have proper natural parameter values nor normalization, thus the VB lower bound terms are `np.nan` for this initial state.

These initialization methods can be used to perform even a bit more complex initializations. For instance, a Gaussian distribution could be initialized with a random mean and variance 0.1. In our PCA model, this can be obtained by

```
>>> X.initialize_from_parameters(np.random.randn(1, 100, D), 10)
```

Note that the shape of the random mean is the sum of the plates `(1, 100)` and the variable shape `(D,)`. In addition, instead of variance, `GaussianARD` uses precision as the second parameter, thus we initialized the variance to $\frac{1}{10}$. This random initialization is important in our PCA model because the default initialization gives `C` and `X` zero mean. If the mean of the other variable was zero when the other is updated, the other variable gets zero mean too. This would lead to an update algorithm where both means remain zeros and effectively no latent space is found. Thus, it is important to give non-zero random initialization for `X` if `C` is updated before `X` the first time. It is typical that at least some nodes need be initialized with some randomness.

By default, nodes are initialized with the method `initialize_from_prior`. The method is not very time consuming but if for any reason you want to avoid that default initialization computation, you can provide `initialize=False` when creating the stochastic node. However, the node does not have a proper state in that case, which leads to errors in VB learning unless the distribution is initialized using the above methods.

2.4.4 Running the inference algorithm

The approximation methods are based on iterative algorithms, which can be run using `update` method. By default, it takes one iteration step updating all nodes once:

```
>>> Q.update()
Iteration 1: loglike=-9.305259e+02 (... seconds)
```

The `loglike` tells the VB lower bound. The order in which the nodes are updated is the same as the order in which the nodes were given when creating `Q`. If you want to change the order or update only some of the nodes, you can give as arguments the nodes you want to update and they are updated in the given order:

```
>>> Q.update(C, X)
Iteration 2: loglike=-8.818976e+02 (... seconds)
```

It is also possible to give the same node several times:

```
>>> Q.update(C, X, C, tau)
Iteration 3: loglike=-8.071222e+02 (... seconds)
```

Note that each call to `update` is counted as one iteration step although not variables are necessarily updated. Instead of doing one iteration step, `repeat` keyword argument can be used to perform several iteration steps:

```
>>> Q.update(repeat=10)
Iteration 4: loglike=-7.167588e+02 (... seconds)
Iteration 5: loglike=-6.827873e+02 (... seconds)
Iteration 6: loglike=-6.259477e+02 (... seconds)
Iteration 7: loglike=-4.725400e+02 (... seconds)
Iteration 8: loglike=-3.270816e+02 (... seconds)
Iteration 9: loglike=-2.208865e+02 (... seconds)
Iteration 10: loglike=-1.658761e+02 (... seconds)
Iteration 11: loglike=-1.469468e+02 (... seconds)
Iteration 12: loglike=-1.420311e+02 (... seconds)
Iteration 13: loglike=-1.405139e+02 (... seconds)
```

The VB algorithm stops automatically if it converges, that is, the relative change in the lower bound is below some threshold:

```
>>> Q.update(repeat=1000)
Iteration 14: loglike=-1.396481e+02 (... seconds)
...
Iteration 488: loglike=-1.224106e+02 (... seconds)
Converged at iteration 488.
```

Now the algorithm stopped before taking 1000 iteration steps because it converged. The relative tolerance can be adjusted by providing `tol` keyword argument to the `update` method:

```
>>> Q.update(repeat=10000, tol=1e-6)
Iteration 489: loglike=-1.224094e+02 (... seconds)
...
Iteration 847: loglike=-1.222506e+02 (... seconds)
Converged at iteration 847.
```

Making the tolerance smaller, may improve the result but it may also significantly increase the iteration steps until convergence.

Instead of using `update` method of the inference engine VB, it is possible to use the `update` methods of the nodes directly as

```
>>> C.update()

or

>>> Q['C'].update()
```

However, this is not recommended, because the `update` method of the inference engine VB is a wrapper which, in addition to calling the nodes' `update` methods, checks for convergence and does a few other useful minor things. But if for any reason these direct update methods are needed, they can be used.

Parameter expansion

Sometimes the VB algorithm converges very slowly. This may happen when the variables are strongly coupled in the true posterior but factorized in the approximate posterior. This coupling leads to zigzagging of the variational parameters which progresses slowly. One solution to this problem is to use parameter expansion. The idea is to add an auxiliary variable which parameterizes the posterior approximation of several variables. Then optimizing this auxiliary variable actually optimizes several posterior approximations jointly leading to faster convergence.

The parameter expansion is model specific. Currently in BayesPy, only state-space models have built-in parameter expansions available. These state-space models contain a variable which is a dot product of two variables (plus some noise):

$$y = \mathbf{c}^T \mathbf{x} + \text{noise}$$

The parameter expansion can be motivated by noticing that we can add an auxiliary variable which rotates the variables \mathbf{c} and \mathbf{x} so that the dot product is unaffected:

$$y = \mathbf{c}^T \mathbf{x} + \text{noise} = \mathbf{c}^T \mathbf{R} \mathbf{R}^{-1} \mathbf{x} + \text{noise} = (\mathbf{R}^T \mathbf{c})^T (\mathbf{R}^{-1} \mathbf{x}) + \text{noise}$$

Now, applying this rotation to the posterior approximations $q(\mathbf{c})$ and $q(\mathbf{x})$, and optimizing the VB lower bound with respect to the rotation leads to parameterized joint optimization of \mathbf{c} and \mathbf{x} .

The available parameter expansion methods are in module `transformations`:

```
>>> from bayespy.inference.vmp import transformations
```

First, you create the rotation transformations for the two variables:

```
>>> rotX = transformations.RotateGaussianARD(X)
>>> rotC = transformations.RotateGaussianARD(C, alpha)
```

Here, the rotation for \mathbf{C} provides the ARD parameters α so they are updated simultaneously. In addition to `RotateGaussianARD`, there are a few other built-in rotations defined, for instance, `RotateGaussian` and `RotateGaussianMarkovChain`. It is extremely important that the model satisfies the assumptions made by the rotation class and the user is mostly responsible for this. The optimizer for the rotations is constructed by giving the two rotations and the dimensionality of the rotated space:

```
>>> R = transformations.RotationOptimizer(rotC, rotX, D)
```

Now, calling `rotate` method will find optimal rotation and update the relevant nodes (\mathbf{X} , \mathbf{C} and α) accordingly:

```
>>> R.rotate()
```

Let us see how our iteration would have gone if we had used this parameter expansion. First, let us re-initialize our nodes and VB algorithm:

```
>>> alpha.initialize_from_prior()
>>> C.initialize_from_prior()
>>> X.initialize_from_parameters(np.random.randn(1, 100, D), 10)
>>> tau.initialize_from_prior()
>>> Q = VB(Y, C, X, alpha, tau)
```

Then, the rotation is set to run after each iteration step:

```
>>> Q.callback = R.rotate
```

Now the iteration converges to the relative tolerance 10^{-6} much faster:

```
>>> Q.update(repeat=1000, tol=1e-6)
Iteration 1: loglike=-9.363500e+02 (... seconds)
...
Iteration 18: loglike=-1.221354e+02 (... seconds)
Converged at iteration 18.
```

The convergence took 18 iterations with rotations and 488 or 847 iterations without the parameter expansion. In addition, the lower bound is improved slightly. One can compare the number of iteration steps in this case because the cost per iteration step with or without parameter expansion is approximately the same. Sometimes the parameter expansion can have the drawback that it converges to a bad local optimum. Usually, this can be solved by updating the nodes near the observations a few times before starting to update the hyperparameters and to use parameter expansion. In any case, the parameter expansion is practically necessary when using state-space models in order to converge to a proper solution in a reasonable time.

2.5 Examining the results

After the results have been obtained, it is important to be able to examine the results easily. The results can be examined either numerically by inspecting numerical arrays or visually by plotting distributions of the nodes. In addition, the posterior distributions can be visualized during the learning algorithm and the results can be saved into a file.

2.5.1 Plotting the results

The module `plot` offers some plotting basic functionality:

```
>>> import bayespy.plot as bpplt
```

The module contains `matplotlib.pyplot` module if the user needs that. For instance, interactive plotting can be enabled as:

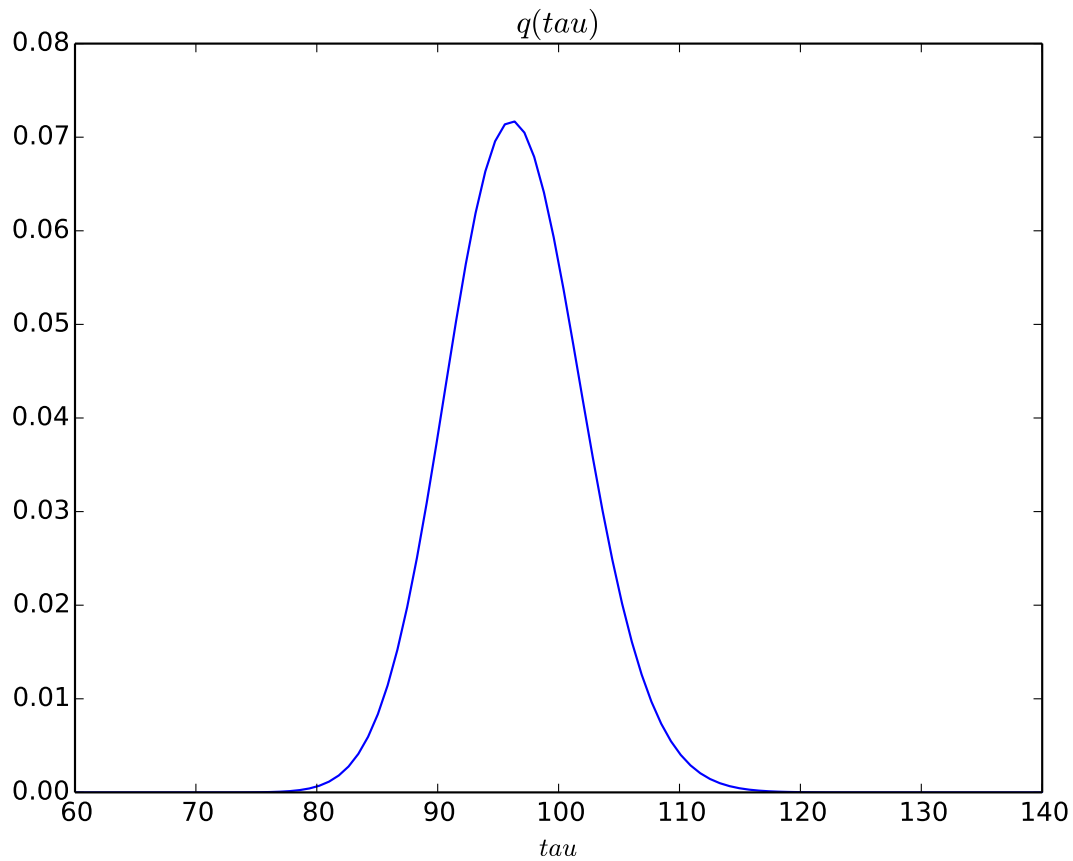
```
>>> bpplt.pyplot.ion()
```

The `plot` module contains some functions but it is not a very comprehensive collection, thus the user may need to write some problem- or model-specific plotting functions. The current collection is:

- `pdf()`: show probability density function of a scalar
- `contour()`: show probability density function of two-element vector
- `hinton()`: show the Hinton diagram
- `plot()`: show value as a function

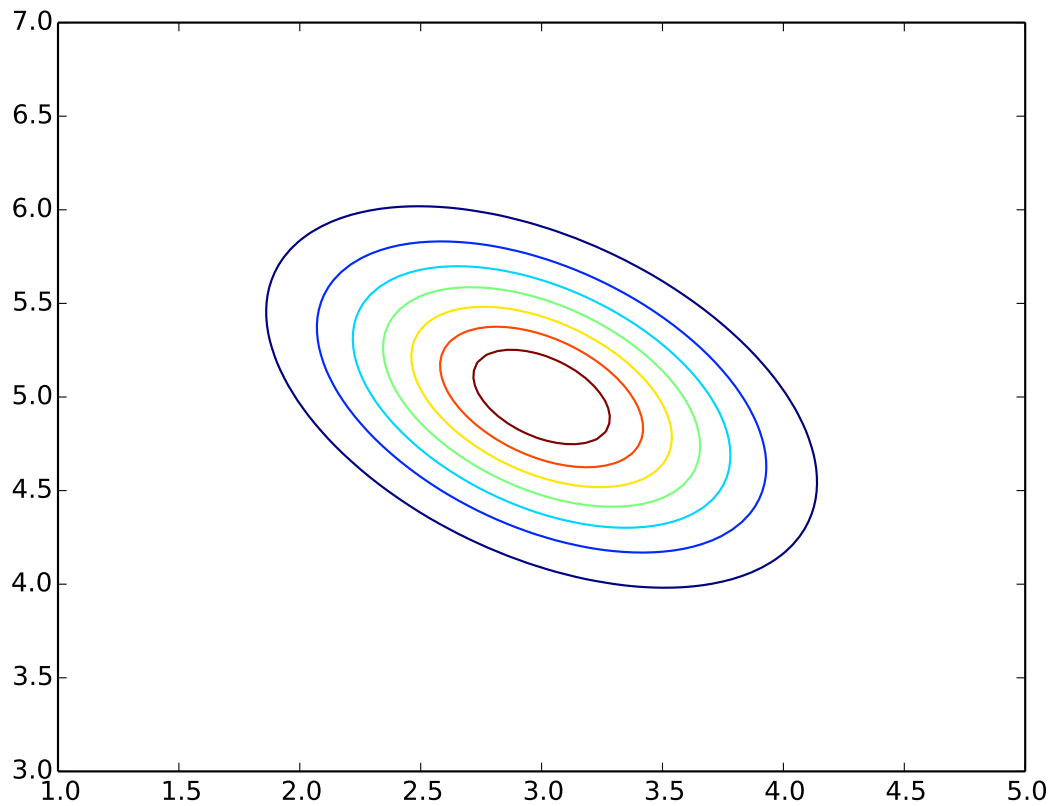
The probability density function of a scalar random variable can be plotted using the function `pdf()`:

```
>>> bpplt.pyplot.figure()
<matplotlib.figure.Figure object at 0x...>
>>> bpplt.pdf(Q['tau'], np.linspace(60, 140, num=100))
[<matplotlib.lines.Line2D object at 0x...>]
```

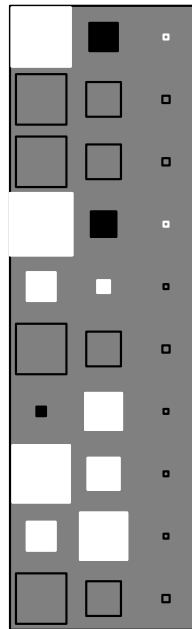
The variable `tau` models the inverse variance of the noise, for which the true value is $0.1^{-2} = 100$. Thus, the posterior captures the true value quite accurately. Similarly, the function `contour()` can be used to plot the probability density function of a 2-dimensional variable, for instance:

```
>>> V = Gaussian([3, 5], [[4, 2], [2, 5]])
>>> bpplt.pyplot.figure()
<matplotlib.figure.Figure object at 0x...>
>>> bpplt.contour(V, np.linspace(1, 5, num=100), np.linspace(3, 7, num=100))
<matplotlib.contour.QuadContourSet object at 0x...>
```



Both `pdf()` and `contour()` require that the user provides the grid on which the probability density function is computed. They also support several keyword arguments for modifying the output, similarly as `plot` and `contour` in `matplotlib.pyplot`. These functions can be used only for stochastic nodes. A few other plot types are also available as built-in functions. A Hinton diagram can be plotted as:

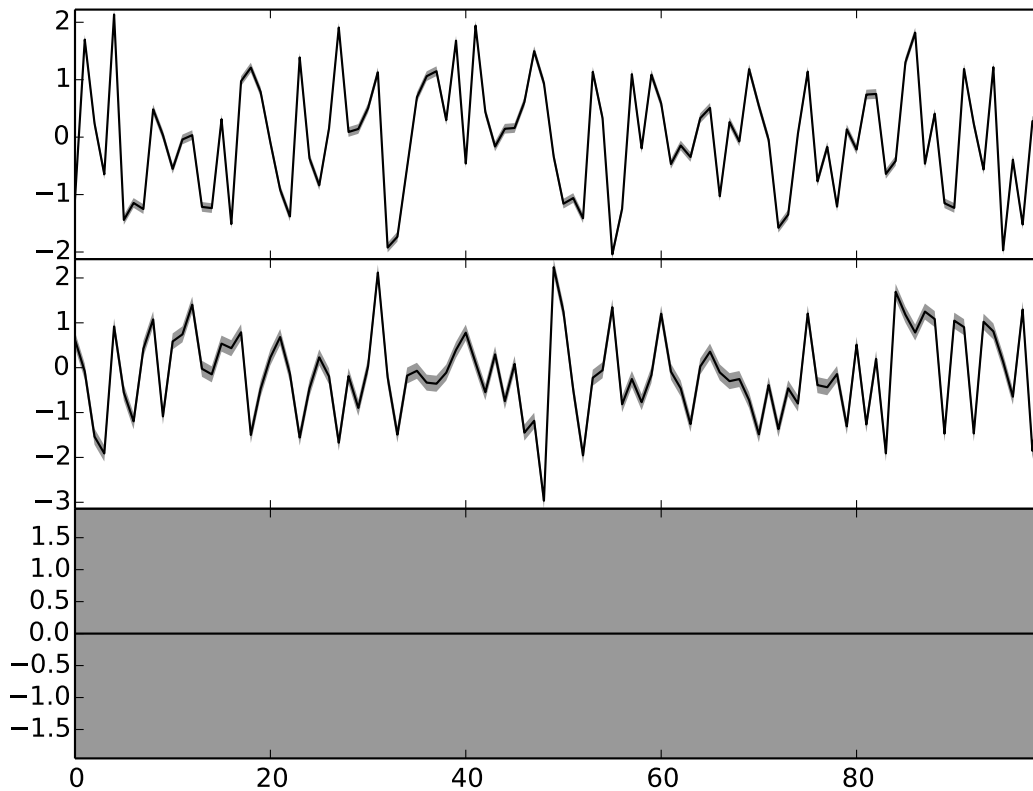
```
>>> bpplt.pyplot.figure()
<matplotlib.figure.Figure object at 0x...>
>>> bpplt.hinton(C)
```



The diagram shows the elements of the matrix C . The size of the filled rectangle corresponds to the absolute value of the element mean, and white and black correspond to positive and negative values, respectively. The non-filled rectangle shows standard deviation. From this diagram it is clear that the third column of C has been pruned out and the rows that were missing in the data have zero mean and column-specific variance. The function `hinton()` is a simple wrapper for node-specific Hinton diagram plotters, such as `gaussian_hinton()` and `dirichlet_hinton()`. Thus, the keyword arguments depend on the node which is plotted.

Another plotting function is `plot()`, which just plots the values of the node over one axis as a function:

```
>>> bpplt.pyplot.figure()
<matplotlib.figure.Figure object at 0x...>
>>> bpplt.plot(X, axis=-2)
```



Now, the `axis` is the second last axis which corresponds to $n = 0, \dots, N - 1$. As $D = 3$, there are three subplots. For Gaussian variables, the function shows the mean and two standard deviations. The plot shows that the third component has been pruned out, thus the method has been able to recover the true dimensionality of the latent space. It also has similar keyword arguments to `plot` function in `matplotlib.pyplot`. Again, `plot()` is a simple wrapper over node-specific plotting functions, thus it supports only some node classes.

2.5.2 Monitoring during the inference algorithm

It is possible to plot the distribution of the nodes during the learning algorithm. This is useful when the user is interested to see how the distributions evolve during learning and what is happening to the distributions. In order to utilize monitoring, the user must set plotters for the nodes that he or she wishes to monitor. This can be done either when creating the node or later at any time.

The plotters are set by creating a plotter object and providing this object to the node. The plotter is a wrapper of one of the plotting functions mentioned above: `PDFPlotter`, `ContourPlotter`, `HintonPlotter` or `FunctionPlotter`. Thus, our example model could use the following plotters:

```
>>> tau.set_plotter(bpplt.PDFPlotter(np.linspace(60, 140, num=100)))
>>> C.set_plotter(bpplt.HintonPlotter())
>>> X.set_plotter(bpplt.FunctionPlotter(axis=-2))
```

These could have been given at node creation as a keyword argument `plotter`:

```
>>> V = Gaussian([3, 5], [[4, 2], [2, 5]],
...               plotter=bpplt.ContourPlotter(np.linspace(1, 5, num=100),
...               np.linspace(3, 7, num=100)))
```

When the plotter is set, one can use the `plot` method of the node to perform plotting:

```
>>> V.plot()
<matplotlib.contour.QuadContourSet object at 0x...>
```

Nodes can also be plotted using the `plot` method of the inference engine:

```
>>> Q.plot('C')
```

This method remembers the figure in which a node has been plotted and uses that every time it plots the same node. In order to monitor the nodes during learning, it is possible to use the keyword argument `plot`:

```
>>> Q.update(repeat=5, plot=True, tol=np.nan)
Iteration 68: loglike=-1.221354e+02 (... seconds)
Iteration 69: loglike=-1.221354e+02 (... seconds)
Iteration 70: loglike=-1.221354e+02 (... seconds)
Iteration 71: loglike=-1.221354e+02 (... seconds)
Iteration 72: loglike=-1.221354e+02 (... seconds)
```

Each node which has a plotter set will be plotted after it is updated. Note that this may slow down the inference significantly if the plotting operation is time consuming.

2.5.3 Posterior parameters and moments

If the built-in plotting functions are not sufficient, it is possible to use `matplotlib.pyplot` for custom plotting. Each node has `get_moments` method which returns the moments and they can be used for plotting. Stochastic exponential family nodes have natural parameter vectors which can also be used. In addition to plotting, it is also possible to just print the moments or parameters in the console.

2.5.4 Saving and loading results

The results of the inference engine can be easily saved and loaded using `VB.save()` and `VB.load()` methods:

```
>>> Q.save(filename='tmp.hdf5')
>>> Q.load(filename='tmp.hdf5')
```

The results are stored in a HDF5 file. The user may set an autosave file in which the results are automatically saved regularly. Autosave filename can be set at creation time by `autosave_filename` keyword argument or later using `VB.set_autosave()` method. If autosave file has been set, the `VB.save()` and `VB.load()` methods use that file by default. In order for the saving to work, all stochastic nodes must have been given (unique) names.

However, note that these methods do *not* save nor load the node definitions. It means that the user must create the nodes and the inference engine and then use `VB.load()` to set the state of the nodes and the inference engine. If there are any differences in the model that was saved and the one which is tried to update using loading, then loading does not work. Thus, the user should keep the model construction unmodified in a Python file in order to be able to load the results later. Or if the user wishes to share the results, he or she must share the model construction Python file with the HDF5 results file.

EXAMPLES

3.1 Regression

3.1.1 Linear regression

```
import numpy as np
k = 2
c = 5
s = 2

x = np.arange(10)
y = k*x + c + s*np.random.randn(10)

from bayespy.nodes import GaussianARD
B = GaussianARD(0, 1e-6, shape=(2,))

X = np.vstack([x, np.ones(len(x))]).T

from bayespy.nodes import SumMultiply
F = SumMultiply('i,i', B, X)

from bayespy.nodes import Gamma
tau = Gamma(1e-3, 1e-3)

Y = GaussianARD(F, tau)
Y.observe(y)

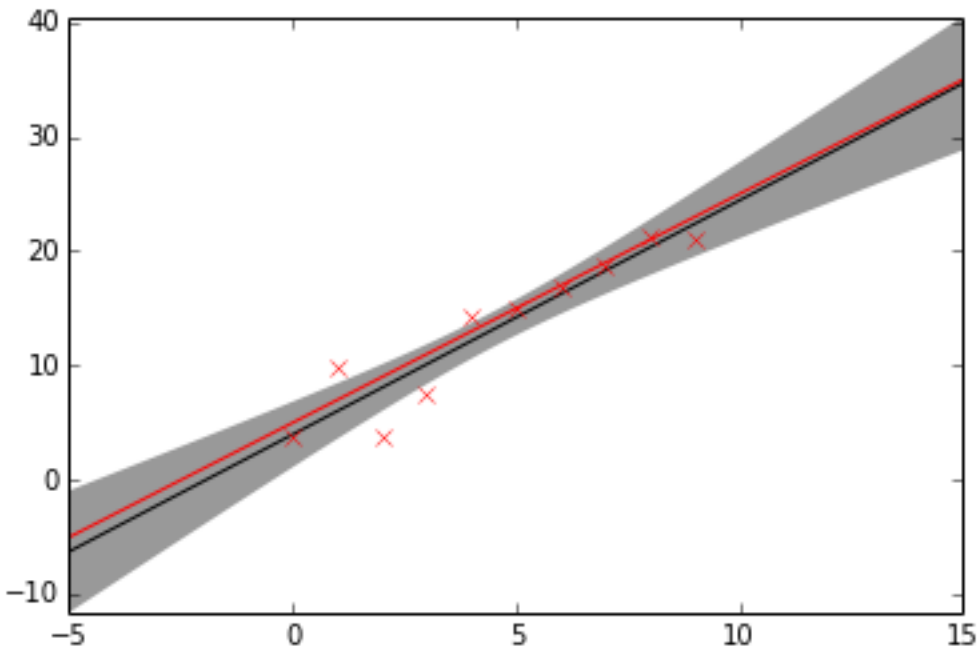
from bayespy.inference import VB
Q = VB(Y, B, tau)

Q.update(repeat=100)

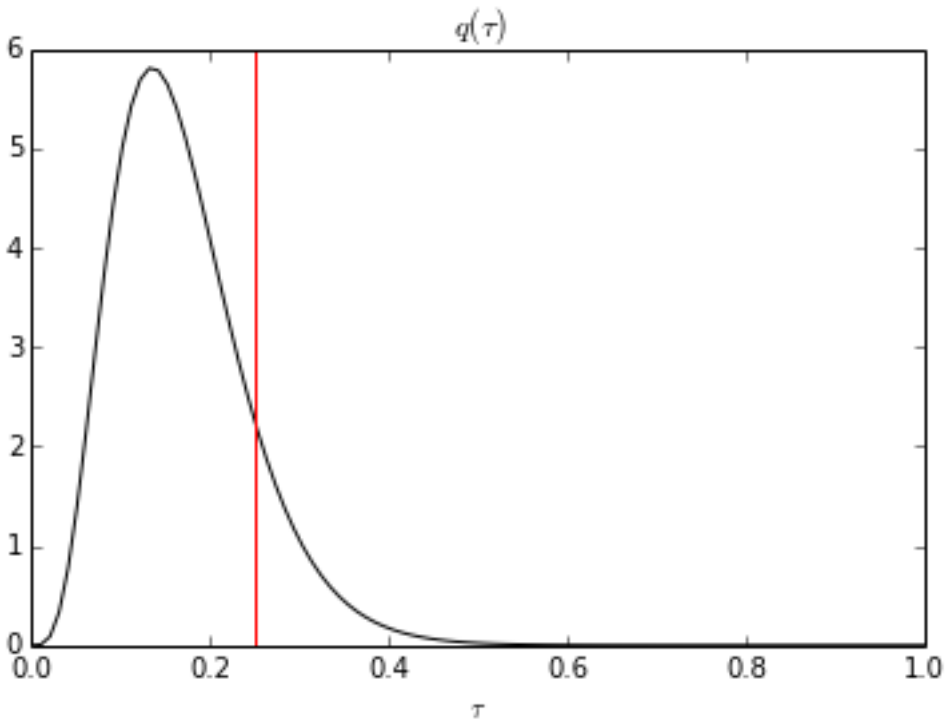
import bayespy.plot as bpplt
# These two lines are needed to enable inline plotting IPython Notebooks
%matplotlib inline
bpplt.pyplot.plot([])

xh = np.linspace(-5, 15, 100)
Xh = np.vstack([xh, np.ones(len(xh))]).T
Fh = SumMultiply('i,i', B, Xh)
bpplt.plot(Fh, x=xh, scale=2)
bpplt.plot(y, x=x, color='r', marker='x', linestyle='None')
bpplt.plot(k*xh+c, x=xh, color='r');
```

```
Iteration 1: loglike=-4.515537e+01 (0.000 seconds)
Iteration 2: loglike=-4.429472e+01 (0.010 seconds)
Iteration 3: loglike=-4.428241e+01 (0.000 seconds)
Iteration 4: loglike=-4.428197e+01 (0.000 seconds)
Iteration 5: loglike=-4.428195e+01 (0.010 seconds)
Converged.
```



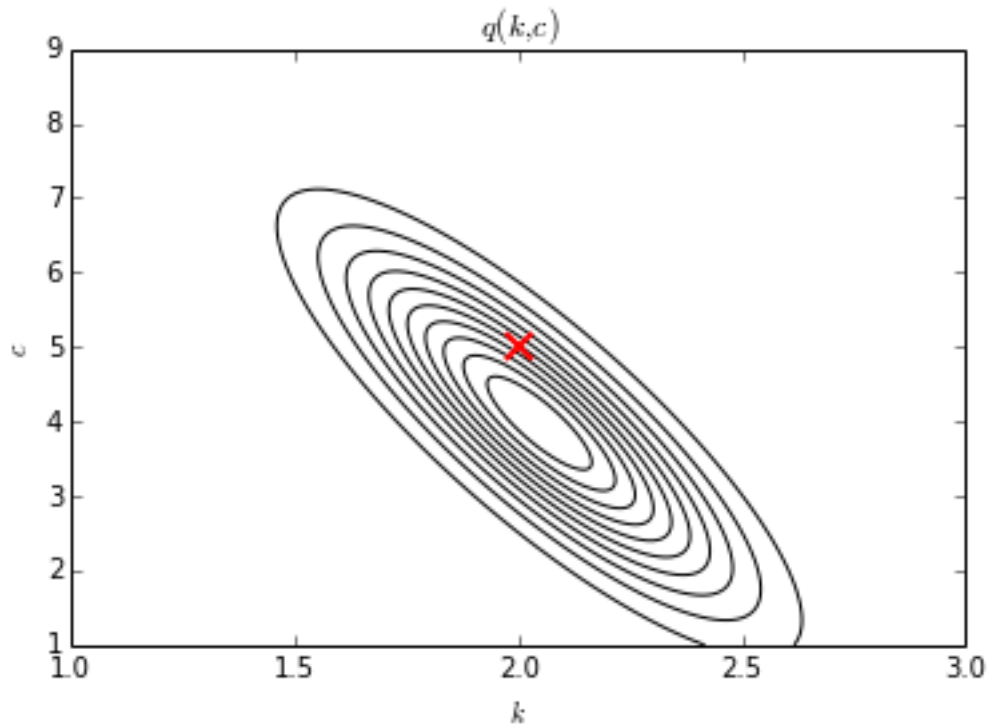
```
bpplt.pdf(tau, np.linspace(1e-6,1,100), color='k')
bpplt.pyplot.axvline(s**(-2), color='r')
# Add labels
bpplt.pyplot.title(r'$q(\tau)$')
bpplt.pyplot.xlabel(r'$\tau$');
```

```

bpplt.contour(B, np.linspace(1,3,1000), np.linspace(1,9,1000), n=10, colors='k')
bpplt.plot(c, x=k, color='r', marker='x', linestyle='None', markersize=10, markedgewidth=2)
# Add labels
bpplt.pyplot.title(r'$q(k,c)$')
bpplt.pyplot.xlabel(r'$k$')
bpplt.pyplot.ylabel(r'$c$');

```



3.1.2 Improving accuracy

```
from bayespy.nodes import GaussianGammaISO
B_tau = GaussianGammaISO(np.zeros(2), 1e-6*np.identity(2), 1e-3, 1e-3)

F_tau = SumMultiply('i,i', B_tau, X)

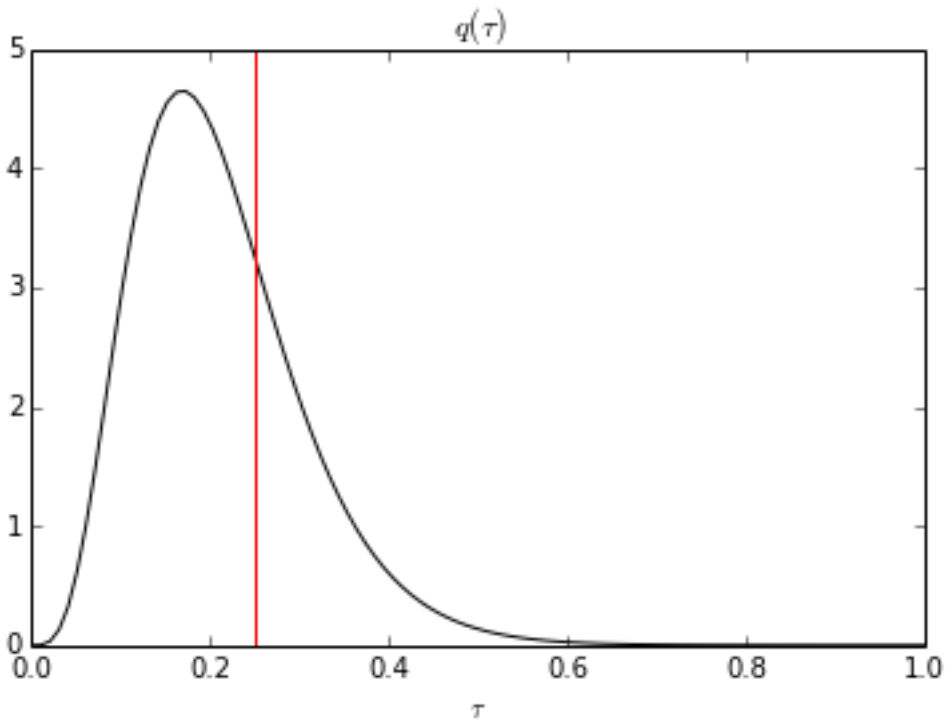
Y = GaussianARD(F_tau, 1)
Y.observe(y)

from bayespy.inference import VB
Q = VB(Y, B_tau)

Q.update(repeat=10)

Iteration 1: loglike=-4.594957e+01 (0.000 seconds)
Iteration 2: loglike=-4.594957e+01 (0.000 seconds)
Converged.

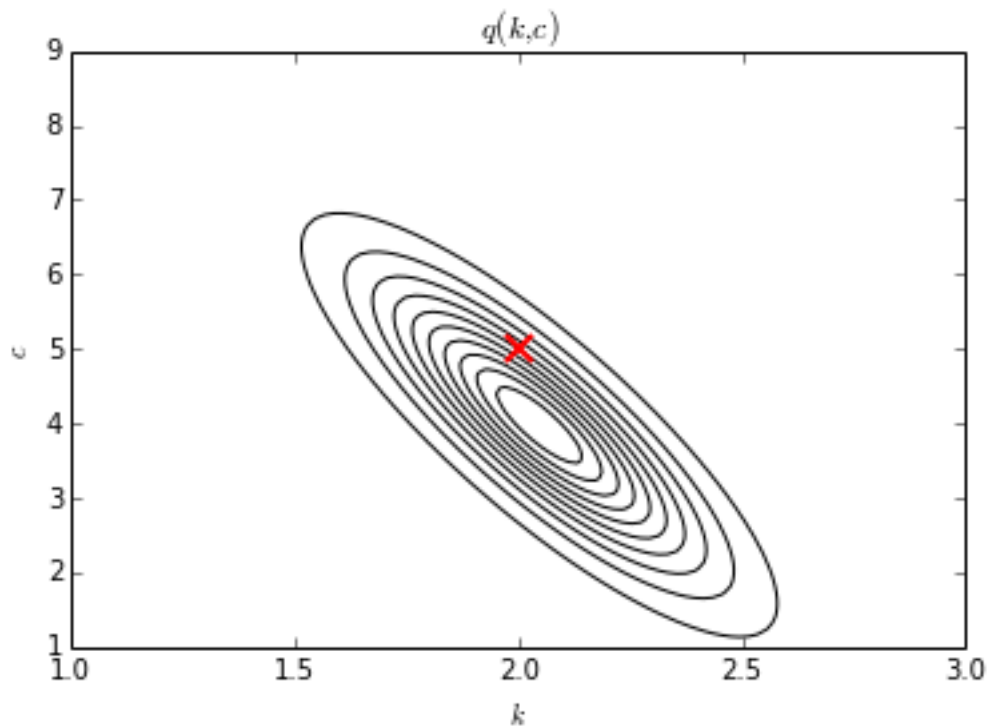
bpplt.pdf(B_tau.get_marginal_logpdf(gaussian=None, gamma=True),
          np.linspace(1e-6, 1, 100), color='k')
bpplt.pyplot.axvline(s**(-2), color='r')
# Add labels
bpplt.pyplot.title(r'$q(\tau)$')
bpplt.pyplot.xlabel(r'$\tau$');
```



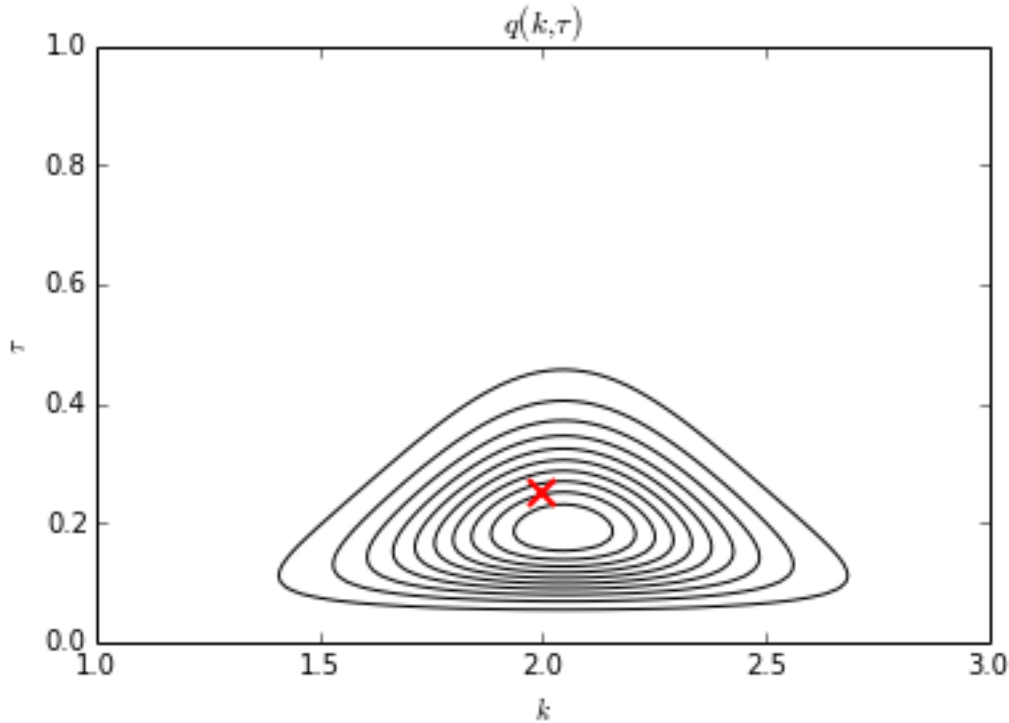
```

bpplt.contour(B_tau.get_marginal_logpdf(gaussian=[0,1], gamma=False),
              np.linspace(1,3,100), np.linspace(1,9,100),
              n=10, colors='k')
# Plot the true value
bpplt.plot(c, x=k, color='r', marker='x', linestyle='None', markersize=10, markeredgewidth=2)
# Add labels
bpplt.pyplot.title(r'$q(k,c)$')
bpplt.pyplot.xlabel(r'$k$')
bpplt.pyplot.ylabel(r'$c$');

```



```
bpplt.contour(B_tau.get_marginal_logpdf(gaussian=[0], gamma=True),
              np.linspace(1, 3, 100), np.linspace(1e-6, 1, 100),
              n=10, colors='k')
bpplt.plot(s**(-2), x=k, color='r', marker='x', linestyle='None', markersize=10, markeredgewidth=2)
bpplt.pyplot.title(r'$q(k, \tau)$')
bpplt.pyplot.xlabel(r'$k$')
bpplt.pyplot.ylabel(r'$\tau$');
```



```
xh = np.linspace(-5, 15, 100)
Xh = np.vstack([xh, np.ones(len(xh))]).T
Fh_tau = SumMultiply('i,i', B_tau, Xh)
bpplt.plot(Fh_tau, x=xh, scale=2)
bpplt.plot(y, x=x, color='r', marker='x', linestyle='None')
bpplt.plot(k*xh+c, x=xh, color='r')
```

```
AttributeError                                Traceback (most recent call last)

<ipython-input-8-bad1c68bbf3d> in <module>()
      2 Xh = np.vstack([xh, np.ones(len(xh))]).T
      3 Fh_tau = SumMultiply('i,i', B_tau, Xh)
----> 4 bpplt.plot(Fh_tau, x=xh, scale=2)
      5 bpplt.plot(y, x=x, color='r', marker='x', linestyle='None')
      6 bpplt.plot(k*xh+c, x=xh, color='r')
```

```
/home/jluttine/workspace/bayespy/bayespy/plot.py in plot(Y, axis, scale, center, **kwargs)
    125         return plot_gaussian(Y, axis=axis, scale=scale, center=center, **kwargs)
    126
--> 127     (mu, var) = Y.get_mean_and_variance()
    128     std = np.sqrt(var)
    129
```

AttributeError: 'SumMultiply' object has no attribute 'get_mean_and_variance'

3.1.3 Multivariate regression

3.1.4 Non-linear regression

3.2 Gaussian mixture model

Do some stuff:

```
from bayespy.nodes import Dirichlet
alpha = Dirichlet([1e-3, 1e-3, 1e-3])
print(alpha._message_to_child())

[array([-666.66994695, -666.66994695, -666.66994695])]
```

Nice!

3.3 Bernoulli mixture model

blaa blaa blaa

```
import numpy as np
D = 10
p0 = [0.1, 0.9, 0.1, 0.9, 0.1, 0.9, 0.1, 0.9, 0.1, 0.9]
p1 = [0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0]
p2 = [1.0, 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, 0.1]
p = np.array([p0, p1, p2])
from bayespy.utils import random
N = 100
z = random.categorical([1/3, 1/3, 1/3], size=N)
x = random.bernoulli(p[z])

from bayespy.nodes import Categorical, Dirichlet
K = 5
R = Dirichlet(K*[1e-3],
              name='R')
Z = Categorical(R,
               plates=(N,1),
               name='Z')

from bayespy.nodes import Mixture, Bernoulli, Beta
P = Beta([1e-1, 1e-1],
         plates=(D,K),
         name='P')
X = Mixture(Z, Bernoulli, P)

X.observe(x)

from bayespy.inference import VB
Q = VB(Z, R, X, P)
P.initialize_from_random()

Q.update(repeat=10)

Iteration 1: loglike=nan (0.005 seconds)
Iteration 2: loglike=nan (0.003 seconds)
```

```

Iteration 3: loglike=nan (0.003 seconds)
Iteration 4: loglike=nan (0.003 seconds)
Iteration 5: loglike=nan (0.003 seconds)
Iteration 6: loglike=nan (0.003 seconds)
Iteration 7: loglike=nan (0.003 seconds)
Iteration 8: loglike=nan (0.003 seconds)
Iteration 9: loglike=nan (0.003 seconds)
Iteration 10: loglike=nan (0.003 seconds)

```

```

/home/jluttine/workspace/bayespy/bayespy/inference/vmp/nodes/dirichlet.py:91: RuntimeWarning: divide
  logp = np.log(p)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/nodes/expfamily.py:71: RuntimeWarning: invalid
  L = L + np.sum(phi_i * u_i, axis=axis_sum)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/nodes/expfamily.py:71: RuntimeWarning: invalid
  L = L + np.sum(phi_i * u_i, axis=axis_sum)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/nodes/mixture.py:229: UserWarning: The natural
  warnings.warn("The natural parameters of mixture distribution ")

```

```

import bayespy.plot.plotting as bpplt
bpplt.beta_hinton(P)
import matplotlib.pyplot as plt
plt.show()

```

```

/home/jluttine/workspace/bayespy/bayespy/plot/plotting.py:204: RuntimeWarning: invalid value encounte
  _w = np.abs(w)

```

3.4 Discrete hidden Markov model

This example is also available as an IPython notebook or a Python script.

3.4.1 Known parameters

This example follows the one presented in [Wikipedia](#). Each day, the state of the weather is either ‘rainy’ or ‘sunny’. The weather follows a first-order discrete Markov process with the following initial state probability and state transition probabilities:

```

from bayespy.nodes import CategoricalMarkovChain
# Initial state probabilities
a0 = [0.6, 0.4] # p(rainy)=0.6, p(sunny)=0.4
# State transition probabilities
A = [[0.7, 0.3], # p(rainy->rainy)=0.7, p(rainy->sunny)=0.3
      [0.4, 0.6]] # p(sunny->rainy)=0.4, p(sunny->sunny)=0.6
# The length of the process
N = 1000
# Markov chain
Z = CategoricalMarkovChain(a0, A, states=N)

```

However, instead of observing this process directly, we observe whether Bob is ‘walking’, ‘shopping’ or ‘cleaning’. The probability of each activity depends on the current weather as follows:

```

from bayespy.nodes import Categorical, Mixture
# Emission probabilities
P = [[0.1, 0.4, 0.5],
      [0.6, 0.3, 0.1]]

```

```
# Observed process
Y = Mixture(Z, Categorical, P)
```

In order to test our method, we'll generate artificial data using this model:

```
# Draw realization of the weather process
weather = Z.random()
# Using this weather, draw realizations of the activities
activity = Mixture(weather, Categorical, P).random()
```

Now, using this data, we set our variable Y to be observed:

```
Y.observe(activity)
```

In order to run inference, we construct variational Bayesian inference engine:

```
from bayespy.inference import VB
Q = VB(Y, Z)
```

Note that we need to give all random variables to VB. In this case, the only random variables were Y and Z . Next we run the inference, that is, compute our posterior distribution:

```
Q.update()

Iteration 1: loglike=-1.091583e+03 (0.090 seconds)
```

In this case, because there is only one unobserved random variable, we recover the exact posterior distribution and there is no need to iterate more than one step.

3.4.2 Unknown parameters

Next, we consider the case when we do not know the parameters of the weather process (initial state probability and state transition probabilities). We give these parameters quite non-informative priors, but it is possible to provide more informative priors if such information is available. First, the weather process:

```
from bayespy.nodes import Dirichlet
# Initial state probabilities
a0 = Dirichlet([0.1, 0.1])
# State transition probabilities
A = Dirichlet([0.1, 0.1],
              [0.1, 0.1])
# Markov chain
Z = CategoricalMarkovChain(a0, A, states=N)
```

Second, the emission probabilities are also given quite non-informative priors:

```
# Emission probabilities
P = Dirichlet([0.1, 0.1, 0.1],
              [0.1, 0.1, 0.1])
# Observed process
Y = Mixture(Z, Categorical, P)
```

We use the same data as before:

```
Y.observe(activity)
```

Because VB takes all the unknown variables, we need to provide A , $a0$ and P also:


```
Q = VB(Y, Z, A, a0, P)
```

If we ran the VB algorithm now, we would get a result where all both states would have identical emission probability distribution. This happens because of a non-random default initialization. `P` is initialized in such a way that both states have the same distribution, and `Z` is initialized in such a way that each state has equal probability. Thus, the VB algorithm won't separate them. In such cases, it is necessary to use a random initialization. In principle, it is possible to use random initialization for either variable and then update the other variable first. In the case of mixture distributions, it might be better to initialize the parameters (`P`) randomly and update the state assignments (`Z`) first.

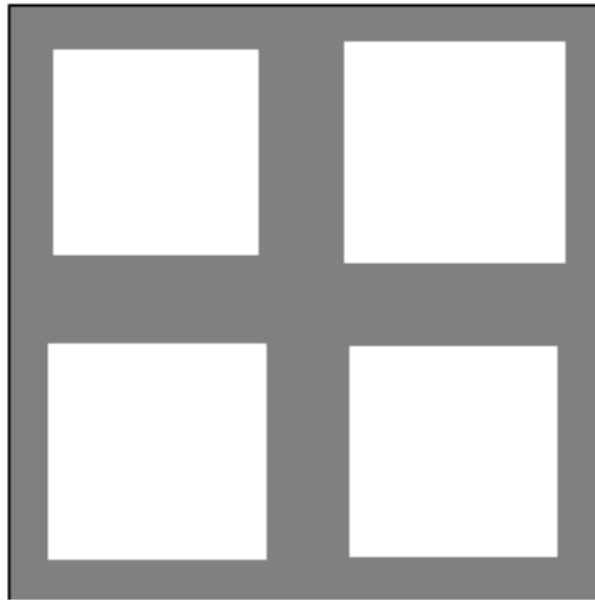
```
P.initialize_from_random()
Q.update(Z, A, a0, P, repeat=20)
```

```
Iteration 1: loglike=-1.115941e+03 (0.090 seconds)
Iteration 2: loglike=-1.115671e+03 (0.090 seconds)
Iteration 3: loglike=-1.115603e+03 (0.100 seconds)
Iteration 4: loglike=-1.115574e+03 (0.090 seconds)
Iteration 5: loglike=-1.115555e+03 (0.090 seconds)
Iteration 6: loglike=-1.115538e+03 (0.100 seconds)
Iteration 7: loglike=-1.115521e+03 (0.090 seconds)
Iteration 8: loglike=-1.115504e+03 (0.090 seconds)
Iteration 9: loglike=-1.115487e+03 (0.090 seconds)
Iteration 10: loglike=-1.115469e+03 (0.090 seconds)
Iteration 11: loglike=-1.115451e+03 (0.100 seconds)
Iteration 12: loglike=-1.115433e+03 (0.090 seconds)
Iteration 13: loglike=-1.115413e+03 (0.090 seconds)
Iteration 14: loglike=-1.115394e+03 (0.090 seconds)
Iteration 15: loglike=-1.115374e+03 (0.090 seconds)
Iteration 16: loglike=-1.115354e+03 (0.100 seconds)
Iteration 17: loglike=-1.115333e+03 (0.090 seconds)
Iteration 18: loglike=-1.115312e+03 (0.090 seconds)
Iteration 19: loglike=-1.115290e+03 (0.090 seconds)
Iteration 20: loglike=-1.115268e+03 (0.090 seconds)
```

In order to update the variables in that order, one may explicitly give the nodes in that order to the `update` method. However, the default update order is the one used when constructing `Q`, which is the same in this case, thus we could have ignored listing the nodes to the `update` method.

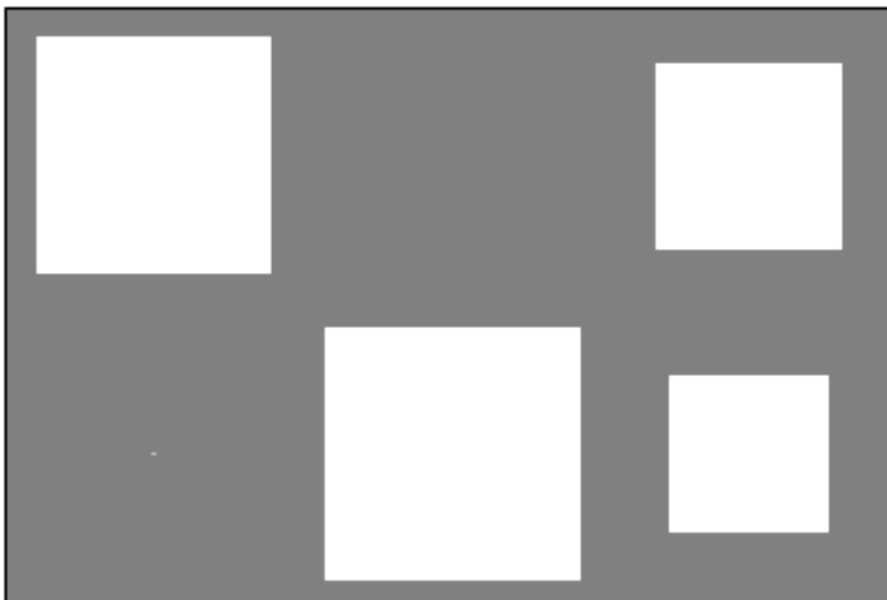
Plot the estimated state transition probabilities:

```
# NOTE: These three lines are just to enable inline plotting in IPython Notebooks.
import matplotlib.pyplot as plt
%matplotlib inline
plt.plot([])
# Plot the state transition matrix
import bayespy.plot.plotting as bpplt
bpplt.dirichlet_hinton(A)
```



Plot the estimated emission probabilities:

```
bpplt.dirichlet_hinton(P)
```



It is interesting that these estimated parameters are very different from the true parameters. This happens because of un-identifiability: different parameters lead to similar marginal distributions over the observed process.

3.5 Hidden Markov model

blaa blaa

3.6 Principal component analysis

Yeah.

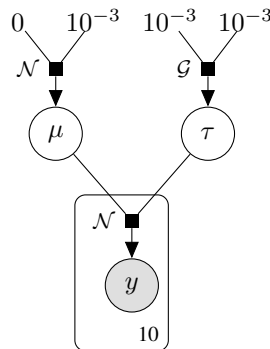


Figure 3.1: Directed factor graph of the example model.

```
from bayespy.nodes import GaussianARD
GaussianARD(0, 1)
```

```
<bayespy.inference.vmp.nodes.gaussian.GaussianARD at 0x7fa3343bce90>
```

3.7 Linear state-space model

This example is also available as an IPython notebook or a Python script.

In linear state-space models a sequence of M -dimensional observations $\mathbf{Y} = (\mathbf{y}_1, \dots, \mathbf{y}_N)$ is assumed to be generated from latent D -dimensional states $\mathbf{X} = (\mathbf{x}_1, \dots, \mathbf{x}_N)$ which follow a first-order Markov process:

$$\begin{aligned}\mathbf{x}_n &= \mathbf{A}\mathbf{x}_{n-1} + \text{noise}, \\ \mathbf{y}_n &= \mathbf{C}\mathbf{x}_n + \text{noise},\end{aligned}$$

where the noise is Gaussian, \mathbf{A} is the $D \times D$ state dynamics matrix and \mathbf{C} is the $M \times D$ loading matrix. Usually, the latent space dimensionality D is assumed to be much smaller than the observation space dimensionality M in order to model the dependencies of high-dimensional observations efficiently.

First, let us generate some toy data:

```
import numpy as np

M = 30
N = 400

w = 0.3
a = np.array([[np.cos(w), -np.sin(w), 0, 0],
               [np.sin(w), np.cos(w), 0, 0],
               [0, 0, 1, 0],
```

```

        [0,          0,          0, 0]])
c = np.random.randn(M, 4)
x = np.empty((N, 4))
f = np.empty((M, N))
y = np.empty((M, N))
x[0] = 10*np.random.randn(4)
f[:, 0] = np.dot(c, x[0])
y[:, 0] = f[:, 0] + 3*np.random.randn(M)
for n in range(N-1):
    x[n+1] = np.dot(a, x[n]) + np.random.randn(4)
    f[:, n+1] = np.dot(c, x[n+1])
    y[:, n+1] = f[:, n+1] + 3*np.random.randn(M)

```

The linear state-space model can be constructed as follows:

```

from bayespy.inference.vmp.nodes.gaussian_markov_chain import GaussianMarkovChain
from bayespy.inference.vmp.nodes.gaussian import GaussianARD
from bayespy.inference.vmp.nodes.gamma import Gamma
from bayespy.inference.vmp.nodes.dot import SumMultiply

D = 10

# Dynamics matrix with ARD
alpha = Gamma(1e-5,
              1e-5,
              plates=(D,),
              name='alpha')
A = GaussianARD(0,
               alpha,
               shape=(D,),
               plates=(D,),
               name='A')

# Latent states with dynamics
X = GaussianMarkovChain(np.zeros(D),          # mean of x0
                       1e-3*np.identity(D),  # prec of x0
                       A,                     # dynamics
                       np.ones(D),            # innovation
                       n=N,                   # time instances
                       name='X',
                       initialize=False)
X.initialize_from_value(np.zeros((N,D))) # just some empty values, X is
                                          # updated first anyway

# Mixing matrix from latent space to observation space using ARD
gamma = Gamma(1e-5,
              1e-5,
              plates=(D,),
              name='gamma')
C = GaussianARD(0,
               gamma,
               shape=(D,),
               plates=(M,1),
               name='C')

# Initialize nodes (must use some randomness for C, and update X before C)
C.initialize_from_random()

# Observation noise

```

```
tau = Gamma(1e-5,
            1e-5,
            name='tau')

# Observations
F = SumMultiply('i,i',
               C,
               X,
               name='F')
Y = GaussianARD(F,
               tau,
               name='Y')
```

An inference machine using variational Bayesian inference with variational message passing is then construed as

```
from bayespy.inference.vmp.vmp import VB
Q = VB(X, C, gamma, A, alpha, tau, Y)
```

Observe the data partially (80% is marked missing):

```
from bayespy.utils import random

# Add missing values randomly (keep only 20%)
mask = random.mask(M, N, p=0.2)
Y.observe(y, mask=mask)
```

Then inference (100 iterations) can be run simply as

```
Q.update(repeat=10)

Iteration 1: loglike=-3.118644e+04 (0.210 seconds)
Iteration 2: loglike=-1.129540e+04 (0.210 seconds)
Iteration 3: loglike=-9.139376e+03 (0.210 seconds)
Iteration 4: loglike=-8.704676e+03 (0.220 seconds)
Iteration 5: loglike=-8.531889e+03 (0.200 seconds)
Iteration 6: loglike=-8.386198e+03 (0.210 seconds)
Iteration 7: loglike=-8.255826e+03 (0.210 seconds)
Iteration 8: loglike=-8.176274e+03 (0.210 seconds)
Iteration 9: loglike=-8.139579e+03 (0.210 seconds)
Iteration 10: loglike=-8.117779e+03 (0.210 seconds)
```

3.7.1 Speeding up with parameter expansion

VB inference can converge extremely slowly if the variables are strongly coupled. Because VMP updates one variable at a time, it may lead to slow zigzagging. This can be solved by using parameter expansion which reduces the coupling. In state-space models, the states \mathbf{x}_n and the loadings \mathbf{C} are coupled through a dot product $\mathbf{C}\mathbf{x}_n$, which is unaltered if the latent space is rotated arbitrarily:

$$\mathbf{y}_n = \mathbf{C}\mathbf{x}_n = \mathbf{C}\mathbf{R}^{-1}\mathbf{R}\mathbf{x}_n.$$

Thus, one intuitive transformation would be $\mathbf{C} \rightarrow \mathbf{C}\mathbf{R}^{-1}$ and $\mathbf{X} \rightarrow \mathbf{R}\mathbf{X}$. In order to keep the dynamics of the latent states unaffected by the transformation, the state dynamics matrix \mathbf{A} must be transformed accordingly:

$$\mathbf{R}\mathbf{x}_n = \mathbf{R}\mathbf{A}\mathbf{R}^{-1}\mathbf{R}\mathbf{x}_{n-1},$$

resulting in a transformation $\mathbf{A} \rightarrow \mathbf{R}\mathbf{A}\mathbf{R}^{-1}$. For more details, refer to *Fast Variational Bayesian Linear State-Space Model (Lutten, 2013).

In BayesPy, the transformations can be used as follows:

```
# Import the parameter expansion module
from bayespy.inference.vmp import transformations

# Rotator of the state dynamics matrix
rotA = transformations.RotateGaussianARD(Q['A'], Q['alpha'])
# Rotator of the states (includes rotation of the state dynamics matrix)
rotX = transformations.RotateGaussianMarkovChain(Q['X'], rotA)
# Rotator of the loading matrix
rotC = transformations.RotateGaussianARD(Q['C'], Q['gamma'])
# Rotation optimizer
R = transformations.RotationOptimizer(rotX, rotC, D)
```

Note that it is crucial to select the correct rotation class which corresponds to the particular model block exactly. The rotation can be performed after each full VB update:

```
for ind in range(10):
    Q.update()
    R.rotate()

Iteration 11: loglike=-8.100983e+03 (0.210 seconds)
Iteration 12: loglike=-7.622913e+03 (0.210 seconds)
Iteration 13: loglike=-7.452057e+03 (0.200 seconds)
Iteration 14: loglike=-7.385975e+03 (0.200 seconds)
Iteration 15: loglike=-7.351449e+03 (0.210 seconds)
Iteration 16: loglike=-7.331026e+03 (0.210 seconds)
Iteration 17: loglike=-7.317997e+03 (0.200 seconds)
Iteration 18: loglike=-7.309212e+03 (0.200 seconds)
Iteration 19: loglike=-7.303074e+03 (0.210 seconds)
Iteration 20: loglike=-7.298661e+03 (0.210 seconds)
```

If you want to implement your own rotations or check the existing ones, you may use debugging utilities:

```
for ind in range(10):
    Q.update()
    R.rotate(check_bound=True,
             check_gradient=True)

Iteration 21: loglike=-7.295401e+03 (0.210 seconds)
Norm of numerical gradient: 3905.05
Norm of function gradient: 3905.05
Gradient relative error = 6.39002e-05 and absolute error = 0.249533
Iteration 22: loglike=-7.292861e+03 (0.210 seconds)
Norm of numerical gradient: 6245.37
```

```
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
warnings.warn("Rotation gradient has relative error %g" % err)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
warnings.warn("Rotation gradient has relative error %g" % err)
```

```
Norm of function gradient: 6245.43
Gradient relative error = 7.56396e-05 and absolute error = 0.472397
Iteration 23: loglike=-7.290841e+03 (0.210 seconds)
Norm of numerical gradient: 3984.43
Norm of function gradient: 3984.43
Gradient relative error = 6.78117e-05 and absolute error = 0.270191
Iteration 24: loglike=-7.289243e+03 (0.210 seconds)
Norm of numerical gradient: 13053.7
```

```

/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)

Norm of function gradient: 13053.8
Gradient relative error = 2.65118e-05 and absolute error = 0.346078
Iteration 25: loglike=-7.287794e+03 (0.200 seconds)
Norm of numerical gradient: 4144.61
Norm of function gradient: 4144.59
Gradient relative error = 7.02612e-05 and absolute error = 0.291205
Iteration 26: loglike=-7.286531e+03 (0.210 seconds)
Norm of numerical gradient: 5821.72

/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)

Norm of function gradient: 5821.73
Gradient relative error = 4.57892e-05 and absolute error = 0.266572
Iteration 27: loglike=-7.285469e+03 (0.210 seconds)
Norm of numerical gradient: 15766.4
Norm of function gradient: 15766.4
Gradient relative error = 3.5184e-05 and absolute error = 0.554724
Iteration 28: loglike=-7.284584e+03 (0.200 seconds)
Norm of numerical gradient: 5782.51

/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)

Norm of function gradient: 5782.51
Gradient relative error = 5.61705e-05 and absolute error = 0.324807
Iteration 29: loglike=-7.283818e+03 (0.210 seconds)
Norm of numerical gradient: 9067.22
Norm of function gradient: 9067.21
Gradient relative error = 2.4973e-05 and absolute error = 0.226435
Iteration 30: loglike=-7.283121e+03 (0.200 seconds)
Norm of numerical gradient: 9594.54

/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)
/home/jluttine/workspace/bayespy/bayespy/inference/vmp/transformations.py:142: UserWarning: Rotation
  warnings.warn("Rotation gradient has relative error %g" % err)

Norm of function gradient: 9594.62
Gradient relative error = 5.43175e-05 and absolute error = 0.521151

```

3.8 Latent Dirichlet allocation

blaa blaa blaa..

DEVELOPER GUIDE

How to document: https://github.com/numpy/numpy/blob/master/doc/HOWTO_DOCUMENT.rst.txt

How to contribute: http://docs.scipy.org/doc/numpy/dev/gitwash/development_workflow.html

4.1 Variational message passing

The general update equation for factorized approximation:

$$\log q(\boldsymbol{\theta}) = \langle \log p(\boldsymbol{\theta} | \text{pa}(\boldsymbol{\theta})) \rangle + \sum_{\mathbf{x} \in \text{ch}(\boldsymbol{\theta})} \langle \log p(\mathbf{x} | \text{pa}(\mathbf{x})) \rangle + \text{const}, \quad (4.1)$$

where $\text{pa}(\boldsymbol{\theta})$ and $\text{ch}(\boldsymbol{\theta})$ are the set of parents and children of $\boldsymbol{\theta}$, respectively. The expectations are over the approximate distribution of all other variables than $\boldsymbol{\theta}$. Actually, not all the variables are needed, because the non-constant part uses only the Markov blanket of $\boldsymbol{\theta}$. Thus, the optimization can be done locally using messages from neighbouring nodes.

The messages are simple for conjugate-exponential models. Exponential-family distributions have the form

$$\log p(\mathbf{x} | \boldsymbol{\Theta}) = \mathbf{u}_{\mathbf{x}}(\mathbf{x})^T \boldsymbol{\phi}_{\mathbf{x}}(\boldsymbol{\Theta}) + g_{\mathbf{x}}(\boldsymbol{\Theta}) + f_{\mathbf{x}}(\mathbf{x}), \quad (4.2)$$

where $\boldsymbol{\Theta} = \{\boldsymbol{\theta}_j\}$ is the set of parents. If a parent has a conjugate prior, (4.2) is linear with respect to the parent's natural statistics. Thus, (4.2) can be re-organized with respect to $\boldsymbol{\theta}_j$ as

$$\log p(\mathbf{x} | \boldsymbol{\Theta}) = \mathbf{u}_{\boldsymbol{\theta}_j}(\boldsymbol{\theta}_j)^T \boldsymbol{\phi}_{\mathbf{x} \rightarrow \boldsymbol{\theta}_j}(\mathbf{x}, \{\boldsymbol{\theta}_k\}_{k \neq j}) + \text{const},$$

where $\mathbf{u}_{\boldsymbol{\theta}_j}$ is the natural statistics of $\boldsymbol{\theta}_j$. Thus, the update equation (4.1) can be given as

$$\log q(\boldsymbol{\theta}_j) = \mathbf{u}_{\boldsymbol{\theta}_j}(\boldsymbol{\theta}_j)^T \left(\langle \boldsymbol{\phi}_{\boldsymbol{\theta}_j} \rangle + \sum_{\mathbf{x} \in \text{ch}(\boldsymbol{\theta}_j)} \langle \boldsymbol{\phi}_{\mathbf{x} \rightarrow \boldsymbol{\theta}_j} \rangle \right) + f_{\boldsymbol{\theta}_j}(\boldsymbol{\theta}_j) + \text{const},$$

where the summation is over all the child nodes of $\boldsymbol{\theta}_j$. Because of the conjugacy, $\langle \boldsymbol{\phi}_{\boldsymbol{\theta}_j} \rangle$ depends (multi)linearly on the expectations of the parents' natural statistics. Similarly, $\langle \boldsymbol{\phi}_{\mathbf{x} \rightarrow \boldsymbol{\theta}_j} \rangle$ depends (multi)linearly on the expectations of the children's and co-parents' natural statistics.

The required expectations can be computed locally by using messages from the parents and the children. The message from a parent node $\boldsymbol{\theta}_j$ to a child node \mathbf{x} is

$$\mathbf{m}_{\boldsymbol{\theta}_j \rightarrow \mathbf{x}} = \langle \mathbf{u}_{\boldsymbol{\theta}_j} \rangle = \tilde{\mathbf{u}}_{\boldsymbol{\theta}_j}(\tilde{\boldsymbol{\phi}}_{\boldsymbol{\theta}_j}),$$

and the message from a child node \mathbf{x} to a parent node $\boldsymbol{\theta}_j$ is

$$\mathbf{m}_{\mathbf{x} \rightarrow \boldsymbol{\theta}_j} = \langle \boldsymbol{\phi}_{\mathbf{x} \rightarrow \boldsymbol{\theta}_j} \rangle = \boldsymbol{\phi}_{\mathbf{x} \rightarrow \boldsymbol{\theta}_j}(\langle \mathbf{u}_{\mathbf{x}} \rangle, \{\mathbf{m}_{\boldsymbol{\theta}_k \rightarrow \mathbf{x}}\}_{k \neq j}).$$

Using the messages, the natural parameters of $q(\boldsymbol{\theta})$ can be updated as

$$\tilde{\boldsymbol{\phi}}_{\boldsymbol{\theta}} = \boldsymbol{\phi}_{\boldsymbol{\theta}}(\{\mathbf{m}_{\mathbf{z} \rightarrow \boldsymbol{\theta}}\}_{\mathbf{z} \in \text{pa}(\boldsymbol{\theta})}) + \sum_{\mathbf{x} \in \text{ch}(\boldsymbol{\theta})} \mathbf{m}_{\mathbf{x} \rightarrow \boldsymbol{\theta}}.$$

4.2 Implementing nodes

USER API

<code>bayespy.nodes</code>	Package for nodes used to construct the model.
<code>bayespy.inference</code>	Package for Bayesian inference engines
<code>bayespy.plot</code>	Functions for plotting nodes.

5.1 bayespy.nodes

Package for nodes used to construct the model.

5.1.1 Stochastic nodes

Nodes for Gaussian variables:

<code>Gaussian(mu, Lambda, **kwargs)</code>	Node for Gaussian variables.
<code>GaussianARD(mu, alpha[, ndim, shape])</code>	Node for Gaussian variables with ARD prior.

bayespy.nodes.Gaussian

class `bayespy.nodes.Gaussian(mu, Lambda, **kwargs)`

Node for Gaussian variables.

The node represents a D -dimensional vector from the Gaussian distribution:

$$\mathbf{x} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Lambda}),$$

where $\boldsymbol{\mu}$ is the mean vector and $\boldsymbol{\Lambda}$ is the precision matrix (i.e., inverse of the covariance matrix).

$$\mathbf{x}, \boldsymbol{\mu} \in \mathbb{R}^D, \quad \boldsymbol{\Lambda} \in \mathbb{R}^{D \times D}, \quad \boldsymbol{\Lambda} \text{ symmetric positive definite}$$

Parameters **mu** : Gaussian-like node or GaussianGammaISO-like node or GaussianWishart-like node or array

Mean vector

Lambda : Wishart-like node or array

Precision matrix

See also:

`Wishart`, `GaussianARD`, `GaussianWishart`, `GaussianGammaARD`, `GaussianGammaISO`

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(mu, Lambda)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>rotate(R[, inv, logdet, Q])</code>	
<code>rotate_matrix(R1, R2[, inv1, logdet1, inv2, ...])</code>	The vector is reshaped into a matrix by stacking the row vectors.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Gaussian.add_plate_axis

`Gaussian.add_plate_axis(to_plate)`

bayespy.nodes.Gaussian.delete

`Gaussian.delete()`
Delete this node and the children

bayespy.nodes.Gaussian.get_mask

`Gaussian.get_mask()`

bayespy.nodes.Gaussian.get_moments

`Gaussian.get_moments()`

bayespy.nodes.Gaussian.get_shape

`Gaussian.get_shape(ind)`

bayespy.nodes.Gaussian.has_plotter

`Gaussian.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.Gaussian.initialize_from_parameters

`Gaussian.initialize_from_parameters(mu, Lambda)`

bayespy.nodes.Gaussian.initialize_from_prior

`Gaussian.initialize_from_prior()`

bayespy.nodes.Gaussian.initialize_from_random

`Gaussian.initialize_from_random()`
Set the variable to a random sample from the current distribution.

bayespy.nodes.Gaussian.initialize_from_value

`Gaussian.initialize_from_value(x, *args)`

bayespy.nodes.Gaussian.load

`Gaussian.load(group)`
Load the state of the node from a HDF5 file.

bayespy.nodes.Gaussian.logpdf

`Gaussian.logpdf(X, mask=True)`
Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Gaussian.lower_bound_contribution

`Gaussian.lower_bound_contribution(gradient=False)`

bayespy.nodes.Gaussian.lowerbound

`Gaussian.lowerbound()`

bayespy.nodes.Gaussian.move_plates

`Gaussian.move_plates(from_plate, to_plate)`

bayespy.nodes.Gaussian.observe

`Gaussian.observe(x, *args, mask=True)`
 Fix moments, compute f and propagate mask.

bayespy.nodes.Gaussian.pdf

`Gaussian.pdf(X, mask=True)`
 Compute the probability density function of this node.

bayespy.nodes.Gaussian.plot

`Gaussian.plot(**kwargs)`
 Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Gaussian.random

`Gaussian.random()`
 Draw a random sample from the distribution.

bayespy.nodes.Gaussian.rotate

`Gaussian.rotate(R, inv=None, logdet=None, Q=None)`

bayespy.nodes.Gaussian.rotate_matrix

`Gaussian.rotate_matrix(R1, R2, inv1=None, logdet1=None, inv2=None, logdet2=None, Q=None)`
 The vector is reshaped into a matrix by stacking the row vectors.
 Computes $R1 * X * R2'$, which is identical to $\text{kron}(R1, R2) * x$ (??)
 Note that this is slightly different from the standard Kronecker product definition because Numpy stacks row vectors instead of column vectors.

Parameters **R1** : ndarray
 A matrix from the left

R2 : ndarray
 A matrix from the right

bayespy.nodes.Gaussian.save

`Gaussian.save(group)`
 Save the state of the node into a HDF5 file.
 group can be the root

bayespy.nodes.Gaussian.set_plotter

Gaussian.set_plotter(plotter)

bayespy.nodes.Gaussian.show

Gaussian.show()

bayespy.nodes.Gaussian.unobserve

Gaussian.unobserve()

bayespy.nodes.Gaussian.update

Gaussian.update()

Attributes

dims
plates

bayespy.nodes.Gaussian.dims

Gaussian.dims = None

bayespy.nodes.Gaussian.plates

Gaussian.plates = None

bayespy.nodes.GaussianARD

class bayespy.nodes.GaussianARD(mu, alpha, ndim=None, shape=None, **kwargs)

Node for Gaussian variables with ARD prior.

The node represents a D -dimensional vector from the Gaussian distribution:

$$\mathbf{x} \sim \mathcal{N}(\boldsymbol{\mu}, \text{diag}(\boldsymbol{\alpha})),$$

where $\boldsymbol{\mu}$ is the mean vector and $\text{diag}(\boldsymbol{\alpha})$ is the diagonal precision matrix (i.e., inverse of the covariance matrix).

$$\mathbf{x}, \boldsymbol{\mu} \in \mathbb{R}^D, \quad \alpha_d > 0 \text{ for } d = 0, \dots, D-1$$

Note: The form of the posterior approximation is a Gaussian distribution with full covariance matrix instead of a diagonal matrix.

Parameters **mu** : Gaussian-like node or GaussianGammaISO-like node or GaussianGammaARD-like node or array

Mean vector

alpha : gamma-like node or array

Diagonal elements of the precision matrix

See also:

`Gamma`, `Gaussian`, `GaussianGammaARD`, `GaussianGammaISO`, `GaussianWishart`

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_mean_and_covariance(mu, Cov)</code>	
<code>initialize_from_parameters(mu, alpha)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function Q(X) of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>rotate(R[, inv, logdet, axis, Q])</code>	
<code>rotate_plates(Q[, plate_axis])</code>	Approximate rotation of a plate axis.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.GaussianARD.add_plate_axis

`GaussianARD.add_plate_axis(to_plate)`

bayespy.nodes.GaussianARD.delete

`GaussianARD.delete()`
Delete this node and the children

bayespy.nodes.GaussianARD.get_mask

`GaussianARD.get_mask()`

bayespy.nodes.GaussianARD.get_moments

`GaussianARD.get_moments()`

bayespy.nodes.GaussianARD.get_shape

`GaussianARD.get_shape(ind)`

bayespy.nodes.GaussianARD.has_plotter

`GaussianARD.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.GaussianARD.initialize_from_mean_and_covariance

`GaussianARD.initialize_from_mean_and_covariance(mu, Cov)`

bayespy.nodes.GaussianARD.initialize_from_parameters

`GaussianARD.initialize_from_parameters(mu, alpha)`

bayespy.nodes.GaussianARD.initialize_from_prior

`GaussianARD.initialize_from_prior()`

bayespy.nodes.GaussianARD.initialize_from_random

`GaussianARD.initialize_from_random()`
Set the variable to a random sample from the current distribution.

bayespy.nodes.GaussianARD.initialize_from_value

`GaussianARD.initialize_from_value(x, *args)`

bayespy.nodes.GaussianARD.load

`GaussianARD.load(group)`
Load the state of the node from a HDF5 file.

bayespy.nodes.GaussianARD.logpdf

`GaussianARD.logpdf(X, mask=True)`
Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.GaussianARD.lower_bound_contribution

`GaussianARD.lower_bound_contribution` (*gradient=False*)

bayespy.nodes.GaussianARD.lowerbound

`GaussianARD.lowerbound` ()

bayespy.nodes.GaussianARD.move_plates

`GaussianARD.move_plates` (*from_plate, to_plate*)

bayespy.nodes.GaussianARD.observe

`GaussianARD.observe` (*x, *args, mask=True*)

Fix moments, compute f and propagate mask.

bayespy.nodes.GaussianARD.pdf

`GaussianARD.pdf` (*X, mask=True*)

Compute the probability density function of this node.

bayespy.nodes.GaussianARD.plot

`GaussianARD.plot` (***kwargs*)

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.GaussianARD.random

`GaussianARD.random` ()

Draw a random sample from the distribution.

bayespy.nodes.GaussianARD.rotate

`GaussianARD.rotate` (*R, inv=None, logdet=None, axis=-1, Q=None*)

bayespy.nodes.GaussianARD.rotate_plates

`GaussianARD.rotate_plates` (*Q, plate_axis=-1*)

Approximate rotation of a plate axis.

Mean is rotated exactly but covariance/precision matrix is rotated approximately.

bayespy.nodes.GaussianARD.save

`GaussianARD.save(group)`
Save the state of the node into a HDF5 file.
group can be the root

bayespy.nodes.GaussianARD.set_plotter

`GaussianARD.set_plotter(plotter)`

bayespy.nodes.GaussianARD.show

`GaussianARD.show()`

bayespy.nodes.GaussianARD.unobserve

`GaussianARD.unobserve()`

bayespy.nodes.GaussianARD.update

`GaussianARD.update()`

Attributes

<code>dims</code>
<code>plates</code>

bayespy.nodes.GaussianARD.dims

`GaussianARD.dims = None`

bayespy.nodes.GaussianARD.plates

`GaussianARD.plates = None`

Nodes for precision and scale variables:

<code>Gamma(a, b, **kwargs)</code>	Node for gamma random variables.
<code>Wishart(n, V, **kwargs)</code>	Node for Wishart random variables.
<code>Exponential(l, **kwargs)</code>	Node for exponential random variables.

bayespy.nodes.Gamma

class `bayespy.nodes.Gamma(a, b, **kwargs)`
Node for gamma random variables.

Parameters **a** : scalar or array

Shape parameter

b : gamma-like node or scalar or array

Rate parameter

Methods

<code>add_plate_axis(to_plate)</code>	
<code>as_diagonal_wishart()</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function Q(X) of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

`bayespy.nodes.Gamma.add_plate_axis`

`Gamma.add_plate_axis (to_plate)`

`bayespy.nodes.Gamma.as_diagonal_wishart`

`Gamma.as_diagonal_wishart ()`

`bayespy.nodes.Gamma.delete`

`Gamma.delete ()`
Delete this node and the children

bayespy.nodes.Gamma.get_mask

`Gamma.get_mask()`

bayespy.nodes.Gamma.get_moments

`Gamma.get_moments()`

bayespy.nodes.Gamma.get_shape

`Gamma.get_shape(ind)`

bayespy.nodes.Gamma.has_plotter

`Gamma.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.Gamma.initialize_from_parameters

`Gamma.initialize_from_parameters(*args)`

bayespy.nodes.Gamma.initialize_from_prior

`Gamma.initialize_from_prior()`

bayespy.nodes.Gamma.initialize_from_random

`Gamma.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Gamma.initialize_from_value

`Gamma.initialize_from_value(x, *args)`

bayespy.nodes.Gamma.load

`Gamma.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Gamma.logpdf

`Gamma.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Gamma.lower_bound_contribution

`Gamma.lower_bound_contribution (gradient=False)`

bayespy.nodes.Gamma.lowerbound

`Gamma.lowerbound ()`

bayespy.nodes.Gamma.move_plates

`Gamma.move_plates (from_plate, to_plate)`

bayespy.nodes.Gamma.observe

`Gamma.observe (x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Gamma.pdf

`Gamma.pdf (X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.Gamma.plot

`Gamma.plot (**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Gamma.random

`Gamma.random ()`

Draw a random sample from the distribution.

bayespy.nodes.Gamma.save

`Gamma.save (group)`

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Gamma.set_plotter

`Gamma.set_plotter (plotter)`

bayespy.nodes.Gamma.show

`Gamma.show()`
Print the distribution using standard parameterization.

bayespy.nodes.Gamma.unobserve

`Gamma.unobserve()`

bayespy.nodes.Gamma.update

`Gamma.update()`

Attributes

<code>dims</code>	tuple() -> empty tuple
<code>plates</code>	

bayespy.nodes.Gamma.dims

`Gamma.dims = (), ()`

bayespy.nodes.Gamma.plates

`Gamma.plates = None`

bayespy.nodes.Wishart

class bayespy.nodes.**Wishart** (*n*, *V*, ***kwargs*)

Node for Wishart random variables.

The random variable $\mathbf{\Lambda}$ is a $D \times D$ positive-definite symmetric matrix.

$$p(\mathbf{\Lambda}) = \text{Wishart}(\mathbf{\Lambda} | N, \mathbf{V})$$

Parameters **n** : scalar or array

N , degrees of freedom, $N > D - 1$.

V : Wishart-like node or (...D,D)-array

V, scale matrix.

Methods

`add_plate_axis(to_plate)`

`delete()`

Delete this node and the children

Continued on next page

Table 5.10 – continued from previous page

<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Wishart.add_plate_axis

`Wishart.add_plate_axis (to_plate)`

bayespy.nodes.Wishart.delete

`Wishart.delete()`
Delete this node and the children

bayespy.nodes.Wishart.get_mask

`Wishart.get_mask()`

bayespy.nodes.Wishart.get_moments

`Wishart.get_moments()`

bayespy.nodes.Wishart.get_shape

`Wishart.get_shape (ind)`

bayespy.nodes.Wishart.has_plotter

`Wishart.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.Wishart.initialize_from_parameters

`Wishart.initialize_from_parameters(*args)`

bayespy.nodes.Wishart.initialize_from_prior

`Wishart.initialize_from_prior()`

bayespy.nodes.Wishart.initialize_from_random

`Wishart.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Wishart.initialize_from_value

`Wishart.initialize_from_value(x, *args)`

bayespy.nodes.Wishart.load

`Wishart.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Wishart.logpdf

`Wishart.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Wishart.lower_bound_contribution

`Wishart.lower_bound_contribution(gradient=False)`

bayespy.nodes.Wishart.lowerbound

`Wishart.lowerbound()`

bayespy.nodes.Wishart.move_plates

`Wishart.move_plates(from_plate, to_plate)`

bayespy.nodes.Wishart.observe

`Wishart.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Wishart.pdf

`Wishart.pdf(X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.Wishart.plot

`Wishart.plot(**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Wishart.random

`Wishart.random()`

Draw a random sample from the distribution.

bayespy.nodes.Wishart.save

`Wishart.save(group)`

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Wishart.set_plotter

`Wishart.set_plotter(plotter)`

bayespy.nodes.Wishart.show

`Wishart.show()`

bayespy.nodes.Wishart.unobserve

`Wishart.unobserve()`

bayespy.nodes.Wishart.update

`Wishart.update()`

Attributes

`dims`
`plates`

bayespy.nodes.Wishart.dims

Wishart.dims = None

bayespy.nodes.Wishart.plates

Wishart.plates = None

bayespy.nodes.Exponential

class bayespy.nodes.Exponential(l, **kwargs)

Node for exponential random variables.

Warning: Use [Gamma](#) instead of this. *Exponential(l)* is equivalent to *Gamma(l, l)*.

Parameters l : gamma-like node or scalar or array

Rate parameter

See also:

[Gamma](#), [Poisson](#)

Notes

For simplicity, this is just a gamma node with the first parent fixed to one. Note that this is a bit inconsistent with the BayesPy philosophy which states that the node does not only define the form of the prior distribution but more importantly the form of the posterior approximation. Thus, one might expect that this node would have exponential posterior distribution approximation. However, it has a gamma distribution. Also, the moments are gamma moments although only $E[x]$ would be the moment of a exponential random variable. All this was done because: a) gamma was already implemented, so there was no need to implement anything, and b) people might easily use Exponential node as a prior definition and expect to get gamma posterior (which is what happens now). Maybe some day a pure Exponential node is implemented and the users are advised to use $\text{Gamma}(1, b)$ if they want to use an exponential prior distribution but gamma posterior approximation.

Methods

<code>add_plate_axis(to_plate)</code>	
<code>as_diagonal_wishart()</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.

Continued on next page

Table 5.12 – continued from previous page

<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Exponential.add_plate_axis

`Exponential.add_plate_axis(to_plate)`

bayespy.nodes.Exponential.as_diagonal_wishart

`Exponential.as_diagonal_wishart()`

bayespy.nodes.Exponential.delete

`Exponential.delete()`
Delete this node and the children

bayespy.nodes.Exponential.get_mask

`Exponential.get_mask()`

bayespy.nodes.Exponential.get_moments

`Exponential.get_moments()`

bayespy.nodes.Exponential.get_shape

`Exponential.get_shape(ind)`

bayespy.nodes.Exponential.has_plotter

`Exponential.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.Exponential.initialize_from_parameters

`Exponential.initialize_from_parameters(*args)`

bayespy.nodes.Exponential.initialize_from_prior

`Exponential.initialize_from_prior()`

bayespy.nodes.Exponential.initialize_from_random

`Exponential.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Exponential.initialize_from_value

`Exponential.initialize_from_value(x, *args)`

bayespy.nodes.Exponential.load

`Exponential.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Exponential.logpdf

`Exponential.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Exponential.lower_bound_contribution

`Exponential.lower_bound_contribution(gradient=False)`

bayespy.nodes.Exponential.lowerbound

`Exponential.lowerbound()`

bayespy.nodes.Exponential.move_plates

`Exponential.move_plates(from_plate, to_plate)`

bayespy.nodes.Exponential.observe

`Exponential.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Exponential.pdf

`Exponential.pdf(X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.Exponential.plot

`Exponential.plot (**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Exponential.random

`Exponential.random()`

Draw a random sample from the distribution.

bayespy.nodes.Exponential.save

`Exponential.save (group)`

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Exponential.set_plotter

`Exponential.set_plotter (plotter)`

bayespy.nodes.Exponential.show

`Exponential.show()`

Print the distribution using standard parameterization.

bayespy.nodes.Exponential.unobserve

`Exponential.unobserve()`

bayespy.nodes.Exponential.update

`Exponential.update()`

Attributes

<code>dims</code>	tuple() -> empty tuple
<code>plates</code>	

bayespy.nodes.Exponential.dims

`Exponential.dims = (), ()`

bayespy.nodes.Exponential.plates

Exponential.plates = None

Nodes for modelling Gaussian and precision variables jointly (useful as prior for Gaussian nodes):

GaussianGammaISO(*args, **kwargs)	Node for Gaussian-gamma (isotropic) random variables.
GaussianGammaARD(mu, alpha, a, b, **kwargs)	Node for Gaussian and gamma random variables with ARD form.
GaussianWishart(*args, **kwargs)	Node for Gaussian-Wishart random variables.

bayespy.nodes.GaussianGammaISO

class bayespy.nodes.GaussianGammaISO(*args, **kwargs)

Node for Gaussian-gamma (isotropic) random variables.

The prior:

$$p(x, \alpha | \mu, \Lambda, a, b)$$

$$p(x | \alpha, \mu, \Lambda) = \mathcal{N}(x | \mu, \alpha \Lambda)$$

$$p(\alpha | a, b) = \mathcal{G}(\alpha | a, b)$$

The posterior approximation $q(x, \alpha)$ has the same Gaussian-gamma form.

Currently, supports only vector variables.

Methods

add_plate_axis(to_plate)	
delete()	Delete this node and the children
get_gaussian_mean_and_variance()	Return the mean and variance of the distribution
get_marginal_logpdf([gaussian, gamma])	Get the (marginal) log pdf of a subset of the variables
get_mask()	
get_moments()	
get_shape(ind)	
has_plotter()	Return True if the node has a plotter
initialize_from_parameters(*args)	
initialize_from_prior()	
initialize_from_random()	Set the variable to a random sample from the current distribution.
initialize_from_value(x, *args)	
load(group)	Load the state of the node from a HDF5 file.
logpdf(X[, mask])	Compute the log probability density function Q(X) of this node.
lower_bound_contribution([gradient])	
lowerbound()	
move_plates(from_plate, to_plate)	
observe(x, *args[, mask])	Fix moments, compute f and propagate mask.
pdf(X[, mask])	Compute the probability density function of this node.
plot(**kwargs)	Plot the node distribution using the plotter of the node
plotmatrix()	Creates a matrix of marginal plots.
random()	Draw a random sample from the distribution.
save(group)	Save the state of the node into a HDF5 file.
set_plotter(plotter)	

Continued on next page

Table 5.15 – continued from previous page

<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.GaussianGammaISO.add_plate_axis

`GaussianGammaISO.add_plate_axis (to_plate)`

bayespy.nodes.GaussianGammaISO.delete

`GaussianGammaISO.delete ()`

Delete this node and the children

bayespy.nodes.GaussianGammaISO.get_gaussian_mean_and_variance

`GaussianGammaISO.get_gaussian_mean_and_variance ()`

Return the mean and variance of the distribution

bayespy.nodes.GaussianGammaISO.get_marginal_logpdf

`GaussianGammaISO.get_marginal_logpdf (gaussian=None, gamma=None)`

Get the (marginal) log pdf of a subset of the variables

Parameters `gaussian` : list or None

Indices of the Gaussian variables to keep or None

`gamma` : bool or None

True if keep the gamma variable, otherwise False or None

Returns function

A function which computes log-pdf

bayespy.nodes.GaussianGammaISO.get_mask

`GaussianGammaISO.get_mask ()`

bayespy.nodes.GaussianGammaISO.get_moments

`GaussianGammaISO.get_moments ()`

bayespy.nodes.GaussianGammaISO.get_shape

`GaussianGammaISO.get_shape (ind)`

bayespy.nodes.GaussianGammaISO.has_plotter

`GaussianGammaISO.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.GaussianGammaISO.initialize_from_parameters

`GaussianGammaISO.initialize_from_parameters(*args)`

bayespy.nodes.GaussianGammaISO.initialize_from_prior

`GaussianGammaISO.initialize_from_prior()`

bayespy.nodes.GaussianGammaISO.initialize_from_random

`GaussianGammaISO.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.GaussianGammaISO.initialize_from_value

`GaussianGammaISO.initialize_from_value(x, *args)`

bayespy.nodes.GaussianGammaISO.load

`GaussianGammaISO.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.GaussianGammaISO.logpdf

`GaussianGammaISO.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.GaussianGammaISO.lower_bound_contribution

`GaussianGammaISO.lower_bound_contribution(gradient=False)`

bayespy.nodes.GaussianGammaISO.lowerbound

`GaussianGammaISO.lowerbound()`

bayespy.nodes.GaussianGammaISO.move_plates

`GaussianGammaISO.move_plates(from_plate, to_plate)`

bayespy.nodes.GaussianGammaISO.observe

`GaussianGammaISO.observe(x, *args, mask=True)`
Fix moments, compute f and propagate mask.

bayespy.nodes.GaussianGammaISO.pdf

`GaussianGammaISO.pdf(X, mask=True)`
Compute the probability density function of this node.

bayespy.nodes.GaussianGammaISO.plot

`GaussianGammaISO.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.GaussianGammaISO.plotmatrix

`GaussianGammaISO.plotmatrix()`
Creates a matrix of marginal plots.

On diagonal, are marginal plots of each variable. Off-diagonal plot (i,j) shows the joint marginal density of x_i and x_j .

bayespy.nodes.GaussianGammaISO.random

`GaussianGammaISO.random()`
Draw a random sample from the distribution.

bayespy.nodes.GaussianGammaISO.save

`GaussianGammaISO.save(group)`
Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.GaussianGammaISO.set_plotter

`GaussianGammaISO.set_plotter(plotter)`

bayespy.nodes.GaussianGammaISO.show

`GaussianGammaISO.show()`
Print the distribution using standard parameterization.

bayespy.nodes.GaussianGammaISO.unobserve

GaussianGammaISO.unobserve()

bayespy.nodes.GaussianGammaISO.update

GaussianGammaISO.update()

Attributes

dims
plates

bayespy.nodes.GaussianGammaISO.dims

GaussianGammaISO.dims = None

bayespy.nodes.GaussianGammaISO.plates

GaussianGammaISO.plates = None

bayespy.nodes.GaussianGammaARD

class bayespy.nodes.GaussianGammaARD(*mu, alpha, a, b, **kwargs*)

Node for Gaussian and gamma random variables with ARD form.

The prior:

$$p(x, \tau | \mu, \alpha, a, b) = p(x | \tau, \mu, \alpha) p(\tau | a, b)$$

$$p(x | \alpha, \mu, \alpha) = \mathcal{N}(x | \mu, \text{diag}(\alpha \tau))$$

$$p(\tau | a, b) = \mathcal{G}(\tau | a, b)$$

The posterior approximation $q(x, \tau)$ has the same Gaussian-gamma form.

Warning: Not yet implemented.

See also:

Gaussian, GaussianARD, Gamma, GaussianGammaISO, GaussianWishart

Methods

add_plate_axis(to_plate)	
delete()	Delete this node and the children
get_mask()	
get_moments()	

Continued on next page

Table 5.17 – continued from previous page

<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.GaussianGammaARD.add_plate_axis

`GaussianGammaARD.add_plate_axis(to_plate)`

bayespy.nodes.GaussianGammaARD.delete

`GaussianGammaARD.delete()`
Delete this node and the children

bayespy.nodes.GaussianGammaARD.get_mask

`GaussianGammaARD.get_mask()`

bayespy.nodes.GaussianGammaARD.get_moments

`GaussianGammaARD.get_moments()`

bayespy.nodes.GaussianGammaARD.get_shape

`GaussianGammaARD.get_shape(ind)`

bayespy.nodes.GaussianGammaARD.has_plotter

`GaussianGammaARD.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.GaussianGammaARD.initialize_from_parameters

GaussianGammaARD.**initialize_from_parameters** (*args)

bayespy.nodes.GaussianGammaARD.initialize_from_prior

GaussianGammaARD.**initialize_from_prior**()

bayespy.nodes.GaussianGammaARD.initialize_from_random

GaussianGammaARD.**initialize_from_random**()

Set the variable to a random sample from the current distribution.

bayespy.nodes.GaussianGammaARD.initialize_from_value

GaussianGammaARD.**initialize_from_value** (x, *args)

bayespy.nodes.GaussianGammaARD.load

GaussianGammaARD.**load** (group)

Load the state of the node from a HDF5 file.

bayespy.nodes.GaussianGammaARD.logpdf

GaussianGammaARD.**logpdf** (X, mask=True)

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.GaussianGammaARD.lower_bound_contribution

GaussianGammaARD.**lower_bound_contribution** (gradient=False)

bayespy.nodes.GaussianGammaARD.lowerbound

GaussianGammaARD.**lowerbound**()

bayespy.nodes.GaussianGammaARD.move_plates

GaussianGammaARD.**move_plates** (from_plate, to_plate)

bayespy.nodes.GaussianGammaARD.observe

GaussianGammaARD.**observe** (x, *args, mask=True)

Fix moments, compute f and propagate mask.

bayespy.nodes.GaussianGammaARD.pdf

`GaussianGammaARD.pdf` (*X*, *mask=True*)
Compute the probability density function of this node.

bayespy.nodes.GaussianGammaARD.plot

`GaussianGammaARD.plot` (***kwargs*)
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.GaussianGammaARD.random

`GaussianGammaARD.random` ()
Draw a random sample from the distribution.

bayespy.nodes.GaussianGammaARD.save

`GaussianGammaARD.save` (*group*)
Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.GaussianGammaARD.set_plotter

`GaussianGammaARD.set_plotter` (*plotter*)

bayespy.nodes.GaussianGammaARD.unobserve

`GaussianGammaARD.unobserve` ()

bayespy.nodes.GaussianGammaARD.update

`GaussianGammaARD.update` ()

Attributes

`dims`
`plates`

bayespy.nodes.GaussianGammaARD.dims

`GaussianGammaARD.dims = None`

bayespy.nodes.GaussianGammaARD.plates

GaussianGammaARD.plates = None

bayespy.nodes.GaussianWishart

class bayespy.nodes.GaussianWishart (*args, **kwargs)

Node for Gaussian-Wishart random variables.

The prior:

$$p(x, \Lambda | \mu, \alpha, V, n)$$

$$p(x | \Lambda, \mu, \alpha) = (N)(x | \mu, \alpha^{-1} \text{Lambda}^{-1})$$

$$p(\Lambda | V, n) = (W)(\Lambda | n, V)$$

The posterior approximation $q(x, \Lambda)$ has the same Gaussian-Wishart form.

Currently, supports only vector variables.

Methods

add_plate_axis(to_plate)	
delete()	Delete this node and the children
get_mask()	
get_moments()	
get_shape(ind)	
has_plotter()	Return True if the node has a plotter
initialize_from_parameters(*args)	
initialize_from_prior()	
initialize_from_random()	Set the variable to a random sample from the current distribution.
initialize_from_value(x, *args)	
load(group)	Load the state of the node from a HDF5 file.
logpdf(X[, mask])	Compute the log probability density function Q(X) of this node.
lower_bound_contribution([gradient])	
lowerbound()	
move_plates(from_plate, to_plate)	
observe(x, *args[, mask])	Fix moments, compute f and propagate mask.
pdf(X[, mask])	Compute the probability density function of this node.
plot(**kwargs)	Plot the node distribution using the plotter of the node
random()	Draw a random sample from the distribution.
save(group)	Save the state of the node into a HDF5 file.
set_plotter(plotter)	
show()	Print the distribution using standard parameterization.
unobserve()	
update()	

bayespy.nodes.GaussianWishart.add_plate_axis

GaussianWishart.add_plate_axis (to_plate)

bayespy.nodes.GaussianWishart.delete

`GaussianWishart.delete()`
Delete this node and the children

bayespy.nodes.GaussianWishart.get_mask

`GaussianWishart.get_mask()`

bayespy.nodes.GaussianWishart.get_moments

`GaussianWishart.get_moments()`

bayespy.nodes.GaussianWishart.get_shape

`GaussianWishart.get_shape(ind)`

bayespy.nodes.GaussianWishart.has_plotter

`GaussianWishart.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.GaussianWishart.initialize_from_parameters

`GaussianWishart.initialize_from_parameters(*args)`

bayespy.nodes.GaussianWishart.initialize_from_prior

`GaussianWishart.initialize_from_prior()`

bayespy.nodes.GaussianWishart.initialize_from_random

`GaussianWishart.initialize_from_random()`
Set the variable to a random sample from the current distribution.

bayespy.nodes.GaussianWishart.initialize_from_value

`GaussianWishart.initialize_from_value(x, *args)`

bayespy.nodes.GaussianWishart.load

`GaussianWishart.load(group)`
Load the state of the node from a HDF5 file.

bayespy.nodes.GaussianWishart.logpdf

`GaussianWishart.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.GaussianWishart.lower_bound_contribution

`GaussianWishart.lower_bound_contribution(gradient=False)`

bayespy.nodes.GaussianWishart.lowerbound

`GaussianWishart.lowerbound()`

bayespy.nodes.GaussianWishart.move_plates

`GaussianWishart.move_plates(from_plate, to_plate)`

bayespy.nodes.GaussianWishart.observe

`GaussianWishart.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.GaussianWishart.pdf

`GaussianWishart.pdf(X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.GaussianWishart.plot

`GaussianWishart.plot(**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.GaussianWishart.random

`GaussianWishart.random()`

Draw a random sample from the distribution.

bayespy.nodes.GaussianWishart.save

`GaussianWishart.save(group)`

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.GaussianWishart.set_plotter

GaussianWishart.**set_plotter** (*plotter*)

bayespy.nodes.GaussianWishart.show

GaussianWishart.**show** ()
Print the distribution using standard parameterization.

bayespy.nodes.GaussianWishart.unobserve

GaussianWishart.**unobserve** ()

bayespy.nodes.GaussianWishart.update

GaussianWishart.**update** ()

Attributes

`dims`
`plates`

bayespy.nodes.GaussianWishart.dims

GaussianWishart.**dims** = None

bayespy.nodes.GaussianWishart.plates

GaussianWishart.**plates** = None

Nodes for discrete count variables:

<code>Bernoulli(p, **kwargs)</code>	Node for Bernoulli random variables.
<code>Binomial(n, p, **kwargs)</code>	Node for binomial random variables.
<code>Categorical(p, **kwargs)</code>	Node for categorical random variables.
<code>Multinomial(n, p, **kwargs)</code>	Node for multinomial random variables.
<code>Poisson(l, **kwargs)</code>	Node for Poisson random variables.

bayespy.nodes.Bernoulli

class bayespy.nodes.**Bernoulli** (*p*, ***kwargs*)
Node for Bernoulli random variables.

The node models a binary random variable $z \in \{0, 1\}$ with prior probability $p \in [0, 1]$ for value one:

$$z \sim \text{Bernoulli}(p).$$

Parameters **p** : beta-like node

Probability of a successful trial

Examples

```

from bayespy.nodes import Bernoulli, Beta
p = Beta([1e-3, 1e-3])
z = Bernoulli(p, plates=(10,))
z.observe([0, 1, 1, 1, 0, 1, 1, 1, 0, 1])
p.update()
import bayespy.plot as bpplt
import numpy as np
bpplt.pdf(p, np.linspace(0, 1, num=100))

```

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function Q(X) of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Bernoulli.add_plate_axis

`Bernoulli.add_plate_axis(to_plate)`

bayespy.nodes.Bernoulli.delete

`Bernoulli.delete()`
Delete this node and the children

bayespy.nodes.Bernoulli.get_mask

`Bernoulli.get_mask()`

bayespy.nodes.Bernoulli.get_moments

`Bernoulli.get_moments()`

bayespy.nodes.Bernoulli.get_shape

`Bernoulli.get_shape(ind)`

bayespy.nodes.Bernoulli.has_plotter

`Bernoulli.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.Bernoulli.initialize_from_parameters

`Bernoulli.initialize_from_parameters(*args)`

bayespy.nodes.Bernoulli.initialize_from_prior

`Bernoulli.initialize_from_prior()`

bayespy.nodes.Bernoulli.initialize_from_random

`Bernoulli.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Bernoulli.initialize_from_value

`Bernoulli.initialize_from_value(x, *args)`

bayespy.nodes.Bernoulli.load

`Bernoulli.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Bernoulli.logpdf

`Bernoulli.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Bernoulli.lower_bound_contribution

`Bernoulli.lower_bound_contribution (gradient=False)`

bayespy.nodes.Bernoulli.lowerbound

`Bernoulli.lowerbound()`

bayespy.nodes.Bernoulli.move_plates

`Bernoulli.move_plates (from_plate, to_plate)`

bayespy.nodes.Bernoulli.observe

`Bernoulli.observe (x, *args, mask=True)`
Fix moments, compute f and propagate mask.

bayespy.nodes.Bernoulli.pdf

`Bernoulli.pdf (X, mask=True)`
Compute the probability density function of this node.

bayespy.nodes.Bernoulli.plot

`Bernoulli.plot (**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Bernoulli.random

`Bernoulli.random()`
Draw a random sample from the distribution.

bayespy.nodes.Bernoulli.save

`Bernoulli.save (group)`
Save the state of the node into a HDF5 file.
group can be the root

bayespy.nodes.Bernoulli.set_plotter

`Bernoulli.set_plotter (plotter)`

`bayespy.nodes.Bernoulli.show`

`Bernoulli.show()`
 Print the distribution using standard parameterization.

`bayespy.nodes.Bernoulli.unobserve`

`Bernoulli.unobserve()`

`bayespy.nodes.Bernoulli.update`

`Bernoulli.update()`

Attributes

<code>dims</code>
<code>plates</code>

`bayespy.nodes.Bernoulli.dims`

`Bernoulli.dims = None`

`bayespy.nodes.Bernoulli.plates`

`Bernoulli.plates = None`

`bayespy.nodes.Binomial`

class `bayespy.nodes.Binomial`(*n*, *p*, ***kwargs*)
 Node for binomial random variables.

The node models the number of successes $x \in \{0, \dots, n\}$ in n trials with probability p for success:

$$x \sim \text{Binomial}(n, p).$$

Parameters **n** : scalar or array

Number of trials

p : beta-like node or scalar or array

Probability of a success in a trial

See also:

`Bernoulli`, `Multinomial`, `Beta`

Examples

```
from bayespy.nodes import Binomial, Beta
p = Beta([1e-3, 1e-3])
x = Binomial(10, p)
x.observe(7)
p.update()
import bayespy.plot as bpplt
import numpy as np
bpplt.pdf(p, np.linspace(0, 1, num=100))
```

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Binomial.add_plate_axis

`Binomial.add_plate_axis(to_plate)`

bayespy.nodes.Binomial.delete

`Binomial.delete()`
Delete this node and the children

bayespy.nodes.Binomial.get_mask

`Binomial.get_mask()`

bayespy.nodes.Binomial.get_moments

`Binomial.get_moments()`

bayespy.nodes.Binomial.get_shape

`Binomial.get_shape(ind)`

bayespy.nodes.Binomial.has_plotter

`Binomial.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.Binomial.initialize_from_parameters

`Binomial.initialize_from_parameters(*args)`

bayespy.nodes.Binomial.initialize_from_prior

`Binomial.initialize_from_prior()`

bayespy.nodes.Binomial.initialize_from_random

`Binomial.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Binomial.initialize_from_value

`Binomial.initialize_from_value(x, *args)`

bayespy.nodes.Binomial.load

`Binomial.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Binomial.logpdf

`Binomial.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Binomial.lower_bound_contribution

`Binomial.lower_bound_contribution(gradient=False)`

bayespy.nodes.Binomial.lowerbound

```
Binomial.lowerbound()
```

bayespy.nodes.Binomial.move_plates

```
Binomial.move_plates(from_plate, to_plate)
```

bayespy.nodes.Binomial.observe

```
Binomial.observe(x, *args, mask=True)
```

Fix moments, compute f and propagate mask.

bayespy.nodes.Binomial.pdf

```
Binomial.pdf(X, mask=True)
```

Compute the probability density function of this node.

bayespy.nodes.Binomial.plot

```
Binomial.plot(**kwargs)
```

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, bayespy.plot.plotting for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Binomial.random

```
Binomial.random()
```

Draw a random sample from the distribution.

bayespy.nodes.Binomial.save

```
Binomial.save(group)
```

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Binomial.set_plotter

```
Binomial.set_plotter(plotter)
```

bayespy.nodes.Binomial.show

```
Binomial.show()
```

Print the distribution using standard parameterization.

bayespy.nodes.Binomial.unobserve

`Binomial.unobserve()`

bayespy.nodes.Binomial.update

`Binomial.update()`

Attributes

<code>dims</code>
<code>plates</code>

bayespy.nodes.Binomial.dims

`Binomial.dims = None`

bayespy.nodes.Binomial.plates

`Binomial.plates = None`

bayespy.nodes.Categorical

class `bayespy.nodes.Categorical(p, **kwargs)`

Node for categorical random variables.

The node models a categorical random variable $x \in \{0, \dots, K - 1\}$ with prior probabilities $\{p_0, \dots, p_{K-1}\}$ for each category:

$$p(x = k) = p_k \quad \text{for } k \in \{0, \dots, K - 1\}.$$

Parameters `p` : Dirichlet-like node or (...K)-array

Probabilities for each category

See also:

`Bernoulli`, `Multinomial`, `Dirichlet`

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	

Continued on next page

Table 5.26 – continued from previous page

<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Categorical.add_plate_axis

`Categorical.add_plate_axis` (*to_plate*)

bayespy.nodes.Categorical.delete

`Categorical.delete()`
Delete this node and the children

bayespy.nodes.Categorical.get_mask

`Categorical.get_mask()`

bayespy.nodes.Categorical.get_moments

`Categorical.get_moments()`

bayespy.nodes.Categorical.get_shape

`Categorical.get_shape` (*ind*)

bayespy.nodes.Categorical.has_plotter

`Categorical.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.Categorical.initialize_from_parameters

`Categorical.initialize_from_parameters` (**args*)

bayespy.nodes.Categorical.initialize_from_prior

`Categorical.initialize_from_prior()`

bayespy.nodes.Categorical.initialize_from_random

`Categorical.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Categorical.initialize_from_value

`Categorical.initialize_from_value(x, *args)`

bayespy.nodes.Categorical.load

`Categorical.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Categorical.logpdf

`Categorical.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Categorical.lower_bound_contribution

`Categorical.lower_bound_contribution(gradient=False)`

bayespy.nodes.Categorical.lowerbound

`Categorical.lowerbound()`

bayespy.nodes.Categorical.move_plates

`Categorical.move_plates(from_plate, to_plate)`

bayespy.nodes.Categorical.observe

`Categorical.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Categorical.pdf

`Categorical.pdf(X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.Categorical.plot

`Categorical.plot(**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Categorical.random

`Categorical.random()`

Draw a random sample from the distribution.

bayespy.nodes.Categorical.save

`Categorical.save(group)`

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Categorical.set_plotter

`Categorical.set_plotter(plotter)`

bayespy.nodes.Categorical.show

`Categorical.show()`

Print the distribution using standard parameterization.

bayespy.nodes.Categorical.unobserve

`Categorical.unobserve()`

bayespy.nodes.Categorical.update

`Categorical.update()`

Attributes

<code>dims</code>
<code>plates</code>

bayespy.nodes.Categorical.dims

`Categorical.dims = None`

bayespy.nodes.Categorical.plates

`Categorical.plates = None`

bayespy.nodes.Multinomial

class bayespy.nodes.**Multinomial** (*n*, *p*, ***kwargs*)

Node for multinomial random variables.

Assume there are K categories and N trials each of which leads a success for exactly one of the categories. Given the probabilities p_0, \dots, p_{K-1} for the categories, multinomial distribution is gives the probability of any combination of numbers of successes for the categories.

The node models the number of successes $x_k \in \{0, \dots, n\}$ in n trials with probability p_k for success in K categories.

$$\text{Multinomial}(\mathbf{x}|N, \mathbf{p}) = \frac{N!}{x_0! \cdots x_{K-1}!} p_0^{x_0} \cdots p_{K-1}^{x_{K-1}}$$

Parameters **n** : scalar or array

N , number of trials

p : Dirichlet-like node or (...,K)-array

p, probabilities of successes for the categories

See also:

`Dirichlet`, `Binomial`, `Categorical`

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.

Continued on next page

Table 5.28 – continued from previous page

```
unobserve()
update()
```

bayespy.nodes.Multinomial.add_plate_axis

```
Multinomial.add_plate_axis(to_plate)
```

bayespy.nodes.Multinomial.delete

```
Multinomial.delete()
```

Delete this node and the children

bayespy.nodes.Multinomial.get_mask

```
Multinomial.get_mask()
```

bayespy.nodes.Multinomial.get_moments

```
Multinomial.get_moments()
```

bayespy.nodes.Multinomial.get_shape

```
Multinomial.get_shape(ind)
```

bayespy.nodes.Multinomial.has_plotter

```
Multinomial.has_plotter()
```

Return True if the node has a plotter

bayespy.nodes.Multinomial.initialize_from_parameters

```
Multinomial.initialize_from_parameters(*args)
```

bayespy.nodes.Multinomial.initialize_from_prior

```
Multinomial.initialize_from_prior()
```

bayespy.nodes.Multinomial.initialize_from_random

```
Multinomial.initialize_from_random()
```

Set the variable to a random sample from the current distribution.

bayespy.nodes.Multinomial.initialize_from_value

`Multinomial.initialize_from_value(x, *args)`

bayespy.nodes.Multinomial.load

`Multinomial.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Multinomial.logpdf

`Multinomial.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Multinomial.lower_bound_contribution

`Multinomial.lower_bound_contribution(gradient=False)`

bayespy.nodes.Multinomial.lowerbound

`Multinomial.lowerbound()`

bayespy.nodes.Multinomial.move_plates

`Multinomial.move_plates(from_plate, to_plate)`

bayespy.nodes.Multinomial.observe

`Multinomial.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Multinomial.pdf

`Multinomial.pdf(X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.Multinomial.plot

`Multinomial.plot(**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Multinomial.random

```
Multinomial.random()
```

Draw a random sample from the distribution.

bayespy.nodes.Multinomial.save

```
Multinomial.save(group)
```

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Multinomial.set_plotter

```
Multinomial.set_plotter(plotter)
```

bayespy.nodes.Multinomial.show

```
Multinomial.show()
```

Print the distribution using standard parameterization.

bayespy.nodes.Multinomial.unobserve

```
Multinomial.unobserve()
```

bayespy.nodes.Multinomial.update

```
Multinomial.update()
```

Attributes

```
dims  
plates
```

bayespy.nodes.Multinomial.dims

```
Multinomial.dims = None
```

bayespy.nodes.Multinomial.plates

```
Multinomial.plates = None
```

bayespy.nodes.Poisson

```
class bayespy.nodes.Poisson(l, **kwargs)
```

Node for Poisson random variables.

The node uses Poisson distribution:

$$p(x) = \text{Poisson}(x|\lambda)$$

where λ is the rate parameter.

Parameters **l** : gamma-like node or scalar or array

λ , rate parameter

See also:

[Gamma](#), [Exponential](#)

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function Q(X) of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

`bayespy.nodes.Poisson.add_plate_axis`

`Poisson.add_plate_axis(to_plate)`

`bayespy.nodes.Poisson.delete`

`Poisson.delete()`

Delete this node and the children

bayespy.nodes.Poisson.get_mask

`Poisson.get_mask()`

bayespy.nodes.Poisson.get_moments

`Poisson.get_moments()`

bayespy.nodes.Poisson.get_shape

`Poisson.get_shape(ind)`

bayespy.nodes.Poisson.has_plotter

`Poisson.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.Poisson.initialize_from_parameters

`Poisson.initialize_from_parameters(*args)`

bayespy.nodes.Poisson.initialize_from_prior

`Poisson.initialize_from_prior()`

bayespy.nodes.Poisson.initialize_from_random

`Poisson.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Poisson.initialize_from_value

`Poisson.initialize_from_value(x, *args)`

bayespy.nodes.Poisson.load

`Poisson.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Poisson.logpdf

`Poisson.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Poisson.lower_bound_contribution

`Poisson.lower_bound_contribution` (*gradient=False*)

bayespy.nodes.Poisson.lowerbound

`Poisson.lowerbound` ()

bayespy.nodes.Poisson.move_plates

`Poisson.move_plates` (*from_plate, to_plate*)

bayespy.nodes.Poisson.observe

`Poisson.observe` (*x, *args, mask=True*)
Fix moments, compute f and propagate mask.

bayespy.nodes.Poisson.pdf

`Poisson.pdf` (*X, mask=True*)
Compute the probability density function of this node.

bayespy.nodes.Poisson.plot

`Poisson.plot` (***kwargs*)
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Poisson.random

`Poisson.random` ()
Draw a random sample from the distribution.

bayespy.nodes.Poisson.save

`Poisson.save` (*group*)
Save the state of the node into a HDF5 file.
group can be the root

bayespy.nodes.Poisson.set_plotter

`Poisson.set_plotter` (*plotter*)

bayespy.nodes.Poisson.show

`Poisson.show()`
 Print the distribution using standard parameterization.

bayespy.nodes.Poisson.unobserve

`Poisson.unobserve()`

bayespy.nodes.Poisson.update

`Poisson.update()`

Attributes

<code>dims</code>	tuple() -> empty tuple
<code>plates</code>	

bayespy.nodes.Poisson.dims

`Poisson.dims = (),`

bayespy.nodes.Poisson.plates

`Poisson.plates = None`

Nodes for probabilities:

<code>Beta(alpha, **kwargs)</code>	Node for beta random variables.
<code>Dirichlet(*args, **kwargs)</code>	Node for Dirichlet random variables.

bayespy.nodes.Beta

class `bayespy.nodes.Beta(alpha, **kwargs)`
 Node for beta random variables.

The node models a probability variable $p \in [0, 1]$ as

$$p \sim \text{Beta}(a, b)$$

where a and b are prior counts for success and failure, respectively.

Parameters `alpha` : (...2)-shaped array

Two-element vector containing a and b

Examples

```
from bayespy.nodes import Bernoulli, Beta
p = Beta([1e-3, 1e-3])
z = Bernoulli(p, plates=(10,))
z.observe([0, 1, 1, 1, 0, 1, 1, 1, 0, 1])
p.update()
import bayespy.plot as bpplt
import numpy as np
bpplt.pdf(p, np.linspace(0, 1, num=100))
```

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function Q(X) of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Beta.add_plate_axis

`Beta.add_plate_axis (to_plate)`

bayespy.nodes.Beta.delete

`Beta.delete()`
Delete this node and the children

bayespy.nodes.Beta.get_mask

`Beta.get_mask()`

bayespy.nodes.Beta.get_moments

`Beta.get_moments()`

bayespy.nodes.Beta.get_shape

`Beta.get_shape(ind)`

bayespy.nodes.Beta.has_plotter

`Beta.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.Beta.initialize_from_parameters

`Beta.initialize_from_parameters(*args)`

bayespy.nodes.Beta.initialize_from_prior

`Beta.initialize_from_prior()`

bayespy.nodes.Beta.initialize_from_random

`Beta.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Beta.initialize_from_value

`Beta.initialize_from_value(x, *args)`

bayespy.nodes.Beta.load

`Beta.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Beta.logpdf

`Beta.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Beta.lower_bound_contribution

`Beta.lower_bound_contribution(gradient=False)`

bayespy.nodes.Beta.lowerbound

`Beta.lowerbound()`

bayespy.nodes.Beta.move_plates

`Beta.move_plates` (*from_plate, to_plate*)

bayespy.nodes.Beta.observe

`Beta.observe` (*x, *args, mask=True*)

Fix moments, compute f and propagate mask.

bayespy.nodes.Beta.pdf

`Beta.pdf` (*X, mask=True*)

Compute the probability density function of this node.

bayespy.nodes.Beta.plot

`Beta.plot` (***kwargs*)

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Beta.random

`Beta.random()`

Draw a random sample from the distribution.

bayespy.nodes.Beta.save

`Beta.save` (*group*)

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Beta.set_plotter

`Beta.set_plotter` (*plotter*)

bayespy.nodes.Beta.show

`Beta.show()`

Print the distribution using standard parameterization.

bayespy.nodes.Beta.unobserve

Beta.unobserve()

bayespy.nodes.Beta.update

Beta.update()

Attributes

dims
plates

bayespy.nodes.Beta.dims

Beta.dims = None

bayespy.nodes.Beta.plates

Beta.plates = None

bayespy.nodes.Dirichlet

class bayespy.nodes.**Dirichlet**(*args, **kwargs)

Node for Dirichlet random variables.

The node models a set of probabilities $\{\pi_0, \dots, \pi_{K-1}\}$ which satisfy $\sum_{k=0}^{K-1} \pi_k = 1$ and $\pi_k \in [0, 1] \forall k = 0, \dots, K-1$.

$$p(\pi_0, \dots, \pi_{K-1}) = \text{Dirichlet}(\alpha_0, \dots, \alpha_{K-1})$$

where α_k are concentration parameters.

The posterior approximation has the same functional form but with different concentration parameters.

Parameters **alpha** : (... ,K)-shaped array

Prior counts α_k

See also:

Beta, Categorical, Multinomial, CategoricalMarkovChain

Methods

add_plate_axis(to_plate)
delete()
get_mask()
get_moments()

Delete this node and the children

Continued on next page

Table 5.35 – continued from previous page

<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Dirichlet.add_plate_axis

`Dirichlet.add_plate_axis(to_plate)`

bayespy.nodes.Dirichlet.delete

`Dirichlet.delete()`
Delete this node and the children

bayespy.nodes.Dirichlet.get_mask

`Dirichlet.get_mask()`

bayespy.nodes.Dirichlet.get_moments

`Dirichlet.get_moments()`

bayespy.nodes.Dirichlet.get_shape

`Dirichlet.get_shape(ind)`

bayespy.nodes.Dirichlet.has_plotter

`Dirichlet.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.Dirichlet.initialize_from_parameters

`Dirichlet.initialize_from_parameters(*args)`

bayespy.nodes.Dirichlet.initialize_from_prior

`Dirichlet.initialize_from_prior()`

bayespy.nodes.Dirichlet.initialize_from_random

`Dirichlet.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Dirichlet.initialize_from_value

`Dirichlet.initialize_from_value(x, *args)`

bayespy.nodes.Dirichlet.load

`Dirichlet.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Dirichlet.logpdf

`Dirichlet.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Dirichlet.lower_bound_contribution

`Dirichlet.lower_bound_contribution(gradient=False)`

bayespy.nodes.Dirichlet.lowerbound

`Dirichlet.lowerbound()`

bayespy.nodes.Dirichlet.move_plates

`Dirichlet.move_plates(from_plate, to_plate)`

bayespy.nodes.Dirichlet.observe

`Dirichlet.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Dirichlet.pdf

`Dirichlet.pdf(X, mask=True)`
Compute the probability density function of this node.

bayespy.nodes.Dirichlet.plot

`Dirichlet.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Dirichlet.random

`Dirichlet.random()`
Draw a random sample from the distribution.

bayespy.nodes.Dirichlet.save

`Dirichlet.save(group)`
Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Dirichlet.set_plotter

`Dirichlet.set_plotter(plotter)`

bayespy.nodes.Dirichlet.show

`Dirichlet.show()`
Print the distribution using standard parameterization.

bayespy.nodes.Dirichlet.unobserve

`Dirichlet.unobserve()`

bayespy.nodes.Dirichlet.update

`Dirichlet.update()`

Continued on next page

Table 5.36 – continued from previous page

Attributes

`dims`
`plates`

`bayespy.nodes.Dirichlet.dims`

`Dirichlet.dims = None`

`bayespy.nodes.Dirichlet.plates`

`Dirichlet.plates = None`

Nodes for dynamic variables:

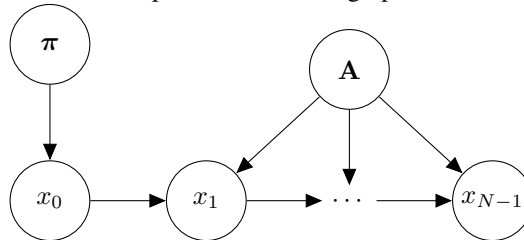
<code>CategoricalMarkovChain(pi, A[, states])</code>	Node for categorical Markov chain random variables.
<code>GaussianMarkovChain(mu, Lambda, A, nu[, n])</code>	Node for Gaussian Markov chain random variables.
<code>SwitchingGaussianMarkovChain(mu, Lambda, B, ...)</code>	Node for Gaussian Markov chain random variables with switching d
<code>VaryingGaussianMarkovChain(mu, Lambda, B, S, nu)</code>	Node for Gaussian Markov chain random variables with time-varyin

`bayespy.nodes.CategoricalMarkovChain`

class `bayespy.nodes.CategoricalMarkovChain` (*pi*, *A*, *states=None*, ***kwargs*)

Node for categorical Markov chain random variables.

The node models a Markov chain which has a discrete set of K possible states and the next state depends only on the previous state and the state transition probabilities. The graphical model is shown below:



where π contains the probabilities for the initial state and \mathbf{A} is the state transition probability matrix. It is possible to have \mathbf{A} varying in time.

$$p(x_0, \dots, x_{N-1}) = p(x_0) \prod_{n=1}^{N-1} p(x_n | x_{n-1}),$$

where

$$\begin{aligned}
 p(x_0 = k) &= \pi_k, \quad \text{for } k \in \{0, \dots, K-1\}, \\
 p(x_n = j | x_{n-1} = i) &= a_{ij}^{(n-1)} \quad \text{for } n = 1, \dots, N-1, i \in \{1, \dots, K-1\}, j \in \{1, \dots, K-1\} \\
 a_{ij}^{(n)} &= [\mathbf{A}_n]_{ij}
 \end{aligned}$$

This node can be used to construct hidden Markov models by using `Mixture` for the emission distribution.

Parameters `pi` : Dirichlet-like node or (...*K*)-array

π , probabilities for the first state. *K*-dimensional Dirichlet.

A : Dirichlet-like node or (*K*,*K*)-array or (...*1*,*K*,*K*)-array or (...*N-1*,*K*,*K*)-array

A, probabilities for state transitions. *K*-dimensional Dirichlet with plates (*K*,) or (...*1*,*K*) or (...*N-1*,*K*).

states : int, optional

N, the length of the chain.

See also:

[Categorical](#), [Dirichlet](#), [GaussianMarkovChain](#), [Mixture](#),
[SwitchingGaussianMarkovChain](#)

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	Print the distribution using standard parameterization.
<code>unobserve()</code>	
<code>update()</code>	

`bayespy.nodes.CategoricalMarkovChain.add_plate_axis`

`CategoricalMarkovChain.add_plate_axis(to_plate)`

`bayespy.nodes.CategoricalMarkovChain.delete`

`CategoricalMarkovChain.delete()`

Delete this node and the children

bayespy.nodes.CategoricalMarkovChain.get_mask

`CategoricalMarkovChain.get_mask()`

bayespy.nodes.CategoricalMarkovChain.get_moments

`CategoricalMarkovChain.get_moments()`

bayespy.nodes.CategoricalMarkovChain.get_shape

`CategoricalMarkovChain.get_shape(ind)`

bayespy.nodes.CategoricalMarkovChain.has_plotter

`CategoricalMarkovChain.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.CategoricalMarkovChain.initialize_from_parameters

`CategoricalMarkovChain.initialize_from_parameters(*args)`

bayespy.nodes.CategoricalMarkovChain.initialize_from_prior

`CategoricalMarkovChain.initialize_from_prior()`

bayespy.nodes.CategoricalMarkovChain.initialize_from_random

`CategoricalMarkovChain.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.CategoricalMarkovChain.initialize_from_value

`CategoricalMarkovChain.initialize_from_value(x, *args)`

bayespy.nodes.CategoricalMarkovChain.load

`CategoricalMarkovChain.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.CategoricalMarkovChain.logpdf

`CategoricalMarkovChain.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.CategoricalMarkovChain.lower_bound_contribution

`CategoricalMarkovChain.lower_bound_contribution` (*gradient=False*)

bayespy.nodes.CategoricalMarkovChain.lowerbound

`CategoricalMarkovChain.lowerbound` ()

bayespy.nodes.CategoricalMarkovChain.move_plates

`CategoricalMarkovChain.move_plates` (*from_plate, to_plate*)

bayespy.nodes.CategoricalMarkovChain.observe

`CategoricalMarkovChain.observe` (*x, *args, mask=True*)

Fix moments, compute f and propagate mask.

bayespy.nodes.CategoricalMarkovChain.pdf

`CategoricalMarkovChain.pdf` (*X, mask=True*)

Compute the probability density function of this node.

bayespy.nodes.CategoricalMarkovChain.plot

`CategoricalMarkovChain.plot` (***kwargs*)

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.CategoricalMarkovChain.random

`CategoricalMarkovChain.random` ()

Draw a random sample from the distribution.

bayespy.nodes.CategoricalMarkovChain.save

`CategoricalMarkovChain.save` (*group*)

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.CategoricalMarkovChain.set_plotter

`CategoricalMarkovChain.set_plotter` (*plotter*)

bayespy.nodes.CategoricalMarkovChain.show

`CategoricalMarkovChain.show()`
 Print the distribution using standard parameterization.

bayespy.nodes.CategoricalMarkovChain.unobserve

`CategoricalMarkovChain.unobserve()`

bayespy.nodes.CategoricalMarkovChain.update

`CategoricalMarkovChain.update()`

Attributes

<code>dims</code> <code>plates</code>
--

bayespy.nodes.CategoricalMarkovChain.dims

`CategoricalMarkovChain.dims = None`

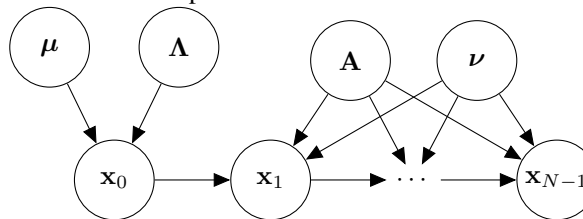
bayespy.nodes.CategoricalMarkovChain.plates

`CategoricalMarkovChain.plates = None`

bayespy.nodes.GaussianMarkovChain

class bayespy.nodes.**GaussianMarkovChain**(*mu*, *Lambda*, *A*, *nu*, *n=None*, ***kwargs*)
 Node for Gaussian Markov chain random variables.

In a simple case, the graphical model can be presented as:



where μ and Λ are the mean and the precision matrix of the initial state, A is the state dynamics matrix and ν is the precision of the innovation noise. It is possible that A and/or ν are different for each transition instead of being constant.

The probability distribution is

$$p(\mathbf{x}_0, \dots, \mathbf{x}_{N-1}) = p(\mathbf{x}_0) \prod_{n=1}^{N-1} p(\mathbf{x}_n | \mathbf{x}_{n-1})$$

where

$$p(\mathbf{x}_0) = \mathcal{N}(\mathbf{x}_0 | \boldsymbol{\mu}, \boldsymbol{\Lambda})$$

$$p(\mathbf{x}_n | \mathbf{x}_{n-1}) = \mathcal{N}(\mathbf{x}_n | \mathbf{A}_{n-1} \mathbf{x}_{n-1}, \text{diag}(\boldsymbol{\nu}_{n-1})).$$

Parameters **mu** : Gaussian-like node or (... ,D)-array

$\boldsymbol{\mu}$, mean of x_0 , D -dimensional with plates (...)

Lambda : Wishart-like node or (... ,D,D)-array

$\boldsymbol{\Lambda}$, precision matrix of x_0 , $D \times D$ -dimensional with plates (...)

A : Gaussian-like node or (D,D)-array or (... ,1,D,D)-array or (... ,N-1,D,D)-array

\mathbf{A} , state dynamics matrix, D -dimensional with plates (D,) or (... ,1,D) or (... ,N-1,D)

nu : gamma-like node or (D,)-array or (... ,1,D)-array or (... ,N-1,D)-array

$\boldsymbol{\nu}$, diagonal elements of the precision of the innovation process, plates (D,) or (... ,1,D) or (... ,N-1,D)

n : int, optional

N , the length of the chain. Must be given if \mathbf{A} and $\boldsymbol{\nu}$ are constant over time.

See also:

[Gaussian](#), [GaussianARD](#), [Wishart](#), [Gamma](#), [SwitchingGaussianMarkovChain](#), [VaryingGaussianMarkovChain](#), [CategoricalMarkovChain](#)

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function Q(X) of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>rotate(R[, inv, logdet])</code>	
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.GaussianMarkovChain.add_plate_axis

GaussianMarkovChain.**add_plate_axis** (*to_plate*)

bayespy.nodes.GaussianMarkovChain.delete

GaussianMarkovChain.**delete** ()
Delete this node and the children

bayespy.nodes.GaussianMarkovChain.get_mask

GaussianMarkovChain.**get_mask** ()

bayespy.nodes.GaussianMarkovChain.get_moments

GaussianMarkovChain.**get_moments** ()

bayespy.nodes.GaussianMarkovChain.get_shape

GaussianMarkovChain.**get_shape** (*ind*)

bayespy.nodes.GaussianMarkovChain.has_plotter

GaussianMarkovChain.**has_plotter** ()
Return True if the node has a plotter

bayespy.nodes.GaussianMarkovChain.initialize_from_parameters

GaussianMarkovChain.**initialize_from_parameters** (*args)

bayespy.nodes.GaussianMarkovChain.initialize_from_prior

GaussianMarkovChain.**initialize_from_prior** ()

bayespy.nodes.GaussianMarkovChain.initialize_from_random

GaussianMarkovChain.**initialize_from_random** ()
Set the variable to a random sample from the current distribution.

bayespy.nodes.GaussianMarkovChain.initialize_from_value

GaussianMarkovChain.**initialize_from_value** (*x*, *args)

bayespy.nodes.GaussianMarkovChain.load

`GaussianMarkovChain.load(group)`
Load the state of the node from a HDF5 file.

bayespy.nodes.GaussianMarkovChain.logpdf

`GaussianMarkovChain.logpdf(X, mask=True)`
Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.GaussianMarkovChain.lower_bound_contribution

`GaussianMarkovChain.lower_bound_contribution(gradient=False)`

bayespy.nodes.GaussianMarkovChain.lowerbound

`GaussianMarkovChain.lowerbound()`

bayespy.nodes.GaussianMarkovChain.move_plates

`GaussianMarkovChain.move_plates(from_plate, to_plate)`

bayespy.nodes.GaussianMarkovChain.observe

`GaussianMarkovChain.observe(x, *args, mask=True)`
Fix moments, compute f and propagate mask.

bayespy.nodes.GaussianMarkovChain.pdf

`GaussianMarkovChain.pdf(X, mask=True)`
Compute the probability density function of this node.

bayespy.nodes.GaussianMarkovChain.plot

`GaussianMarkovChain.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.GaussianMarkovChain.random

`GaussianMarkovChain.random()`
Draw a random sample from the distribution.

`GaussianMarkovChain.rotate` (R , $inv=None$, $logdet=None$)

GaussianMarkovChain.**save** (*group*)
 Save the state of the node into a HDF5 file.
group can be the root

GaussianMarkovChain.**set_plotter** (*plotter*)

```
GaussianMarkovChain.show()
```

```
GaussianMarkovChain.unobserve()
```

```
GaussianMarkovChain.update()
```

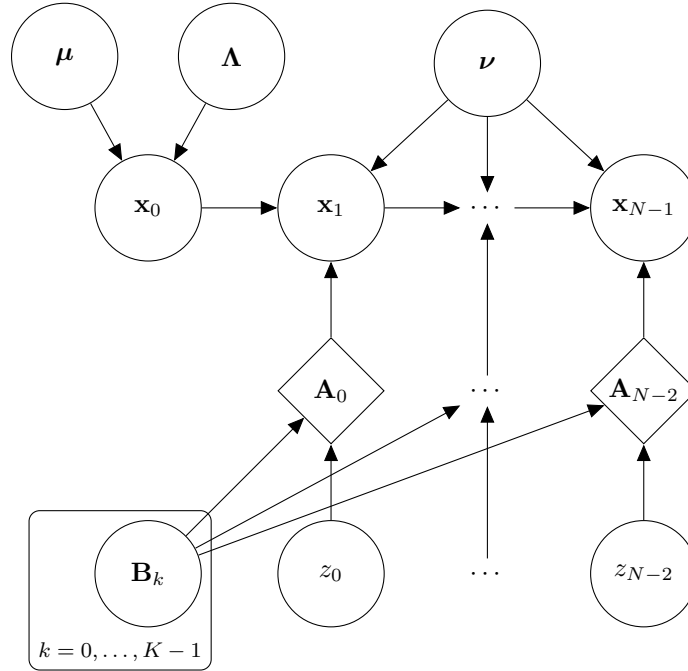
dims
plates

```
GaussianMarkovChain.dims = None
```

```
GaussianMarkovChain.plates = None
```

```
class bayespy.nodes.SwitchingGaussianMarkovChain(mu, Lambda, B, Z, nu, n=None,
                                                **kwargs)
    Node for Gaussian Markov chain random variables with switching dynamics.
```

The node models a sequence of Gaussian variables :math:\mathbf{x}_0, \dots, \mathbf{x}_{N-1} with linear Markovian dynamics. The dynamics may change in time, which is obtained by having a set of matrices and at each time selecting one of them as the state dynamics matrix. The graphical model can be presented as:



where μ and Λ are the mean and the precision matrix of the initial state, ν is the precision of the innovation noise, and \mathbf{A}_n are the state dynamics matrix obtained by selecting one of the matrices $\{\mathbf{B}_k\}_{k=0}^{K-1}$ at each time. The selections are provided by $z_n \in \{0, \dots, K-1\}$. The probability distribution is

$$p(\mathbf{x}_0, \dots, \mathbf{x}_{N-1}) = p(\mathbf{x}_0) \prod_{n=1}^{N-1} p(\mathbf{x}_n | \mathbf{x}_{n-1})$$

where

$$\begin{aligned} p(\mathbf{x}_0) &= \mathcal{N}(\mathbf{x}_0 | \mu, \Lambda) \\ p(\mathbf{x}_n | \mathbf{x}_{n-1}) &= \mathcal{N}(\mathbf{x}_n | \mathbf{A}_{n-1} \mathbf{x}_{n-1}, \text{diag}(\nu)), \quad \text{for } n = 1, \dots, N-1, \\ \mathbf{A}_n &= \mathbf{B}_{z_n}, \quad \text{for } n = 0, \dots, N-2. \end{aligned}$$

Parameters **mu** : Gaussian-like node or (... ,D)-array

μ , mean of x_0 , D -dimensional with plates (...)

Lambda : Wishart-like node or (... ,D,D)-array

Λ , precision matrix of x_0 , $D \times D$ -dimensional with plates (...)

B : Gaussian-like node or (... ,D,D,K)-array

$\{\mathbf{B}_k\}_{k=0}^{K-1}$, a set of state dynamics matrix, $D \times K$ -dimensional with plates (... ,D)

Z : categorical-like node or (... ,N-1)-array

$\{z_0, \dots, z_{N-2}\}$, time-dependent selection, K -categorical with plates (... ,N-1)

nu : gamma-like node or (... ,D)-array

ν , diagonal elements of the precision of the innovation process, plates (... ,D)

n : int, optional

N , the length of the chain. Must be given if \mathbf{Z} does not have plates over the time domain (which would not make sense).

See also:

[Gaussian](#), [GaussianARD](#), [Wishart](#), [Gamma](#), [GaussianMarkovChain](#), [VaryingGaussianMarkovChain](#), [Categorical](#), [CategoricalMarkovChain](#)

Notes

Equivalent model block can be constructed with [GaussianMarkovChain](#) by explicitly using [Gate](#) to select the state dynamics matrix. However, that approach is not very efficient for large datasets because it does not utilize the structure of \mathbf{A}_n , thus it explicitly computes huge moment arrays.

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>rotate(R[, inv, logdet])</code>	
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.SwitchingGaussianMarkovChain.add_plate_axis

`SwitchingGaussianMarkovChain.add_plate_axis(to_plate)`

bayespy.nodes.SwitchingGaussianMarkovChain.delete

`SwitchingGaussianMarkovChain.delete()`
Delete this node and the children

bayespy.nodes.SwitchingGaussianMarkovChain.get_mask

`SwitchingGaussianMarkovChain.get_mask()`

bayespy.nodes.SwitchingGaussianMarkovChain.get_moments

`SwitchingGaussianMarkovChain.get_moments()`

bayespy.nodes.SwitchingGaussianMarkovChain.get_shape

`SwitchingGaussianMarkovChain.get_shape(ind)`

bayespy.nodes.SwitchingGaussianMarkovChain.has_plotter

`SwitchingGaussianMarkovChain.has_plotter()`

Return True if the node has a plotter

bayespy.nodes.SwitchingGaussianMarkovChain.initialize_from_parameters

`SwitchingGaussianMarkovChain.initialize_from_parameters(*args)`

bayespy.nodes.SwitchingGaussianMarkovChain.initialize_from_prior

`SwitchingGaussianMarkovChain.initialize_from_prior()`

bayespy.nodes.SwitchingGaussianMarkovChain.initialize_from_random

`SwitchingGaussianMarkovChain.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.SwitchingGaussianMarkovChain.initialize_from_value

`SwitchingGaussianMarkovChain.initialize_from_value(x, *args)`

bayespy.nodes.SwitchingGaussianMarkovChain.load

`SwitchingGaussianMarkovChain.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.SwitchingGaussianMarkovChain.logpdf

`SwitchingGaussianMarkovChain.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.SwitchingGaussianMarkovChain.lower_bound_contribution

SwitchingGaussianMarkovChain.**lower_bound_contribution** (*gradient=False*)

bayespy.nodes.SwitchingGaussianMarkovChain.lowerbound

SwitchingGaussianMarkovChain.**lowerbound** ()

bayespy.nodes.SwitchingGaussianMarkovChain.move_plates

SwitchingGaussianMarkovChain.**move_plates** (*from_plate, to_plate*)

bayespy.nodes.SwitchingGaussianMarkovChain.observe

SwitchingGaussianMarkovChain.**observe** (*x, *args, mask=True*)

Fix moments, compute f and propagate mask.

bayespy.nodes.SwitchingGaussianMarkovChain.pdf

SwitchingGaussianMarkovChain.**pdf** (*X, mask=True*)

Compute the probability density function of this node.

bayespy.nodes.SwitchingGaussianMarkovChain.plot

SwitchingGaussianMarkovChain.**plot** (***kwargs*)

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, bayespy.plot.plotting for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.SwitchingGaussianMarkovChain.random

SwitchingGaussianMarkovChain.**random** ()

Draw a random sample from the distribution.

bayespy.nodes.SwitchingGaussianMarkovChain.rotate

SwitchingGaussianMarkovChain.**rotate** (*R, inv=None, logdet=None*)

bayespy.nodes.SwitchingGaussianMarkovChain.save

SwitchingGaussianMarkovChain.**save** (*group*)

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.SwitchingGaussianMarkovChain.set_plotter

`SwitchingGaussianMarkovChain.set_plotter(plotter)`

bayespy.nodes.SwitchingGaussianMarkovChain.show

`SwitchingGaussianMarkovChain.show()`

bayespy.nodes.SwitchingGaussianMarkovChain.unobserve

`SwitchingGaussianMarkovChain.unobserve()`

bayespy.nodes.SwitchingGaussianMarkovChain.update

`SwitchingGaussianMarkovChain.update()`

Attributes

<code>dims</code>
<code>plates</code>

bayespy.nodes.SwitchingGaussianMarkovChain.dims

`SwitchingGaussianMarkovChain.dims = None`

bayespy.nodes.SwitchingGaussianMarkovChain.plates

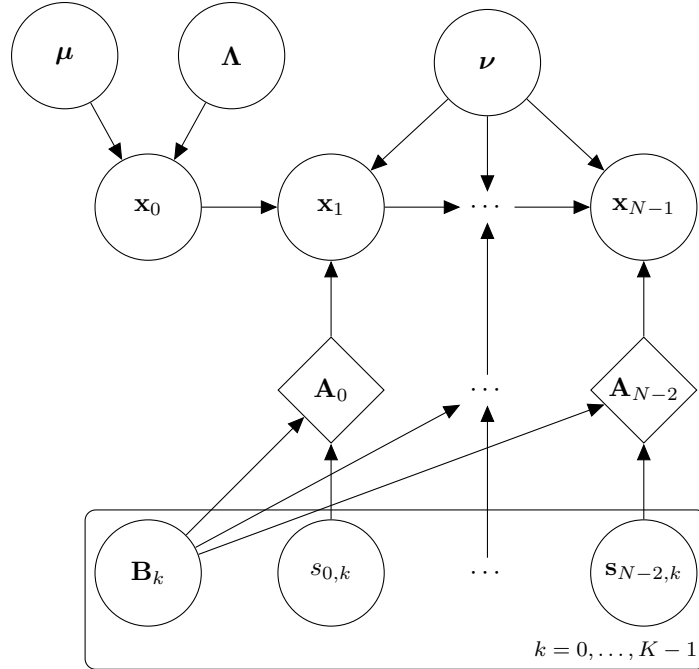
`SwitchingGaussianMarkovChain.plates = None`

bayespy.nodes.VaryingGaussianMarkovChain

class `bayespy.nodes.VaryingGaussianMarkovChain(mu, Lambda, B, S, nu, n=None, **kwargs)`

Node for Gaussian Markov chain random variables with time-varying dynamics.

The node models a sequence of Gaussian variables $\mathbf{x}_0, \dots, \mathbf{x}_{N-1}$ with linear Markovian dynamics. The time variability of the dynamics is obtained by modelling the state dynamics matrix as a linear combination of a set of matrices with time-varying linear combination weights [R6]. The graphical model can be presented as:



where μ and Λ are the mean and the precision matrix of the initial state, ν is the precision of the innovation noise, and \mathbf{A}_n are the state dynamics matrix obtained by mixing matrices \mathbf{B}_k with weights $s_{n,k}$.

The probability distribution is

$$p(\mathbf{x}_0, \dots, \mathbf{x}_{N-1}) = p(\mathbf{x}_0) \prod_{n=1}^{N-1} p(\mathbf{x}_n | \mathbf{x}_{n-1})$$

where

$$\begin{aligned} p(\mathbf{x}_0) &= \mathcal{N}(\mathbf{x}_0 | \mu, \Lambda) \\ p(\mathbf{x}_n | \mathbf{x}_{n-1}) &= \mathcal{N}(\mathbf{x}_n | \mathbf{A}_{n-1} \mathbf{x}_{n-1}, \text{diag}(\nu)), \quad \text{for } n = 1, \dots, N-1, \\ \mathbf{A}_n &= \sum_{k=0}^{K-1} s_{n,k} \mathbf{B}_k, \quad \text{for } n = 0, \dots, N-2. \end{aligned}$$

Parameters **mu** : Gaussian-like node or (... ,D)-array

μ , mean of x_0 , D -dimensional with plates (...)

Lambda : Wishart-like node or (... ,D,D)-array

Λ , precision matrix of x_0 , $D \times D$ -dimensional with plates (...)

B : Gaussian-like node or (... ,D,D,K)-array

$\{\mathbf{B}_k\}_{k=0}^{K-1}$, a set of state dynamics matrix, $D \times K$ -dimensional with plates (... ,D)

S : Gaussian-like node or (... ,N-1,K)-array

$\{s_0, \dots, s_{N-2}\}$, time-varying weights of the linear combination, K -dimensional with plates (... ,N-1)

nu : gamma-like node or (... ,D)-array

ν , diagonal elements of the precision of the innovation process, plates (... ,D)

n : int, optional

N , the length of the chain. Must be given if **S** does not have plates over the time domain (which would not make sense).

See also:

`Gaussian`, `GaussianARD`, `Wishart`, `Gamma`, `GaussianMarkovChain`, `SwitchingGaussianMarkovChain`

Notes

Equivalent model block can be constructed with `GaussianMarkovChain` by explicitly using `SumMultiply` to compute the linear combination. However, that approach is not very efficient for large datasets because it does not utilize the structure of \mathbf{A}_n , thus it explicitly computes huge moment arrays.

References

[R6]

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>rotate(R[, inv, logdet])</code>	
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>show()</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.VaryingGaussianMarkovChain.add_plate_axis

`VaryingGaussianMarkovChain.add_plate_axis(to_plate)`

bayespy.nodes.VaryingGaussianMarkovChain.delete

`VaryingGaussianMarkovChain.delete()`
Delete this node and the children

bayespy.nodes.VaryingGaussianMarkovChain.get_mask

`VaryingGaussianMarkovChain.get_mask()`

bayespy.nodes.VaryingGaussianMarkovChain.get_moments

`VaryingGaussianMarkovChain.get_moments()`

bayespy.nodes.VaryingGaussianMarkovChain.get_shape

`VaryingGaussianMarkovChain.get_shape(ind)`

bayespy.nodes.VaryingGaussianMarkovChain.has_plotter

`VaryingGaussianMarkovChain.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.VaryingGaussianMarkovChain.initialize_from_parameters

`VaryingGaussianMarkovChain.initialize_from_parameters(*args)`

bayespy.nodes.VaryingGaussianMarkovChain.initialize_from_prior

`VaryingGaussianMarkovChain.initialize_from_prior()`

bayespy.nodes.VaryingGaussianMarkovChain.initialize_from_random

`VaryingGaussianMarkovChain.initialize_from_random()`
Set the variable to a random sample from the current distribution.

bayespy.nodes.VaryingGaussianMarkovChain.initialize_from_value

`VaryingGaussianMarkovChain.initialize_from_value(x, *args)`

bayespy.nodes.VaryingGaussianMarkovChain.load

`VaryingGaussianMarkovChain.load(group)`
Load the state of the node from a HDF5 file.

bayespy.nodes.VaryingGaussianMarkovChain.logpdf

VaryingGaussianMarkovChain.**logpdf** (*X*, *mask=True*)
Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.VaryingGaussianMarkovChain.lower_bound_contribution

VaryingGaussianMarkovChain.**lower_bound_contribution** (*gradient=False*)

bayespy.nodes.VaryingGaussianMarkovChain.lowerbound

VaryingGaussianMarkovChain.**lowerbound** ()

bayespy.nodes.VaryingGaussianMarkovChain.move_plates

VaryingGaussianMarkovChain.**move_plates** (*from_plate*, *to_plate*)

bayespy.nodes.VaryingGaussianMarkovChain.observe

VaryingGaussianMarkovChain.**observe** (*x*, **args*, *mask=True*)
Fix moments, compute f and propagate mask.

bayespy.nodes.VaryingGaussianMarkovChain.pdf

VaryingGaussianMarkovChain.**pdf** (*X*, *mask=True*)
Compute the probability density function of this node.

bayespy.nodes.VaryingGaussianMarkovChain.plot

VaryingGaussianMarkovChain.**plot** (***kwargs*)
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.VaryingGaussianMarkovChain.random

VaryingGaussianMarkovChain.**random** ()
Draw a random sample from the distribution.

bayespy.nodes.VaryingGaussianMarkovChain.rotate

VaryingGaussianMarkovChain.**rotate** (*R*, *inv=None*, *logdet=None*)

bayespy.nodes.VaryingGaussianMarkovChain.save

`VaryingGaussianMarkovChain.save(group)`
Save the state of the node into a HDF5 file.
group can be the root

bayespy.nodes.VaryingGaussianMarkovChain.set_plotter

`VaryingGaussianMarkovChain.set_plotter(plotter)`

bayespy.nodes.VaryingGaussianMarkovChain.show

`VaryingGaussianMarkovChain.show()`

bayespy.nodes.VaryingGaussianMarkovChain.unobserve

`VaryingGaussianMarkovChain.unobserve()`

bayespy.nodes.VaryingGaussianMarkovChain.update

`VaryingGaussianMarkovChain.update()`

Attributes

<code>dims</code>
<code>plates</code>

bayespy.nodes.VaryingGaussianMarkovChain.dims

`VaryingGaussianMarkovChain.dims = None`

bayespy.nodes.VaryingGaussianMarkovChain.plates

`VaryingGaussianMarkovChain.plates = None`

Other stochastic nodes:

<code>Mixture(z, node_class, *params[, cluster_plate])</code>	Node for exponential family mixture variables.
---	--

bayespy.nodes.Mixture

class `bayespy.nodes.Mixture(z, node_class, *params, cluster_plate=-1, **kwargs)`
Node for exponential family mixture variables.

The node represents a random variable which is sampled from a mixture distribution. It is possible to mix any

exponential family distribution. The probability density function is

$$p(x|z = k, \theta_0, \dots, \theta_{K-1}) = \phi(x|\theta_k),$$

where ϕ is the probability density function of the mixed exponential family distribution and $\theta_0, \dots, \theta_{K-1}$ are the parameters of each cluster. For instance, ϕ could be the Gaussian probability density function \mathcal{N} and $\theta_k = \{\mu_k, \Lambda_k\}$ where μ_k and Λ_k are the mean vector and precision matrix for cluster k .

Parameters **z** : categorical-like node or array

z, cluster assignment

node_class : stochastic exponential family node class

Mixed distribution

params : types specified by the mixed distribution

Parameters of the mixed distribution. If some parameters should vary between clusters, those parameters' plate axis *cluster_plate* should have a size which equals the number of clusters. For parameters with shared values, that plate axis should have length 1. At least one parameter should vary between clusters.

cluster_plate : int, optional

Negative integer defining which plate axis is used for the clusters in the parameters. That plate axis is ignored from the parameters when considering the plates for this node. By default, mix over the last plate axis.

See also:

`Categorical`, `CategoricalMarkovChain`

Examples

A simple 2-dimensional Gaussian mixture model with three clusters for 100 samples can be constructed, for instance, as:

```
from bayespy.nodes import (Dirichlet, Categorical, Mixture,
                           Gaussian, Wishart)
alpha = Dirichlet([1e-3, 1e-3, 1e-3])
Z = Categorical(alpha, plates=(100,))
mu = Gaussian(np.zeros(2), 1e-6*np.identity(2), plates=(3,))
Lambda = Wishart(2, 1e-6*np.identity(2), plates=(3,))
X = Mixture(Z, Gaussian, mu, Lambda)
```

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.

Table 5.47 – continued from previous p

<code>initialize_from_value(x, *args)</code>	
<code>integrated_logpdf_from_parents(x, index)</code>	Approximates the posterior predictive pdf int $p(x parents)$ $q(parents)$ $dparent$
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.nodes.Mixture.add_plate_axis

`Mixture.add_plate_axis (to_plate)`

bayespy.nodes.Mixture.delete

`Mixture.delete ()`
Delete this node and the children

bayespy.nodes.Mixture.get_mask

`Mixture.get_mask ()`

bayespy.nodes.Mixture.get_moments

`Mixture.get_moments ()`

bayespy.nodes.Mixture.get_shape

`Mixture.get_shape (ind)`

bayespy.nodes.Mixture.has_plotter

`Mixture.has_plotter ()`
Return True if the node has a plotter

bayespy.nodes.Mixture.initialize_from_parameters

`Mixture.initialize_from_parameters (*args)`

bayespy.nodes.Mixture.initialize_from_prior

`Mixture.initialize_from_prior()`

bayespy.nodes.Mixture.initialize_from_random

`Mixture.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.nodes.Mixture.initialize_from_value

`Mixture.initialize_from_value(x, *args)`

bayespy.nodes.Mixture.integrated_logpdf_from_parents

`Mixture.integrated_logpdf_from_parents(x, index)`

Approximates the posterior predictive pdf $\int p(x|\text{parents}) q(\text{parents}) d\text{parents}$ in log-scale as $\int q(\text{parents}_i) \exp(\int q(\text{parents}_i) \log p(x|\text{parents}) d\text{parents}_i) d\text{parents}_i$.

bayespy.nodes.Mixture.load

`Mixture.load(group)`

Load the state of the node from a HDF5 file.

bayespy.nodes.Mixture.logpdf

`Mixture.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.nodes.Mixture.lower_bound_contribution

`Mixture.lower_bound_contribution(gradient=False)`

bayespy.nodes.Mixture.lowerbound

`Mixture.lowerbound()`

bayespy.nodes.Mixture.move_plates

`Mixture.move_plates(from_plate, to_plate)`

bayespy.nodes.Mixture.observe

`Mixture.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.nodes.Mixture.pdf

`Mixture.pdf(X, mask=True)`

Compute the probability density function of this node.

bayespy.nodes.Mixture.plot

`Mixture.plot(**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Mixture.random

`Mixture.random()`

Draw a random sample from the distribution.

bayespy.nodes.Mixture.save

`Mixture.save(group)`

Save the state of the node into a HDF5 file.

group can be the root

bayespy.nodes.Mixture.set_plotter

`Mixture.set_plotter(plotter)`

bayespy.nodes.Mixture.unobserve

`Mixture.unobserve()`

bayespy.nodes.Mixture.update

`Mixture.update()`

Attributes

<code>dims</code>
<code>plates</code>

bayespy.nodes.Mixture.dims

`Mixture.dims = None`

`bayespy.nodes.Mixture.plates`

`Mixture.plates = None`

5.1.2 Deterministic nodes

<code>Dot(*args, **kwargs)</code>	Node for computing inner product of several Gaussian vectors.
<code>SumMultiply(*args[, iterator_axis])</code>	Node for computing general products and sums of Gaussian nodes.
<code>Gate(Z, X[, gated_plate, moments])</code>	Deterministic gating of one node.

`bayespy.nodes.Dot`

`bayespy.nodes.Dot(*args, **kwargs)`

Node for computing inner product of several Gaussian vectors.

This is a simple wrapper of the much more general `SumMultiply`. For now, it is here for backward compatibility.

`bayespy.nodes.SumMultiply`

class `bayespy.nodes.SumMultiply(*args, iterator_axis=None, **kwargs)`

Node for computing general products and sums of Gaussian nodes.

The node is similar to *numpy.einsum*, which is a very general function for computing dot products, sums, products and other sums of products of arrays.

For instance, the equivalent of

```
np.einsum('abc,bd,ca->da', X, Y, Z)
```

would be given as

```
SumMultiply('abc,bd,ca->da', X, Y, Z)
```

or

```
SumMultiply(X, [0,1,2], Y, [1,3], Z, [2,0], [3,0])
```

which is similar to the other syntax of *numpy.einsum*.

This node operates similarly as *numpy.einsum*. However, you must use all the elements of each node, that is, an operation like `np.einsum('ii->i',X)` is not allowed. Thus, for each node, each axis must be given unique id. The id identifies which axes correspond to which axes between the different nodes. Also, Ellipsis ('...') is not yet supported for simplicity. It would also have some problems with constant inputs (because how to determine ndim), so let us just forget it for now.

Each output axis must appear in the input mappings.

The keys must refer to variable dimension axes only, not plate axes.

The input nodes may be Gaussian-gamma (isotropic) nodes.

The output message is Gaussian-gamma (isotropic) if any of the input nodes is Gaussian-gamma.

Notes

This operation can be extremely slow if not used wisely. For large and complex operations, it is sometimes more efficient to split the operation into multiple nodes. For instance, the example above could probably be computed faster by

```
XZ = SumMultiply(X, [0,1,2], Z, [2,0], [0,1])
F = SumMultiply(XZ, [0,1], Y, [1,2], [2,0])
```

because the third axis ('c') could be summed out already in the first operation. This same effect applies also to `numpy.einsum` in general.

Examples

Sum over the rows: 'ij->j'

Inner product of three vectors: 'i,i,i'

Matrix-vector product: 'ij,j->i'

Matrix-matrix product: 'ik,kj->ij'

Outer product: 'i,j->ij'

Vector-matrix-vector product: 'i,ij,j'

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_parameters()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>lower_bound_contribution([gradient])</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>set_plotter(plotter)</code>	

bayespy.nodes.SumMultiply.add_plate_axis

`SumMultiply.add_plate_axis(to_plate)`

bayespy.nodes.SumMultiply.delete

`SumMultiply.delete()`
Delete this node and the children

bayespy.nodes.SumMultiply.get_mask

`SumMultiply.get_mask()`

bayespy.nodes.SumMultiply.get_moments

`SumMultiply.get_moments()`

bayespy.nodes.SumMultiply.get_parameters

`SumMultiply.get_parameters()`

bayespy.nodes.SumMultiply.get_shape

`SumMultiply.get_shape(ind)`

bayespy.nodes.SumMultiply.has_plotter

`SumMultiply.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.SumMultiply.lower_bound_contribution

`SumMultiply.lower_bound_contribution(gradient=False)`

bayespy.nodes.SumMultiply.move_plates

`SumMultiply.move_plates(from_plate, to_plate)`

bayespy.nodes.SumMultiply.plot

`SumMultiply.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.SumMultiply.set_plotter

`SumMultiply.set_plotter(plotter)`

Attributes

`plates`

bayespy.nodes.SumMultiply.plates

`SumMultiply.plates = None`

bayespy.nodes.Gate

class bayespy.nodes.**Gate** (*Z, X, gated_plate=-1, moments=None, **kwargs*)
 Deterministic gating of one node.

Gating is performed over one plate axis.

Note: You should not use gating for several variables which parents of a same node if the gates use the same gate assignments. In such case, the results will be wrong. The reason is a general one: A stochastic node may not be a parent of another node via several paths unless at most one path has no other stochastic nodes between them.

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>lower_bound_contribution([gradient])</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>set_plotter(plotter)</code>	

bayespy.nodes.Gate.add_plate_axis

`Gate.add_plate_axis (to_plate)`

bayespy.nodes.Gate.delete

`Gate.delete ()`
 Delete this node and the children

bayespy.nodes.Gate.get_mask

`Gate.get_mask ()`

bayespy.nodes.Gate.get_moments

`Gate.get_moments ()`

bayespy.nodes.Gate.get_shape

`Gate.get_shape (ind)`

bayespy.nodes.Gate.has_plotter

`Gate.has_plotter()`
Return True if the node has a plotter

bayespy.nodes.Gate.lower_bound_contribution

`Gate.lower_bound_contribution(gradient=False)`

bayespy.nodes.Gate.move_plates

`Gate.move_plates(from_plate, to_plate)`

bayespy.nodes.Gate.plot

`Gate.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.nodes.Gate.set_plotter

`Gate.set_plotter(plotter)`

Attributes

`plates`

bayespy.nodes.Gate.plates

`Gate.plates = None`

5.2 bayespy.inference

Package for Bayesian inference engines

5.2.1 Inference engines

`VB(*nodes[, tol, autosave_filename, ...])` Variational Bayesian (VB) inference engine

bayespy.inference.VB

class bayespy.inference.VB(*nodes, tol=1e-05, autosave_filename=None, autosave_iterations=0, callback=None)

Variational Bayesian (VB) inference engine

Parameters nodes : nodes

Nodes that form the model. Must include all at least all stochastic nodes of the model.

tol : double, optional

Convergence criterion. Tolerance for the relative change in the VB lower bound.

autosave_filename : string, optional

Filename for automatic saving

autosave_iterations : int, optional

Iteration interval between each automatic saving

callback : callable, optional

Function which is called after each update iteration step

Methods

compute_lowerbound()	
compute_lowerbound_terms(*nodes)	
get_iteration_by_nodes()	
load(*nodes[, filename])	
loglikelihood_lowerbound()	
plot(*nodes)	Plot the distribution of the given nodes (or all nodes)
plot_iteration_by_nodes()	Plot the cost function per node during the iteration.
save([filename])	
set_autosave(filename[, iterations])	
update(*nodes[, repeat, plot, tol, verbose])	

bayespy.inference.VB.compute_lowerbound

VB.compute_lowerbound()

bayespy.inference.VB.compute_lowerbound_terms

VB.compute_lowerbound_terms(*nodes)

bayespy.inference.VB.get_iteration_by_nodes

VB.get_iteration_by_nodes()

bayespy.inference.VB.load

VB.load(*nodes, filename=None)

bayespy.inference.VB.loglikelihood_lowerbound

`VB.loglikelihood_lowerbound()`

bayespy.inference.VB.plot

`VB.plot(*nodes)`
Plot the distribution of the given nodes (or all nodes)

bayespy.inference.VB.plot_iteration_by_nodes

`VB.plot_iteration_by_nodes()`
Plot the cost function per node during the iteration.
Handy tool for debugging.

bayespy.inference.VB.save

`VB.save(filename=None)`

bayespy.inference.VB.set_autosave

`VB.set_autosave(filename, iterations=None)`

bayespy.inference.VB.update

`VB.update(*nodes, repeat=1, plot=False, tol=None, verbose=True)`

5.2.2 Parameter expansions

<code>vmp.transformations.RotationOptimizer(...)</code>	Optimizer for rotation parameter expansion in state-space models
<code>vmp.transformations.RotateGaussian(X)</code>	Rotation parameter expansion for <code>bayespy.nodes.VaryingGaussian</code>
<code>vmp.transformations.RotateGaussianARD(X, *alpha)</code>	Rotation parameter expansion for <code>bayespy.nodes.VaryingGaussian</code>
<code>vmp.transformations.RotateGaussianMarkovChain(X, ...)</code>	Rotation parameter expansion for <code>bayespy.nodes.VaryingGaussian</code>
<code>vmp.transformations.RotateSwitchingMarkovChain(X, ...)</code>	Rotation for <code>bayespy.nodes.SwitchingGaussian</code>
<code>vmp.transformations.RotateVaryingMarkovChain(X, ...)</code>	Rotation for <code>bayespy.nodes.SwitchingGaussian</code>
<code>vmp.transformations.RotateMultiple(*rotators)</code>	Identical parameter expansion for several nodes simultaneously

bayespy.inference.vmp.transformations.RotationOptimizer

class `bayespy.inference.vmp.transformations.RotationOptimizer(block1, block2, D)`
Optimizer for rotation parameter expansion in state-space models

Rotates one model block with \mathbf{R} and one model block with \mathbf{R}^{-1} .

Parameters `block1` : rotator object

The first rotation parameter expansion object

block2 : rotator object

The second rotation parameter expansion object

D : int

Dimensionality of the latent space

References

[R4], [R5]

Methods

`rotate([maxiter, check_gradient, verbose, ...])` Optimize the rotation of two separate model blocks jointly.

`bayespy.inference.vmp.transformations.RotationOptimizer.rotate`

`RotationOptimizer.rotate(maxiter=10, check_gradient=False, verbose=False, check_bound=False)`

Optimize the rotation of two separate model blocks jointly.

If some variable is the dot product of two Gaussians, rotating the two Gaussians optimally can make the inference algorithm orders of magnitude faster.

First block is rotated with \mathbf{R} and the second with \mathbf{R}^{-T} .

Blocks must have methods: `bound(U,s,V)` and `rotate(R)`.

`bayespy.inference.vmp.transformations.RotateGaussian`

`class bayespy.inference.vmp.transformations.RotateGaussian(X)`

Rotation parameter expansion for `bayespy.nodes.Gaussian`

Methods

`bound(R[, logdet, inv])`
`get_bound_terms(R[, logdet, inv])`
`nodes()`
`rotate(R[, inv, logdet])`
`setup()` This method should be called just before optimization.

`bayespy.inference.vmp.transformations.RotateGaussian.bound`

`RotateGaussian.bound(R, logdet=None, inv=None)`

`bayespy.inference.vmp.transformations.RotateGaussian.get_bound_terms`

`RotateGaussian.get_bound_terms(R, logdet=None, inv=None)`

bayespy.inference.vmp.transformations.RotateGaussian.nodes

`RotateGaussian.nodes()`

bayespy.inference.vmp.transformations.RotateGaussian.rotate

`RotateGaussian.rotate(R, inv=None, logdet=None)`

bayespy.inference.vmp.transformations.RotateGaussian.setup

`RotateGaussian.setup()`

This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateGaussianARD

class bayespy.inference.vmp.transformations.**RotateGaussianARD** (*X, *alpha, axis=-1, precompute=False*)

Rotation parameter expansion for `bayespy.nodes.GaussianARD`

The model:

$\alpha \sim N(a, b)$ $X \sim N(\mu, \alpha)$

X can be an array (e.g., `GaussianARD`).

Transform $q(X)$ and $q(\alpha)$ by rotating X.

Requirements: * X and alpha do not contain any observed values

Methods

<code>bound(R[, logdet, inv, Q])</code>	
<code>get_bound_terms(R[, logdet, inv, Q])</code>	
<code>nodes()</code>	
<code>rotate(R[, inv, logdet, Q])</code>	
<code>setup([plate_axis])</code>	This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateGaussianARD.bound

`RotateGaussianARD.bound(R, logdet=None, inv=None, Q=None)`

bayespy.inference.vmp.transformations.RotateGaussianARD.get_bound_terms

`RotateGaussianARD.get_bound_terms(R, logdet=None, inv=None, Q=None)`

bayespy.inference.vmp.transformations.RotateGaussianARD.nodes

`RotateGaussianARD.nodes()`

bayespy.inference.vmp.transformations.RotateGaussianARD.rotate

`RotateGaussianARD.rotate(R, inv=None, logdet=None, Q=None)`

bayespy.inference.vmp.transformations.RotateGaussianARD.setup

`RotateGaussianARD.setup(plate_axis=None)`

This method should be called just before optimization.

For efficiency, sum over axes that are not in mu, alpha nor rotation.

If using Q, set rotate_plates to True.

bayespy.inference.vmp.transformations.RotateGaussianMarkovChain

`class bayespy.inference.vmp.transformations.RotateGaussianMarkovChain(X, *args)`

Rotation parameter expansion for `bayespy.nodes.GaussianMarkovChain`

Assume the following model.

Constant, unit isotropic innovation noise. Unit variance only?

Maybe: Assume innovation noise with unit variance? Would it help make this function more general with respect to A.

TODO: Allow constant A or not rotating A.

A may vary in time.

Shape of A: (N,D,D) Shape of AA: (N,D,D,D)

No plates for X.

Methods

<code>bound(R[, logdet, inv])</code>	
<code>get_bound_terms(R[, logdet, inv])</code>	
<code>nodes()</code>	
<code>rotate(R[, inv, logdet])</code>	
<code>setup()</code>	This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateGaussianMarkovChain.bound

`RotateGaussianMarkovChain.bound(R, logdet=None, inv=None)`

bayespy.inference.vmp.transformations.RotateGaussianMarkovChain.get_bound_terms

`RotateGaussianMarkovChain.get_bound_terms(R, logdet=None, inv=None)`

bayespy.inference.vmp.transformations.RotateGaussianMarkovChain.nodes

`RotateGaussianMarkovChain.nodes()`

bayespy.inference.vmp.transformations.RotateGaussianMarkovChain.rotate

`RotateGaussianMarkovChain.rotate` (*R*, *inv=None*, *logdet=None*)

bayespy.inference.vmp.transformations.RotateGaussianMarkovChain.setup

`RotateGaussianMarkovChain.setup` ()

This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain

class `bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain` (*X*, *B*, *Z*,
B_rotator)

Rotation for `bayespy.nodes.VaryingGaussianMarkovChain`

Assume the following model.

Constant, unit isotropic innovation noise.

$$A_n = B_{z_n}$$

Gaussian *B*: (... , *K*, *D*) x (*D*) Categorical *Z*: (... , *N*-1) x (*K*) GaussianMarkovChain *X*: (...) x (*N*,*D*)

No plates for *X*.

Methods

`bound`(*R*[, *logdet*, *inv*])

`get_bound_terms`(*R*[, *logdet*, *inv*])

`nodes`()

`rotate`(*R*[, *inv*, *logdet*])

`setup`()

This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain.bound

`RotateSwitchingMarkovChain.bound` (*R*, *logdet=None*, *inv=None*)

bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain.get_bound_terms

`RotateSwitchingMarkovChain.get_bound_terms` (*R*, *logdet=None*, *inv=None*)

bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain.nodes

`RotateSwitchingMarkovChain.nodes` ()

bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain.rotate

`RotateSwitchingMarkovChain.rotate` (*R*, *inv=None*, *logdet=None*)

bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain.setup

`RotateSwitchingMarkovChain.setup()`
 This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateVaryingMarkovChain

class bayespy.inference.vmp.transformations.**RotateVaryingMarkovChain** (*X, B, S, B_rotator*)

Rotation for `bayespy.nodes.SwitchingGaussianMarkovChain`

Assume the following model.

Constant, unit isotropic innovation noise.

$$A_n = \sum_k B_k s_{kn}$$

Gaussian B: (1,D) x (D,K) Gaussian S: (N,1) x (K) MC X: () x (N+1,D)

No plates for X.

Methods

<code>bound(R[, logdet, inv])</code>	
<code>get_bound_terms(R[, logdet, inv])</code>	
<code>nodes()</code>	
<code>rotate(R[, inv, logdet])</code>	
<code>setup()</code>	This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateVaryingMarkovChain.bound

`RotateVaryingMarkovChain.bound(R, logdet=None, inv=None)`

bayespy.inference.vmp.transformations.RotateVaryingMarkovChain.get_bound_terms

`RotateVaryingMarkovChain.get_bound_terms(R, logdet=None, inv=None)`

bayespy.inference.vmp.transformations.RotateVaryingMarkovChain.nodes

`RotateVaryingMarkovChain.nodes()`

bayespy.inference.vmp.transformations.RotateVaryingMarkovChain.rotate

`RotateVaryingMarkovChain.rotate(R, inv=None, logdet=None)`

bayespy.inference.vmp.transformations.RotateVaryingMarkovChain.setup

`RotateVaryingMarkovChain.setup()`
 This method should be called just before optimization.

bayespy.inference.vmp.transformations.RotateMultiple

class bayespy.inference.vmp.transformations.RotateMultiple(*rotators)

Identical parameter expansion for several nodes simultaneously

Performs the same rotation for multiple nodes and combines the cost effect.

Methods

```
bound(R[, logdet, inv])
get_bound_terms(R[, logdet, inv])
nodes()
rotate(R[, inv, logdet])
setup()
```

bayespy.inference.vmp.transformations.RotateMultiple.bound

RotateMultiple.bound(R, logdet=None, inv=None)

bayespy.inference.vmp.transformations.RotateMultiple.get_bound_terms

RotateMultiple.get_bound_terms(R, logdet=None, inv=None)

bayespy.inference.vmp.transformations.RotateMultiple.nodes

RotateMultiple.nodes()

bayespy.inference.vmp.transformations.RotateMultiple.rotate

RotateMultiple.rotate(R, inv=None, logdet=None)

bayespy.inference.vmp.transformations.RotateMultiple.setup

RotateMultiple.setup()

5.3 bayespy.plot

Functions for plotting nodes.

5.3.1 Functions

pdf(Z, x, *args[, name])	Plot probability density function of a scalar variable.
contour(Z, x, y[, n])	Plot 2-D probability density function of a 2-D variable.
plot(Y[, axis, scale, center])	Plot a variable or an array as 1-D function with errorbars
hinton(X, **kwargs)	Plot the Hinton diagram of a node

bayespy.plot.pdf

`bayespy.plot.pdf` (*Z*, *x*, **args*, *name=None*, ***kwargs*)
 Plot probability density function of a scalar variable.

Parameters *Z* : node or function

Stochastic node or log pdf function

x : array

Grid points

bayespy.plot.contour

`bayespy.plot.contour` (*Z*, *x*, *y*, *n=None*, ***kwargs*)
 Plot 2-D probability density function of a 2-D variable.

Parameters *Z* : node or function

Stochastic node or log pdf function

x : array

Grid points on x axis

y : array

Grid points on y axis

bayespy.plot.plot

`bayespy.plot.plot` (*Y*, *axis=-1*, *scale=2*, *center=False*, ***kwargs*)
 Plot a variable or an array as 1-D function with errorbars

bayespy.plot.hinton

`bayespy.plot.hinton` (*X*, ***kwargs*)
 Plot the Hinton diagram of a node

The keyword arguments depend on the node type. For some node types, the diagram also shows uncertainty with non-filled rectangles.

Parameters *X* : node

Notes

The function is a simple wrapper for node specific Hinton diagram plotting functions:

<code>gaussian_hinton(X[, rows, cols, scale])</code>	Plot the Hinton diagram of a Gaussian node
<code>beta_hinton(P)</code>	Plot a beta distributed random variable as a Hinton diagram
<code>dirichlet_hinton(P[, square])</code>	Plot a beta distributed random variable as a Hinton diagram

5.3.2 Plotters

<code>Plotter(plotter, *args, **kwargs)</code>	Wrapper for plotting functions and base class for node plotters
<code>PDFPlotter(x_grid, **kwargs)</code>	Plotter of probability density function of a scalar node
<code>ContourPlotter(x1_grid, x2_grid, **kwargs)</code>	Plotter of probability density function of a two-dimensional node
<code>HintonPlotter(**kwargs)</code>	Plotter of the Hinton diagram of a node
<code>FunctionPlotter(**kwargs)</code>	Plotter of a node as a 1-dimensional function
<code>GaussianTimeseriesPlotter(**kwargs)</code>	Plotter of a Gaussian node as a timeseries
<code>CategoricalMarkovChainPlotter(**kwargs)</code>	Plotter of a Categorical timeseries

bayespy.plot.Plotter

class bayespy.plot.**Plotter** (*plotter, *args, **kwargs*)

Wrapper for plotting functions and base class for node plotters

The purpose of this class is to collect all the parameters needed by a plotting function and provide a callable interface which needs only the node as the input.

Plotter instances are callable objects that plot a given node using a specified plotting function.

Parameters **plotter** : function

Plotting function to use

args : defined by the plotting function

Additional inputs needed by the plotting function

kwargs : defined by the plotting function

Additional keyword arguments supported by the plotting function

Examples

First, create a gamma variable:

```
>>> import numpy as np
>>> from bayespy.nodes import Gamma
>>> x = Gamma(4, 5)
```

The probability density function can be plotted as:

```
>>> import bayespy.plot as bpplt
>>> bpplt.pdf(x, np.linspace(0.1, 10, num=100))
[<matplotlib.lines.Line2D object at 0x...>]
```

However, this can be problematic when one needs to provide a plotting function for the inference engine as the inference engine gives only the node as input. Thus, we need to create a simple plotter wrapper:

```
>>> p = bpplt.Plotter(bpplt.pdf, np.linspace(0.1, 10, num=100))
```

Now, this callable object `p` needs only the node as the input:

```
>>> p(x)
[<matplotlib.lines.Line2D object at 0x...>]
```

Thus, it can be given to the inference engine to use as a plotting function:

```
>>> x = Gamma(4, 5, plotter=p)
>>> x.plot()
[<matplotlib.lines.Line2D object at 0x...>]
```

Methods

<code>__call__(X)</code>	Plot the node using the specified plotting function
--------------------------	---

`bayespy.plot.Plotter.__call__`

`Plotter.__call__(X)`

Plot the node using the specified plotting function

Parameters **X** : node

The plotted node

`bayespy.plot.PDFPlotter`

class `bayespy.plot.PDFPlotter(x_grid, **kwargs)`

Plotter of probability density function of a scalar node

Parameters **x_grid** : array

Numerical grid on which the density function is computed and plotted

See also:

[pdf](#)

Methods

<code>__call__(X)</code>	Plot the node using the specified plotting function
--------------------------	---

`bayespy.plot.PDFPlotter.__call__`

`PDFPlotter.__call__(X)`

Plot the node using the specified plotting function

Parameters **X** : node

The plotted node

`bayespy.plot.ContourPlotter`

class `bayespy.plot.ContourPlotter(x1_grid, x2_grid, **kwargs)`

Plotter of probability density function of a two-dimensional node

Parameters **x1_grid** : array

Grid for the first dimension

x2_grid : array

Grid for the second dimension

See also:

[contour](#)

Methods

`__call__(X)` Plot the node using the specified plotting function

`bayespy.plot.ContourPlotter.__call__`

`ContourPlotter.__call__(X)`
 Plot the node using the specified plotting function

Parameters `X` : node

The plotted node

`bayespy.plot.HintonPlotter`

class `bayespy.plot.HintonPlotter(**kwargs)`
 Plotter of the Hinton diagram of a node

See also:

`hinton`

Methods

`__call__(X)` Plot the node using the specified plotting function

`bayespy.plot.HintonPlotter.__call__`

`HintonPlotter.__call__(X)`
 Plot the node using the specified plotting function

Parameters `X` : node

The plotted node

`bayespy.plot.FunctionPlotter`

class `bayespy.plot.FunctionPlotter(**kwargs)`
 Plotter of a node as a 1-dimensional function

See also:

`plot`

Methods

`__call__(X)` Plot the node using the specified plotting function

bayespy.plot.FunctionPlotter.__call__

FunctionPlotter.__call__(X)

Plot the node using the specified plotting function

Parameters X : node

The plotted node

bayespy.plot.GaussianTimeseriesPlotter

class bayespy.plot.GaussianTimeseriesPlotter(**kwargs)

Plotter of a Gaussian node as a timeseries

Methods

__call__(X) Plot the node using the specified plotting function

bayespy.plot.GaussianTimeseriesPlotter.__call__

GaussianTimeseriesPlotter.__call__(X)

Plot the node using the specified plotting function

Parameters X : node

The plotted node

bayespy.plot.CategoricalMarkovChainPlotter

class bayespy.plot.CategoricalMarkovChainPlotter(**kwargs)

Plotter of a Categorical timeseries

Methods

__call__(X) Plot the node using the specified plotting function

bayespy.plot.CategoricalMarkovChainPlotter.__call__

CategoricalMarkovChainPlotter.__call__(X)

Plot the node using the specified plotting function

Parameters X : node

The plotted node

DEVELOPER API

Moments, Distributions, `utils.misc`, `utils.random` etc ...?

6.1 Nodes

Base classes and special nodes:

<code>node.Node(*parents, **kwargs)</code>	Base class for all nodes.
<code>stochastic.Stochastic(*args[, initialize, dims])</code>	Base class for nodes that are stochastic.
<code>expfamily.ExponentialFamily(*args, **kwargs)</code>	A base class for nodes using natural parameterization ϕ .
<code>deterministic.Deterministic(*args, **kwargs)</code>	Base class for deterministic nodes.
<code>constant.Constant(moments, x, **kwargs)</code>	Node for presenting constant values.

6.1.1 `bayespy.inference.vmp.nodes.node.Node`

class `bayespy.inference.vmp.nodes.node.Node(*parents, **kwargs)`

Base class for all nodes.

mask dims plates parents children name

Sub-classes must implement: 1. For computing the message to children:

`get_moments(self):`

2. For computing the message to parents: `_get_message_and_mask_to_parent(self, index)`

Sub-classes may need to re-implement: 1. If they manipulate plates:

`_compute_mask_to_parent(index, mask)` `_plates_to_parent(self, index)` `_plates_from_parent(self, index)`

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter

Continued on next page

Table 6.2 – continued from previous page

<code>move_plates(from_plate, to_plate)</code>	
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>set_plotter(plotter)</code>	

bayespy.inference.vmp.nodes.node.Node.add_plate_axis

`Node.add_plate_axis (to_plate)`

bayespy.inference.vmp.nodes.node.Node.delete

`Node.delete ()`
Delete this node and the children

bayespy.inference.vmp.nodes.node.Node.get_mask

`Node.get_mask ()`

bayespy.inference.vmp.nodes.node.Node.get_moments

`Node.get_moments ()`

bayespy.inference.vmp.nodes.node.Node.get_shape

`Node.get_shape (ind)`

bayespy.inference.vmp.nodes.node.Node.has_plotter

`Node.has_plotter ()`
Return True if the node has a plotter

bayespy.inference.vmp.nodes.node.Node.move_plates

`Node.move_plates (from_plate, to_plate)`

bayespy.inference.vmp.nodes.node.Node.plot

`Node.plot (**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.inference.vmp.nodes.node.Node.set_plotter

`Node.set_plotter (plotter)`

Attributes

`plates`

`bayespy.inference.vmp.nodes.node.Node.plates`

`Node.plates = None`

6.1.2 bayespy.inference.vmp.nodes.stochastic.Stochastic

`class bayespy.inference.vmp.nodes.stochastic.Stochastic(*args, initialize=True, dims=None, **kwargs)`

Base class for nodes that are stochastic.

u observed

Sub-classes must implement: `_compute_message_to_parent(parent, index, u_self, *u_parents)` `_update_distribution_and_lowerbound(self, m, *u)` `lowerbound(self)` `_compute_dims` `initialize_from_prior()`

If you want to be able to observe the variable: `_compute_fixed_moments_and_f`

Sub-classes may need to re-implement: 1. If they manipulate plates:

`_compute_mask_to_parent(index, mask)` `_plates_to_parent(self, index)` `_plates_from_parent(self, index)`

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x[, mask])</code>	Fix moments, compute f and propagate mask.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>unobserve()</code>	
<code>update()</code>	

`bayespy.inference.vmp.nodes.stochastic.Stochastic.add_plate_axis`

`Stochastic.add_plate_axis(to_plate)`

bayespy.inference.vmp.nodes.stochastic.Stochastic.delete

`Stochastic.delete()`
Delete this node and the children

bayespy.inference.vmp.nodes.stochastic.Stochastic.get_mask

`Stochastic.get_mask()`

bayespy.inference.vmp.nodes.stochastic.Stochastic.get_moments

`Stochastic.get_moments()`

bayespy.inference.vmp.nodes.stochastic.Stochastic.get_shape

`Stochastic.get_shape(ind)`

bayespy.inference.vmp.nodes.stochastic.Stochastic.has_plotter

`Stochastic.has_plotter()`
Return True if the node has a plotter

bayespy.inference.vmp.nodes.stochastic.Stochastic.load

`Stochastic.load(group)`
Load the state of the node from a HDF5 file.

bayespy.inference.vmp.nodes.stochastic.Stochastic.lowerbound

`Stochastic.lowerbound()`

bayespy.inference.vmp.nodes.stochastic.Stochastic.move_plates

`Stochastic.move_plates(from_plate, to_plate)`

bayespy.inference.vmp.nodes.stochastic.Stochastic.observe

`Stochastic.observe(x, mask=True)`
Fix moments, compute f and propagate mask.

bayespy.inference.vmp.nodes.stochastic.Stochastic.plot

`Stochastic.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.inference.vmp.nodes.stochastic.Stochastic.random

```
Stochastic.random()
```

Draw a random sample from the distribution.

bayespy.inference.vmp.nodes.stochastic.Stochastic.save

```
Stochastic.save(group)
```

Save the state of the node into a HDF5 file.

group can be the root

bayespy.inference.vmp.nodes.stochastic.Stochastic.set_plotter

```
Stochastic.set_plotter(plotter)
```

bayespy.inference.vmp.nodes.stochastic.Stochastic.unobserve

```
Stochastic.unobserve()
```

bayespy.inference.vmp.nodes.stochastic.Stochastic.update

```
Stochastic.update()
```

Attributes

`plates`

bayespy.inference.vmp.nodes.stochastic.Stochastic.plates

```
Stochastic.plates = None
```

6.1.3 bayespy.inference.vmp.nodes.expfamily.ExponentialFamily

```
class bayespy.inference.vmp.nodes.expfamily.ExponentialFamily(*args, **kwargs)
```

A base class for nodes using natural parameterization *phi*.

phi

Sub-classes must implement the following static methods: `_compute_message_to_parent(index, u_self, *u_parents)` `_compute_phi_from_parents(*u_parents, mask)` `_compute_moments_and_cgf(phi, mask)` `_compute_fixed_moments_and_f(x, mask=True)`

Sub-classes may need to re-implement: 1. If they manipulate plates:

```
_compute_mask_to_parent(index, mask) _plates_to_parent(self, index) _plates_from_parent(self, index)
```

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>initialize_from_parameters(*args)</code>	
<code>initialize_from_prior()</code>	
<code>initialize_from_random()</code>	Set the variable to a random sample from the current distribution.
<code>initialize_from_value(x, *args)</code>	
<code>load(group)</code>	Load the state of the node from a HDF5 file.
<code>logpdf(X[, mask])</code>	Compute the log probability density function $Q(X)$ of this node.
<code>lower_bound_contribution([gradient])</code>	
<code>lowerbound()</code>	
<code>move_plates(from_plate, to_plate)</code>	
<code>observe(x, *args[, mask])</code>	Fix moments, compute f and propagate mask.
<code>pdf(X[, mask])</code>	Compute the probability density function of this node.
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>random()</code>	Draw a random sample from the distribution.
<code>save(group)</code>	Save the state of the node into a HDF5 file.
<code>set_plotter(plotter)</code>	
<code>unobserve()</code>	
<code>update()</code>	

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.add_plate_axis

`ExponentialFamily.add_plate_axis(to_plate)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.delete

`ExponentialFamily.delete()`
Delete this node and the children

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.get_mask

`ExponentialFamily.get_mask()`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.get_moments

`ExponentialFamily.get_moments()`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.get_shape

`ExponentialFamily.get_shape(ind)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.has_plotter

`ExponentialFamily.has_plotter()`
Return True if the node has a plotter

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.initialize_from_parameters

`ExponentialFamily.initialize_from_parameters(*args)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.initialize_from_prior

`ExponentialFamily.initialize_from_prior()`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.initialize_from_random

`ExponentialFamily.initialize_from_random()`

Set the variable to a random sample from the current distribution.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.initialize_from_value

`ExponentialFamily.initialize_from_value(x, *args)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.load

`ExponentialFamily.load(group)`

Load the state of the node from a HDF5 file.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.logpdf

`ExponentialFamily.logpdf(X, mask=True)`

Compute the log probability density function $Q(X)$ of this node.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.lower_bound_contribution

`ExponentialFamily.lower_bound_contribution(gradient=False)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.lowerbound

`ExponentialFamily.lowerbound()`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.move_plates

`ExponentialFamily.move_plates(from_plate, to_plate)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.observe

`ExponentialFamily.observe(x, *args, mask=True)`

Fix moments, compute f and propagate mask.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.pdf

`ExponentialFamily.pdf(X, mask=True)`
 Compute the probability density function of this node.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.plot

`ExponentialFamily.plot(**kwargs)`
 Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.random

`ExponentialFamily.random()`
 Draw a random sample from the distribution.

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.save

`ExponentialFamily.save(group)`
 Save the state of the node into a HDF5 file.

group can be the root

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.set_plotter

`ExponentialFamily.set_plotter(plotter)`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.unobserve

`ExponentialFamily.unobserve()`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.update

`ExponentialFamily.update()`

Attributes

`dims`
`plates`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.dims

`ExponentialFamily.dims = None`

bayespy.inference.vmp.nodes.expfamily.ExponentialFamily.plates

ExponentialFamily.plates = None

6.1.4 bayespy.inference.vmp.nodes.deterministic.Deterministic

class bayespy.inference.vmp.nodes.deterministic.Deterministic(*args, **kwargs)

Base class for deterministic nodes.

Sub-classes must implement: 1. For implementing the deterministic function:

 _compute_moments(self, *u)

2. One of the following options: a) Simple methods:

 _compute_message_to_parent(self, index, m, *u) not? _compute_mask_to_parent(self, index, mask)

(a) More control with: _compute_message_and_mask_to_parent(self, index, m, *u)

Sub-classes may need to re-implement: 1. If they manipulate plates:

 _compute_mask_to_parent(index, mask) _plates_to_parent(self, index) _plates_from_parent(self, index)

Methods

add_plate_axis(to_plate)	
delete()	Delete this node and the children
get_mask()	
get_moments()	
get_shape(ind)	
has_plotter()	Return True if the node has a plotter
lower_bound_contribution([gradient])	
move_plates(from_plate, to_plate)	
plot(**kwargs)	Plot the node distribution using the plotter of the node
set_plotter(plotter)	

bayespy.inference.vmp.nodes.deterministic.Deterministic.add_plate_axis

Deterministic.add_plate_axis(to_plate)

bayespy.inference.vmp.nodes.deterministic.Deterministic.delete

Deterministic.delete()

Delete this node and the children

bayespy.inference.vmp.nodes.deterministic.Deterministic.get_mask

Deterministic.get_mask()

bayespy.inference.vmp.nodes.deterministic.Deterministic.get_moments

`Deterministic.get_moments()`

bayespy.inference.vmp.nodes.deterministic.Deterministic.get_shape

`Deterministic.get_shape(ind)`

bayespy.inference.vmp.nodes.deterministic.Deterministic.has_plotter

`Deterministic.has_plotter()`
Return True if the node has a plotter

bayespy.inference.vmp.nodes.deterministic.Deterministic.lower_bound_contribution

`Deterministic.lower_bound_contribution(gradient=False)`

bayespy.inference.vmp.nodes.deterministic.Deterministic.move_plates

`Deterministic.move_plates(from_plate, to_plate)`

bayespy.inference.vmp.nodes.deterministic.Deterministic.plot

`Deterministic.plot(**kwargs)`
Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.inference.vmp.nodes.deterministic.Deterministic.set_plotter

`Deterministic.set_plotter(plotter)`

Attributes

`plates`

bayespy.inference.vmp.nodes.deterministic.Deterministic.plates

`Deterministic.plates = None`

6.1.5 bayespy.inference.vmp.nodes.constant.Constant

class `bayespy.inference.vmp.nodes.constant.Constant(moments, x, **kwargs)`
Node for presenting constant values.

The node wraps arrays into proper node type.

Methods

<code>add_plate_axis(to_plate)</code>	
<code>delete()</code>	Delete this node and the children
<code>get_mask()</code>	
<code>get_moments()</code>	
<code>get_shape(ind)</code>	
<code>has_plotter()</code>	Return True if the node has a plotter
<code>move_plates(from_plate, to_plate)</code>	
<code>plot(**kwargs)</code>	Plot the node distribution using the plotter of the node
<code>set_plotter(plotter)</code>	

bayespy.inference.vmp.nodes.constant.Constant.add_plate_axis

`Constant.add_plate_axis(to_plate)`

bayespy.inference.vmp.nodes.constant.Constant.delete

`Constant.delete()`
Delete this node and the children

bayespy.inference.vmp.nodes.constant.Constant.get_mask

`Constant.get_mask()`

bayespy.inference.vmp.nodes.constant.Constant.get_moments

`Constant.get_moments()`

bayespy.inference.vmp.nodes.constant.Constant.get_shape

`Constant.get_shape(ind)`

bayespy.inference.vmp.nodes.constant.Constant.has_plotter

`Constant.has_plotter()`
Return True if the node has a plotter

bayespy.inference.vmp.nodes.constant.Constant.move_plates

`Constant.move_plates(from_plate, to_plate)`

bayespy.inference.vmp.nodes.constant.Constant.plot

`Constant.plot (**kwargs)`

Plot the node distribution using the plotter of the node

Because the distributions are in general very difficult to plot, the user must specify some functions which performs the plotting as wanted. See, for instance, `bayespy.plot.plotting` for available plotters, that is, functions that perform plotting for a node.

bayespy.inference.vmp.nodes.constant.Constant.set_plotter

`Constant.set_plotter (plotter)`

Attributes

`plates`

bayespy.inference.vmp.nodes.constant.Constant.plates

`Constant.plates = None`

6.2 Moments

TODO

INDICES AND TABLES

- *genindex*
- *modindex*
- *search*

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b

`bayespy.inference`, [132](#)
`bayespy.nodes`, [47](#)
`bayespy.plot`, [140](#)

Symbols

`__call__()` (bayespy.plot.CategoricalMarkovChainPlotter method), 145
`__call__()` (bayespy.plot.ContourPlotter method), 144
`__call__()` (bayespy.plot.FunctionPlotter method), 145
`__call__()` (bayespy.plot.GaussianTimeseriesPlotter method), 145
`__call__()` (bayespy.plot.HintonPlotter method), 144
`__call__()` (bayespy.plot.PDFPlotter method), 143
`__call__()` (bayespy.plot.Plotter method), 143

A

`add_plate_axis()` (bayespy.inference.vmp.nodes.constant.Constant method), 157
`add_plate_axis()` (bayespy.inference.vmp.nodes.deterministic.Deterministic method), 155
`add_plate_axis()` (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 152
`add_plate_axis()` (bayespy.inference.vmp.nodes.node.Node method), 148
`add_plate_axis()` (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 149
`add_plate_axis()` (bayespy.nodes.Bernoulli method), 79
`add_plate_axis()` (bayespy.nodes.Beta method), 98
`add_plate_axis()` (bayespy.nodes.Binomial method), 83
`add_plate_axis()` (bayespy.nodes.Categorical method), 87
`add_plate_axis()` (bayespy.nodes.CategoricalMarkovChain method), 106
`add_plate_axis()` (bayespy.nodes.Dirichlet method), 102
`add_plate_axis()` (bayespy.nodes.Exponential method), 64
`add_plate_axis()` (bayespy.nodes.Gamma method), 56
`add_plate_axis()` (bayespy.nodes.Gate method), 131
`add_plate_axis()` (bayespy.nodes.Gaussian method), 48
`add_plate_axis()` (bayespy.nodes.GaussianARD method), 52
`add_plate_axis()` (bayespy.nodes.GaussianGammaARD method), 72
`add_plate_axis()` (bayespy.nodes.GaussianGammaISO method), 68
`add_plate_axis()` (bayespy.nodes.GaussianMarkovChain method), 111

`add_plate_axis()` (bayespy.nodes.GaussianWishart method), 75
`add_plate_axis()` (bayespy.nodes.Mixture method), 125
`add_plate_axis()` (bayespy.nodes.Multinomial method), 91
`add_plate_axis()` (bayespy.nodes.Poisson method), 94
`add_plate_axis()` (bayespy.nodes.SumMultiply method), 129
`add_plate_axis()` (bayespy.nodes.SwitchingGaussianMarkovChain method), 115
`add_plate_axis()` (bayespy.nodes.VaryingGaussianMarkovChain method), 120
`add_plate_axis()` (bayespy.nodes.Wishart method), 60
`as_diagonal_wishart()` (bayespy.nodes.Exponential method), 64
`as_diagonal_wishart()` (bayespy.nodes.Gamma method), 56

B

`bayespy.inference` (module), 132
`bayespy.nodes` (module), 47
`bayespy.plot` (module), 140
Bernoulli (class in bayespy.nodes), 78
Beta (class in bayespy.nodes), 97
Binomial (class in bayespy.nodes), 82
`bound()` (bayespy.inference.vmp.transformations.RotateGaussian method), 135
`bound()` (bayespy.inference.vmp.transformations.RotateGaussianARD method), 136
`bound()` (bayespy.inference.vmp.transformations.RotateGaussianMarkovChain method), 137
`bound()` (bayespy.inference.vmp.transformations.RotateMultiple method), 140
`bound()` (bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain method), 138
`bound()` (bayespy.inference.vmp.transformations.RotateVaryingMarkovChain method), 139

C

Categorical (class in bayespy.nodes), 86
CategoricalMarkovChain (class in bayespy.nodes), 105
CategoricalMarkovChainPlotter (class in bayespy.plot), 145

compute_lowerbound() (bayespy.inference.VB method), 133
 compute_lowerbound_terms() (bayespy.inference.VB method), 133
 Constant (class in bayespy.inference.vmp.nodes.constant), 156
 contour() (in module bayespy.plot), 141
 ContourPlotter (class in bayespy.plot), 143

D

delete() (bayespy.inference.vmp.nodes.constant.Constant method), 157
 delete() (bayespy.inference.vmp.nodes.deterministic.Deterministic method), 155
 delete() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 152
 delete() (bayespy.inference.vmp.nodes.node.Node method), 148
 delete() (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 150
 delete() (bayespy.nodes.Bernoulli method), 79
 delete() (bayespy.nodes.Beta method), 98
 delete() (bayespy.nodes.Binomial method), 83
 delete() (bayespy.nodes.Categorical method), 87
 delete() (bayespy.nodes.CategoricalMarkovChain method), 106
 delete() (bayespy.nodes.Dirichlet method), 102
 delete() (bayespy.nodes.Exponential method), 64
 delete() (bayespy.nodes.Gamma method), 56
 delete() (bayespy.nodes.Gate method), 131
 delete() (bayespy.nodes.Gaussian method), 48
 delete() (bayespy.nodes.GaussianARD method), 52
 delete() (bayespy.nodes.GaussianGammaARD method), 72
 delete() (bayespy.nodes.GaussianGammaISO method), 68
 delete() (bayespy.nodes.GaussianMarkovChain method), 111
 delete() (bayespy.nodes.GaussianWishart method), 76
 delete() (bayespy.nodes.Mixture method), 125
 delete() (bayespy.nodes.Multinomial method), 91
 delete() (bayespy.nodes.Poisson method), 94
 delete() (bayespy.nodes.SumMultiply method), 129
 delete() (bayespy.nodes.SwitchingGaussianMarkovChain method), 115
 delete() (bayespy.nodes.VaryingGaussianMarkovChain method), 121
 delete() (bayespy.nodes.Wishart method), 60
 Deterministic (class in bayespy.inference.vmp.nodes.deterministic), 155
 dims (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily attribute), 154
 dims (bayespy.nodes.Bernoulli attribute), 82

dims (bayespy.nodes.Beta attribute), 101
 dims (bayespy.nodes.Binomial attribute), 86
 dims (bayespy.nodes.Categorical attribute), 89
 dims (bayespy.nodes.CategoricalMarkovChain attribute), 109
 dims (bayespy.nodes.Dirichlet attribute), 105
 dims (bayespy.nodes.Exponential attribute), 66
 dims (bayespy.nodes.Gamma attribute), 59
 dims (bayespy.nodes.Gaussian attribute), 51
 dims (bayespy.nodes.GaussianARD attribute), 55
 dims (bayespy.nodes.GaussianGammaARD attribute), 74
 dims (bayespy.nodes.GaussianGammaISO attribute), 71
 dims (bayespy.nodes.GaussianMarkovChain attribute), 113
 dims (bayespy.nodes.GaussianWishart attribute), 78
 dims (bayespy.nodes.Mixture attribute), 127
 dims (bayespy.nodes.Multinomial attribute), 93
 dims (bayespy.nodes.Poisson attribute), 97
 dims (bayespy.nodes.SwitchingGaussianMarkovChain attribute), 118
 dims (bayespy.nodes.VaryingGaussianMarkovChain attribute), 123
 dims (bayespy.nodes.Wishart attribute), 63
 Dirichlet (class in bayespy.nodes), 101
 Dot() (in module bayespy.nodes), 128

E

Exponential (class in bayespy.nodes), 63
 ExponentialFamily (class in bayespy.inference.vmp.nodes.expfamily), 151

F

FunctionPlotter (class in bayespy.plot), 144

G

Gamma (class in bayespy.nodes), 55
 Gate (class in bayespy.nodes), 131
 Gaussian (class in bayespy.nodes), 47
 GaussianARD (class in bayespy.nodes), 51
 GaussianGammaARD (class in bayespy.nodes), 71
 GaussianGammaISO (class in bayespy.nodes), 67
 GaussianMarkovChain (class in bayespy.nodes), 109
 GaussianTimeseriesPlotter (class in bayespy.plot), 145
 GaussianWishart (class in bayespy.nodes), 75
 get_bound_terms() (bayespy.inference.vmp.transformations.RotateGaussian method), 135
 get_bound_terms() (bayespy.inference.vmp.transformations.RotateGaussian method), 136
 get_bound_terms() (bayespy.inference.vmp.transformations.RotateGaussian method), 137
 get_bound_terms() (bayespy.inference.vmp.transformations.RotateMultiple method), 140

[get_bound_terms\(\) \(bayespy.inference.vmp.transformations.RotatoSwitchingMarkovChain method\), 138](#)
[get_bound_terms\(\) \(bayespy.inference.vmp.transformations.RotatoVaryingMarkovChain method\), 139](#)
[get_gaussian_mean_and_variance\(\) \(bayespy.nodes.GaussianGammaISO method\), 68](#)
[get_iteration_by_nodes\(\) \(bayespy.inference.VB method\), 133](#)
[get_marginal_logpdf\(\) \(bayespy.nodes.GaussianGammaISO method\), 68](#)
[get_mask\(\) \(bayespy.inference.vmp.nodes.constant.Constant method\), 157](#)
[get_mask\(\) \(bayespy.inference.vmp.nodes.deterministic.Deterministic method\), 155](#)
[get_mask\(\) \(bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method\), 152](#)
[get_mask\(\) \(bayespy.inference.vmp.nodes.node.Node method\), 148](#)
[get_mask\(\) \(bayespy.inference.vmp.nodes.stochastic.Stochastic method\), 150](#)
[get_mask\(\) \(bayespy.nodes.Bernoulli method\), 80](#)
[get_mask\(\) \(bayespy.nodes.Beta method\), 98](#)
[get_mask\(\) \(bayespy.nodes.Binomial method\), 83](#)
[get_mask\(\) \(bayespy.nodes.Categorical method\), 87](#)
[get_mask\(\) \(bayespy.nodes.CategoricalMarkovChain method\), 107](#)
[get_mask\(\) \(bayespy.nodes.Dirichlet method\), 102](#)
[get_mask\(\) \(bayespy.nodes.Exponential method\), 64](#)
[get_mask\(\) \(bayespy.nodes.Gamma method\), 57](#)
[get_mask\(\) \(bayespy.nodes.Gate method\), 131](#)
[get_mask\(\) \(bayespy.nodes.Gaussian method\), 48](#)
[get_mask\(\) \(bayespy.nodes.GaussianARD method\), 52](#)
[get_mask\(\) \(bayespy.nodes.GaussianGammaARD method\), 72](#)
[get_mask\(\) \(bayespy.nodes.GaussianGammaISO method\), 68](#)
[get_mask\(\) \(bayespy.nodes.GaussianMarkovChain method\), 111](#)
[get_mask\(\) \(bayespy.nodes.GaussianWishart method\), 76](#)
[get_mask\(\) \(bayespy.nodes.Mixture method\), 125](#)
[get_mask\(\) \(bayespy.nodes.Multinomial method\), 91](#)
[get_mask\(\) \(bayespy.nodes.Poisson method\), 95](#)
[get_mask\(\) \(bayespy.nodes.SumMultiply method\), 129](#)
[get_mask\(\) \(bayespy.nodes.SwitchingGaussianMarkovChain method\), 116](#)
[get_mask\(\) \(bayespy.nodes.VaryingGaussianMarkovChain method\), 121](#)
[get_mask\(\) \(bayespy.nodes.Wishart method\), 60](#)
[get_moments\(\) \(bayespy.inference.vmp.nodes.constant.Constant method\), 157](#)
[get_moments\(\) \(bayespy.inference.vmp.nodes.deterministic.Deterministic method\), 156](#)
[get_moments\(\) \(bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method\), 152](#)
[get_moments\(\) \(bayespy.inference.vmp.nodes.node.Node method\), 148](#)
[get_moments\(\) \(bayespy.inference.vmp.nodes.stochastic.Stochastic method\), 150](#)
[get_moments\(\) \(bayespy.nodes.Bernoulli method\), 80](#)
[get_moments\(\) \(bayespy.nodes.Beta method\), 99](#)
[get_moments\(\) \(bayespy.nodes.Binomial method\), 84](#)
[get_moments\(\) \(bayespy.nodes.Categorical method\), 87](#)
[get_moments\(\) \(bayespy.nodes.CategoricalMarkovChain method\), 107](#)
[get_moments\(\) \(bayespy.nodes.Dirichlet method\), 102](#)
[get_moments\(\) \(bayespy.nodes.Exponential method\), 64](#)
[get_moments\(\) \(bayespy.nodes.Gamma method\), 57](#)
[get_moments\(\) \(bayespy.nodes.Gate method\), 131](#)
[get_moments\(\) \(bayespy.nodes.Gaussian method\), 48](#)
[get_moments\(\) \(bayespy.nodes.GaussianARD method\), 53](#)
[get_moments\(\) \(bayespy.nodes.GaussianGammaARD method\), 72](#)
[get_moments\(\) \(bayespy.nodes.GaussianGammaISO method\), 68](#)
[get_moments\(\) \(bayespy.nodes.GaussianMarkovChain method\), 111](#)
[get_moments\(\) \(bayespy.nodes.GaussianWishart method\), 76](#)
[get_moments\(\) \(bayespy.nodes.Mixture method\), 125](#)
[get_moments\(\) \(bayespy.nodes.Multinomial method\), 91](#)
[get_moments\(\) \(bayespy.nodes.Poisson method\), 95](#)
[get_moments\(\) \(bayespy.nodes.SumMultiply method\), 130](#)
[get_moments\(\) \(bayespy.nodes.SwitchingGaussianMarkovChain method\), 116](#)
[get_moments\(\) \(bayespy.nodes.VaryingGaussianMarkovChain method\), 121](#)
[get_moments\(\) \(bayespy.nodes.Wishart method\), 60](#)
[get_parameters\(\) \(bayespy.nodes.SumMultiply method\), 130](#)
[get_shape\(\) \(bayespy.inference.vmp.nodes.constant.Constant method\), 157](#)
[get_shape\(\) \(bayespy.inference.vmp.nodes.deterministic.Deterministic method\), 156](#)
[get_shape\(\) \(bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method\), 152](#)
[get_shape\(\) \(bayespy.inference.vmp.nodes.node.Node method\), 148](#)
[get_shape\(\) \(bayespy.inference.vmp.nodes.stochastic.Stochastic method\), 150](#)
[get_shape\(\) \(bayespy.nodes.Bernoulli method\), 80](#)
[get_shape\(\) \(bayespy.nodes.Beta method\), 99](#)
[get_shape\(\) \(bayespy.nodes.Binomial method\), 84](#)
[get_shape\(\) \(bayespy.nodes.Categorical method\), 87](#)

[get_shape\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), [107](#)
[get_shape\(\)](#) (bayespy.nodes.Dirichlet method), [102](#)
[get_shape\(\)](#) (bayespy.nodes.Exponential method), [64](#)
[get_shape\(\)](#) (bayespy.nodes.Gamma method), [57](#)
[get_shape\(\)](#) (bayespy.nodes.Gate method), [131](#)
[get_shape\(\)](#) (bayespy.nodes.Gaussian method), [48](#)
[get_shape\(\)](#) (bayespy.nodes.GaussianARD method), [53](#)
[get_shape\(\)](#) (bayespy.nodes.GaussianGammaARD method), [72](#)
[get_shape\(\)](#) (bayespy.nodes.GaussianGammaISO method), [68](#)
[get_shape\(\)](#) (bayespy.nodes.GaussianMarkovChain method), [111](#)
[get_shape\(\)](#) (bayespy.nodes.GaussianWishart method), [76](#)
[get_shape\(\)](#) (bayespy.nodes.Mixture method), [125](#)
[get_shape\(\)](#) (bayespy.nodes.Multinomial method), [91](#)
[get_shape\(\)](#) (bayespy.nodes.Poisson method), [95](#)
[get_shape\(\)](#) (bayespy.nodes.SumMultiply method), [130](#)
[get_shape\(\)](#) (bayespy.nodes.SwitchingGaussianMarkovChain method), [116](#)
[get_shape\(\)](#) (bayespy.nodes.VaryingGaussianMarkovChain method), [121](#)
[get_shape\(\)](#) (bayespy.nodes.Wishart method), [60](#)

H

[has_plotter\(\)](#) (bayespy.inference.vmp.nodes.constant.Constant method), [157](#)
[has_plotter\(\)](#) (bayespy.inference.vmp.nodes.deterministic.Deterministic method), [156](#)
[has_plotter\(\)](#) (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), [152](#)
[has_plotter\(\)](#) (bayespy.inference.vmp.nodes.node.Node method), [148](#)
[has_plotter\(\)](#) (bayespy.inference.vmp.nodes.stochastic.Stochastic method), [150](#)
[has_plotter\(\)](#) (bayespy.nodes.Bernoulli method), [80](#)
[has_plotter\(\)](#) (bayespy.nodes.Beta method), [99](#)
[has_plotter\(\)](#) (bayespy.nodes.Binomial method), [84](#)
[has_plotter\(\)](#) (bayespy.nodes.Categorical method), [87](#)
[has_plotter\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), [107](#)
[has_plotter\(\)](#) (bayespy.nodes.Dirichlet method), [102](#)
[has_plotter\(\)](#) (bayespy.nodes.Exponential method), [64](#)
[has_plotter\(\)](#) (bayespy.nodes.Gamma method), [57](#)
[has_plotter\(\)](#) (bayespy.nodes.Gate method), [132](#)
[has_plotter\(\)](#) (bayespy.nodes.Gaussian method), [49](#)
[has_plotter\(\)](#) (bayespy.nodes.GaussianARD method), [53](#)
[has_plotter\(\)](#) (bayespy.nodes.GaussianGammaARD method), [72](#)
[has_plotter\(\)](#) (bayespy.nodes.GaussianGammaISO method), [69](#)
[has_plotter\(\)](#) (bayespy.nodes.GaussianMarkovChain method), [111](#)
[has_plotter\(\)](#) (bayespy.nodes.GaussianWishart method), [76](#)
[has_plotter\(\)](#) (bayespy.nodes.Mixture method), [125](#)
[has_plotter\(\)](#) (bayespy.nodes.Multinomial method), [91](#)
[has_plotter\(\)](#) (bayespy.nodes.Poisson method), [95](#)
[has_plotter\(\)](#) (bayespy.nodes.SumMultiply method), [130](#)
[has_plotter\(\)](#) (bayespy.nodes.SwitchingGaussianMarkovChain method), [116](#)
[has_plotter\(\)](#) (bayespy.nodes.VaryingGaussianMarkovChain method), [121](#)
[has_plotter\(\)](#) (bayespy.nodes.Wishart method), [60](#)
[hinton\(\)](#) (in module bayespy.plot), [141](#)
[HintonPlotter](#) (class in bayespy.plot), [144](#)

I

[initialize_from_mean_and_covariance\(\)](#) (bayespy.nodes.GaussianARD method), [53](#)
[initialize_from_parameters\(\)](#) (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), [153](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Bernoulli method), [80](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Beta method), [99](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Binomial method), [84](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Categorical method), [87](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), [107](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Dirichlet method), [103](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Exponential method), [64](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Gamma method), [57](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.Gaussian method), [49](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.GaussianARD method), [53](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.GaussianGammaARD method), [73](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.GaussianGammaISO method), [69](#)
[initialize_from_parameters\(\)](#) (bayespy.nodes.GaussianMarkovChain method), [111](#)

<code>initialize_from_parameters()</code> (<code>bayespy.nodes.GaussianWishart</code> method), 76	<code>initialize_from_prior()</code> (<code>bayespy.nodes.VaryingGaussianMarkovChain</code> method), 121
<code>initialize_from_parameters()</code> (<code>bayespy.nodes.Mixture</code> method), 125	<code>initialize_from_prior()</code> (<code>bayespy.nodes.Wishart</code> method), 61
<code>initialize_from_parameters()</code> (<code>bayespy.nodes.Multinomial</code> method), 91	<code>initialize_from_random()</code> (<code>bayespy.inference.vmp.nodes.expfamily.ExponentialFamily</code> method), 153
<code>initialize_from_parameters()</code> (<code>bayespy.nodes.Poisson</code> method), 95	<code>initialize_from_random()</code> (<code>bayespy.nodes.Bernoulli</code> method), 80
<code>initialize_from_parameters()</code> (<code>bayespy.nodes.SwitchingGaussianMarkovChain</code> method), 116	<code>initialize_from_random()</code> (<code>bayespy.nodes.Beta</code> method), 99
<code>initialize_from_parameters()</code> (<code>bayespy.nodes.VaryingGaussianMarkovChain</code> method), 121	<code>initialize_from_random()</code> (<code>bayespy.nodes.Binomial</code> method), 84
<code>initialize_from_parameters()</code> (<code>bayespy.nodes.Wishart</code> method), 61	<code>initialize_from_random()</code> (<code>bayespy.nodes.Categorical</code> method), 88
<code>initialize_from_prior()</code> (<code>bayespy.inference.vmp.nodes.expfamily.ExponentialFamily</code> method), 153	<code>initialize_from_random()</code> (<code>bayespy.nodes.CategoricalMarkovChain</code> method), 107
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Bernoulli</code> method), 80	<code>initialize_from_random()</code> (<code>bayespy.nodes.Dirichlet</code> method), 103
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Beta</code> method), 99	<code>initialize_from_random()</code> (<code>bayespy.nodes.Exponential</code> method), 65
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Binomial</code> method), 84	<code>initialize_from_random()</code> (<code>bayespy.nodes.Gamma</code> method), 57
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Categorical</code> method), 88	<code>initialize_from_random()</code> (<code>bayespy.nodes.Gaussian</code> method), 49
<code>initialize_from_prior()</code> (<code>bayespy.nodes.CategoricalMarkovChain</code> method), 107	<code>initialize_from_random()</code> (<code>bayespy.nodes.GaussianARD</code> method), 53
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Dirichlet</code> method), 103	<code>initialize_from_random()</code> (<code>bayespy.nodes.GaussianGammaARD</code> method), 73
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Exponential</code> method), 65	<code>initialize_from_random()</code> (<code>bayespy.nodes.GaussianGammaISO</code> method), 69
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Gamma</code> method), 57	<code>initialize_from_random()</code> (<code>bayespy.nodes.GaussianMarkovChain</code> method), 111
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Gaussian</code> method), 49	<code>initialize_from_random()</code> (<code>bayespy.nodes.GaussianWishart</code> method), 76
<code>initialize_from_prior()</code> (<code>bayespy.nodes.GaussianARD</code> method), 53	<code>initialize_from_random()</code> (<code>bayespy.nodes.Mixture</code> method), 126
<code>initialize_from_prior()</code> (<code>bayespy.nodes.GaussianGammaARD</code> method), 73	<code>initialize_from_random()</code> (<code>bayespy.nodes.Multinomial</code> method), 91
<code>initialize_from_prior()</code> (<code>bayespy.nodes.GaussianGammaISO</code> method), 69	<code>initialize_from_random()</code> (<code>bayespy.nodes.Poisson</code> method), 95
<code>initialize_from_prior()</code> (<code>bayespy.nodes.GaussianMarkovChain</code> method), 111	<code>initialize_from_random()</code> (<code>bayespy.nodes.SwitchingGaussianMarkovChain</code> method), 116
<code>initialize_from_prior()</code> (<code>bayespy.nodes.GaussianWishart</code> method), 76	<code>initialize_from_random()</code> (<code>bayespy.nodes.VaryingGaussianMarkovChain</code> method), 121
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Mixture</code> method), 126	<code>initialize_from_random()</code> (<code>bayespy.nodes.Wishart</code> method), 61
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Multinomial</code> method), 91	
<code>initialize_from_prior()</code> (<code>bayespy.nodes.Poisson</code> method), 95	
<code>initialize_from_prior()</code> (<code>bayespy.nodes.SwitchingGaussianMarkovChain</code> method), 116	

[initialize_from_value\(\)](#) (bayespy.inference.vmp.nodes.exponential.ExponentialFamily method), 153
[initialize_from_value\(\)](#) (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 150
[initialize_from_value\(\)](#) (bayespy.nodes.Bernoulli method), 80
[initialize_from_value\(\)](#) (bayespy.nodes.Beta method), 99
[initialize_from_value\(\)](#) (bayespy.nodes.Binomial method), 84
[initialize_from_value\(\)](#) (bayespy.nodes.Categorical method), 88
[initialize_from_value\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), 107
[initialize_from_value\(\)](#) (bayespy.nodes.Dirichlet method), 103
[initialize_from_value\(\)](#) (bayespy.nodes.Exponential method), 65
[initialize_from_value\(\)](#) (bayespy.nodes.Gamma method), 57
[initialize_from_value\(\)](#) (bayespy.nodes.Gaussian method), 49
[initialize_from_value\(\)](#) (bayespy.nodes.GaussianARD method), 53
[initialize_from_value\(\)](#) (bayespy.nodes.GaussianGammaARD method), 73
[initialize_from_value\(\)](#) (bayespy.nodes.GaussianGammaISO method), 69
[initialize_from_value\(\)](#) (bayespy.nodes.GaussianMarkovChain method), 111
[initialize_from_value\(\)](#) (bayespy.nodes.GaussianWishart method), 76
[initialize_from_value\(\)](#) (bayespy.nodes.Mixture method), 126
[initialize_from_value\(\)](#) (bayespy.nodes.Multinomial method), 92
[initialize_from_value\(\)](#) (bayespy.nodes.Poisson method), 95
[initialize_from_value\(\)](#) (bayespy.nodes.SwitchingGaussianMarkovChain method), 116
[initialize_from_value\(\)](#) (bayespy.nodes.VaryingGaussianMarkovChain method), 121
[initialize_from_value\(\)](#) (bayespy.nodes.Wishart method), 61
[integrated_logpdf_from_parents\(\)](#) (bayespy.nodes.Mixture method), 126
L
[load\(\)](#) (bayespy.inference.VB method), 133
[load\(\)](#) (bayespy.inference.vmp.nodes.exponential.ExponentialFamily method), 153
[load\(\)](#) (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 150
[load\(\)](#) (bayespy.nodes.Bernoulli method), 80
[load\(\)](#) (bayespy.nodes.Beta method), 99
[load\(\)](#) (bayespy.nodes.Binomial method), 84
[load\(\)](#) (bayespy.nodes.Categorical method), 88
[load\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), 107
[load\(\)](#) (bayespy.nodes.Dirichlet method), 103
[load\(\)](#) (bayespy.nodes.Exponential method), 65
[load\(\)](#) (bayespy.nodes.Gamma method), 57
[load\(\)](#) (bayespy.nodes.Gaussian method), 49
[load\(\)](#) (bayespy.nodes.GaussianARD method), 53
[load\(\)](#) (bayespy.nodes.GaussianGammaARD method), 73
[load\(\)](#) (bayespy.nodes.GaussianGammaISO method), 69
[load\(\)](#) (bayespy.nodes.GaussianMarkovChain method), 111
[load\(\)](#) (bayespy.nodes.GaussianWishart method), 76
[load\(\)](#) (bayespy.nodes.Mixture method), 126
[load\(\)](#) (bayespy.nodes.Multinomial method), 92
[load\(\)](#) (bayespy.nodes.Poisson method), 95
[load\(\)](#) (bayespy.nodes.SwitchingGaussianMarkovChain method), 116
[load\(\)](#) (bayespy.nodes.VaryingGaussianMarkovChain method), 121
[load\(\)](#) (bayespy.nodes.Wishart method), 61
[loglikelihood_lowerbound\(\)](#) (bayespy.inference.VB method), 134
[logpdf\(\)](#) (bayespy.inference.vmp.nodes.exponential.ExponentialFamily method), 153
[logpdf\(\)](#) (bayespy.nodes.Bernoulli method), 80
[logpdf\(\)](#) (bayespy.nodes.Beta method), 99
[logpdf\(\)](#) (bayespy.nodes.Binomial method), 84
[logpdf\(\)](#) (bayespy.nodes.Categorical method), 88
[logpdf\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), 107
[logpdf\(\)](#) (bayespy.nodes.Dirichlet method), 103
[logpdf\(\)](#) (bayespy.nodes.Exponential method), 65
[logpdf\(\)](#) (bayespy.nodes.Gamma method), 57
[logpdf\(\)](#) (bayespy.nodes.Gaussian method), 49
[logpdf\(\)](#) (bayespy.nodes.GaussianARD method), 53
[logpdf\(\)](#) (bayespy.nodes.GaussianGammaARD method), 73
[logpdf\(\)](#) (bayespy.nodes.GaussianGammaISO method), 69
[logpdf\(\)](#) (bayespy.nodes.GaussianMarkovChain method), 111
[logpdf\(\)](#) (bayespy.nodes.GaussianWishart method), 76
[logpdf\(\)](#) (bayespy.nodes.Mixture method), 126
[logpdf\(\)](#) (bayespy.nodes.Multinomial method), 92
[logpdf\(\)](#) (bayespy.nodes.Poisson method), 95
[logpdf\(\)](#) (bayespy.nodes.SwitchingGaussianMarkovChain method), 116
[logpdf\(\)](#) (bayespy.nodes.VaryingGaussianMarkovChain method), 121
[logpdf\(\)](#) (bayespy.nodes.Wishart method), 61
[lower_bound_contribution\(\)](#) (bayespy.inference.vmp.nodes.deterministic.Deterministic method), 156

[lower_bound_contribution\(\)](#)
 (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), [61](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Bernoulli method), [81](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Beta method), [99](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Binomial method), [84](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Categorical method), [88](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.CategoricalMarkovChain method), [108](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Dirichlet method), [103](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Exponential method), [65](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Gamma method), [58](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Gate method), [132](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Gaussian method), [49](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.GaussianARD method), [54](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.GaussianGammaARD method), [73](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.GaussianGammaISO method), [69](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.GaussianMarkovChain method), [112](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.GaussianWishart method), [77](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Mixture method), [126](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Multinomial method), [92](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Poisson method), [96](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.SumMultiply method), [130](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.SwitchingGaussianMarkovChain method), [117](#)
[lower_bound_contribution\(\)](#)
 (bayespy.nodes.VaryingGaussianMarkovChain method), [122](#)
[lower_bound_contribution\(\)](#) (bayespy.nodes.Wishart method), [61](#)
[lowerbound\(\)](#) (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), [153](#)
[lowerbound\(\)](#) (bayespy.inference.vmp.nodes.stochastic.Stochastic method), [150](#)
[lowerbound\(\)](#) (bayespy.nodes.Bernoulli method), [81](#)
[lowerbound\(\)](#) (bayespy.nodes.Beta method), [100](#)
[lowerbound\(\)](#) (bayespy.nodes.Binomial method), [85](#)
[lowerbound\(\)](#) (bayespy.nodes.Categorical method), [88](#)
[lowerbound\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), [108](#)
[lowerbound\(\)](#) (bayespy.nodes.Dirichlet method), [103](#)
[lowerbound\(\)](#) (bayespy.nodes.Exponential method), [65](#)
[lowerbound\(\)](#) (bayespy.nodes.Gamma method), [58](#)
[lowerbound\(\)](#) (bayespy.nodes.Gaussian method), [49](#)
[lowerbound\(\)](#) (bayespy.nodes.GaussianARD method), [54](#)
[lowerbound\(\)](#) (bayespy.nodes.GaussianGammaARD method), [73](#)
[lowerbound\(\)](#) (bayespy.nodes.GaussianGammaISO method), [69](#)
[lowerbound\(\)](#) (bayespy.nodes.GaussianMarkovChain method), [112](#)
[lowerbound\(\)](#) (bayespy.nodes.GaussianWishart method), [77](#)
[lowerbound\(\)](#) (bayespy.nodes.Mixture method), [126](#)
[lowerbound\(\)](#) (bayespy.nodes.Multinomial method), [92](#)
[lowerbound\(\)](#) (bayespy.nodes.Poisson method), [96](#)
[lowerbound\(\)](#) (bayespy.nodes.SwitchingGaussianMarkovChain method), [117](#)
[lowerbound\(\)](#) (bayespy.nodes.VaryingGaussianMarkovChain method), [122](#)
[lowerbound\(\)](#) (bayespy.nodes.Wishart method), [61](#)

M

[Mixture](#) (class in bayespy.nodes), [123](#)
[move_plates\(\)](#) (bayespy.inference.vmp.nodes.constant.Constant method), [157](#)
[move_plates\(\)](#) (bayespy.inference.vmp.nodes.deterministic.Deterministic method), [156](#)
[move_plates\(\)](#) (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), [153](#)
[move_plates\(\)](#) (bayespy.inference.vmp.nodes.node.Node method), [148](#)
[move_plates\(\)](#) (bayespy.inference.vmp.nodes.stochastic.Stochastic method), [150](#)
[move_plates\(\)](#) (bayespy.nodes.Bernoulli method), [81](#)
[move_plates\(\)](#) (bayespy.nodes.Beta method), [100](#)
[move_plates\(\)](#) (bayespy.nodes.Binomial method), [85](#)
[move_plates\(\)](#) (bayespy.nodes.Categorical method), [88](#)
[move_plates\(\)](#) (bayespy.nodes.CategoricalMarkovChain method), [108](#)
[move_plates\(\)](#) (bayespy.nodes.Dirichlet method), [103](#)
[move_plates\(\)](#) (bayespy.nodes.Exponential method), [65](#)

move_plates() (bayespy.nodes.Gamma method), 58
 move_plates() (bayespy.nodes.Gate method), 132
 move_plates() (bayespy.nodes.Gaussian method), 49
 move_plates() (bayespy.nodes.GaussianARD method), 54
 move_plates() (bayespy.nodes.GaussianGammaARD method), 73
 move_plates() (bayespy.nodes.GaussianGammaISO method), 69
 move_plates() (bayespy.nodes.GaussianMarkovChain method), 112
 move_plates() (bayespy.nodes.GaussianWishart method), 77
 move_plates() (bayespy.nodes.Mixture method), 126
 move_plates() (bayespy.nodes.Multinomial method), 92
 move_plates() (bayespy.nodes.Poisson method), 96
 move_plates() (bayespy.nodes.SumMultiply method), 130
 move_plates() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
 move_plates() (bayespy.nodes.VaryingGaussianMarkovChain method), 122
 move_plates() (bayespy.nodes.Wishart method), 61
 Multinomial (class in bayespy.nodes), 90

N

Node (class in bayespy.inference.vmp.nodes.node), 147
 nodes() (bayespy.inference.vmp.transformations.RotateGaussian method), 136
 nodes() (bayespy.inference.vmp.transformations.RotateGaussianARD method), 136
 nodes() (bayespy.inference.vmp.transformations.RotateGaussianMarkovChain method), 137
 nodes() (bayespy.inference.vmp.transformations.RotateMultiply method), 140
 nodes() (bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain method), 138
 nodes() (bayespy.inference.vmp.transformations.RotateVaryingMarkovChain method), 139

O

observe() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 153
 observe() (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 150
 observe() (bayespy.nodes.Bernoulli method), 81
 observe() (bayespy.nodes.Beta method), 100
 observe() (bayespy.nodes.Binomial method), 85
 observe() (bayespy.nodes.Categorical method), 88
 observe() (bayespy.nodes.CategoricalMarkovChain method), 108
 observe() (bayespy.nodes.Dirichlet method), 103
 observe() (bayespy.nodes.Exponential method), 65
 observe() (bayespy.nodes.Gamma method), 58

observe() (bayespy.nodes.Gaussian method), 50
 observe() (bayespy.nodes.GaussianARD method), 54
 observe() (bayespy.nodes.GaussianGammaARD method), 73
 observe() (bayespy.nodes.GaussianGammaISO method), 70
 observe() (bayespy.nodes.GaussianMarkovChain method), 112
 observe() (bayespy.nodes.GaussianWishart method), 77
 observe() (bayespy.nodes.Mixture method), 126
 observe() (bayespy.nodes.Multinomial method), 92
 observe() (bayespy.nodes.Poisson method), 96
 observe() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
 observe() (bayespy.nodes.VaryingGaussianMarkovChain method), 122
 observe() (bayespy.nodes.Wishart method), 61

P

pdf() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 154
 pdf() (bayespy.nodes.Bernoulli method), 81
 pdf() (bayespy.nodes.Beta method), 100
 pdf() (bayespy.nodes.Binomial method), 85
 pdf() (bayespy.nodes.Categorical method), 88
 pdf() (bayespy.nodes.CategoricalMarkovChain method), 108
 pdf() (bayespy.nodes.Dirichlet method), 104
 pdf() (bayespy.nodes.Exponential method), 65
 pdf() (bayespy.nodes.Gamma method), 58
 pdf() (bayespy.nodes.Gaussian method), 50
 pdf() (bayespy.nodes.GaussianARD method), 54
 pdf() (bayespy.nodes.GaussianGammaARD method), 74
 pdf() (bayespy.nodes.GaussianGammaISO method), 70
 pdf() (bayespy.nodes.GaussianMarkovChain method), 112
 pdf() (bayespy.nodes.GaussianWishart method), 77
 pdf() (bayespy.nodes.Mixture method), 127
 pdf() (bayespy.nodes.Multinomial method), 92
 pdf() (bayespy.nodes.Poisson method), 96
 pdf() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
 pdf() (bayespy.nodes.VaryingGaussianMarkovChain method), 122
 pdf() (bayespy.nodes.Wishart method), 62
 pdf() (in module bayespy.plot), 141
 PDFPlotter (class in bayespy.plot), 143
 plates (bayespy.inference.vmp.nodes.constant.Constant attribute), 158
 plates (bayespy.inference.vmp.nodes.deterministic.Deterministic attribute), 156
 plates (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily attribute), 155

- plates (bayespy.inference.vmp.nodes.node.Node attribute), 149
 - plates (bayespy.inference.vmp.nodes.stochastic.Stochastic attribute), 151
 - plates (bayespy.nodes.Bernoulli attribute), 82
 - plates (bayespy.nodes.Beta attribute), 101
 - plates (bayespy.nodes.Binomial attribute), 86
 - plates (bayespy.nodes.Categorical attribute), 90
 - plates (bayespy.nodes.CategoricalMarkovChain attribute), 109
 - plates (bayespy.nodes.Dirichlet attribute), 105
 - plates (bayespy.nodes.Exponential attribute), 67
 - plates (bayespy.nodes.Gamma attribute), 59
 - plates (bayespy.nodes.Gate attribute), 132
 - plates (bayespy.nodes.Gaussian attribute), 51
 - plates (bayespy.nodes.GaussianARD attribute), 55
 - plates (bayespy.nodes.GaussianGammaARD attribute), 75
 - plates (bayespy.nodes.GaussianGammaISO attribute), 71
 - plates (bayespy.nodes.GaussianMarkovChain attribute), 113
 - plates (bayespy.nodes.GaussianWishart attribute), 78
 - plates (bayespy.nodes.Mixture attribute), 128
 - plates (bayespy.nodes.Multinomial attribute), 93
 - plates (bayespy.nodes.Poisson attribute), 97
 - plates (bayespy.nodes.SumMultiply attribute), 130
 - plates (bayespy.nodes.SwitchingGaussianMarkovChain attribute), 118
 - plates (bayespy.nodes.VaryingGaussianMarkovChain attribute), 123
 - plates (bayespy.nodes.Wishart attribute), 63
 - plot() (bayespy.inference.VB method), 134
 - plot() (bayespy.inference.vmp.nodes.constant.Constant method), 158
 - plot() (bayespy.inference.vmp.nodes.deterministic.Deterministic method), 156
 - plot() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 154
 - plot() (bayespy.inference.vmp.nodes.node.Node method), 148
 - plot() (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 150
 - plot() (bayespy.nodes.Bernoulli method), 81
 - plot() (bayespy.nodes.Beta method), 100
 - plot() (bayespy.nodes.Binomial method), 85
 - plot() (bayespy.nodes.Categorical method), 89
 - plot() (bayespy.nodes.CategoricalMarkovChain method), 108
 - plot() (bayespy.nodes.Dirichlet method), 104
 - plot() (bayespy.nodes.Exponential method), 66
 - plot() (bayespy.nodes.Gamma method), 58
 - plot() (bayespy.nodes.Gaussian method), 50
 - plot() (bayespy.nodes.GaussianARD method), 54
 - plot() (bayespy.nodes.GaussianGammaARD method), 74
 - plot() (bayespy.nodes.GaussianGammaISO method), 70
 - plot() (bayespy.nodes.GaussianMarkovChain method), 112
 - plot() (bayespy.nodes.GaussianWishart method), 77
 - plot() (bayespy.nodes.Mixture method), 127
 - plot() (bayespy.nodes.Multinomial method), 92
 - plot() (bayespy.nodes.Poisson method), 96
 - plot() (bayespy.nodes.SumMultiply method), 130
 - plot() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
 - plot() (bayespy.nodes.VaryingGaussianMarkovChain method), 122
 - plot() (bayespy.nodes.Wishart method), 62
 - plot() (in module bayespy.plot), 141
 - plot_iteration_by_nodes() (bayespy.inference.VB method), 134
 - plotmatrix() (bayespy.nodes.GaussianGammaISO method), 70
 - Plotter (class in bayespy.plot), 142
 - Poisson (class in bayespy.nodes), 93
- ## R
- random() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 154
 - random() (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 151
 - random() (bayespy.nodes.Bernoulli method), 81
 - random() (bayespy.nodes.Beta method), 100
 - random() (bayespy.nodes.Binomial method), 85
 - random() (bayespy.nodes.Categorical method), 89
 - random() (bayespy.nodes.CategoricalMarkovChain method), 108
 - random() (bayespy.nodes.Dirichlet method), 104
 - random() (bayespy.nodes.Exponential method), 66
 - random() (bayespy.nodes.Gamma method), 58
 - random() (bayespy.nodes.Gaussian method), 50
 - random() (bayespy.nodes.GaussianARD method), 54
 - random() (bayespy.nodes.GaussianGammaARD method), 74
 - random() (bayespy.nodes.GaussianGammaISO method), 70
 - random() (bayespy.nodes.GaussianMarkovChain method), 112
 - random() (bayespy.nodes.GaussianWishart method), 77
 - random() (bayespy.nodes.Mixture method), 127
 - random() (bayespy.nodes.Multinomial method), 93
 - random() (bayespy.nodes.Poisson method), 96
 - random() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
 - random() (bayespy.nodes.VaryingGaussianMarkovChain method), 122
 - random() (bayespy.nodes.Wishart method), 62

- rotate() (bayespy.inference.vmp.transformations.RotateGaussian method), 136
- rotate() (bayespy.inference.vmp.transformations.RotateGaussianARD method), 137
- rotate() (bayespy.inference.vmp.transformations.RotateGaussianMarkovChain method), 138
- rotate() (bayespy.inference.vmp.transformations.RotateMultiple method), 140
- rotate() (bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain method), 138
- rotate() (bayespy.inference.vmp.transformations.RotateVaryingMarkovChain method), 139
- rotate() (bayespy.inference.vmp.transformations.RotationOptimizer method), 135
- rotate() (bayespy.nodes.Gaussian method), 50
- rotate() (bayespy.nodes.GaussianARD method), 54
- rotate() (bayespy.nodes.GaussianMarkovChain method), 113
- rotate() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
- rotate() (bayespy.nodes.VaryingGaussianMarkovChain method), 122
- rotate_matrix() (bayespy.nodes.Gaussian method), 50
- rotate_plates() (bayespy.nodes.GaussianARD method), 54
- RotateGaussian (class in bayespy.inference.vmp.transformations), 135
- RotateGaussianARD (class in bayespy.inference.vmp.transformations), 136
- RotateGaussianMarkovChain (class in bayespy.inference.vmp.transformations), 137
- RotateMultiple (class in bayespy.inference.vmp.transformations), 140
- RotateSwitchingMarkovChain (class in bayespy.inference.vmp.transformations), 138
- RotateVaryingMarkovChain (class in bayespy.inference.vmp.transformations), 139
- RotationOptimizer (class in bayespy.inference.vmp.transformations), 134
- save() (bayespy.inference.VB method), 134
- save() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 154
- save() (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 151
- save() (bayespy.nodes.Bernoulli method), 81
- save() (bayespy.nodes.Beta method), 100
- save() (bayespy.nodes.Binomial method), 85
- save() (bayespy.nodes.Categorical method), 89
- save() (bayespy.nodes.CategoricalMarkovChain method), 108
- save() (bayespy.nodes.Dirichlet method), 104
- save() (bayespy.nodes.Exponential method), 66
- save() (bayespy.nodes.Gamma method), 58
- save() (bayespy.nodes.Gaussian method), 50
- save() (bayespy.nodes.GaussianARD method), 55
- save() (bayespy.nodes.GaussianGammaARD method), 74
- save() (bayespy.nodes.GaussianGammaISO method), 70
- save() (bayespy.nodes.GaussianMarkovChain method), 113
- save() (bayespy.nodes.GaussianWishart method), 77
- save() (bayespy.nodes.Mixture method), 127
- save() (bayespy.nodes.Multinomial method), 93
- save() (bayespy.nodes.Poisson method), 96
- save() (bayespy.nodes.SwitchingGaussianMarkovChain method), 117
- save() (bayespy.nodes.VaryingGaussianMarkovChain method), 123
- save() (bayespy.nodes.Wishart method), 62
- set_autosave() (bayespy.inference.VB method), 134
- set_plotter() (bayespy.inference.vmp.nodes.constant.Constant method), 158
- set_plotter() (bayespy.inference.vmp.nodes.deterministic.Deterministic method), 156
- set_plotter() (bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method), 154
- set_plotter() (bayespy.inference.vmp.nodes.node.Node method), 148
- set_plotter() (bayespy.inference.vmp.nodes.stochastic.Stochastic method), 151
- set_plotter() (bayespy.nodes.Bernoulli method), 81
- set_plotter() (bayespy.nodes.Beta method), 100
- set_plotter() (bayespy.nodes.Binomial method), 85
- set_plotter() (bayespy.nodes.Categorical method), 89
- set_plotter() (bayespy.nodes.CategoricalMarkovChain method), 108
- set_plotter() (bayespy.nodes.Dirichlet method), 104
- set_plotter() (bayespy.nodes.Exponential method), 66
- set_plotter() (bayespy.nodes.Gamma method), 58
- set_plotter() (bayespy.nodes.Gate method), 132
- set_plotter() (bayespy.nodes.Gaussian method), 51
- set_plotter() (bayespy.nodes.GaussianARD method), 55
- set_plotter() (bayespy.nodes.GaussianGammaARD method), 74
- set_plotter() (bayespy.nodes.GaussianGammaISO method), 70
- set_plotter() (bayespy.nodes.GaussianMarkovChain method), 113
- set_plotter() (bayespy.nodes.GaussianWishart method), 78

S

[set_plotter\(\) \(bayespy.nodes.Mixture method\), 127](#)
[set_plotter\(\) \(bayespy.nodes.Multinomial method\), 93](#)
[set_plotter\(\) \(bayespy.nodes.Poisson method\), 96](#)
[set_plotter\(\) \(bayespy.nodes.SumMultiply method\), 130](#)
[set_plotter\(\) \(bayespy.nodes.SwitchingGaussianMarkovChain method\), 118](#)
[set_plotter\(\) \(bayespy.nodes.VaryingGaussianMarkovChain method\), 123](#)
[set_plotter\(\) \(bayespy.nodes.Wishart method\), 62](#)
[setup\(\) \(bayespy.inference.vmp.transformations.RotateGaussianMarkovChain method\), 136](#)
[setup\(\) \(bayespy.inference.vmp.transformations.RotateGaussianMarkovChain method\), 137](#)
[setup\(\) \(bayespy.inference.vmp.transformations.RotateGaussianMarkovChain method\), 138](#)
[setup\(\) \(bayespy.inference.vmp.transformations.RotateMultipleMarkovChain method\), 140](#)
[setup\(\) \(bayespy.inference.vmp.transformations.RotateSwitchingMarkovChain method\), 139](#)
[setup\(\) \(bayespy.inference.vmp.transformations.RotateVaryingMarkovChain method\), 139](#)
[show\(\) \(bayespy.nodes.Bernoulli method\), 82](#)
[show\(\) \(bayespy.nodes.Beta method\), 100](#)
[show\(\) \(bayespy.nodes.Binomial method\), 85](#)
[show\(\) \(bayespy.nodes.Categorical method\), 89](#)
[show\(\) \(bayespy.nodes.CategoricalMarkovChain method\), 109](#)
[show\(\) \(bayespy.nodes.Dirichlet method\), 104](#)
[show\(\) \(bayespy.nodes.Exponential method\), 66](#)
[show\(\) \(bayespy.nodes.Gamma method\), 59](#)
[show\(\) \(bayespy.nodes.Gaussian method\), 51](#)
[show\(\) \(bayespy.nodes.GaussianARD method\), 55](#)
[show\(\) \(bayespy.nodes.GaussianGammaISO method\), 70](#)
[show\(\) \(bayespy.nodes.GaussianMarkovChain method\), 113](#)
[show\(\) \(bayespy.nodes.GaussianWishart method\), 78](#)
[show\(\) \(bayespy.nodes.Multinomial method\), 93](#)
[show\(\) \(bayespy.nodes.Poisson method\), 97](#)
[show\(\) \(bayespy.nodes.SwitchingGaussianMarkovChain method\), 118](#)
[show\(\) \(bayespy.nodes.VaryingGaussianMarkovChain method\), 123](#)
[show\(\) \(bayespy.nodes.Wishart method\), 62](#)
[Stochastic \(class in bayespy.inference.vmp.nodes.stochastic\), 149](#)
[SumMultiply \(class in bayespy.nodes\), 128](#)
[SwitchingGaussianMarkovChain \(class in bayespy.nodes\), 113](#)

U

[unobserve\(\) \(bayespy.inference.vmp.nodes.expfamily.ExponentialFamily method\), 154](#)
[unobserve\(\) \(bayespy.inference.vmp.nodes.stochastic.Stochastic method\), 151](#)
[unobserve\(\) \(bayespy.nodes.Bernoulli method\), 82](#)
[unobserve\(\) \(bayespy.nodes.Beta method\), 101](#)
[unobserve\(\) \(bayespy.nodes.Binomial method\), 86](#)
[unobserve\(\) \(bayespy.nodes.Categorical method\), 89](#)
[unobserve\(\) \(bayespy.nodes.CategoricalMarkovChain method\), 109](#)
[unobserve\(\) \(bayespy.nodes.Dirichlet method\), 104](#)
[unobserve\(\) \(bayespy.nodes.Exponential method\), 66](#)
[unobserve\(\) \(bayespy.nodes.Gamma method\), 59](#)
[unobserve\(\) \(bayespy.nodes.Gaussian method\), 51](#)
[unobserve\(\) \(bayespy.nodes.GaussianARD method\), 55](#)
[unobserve\(\) \(bayespy.nodes.GaussianGammaARD method\), 74](#)
[unobserve\(\) \(bayespy.nodes.GaussianGammaISO method\), 71](#)
[unobserve\(\) \(bayespy.nodes.GaussianMarkovChain method\), 113](#)
[unobserve\(\) \(bayespy.nodes.GaussianWishart method\), 78](#)
[unobserve\(\) \(bayespy.nodes.Mixture method\), 127](#)
[unobserve\(\) \(bayespy.nodes.Multinomial method\), 93](#)
[unobserve\(\) \(bayespy.nodes.Poisson method\), 97](#)

`update()` (`bayespy.nodes.SwitchingGaussianMarkovChain` method), [118](#)

`update()` (`bayespy.nodes.VaryingGaussianMarkovChain` method), [123](#)

`update()` (`bayespy.nodes.Wishart` method), [62](#)

V

`VaryingGaussianMarkovChain` (class in `bayespy.nodes`), [118](#)

`VB` (class in `bayespy.inference`), [133](#)

W

`Wishart` (class in `bayespy.nodes`), [59](#)