

Graph_Sampler:

A Network Inference and Simulation Program

by Frédéric Y. Bois

User's Manual, software version 2.0.0

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contact:

Frederic Bois

fbois@member.fsf.org

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2 Overview

Graph_Sampler is an inference and simulation tool for networks (understood as graphs). It can *simulate* random graphs for general directed graphs (eventually cyclic) (see [\[Bibliographic References\]](#), [page 25](#)) or for directed acyclic graphs (Bayesian networks). The graphs are generated by Markov chain Monte Carlo simulations and their structure can be specified to follow probabilistic properties through the use of prior distributions. In the case of Bayesian networks, you can also *infer* about their probable structure through the joint use of priors and data about node values (via a likelihood function).

2.1 General procedure

You write an input files and run compiled `graph_sampler` program. The input files specifies the kind of graph to simulate, some simulation parameters and output options, the priors you want, the eventual data and their likelihood (see [Chapter 4 \[Running Graph_Sampler\]](#), [page 13](#)). The simulation output is written to standard ASCII files.

No knowledge of computer programming is required, unless you want to tailor the program to special needs (in which case you may want to contact us).

2.2 New features

- Version 1.1.0 allows you to set the relative weight of data though the parameter `gamma_zellner`.

3 Installation

3.1 System requirements

Graph_Sampler is written in ANSI-standard C language. We are distributing the source code and you should be able to compile it for any system, provided you have an ANSI C compliant compiler.

On any system we recommend the GNU gcc compiler (freeware). An automated compilation script (called **Makefile**) is provided and can be used if the standard command **make** is available to you. We also recommend that you install the GNU Scientific Library prior to installing *Graph_Sampler*, so that it can make use of the Mersenne twister and Tausworthe pseudo-random number generators it provides.

If you want to modify the input file parser you will need **lex** and **yacc** (that is for experienced C programmers).

3.2 Distribution

Graph_Sampler source code is available on Internet through:

<https://sites.google.com/site/utcchairmmbstpt/software>.

3.3 Machine-specific installation

3.3.1 Unix and GNU/Linux operating systems

To install on a Unix or GNU/Linux machine, download (in binary mode) the distributed archive file to your machine. Place it in a directory where there is no existing **graph_sampler** subdirectory that could be erased (make sure you check that). Decompress the archive with GNU gunzip (**gunzip <archive-name>.tar.gz**). Untar the decompressed archive with tar (**tar xf <archive-name>.tar**) (do **man tar** for further help). Many other archiving tools can be used in place of gunzip and tar. Move to the **graph_sampler** directory just created and issue the following commands:

```
make
```

This command compiles the **graph_sampler** program.

If you do not have the GNU Scientific Library installed, or do not want to use it, you should compile with the command **make -f Makefile_no_gsl**.

You can also compile this manual as an info file with the command **make info** or as an html file with **make html**.

3.3.2 Other operating systems

Under other operating systems (Windows, etc.) or if everything else fails you should be able to both uncompress and untar the archive with widely distributed archiving tools. Refer to the documentation of your C compiler to create an executable file from the source code files provided.

You are now ready to use *Graph_Sampler*.

4 Running Graph_Sampler

After having compiled `graph_sampler`, you are ready to run it. For this you need to write an input file. This chapter explains how to write such files with the proper syntax.

In Unix the command-line syntax to run that executable is simply:

```
graph_sampler [input-file [output-prefix]]
```

where the brackets indicate optional arguments. If no input file or/and output prefix are specified, the program will use defaults. The default input file name is `script.txt`, the output files created depend on flag you set in the input file (see below) and their name is printed on exit. The default output file names are `best_graph.out`, `graph_samples.out`, `degree_count.out`, `motifs_count.out`, `edge_p.out`, `results_mcmc.bin` and `missing_data.out` (the latter is created only if “NA” data are specified). If you only specify an input file name, the output file names will still be the default ones. If you specify both an input file name and an output prefix, the default output file names will be prefixed by it (*i.e.*, with the prefix `my` the edge probabilities output file will be named `my_edge_p.out`).

When the program starts, it announces which model description file was used to create it. While the input file is read or while simulations are running, some informations will be printed on your computer screen. They can help you check that the input file is correctly interpreted and that the program runs as it should. *Graph_Sampler* can also post error messages, which should be self-explanatory. Where appropriate, they show the line number in the input file where the error occurred.

The program ends (if everything went fine) by giving you the name of the output file generated. If you want to run the program in batch mode (in the background), you may want to redirect the screen output and error messages; refer for this to the `man` pages for your command shell.

4.1 Input file syntax

An input file specifies the kind of graph to simulate, some simulation parameters and output options, the priors you want, the eventual data and their likelihood. All that is done through the specification of predefined variables, using some keywords, user defined variables, numbers and operators.

A *Graph_Sampler* input file is a text (ASCII) file that obeys a relatively simple syntax:

- An input file can contain statements, matrix definitions and comments.
- Statements and matrix definitions must end with `;` and can span several lines. They can be placed in any order, except that matrix sizes (defined by specific predefined variables) must be defined before the corresponding matrix definition.
- Comments start with the pound sign `#` and go up to the end of line. They are ignored.

Example:

```
# this is a comment, comments are useful
```

- Variables are user defined symbols whose name must start with a letter, followed eventually by other letters, numbers and `_`. Letters can be upper-case or lower-case. Variable names are case sensitive. Example:

```
Xa_2
```

Note that unassigned variables have a default value of zero.

- Predefined variables are reserved names that *Graph_Sampler* understands. An exhaustive list of the predefined variables is given in the next section. Predefined variables not explicitly assigned have (hopefully useful) default values which may differ from zero (refer to their description, below). Example:

```
n_nodes
```

- Expressions are numbers (as in C) or formulae including numbers and/or user defined variables, operators ('+', '-', '*', '/') or parentheses. Formulae are computed at they appear, with usual precedences. The division is always a real division (not an integer division). Example:

```
(5 + 6) * (3.4 / 1.1E-8) + Xa_2;
```

- Statements are in the format:

```
<variable> = <expression>;
```

Example:

```
X_a2 = 5000;
n_nodes = 6 * Xa_2;
```

- White space consist of space, tab or carriage return. Several white space characers in a row are treated as just one white space. Example:

```
Xa_2 =      (2   + 3)   /
            (25. - 5.76);
```

- Lists are comma separated lists of expressions. Example:

```
1, 2, 2+1, 2*2, 5, Xa_2
```

- Array definitions can only be used with predefined variables at the lefthand side. They are in the forms: `<variable> = array{<list of expressions>;}`.

The term **array** is a reserved keyword (see the list of those keywords below). Example:

```
n_data_levels = array{2, 2, 1+1};
```

- Matrix definitions can only be used with predefined variables at the lefthand side. They are in the forms:

```
<variable> = matrix{<list of expressions>;}
```

The term **matrix** is a reserved keyword (see the list of those keywords below). Example:

```
data = matrix{
1,   2,  2+1,
2*2, 5,  Xa_2};
```

That is the general form. Some matrices can accept keywords such as **empty**, **full**, **equanimous**, or **random** instead of a list of expression inside the curly braces (see the specification of each predefined matrix, below).

4.2 Predefined variables

Here are, grouped by topic, the predefined variables that *Graph_Sampler* understands (they may have different synonyms, in general a long and a short form, separed by commas):

4.2.1 Global control variables

autocycle

The `autocycle` variable should be set to 1 (`true`) if edges from a node to itself are allowed, and to 0 (`false`) otherwise. Its default value is `false`. Setting it to `true` is incompatible with specifying `bbn` to `true` (loops are not allowed in Bayesian networks).

bayesian_network, bbn

The predefined variable `bayesian_network` indicate whether the graphs to sample are Bayesian networks (in that case it should be set to 1 or `true`) or general directed graphs (in which case it should set to 0 or `false`). General directed graphs can only be simulated on the basis of priors. For Bayesian networks both simulation and structural inference can be performed. The default value for `bayesian_network` is `false`.

Example:

```
bayesian_network = true; # bayesian_network = 1 would also work
```

dynamic_bayesian_network

If `dynamic_bayesian_network` is set to 1 or `true` the graphs sampled are dynamic Bayesian networks (DBNs). Both simulation and structural inference can be performed. In DBNs, the data are supposed to be collected at different discrete times, and the node states (values) at a given time can influence the nodes values at subsequent times. That allows the modeling of loops (*e.g.*, a node at time t can be its own parent at time $t+1$) (see [\[Bibliographic References\]](#), page 25). Currently, in *graph_sampler*, edges can only connect nodes from one time to the next (no connection to node values at the same time or times ulterior to the next). The pattern of edges from one time to the next is also constant and valid for all time pairs (the dependence structure is not allowed to change with time). The initial adjacency matrix specified, together with the priors on edges refer to edges between subsequent times and do not need to respect acyclicity (again, for example, a 1 on the diagonal of the adjacency matrix means that the corresponding node at time t is the parent of itself, but at time $t+1$). Despite the free structure of the adjacency matrix sampled, acyclicity is always maintained in such DBNs, and the adjacency matrices given just need to be “unrolled” in time. The default value for `dynamic_bayesian_network` is `false`.

n_nodes, nNodes

The number of nodes in the network considered is specified by setting `n_nodes` to an integer (not long integer) value. `n_nodes` must be set before the initial adjacency or prior on edges’ probability matrices are defined. The default value for `n_nodes` is 0, which raises an error message, because `n_nodes` should be set to a meaningful value.

initial_adjacency

The starting value of the graph adjacency matrix is defined by setting `initial_adjacency`, a square matrix of dimension `n_nodes`. Matrix elements should be either 0 or 1. Element $[i,j]$ is set to 1 if an edge (link) goes from node i to node j . Setting it to 0 indicates no edge between the two nodes.

Example:

```
n_nodes = 3;
initial_adjacency = matrix {0, 0, 0,
```

```
1, 0, 0,
1, 0, 0};
```

`initial_adjacency` definition can also use an extended syntax:

```
initial_adjacency = matrix{empty | full | random};.
```

where “|” means “or”.

- If the keyword `empty` is used, all elements will be set to zero.
- If `full` is used all elements will be set to 1 when `bayesian_network` is `false`. If `bayesian_network` is `true` the diagonal elements will be set to zero and the others to 1. If you want it to work with Bayesian networks, you should set `bayesian_network` to `true` before defining `initial_adjacency`, because its default value is `false`.
- If `random` is used all elements will be set randomly to 0 or 1 (with equal probability) when `bayesian_network` is `false`. If `bayesian_network` is `true` the diagonal elements will be set to zero and the others to 0 or 1. If you want it to work with Bayesian networks, you should set `bayesian_network` to `true` before defining `initial_adjacency`, because its default value is `false`.

`nRuns, n_runs`

The total number of iterations to be performed by the MCMC sampler is specified by setting `nRuns` to a an integer or a floating point number inferior to the maximum long integer value on your machine. Its default value is 1000000000 (yes, a billion).

`nBurnin, n_burn_in`

A certain number of “burn-in” iterations can be specified by setting `n_burn_in` to a long integer value. In that case the MCMC chain recording, and computation of summary outputs (such as the edge probabilities) starts only after `n_burn_in` iteration. Its default value is zero. This is typically used to discard the part of the MCMC chain that is not at equilibrium. However, checking that equilibrium is attained is best done, in our opinion, by running multiple independent chains and using Gelman and Rubin \hat{R} diagnostic (see [\[Bibliographic References\]](#), page 25 and other relevant statistical literature).

`perk_scale`

Tempered MCMC sampling is performed if a `perk_scale` is specified (Geyer and Thompson, Journal of the American Statistical Association, 1995, 90:909-920). The `perk_scale` defines a set of inverse temperatures (between 0 and 1) to be used in tempered MCMC.

```
perk_scale = array {0.1, 0.5, 0.9, 1};
```

This option slows effective sampling (which occurs at perk equal to 1) by a factor equal to the number of perk factors provided, but it improves mixing and convergence dramatically. Perks (inverse temperatures) are sampled at the start of each adjacency matrix updating. Therefore if a perk of zero is specified, the Markov chain should regenerate when it hits this perk (which corresponds to an infinite temperature). Samples obtained at perk 1.0 between two random hits of perk zero should therefore be from the exact target distribution (*i.e.*, obtained at convergence). If recording the chain is requested (`save_chain` set to `true`) perks are output to the file `inverse_temperatures.out`. You can use it to trace back which graph samples were obtained at which temperature.

random_generator

If you have linked *Graph_Sampler* with GNU Scientific Library (gsl) you can choose between two extremely long period random number generators provided by the library: either the “Mersenne twister” generator (gsl_rng_mt19937) or the “Tausworthe generator” (gsl_rng_taus2). To that effect you can set the variable **random_generator** to either the **mersenne_twister** keyword or the **tausworthe** keyword. By default the Mersenne twister is used.

Example:

```
random_generator = tausworthe;
```

If you have have compiled *Graph_Sampler* with the NO_LIBGSL option, the GNU Scientific Library is not available. In that case the Park and Millers minimal standard MINSTD generator (a good one though) is used instead. Setting the **random_generator** variable is ignored in that case.

seed, random_seed

The starting value of the pseudo-random generator **seed** can be explicitly set to any real or integer number superior to zero. That allows repeating exactly the same sequence random numbers. That is required to generate different chains for the same problem in order to check the convergence of the MCMC simulations. If it is not set by the user, **seed** has a default value of 314159265.3589793.

Example:

```
random_seed = 123.456;
```

4.2.2 Variables specifying priors

hyper_pB

The matrix **hyper_pB** is a square matrix of dimension **n_nodes** which specifies a prior distribution on edge probabilities. Each element $[i,j]$ of **hyper_pB** is the parameter p (a real of double format) of a Bernoulli distribution for the presence of an edge from node i to node j . In the case of Bayesian networks, p values should be 0 on the first diagonal.

Example:

```
bayesian_network = true;
hyper_pB = matrix {0, 0.1, 0.1,
                  0.9, 0, 0.1,
                  0.9, 0.1, 0 };
```

hyper_pB definition can also use an extended syntax:

```
hyper_pB = matrix{equanimous};.
```

If the keyword **equanimous** is used, all elements of **hyper_pB** will be set to 0.5 when **bayesian_network** is **false**. If **bayesian_network** is **true** the diagonal elements will be set to zero and the others to 0.5. If you want it to work with Bayesian networks, you should set **bayesian_network** to **true** before defining **hyper_pB**, because its default value is **false**.

Internally, **hyper_pB** is always used. If it is not defined by the user, p values will default to 0.5 (with zeroes on the diagonal if **bayesian_network** is **true**), so that the prior is

neutral (equal probability for the absence or presence of any edge). The use of the keyword `equanimous` is equivalent, with the advantage of being explicit.

In the case of a Bayesian network, nodes which have been assigned a zero probability of having parents (a column of zero in the `hyper_pB` matrix) are understood to be special “control” nodes for which the likelihood will not be computed. Such nodes will typically correspond to experimental design variables. Their likelihood is not computed. They condition the likelihood of their eventual children node and then take the values assigned to them in the input file (in which case the “data” are rather forcing values than actual observations).

`concordance_prior`, `bPriorConcordance`

The flag `concordance_prior` set to 1 or `true` indicates that a concordance prior should be used (in addition to the baseline Bernoulli prior on individual edges). By default `concordance_prior` is `false`. A concordance prior is an unnormalized score of the edge-wise difference between a reference adjacency matrix and the matrix being examined (see below `edge_requirements`). Beware that you should probably not use it in conjunction with an informative Bernoulli prior on edges, since both priors specify (explicitly in the case of Bernoulli) individual edge probabilities. Leaving the Bernoulli prior unspecified will be fine in that case as it will be assigned a non-informative default value.

`edge_requirements`

The matrix `edge_requirements` is a square matrix of dimension `n_nodes` which specifies the concordance between the edges of a reference adjacency matrix and the current one. Each element $[i,j]$ of `edge_requirements` can take a value of 1, -1, or 0.

- The value 1 indicates that an edge from node i to node j is desired (rather than strictly required). The presence of that edge in the adjacency matrix evaluated raises its score by `lambda_concordance` (see below).
- The value -1 indicates that an edge from node i to node j is not desired. The presence of that edge in the adjacency matrix evaluated lowers its score. In the case of Bayesian networks, diagonal values should be -1, otherwise Hell might break loose.
- A value of 0 indicates no preference: the score is unaffected by the presence or absence of an edge from node i to node j . The presence of that edge in the adjacency matrix evaluated raises its score.

Example:

```
concordance_prior = true;
edge_requirements = matrix {-1, -1,  0,
                           1, -1, -1,
                           1, -1, -1};
```

By default, all elements of `edge_requirements` will be set to 0 when `bayesian_network` is `false`. If `bayesian_network` is `true` the diagonal elements will be set to -1 and the others to 0. If you want it to work with Bayesian networks, you should set `bayesian_network` before defining `edge_requirements`, because its default value is `false`.

lambda_concordance, lambda_concord

The parameter `lambda_concord` is used to weight the differences between the reference adjacency matrix and the current adjacency matrix when `bPriorConcordance` is `true`. It should be set to a double (typically superior to zero). Its default value is 1.

degree_prior, bPriorDegreeNode

The flag `degree_prior` set to 1 or `true` indicates that an exponential prior is placed on the distribution of the nodes' degrees (the number of incoming and outgoing edges for a given node) (see [Bibliographic References], page 25). It comes in addition to the baseline Bernoulli prior on individual edges. By default it is `false`.

gamma_degree

If `bPriorDegreeNode` is `true`, `gamma_degree` specifies the parameter of the exponential prior on degree counts. It should be set to a double (typically superior to zero). Its default value is 1.

edge_count_prior

The variable `edge_count_prior` can be set to a number between 0 and the maximum number of edges possible (`n_nodes` squared, in a general graph, and `n_nodes` times (`n_nodes` - 1) in a Bayesian network) to impose a binomial prior on the total number of edges in the graph. The number given should be the *a priori* expected value for the edge count. The variable `n_nodes` must be set before setting `edge_count_prior`.

Example:

```
n_nodes = 20;
edge_count_prior = 50;
```

motif_prior, bPriorMotif

The flag `bPriorMotif` set to 1 or `true` indicates that a beta-binomial prior is placed on the count of triangular feed-forward and feedback loops in the network (see [Bibliographic References], page 25). It comes in addition to the baseline Bernoulli prior on individual edges and is incompatible with Bayesian networks (an error message will be issued). By default it is `false`.

alpha_motif

If `bPriorMotif` is `true`, `alpha_motif` specifies the first parameter of the beta-binomial prior on loops' counts. It should be set to an integer superior to zero. Its default value is 1.

beta_motif

If `bPriorMotif` is `true`, `beta_motif` specifies the first parameter of the beta-binomial prior on loops' counts. It should be set to an integer superior to zero. Its default value is 1.

4.2.3 Variables specifying data and likelihood**n_data, nData**

If `bayesian_network` is `true`, data can be input to infer on the probability of the presence of edges on the basis of priors and data likelihood, in a fully Bayesian framework. The

predefined variable `nData` should be set to an integer equal to the number of data points per node. Its default is zero. If no data are provided while `bayesian_network` is `true`, simulations will proceed simply on the basis of priors distributions.

data

After `n_nodes`, `nData` and `bayesian_network` have been defined, a data matrix can also be defined (actually if `nData` is different from zero a data matrix must be defined). `data` has no default value. The matrix of data should have `n_nodes` rows and each row should be a vector of `nData` values (integers, doubles or “NA” in the case of missing data). A warning is issued if a node has only missing data (that is likely to lead to identifiability problems).

Example:

```
n_nodes = 3;
bayesian_network = true;
n_data = 4;
data = matrix {1.1, 1.3, 1.4, 1.35,
               2.1, NA, 2.5, 2.45,
               3.4, 3.6, 3.8, 3.85};
```

If missing data are entered (as “NA”), they will be replaced in the computation by imputed values (imputation is performed by MCMC sampling). A sub-sample (at the moment a thousand) of the imputed data value is written to a text file (named `missing_data.out`)

likelihood

If data are supplied, their likelihood function must also be specified with the following syntax:

```
likelihood = dirichlet | normal_gamma | zellner;.
```

where “|” means “or”.

- The keyword `dirichlet` should be used for discrete data only. It specifies a Dirichlet-multinomial model (See [\[Bibliographic References\]](#), [page 25](#), [\[Bibliographic References\]](#), [page 25](#), [\[Bibliographic References\]](#), [page 25](#)). In that case the data have to be coded by integers from zero to n . The number of levels for each node has to be specified using an `[nData_levels]`, [page 20](#) declaration. The Dirichlet hyper-parameters are internally set to one, specify a uniform prior on configurations of parents for any node.
- The keyword `normal_gamma` specifies a vague normal-gamma prior for the regression parameters describing the dependance of children nodes with respect to their parents. Such a prior and model can be used for continuous or discrete data.
- The keyword `zellner` specifies a Zellner prior for the normal regression model (based on our experience, we do not recommend it though). One of its drawbacks is that any node cannot have more parents than there are data about it (arguably, an artificial constraint).

n_data_levels, nData_levels

If a Dirichlet-multinomial model is used, discrete data have to be specified for each node. Such data have to be coded as integers from zero to n , n being the number of levels for a given node. Those levels are specified using the `n_data_levels` [\[array\]](#), [page 22](#) declaration.


```
n_data_levels = array{2, 2, 3, 2, 4};
```

`alpha_normal_gamma`

The parameter `alpha_normal_gamma` corresponds to the prior shape of the Gamma distribution of the data precision in the Normal-Gamma regression model. It can be set to any positive floating point value. By default its value is 1.5, which works well in our hands. You may want to tailor it to your needs.

`beta_normal_gamma`

The parameter `beta_normal_gamma` corresponds to the prior rate of the Gamma distribution of the data precision in the Normal-Gamma regression model. It can be set to any positive floating point value. By default its value is 1000, which is rather vague and works well in our hands.

`gamma_zellner`

The tuning parameter `gamma_zellner` can be set to any positive floating point value. When it is equal to the number of data points per node, the data and Zellner prior on the regression parameters have equal weight. By default its value is 1.0.

4.2.4 Variables specifying outputs

`save_chain, bsave_the_chain`

The MCMC sampling chain can be saved in binary format to a file (named `results_mcmc.bin`) by setting `save_chain` to 1 or `true`. By default, the chain is not saved. Beware, MCMC chains can be very large, even though the recording format is very compact: `results_mcmc.bin` starts with the number of nodes in the graph (as a binary integer, *i.e.* a byte), followed by the value of the adjacency matrix (`n_nodes` by `n_nodes` bytes) at the end of burn-in period, followed by a one-byte encoding of the difference between successive adjacency matrices. The difference d between adjacency matrices (equal to -1 for removing an edge, +1 for adding an edge) and its location $[i, j]$ are encoded as: $(i + j * n_nodes + 1) * d$. No difference is encoded as zero. The `results_mcmc.bin` file can be used to recreate the successive adjacency matrices sampled.

`n_saved_adjacency, nSaved_adjacency`

The user can request the output of a number `n_saved_adjacency` (integer) of randomly generated adjacency matrices. Those matrices are saved at regularly spaced iterations along the MCMC chain (after the burn-in period) in the file `graph_samples.out` in text format, along with the logarithms of the prior probability, data likelihood (if data were specified) and posterior probability. A value of 1 for element $[i, j]$ (that is, on the i th row and j th column) indicates that node i is parent of node j . By default `n_saved_adjacency` is zero and no matrices are recorded.

`save_best_graph, bsave_best_graph`

By setting `save_best_graph` to `true`, the user can request the output of the adjacency matrix of the graph having the highest posterior probability among all random graphs generated after the burn-in period. That matrix is saved in the file `best_graph.out` in text

format, along with the logarithmes of its prior probability, data likelihood (if data were specified) and posterior probability. By default `saved_best_graph` is `false`.

`save_the_edge_probabilities, bsave_the_edge_probabilities`

Setting `save_the_edge_probabilities` to `true`, forces the output of a matrix of the individual edge probabilities in the file `edge_p.out`, in text format. By default `save_the_edge_probabilities` is `false`.

`save_the_degree_counts, bsave_the_degree_counts`

Setting `save_the_degree_counts` to `true`, forces the output of a count of the nodes' degrees in the graphs sampled after the burn-in period to the file `degree_count.out`, in text format. By default `saved_the_degree_counts` is `false`.

`save_the_motifs_probabilities, bsave_the_motifs_probabilities`

Setting `save_the_motifs_probabilities` to `true`, forces the output (to the file `motifs_count.out`, in text format) of a count of triangular feed-forward and feedback loops in the graphs sampled after the burn-in period. By default `saved_the_motifs_probabilities` is `false`.

4.3 Reserved keywords

The following keywords can be used in Graph_Sampler input files:

array keyword

This keyword is used for vector definition. Example:

```
n_data_levels = array {2, 2, 1+1};
```

dirichlet keyword

This keyword should be used in the case of discrete data, to specify a Dirichlet prior (syntax: `likelihood = dirichlet;`).

empty keyword

This keyword can be used to create an empty initial adjacency matrix (syntax: `matrix{empty};`).

equanimous keyword

This keyword can be used to create a prior matrix on edge probabilities (`hyper_pB`) with all elements set to 0.5 when `bayesian_network` is `false`. If `bayesian_network` is `true` the diagonal elements will be set to zero and the others to 0.5. (syntax: `matrix{equanimous};`).

false (or False or FALSE) keyword

This keyword is equivalent to zero and can be used when assigning variables.

full keyword

This keyword can be used to create a full initial adjacency matrix (all elements at 1, except a zeroed diagonal in Bayesian networks) (syntax: `matrix{full};`).

matrix keyword

This keyword is used for matrix definition. Example:

```
data = matrix {1.1, 1.3, 1.4, 1.35,  
              2.1, 2.4, 2.5, 2.45,  
              3.4, 3.6, 3.8, 3.85};
```

mersenne_twister keyword

This keyword can be used to specify that the Mersenne twister pseudo-random number generator will be used (syntax: `random_generator = mersenne_twister;`).

NA keyword

This keyword should be used instead of a number to indicate that a data value is missing. It can only be used within a data matrix.

normal_gamma keyword

This keyword should be used in the case of continuous data, to specify a Normal-Gamma prior (syntax: `likelihood = normal_gamma;`).

random keyword

This keyword can be used to create a random initial adjacency matrix (all elements 0 or 1 at random, except a zeroed diagonal in Bayesian networks) (syntax: `matrix{random};`).

true (or True or TRUE) keyword

This keyword is equivalent to 1 and can be used when assigning variables.

tausworthe keyword

This keyword can be used to specify that the Tausworthe pseudo-random number generator will be used (syntax: `random_generator = tausworthe;`).

zellner keyword

This keyword should be used in the case of continuous data, to specify a Zellner prior (syntax: `likelihood = zellner;`).

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