Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II. *doi: 10.18637/jss.v000.i00*

Making, Updating, and Querying Causal Models using **`CausalQueries`**

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Abstract

The R package `CausalQueries` can be used to make, update, and query causal models defined on binary nodes. Users provide a causal statement of the form `X -> M <- Y; M <-> Y` which is interpreted as a structural causal model over a collection of binary nodes. Then `CausalQueries` allows users to (1) identify the set of principal strata—causal types—required to characterize all possible causal relations between nodes that are consistent with the causal statement (2) determine a set of parameters needed to characterize distributions over these causal types (3) update beliefs over distributions of causal types, using a `stan` model plus data, and (4) pose a wide range of causal queries of the model, using either the prior distribution, the posterior distribution, or a user-specified candidate vector of parameters.

Keywords: causal model, Bayesian updating, DAG, Stan.

1. Introduction: Causal models

`CausalQueries` is an R package that lets users make, update, and query causal models. Users provide a structural causal model in the form of a statement that reports a set of binary variables and the relations of causal ancestry between them. Once such a statement is provided to `make_model()`, `CausalQueries` generates a parameter vector that fully describes a probability distribution over all possible types of causal relations between variables ("causal types"). Given a prior distribution over parameters—equivalently, over causal models consistent with the structural model— and data on some or all nodes, `update_model()` deploys a Stan (Carpenter, Gelman, Hoffman, Lee, Goodrich, Betancourt, Brubaker, Guo, Li, and Riddell 2017) model to generate a posterior distribution over causal models. The function `query_model()` can then be used to ask a wide range of causal queries, using either the prior distribution, the posterior distribution, or a user-specified candidate vector of parameters.

In the next section we provide a motivating example. We then describe how the package relates to existing available software. Section 4 gives an overview of the statistical model behind the package. Section 5, Section 6, and Section 7 then describe, in turn, the functionality for making, updating, and querying causal models. We provide further computation details in the final section.

2. Motivating example

Before providing details on package functionality, we illustrate the three core functions of the package by showing how to use `CausalQueries` to replicate the analysis in (Chickering and Pearl 1996; see also Humphreys and Jacobs 2023). Chickering and Pearl (1996) seek to draw inferences on causal effects in the presence of imperfect compliance. We have access to an instrument Z (a randomly assigned prescription for cholesterol medication), which is a cause of X (treatment uptake) but otherwise unrelated to Y (cholesterol). We imagine we are interested in three specific queries. The first is the average causal effect of X on Y. The second is the average effect for units for which $X = 0$ and $Y = 0$. The last is the average effect for "compliers": units for which X responds positively to Z. Thus two of these queries are conditional queries, with one conditional on a counterfactual quantity.

The data on Z, X, and Y is given in Chickering and Pearl (1996) and is also included in the `CausalQueries` package. The data is complete for all units and looks as follows:

```
R> data("lipids_data")
R>
R> lipids_data

#>    event strategy count
#> 1 Z0X0Y0      ZXY   158
#> 2 Z1X0Y0      ZXY    52
#> 3 Z0X1Y0      ZXY     0
#> 4 Z1X1Y0      ZXY    23
#> 5 Z0X0Y1      ZXY    14
#> 6 Z1X0Y1      ZXY    12
#> 7 Z0X1Y1      ZXY     0
#> 8 Z1X1Y1      ZXY    78
```

This data is reported in "compact form," meaning it records the number of units ("count") that display each possible pattern of outcomes on the three variables ("event"). The "strategy" column records the set of variables for which data has been recorded. In this illustration the data is complete and so the implied strategy is `ZXY` for all units.

`CausalQueries` then allows users to create the model, input data, and update the model as follows:

```
R> lipids_model <-
+   make_model("Z -> X -> Y; X <-> Y") |>
+   update_model(lipids_data)
```

Finally, the model can then be queried:

```
R> lipids_queries <-
+   lipids_model  |>
+   query_model(query = "Y[X=1] - Y[X=0]",
+               given = c("All",  "X==0 & Y==0", "X[Z=1] > X[Z=0]"),
+               using = "posteriors")
```

Here three distinct queries are posed, with the queries differing in the type of conditioning imposed.

The output is a data frame with estimates, posterior standard deviations, and credibility intervals. Table 1 shows the output from the analysis of the lipids data. Rows 1 and 2 in the table replicate results in Chickering and Pearl (1996); row 3 returns inferences for complier average effects.

Table 1: Replication of Chickering and Pearl (1996).

query	given	mean	sd	cred.low	cred.high
Y[X=1] - Y[X=0]	-	0.55	0.10	0.37	0.73
Y[X=1] - Y[X=0]	X==0 & Y==0	0.64	0.15	0.37	0.88
Y[X=1] - Y[X=0]	X[Z=1] > X[Z=0]	0.70	0.05	0.59	0.80

As we describe below, the same basic procedure of making, updating, and querying models, can be used (up to computational constraints) for arbitrary causal models, for different types of data structures, and for all causal queries that can be posed of the causal model.

3. Connections to existing packages

The literature on causal inference and its software ecosystem is large, spanning the social and natural sciences as well as computer science and applied mathematics. Here we contextualize the scope and functionality of `CausalQueries` within the subset of the causal inference domain addressing the evaluation of causal queries on causal models encoded as directed acyclic graphs (DAGs) or structural equation models (SEMs). Table 2 provides an overview of relevant software and discusses key connections, advantages and disadvantages with respect to `CausalQueries`.

Table 2: Related software.

Software	Source	Language	Availability	Scope
`causalnex`	Beaumont, Horsburgh, Pilgerstorfer, Droth, Oentaryo, Ler, Nguyen, Ferreira, Patel, and Leong (2021)	Python	• pip	• causal structure learning • querying marginal distributions • discrete data
`pclag`	Kalisch, Mächler, Colombo, Maathuis, and Bühlmann (2012)	R	• CRAN • GitHub	• causal structure learning • ATEs under linear conditional expectations, no hidden selection
`DoWhy`	Sharma and Kiciman (2020)	Python	• pip	• identification • average and conditional causal effects • robustness checks
`autobounds`	Duarte, Finkelstein, Knox, Mummolo, and Shpitser (2023)	Python	• Docker • GitHub	• bounding causal effects • partial identification • DAG canonicalization • binary data
`causaloptim`	Sachs, Jonzon, Sjölander, and Gabriel (2023)	R	• CRAN • GitHub	• bounding causal effects • non-identified queries • binary data

`causalnex` is a comprehensive software that offers a suite of functions for the discovery and querying of causal models. Like `CausalQueries`, it uses Bayesian methods and allows users to use "`do` calculus" (Pearl 2009). The parameters of focus are conditional probability distribution tables rather than principal strata (causal types). This approach limits the types of queries that can be posed and the kinds of expert information that can be incorporated. For instance, knowledge of conditional probability distributions are not sufficient to make claims about (or provide priors with respect to) effect monotonicity, complier effects, or the "probability of causation" (Dawid, Musio, and Murtas 2017). However it makes it possible to address simple queries efficiently with much larger models.

Like `causalnex`, `pclag` places particular emphasis on learning about causal structures, utilizing the resultant DAGs to recover average treatment effects (ATEs) across all learned Markov-equivalent classes implied by observed data that satisfy linearity of conditional expectations. This approach again is more restrictive than `CausalQueries` in the queries it allows.

DoWhy is a feature-rich framework that emphasizes causal identification, causal effect estimation, and assumption validation. Given a user-specified DAG, it deploys do-calculus to find expressions that identify desired causal-effects via Back-door, Front-door, IV and mediation identification criteria and leverages the identified expression and standard estimators to estimate the desired estimand. Following estimation, DoWhy deploys a comprehensive refutation engine implementing a large set of robustness tests. While this approach allows it to efficiently handle varied data types on large causal models, the decision to not parameterize the DAG itself places substantial limitations on the types of queries that can be posed.

The packages bearing the greatest resemblance to CausalQueries for model definition are autobounds and causaloptim. Dealing with discrete causal models, their definitions of principal strata (causal types) and the resultant set of causal relations on the DAG are very close to those of CausalQueries. Differences in model definition arise for disturbance terms and confounding being defined implicitly by the causal statement in CausalQueries vs explicitly via separate disturbance nodes in autobounds and causaloptim. While CausalQueries assumes canonical form for input DAGs, autobounds and causaloptim facilitate canonicalization. The essential difference between the methods; however, lies in their approach to evaluating queries.

Both autobounds and causaloptim build on seminal approaches in Balke and Pearl (1997) to construct bounds on queries, using constrained polynomial and linear optimization respectively. In contrast, CausalQueries utilizes Bayesian inference to generate a posterior over the causal model which is then queried (consistent with Chickering and Pearl 1996; Zhang, Tian, and Bareinboim 2022). A key difference is the target of inference. The polynomial and linear programming approach to querying is in principle suited to handling larger causal models, though given their similarity in model parameterization, autobounds, causaloptim and CausalQueries face similar constraints induced by parameter spaces expanding rapidly with model size. The Bayesian approach to model updating and querying holds the efficiency advantage that a model can be updated once and queried arbitrarily, while expensive optimization runs are required for each separate query in autobounds and causaloptim.

Summarizing, the particular strength of CausalQueries is to allow users to specify arbitrary DAGs, to specify arbitrary queries defined on the DAG, and use the same canonical procedure to form Bayesian posteriors over those queries whether or not the queries are identified. Thus, for example, if researchers are interested in learning about a quantity like the local average treatment effect and their model satisfies the conditions in Angrist, Imbens, and Rubin (1996), then updating will recover valid estimates as data grows even if researchers are unaware that the local average treatment effect is identified and are ignorant of bespoke estimation procedure proposed by Angrist *et al.* (1996).

There are two broad limitations on the sets of models handled natively by CausalQueries. First, CausalQueries is designed for models with a relatively small number of binary nodes. Because there is no compromise made on the space of possible causal relations implied by a given model, the parameter space grows very rapidly with the complexity of the causal model. The complexity growth depends on the causal structure and grows rapidly with the number of parents affecting a given child. A chain model of the form $A \to B \to C \to D \to E$ has just 40 parameters. A model in which A, B, C, D are all direct ancestors of E has $65,544$ parameters. Moving from binary to nonbinary nodes has similar effects. The restriction to binary nodes is for computational and not conceptual reasons.[1]

Second, the package is geared towards learning about populations from independently sampled units from populations. Thus the basic setup does not address problems of clustering, hierarchical structures, or purposive sampling. The broader framework can however be used for these purposes (see section 9.4 of Humphreys and Jacobs 2023). The targets of inference are usually case-level quantities or population quantities and `CausalQueries` is not well suited for estimating sample quantities.

4. Statistical model

The core conceptual framework used by `CausalQueries` is that described in Pearl's *Causality* (Pearl 2009). It can be summarized as follows (using notation from Humphreys and Jacobs 2023):

Definition 1 *A "**causal model**" is:*

1. *an ordered collection of "endogenous nodes"* $Y = \{Y_1, Y_2, \dots, Y_n\}$
2. *an ordered collection of "exogenous nodes"* $\Theta = \{\theta^{Y_1}, \theta^{Y_1}, \dots, \theta^{Y_n}\}$
3. *a collection of functions* $F = \{f_{Y_1}, f_{Y_2}, \dots, f_{Y_n}\}$ *with* f_{Y_j} *specifying, for each* j*, how outcome* Y_j *depends on* θ_j *and realizations of endogenous nodes prior to* Y_j*.*
4. *a probability distribution,* λ*, over* Θ*.*

By default, `CausalQueries` assumes endogenous nodes to be binary. When we specify a causal structure we specify which endogenous nodes are (possibly) direct causes of a node, Y_j, given other nodes in the model. These nodes are called the parents of Y_j, PA_j (we use upper case PA_j to indicate the collection of nodes and use lower case pa_j to indicate a particular set of values that these nodes might take on). With discrete valued nodes, it is possible to identify all possible ways that a node might respond to its parents. We refer to the ways that a node responds as "nodal type."

If node i can take on k_i possible values then the set of possible values that can be taken on by parents of j is $m_j := \prod_{i \in PA_j} k_i$. Then there are $k_j^{m_j}$ different ways that node j might respond to its parents. In the case of binary nodes, this becomes $2^{\left(2^{|PA_j|}\right)}$. Thus for an endogenous node with no parents, there are 2 nodal types, for a binary node with one binary parent there are four types, for a binary node with 2 parents there are 16, and so on.

The set of all possible causal reactions of a given unit to all possible values of parents is then given by its collection of nodal types at each node. We call this collection a unit's "causal

[1] For more on computation constraints and strategies to update and query large models see the associated package `CausalQueriesTools` available via `devtools::install_github("till-tietz/CausalQueriesTools")`. The core approach used here is to divide large causal models into modules, update on modules and reassemble to pose queries. Also, see section 9.4.1 of Humphreys and Jacobs (2023) for an approach that codes non-binary data as a profile of outcomes on multiple binary nodes.

type", θ. These causal types correspond to the principal strata, familiar, for instance, from the study of instrumental variables (Frangakis and Rubin 2002).

The approach used by `CausalQueries` is to let the domain of exogenous nodes θ^{Y_j} be co-extensive with the number of nodal types for Y_j. Function f^j then determines the value of y by simply reporting the value of Y_j implied by the nodal type and the values of the parents of Y_j. Thus if $\theta^j_{pa_j}$ is the value for j when parents have values pa_j, then we have that $f_{Y_j}(\theta^j, pa_j) = \theta^j_{pa_j}$. The practical implication is that, given the causal structure, learning about the model reduces to learning about the distribution, λ, over the nodal types.

In cases in which there is no unobserved confounding, we take the probability distributions over the nodal types for different nodes to be independent: $\theta^i \perp\!\!\!\perp \theta^j, i \neq j$. In this case we use a categorical distribution to specify $\lambda^j_x := \Pr(\theta^j = \theta^j_x)$. From independence then we have that the probability of a given causal type θ_x is $\prod_{i=1}^n \lambda^i_x$. For instance $\Pr(\theta = (\theta^X_1, \theta^Y_{01})) = \Pr(\theta^X = \theta^X_1) \Pr(\theta^Y = \theta^Y_{01}) = \lambda^X_1 \lambda^Y_{01}$.

In cases in which there is confounding, the logic is the same except that we need to specify enough parameters to capture the joint distribution over nodal types for different nodes. We do this by making use of the causal structure.

As an example, for the Lipids model, the joint distribution of nodal types can be simplified as in Equation 1.

$$\Pr(\theta^Z = \theta^Z_1, \theta^X = \theta^X_{10}, \theta^Y = \theta^Y_{11}) = \Pr(\theta^Z = \theta^Z_1) \Pr(\theta^X = \theta^X_{10}) \Pr(\theta^Y = \theta^Y_{11} | \theta^X = \theta^X_{10}) \quad (1)$$

And so, for this model, λ would include parameters that represent $\Pr(\theta^Z)$ and $\Pr(\theta^X)$ but also the conditional probability $\Pr(\theta^Y | \theta^X)$:

$$\Pr(\theta^Z = \theta^Z_1, \theta^X = \theta^X_{10}, \theta^Y = \theta^Y_{11}) = \lambda^Z_1 \lambda^X_{10} \lambda^{Y|\theta^X_{10}}_{11} \quad (2)$$

Representing beliefs *over causal models* thus requires specifying a probability distribution over λ. This might be a degenerate distribution if users want to specify a particular model. `CausalQueries` also allows users to specify parameters, α of a Dirichlet distribution over λ^j, for each node Y^j (and similarly for conditional distributions in the case of confounding). If all entries of α are 0.5 this corresponds to Jeffreys priors. The default behavior is for `CausalQueries` to assume a uniform distribution – that is, that all nodal types are equally likely – which corresponds to α being a vector of 1s.[2]

Updating is then done with respect to beliefs over λ. In the Bayesian approach we have:

$$p(\lambda | D) = \frac{p(D|\lambda) p(\lambda)}{\int_{\lambda'} p(D|\lambda') p(\lambda')}$$

where $p(D|\lambda')$ is calculated under the assumption that units are exchangeable and independently drawn. In practice this means that the probability that two units have causal

[2]We note that, while flexible, using the Dirichlet distribution does constrain the types of priors that can be represented; see Irons and Cinelli (2023) for a discussion of constraints and an approach to incorporating still richer prios using multiple Beta distributions.

types θ_i and θ_j is simply $\lambda'_i\lambda'_j$. Since a causal type fully determines an outcome vector $d = \{y_1, y_2, \dots, y_n\}$, the probability of a given outcome ("event"), w_d, is given simply by the probability that the causal type is among those that yield outcome d. Thus, from λ we can calculate a vector of event probabilities, $w(\lambda)$, for each vector of outcomes, and under independence, we have:

$$D \sim \text{Multinomial}(w(\lambda), N)$$

Thus for instance in the case of an $X \rightarrow Y$ model, and letting w_{xy} denote the probability of a data type $X = x, Y = y$, the event probabilities are:

$$w(\lambda) = \begin{cases} w_{00} & = & \lambda^X_0(\lambda^Y_{00} + \lambda^Y_{01}) \\ w_{01} & = & \lambda^X_0(\lambda^Y_{11} + \lambda^Y_{10}) \\ w_{10} & = & \lambda^X_1(\lambda^Y_{00} + \lambda^Y_{10}) \\ w_{11} & = & \lambda^X_1(\lambda^Y_{11} + \lambda^Y_{01}) \end{cases}$$

For a more complex example Table 3 illustrates key values for the Lipids model. We see here that we have two types for node Z, four for X (representing the strata familiar from instrumental variables analysis: never takers, always takers, defiers, and compliers) and 4 for Y. For Z and X we have parameters corresponding to probability of these nodal types. For instance `Z.0` is the probability that $Z = 0$. `Z.1` is the complementary probability that $Z = 1$. Things are a little more complicated for distributions on nodal types for Y however: because of confounding between X and Y we have parameters that capture the conditional probability of the nodal types for Y *given* the nodal types for X. We see there are four sets of these parameters.

Table 3: Nodal types and parameters for Lipids model.

node	nodal_type	param_set	param_names	param_value	priors
Z	0	Z	Z.0	0.57	1
Z	1	Z	Z.1	0.43	1
X	00	X	X.00	0.24	1
X	10	X	X.10	0.30	1
X	01	X	X.01	0.20	1
X	11	X	X.11	0.27	1
Y	00	Y.X.00	Y.00_X.00	0.71	1
Y	10	Y.X.00	Y.10_X.00	0.19	1
Y	01	Y.X.00	Y.01_X.00	0.00	1
Y	11	Y.X.00	Y.11_X.00	0.10	1
Y	00	Y.X.01	Y.00_X.01	0.15	1
Y	10	Y.X.01	Y.10_X.01	0.40	1
Y	01	Y.X.01	Y.01_X.01	0.39	1
Y	11	Y.X.01	Y.11_X.01	0.06	1
Y	00	Y.X.10	Y.00_X.10	0.17	1
Y	10	Y.X.10	Y.10_X.10	0.65	1

Y	01	Y.X.10	Y.01_X.10	0.14	1
Y	11	Y.X.10	Y.11_X.10	0.04	1
Y	00	Y.X.11	Y.00_X.11	0.24	1
Y	10	Y.X.11	Y.10_X.11	0.71	1
Y	01	Y.X.11	Y.01_X.11	0.04	1
Y	11	Y.X.11	Y.11_X.11	0.01	1

The next to final column shows a sample set of parameter values. Together, the parameters describe a full joint probability distribution over types for Z, X and Y that is faithful to the graph.

These parameters again imply a probability distribution over data types. For instance the probability of data type $Z = 0, X = 0, Y = 0$ is:

$$w_{000} = \Pr(Z = 0, X = 0, Y = 0) = \lambda^Z_0 \lambda^X_{00} (\lambda^{Y|\lambda^X_{00}}_{00} + \lambda^{Y|\lambda^X_{00}}_{01}) + \lambda^Z_0 \lambda^X_{01} (\lambda^{Y|\lambda^X_{01}}_{00} + \lambda^{Y|\lambda^X_{01}}_{01})$$

The value of the `CausalQueries` package is that it allows users to specify arbitrary models of this form, figure out all the implied nodal types and causal types, and then update given priors and data by calculating event probabilities implied by all possible parameter vectors and in turn the likelihood of the data given the model. In addition, the package allows for arbitrary querying of a model to assess the values of estimands of interest that are a function of the values or counterfactual values of nodes, *conditional* on values or counterfactual values of nodes.

The following sections review key functionality for making, updating, and querying causal models.

5. Making models

A model is defined in one step in `CausalQueries` using a `dagitty` type syntax (Textor, van der Zander, Gilthorpe, Liśkiewicz, and Ellison 2016) in which the model structure is provided in the form of a causal statement. For instance:

```
R> model <- make_model("X -> M -> Y <- X")
```

The statement provides the names of nodes as well as arrows ("`->`" or "`<-`") connecting nodes and indicating whether one node is a potential cause of another, i.e., whether a given node is a "parent" or "child" of another. Formally, a statement like this is interpreted as:

1. Functional equations:
   - $Y = f_Y(M, X, \theta^Y)$
   - $M = f_M(X, \theta^M)$
   - $X = f_X(\theta^X)$
2. Distributions on Θ:

   - $\Pr(\theta^i = \theta^i_k) = \lambda^i_k$

3. Independence assumptions:

   - $\theta_i \perp\!\!\!\perp \theta_j, i \neq j$

In addition, as we did in the Chickering and Pearl (1996) example, it is possible to use two-headed arrows ("`<->`") to indicate "unobserved confounding," that is, the presence of an unobserved variable that might influence two or more observed variables. In this case, condition 3 above is relaxed, and the exogenous nodes associated with confounded variables have a joint distribution. We describe how this is done in greater detail in Section 5.3.1.

5.1. Graphing

Plotting the model can help check that you have defined the structure of the model correctly. `CausalQueries` provides simple graphing tools that draw on functionality from the `dagitty`, `ggplot2`, and `ggdag` packages.

Once defined, a model can be graphed by calling the `plot()` method on the objects with class `causal_model`. This method is a wrapper for the `plot_model()` function and accepts additional options described in `?plot_model`.

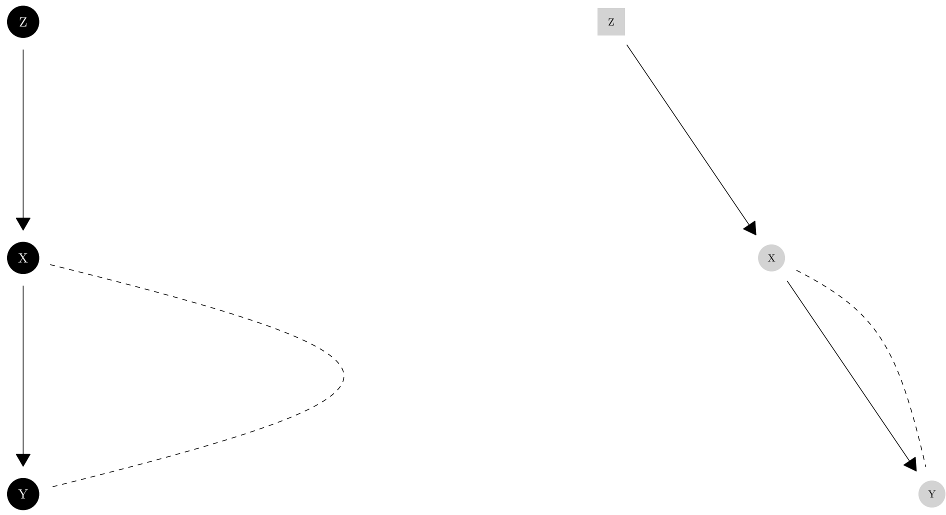
Figure 1 shows figures generated by plotting `lipids_model` with and without options. The plots have class `c("gg", "ggplot")` and so will accept any additional layers available for the objects of class `ggplot`.

```
R> lipids_model |> plot()
R>
R> lipids_model |>
+   plot(x_coord = 1:3,
+        y_coord = 3:1,
+        textcol = "black",
+        textsize = 3,
+        shape = c(15, 16, 16),
+        nodecol = "lightgrey",
+        nodesize = 10)
```

5.2. Model inspection

When a model is defined, `CausalQueries` generates a set of internal objects that are used for all inferential tasks. These include default parameter values and default priors, as well as matrices that map from parameters to causal types, and from causal types to data types. These objects generally do not need to be examined by the users, however `CausalQueries` provides a pair of functions, `inspect()` and `grab()`, that lets users quickly examine these elements

Table 4 summarizes features of a causal model that can be examined using `inspect()`.



(a) Without options (b) With options

Figure 1: Examples of model graphs.

Table 4: Elements of a model that can be inspected using `inspect()`.

Element	Description
`statement`	A character string describing causal relations using dagitty syntax.
`nodes`	A list containing the nodes in the model.
`parents_df`	A table listing nodes, whether they are root nodes or not, and the number and names of parents they have.
`parameters`	A vector of 'true' parameters.
`parameter_names`	A vector of names of parameters.
`parameter_mapping`	A matrix mapping from parameters into data types.
`parameter_matrix`	A matrix mapping from parameters into causal types.
`parameters_df`	A data frame containing parameter information.
`causal_types`	A data frame listing causal types and the nodal types that produce them.
`nodal_types`	A list with the nodal types of the model.
`data_types`	A list with all data types consistent with the model; for options see `?get_all_data_types`.
`ambiguities_matrix`	A matrix mapping from causal types into data types.
`type_prior`	A matrix of type probabilities using priors.
`prior_hyperparameters`	A vector of alpha values used to parameterize Dirichlet prior distributions; optionally provide node names to reduce output, e.g., `inspect(prior_hyperparameters, nodes = c('M', 'Y'))`.

Element	Description
`prior_event_probabilities`	A vector of data (event) probabilities given a single realization of parameters; for options see `?get_event_probabilities`.
`prior_distribution`	A data frame of the parameter prior distribution.
`posterior_distribution`	A data frame of the parameter posterior distribution.
`posterior_event_probabilities`	A sample of data (event) probabilities from the posterior.
`type_distribution`	A matrix of type probabilities using posteriors.
`data`	A data frame with data that was provided to update the model.
`stanfit`	A `stanfit` object generated by Stan; prints `stanfit` summary with updated parameter names.
`stan_summary`	A list of Stan outputs that includes `stanfit`, `data`, and, if requested when updating the model, posterior `event_probabilities` and `type_distribution`; prints `stanfit` summary with updated parameter names.

5.3. Tailoring models

When a causal statement is provided to `make_model()`, a model is formed with a set of default assumptions: in particular, no restrictions are placed on nodal types and flat priors are assumed over all parameters. These features can be adjusted after a model is formed using `set_confounds`, `set_restrictions`, `set_priors`, and `set_parameters`.

Allowing confounding

Unobserved confounding between two (or more) nodes arises when the nodal types for the nodes are not independent. For instance, in the $X \rightarrow Y$ graph, there are 2 nodal types for X and 4 for Y. There are thus 8 joint nodal types (or causal types), as shown in Table 5.

Table 5: Nodal types in $X \rightarrow Y$ model.

	θ_0^X	θ_1^X	$\sum$
θ_{00}^Y	$\Pr(\theta_0^X, \theta_{00}^Y)$	$\Pr(\theta_1^X, \theta_{00}^Y)$	$\Pr(\theta_{00}^Y)$
θ_{10}^Y	$\Pr(\theta_0^X, \theta_{10}^Y)$	$\Pr(\theta_1^X, \theta_{10}^Y)$	$\Pr(\theta_{10}^Y)$
θ_{01}^Y	$\Pr(\theta_0^X, \theta_{01}^Y)$	$\Pr(\theta_1^X, \theta_{01}^Y)$	$\Pr(\theta_{01}^Y)$
θ_{11}^Y	$\Pr(\theta_0^X, \theta_{11}^Y)$	$\Pr(\theta_1^X, \theta_{11}^Y)$	$\Pr(\theta_{11}^Y)$
$\sum$	$\Pr(\theta_0^X)$	$\Pr(\theta_1^X)$	1

Table 5 has eight interior elements so that an unconstrained joint distribution would have seven degrees of freedom. A no-confounding assumption means that $\Pr(\theta^X, \theta^Y) =$

$\Pr(\theta^X)\Pr(\theta^Y)$. In this case, it is sufficient to put a distribution on the marginals, and there would be 3 degrees of freedom for Y and 1 for X, totaling 4 rather than 7.

To allow for an unconstrained joint distribution the parameters data frame for this model would have two parameter families for parameters associated with the node Y. Each family captures the conditional distribution of Y's nodal types, given X. For instance the parameter `Y01_X.1` can be interpreted as $\Pr(\theta^Y = \theta^Y_{01}|\theta^X = 1)$. See again Table 3 for an example of a parameter matrix with confounding.

The confounding structure can affect the number of parameters given the underlying DAG. Table 6 illustrates the number of independent parameters required given different types of confounding.

Table 6: Number of different independent parameters (degrees of freedom) for different three-node models.

Model	Degrees of freedom
`X -> Y <- W`	17
`X -> Y <- W; X <-> W`	18
`X -> Y <- W; X <-> Y; W <-> Y`	62
`X -> Y <- W; X <-> Y; W <-> Y; X <-> W`	63
`X -> W -> Y <- X`	19
`X -> W -> Y <- X; W <-> Y`	64
`X -> W -> Y <- X; X <-> W; W <-> Y`	67
`X -> W -> Y <- X; X <-> W; W <-> Y; X <-> Y`	127

Setting restrictions

Sometimes it is helpful to constrain the set of types. In `CausalQueries` this is done at the level of nodal types, with restrictions on causal types following restrictions on nodal types.

To illustrate, in analyses of data with imperfect compliance, as in our Lipids model example, it is common to impose a monotonicity assumption: that X does not respond negatively to Z. This is one of the conditions needed to interpret instrumental variables estimates as (consistent) estimates of the complier average treatment effect. In `CausalQueries` we can impose this assumption as follows:

```
R> model_restricted <-
+  lipids_model |>
+  set_restrictions("X[Z=1] < X[Z=0]")
```

In words: we restrict the model by removing types for which X decreases in Z. If we wanted to retain only this nodal type rather than remove it, we could do so by passing `keep = TRUE` as an argument to the `set_restrictions()` function call. Users can use `inspect(model, "parameter_matrix")` to view the resulting parameter matrix in which both the set of parameters and the set of causal types are restricted.

Restrictions in `CausalQueries` can be set in many other ways:

- Using nodal type labels:

```
R> model <-
+   lipids_model |>
+   set_restrictions(labels = list(X = "01", Y = c("00", "01", "11")),
+                    keep = TRUE)
```

- Using wildcards in nodal type labels:

```
R> model <- lipids_model |>
+   set_restrictions(labels = list(Y = "?0"))
```

- In models with confounding, restrictions can be added to nodal types conditional on the values of other nodal types using a `given` argument:

```
R> model <- lipids_model |>
+   set_restrictions(labels = list(Y = c('00', '11')), given = 'X.00')
```

Setting restrictions sometimes involves using causal syntax (see Section 7.2 for a guide to the syntax used by `CausalQueries`). The help file in `?set_restrictions` provides further details and examples of restrictions users can set.

Setting Priors

Priors on model parameters can be added to the parameters data frame and interpreted as alpha parameters of a Dirichlet distribution. The Dirichlet distribution is a probability distribution over an $n-1$ dimensional unit simplex. It can be considered a generalization of the Beta distribution and is parametrized by an n-dimensional positive vector α. Thus, for example a Dirichlet with $\alpha = (1, 1, 1, 1, 1)$ gives a probability distribution over all non-negative 5-dimensional vectors that sum to 1, e.g. $(0.1, 0.1, 0.1, 0.1, 0.6)$ or $(0.1, 0.2, 0.3, 0.3, 0.1)$. This particular value for α implies that all such vectors are equally likely. Other values for α can be used to control the expectation and certainty for each dimension. For instance, the vector $\alpha = (100, 1, 1, 1, 100)$ would result in more weight on distributions that are close to $(0.5, 0, 0, 0, 0.5)$.

In `CausalQueries`, priors are generally specified over the distribution of nodal types.[3] For instance, in a model represented by $X \rightarrow Y$, we have one Dirichlet distribution over the two types for θ^X and one Dirichlet distribution over the four types for θ^Y.

Importantly, it is implicitly assumed that priors are independent across families. Thus, for instance, in a model represented by $X \rightarrow Y$, we specify beliefs over λ^X and over λ^Y separately. `CausalQueries` does not let users specify correlated beliefs over these parameters.[4]

Prior hyperparameters are set to unity by default, corresponding to uniform priors. Users can retrieve the model's priors as follows:

[3] If there is confounding in the model, priors are specified over the conditional distribution of nodal types.

[4] Users can specify beliefs about λ^Y given θ^X if a model involves possible confounding. But this statement is about beliefs over a joint distribution, not jointly distributed beliefs.

```
R> lipids_model |>
+   inspect("prior_hyperparameters", nodes = "X")
```

```
#>
#> Alpha parameter values used for Dirichlet prior distributions:
#>
#> X.00 X.10 X.01 X.11
#>    1    1    1    1
```

Alternatively users can set Jeffreys priors using `set_priors()` as follows:

```
R> model <- lipids_model |>
+   set_priors(distribution = "jeffreys")
```

Users can also provide custom priors. The simplest way to specify custom priors is to add them as a vector of numbers using `set_priors()`. For instance:

```
R> lipids_model |>
+   set_priors(node = "X", alphas = 1:4) |>
+   inspect("prior_hyperparameters", nodes = "X")
```

```
#>
#> Alpha parameter values used for Dirichlet prior distributions:
#>
#> X.00 X.10 X.01 X.11
#>    1    2    3    4
```

The priors here should be interpreted as indicating $\alpha_X = (1, 2, 3, 4)$, which implies a distribution over $(\lambda^X_{00}, \lambda^X_{10}, \lambda^X_{01}, \lambda^X_{11})$ with expectation $\left(\frac{1}{10}, \frac{2}{10}, \frac{3}{10}, \frac{4}{10}\right)$.

Providing priors as a vector of numbers for larger models can be hard. For that reason, `set_priors()` allows for more targeted modifications of the parameter vector. For instance:

```
R> lipids_model |>
+   set_priors(statement = "X[Z=1] > X[Z=0]", alphas = 3) |>
+   inspect("prior_hyperparameters", nodes = "X")
```

```
#>
#> Alpha parameter values used for Dirichlet prior distributions:
#>
#> X.00 X.10 X.01 X.11
#>    1    1    3    1
```

Setting priors requires mapping alpha values to parameters, and so the problem of altering priors reduces to selecting rows of the `parameters_df` data frame at which to alter values. When specifying a causal statement as above, `CausalQueries` internally identifies nodal types consistent with the statement, which identifies parameters to alter priors for.

We can achieve the same result as above by specifying nodal types for which we would like to adjust the priors. `set_priors()` allows for the specification of any non-redundant combination of arguments on the `param_names`, `node`, `nodal_type`, `param_set`, and `given` columns of `parameters_df` to identify parameters to set priors for uniquely. Alternatively, a fully formed subsetting statement may be supplied to `alter_at`. Since all these arguments are mapped to the parameters they identify internally, they may be used interchangeably.[5]

While highly targeted prior setting is convenient and flexible, it should be used cautiously. Setting priors on specific parameters in complex models, especially models involving confounding, may strongly affect inferences. Furthermore, note that flat priors over nodal types do not necessarily translate into flat priors over queries. Flat priors over parameters in a parameter family put equal weight on each nodal type, which can translate into strong assumptions on causal quantities of interest. For instance, in an $X \rightarrow Y$ model in which negative effects are ruled out, the average causal effect implied by flat priors is 1/3. This can be seen by querying the model as follows:

```
R> query <-
+   make_model("X -> Y") |>
+   set_restrictions(decreasing("X", "Y")) |>
+   query_model("Y[X=1] - Y[X=0]", using = "priors")
```

More subtly, the *structure* of a model, coupled with flat priors, has substantive importance for priors on causal quantities. For instance, with flat priors, prior on the probability that X has a positive effect on Y in the model $X \rightarrow Y$ is centered on 1/4. But prior on the probability that X positively affects Y in the model $X \rightarrow M \rightarrow Y$ is centered on 1/8.

Caution regarding priors is essential when models are not identified, as is the case for many models considered here. For some quantities, the marginal posterior distribution reflects the marginal prior distribution (Poirier 1998).

Setting Parameters

By default, models have a vector of parameter values included in the `parameters_df` data frame. These are useful for generating data or for situations, such as process tracing, when one wants to make inferences about causal types (θ), given case-level data, under the assumption that the model is known.

The logic for setting parameters is similar to that for setting priors. The critical difference is that whereas the α value placed on nodal types can be any positive number—capturing our certainty over the parameter value—the parameter values must lie in the unit interval, $[0, 1]$. If passed parameter values do not lie in the unit interval, they are normalized so that they do.

[5] See `?set_priors` and `?make_priors` for many more examples.

The causal model below has two parameter sets, one for X and one for Y, with two nodal types for X and four for Y. The key feature of the parameters is that they must sum to 1 within each parameter set.

```
R> make_model("X -> Y") |>
+  inspect("parameters")
```

```
#>
#> Model parameters with associated probabilities:
#>
#>  X.0  X.1 Y.00 Y.10 Y.01 Y.11
#> 0.50 0.50 0.25 0.25 0.25 0.25
```

The example below illustrates a change in the value of the parameter that corresponds to a positive effect of X on Y. Here, the nodal type `Y.Y01` is set to be 0.7, while the other nodal types of this parameter set were re-normalized so that the parameters in the set still sum up to one.

```
R> make_model("X -> Y") |>
+  set_parameters(statement = "Y[X=1] > Y[X=0]", parameters = .7) |>
+  inspect("parameters")
```

```
#>
#> Model parameters with associated probabilities:
#>
#>  X.0  X.1 Y.00 Y.10 Y.01 Y.11
#>  0.5  0.5  0.1  0.1  0.7  0.1
```

5.4. Drawing and manipulating data

Once a model has been defined, it is possible to simulate data from the model using the `make_data()` function. For instance, this can be useful for assessing a model's expected performance given data drawn from some speculated set of parameter values.

Drawing data basics

Generating data requires a specification of parameter values. The parameter values in the parameters dataframe are used by default. Otherwise users can provide parameters on the fly.

```
R> sample_data_1 <-
+  lipids_model |>
+  make_data(n = 4)
```

However, users can also specify parameters directly or draw parameters from a prior or posterior distribution. For instance:

```
R> lipids_model |>
+  make_data(n = 3, param_type = "prior_draw")
```

```
#>   Z X Y
#> 1 0 1 0
#> 2 1 1 0
#> 3 1 1 1
```

The resulting data is ordered by data type, as shown in the example above.

Drawing incomplete data

`CausalQueries` can be used when researchers have gathered different amounts of data for different nodes. For instance, a researcher could collect data on X and Y for all units, but data on M only for some. The function `make_data()` allows users to draw data like this if they specify a data strategy indicating the probabilities of observing data on different nodes, possibly as a function of prior nodes observed.

```
R> sample_data_2 <-
+  lipids_model |>
+  make_data(n = 8,
+            nodes = list(c("Z", "Y"), "X"),
+            probs = list(1, .5),
+            subsets = list(TRUE, "Z==1 & Y==0"))
```

```
#> # A tibble: 2 x 5
#>   node_names nodes      n_steps probs subsets
#>   <chr>      <list>     <lgl>   <dbl> <chr>
#> 1 Z, Y       <chr [2]> NA        1    TRUE
#> 2 X          <chr [1]> NA        0.5  Z==1 & Y==0
```

```
R> sample_data_2
```

```
#>   Z  X Y
#> 1 0 NA 0
#> 2 0 NA 1
#> 3 0 NA 1
#> 4 0 NA 1
#> 5 0 NA 1
#> 6 0 NA 1
#> 7 1 NA 1
#> 8 1 NA 1
```

Reshaping data

Whereas data usually comes in "long form", with one row per observation, the data passed to Stan during model updating is in a "compact" form. The latter records only the number of units of each data type, grouped by data "strategy"—an indicator of the nodes for which researchers gathered data. `CausalQueries` includes functions that let users move between these two forms.

```
R> sample_data_2 |>
+  collapse_data(lipids_model)
```

```
#>   event strategy count
#> 1  Z0Y0       ZY     1
#> 2  Z1Y0       ZY     0
#> 3  Z0Y1       ZY     5
#> 4  Z1Y1       ZY     2
```

In the same way, it is possible to move from compact to long data using `expand_data()`. Note that `NA`'s are interpreted as data not being sought.

6. Updating models

The approach used by the `CausalQueries` package to update parameter values given observed data relies on the Stan programming language (Carpenter *et al.* 2017). Below we explain the data required by the generic Stan program implemented in the package, the structure of that program, and then show how to use the package to produce posterior draws of parameters.

6.1. Data for Stan

We use a generic Stan program that works for all binary causal models. The main advantage of the generic program is that it allows us to pass the details of the causal model as data inputs to Stan instead of generating individual Stan programs for each causal model. Appendix B provides the complete Stan model code.

The data required by the Stan program includes vectors of observed data and priors on parameters, as well as a set of matrices needed for the mapping between events, data types, causal types, and parameters. In addition, data passed to `stan` includes counts of all relevant quantities as well as start and end positions of parameters pertaining to specific nodes and distinct data strategies.

The internal function `prep_stan_data()` takes the model and data as arguments and produces a list with all objects that are required by the generic Stan program. Package users do not need to call the `prep_stan_data()` function directly.

6.2. How the Stan program works

The Stan model involves the following elements: (1) a specification of priors over sets of parameters, (2) a mapping from parameters to event probabilities, and (3) a likelihood function. Below, we describe each of those elements in more detail.

Probability distributions over parameter sets

The causal structure provided by a DAG allows us to reduce the problem of generating a probability distribution over all parameters to one of generating distributions over "sets" of parameters. Without unobserved confounding, these sets correspond to the nodal types for each node: we have a probability distribution over the set of nodal types.

Thus for instance we have two parameter sets in the $X \rightarrow Y$ model. We have a 2-dimensional Dirichlet distribution over the X nodal types, $(\lambda^X_0, \lambda^X_1) \sim Dirichlet(\alpha^X_0, \alpha^X_1)$. , and a 4-dimensional Dirichlet over the Y nodal types, $(\lambda^Y_{00}, \lambda^Y_{10}, \lambda^Y_{01}, \lambda^Y_{11}) \sim Dirichlet(\alpha^Y_{00}, \alpha^Y_{10}, \alpha^Y_{01}, \alpha^Y_{11})$.

In cases with confounding, these are sets of nodal types for a given node *given* values of other nodes.

Event probabilities

We calculate the probability of data types for any candidate parameter vector λ. This is done using a matrix that maps from parameters into data types.

In cases without confounding, there is a column for each data type; the matrix indicates which nodes in each set "contribute" to the data type, and the probability of the data type is found by summing within sets and taking the product over sets. To illustrate, we can examine the parameter mapping matrix for a simple model using the `inspect()` function as follows:

```
R> make_model("X -> Y") |>
+  inspect("parameter_mapping")
```

```
#>
#> Parameter mapping matrix:
#>
#>   Maps from parameters to data types, with
#>   possibly multiple columns for each data type
#>   in cases with confounding.
#>
#>      X0Y0 X1Y0 X0Y1 X1Y1
#> X.0     1    0    1    0
#> X.1     0    1    0    1
#> Y.00    1    1    0    0
#> Y.10    0    1    1    0
#> Y.01    1    0    0    1
#> Y.11    0    0    1    1
```

In this model, the probability of data type `X0Y0`, w_{00} is $\lambda^X_0 \times \lambda^Y_{00} + \lambda^X_0 \times \lambda^Y_{01}$. This formula can be read from the parameter mapping matrix by combining a parameter vector with the first column of the matrix, taking the product of the probability of `X.0` and the *sum* of the probabilities for `Y.00` and `Y.01`.

In cases with confounding, the approach is similar, except that the parameter mapping matrix can contain multiple columns for each data type to capture non-independence between nodes.

In the case of incomplete data, we first identify the set of data strategies, where a collection of a data strategy might be of the form "gather data on X and M, but not Y, for n_1 cases and gather data on X and Y, but not M, for n_2 cases." Within a data strategy, the probability of an observed event is given by summing the probabilities of the types that could give rise to a particular pattern of incomplete data.

Data probability

Once we have the event probabilities in hand for each data strategy, we are ready to calculate the probability of the data. For a given data strategy, this is given by a multinomial distribution with these event probabilities. When there is incomplete data, and so there are multiple data strategies, the probability of the data is given by the product of the multinomial probabilities for data generated by each strategy.

6.3. Implementation

The function `update_model(model, data)` is used to update a model, that is, append a posterior distribution over model parameters to the model. The `data` argument provides a data frame containing some or all of the nodes in the model. The function `update_model()` relies on `rstan::sampling()` to draw from the posterior distribution, and one can pass any additional arguments accepted by `rstan::sampling()`. Given that model updating can sometimes be slow for complex models, we show in Appendix A how users can utilize parallelization to improve computation speed. Appendix C provides an overview of model updating benchmarks, evaluating the effects of model complexity and data size on updating times.

Note that if no data is passed to `update_model()` the Stan model is still implemented and the posterior distribution appended to the model can be interpreted as draws from the prior distribution.

6.4. Incomplete and censored data

`CausalQueries` assumes that missing data is missing at random, conditional on observed data. For instance, in an $X \rightarrow M \rightarrow Y$ model, a researcher might have chosen to collect data on M in a random set of cases in which $X = 1$ and $Y = 1$. If there are positive relations at each stage, one may be more likely to observe M in cases in which $M = 1$. However, the observation of M is still random and conditional on the observed X and Y data. The Stan model in `CausalQueries` takes account of this kind of sampling by assessing the probability of observing a particular pattern of data within each data strategy.[6]

In addition, it is possible to indicate when data has been censored and for the Stan model to take this into account also. For instance, consider a situation in which we only observe

[6]For further discussion, see Section 9.2.3.2 in Humphreys and Jacobs (2023).

X in cases when $X = 1$ and not when $X = 0$. This kind of sampling is non-random and conditional on observables. It can be taken into account, however, by indicating to Stan that the probability of observing a particular data type is 0, regardless of parameter values. This can done using the `censored_types` argument in `update_model()`.

To illustrate, in the example below, we observe perfectly correlated data for X and Y. If we are aware that data in which $X \neq Y$ has been censored, then when we update, we do not move towards a belief that X causes Y.

```
R> data <- data.frame(X = rep(0:1, 5), Y = rep(0:1, 5))
R>
R> list(
+  uncensored =
+    update_model(make_model("X -> Y"),
+                 data),
+  censored =
+    update_model(make_model("X -> Y"),
+                 data,
+                 censored_types = c("X1Y0",  "X0Y1"))
+  ) |>
+  query_model("Y[X=1] - Y[X=0]", using = "posteriors") |>
+  subset(select = c("model", "query", "mean", "sd"))
```

```
#>
#> Causal queries generated by query_model
#>
#> |model      |query           |  mean|   sd|
#> |:----------|:---------------|-----:|----:|
#> |uncensored |Y[X=1] - Y[X=0] | 0.595| 0.20|
#> |censored   |Y[X=1] - Y[X=0] | 0.012| 0.32|
```

6.5. Output

The primary output from `update_model()` is a model with an attached posterior distribution over model parameters stored as a data frame in the model list. This posterior distribution can be directly accessed using the `inspect()` function as follows:

```
R> model <-
+  make_model("X -> Y")  |>
+  update_model()
R>
R> posterior <- grab(model, "posterior_distribution")
```

In addition, a distribution of causal types is stored by default; the `stanfit` object and a distribution over event probabilities are optionally saved as follows:

```
R> lipids_model <-
+  lipids_model |>
+  update_model(keep_fit = TRUE,
+               keep_event_probabilities = TRUE)
```

The summary of the Stan model can be accessed using `inspect()` function and is saved in the updated model object by default. This provides two measures to help assess convergence.

```
R> make_model("X -> Y")  |>
+  update_model(keep_type_distribution = FALSE) |>
+  inspect("stan_summary")

#>
#> Stan model summary:
#>
#> Inference for Stan model: simplexes.
#> 4 chains, each with iter=2000; warmup=1000; thin=1;
#> post-warmup draws per chain=1000, total post-warmup draws=4000.
#>
#>            mean se_mean   sd   2.5%   25%   50%   75% 97.5% n_eff Rhat
#> X.0        0.50    0.01 0.29   0.03  0.26  0.49  0.75  0.98  2923    1
#> X.1        0.50    0.01 0.29   0.02  0.25  0.51  0.74  0.97  2923    1
#> Y.00       0.25    0.00 0.19   0.01  0.09  0.21  0.37  0.70  1937    1
#> Y.10       0.25    0.00 0.19   0.01  0.09  0.21  0.37  0.71  4123    1
#> Y.01       0.25    0.00 0.19   0.01  0.09  0.20  0.36  0.70  4149    1
#> Y.11       0.25    0.00 0.19   0.01  0.09  0.21  0.37  0.70  4807    1
#> lp__      -7.48    0.04 1.63 -11.77 -8.31 -7.10 -6.27 -5.44  1536    1
#>
#> Samples were drawn using NUTS(diag_e) at Mon Oct 28 21:15:52 2024.
#> For each parameter, n_eff is a crude measure of effective sample size,
#> and Rhat is the potential scale reduction factor on split chains (at
#> convergence, Rhat=1).
```

This summary provides information on the distribution of parameters and convergence diagnostics, summarized in the `Rhat` column. The last row shows the unnormalized log density on Stan's unconstrained space, which is intended to diagnose sampling efficiency and evaluate approximations.[7] This summary can also include summaries for the transformed parameters if users retain these.[8]

If users wish to run more advanced diagnostics of performance, they can retain and access the "raw" Stan output as follows:

```
R> model <-
+  make_model("X -> Y") |>
+  update_model(refresh = 0, keep_fit = TRUE)
```

[7] See Stan documentation for more details.
[8] See **?@tbl-additional** for options.

Note that the raw output uses labels from the generic Stan model: `lambda` for the vector of parameters, corresponding to the parameters in the parameters data frame (`inspect(model, "parameters_df")`), a vector `types` for the causal types (`inspect(model, "causal_types")`) and `event_probabilities` for the event probabilities (`inspect(model, "event_probabilities")`).

```
R> model |>
+  inspect("stanfit")
```

```
#>
#> Stan model summary:
#> Inference for Stan model: simplexes.
#> 4 chains, each with iter=2000; warmup=1000; thin=1;
#> post-warmup draws per chain=1000, total post-warmup draws=4000.
#>
#>              mean se_mean   sd   2.5%   25%   50%   75% 97.5% n_eff Rhat
#> lambdas[1]   0.49    0.01 0.29   0.03  0.25  0.49  0.74  0.98  3090    1
#> lambdas[2]   0.51    0.01 0.29   0.02  0.26  0.51  0.75  0.97  3090    1
#> lambdas[3]   0.25    0.00 0.20   0.01  0.09  0.21  0.37  0.73  2170    1
#> lambdas[4]   0.25    0.00 0.19   0.01  0.09  0.20  0.37  0.70  4339    1
#> lambdas[5]   0.25    0.00 0.19   0.01  0.09  0.20  0.37  0.72  4464    1
#> lambdas[6]   0.25    0.00 0.19   0.01  0.10  0.21  0.37  0.71  4361    1
#> types[1]     0.12    0.00 0.13   0.00  0.03  0.08  0.18  0.48  2250    1
#> types[2]     0.13    0.00 0.14   0.00  0.03  0.08  0.19  0.50  2477    1
#> types[3]     0.12    0.00 0.13   0.00  0.03  0.08  0.17  0.49  3938    1
#> types[4]     0.12    0.00 0.13   0.00  0.03  0.08  0.18  0.49  3713    1
#> types[5]     0.12    0.00 0.13   0.00  0.03  0.08  0.18  0.49  3755    1
#> types[6]     0.12    0.00 0.13   0.00  0.03  0.08  0.18  0.49  3365    1
#> types[7]     0.13    0.00 0.13   0.00  0.03  0.08  0.18  0.48  3414    1
#> types[8]     0.13    0.00 0.13   0.00  0.03  0.08  0.19  0.48  3652    1
#> lp__        -7.57    0.05 1.73 -11.87 -8.44 -7.14 -6.29 -5.43  1250    1
#>
#> Samples were drawn using NUTS(diag_e) at Mon Oct 28 21:15:52 2024.
#> For each parameter, n_eff is a crude measure of effective sample size,
#> and Rhat is the potential scale reduction factor on split chains (at
#> convergence, Rhat=1).
```

Users can then pass the Stan fit object to other diagnostic packages such as `bayesplot`.

7. Queries

`CausalQueries` provides functionality to pose and answer elaborate causal queries. The key approach is to code causal queries as functions of causal types and return a distribution over the queries implied by the distribution over causal types.

7.1. Calculating factual and counterfactual quantities

An essential step in calculating most queries is assessing what outcomes will arise for causal types given different interventions on nodes. In practice, we map from causal types to data types by propagating realized values on nodes forward in the DAG, moving from exogenous or intervened upon nodes to their descendants in generational order. An internal function, `realise_outcomes()`, achieves this by traversing the DAG while recording the values implied by realizations on the node's parents for each node's nodal types.

To illustrate, consider the first causal type of a $X \to Y$ model:

1. θ^X_0 implies that, absent intervention on X, X has a realized value of 0; θ^Y_{00} implies that, absent intervention on Y, Y has a realized value of 0 regardless of X
2. We substitute for Y the value implied by the 00 nodal type given a 0 value on X, which in turn is 0.

Calling the function `realise_outcomes()` on this model yields the outcomes implied by all causal types:

```
R> make_model("X -> Y") |>
+  realise_outcomes()

#>      X Y
#> 0.00 0 0
#> 1.00 1 0
#> 0.10 0 1
#> 1.10 1 0
#> 0.01 0 0
#> 1.01 1 1
#> 0.11 0 1
#> 1.11 1 1
```

The output above shows realized values with row names indicating corresponding causal types. Intervening on X (see Pearl 2009) with $do(X = 1)$ yields:

```
R> make_model("X -> Y") |>
+  realise_outcomes(dos = list(X = 1))

#>      X Y
#> 0.00 1 0
#> 1.00 1 0
#> 0.10 1 0
#> 1.10 1 0
#> 0.01 1 1
#> 1.01 1 1
#> 0.11 1 1
#> 1.11 1 1
```

In the same way, `realise_outcomes()` can return the realized values on all nodes for each causal type given arbitrary interventions.

7.2. Causal syntax

`CausalQueries` provides syntax for the formulation of various causal queries including queries on all rungs of the "causal ladder" (Pearl 2009): prediction, such as the proportion of units where Y equals 1; intervention, such as the probability that $Y = 1$ when X is *set* to 1; counterfactuals, such as the probability that Y would be 1 were $X = 1$ given we know Y is 0 when X was observed to be 0. Queries can be posed at the population level or case level and can be unconditional (e.g., what is the effect of X on Y for all units) or conditional (for example, the effect of X on Y for units for which Z affects X). This syntax enables users to write arbitrary causal queries to interrogate their models.

The heart of querying is figuring out which causal types correspond to particular queries. Users may employ logical statements to ask questions about observed conditions without intervention for factual queries. Take, for example, the query mentioned above about the proportion of units where Y equals 1, expressed as `"Y == 1"`. In this case, the logical operator `==` indicates that `CausalQueries` should consider units that fulfill the condition of strict equality where Y equals 1.[9] When this query is posed, the `get_query_types()` function identifies all types that give rise to $Y = 1$, absent any interventions.

```
R> make_model("X -> Y")  |>
+  get_query_types("Y==1")
```

```
#>
#> Causal types satisfying query's condition(s)
#>
#>  query =  Y==1
#>
#> X0.Y10  X1.Y01
#> X0.Y11  X1.Y11
#>
#>
#>  Number of causal types that meet condition(s) =  4
#>  Total number of causal types in model =  8
```

The key to forming causal queries is being able to ask about the values of variables, given that the values of some other variables are "controlled." This corresponds to the application of the *do* operator in Pearl (2009). In `CausalQueries`, this is done by putting square brackets, `[ ]`, around variables that are intervened upon.

For instance, consider the query `Y[X=0]==1`. This query asks about the types for which Y equals 1 when X is set to 0. Since X is set to zero, X is placed inside the brackets. Given

[9] `CausalQueries` also accepts = as a shorthand for ==. However, == is preferred as it is the conventional logical operator.

that Y equals 1 is a condition about potentially observed values, it is expressed using the logical operator ==.

The set of causal types that meets this query is quite different:

```
R> make_model("X -> Y")  |>
+  get_query_types("Y[X=1]==1")
```

```
#>
#> Causal types satisfying query's condition(s)
#>
#>  query =  Y[X=1]==1
#>
#> X0.Y01  X1.Y01
#> X0.Y11  X1.Y11
#>
#>
#>  Number of causal types that meet condition(s) =  4
#>  Total number of causal types in model =  8
```

When a node has multiple parents, it is possible to set the values of none, some, or all of the parents. For instance if $X1$ and $X2$ are parents of Y then `Y==1`, `Y[X1=1]==1`, and `Y[X1=1, X2=1]==1` queries cases for which $Y = 1$ when, respectively, neither parents values are controlled, when $X1$ is set to 1 but $X2$ is not controlled, and when both $X1$ and $X2$ are set to 1. For instance:

```
R> make_model("X1 -> Y <- X2")  |>
+  get_query_types("X1==1 & X2==1 & (Y[X1=1, X2=1] > Y[X1=0, X2=0])")
```

```
#>
#> Causal types satisfying query's condition(s)
#>
#>  query =  X1==1&X2==1&(Y[X1=1,X2=1]>Y[X1=0,X2=0])
#>
#> X11.X21.Y0001  X11.X21.Y0101
#> X11.X21.Y0011  X11.X21.Y0111
#>
#>
#>  Number of causal types that meet condition(s) =  4
#>  Total number of causal types in model =  64
```

In this case, the aim is to identify the types for which in fact $X1 = 1$ and $X2 = 1$ *in addition* $Y = 0$ when $X1 = X2 = 0$, and $Y = 1$ when $X1 = X2 = 1$.

Conditional queries

Many queries of interest are "conditional" queries. For example, the effect of X on Y for units for which $W = 1$ or the effect of X on Y for units for which Z positively affects X. Such conditional queries are posed in `CausalQueries` by providing a `given` statement and the `query` statement. The entire query then becomes: for what units does the `query` condition hold among those units for which the `given` condition holds? The two parts can each be calculated using `get_query_types`. Thus, for instance, in an $X \rightarrow Y$ model, the probability that X causes Y given $X = 1 \,\&\, Y = 1$ is the probability of causal `X1.Y11` type divided by the sum of the probabilities of types `X1.Y11` and `X1.Y01`. In practice, this is done automatically for users when they call `query_model()` or `query_distribution()`.

Complex expressions

Many queries involve complex statements over multiple sets of types. These can be formed with the aid of relational operators. For example, you can make queries about cases where X has a positive effect on Y, i.e., whether Y is greater when X is set to 1 compared to when X is set to 0, expressed as `"Y[X=1] > Y[X=0]"`. The query "X has some effect on Y" is given by `"Y[X=1] != Y[X=0]"`.

Linear operators can also be used over a set of simple statements. Thus `"Y[X=1] - Y[X=0]"` returns the average treatment effect. In essence, rather than returning a `TRUE` or `FALSE` for the two parts of the query, the case memberships are forced to numeric values (1 or 0), and the differences are taken, which can be a 1, 0 or -1 depending on the causal type. Averaging provides the share of cases with positive effects, less the share of cases with negative effects.

```
R> make_model("X -> Y") |>
+   get_query_types("Y[X=1] - Y[X=0]")

#> X0.Y00 X1.Y00 X0.Y10 X1.Y10 X0.Y01 X1.Y01 X0.Y11 X1.Y11
#>      0      0     -1     -1      1      1      0      0
```

Nested queries

`CausalQueries` lets users pose nested "complex counterfactual" queries. For instance `"Y[M=M[X=0], X=1]==1"` queries the types for which Y equals 1 when X is set to 1, while keeping M constant at the value it would take if X were 0.

7.3. Quantifying queries

Giving a *quantitative* answer to a query requires placing probabilities over the causal types that correspond to a query.

Queries by hand

Queries can be calculated directly from the prior distribution or the posterior distribution provided by Stan. For instance, the following call plots the posterior distribution for the probability that Y is increasing in X for the $X \rightarrow Y$ model. The resulting plot is shown in Figure 2.

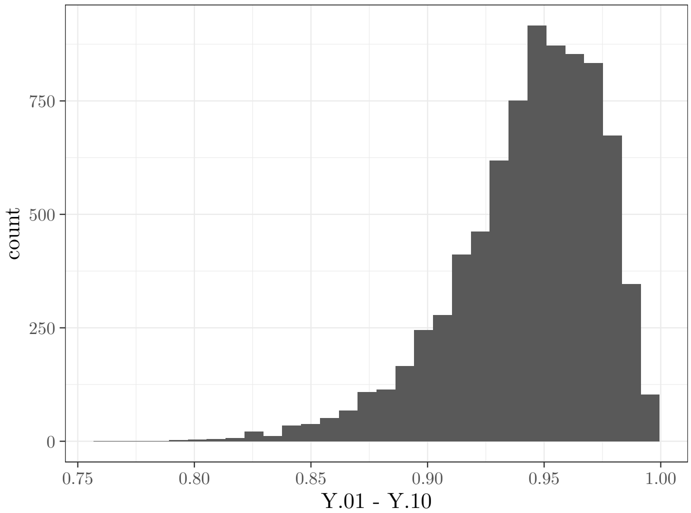


Figure 2: Posterior on "Probability Y is increasing in X".

```
R> data  <- data.frame(X = rep(0:1, 50), Y = rep(0:1, 50))
R>
R> model <-
+  make_model("X -> Y") |>
+  update_model(data, iter  = 4000, refresh = 0)
R>
R> model |>
+  inspect("posterior_distribution")  |>
+  ggplot(aes(Y.01 - Y.10)) + geom_histogram()

#>
#> Summary statistics of model parameters posterior distributions:
#>
#>   Distributions matrix dimensions are
#>   8000 rows (draws) by 6 cols (parameters)
#>
#>      mean   sd
#> X.0  0.50 0.05
#> X.1  0.50 0.05
#> Y.00 0.02 0.02
#> Y.10 0.01 0.01
#> Y.01 0.95 0.03
#> Y.11 0.02 0.02
```

Query distribution

It is generally helpful to use causal syntax to define the query and calculate the query with respect to the prior or posterior probability distributions. This can be done for a list of queries using `query_distribution()` function as follows:

```
R> queries <-
+  make_model("X -> Y") |>
+  query_distribution(
+    query = list(increasing = "(Y[X=1] > Y[X=0])",
+                 ATE = "(Y[X=1] - Y[X=0])"),
+    using = "priors")
```

The command `query_distribution()` can also be used when one is interested in assessing the value of a query for a *particular case*. In a sense, this is equivalent to posing a conditional query, querying conditional on values in a case. For instance, we might consult our posterior for the Lipids model and ask about the effect of X on Y for a case in which $Z = 1$, $X = 1$ and $Y = 1$.

```
R> lipids_model |>
+  query_model(query = "Y[X=1] - Y[X=0]",
+              given = "X==1 & Y==1 & Z==1",
+              using = "posteriors")  |>
+  subset(select = c("query", "mean", "sd"))
```

```
#>
#> Causal queries generated by query_model
#>
#> |query            | mean|    sd|
#> |:---------------|----:|-----:|
#> |Y[X=1] - Y[X=0] |  0.5| 0.237|
```

The result is what we should now believe for all cases in which $Z = 1$, $X = 1$, and $Y = 1$. It is the expected average effect among cases with this data type, so this expectation has an uncertainty attached reflecting our uncertainty about the expectation.

This is, in principle, different from what we would infer if we were presented with a new case. When inquiring about a new case, we need to *update* on the given information observed in the new case. This *new* case-level inference is calculated if the `case_level = TRUE` argument is specified. For a query Q and given D this returns the value $\frac{\int \pi(Q\&D|\lambda_i)p(\lambda_i)d\lambda_i}{\int \pi(D|\lambda_i)p(\lambda_i)d\lambda_i}$ which may differ from the mean of the distribution $\frac{\pi(Q\&D|\lambda)}{\pi(D|\lambda)}$, $\int \frac{\pi(Q\&D|\lambda_i)}{\pi(D|\lambda_i)} p(\lambda_i)d\lambda_i$.

To illustrate the difference, consider an $X \to M \to Y$ model where we are quite certain that X causes Y, but unsure whether this effect works through two positive or two negative effects. If asked what we would think about effects in cases $M = 0$ (or with $M = 1$), we have little basis to know whether these are cases in which effects are more or less likely. However, if we randomly find a case and we observe that $M = 0$, our understanding of the causal model evolves, leading us to believe there is (or is not) an effect in this specific case. The case-level query gives a single value without posterior standard deviation, representing the belief about this new case.

```
R> make_model("X -> M -> Y") |>
```

```
+  update_model(data.frame(X = rep(0:1, 8), Y = rep(0:1, 8)), iter = 4000) |>
+  query_model("Y[X=1] > Y[X=0]",
+            given = "X==1 & Y==1 & M==1",
+            using = "posteriors",
+            case_level = c(TRUE, FALSE))  |>
+  subset(select = c("query", "case_level", "mean", "sd"))
```

```
#>
#> Causal queries generated by query_model
#>
#> |query           |case_level |  mean|    sd|
#> |:---------------|:----------|-----:|-----:|
#> |Y[X=1] > Y[X=0] |TRUE       | 0.672|    NA|
#> |Y[X=1] > Y[X=0] |FALSE      | 0.419| 0.329|
```

Batch queries

The function `query_model()` can also be used to query multiple models. The function takes a list of models, causal queries, and conditions as inputs. It then calculates population or case level estimands given prior or posterior distributions and reports summaries of these distributions. The result is a data frame that can be displayed as a table or used for graphing.

Table 7 returns to the Lipids data and shows the output from a single call to `query_model()` with the `expand_grid` argument set to `TRUE` to generate all combinations of list elements.

```
R> models <- list(
+  A = lipids_model |>
+    update_model(data = lipids_data, refresh = 0),
+  B = lipids_model |> set_restrictions("X[Z=1] < X[Z=0]") |>
+    update_model(data = lipids_data, refresh = 0))
R>
R> queries <-
+  query_model(
+    models,
+    query = list(ATE = "Y[X=1] - Y[X=0]",
+                 POS = "Y[X=1] > Y[X=0]"),
+    given = c(TRUE,  "Y==1 & X==1"),
+    case_level = c(FALSE, TRUE),
+    using = c("priors", "posteriors"),
+    expand_grid = TRUE)
```

Table 7: Results for two queries on two models.

model	query	given	using	case_level	mean	sd

A	ATE	-	priors	FALSE	0.00	0.20
B	ATE	-	priors	FALSE	0.00	0.23
A	ATE	-	posteriors	FALSE	0.56	0.10
B	ATE	-	posteriors	FALSE	0.56	0.10
A	ATE	Y==1 & X==1	priors	FALSE	0.50	0.22
B	ATE	Y==1 & X==1	priors	FALSE	0.49	0.24
A	ATE	Y==1 & X==1	posteriors	FALSE	0.95	0.04
B	ATE	Y==1 & X==1	posteriors	FALSE	0.95	0.04
A	POS	-	priors	FALSE	0.25	0.12
B	POS	-	priors	FALSE	0.25	0.14
A	POS	-	posteriors	FALSE	0.61	0.10
B	POS	-	posteriors	FALSE	0.61	0.10
A	POS	Y==1 & X==1	priors	FALSE	0.50	0.22
B	POS	Y==1 & X==1	priors	FALSE	0.49	0.24
A	POS	Y==1 & X==1	posteriors	FALSE	0.95	0.04
B	POS	Y==1 & X==1	posteriors	FALSE	0.95	0.04
A	ATE	-	priors	TRUE	0.00	NA
B	ATE	-	priors	TRUE	0.00	NA
A	ATE	-	posteriors	TRUE	0.56	NA
B	ATE	-	posteriors	TRUE	0.56	NA
A	ATE	Y==1 & X==1	priors	TRUE	0.50	NA
B	ATE	Y==1 & X==1	priors	TRUE	0.49	NA
A	ATE	Y==1 & X==1	posteriors	TRUE	0.95	NA
B	ATE	Y==1 & X==1	posteriors	TRUE	0.95	NA
A	POS	-	priors	TRUE	0.25	NA
B	POS	-	priors	TRUE	0.25	NA
A	POS	-	posteriors	TRUE	0.61	NA
B	POS	-	posteriors	TRUE	0.61	NA
A	POS	Y==1 & X==1	priors	TRUE	0.50	NA
B	POS	Y==1 & X==1	priors	TRUE	0.49	NA
A	POS	Y==1 & X==1	posteriors	TRUE	0.95	NA
B	POS	Y==1 & X==1	posteriors	TRUE	0.95	NA

8. Conclusion

M TO ADD TEXT HERE

Computational details and software requirements

Version	• 1.1.1
Availability	• Stable Release: https://cran.rstudio.com/web/packages/CausalQueries/index.html • Development: https://github.com/integrated-inferences/CausalQueries
Issues	• https://github.com/integrated-inferences/CausalQueries/issues
Operating Systems	• Linux • MacOS • Windows
Testing Environments OS	• Ubuntu 22.04.2 • Debian 12.2 • MacOS • Windows
Testing Environments R	• R 4.3.1 • R 4.3.0 • R 4.2.3 • r-devel
R Version	• R(>= 3.4.0)
Compiler	• either of the below or similar: • g++ • clang++
Stan requirements	• inline • Rcpp (>= 0.12.0) • RcppEigen (>= 0.3.3.3.0) • RcppArmadillo (>= 0.12.6.4.0) • RcppParallel (>= 5.1.4) • BH (>= 1.66.0) • StanHeaders (>= 2.26.0) • rstan (>= 2.26.0)
R-Packages Depends	• dplyr • methods
R-Packages Imports	• dagitty (>= 0.3-1) • dirmult (>= 0.1.3-4) • stats (>= 4.1.1) • rlang (>= 0.2.0) • rstan (>= 2.26.0) • rstantools (>= 2.0.0) • stringr (>= 1.4.0) • ggdag (>= 0.2.4) • latex2exp (>= 0.9.4) • ggplot2 (>= 3.3.5) • lifecycle (>= 1.0.1)

The results in this paper were obtained using R~3.4.1 with the **MASS**~7.3.47 package. R itself and all packages used are available from the Comprehensive R Archive Network (CRAN) at https://CRAN.R-project.org/.

Acknowledgments

We thank Ben Goodrich, who provided generous insights on using `stan` for this project. We thank Alan M Jacobs for key work in developing the framework underlying the package. Our thanks to Cristian-Liviu Nicolescu, who provided wonderful feedback on the use of the package and a draft of this paper. Our thanks to Jasper Cooper for contributions to the generic function to create Stan code, to Clara Bicalho, who helped figure out the syntax for causal statements, to Julio S. Solís Arce who made many vital contributions figuring out how to simplify the specification of priors, and to Merlin Heidemanns who figured out the `rstantools` integration and made myriad code improvements.

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Appendix A: Parallelization

If users have access to multiple cores, parallel processing can be implemented by including this line before running `CausalQueries`:

```
R> library(parallel)
R>
R> options(mc.cores = parallel::detectCores())
```

Additionally, parallelizing across models or data while running MCMC chains in parallel can be achieved by setting up a nested parallel process. With 8 cores one can run two updating processes with three parallel chains each simultaneously. More generally the number of parallel processes at the upper level of the nested parallel structure are given by $\lfloor \frac{cores}{chains+1} \rfloor$.

```
R> library(future)
R> library(future.apply)
R>
R> chains <- 3
R> cores <- 8
R>
R> future::plan(list(
+      future::tweak(future::multisession,
+                    workers = floor(cores/(chains + 1))),
+      future::tweak(future::multisession,
+                    workers = chains)
+    ))
R>
R> model <- make_model("X -> Y")
R> data <- list(data_1 = data.frame(X=0:1, Y=0:1),
+             data_2 = data.frame(X=0:1, Y=1:0))
R>
R> results <-
+future.apply::future_lapply(
+  data,
+  function(d) {
+    update_model(
+      model = model,
+      data = d,
+      chains = chains,
+      refresh = 0
+    )},
+ future.seed = TRUE)
```

Appendix B: Stan code

Updating is performed using a generic Stan model. The data provided to Stan is generated by the internal function `prep_stan_data()`, which returns a list of objects that Stan expects to receive. The code for the Stan model is shown below. After defining a helper function, the code starts with a block declaring what input data is to be expected. Then, the parameters and the transformed parameters are characterized. Then, the likelihoods and priors are provided. At the end, a block for generated quantities is used to append a posterior distribution of causal types to the model.

```
S4 class stanmodel 'simplexes' coded as follows:
functions{
  row_vector col_sums(matrix X) {
    row_vector[cols(X)] s ;
    s = rep_row_vector(1, rows(X)) * X ;
    return s ;
  }
}
data {
int<lower=1> n_params;
int<lower=1> n_paths;
int<lower=1> n_types;
int<lower=1> n_param_sets;
int<lower=1> n_nodes;
array[n_param_sets] int<lower=1> n_param_each;
int<lower=1> n_data;
int<lower=1> n_events;
int<lower=1> n_strategies;
int<lower=0, upper=1> keep_type_distribution;
vector<lower=0>[n_params] lambdas_prior;
array[n_param_sets] int<lower=1> l_starts;
array[n_param_sets] int<lower=1> l_ends;
array[n_nodes] int<lower=1> node_starts;
array[n_nodes] int<lower=1> node_ends;
array[n_strategies] int<lower=1> strategy_starts;
array[n_strategies] int<lower=1> strategy_ends;
matrix[n_params, n_types] P;
matrix[n_params, n_paths] parmap;
matrix[n_paths, n_data] map;
matrix<lower=0,upper=1>[n_events,n_data] E;
array[n_events] int<lower=0> Y;
}
parameters {
vector<lower=0>[n_params - n_param_sets] gamma;
}
transformed parameters {
vector<lower=0, upper=1>[n_params] lambdas;
```

```
vector<lower=1>[n_param_sets] sum_gammas;
matrix[n_params, n_paths] parlam;
matrix[n_nodes, n_paths] parlam2;
vector<lower=0, upper=1>[n_paths] w_0;
vector<lower=0, upper=1>[n_data] w;
vector<lower=0, upper=1>[n_events] w_full;
// Cases in which a parameter set has only one value need special handling
// they have no gamma components and sum_gamma needs to be made manually
for (i in 1:n_param_sets) {
  if (l_starts[i] >= l_ends[i]) {
    sum_gammas[i] = 1;
    lambdas[l_starts[i]] = 1;
    }
  else if (l_starts[i] < l_ends[i]) {
    sum_gammas[i] =
    1 + sum(gamma[(l_starts[i] - (i-1)):(l_ends[i] - i)]);
    lambdas[l_starts[i]:l_ends[i]] =
    append_row(1, gamma[(l_starts[i] - (i-1)):(l_ends[i] - i)]) /
      sum_gammas[i];
    }
  }
// Mapping from parameters to data types
// (usual case): [n_par * n_data] * [n_par * n_data]
parlam  = rep_matrix(lambdas, n_paths) .* parmap;
// Sum probability over nodes on each path
for (i in 1:n_nodes) {
 parlam2[i,] = col_sums(parlam[(node_starts[i]):(node_ends[i]),]);
 }
// then take product  to get probability of data type on path
for (i in 1:n_paths) {
  w_0[i] = prod(parlam2[,i]);
 }
 // last (if confounding): map to n_data columns instead of n_paths
 w = map'*w_0;
  // Extend/reduce to cover all observed data types
 w_full = E * w;
}
model {
// Dirichlet distributions
for (i in 1:n_param_sets) {
  target += dirichlet_lpdf(lambdas[l_starts[i]:l_ends[i]]  |
    lambdas_prior[l_starts[i] :l_ends[i]]);
  target += -n_param_each[i] * log(sum_gammas[i]);
 }
// Multinomials
// Note with censoring event_probabilities might not sum to 1
for (i in 1:n_strategies) {
```

```
  target += multinomial_lpmf(
  Y[strategy_starts[i]:strategy_ends[i]] |
    w_full[strategy_starts[i]:strategy_ends[i]]/
     sum(w_full[strategy_starts[i]:strategy_ends[i]]));
 }
}
// Option to export distribution of causal types
generated quantities{
vector[n_types] types;
if (keep_type_distribution == 1){
for (i in 1:n_types) {
   types[i] = prod(P[, i].*lambdas + 1 - P[,i]);
}}
 if (keep_type_distribution == 0){
    types = rep_vector(1, n_types);
 }
}
```

Appendix C: Benchmarks

We present a brief summary of model updating benchmarks. Note that these benchmarks are not generally reproducible and depend on the specifications of the hardware system used to produce them. The first benchmark considers the effect of model complexity on updating time. The second benchmark considers the effect of data size on updating time. We run four parallel chains for each model. The results of the benchmarks are presented in Table 9 and Table 10.

Table 9: Benchmark 1.

Model	Number of Model Parameters	`update_model()` Run-Time (seconds)
$X1 \rightarrow Y$	6	7.0
$X1 \rightarrow Y; X2 \rightarrow Y$	20	8.4
$X1 \rightarrow Y; X2 \rightarrow Y; X3 \rightarrow Y$	262	22.9

Table 10: Benchmark 2.

Model	Number of Observations	`update_model()` Run-Time (seconds) |
$X1 \rightarrow Y$	10	5.8
$X1 \rightarrow Y$	100	6.5
$X1 \rightarrow Y$	1000	7.0
$X1 \rightarrow Y$	10000	10.6
$X1 \rightarrow Y$	100000	22.9

Increasing the number of parents in a model greatly increases the number of parameters and computational time. The results suggests the computational time is convex in the number of parents and approximately linear in the number of parameters. Unless model restrictions are imposed four parents would yield 65,536 parameters. The rapid growth of the parameter space with increasing model complexity places limits on feasible computability without further recourse to specialized methods for handling large causal models. In contrast, the results suggest that computational time is concave in the size of the data.

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Journal of Statistical Software http://www.jstatsoft.org/
published by the Foundation for Open Access Statistics http://www.foastat.org/
MMMMMM YYYY, Volume VV, Issue II *Submitted:* yyyy-mm-dd
`doi:10.18637/jss.v000.i00` *Accepted:* yyyy-mm-dd