

Getting Started with because

Achaz von Hardenberg

2025-12-13

Getting started

because is an R package designed to easily perform causal inference with Bayesian Structural Equation Models in JAGS. The package integrates the methods proposed by von Hardenberg & Gonzalez-Voyer (2025) to fit Phylogenetic Bayesian Structural Equation Models (Because) and extends them to other types of covariance structures (eg. spatial autocorrelation, genetic relatedness etc.).

because main features:

- Causal Inference with D-Separation: Testing conditional independencies implied by your causal model.
- Phylogenetic Path Analysis: Using the Phylogenetic Bayesian Structural Equation Model approach (Because, von Hardenberg & Gonzalez-Voyer, 2025).
- *Alternative Covariance structures*: Spatial, genetic, social, or other correlation structures. *Alternative distribution families: Modeling non-Gaussian data.
 - Gaussian (continuous data)
 - Binomial (binary/proportion data)
 - Multinomial (unordered categorical data)
 - Ordinal (ordered categorical data)
 - Poisson (count data)
 - Negative Binomial (overdispersed count data)
 - Zero inflated Poisson (ZIP) and negative binomial (ZINB)
- *Advanced Model Specifications*: random effects (mixed models, nested designs), polynomial terms, interaction terms, categorical predictors, measurement error, missing data, phylogenetic uncertainty.
- *Hierarchical Data*: Multi-level data with variables at different hierarchical levels.
- *Latent Variables and MAG*: Measurement error models and causal inference in the presence of latent variables using the MAG approach by Shipley & Doua (2021).
- *Model Diagnostics*: Checking convergence, comparing models, and interpreting results.

Quick Start

Installation

Before using **because**, you need to have **JAGS** (Just Another Gibbs Sampler) installed on your machine.

- **macOS**: `brew install jags` or download from SourceForge.
- **Windows**: Download installer from SourceForge.
- **Linux**: `sudo apt-get install jags`.

After installing JAGS, you can install **because** from GitHub.

To install the **stable release** (v0.9.3):

```
remotes::install_github("achazhardenberg/because@v0.9.3", build_vignettes = TRUE)
```

To install the **latest development version**:

```
remotes::install_github("achazhardenberg/because", build_vignettes = TRUE)
```

Finally, load the package:

```
library(because)
```

Your First Model

The main function in `because` is `because()`, which compiles and fits your specified Structural Equation Model in JAGS. The function is very rich with functionalities allowing to model complex models with different error structures and hierarchically structured data. However, here, to show the basic workflow, we will use `because()` to fit a simple linear model involving only two variables. Having only two variables this is not a typical SEM being equivalent to a simple linear regression which can not be used to infer causality, but it serves to illustrate the basic usage of the package.

Let's start simulating two variables X and Y where Y is correlated to X :

```
# set seed for reproducibility
set.seed(67)

# Simulate predictor
X <- rnorm(n = 100, mean = 50, sd = 10)

# Generate response with the chosen intercept (alpha) and slope (beta)
alpha <- 20
Y <- alpha + beta * X + rnorm(n, mean = 0, sd = 10)

# Combine into data frame
sim.dat <- data.frame(X, Y)

# Fit linear model with lm() function for comparison
summary(lm(Y ~ X, data = sim.dat))
```

Now we can fit the same model using `because`. We need to specify the structural equations (in this case only one) using R's formula syntax and then call `because()` passing the equation and the data frame:

```
# Define the equations
equations <- list(Y ~ X)

# Fit the model
fit <- because(
  equations = equations,
  data = sim.dat
)

# View results
summary(fit)
```

To check for convergence of the MCMC chains, you can look at the `Rhat` values in the summary output (should be < 1.1). You can also plot the trace plots of the MCMC samples:

```
# Plot trace plots
plot(fit$samples)
```

`fit$samples` is an MCMC object, so you can use all coda functions to analyze and plot the MCMC samples.

You can see how `because()` translates your model into JAGS syntax calling `fit$model` or, before fitting it, using `because_model()`:

```
# Generate JAGS model code
jags_model_code <- because_model(
  equations = equations
)

cat(jags_model_code$model)
```

When specifying the equations you can include multiple predictors as well as factors, interaction terms and polynomial terms following the conventional R formula syntax.

Next: Causal Inference with D-Separation

One of the main features of `because` is the ability to test your causal model's fit to the data using d-separation tests. D-separation tests evaluate whether the conditional independencies implied by your causal model hold in the data (Shiple, 2016). If they do not, this suggests that your model may be misspecified and that you may need to add or remove paths. More details on d-separation tests, how to interpret them and a full tutorial can be found in the D-Separation Tests vignette.