

Introduction to R

Module 7: Intro to Bayesian Methods in R

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Conceptual Introduction



Thought Experiment

Question

Imagine I'm conducting a raffle. I have a large bowl, and inside of it are many raffle entries, each with different numbers on them.

- Let the variable x represent the number drawn from the bowl.
- Before reaching into the bowl, I want to know:
"What is the probability that I'm going to pick up a number less than 10 from the bowl?"
- That is, what is $p(x \leq 10)$?
 - ***Does this probability change if I tell you that all the numbers in the bowl have at least 3 digits (ie are ≥ 100)?***



Thought Experiment

Answer

Classical Statistics: No.

- Probability is defined as: $\lim_{n \rightarrow \infty} \frac{n_S}{n}$, where n is the number of times I repeat the experiment and n_S is the number of times a number $x \leq 10$ is drawn.
- $p(x \leq 10)$ was always equal to zero, all that changed was your knowledge of the experiment.

Bayesian Statistics: Almost certainly.

- Probability is a measure of subjective belief about how likely an event is, based on prior understanding and new information.
- Prior \rightarrow Information \rightarrow Posterior



Epistemological difference

- Bayesian statistics integrates the epistemological uncertainty of statistical estimation into its core procedures. It's fundamental goal is to assess and improve the accuracy of one's beliefs based on a set of identifying statistical assumptions.
- Classical statistics attempts to instead conduct inference on the (unknown) underlying reality, based on its own set of identifying assumptions.

NOT mutually exclusive



Bayes Rule

The cornerstone of the Bayesian approach (and the source of its name) is the conditional likelihood theorem known as **Bayes' rule**.

In its simplest form, Bayes' Rule states that for two events A and B (with $P(B) \neq 0$):

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

Or, if A can take on multiple values, we have the **extended form**:

$$p(A_i|B) = \frac{p(B|A_i)P(A_i)}{\sum_j p(B|A_j)P(A_j)}$$



Bayesian Inference with Bayes' Rule

Adapting Bayes' Rule to the case of a parameter value, θ and observed data y , we have:

$$p(\theta | y) = \frac{f(\theta, y)}{f(y)} = \frac{f(y | \theta)p(\theta)}{\int f(y | \theta)p(\theta)d\theta} \underbrace{\propto}_{\text{proportional to}} f(y|\theta)p(\theta)$$

Adding a bit of terminology:

- $p(\theta)$ is the **prior** distribution: our initial subjective belief about the probability distribution of θ .
- $f(y|\theta)$ you may recognize from Maximum Likelihood estimation as:
 - $f(y|\theta) = \prod_{i=1}^n f(y_i|\theta) = \mathcal{L}(\theta)$, the **likelihood function**.
- Finally, $p(\theta|y)$ is our **posterior** (post-experiment) belief about the probability distribution of θ .



Bayesian Inference with Bayes' Rule

$$\underbrace{p(\theta | y)}_{\text{posterior}} = \frac{\underbrace{f(y | \theta)}_{\text{likelihood}} \underbrace{p(\theta)}_{\text{prior}}}{\underbrace{\int f(y | \theta) p(\theta) d\theta}_{\text{average likelihood}}} \propto \underbrace{f(y | \theta)}_{\text{likelihood}} \underbrace{p(\theta)}_{\text{prior}}$$

proportional to

Hence we have the basic statement:

$$\textit{Posterior} \propto \textit{Likelihood} \times \textit{Prior}$$

- This is commonly summarized as saying that the posterior belief is a compromise between the data and prior belief.



Priors

Given this *compromise with prior beliefs*, Bayesian analysis is often attacked as subjective and a lot of emphasis is placed on the role of prior beliefs. **But fear not!**

- First, as the data sample increases, the data becomes the determining factor of the posterior probability.
- Moreover, if desired, we can easily specify priors that have *no effect* on the posterior estimates.



Types of Priors

Different types of priors include:

- **Uninformative (or “flat”) priors:** Priors that have no impact on posterior values (ie assuming total ignorance about the possible parameter value).
 - A classic uninformative prior is the uniform prior, which treats all possible parameter values as equally likely: $p(\theta) = c \forall \theta \in \Theta$
- **Informative priors:** Priors where we use prior knowledge to specify a prior with a best-guess of the prior mean and distribution for a parameter value.
- **Weakly informative or regularizing priors:** Priors which are deliberately less informative than our actual knowledge, affecting estimates less than informative priors but at least incorporating *very conservative* information into the production of posterior estimates.



Intuition about priors

Think for instance of inference about possible life expectancy:

- We could specify an uninformative prior that says allows for any possible lifespan (even living to 1 million years old).
- We could specify some skewed normal distribution that approximates our current estimates of the distribution of current lifespans.
- Or we could specify some weaker prior that for instance allows life expectancy to be more dispersed and ages to reach, say 150 or 200 years old.
 - Weakly informative priors don't use our best understanding of life expectancy, but at least "tells" our analysis that some possibilities are very implausible.

In almost all circumstances, a weak prior should be preferred.



Prior Example:

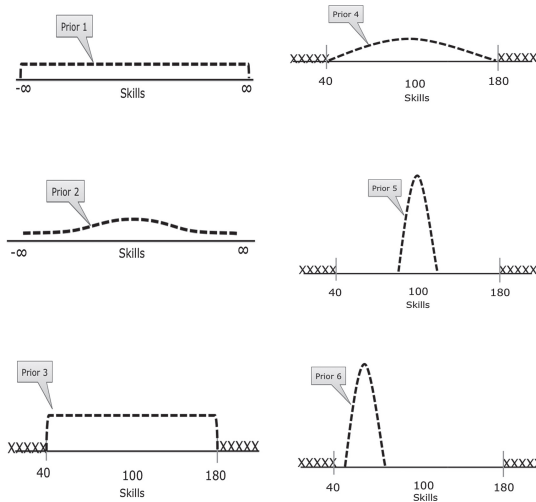


Figure 1: From van de Schoot et al 2014



Bayesian Computation

One major feature of Bayesian inference that I haven't mentioned so far is the intractability of analytic solutions for estimating posterior distributions in most circumstances.

Recall:

$$p(\theta | y) = \frac{f(\theta, y)}{f(y)} = \frac{f(y | \theta)p(\theta)}{\int f(y | \theta)p(\theta)d\theta}$$

For models that are more complex or that involve high-dimensional data, closed-form solutions are not available for the integral in the denominator.

Hence, Bayesian analysis instead typically relies on numerical methods, usually Markov Chain Monte Carlo (MCMC) methods.



MCMC Methods

This method relies on sequentially sampling values of θ from an approximation of the posterior distribution and then correcting the approximation to create better subsequent samples.

- Because the approximated distribution used in 1 step relies on the sample from the previous step, the simulation forms a **Markov chain**.
- A critical property then is **convergence**: Have our simulations converged to the real target distribution?
 - Typically instead of running one really long “chain”, researchers use multiple short chains.
 - The aggregate can not only converge faster, but can provide a better sense of convergence through the noisiness between multiple chains.



Hypothesis Testing in Bayesian Analysis?

Another point of divergence for Bayesian vs. frequentist data analysis is even more dramatic:

- Largely, there is no place for null-hypothesis significance testing (NHST) in Bayesian analysis
 - Bayesian analysis has *something* similar called a **Bayes' factor**, which essentially assigns a prior probability to the likelihood ratio of a null and alternative model and then estimates it's posterior probability.
 - But Bayes factors are heavily criticized by leading Bayesians like Andrew Gelman and Donald Rubin, because it is highly sensitive to prior probabilities and model structures, among other issues.
- Instead, analysis is oriented around estimation of the posterior distribution of parameters (or predictions).



Bayesian Inference with Credible Intervals

Without NHST to tell us if our results are significant, does that mean we just get point estimates and no way to assess how reliable they are? **No!**

- Recall that we are estimating the posterior *distribution* of a parameter (or predicted outcome).
- Hence, we can easily produce a 95% interval for the parameter, simply using the quantiles of the posterior CDF.

In Bayesian analysis, we replace the $100(1 - \alpha)\%$ frequentist confidence interval with the $100(1 - \alpha)\%$ **credible interval**.



Bayesian Inference with Credible Intervals

A credible interval, however, has a much more appealing interpretation than a confidence interval.

- A confidence interval has the interpretation that, in repeated samples, the true parameter lies within the confidence region 95% of the time.
- A credible interval is what people *think* a confidence interval should mean: there is a 95% chance that the true value lies within the 95% credible interval.



Bayesian Regression with rstanarm



Stan

Probably the best approach to doing Bayesian analysis in any software environment is with [rstan](#), which is an R interface to the Stan programming language designed for Bayesian analysis.

- To use [rstan](#), you will first need to install **RTools** from [this link](#).
- Then install the package [rstan](#) from RStudio (make sure to set `dependencies=TRUE` when installing).



Parallelization support

Once you've setup `rstan`, there is one more thing you should typically do: tell it to run on multiple cores.

- `rstan` includes support for basic parallelization that speeds up execution tremendous for larger / more complex regressions.

```
library(rstan)
rstan_options (auto_write=TRUE)
# Run on multiple cores
options (mc.cores=parallel::detectCores ())
```



A Stan regression example

Now that you're **hopefully** excited about rstan, let's look at an example of a rstan regression from the package documentation:

```
# Create schools.stan -----  
data {  
  int<lower=0> J;          // number of schools  
  real y[J];              // estimated treatment effects  
  real<lower=0> sigma[J]; // s.e. of effect estimates  
}  
parameters {  
  real mu;  
  real<lower=0> tau;  
  vector[J] eta;  
}
```



A Stan regression example

```
## Still creating schools.stan
transformed parameters {
  vector[J] theta;
  theta = mu + tau * eta;
}

model {
  target += normal_lpdf(eta | 0, 1);
  target += normal_lpdf(y | theta, sigma);
}

# End of schools.stan -----

## Run Stan regression using schools.stan
fit1 <- stan(
  file = "schools.stan", # Stan program
```

Making RStan easy

Oops! That was a lot of code! And there's still a bit more left out. Luckily, there are a couple of packages that exist to make your life easier:

- First, there is [rstanarm](#), which was created by the developers of Stan and rstan to make running a Bayesian regression with rstan much more like you would run a normal frequentist regression.
- Another very similar package to rstanarm is [brms](#), which also makes running Bayesian regression much simpler and 'R-like'.



Short comparison of rstanarm and brms

rstanarm is faster, has better posterior checking, and is a bit simpler to use.

brms is generally a bit more flexible, with support for some regression types missing in rstanarm, more flexible specification of priors, and support for more types of error correlational structures.

- My sense is that **rstanarm** is the more popular choice, so that's what we'll use here.



Using rstanarm

With rstanarm, most regressions you run using the function `stan_glm()`

- Since generalized linear models (GLMs) incorporates models like linear regression, probit, logit, Poisson, binomial, exponential, etc)

Syntax:

```
mybayesreg <- stan_glm(y ~ X1 + x2 + x3 ...,  
                      family = myfamily, data = mydata,  
                      prior = myprior)
```



Options with stan_glm

Family (with a possible **link** argument needed as well) defines the type of regression you want:

- Linear regression: `family = gaussian`
- Logit: `family = binomial(link = "logit")`
- Probit: `family = binomial(link = "probit")`
- Poisson: `family = poisson`
- More options can be read from the main [GLM page](#)

Prior distributions:

- **Flat priors** can be set by using `prior = NULL`
- *[Weakly]* Informative Priors can be specified by using `prior =` with one of:
 - *normal, student_t, cauchy, laplace* and more found [here](#)



A Titanic survival example with rstanarm

```
titanic <- import("https://raw.githubusercontent.com/vincentarelbundock/corpusdata/master/titanic.csv")  
# Display titanic data  
glimpse(titanic, width = 50)
```

```
## Observations: 1,313  
## Variables: 7  
## $ V1      <chr> "1", "2", "3", "4", "5", "6"...  
## $ Name    <chr> "Allen, Miss Elisabeth Walto...  
## $ PClass  <chr> "1st", "1st", "1st", "1st", ...  
## $ Age     <dbl> 29.00, 2.00, 30.00, 25.00, 0...  
## $ Sex     <chr> "female", "female", "male", ...  
## $ Survived <int> 1, 0, 0, 0, 1, 1, 1, 0, 1, 0...  
## $ SexCode  <int> 1, 1, 0, 1, 0, 0, 1, 0, 1, 0...
```



A Titanic survival example with rstanarm

```
# Recode Class
titanic$class <- recode(titanic$PClass, "*"="NA",
  "1st"="1", "2nd"="2", "3rd"="3")
titanic$class[titanic$class == "NA"] <- NA
titanic$class <- as.numeric(titanic$class)

TitanicLinear <- stan_glm(Survived ~ Age +
  SexCode + as.factor(class),
  data = titanic, family = gaussian)
```



Summary data from stan_glm

```
summary(TitanicLinear)
```

Model Info:

```
function:    stan_glm
family:      gaussian [identity]
formula:     Survived ~ Age + SexCode + as.factor(class)
algorithm:   sampling
priors:      see help('prior_summary')
sample:      4000 (posterior sample size)
observations: 756
predictors:  5
```

Estimates:

	mean	sd	2.5%	25%	50%	75%	97.5%
(Intercept)	0.6	0.1	0.5	0.6	0.6	0.7	0.7
Age	0.0	0.0	0.0	0.0	0.0	0.0	0.0
SexCode	0.5	0.0	0.4	0.5	0.5	0.5	0.6
as.factor(class)2	-0.2	0.0	-0.3	-0.2	-0.2	-0.2	-0.1
as.factor(class)3	-0.4	0.0	-0.5	-0.4	-0.4	-0.4	-0.3
sigma	0.4	0.0	0.4	0.4	0.4	0.4	0.4
mean_PPD	0.4	0.0	0.4	0.4	0.4	0.4	0.5
log-posterior	-364.8	1.8	-369.3	-365.7	-364.5	-363.6	-362.5

Diagnostics:

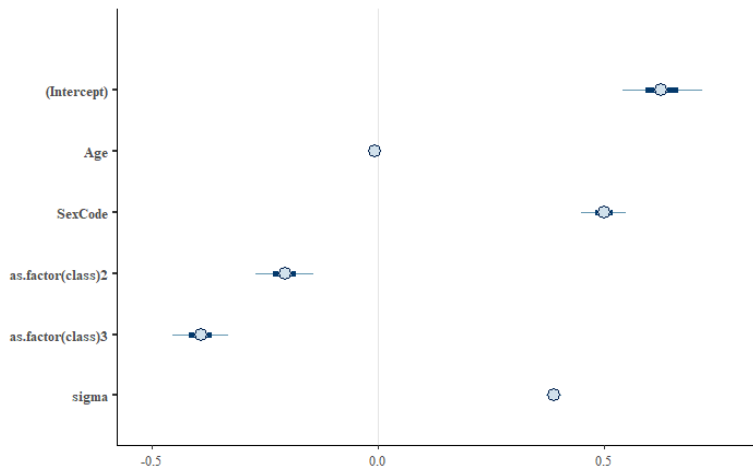
	mcse	Rhat	n_eff
(Intercept)	0.0	1.0	2140
Age	0.0	1.0	3102
SexCode	0.0	1.0	4000
as.factor(class)2	0.0	1.0	2575
as.factor(class)3	0.0	1.0	2386
sigma	0.0	1.0	4000
mean_PPD	0.0	1.0	4000
log-posterior	0.0	1.0	1847

For each parameter, mcse is Monte Carlo standard error, 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).



Viewing credible intervals

```
plot(TitanicLinear)
```



Credible intervals

You can also easily get print the credible intervals with the function `posterior_interval()`

```
posterior_interval(TitanicLinear, prob=0.95)
```

##	2.5%	97.5%
## (Intercept)	0.523751542	0.737444739
## Age	-0.008300092	-0.003851192
## SexCode	0.445067973	0.557727558
## as.factor(class)2	-0.285124975	-0.129082331
## as.factor(class)3	-0.470729826	-0.317873502
## sigma	0.369249759	0.410457494



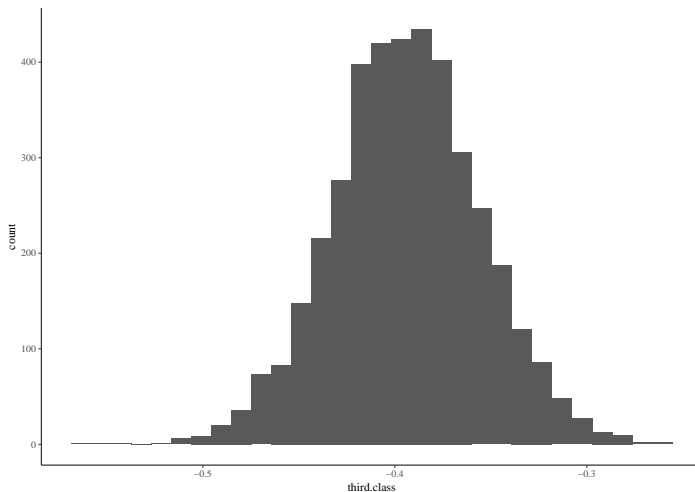
Plotting the posterior distribution

You can also easily plot the posterior distribution of a parameter in R.

```
Titanic_posterior <- TitanicLinear %>% as.tibble() %>%  
  rename(sec.class = "as.factor(class)2",  
         third.class = "as.factor(class)3")  
  
ggplot(Titanic_posterior, aes(x=third.class)) +  
  geom_histogram()
```



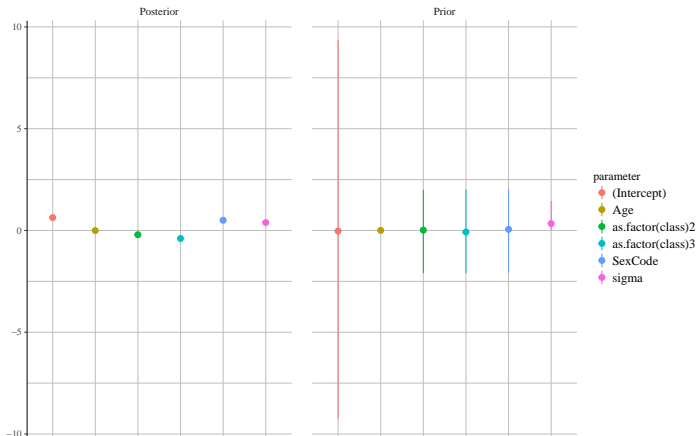
Plotting the posterior distribution



Juxtaposing the prior and the posterior

```
##
```

```
## Drawing from prior...
```



Model Testing



Model testing basics

There are a number of different regression diagnostics after performing Bayesian regression to help infer if the model converged, how well it performs, and even compare between models.

Today, we'll cover some of them included with rstanarm as well as the very useful [shinystan package](#).



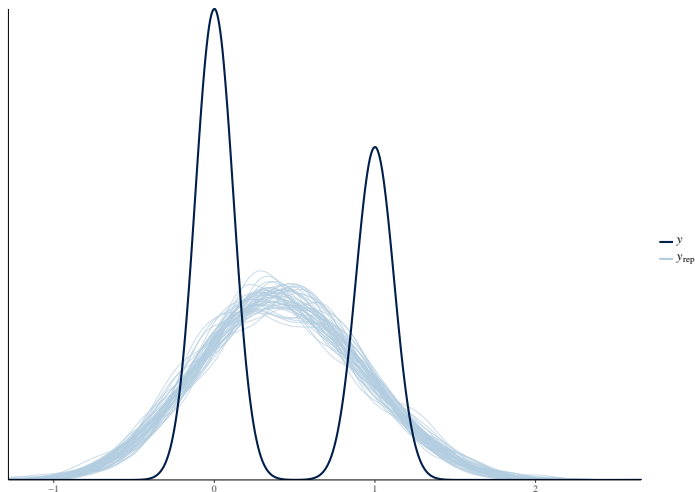
Graphical posterior predictive analysis

To check the predictive accuracy of the posterior distribution, you can use the function `pp_check()`, which plots simulated y values from the posterior distribution against the actual values of y .

```
pp_check(TitanicLinear)
```



Graphical posterior predictive analysis



Regularization and Predictive Accuracy

A critical issue in both Bayesian and frequentist estimation is how to balance predictive accuracy with parsimony. Put another, the researcher should be concerned with not overfitting the data while still creating a compelling model.

The basic approach in frequentist method is to use the Akaike information criterion (AIC):

Expected Log Predictive Density:

$$elpd_{AIC} = \log p(y|\hat{\theta}_{MLE}) - k$$

- Where θ_{MLE} is the maximum likelihood estimator of θ ,
- $\log p(y|\hat{\theta}_{MLE})$ is the log likelihood given θ_{MLE} ,
- and k is the number of parameters in the model.

The most basic Bayesian adaptation of the AIC is the Deviance information criterion (DIC):



Watanabe-Akaike information criterion

An improvement over the DIC is the Watanabe-Akaike information criterion:

$$el\hat{p}d_{WAIC} = \sum_{i=1}^n \log p(y_i) - \sum_{i=1}^n \log V[p(y_i)]$$

The WAIC has the advantages of: - Averaging the likelihood over the posterior distribution rather than using the mean - Does not assume a multivariate Gaussian posterior distribution, as does the DIC (and AIC)



WAIC example

```
loo(TitanicLinear)
```

```
## Computed from 4000 by 756 log-likelihood matrix
##
##           Estimate      SE
## elpd_loo    -360.7  19.3
## p_loo         6.2   0.4
## looic        721.3  38.6
##
## All Pareto k estimates are good (k < 0.5)
## See help('pareto-k-diagnostic') for details.
```



Leave One Out Cross Validation

Another method alongside WAIC for comparing out-of-sample predictive ability is to apply leave-one-out cross-validation (LOO), which assesses predictive ability posterior simulations in which the data is iteratively partitioned in training and prediction sets.

Expected Log Predictive Density:

$$el\hat{p}d_{LOO} = \sum_{i=1}^n \log p(y_i | y_{-i})$$



LOO example

```
loo(TitanicLinear)
```

```
## Computed from 4000 by 756 log-likelihood matrix
##
##           Estimate    SE
## elpd_loo    -360.7  19.3
## p_loo         6.2   0.4
## looic        721.3  38.6
##
## All Pareto k estimates are good (k < 0.5)
## See help('pareto-k-diagnostic') for details.
```



Comparing models

```
Titanic_probit <- stan_glm(Survived ~ Age +
  SexCode + as.factor(class),
  data = titanic, family = binomial(link=probit))
Loo_probit <- loo(Titanic_probit)

Titanic_logit <- stan_glm(Survived ~ Age +
  SexCode + as.factor(class),
  data = titanic, family = binomial(link=logit))
Loo_logit <- loo(Titanic_logit)

compare_models(Loo_probit, Loo_logit)
```

```
## elpd_diff      se
##          1.4      0.8
```



Many more diagnostics with shinystan

Probably the most popular diagnostic for Bayesian regression in R is the functionality from the [shinystan package](#).

- Shinystan launches a “Shiny” web application to show you model diagnostics, so it can’t be done inside of a RMarkdown document (but works just fine if called from the console.)

```
# Don't do in RMarkdown  
launch_shinystan(TitanicLinear)
```

