Bayesian Data Analysis

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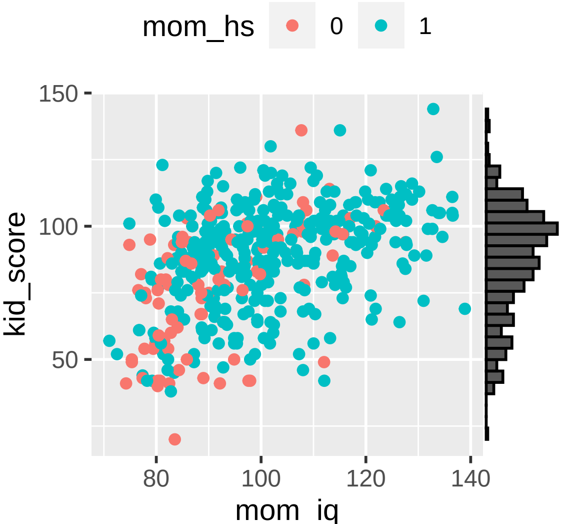
Bayesian Linear Regression with JAGS

Data: Cognitive Test Scores

Data are available on the cognitive test scores of three- and four-year-old children in the USA. - The sample contains 434 observations - Information also provided about his/her mother's IQ and whether or not the mother graduated from highschool.



Simple Linear Regression Model

We will assume a normal model for the data such that

$$y_i|\mu, \sigma^2 \sim N(\mu_i, \sigma^2)$$

Let's start simple and consider the expected value for y_i as a function of one explanatory variable (mother's IQ) such that

$$\mu_i = \alpha + \beta(x_i - \mathrm{m}ean(x_i))$$

where the predictor is mean centered.

This could also be specified as

$$y_i = \alpha + \beta(x_i - \mathrm{m}ean(x_i)) + \epsilon_i$$

$$\epsilon_i \sim N(0, \sigma^2)$$

Prior Choice

We will need to specify priors for α, β and σ.

Before seeing the data would could assume that the value of the intercept (α) is unlikely to be to beyond the range of possible IQ values (1, 200). So let's assume an expected value of 100 and a standard deviation of 30.

$\alpha \sim N(100, 30^2)$

For the slope (β), before seeing the data I have no idea about whether the mother's IQ affects the kid's IQ, so it is reasonable to consider a value of 0 for the slope. Realistically I think we are unlikely to see the value of the slope going anywhere beyond the range (-4,4), so let's assume a standard deviation for the slope of 2.

$\beta \sim N(0, 2^2)$

Prior Choice

For σ we can consider some uninformative or weakly informative priors commonly used for variance parameters:

- Gamma prior $gamma(\epsilon, \epsilon)$ on the precision $(\tau = \frac{1}{\sigma^2})$

$\tau \sim Ga(0.1, 0.1)$

- Uniform prior on the standard deviation

$\sigma \sim U(0, 50)$

- Cauchy (half-t) prior on the standard deviation

$\sigma \sim ht(30, 10^2, 1)$

JAGS model specification

```
lrmodel1 ="
model{
    for (i in 1:n){
        y.i[i] ~ dnorm(mu.i[i], sigma^-2)
        mu.i[i] <- alpha + beta*(x.i[i] - mean(x.i))
    }

#Priors
alpha ~ dnorm(80, 30^-2)
beta ~ dnorm(0, 2^-2)
sigma ~ dt(30,10^-2,1)T(0,) #truncated t-distribution
}
"
```

Model Fitting

```r
library(rjags)
library(R2jags)

jags.data <- list(y.i = kidiq$kid_score,
                  x.i = kidiq$mom_iq,
                  n = nrow(kidiq))

parnames <- c("alpha","beta","sigma","mu.i")

mod1 <- jags(data = jags.data,
            parameters.to.save=parnames,
            model.file = textConnection(lrmodel1))
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 434
##    Unobserved stochastic nodes: 3
##    Total graph size: 1881
##
## Initializing model
```

Output - Parameter Uncertainty

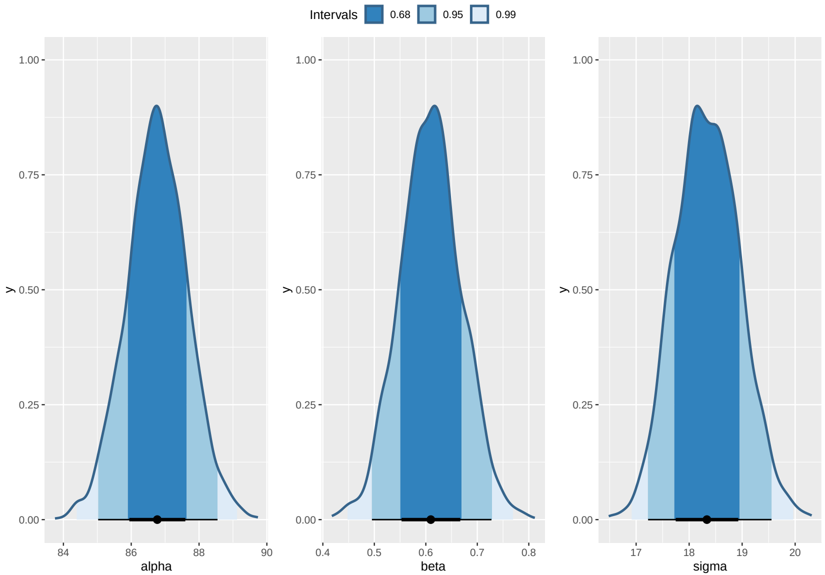
```
m1 <- mod1$BUGSoutput$sims.matrix

par_samps <- m1 %>% spread_draws(alpha,beta,sigma)

par_summary <- m1 %>%
                gather_rvars(alpha,beta,sigma) %>%
                median_qi(.value)
par_summary
```

```
## # A tibble: 3 x 7
##   .variable .value .lower .upper .width .point .interval
##   <chr>      <dbl>  <dbl>  <dbl>  <dbl> <chr>  <chr>
## 1 alpha     86.8   85.0   88.5     0.95 median qi
## 2 beta       0.610  0.495  0.727   0.95 median qi
## 3 sigma     18.3   17.2   19.6     0.95 median qi
```

Output - Parameter Uncertainty



Output - Parameter Uncertainty

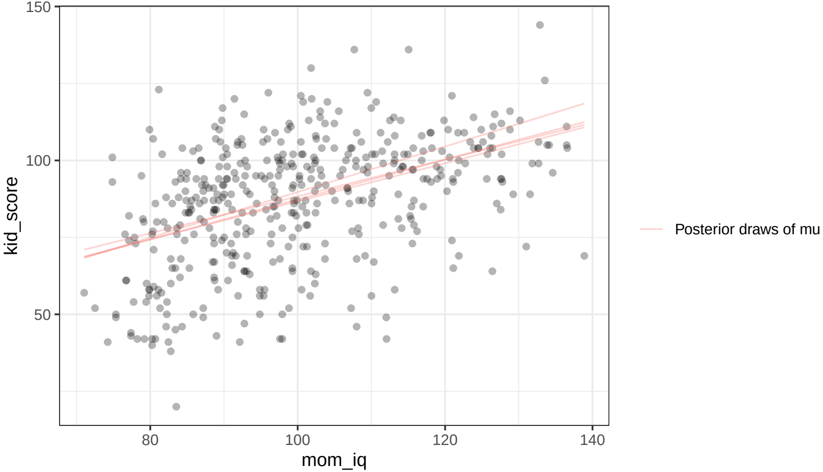
```
mu_ind <- 1:nrow(kidiq)
mu_samps <- m1 %>% spread_draws(mu.i[mu_ind])
mu_summary <- mu_samps %>%
                median_qi(.width = 0.95)
mu_summary[1:5,]
```

```
## # A tibble: 5 x 7
##   mu_ind  mu.i .lower .upper .width .point .interval
##    <int> <dbl>  <dbl>  <dbl>  <dbl> <chr>  <chr>
## 1      1  99.6   96.6 103.     0.95 median qi
## 2      2  80.3   78.1   82.4   0.95 median qi
## 3      3  96.2   93.7   98.7   0.95 median qi
## 4      4  86.4   84.7   88.2   0.95 median qi
## 5      5  82.3   80.4   84.3   0.95 median qi
```

Posterior Draws of μ_i

For each draw (simulation) $s = 1, \ldots, S$ of the parameters from the posterior distribution we can obtain $\mu_i^{(s)} = \beta_0^{(s)} + \beta_1^{(s)}(x_i - mean(x_i))$

5 draws



Posterior Draws of μ_i

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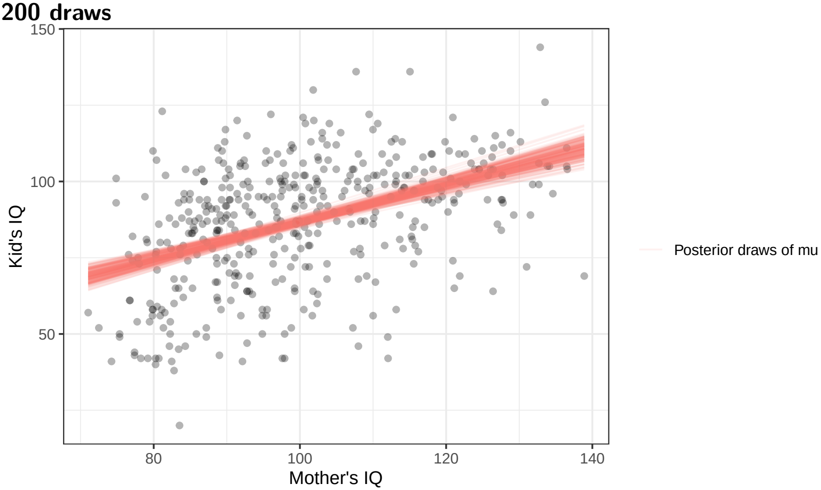
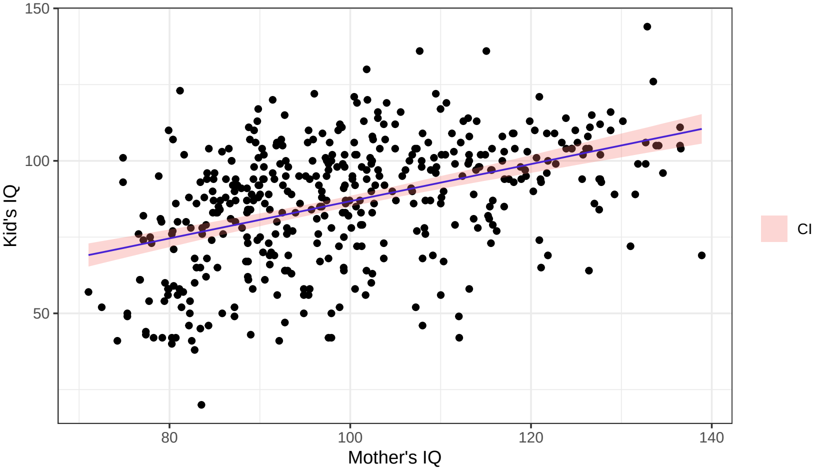
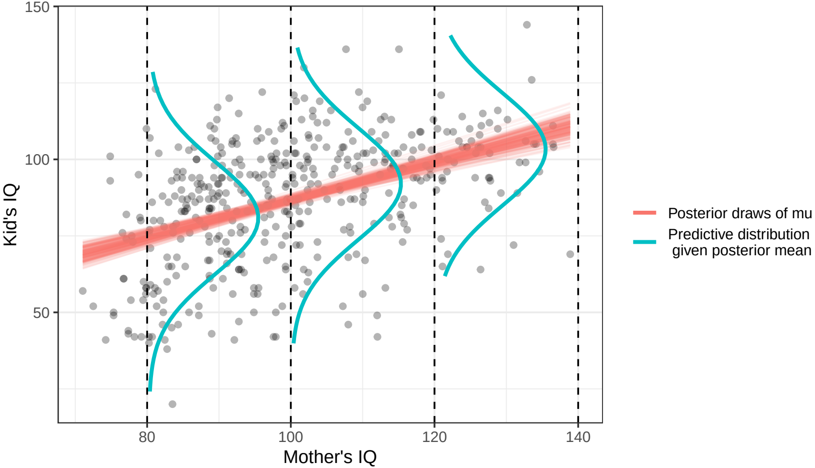


Point Estimate + Credible Interval



Predictive Distribution

The posterior predictive distribution is the distribution of possible unobserved values conditional on the observed values.



Credible interval vs prediction interval

A Bayesian “credible interval”, is an interval associated with the posterior distribution of a parameter, for example, the expected value of the Kid’s IQ given a mother’s IQ of 120 (μ). If I give an 80% interval there should be an 80% chance that the expected value of the Kid IQ lies within the interval.

A prediction interval is an interval associated with a random variable yet to be observed, for example, an unobserved Kid’s IQ, given a mother’s IQ of 120 ($\tilde{y}$). If I give an 80% interval there should be an 80% chance that the actual Kid IQ lies within the interval.

```
lrmodel1 ="
model{
....
## predictive distribution
  mu_pred <- alpha + beta*(120 - mean(x.i))
    ytilde ~ dnorm(mu_pred, sigma^-2)
}
"
```

Credible interval vs prediction interval

Let's consider the difference between the credible interval and the prediction interval for the Kid's IQ when the Mother's IQ = 120.

```
m1 <- mod1$BUGSoutput$sims.matrix

par_samps <- m1 %>% spread_draws(mu_pred,ytilde)

par_summary <- m1 %>%
                gather_rvars(mu_pred,ytilde) %>%
                median_qi(.value)
par_summary
```

```
## # A tibble: 2 x 7
##   .variable .value .lower .upper .width .point .interval
##   <chr>      <dbl>  <dbl>  <dbl>  <dbl> <chr>  <chr>
## 1 mu_pred     98.9   96.1   102.   0.95 median qi
## 2 ytilde      99.5   62.6   134.   0.95 median qi
```

What do you notice about the width of the intervals?

Extending the regression model

Suppose now we want to see if there's a "highschool" effect on the relationship between Mother's IQ and Kid's IQ.

Some possible choices:

- Model 2A: Add the highschool variable in as a covariate, this will lead to a varying intercepts model with α_1 for highschool = no and α_2 for highschool = yes.
- Model 2B: Add the highschool variable in as a covariate and as an interaction with Mother's IQ, this will lead to a varying intercepts and slopes model with α_1 and β_1 for highscool = no and α_2 and β_2 for highscool = yes.

Let's consider model 2B. The specification of this model could be written as

$$y_i|\mu,\sigma^2 \sim N(\mu_i,\sigma^2)$$

$$\mu_i = \underbrace{\alpha_{j[i]} + \beta_{j[i]}}_{\text{j[i] = HS for obs i}} (x_i - mean(x_i))$$

$$\alpha_j \sim N(100, 30^2), \text{ for } j = 1,2$$

$$\beta_j \sim N(0, 2^2), \text{ for } j = 1,2$$

JAGS model specification

```
lrmodel2 ="
model{
    for (i in 1:n){
        y.i[i] ~ dnorm(mu.i[i], sigma^-2)
        mu.i[i] <- alpha.j[hs_index[i]] + beta.j[hs_index[i]]*(x.i[i] - mean(x.i))
    }

#Priors
for(j in 1:m)
{
alpha.j[j] ~ dnorm(80, 30^-2)
beta.j[j] ~ dnorm(0, 2^-2)
}
sigma ~ dt(30,10^-2,1)T(0,) #truncated t-distribution
}
"
```

```
jags.data <- list(y.i = kidiq$kid_score,
                  x.i = kidiq$mom_iq,
                  hs_index = as.numeric(kidiq$mom_hs + 1),
                  n = nrow(kidiq),
                  m = 2)
```

Output

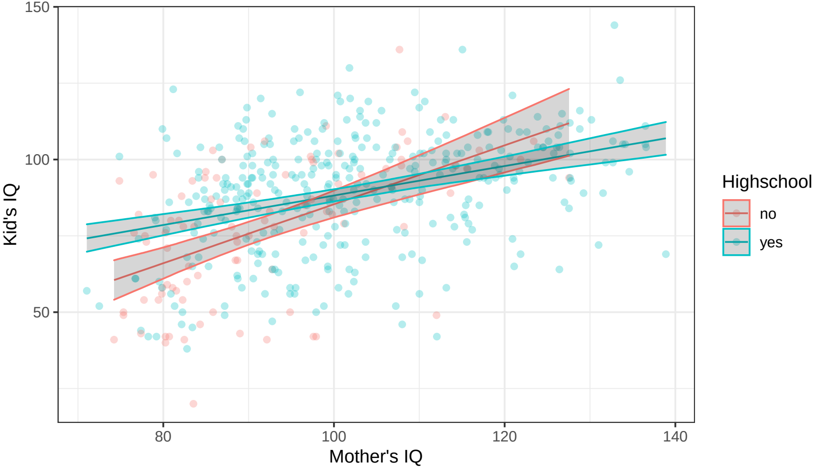
```r
m2 <- mod2$BUGSoutput$sims.matrix

par_samps <- m2 %>% spread_draws(alpha.j[1:2],beta.j[1:2])

par_summary <- m2 %>%
                gather_rvars(alpha.j[1:2],beta.j[1:2]) %>%
                median_qi(.value)
par_summary
```

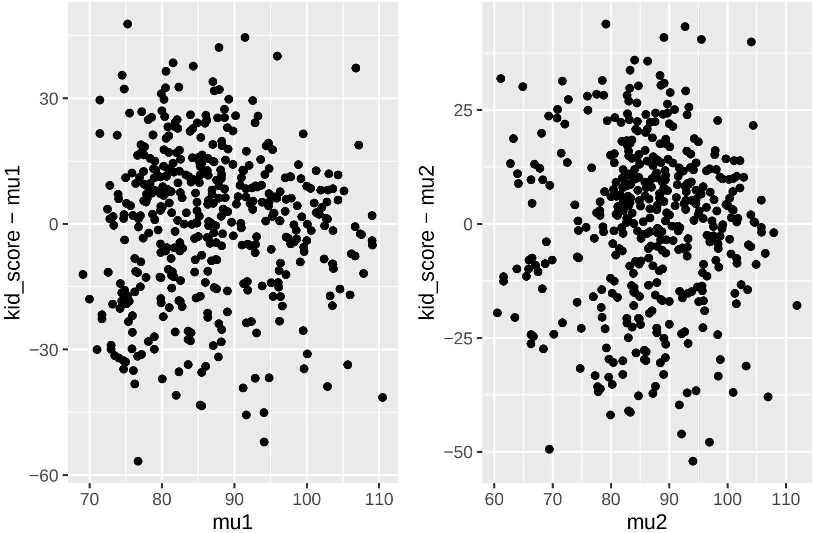
```
## # A tibble: 4 x 8
##   `1:2` .variable .value .lower .upper .width .point .interval
##   <int> <chr>      <dbl>  <dbl>  <dbl>  <dbl> <chr>  <chr>
## 1     1 alpha.j   85.4   81.0   89.8     0.95 median qi
## 2     2 alpha.j   88.2   86.3   90.2     0.95 median qi
## 3     1 beta.j     0.963  0.682  1.26    0.95 median qi
## 4     2 beta.j     0.483  0.350  0.616   0.95 median qi
```

Visualising the results



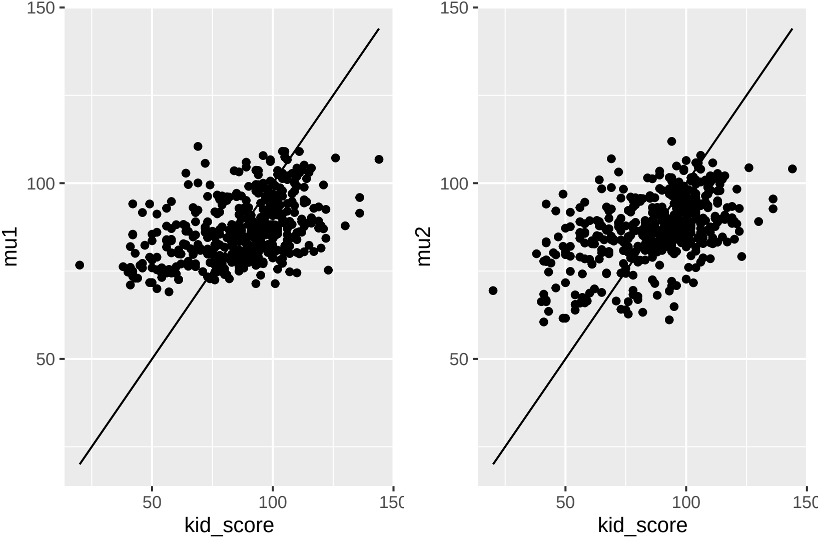
Which model do we choose?

Firstly, let's have a look at the residuals for each model



Which model do we choose?

Let’s also consider the observed values vs the model-based estimates.



Model information criteria

You might have come across these before: Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC)

- The general idea is that the score on the likelihood is a good measure of model fit, except for the fact that more complex models will generally have higher likelihood scores
- If we penalise these scores by some measure of the complexity of the model then we can compare models across complexities
- The usual measure of complexity is some function of the number of parameters
- Because these are relative model comparisons, the best model according to an IC might still be useless.

Model information criteria

To calculate an IC, the likelihood score gets transformed into the deviance (remember JAGS monitors the “deviance” parameter), which is minus twice the log-likelihood score and then add a model complexity term is added.

- The two most common ICs are:

AIC : $-2 \log L + 2p$

BIC : $-2 \log L + p \log(n)$

where p is the number of parameters and n is the number of observations

- Smaller values indicate the preferred model.

Model information criteria

For Bayesian models it's hard to know which value of L to use, seeing as at each iteration we get a different likelihood score. Two specific versions of IC have been developed.

- The first, called the Deviance Information Criteria (DIC) is calculated via:

DIC: -2 log Lmax $+$ 2 p_D

where pD is the effective number of parameters

- The second called the Widely Applicable Information Criterion (WAIC) which is calculated as:

WAIC: -2 log Lmax $+$ p_{WAIC}

Here p_{WAIC} is a measure of the variability of the likelihood scores

Which IC to use?

- WAIC and DIC are built for Bayesian hierarchical models
- DIC is included by default in the R2jags package
- WAIC is included in the loo package which is installed alongside Stan
- WAIC is considered superior as it also provides uncertainties on the values. Most of the others just give a single value

Obtaining DIC and WAIC from JAGS

- DIC is easy to obtain from JAGS

```
DIC.m1 = mod1$BUGSoutput$DIC
DIC.m1
```

```
## [1] 3757.357
```

```
DIC.m2 = mod2$BUGSoutput$DIC
DIC.m2
```

```
## [1] 3745.361
```

- WAIC takes a little bit more work but there's some code here that illustrates how to do it.

```
##   waic p_waic
## 3757.2    2.9
```

```
##   waic p_waic
## 3745.1    4.9
```

Cross Validation

Cross validation (CV) works by:

1. Removing part of the data
2. Fitting the model to the remaining part
3. Predicting the values of the removed part
4. Comparing the predictions with the true (left-out) values

It's often fitted repeatedly

- as in k-fold CV where the data are divided up into k groups, and each group is left out in turn.
- In smaller data sets, people perform leave-one-out cross-validation (LOO-CV)