

Report Title: Example Report

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1 Executive Summary

In the UK it is a criminal offence to drive a motor vehicle with a blood or breath alcohol concentration above the prescribed limit. When a person is arrested for driving under the influence of alcohol it is not usually possible to perform an accurate test of the level of alcohol in the blood or breath immediately. Breath tests can be used as an initial screening tool at the scene, but these are not sufficiently accurate for prosecution. Instead, people are taken to a police station or hospital, where the test can be carried out using proper laboratory protocols. As the body clears alcohol from the blood through time this means that if the individual was over the limit, the measured blood alcohol concentration (BAC) will be lower at the time of measurement than it was when the person was driving a motor vehicle. To deal with this situation, If the BAC after time t (hours) is measured as C_t (g/kg), the BAC at time 0 is estimated as $C_0 = C_t - \beta t$, where β (g/kg/h) is BAC elimination rate.

The key point is how to find a precise β to estimate C_0 . Forensic scientists currently 2.5% percentile of β distribution constructing from samples as the estimated β value for every individuals. This method is obviously not rigorous for the courts.

In this report, we introduce a Bayesian regression model with considering the heterogeneity between individuals, the model gives a posterior distribution of β by using both samples and prior knowledge. Then we randomly simulate 4000 β values from posterior distribution and find out the probability of the person's BAC over limit while driving.

In real world, β estimation is quite difficult, it depends on the individuals' liver condition, drinking habits, genetic, diet, etc. As we don't have corresponding data, in our regression model of β is mainly dominate by gender, but we still find some useful variables like 'gender' and 'drinking time'

When it is too late to use a blood or breath test and the only information available is eyewitness testimony of the quantity of alcohol consumed. We have to use Widmark's equation:

$$C_t = \frac{A}{Weight \times V_d} - \beta t$$

where A is Amount of Alcohol Consumed (g), V_d is the volume of distribution that need to be found.

Forensic scientists use the same method again to estimate V_d separately with β . But V_d and β are not independent, so we build a joint Bayesian regression model, which can simulate them together to solve with the correlation. Then again after simulation, each C_t is calculated by each pair of β and V_d , so expert witness can still find a probability of C_t exceeding the limit.

2 Data Description

β true values are converted to positive to convenient calculation.

It is important to normalized all numerical variables. Centering the covariates can reduce autocorrelation ρ_k of lag k which is defined as:

$$\rho_k = \frac{Cov(\theta^i, \theta^{i+k})}{\theta^2},$$

ρ_k measures how similar the sample at position i is to the sample at position $i + k$. As a random walk process, θ_i should be similar to θ_{i+1} , less similar to θ_{i+2} , independent with θ_{i+k} for large k . So if ρ_k is large means the chains hardly move, can't converge.

To make it more clear, we will use Effective Sample Size (ESS) to explain:

$$n_{\text{eff}} = \frac{n}{1 + 2 \sum_{k=1}^{\infty} \rho_k}.$$

' n_{eff} ' is large means the MCMC method converge faster (for example if we set 4 chains with each chains 2000 iterations, 500 burn-in, the $n_{\text{eff}} = 4000$ means the number of independent samples is 4000 out of 8000). Larger n_{eff} in same number of iterations means smaller variance of estimated exoectation since:

$$V(\hat{E}(\beta)) \approx \frac{\sigma^2}{n_{\text{eff}}}.$$

Also Since β is a small value, the coefficients of large value variables are pretty small, near 0, which will make β estimation worse, so normalization for variables is necessary.

Then we prefer to β to $\log(\beta)$ since the original β distribution has heavy tail, all outliers (if have) can be scaled. As shown in figure 1, β forms a good normal distribution shape after log-transferring. After simulation we can take exponential of the results.

Since β is a constant rate, measured when the BAC curve reaches peak and starts to decrease, so variables like AAC and Maximum BAC will not be used, since they are correlated with the value of BAC, not BAC elimination rate.

From the dataset, most data comes from age smaller than 30 (85/100), so even though age is sufficient variable for β the model can't really recognize it. Research shows that age doesn't really matter unless the subject has age-related liver disease, but because of moral and ethical, we don't find much research of alcohol test on elderly person with liver disease.

'BAC Peak time' is converted to hours.

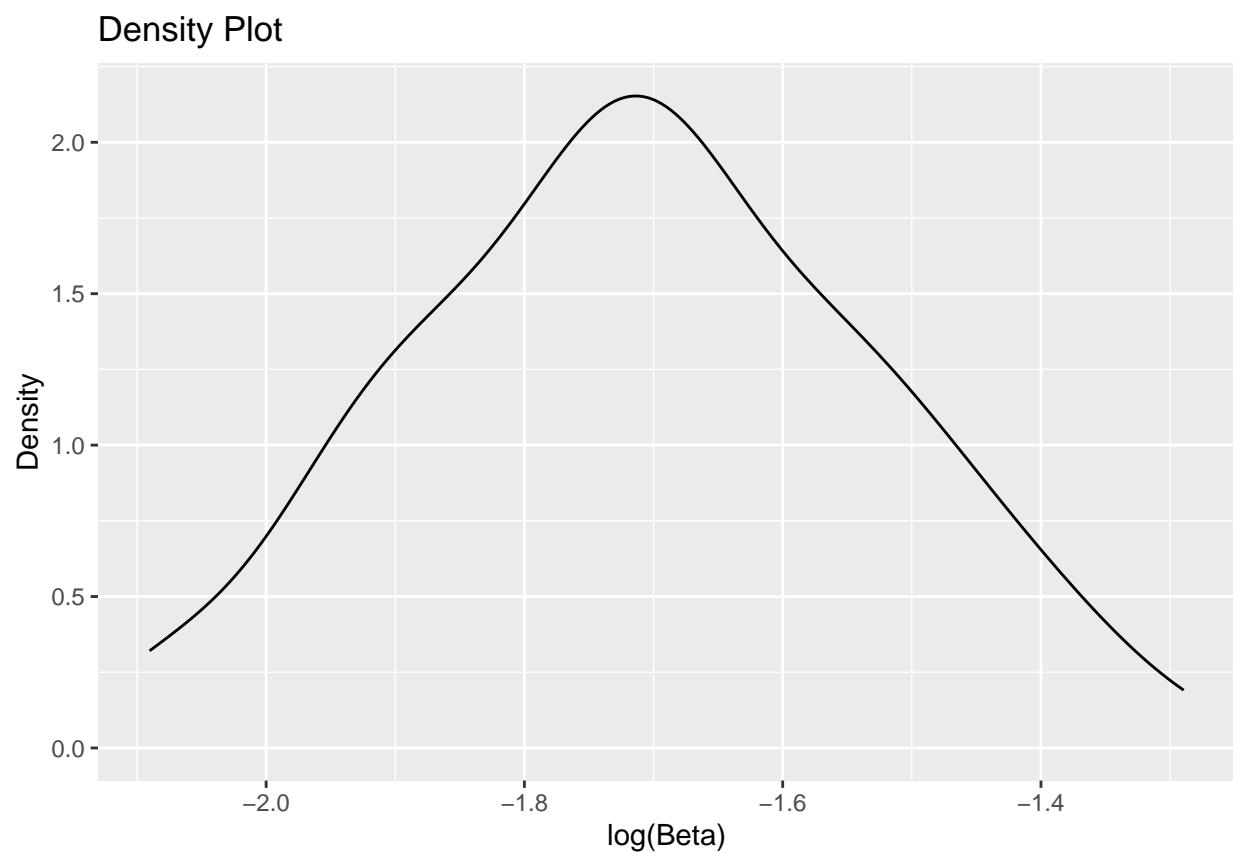


Figure 1: $\log(\beta)$ distribution.

3 Bayesian regression model

3.1 Advantages and disadvantages of exists method for β

Although the forensic scientists' method is easy to calculate and conservative enough, But:

- The courts will be forced to make decisions under estimated β if we only give a single estimation of β , since the calculated C_0 is either over or under the legal limit.
- Differences between individuals are ignored, for example age and sex, which may affect β .
- β value at 2.5% is over conservative and most uncertainties are hiding.

So we don't suggest it.

3.2 Reasons for BRM and advantage

Comparing with fitting linear regression model for β_i , which can be expressed as:

$$\hat{\beta}_{i,j} = \hat{\gamma}_1 \text{female}_j + \hat{\gamma}_2 \text{male}_j + \hat{\gamma}_3 \text{weight}_j + \hat{\gamma}_4 \text{height}_j + \varepsilon_i$$

and giving a exact value of $\hat{\beta}_i$ for i_{th} estimation of $\hat{\beta}$ under σ_i^2 for j_{th} individuals, BRM can model uncertainty from each coefficient $\hat{\gamma}$. We provide priors and sample likelihoods for each variables' coefficients, BRM will apply bayesian rule to each and output simulation results of each coefficients, not only for $\hat{\beta}$. $\hat{\beta}$ s are calculated from simulation results of $\hat{\gamma}_j$, which is:

$$\hat{\beta}_{i,j} = \hat{\gamma}_{1,i} \text{female}_j + \hat{\gamma}_{2,i} \text{male}_j + \hat{\gamma}_{3,i} \text{weight}_j + \hat{\gamma}_{4,i} \text{height}_j + \varepsilon_i$$

where

$$\varepsilon_{\beta,i} \sim \mathcal{N}(0, \sigma_{\beta}^2).$$

Since we have log-transformed β data points, we will take exponential of $\hat{\beta}_{i,j}$ to get actual value.

3.3 How BRM works

We use *brm* package in R to do this.

The principle theorem behind BRM is Bayes' Rule:

$$p(\theta | \text{data}) = \frac{p(\text{data} | \theta) p(\theta)}{p(\text{data})}.$$

The θ in the equation is the coefficients of γ_j . For most real models, we can't compute this posterior $p(\theta | \text{data})$ analytically. Markov Chain Monte Carlo (MCMC) helps us draw samples from it, which we can then summarize. BRM uses Hamiltonian Monte Carlo (One of MCMC), which is better than standard MCMC (like Metropolis-Hastings) since it is faster and cost less.

After setting priors for γ_j , we need specify a family for β as the likelihood of the observed data. In our sample, we have already taken $\log(\beta)$, so it is better to use the most common normal distribution likelihood, it is normal and can express β values good without restrict samples' shape.

Also for the MCMC simulation method, we set 4 chains, each chains 4000 draws with 1000 burn-in draws. Since MCMC is a random walk method through parameter space. One chain is a single run of the MCMC algorithm that generates a sequence of samples, so we need more chains to check the convergence and ensure that all chains convergent to same mode.

For 1000 burn-in draws, since MCMC starts from an initial value which often far from the true posterior region, so the chains need some steps to walk to the correct trace. As figure 2 shows, it is an example of the MCMC process of 'sexfemale' when using 4 chains, 100 draws. Clearly that if we keep the first 25 draws, the results will be affected.

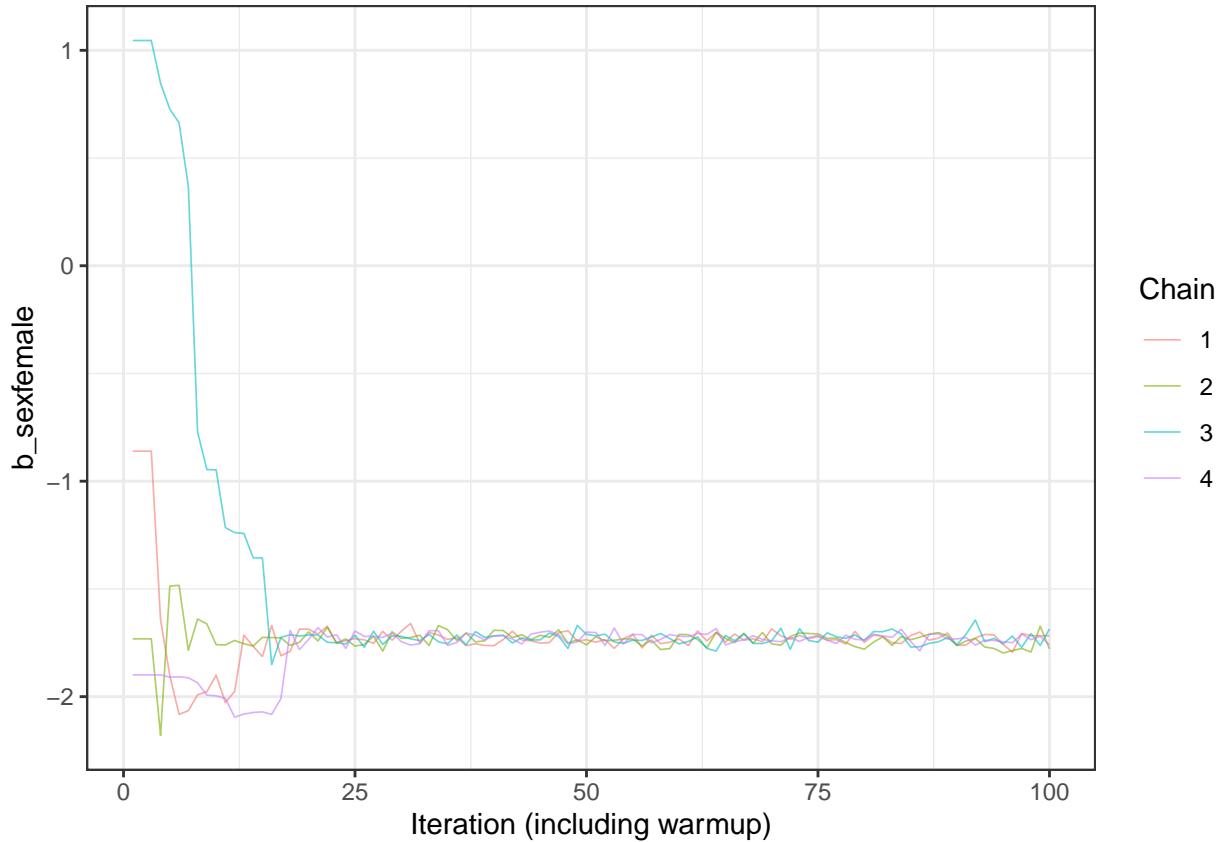


Figure 2: MCMC Simulations Traceplot.

3.4 Model Selection

3.4.1 Key Variables

We remove the intercept and use gender (male and female) to be the two baselines. Since β for male and female are in different range.

- Gender: Female's BAC elimination rate is larger than male on average (figure 3), it is explained by liver weight represents a greater fraction of lean body mass in the female gender [2].
- Drinking time: If the person keep drinking after BAC reaches peak, the measured β will be smaller since β is measured starting at BAC peak time till the end, there will be fluctuations on the BAC plots. We will use total drinking time as the indicator.
- Weight: Basically higher weight often leads lager size of liver and larger amount of total body water.
- Height: Height also affect the amount of total body water.

3.4.2 Priors

Before fitting the Bayesian regression model, appropriate priors need to be specified for all regression coefficients and the residual standard deviation. We use weakly informative priors, which have small effects on the posterior. The selected priors are summarized as follows:

Table 1: Weakly informative priors used in the Bayesian regression model

Parameter	Prior
Regression coefficient for male	Normal(0, 2)
Regression coefficient for female	Normal(0, 2)
Regression coefficients (others)	Normal(0, 0.5)
Residual SD	Exponential(1)

All variables have been standardized and we do not expect $\log(\cdot)$ to have a linear relationship with the variables, so zero-mean normal priors are appropriate. We consider gender to be one of the main factors influencing alcohol elimination rates [1], so we set relatively wide priors Normal(0, 2) for the sex coefficients, allowing their effects to vary within a reasonable range. For other standardized variables (such as weight and height), since their impacts on β are considered relatively small, we used more shrinkage weakly informative priors Normal(0, 0.5) to prevent unreasonably large effects.

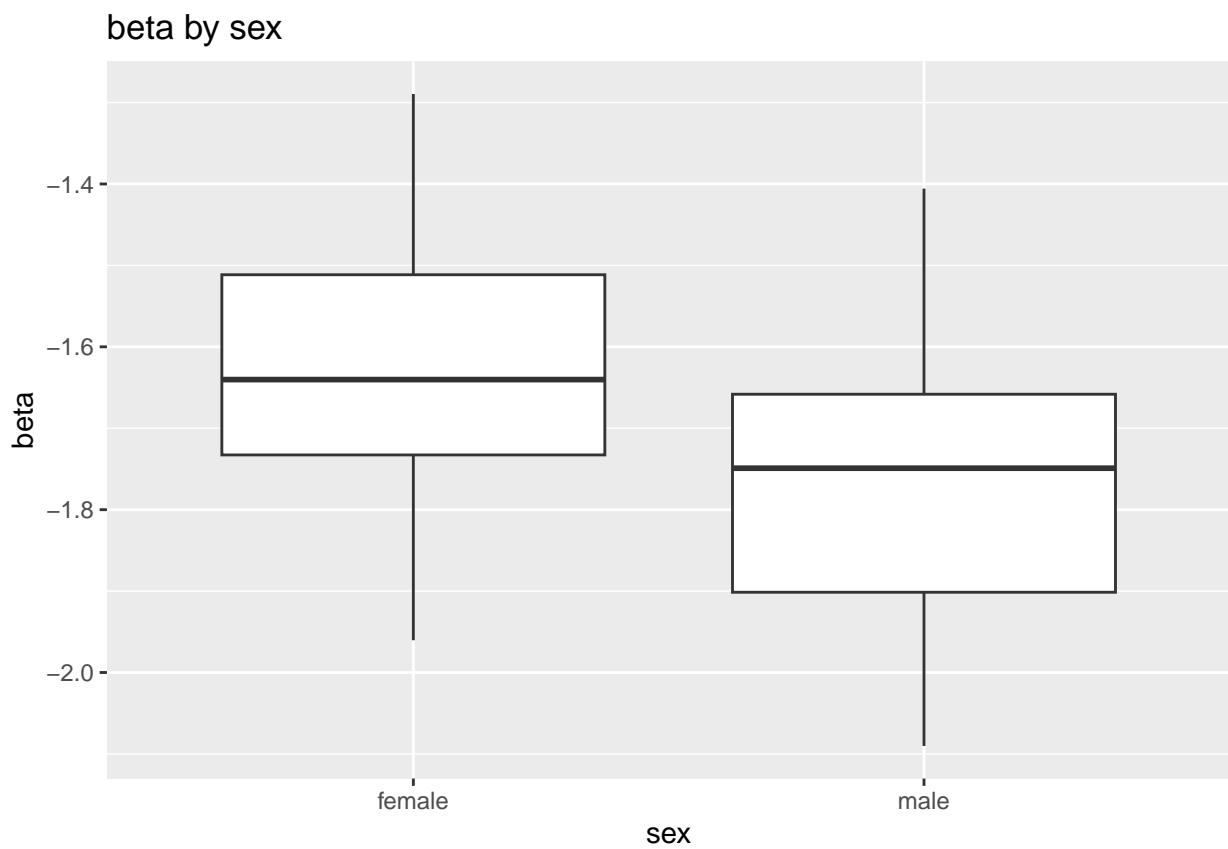


Figure 3: Box plot of beta respect to gender.

The residual standard deviation is given an Exponential(1) prior, which is a commonly used positive weakly informative prior that can avoid unreasonably high noise.

If future research involves different populations, larger sample sizes, or additional biological information, the prior distributions can be adjusted accordingly to ensure they are applicable to any new datasets.

3.5 Model Results

3.5.1 Fitting result

After 4000 iterations in 4 chains, Table 2 gives the posterior summary. Rhat compares within-chain variance and between-chain variance, all less than 1.01 means chains are well-mixed.

Figure 3 shows posterior results for each variables' coefficients, all coefficients show good normal patterns since we all chains have converged and warm-up length is enough. Since the β is log-transformed, the value of 'b_sexfemale' and 'b_sexmale' is not typical value of β like 0.19 when other coefficients are all near zero. Also σ value is estimated under log-transformed β .

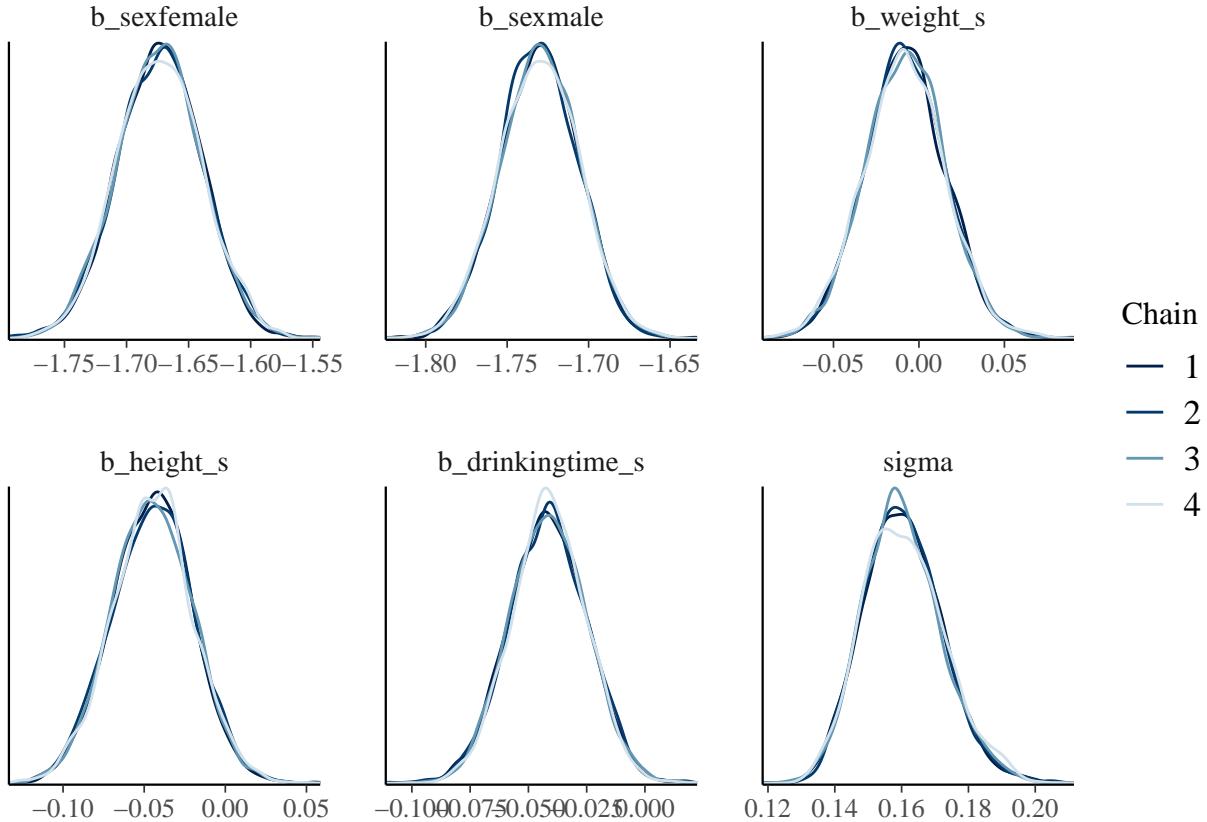


Figure 4: Posterior density of 4 chains for all coefficients.

Figure 4 shows the trace plots for all variable coefficients, it can be seen that all 4 chains mix well and all values are picking after convergent.

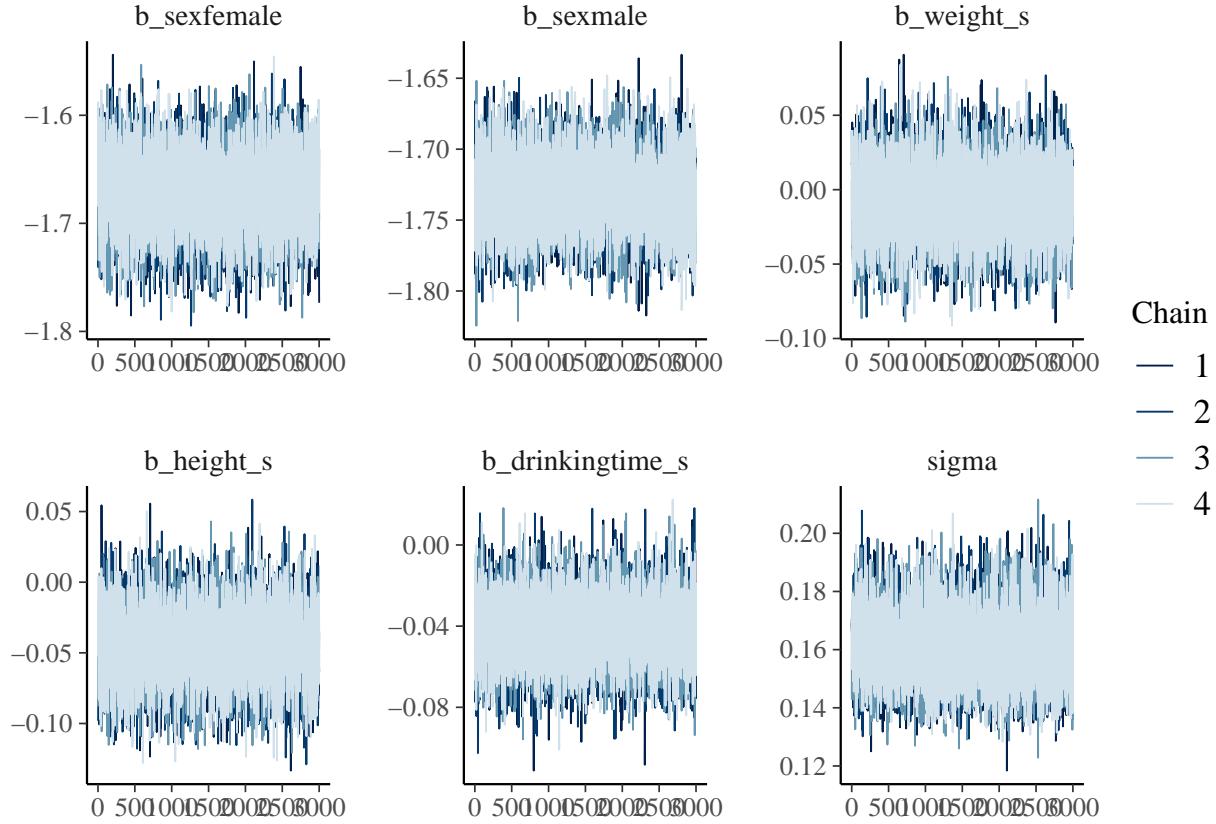


Figure 5: Traceplot of all coefficients and variance sigma.

Table 2: Posterior Summary from BRM

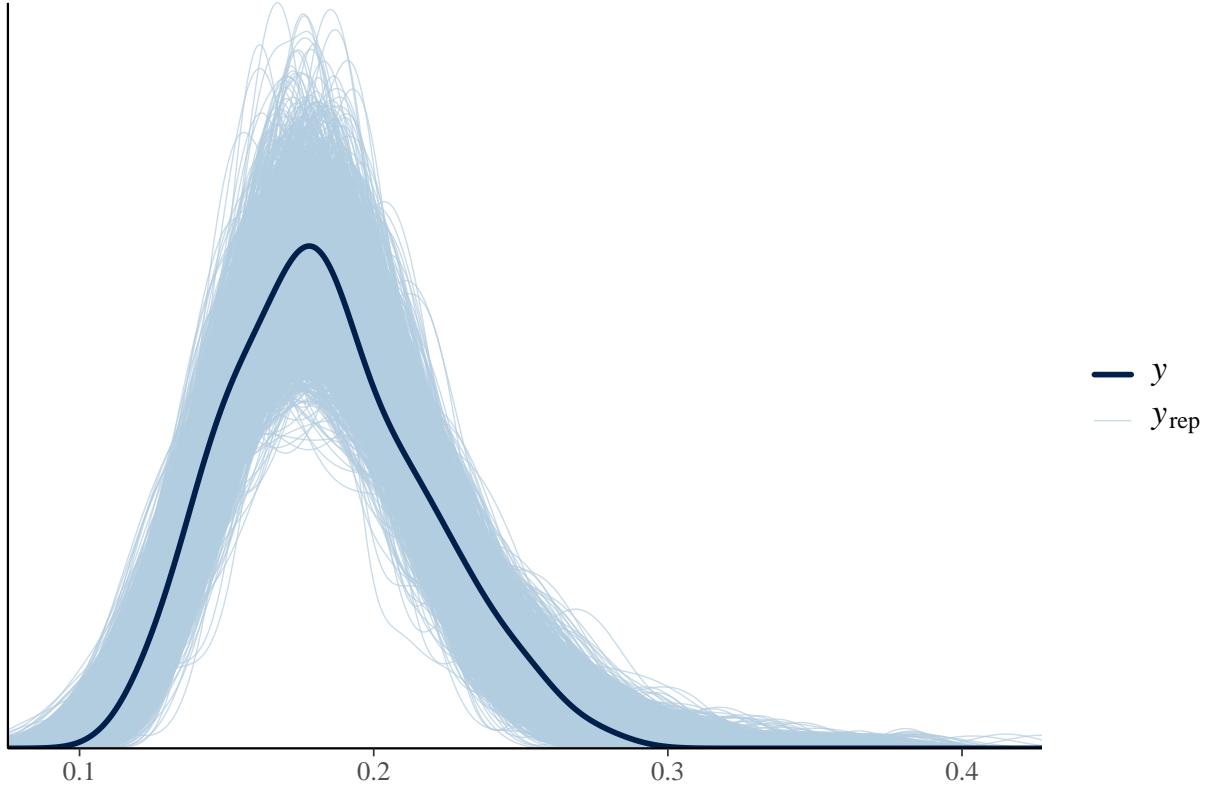
	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sexfemale	-1.673	0.034	-1.740	-1.606	1	8576.353	8334.303
sexmale	-1.730	0.024	-1.778	-1.684	1	8742.778	8309.203
weight_s	-0.008	0.024	-0.054	0.038	1	8392.999	8129.812
height_s	-0.045	0.025	-0.094	0.003	1	7596.179	8023.806
drinkingtime_s	-0.041	0.016	-0.073	-0.010	1	11330.326	8349.984

3.5.2 PPC Density

Figure 5 is the Posterior Predictive Check (PPC) density plot comparing with true value of β (Here we have taken exponential of both true value and predicted value). Notice that predicted posterior distribution matches β sample distribution pretty well, which get the mean, spread, skew both right

even at right tail.

PPC density

**Figure 6:** PPC density of 2000 predict results from posterior.

3.6 Model Testing

We take 12000 number of draws from the posterior distribution.

3.6.1 LOO-PIT QQ plot

The Leave-One-Out Probability Integral Transform Quantile-Quantile plot (LOO-PIT QQ plot) can check if the predictions calibrated correctly and if the predictive distributions biased, which is defined as:

$$\text{LOO-PIT}_i = P(\tilde{y}_i \leq y_i | y_{-i}).$$

Here we still use Monte Carlo method to simulate it, as:

$$\text{LOO-PIT}_i = \frac{1}{S} \sum_{s=1}^S \mathbf{1}(\tilde{y}_{i,-i}^{(s)} \leq y_i)$$

where S is the number of posterior draws.

We will use it to check if our posterior is under or over dispersion, the good model's PIT plot should be flat over $Uniform(0,1)$. For our model, the PIT histogram (Figure 4) is flat everywhere except probability near 0.55 and 0.8, which are acceptable by the randomness of MCMC method. A U-shape (points over dot line at two tails) in PIT plots means overestimates variance, it doesn't appear in our plot gives evidence of our choices on variables and likelihood family.

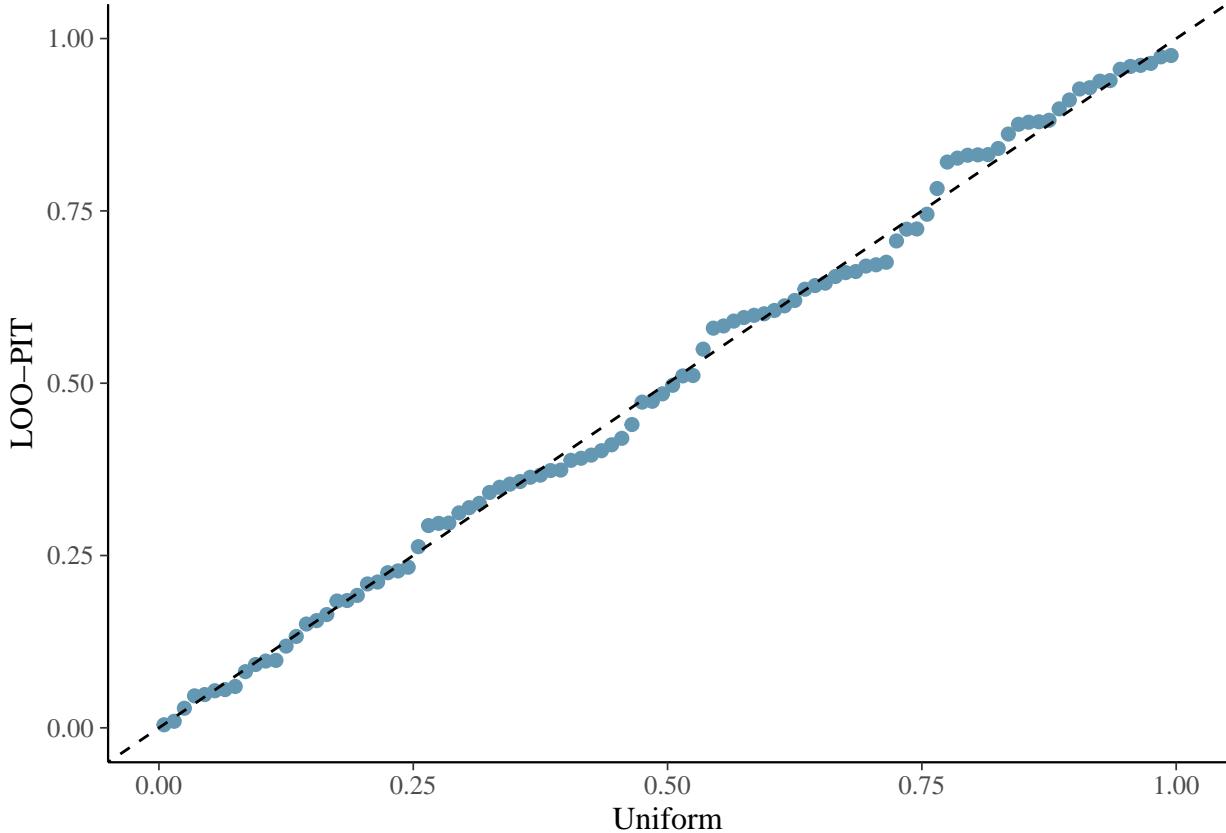


Figure 7: Probability Integral Transform (PIT) histogram.

3.6.2 Coverage rate and Errors

Table 3 shows the coverage rate of 95% and 50% predicted intervals, which means 98 and 52 individuals' real β value is inside the intervals. The MAE and RMSE are both relatively small.

Table 3: Testing table

Metric	Value
95% predictive interval coverage	0.980
50% predictive interval coverage	0.510

Metric	Value
Mean Absolute Error	0.023
Root Mean Square Error	0.028

3.6.3 Cross-Validation

We do two kinds of Cross-Validation: LOO and Kfold (table 4). The two methods show similar results means the model is stable and the p value is near the number of variables (5) shows the model is not over-fitting.

Table 4: Cross-validation Comparison (LOO vs 10-fold)

Method	elpd	elpd_SE	p	p_SE	IC	IC_SE
LOO	38.672	6.321	5.636	0.857	-77.344	12.643
K-fold	36.873	6.478	7.435	1.176	-73.747	12.955

4 Example

Now we will apply our model on an individual example: A 70 year old female (weight: 70kg, height: 160cm) is arrested after being stopped by the police while driving. She provides a blood sample to the police 2 hours after her arrest which gives a reading of $C_t = 0.15\text{g/kg}$. The legal limit is $x = 0.47\text{g/kg}$.

Since there is no ‘drinking time’ data here, we will use a simplified model with only ‘sex’, ‘height’, ‘weight’ variables. We have standardized height and weight by using sample’s mean and variance.

As figure 7 shows, this is the posterior density of C_0 calculated by presicted posterior density of $\hat{\beta}$ the dot line is the legal limit $C_0 = 0.47$, it can be seen that most density is larger than 0.47, so obviously the 70 year old female is over the drink driving limit.

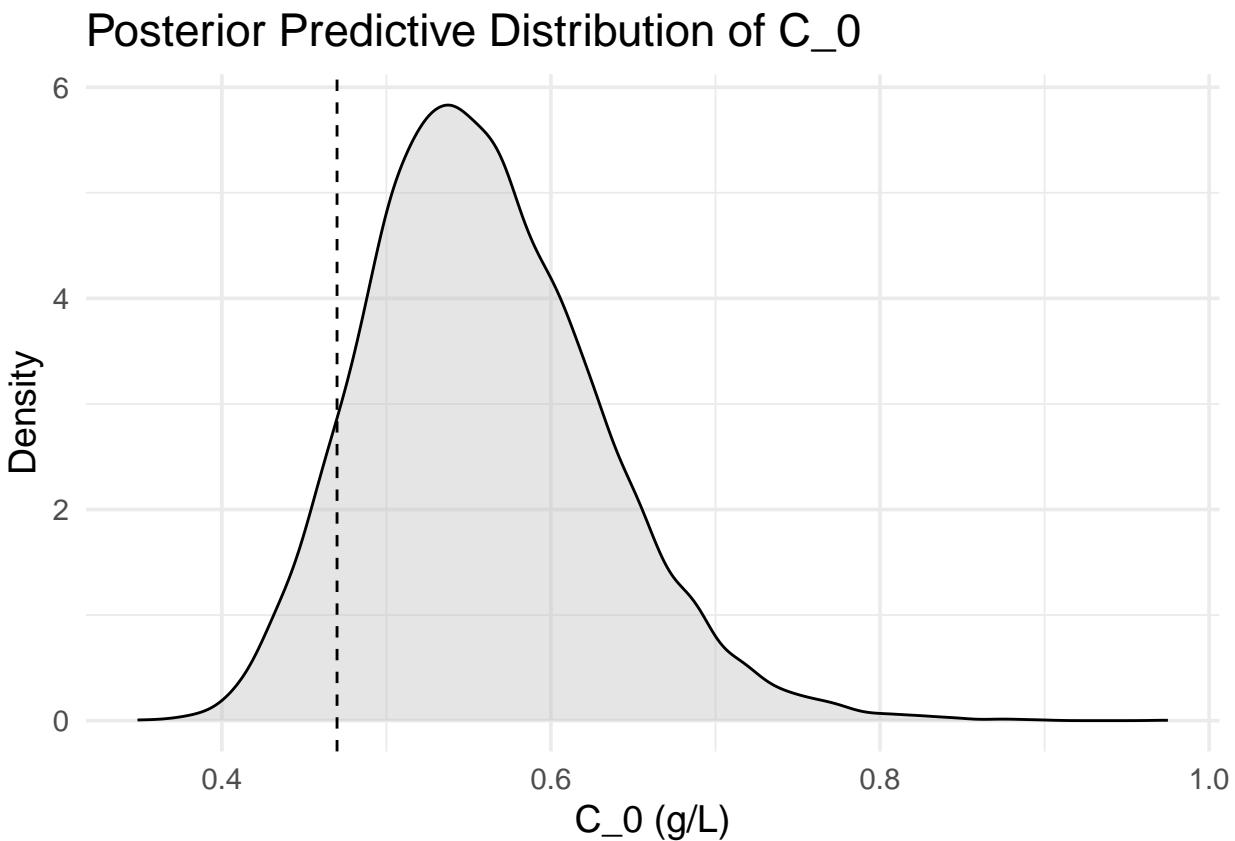


Figure 8: Posterior Predictive Distribution of C_0 , $\text{message}=FALSE$, $\text{warning}=FALSE$, with limit $C_0 = 0.47$ (dot line).

To make the result clear, it is better to give Table 5 to the courts and illustrate:

There is 91.4% probability that the 70 year old female is over the drink driving limit, with both mean, median and mode value over the limit.

The results also show that the original method is not reasonable since 2.5% percentile is over-conservative even in this case.

Table 5: Example results

Statistic	Value
Mean	0.559
Median	0.553
Mode	0.538
2.5%	0.438
25%	0.509
75%	0.603
97.5%	0.713
$P(C_0 > 0.47)$	0.911

5 Widmark's Equation and V_d

When it is too late to use a blood or breath test and the only information available is eyewitness testimony of the quantity of alcohol consumed. We have to use Widmark's equation:

$$C_t = \frac{A}{Weight \times V_d} - \beta t.$$

Since there are many versions of Widmark's equation, it can also write as:

$$C_t = \frac{F \times A}{Weight \times \rho} - \beta t$$

where

$$\rho = \frac{TBW}{weight \times F_{water}}$$

is known as Widmark's rho factor.

F is the fraction of the dose that reaches the systemic circulation, F_{water} is know as the water content of the blood sample, TBW is Total Body Water.

We assume that all different part between two equations are included in V_d . The unit of C_t is g/kg in our dataset, the unit of the first term is g/L, but it is not a problem since the density of water is 1, we just ignore the 1.

5.1 V_d , TBW and ρ

All information in this part are from 'Total body water is the preferred method to use in forensic blood-alcohol calculations rather than ethanol's volume of distribution'[5].

TBW is calculated by:

$$TBW_{Men}(L) = 2.447 - (0.09516 \times age) + (0.1074 \times height) + (0.3362 \times weight)$$

$$TBW_{Women}(L) = -2.097 + (0.1069 \times height) + (0.2466 \times weight).$$

Now subbing the ρ expression in the C_t equation, and comparing with our equation, V_d is actually calculated by:

$$V_d = \frac{TBW}{weight} \times \frac{1}{F_{water}} \times \frac{1}{F} = \eta \times \frac{TBW}{weight}$$

and we need to estimate η value since TBW is a value that can be determined in our dataset. we will use:

$$\hat{V}_{d,i,j} = \hat{\eta}_{1,i} \left(\frac{\text{TBW}}{\text{weight}_{\text{male}}} \right)_j + \hat{\eta}_{2,i} \left(\frac{\text{TBW}}{\text{weight}_{\text{female}}} \right)_j + \varepsilon_i$$

to estimate \hat{V}_d where i is the i_{th} iterations (we will again use BRM, but as a joint model with β to deal with the correlation, we will explain it in next part.), j is the j_{th} individuals, η is the coefficients that need to be predicted.

5.2 Correlations between β and V_d

To show that the correlation can't be ignored, figure 9 gives the correlations between true β and V_d is -0.415 , which is relatively big.

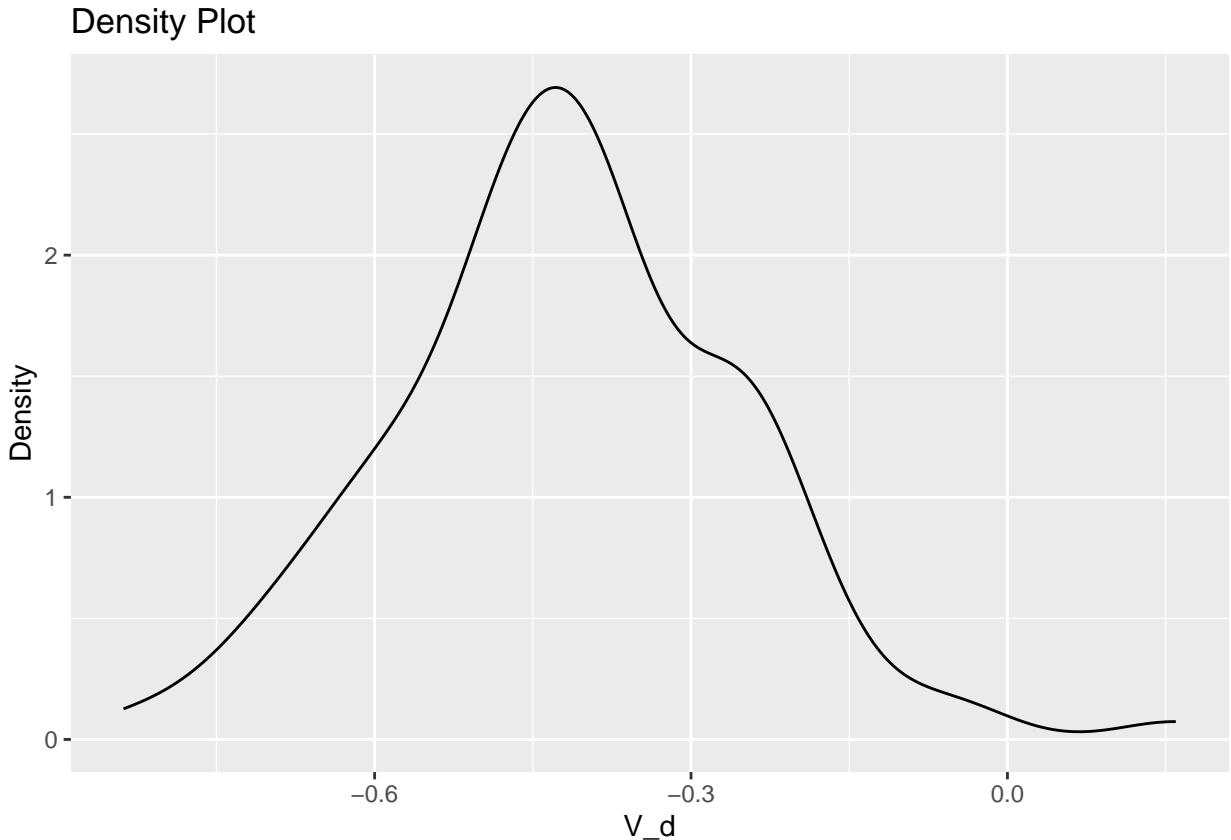


Figure 9: Correlation plot betweenem V_d and Beta

6 Joint Bayesian regression model for β and V_d

6.1 Advantages and disadvantages for exists method for V_d

The exists method is easy to calculate. But as we showed before, the correlation between β and V_d is relatively large and can't be ignored, especially for the courts since we need the calculated C_t as precise as possible.

6.2 Overview of V_d

V_d is calculated by true value β (with our log-transformed). We will not log-transformed V_d since the density of V_d can't be improved by taking log.

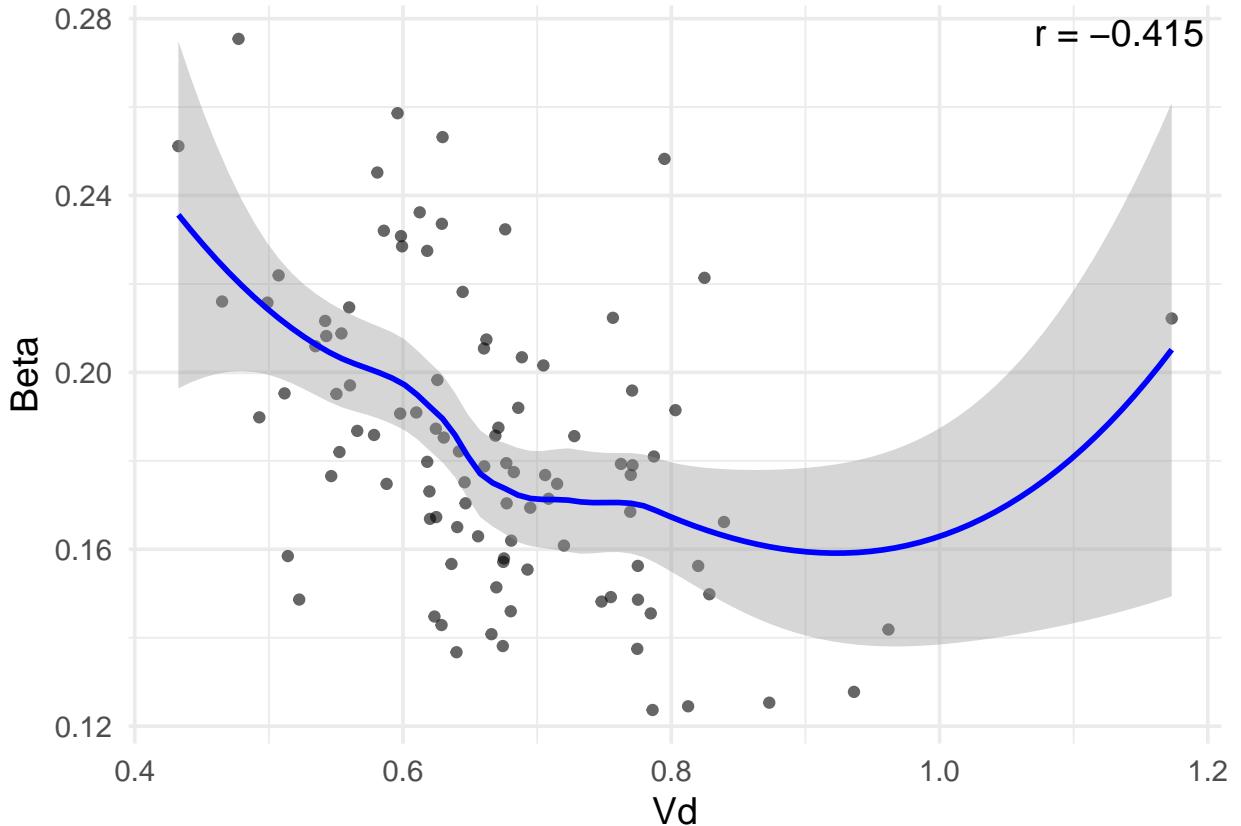


Figure 10: Density plot of V_d

6.3 Modeling

The mathematical expression of the joint model can be expressed as:

$$\hat{\beta}_{i,j} = \hat{\gamma}_{1,i} \text{female}_j + \hat{\gamma}_{2,i} \text{male}_j + \hat{\gamma}_{3,i} \text{weight}_j + \hat{\gamma}_{4,i} \text{height}_j + \varepsilon_{\beta,i}^2.$$

and

$$\hat{V}_{d,i,j} = \hat{\eta}_{1,i} \left(\frac{\text{TBW}}{\text{weight}_{\text{male}}} \right)_j + \hat{\eta}_{2,i} \left(\frac{\text{TBW}}{\text{weight}_{\text{female}}} \right)_j + \varepsilon_{V_d,i}$$

where

$$\begin{pmatrix} \varepsilon_{\beta,i} \\ \varepsilon_{V_d,i} \end{pmatrix} \sim \mathcal{N} \left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{\beta}^2 & \rho \sigma_{\beta} \sigma_{V_d} \\ \rho \sigma_{\beta} \sigma_{V_d} & \sigma_{V_d}^2 \end{pmatrix} \right).$$

6.3.1 Model Selection (priors)

The prior for β 's variables' coefficients is unchanged. And the prior for η is easy to calculated since $\eta = \frac{1}{F_{\text{water}}} \times \frac{1}{F}$.

The Blood water content F_{water} is easy to determine by desiccation and the mean reported values for men and women are 0.825% w/v and 0.838% w/v respectively. The small sex difference is mainly attributed to lower haematocrit in female blood samples[].

The fraction of the alcohol dose that reaches the systemic circulation F is typically 0.7–0.9. So:

- Prior for $\frac{\text{TBW}}{\text{weight}_{\text{male}}}$ is $\text{Normal}(\frac{1}{0.825} \times \frac{1}{0.8}, 2) = \text{Normal}(1.51, 2)$
- Prior for $\frac{\text{TBW}}{\text{weight}_{\text{male}}}$ is $\text{Normal}(\frac{1}{0.848} \times \frac{1}{0.8}, 2) = \text{Normal}(1.49, 2)$

The mean value of two priors is actually near to the linear regression results of single V_d model (1.41 for male and 1.3 for female).

Priors for others are still weak informative priors. Settings for others are not changed (4 chains, 4000 iterations, 1000 warm-up).

6.4 Results

Table 6 below is the results table, all Rhat and ESS are in good range. The expected estimated correlation –0.46 in the model is also near the sample's V_d - β correlation –0.415 (the log-transformation of β doesn't affect the correlation.)

Table 6: Joint model results

Parameter	Estimate	Est.Error	Rhat	Bulk_ESS	Tail_ESS	Group
beta_sexfemale	-1.6666	0.0329	1.0003	8557.968	8235.323	Beta
beta_sexmale	-1.7338	0.0238	1.0001	9338.400	7981.624	Beta

Parameter	Estimate	Est.Error	Rhat	Bulk_ESS	Tail_ESS	Group
beta_weight_s	-0.0011	0.0207	1.0001	9760.305	9063.246	Beta
beta_height_s	-0.0467	0.0222	1.0002	8576.352	8465.325	Beta
beta_drinkingtime_s	-0.0310	0.0147	1.0004	13093.717	9322.180	Beta
Vd_T_Vd:sexfemale	1.2965	0.0367	0.9999	12033.571	9305.396	Vd
Vd_T_Vd:sexmale	1.4090	0.0303	1.0003	10370.123	8750.799	Vd
sigma_beta	0.1611	0.0120	1.0002	10005.001	9157.256	Beta
sigma_Vd	0.1139	0.0082	1.0009	10783.056	9166.474	Vd
rescor(beta,Vd)	-0.4635	0.0800	1.0001	9939.374	9178.082	Correlation

Figure 10 shows the joint posterior distribution of β and V_d . It is a good multivariate gaussian (2d).

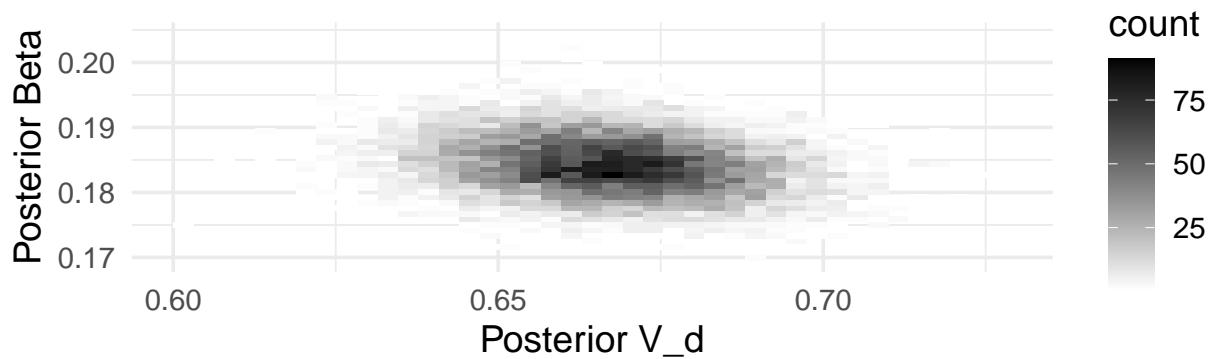


Figure 11: Joint posterior distribution

6.5 Testing

Table 7 is the LOO and Kfold results, the p values (11.0479 and 10.691) means the validation results are good since we have 10 parameters.

Table 7: Cross-validation Comparison (LOO vs 10-fold)

Method	elpd	elpd_SE	p	p_SE	IC	IC_SE
LOO	123.879	14.300	11.473	3.233	-247.759	28.600
K-fold	120.543	15.273	14.810	4.471	-241.086	30.547

Table 8 shows the MSE of β , V_d and calculated C_0 from joint posterior distribution comparing with true value, and also a MSE for single β model to test if the results worse when take in V_d . The estimation result for β is better than before (because of the correlation, V_d explain some variation of β).

Table 8: Prediction Error and Coverage Rate

Metric	Estimate
MSE_Vd	0.0865
MSE_beta (joint model)	0.0232
MSE_beta (model C)	0.0232
MSE_C0	0.1705
Vd Coverage (95%)	0.9600
Vd Coverage (50%)	0.5200
C0 Coverage (95%)	1.0000
C0 Coverage (50%)	0.7100

7 Conclusion

7.1 Limitation

- Based on the variables we have in this sample and small sample size, the model doesn't explain much variation.

Since the BAC elimination rate β really depends on individuals. We can't really know what drugs the person is taking or how often the person taking alcohol or health condition of the person, even we know it is still very hard to model all variation, obviously it will cost much. (So in some sense, the original method is an efficient method if they can split the β by gender, since it is easy and quick method compare to our model model.)

- The model is sensitive with priors.

It is better to choose priors by what the courts want, like make the range of priors for β narrower (less variance) or give more space to the courts so using a flat prior. In this case we only have 100 data points, so any choice of prior will affect the posterior. We use non-informative priors, it may cause slower converge. In practice, it is hard to set priors since again β is quite random.

7.2 Suggestion

When using the model, it is necessary to know when the person is arrested and when the person stop drinking. Although β is a constant rate, if the person is arrested before the BAC reaching peak (point at left hand side of the BAC peak point) and measured when the BAC starting decreasing (point at right hand side of the BAC peak point), then if we use β value to find BAC value at driving time (arrest time) is not suitable since the calculated BAC value will be higher than true value.

We suggest double blood samples method in practice:

'If a driver is not apprehended sitting behind the wheel, the traffic police in Sweden often submit double blood samples taken about 1 h apart. The mean result at each sampling time can be used to calculate the rate of elimination of alcohol assuming the existence of the post-absorptive declining phase and operation of zero-order kinetics. From a long experience with investigating drunken driving cases, the first blood sample is usually obtained 60 min after an arrest is made depending on location throughout the country where the individual is apprehended and the availability of a physician or nurse to draw blood.'[6]

8 Reference

<https://www.sciencedirect.com/science/article/pii/S0379073810000770?via%3Dihub>

P.Y. Kwo, V.A. Ramchandani, S. O'Connor, D. Amann, L.G. Carr, K. Sandrasegaran, K.K. Kopecky, T.K. Li Gender differences in alcohol metabolism: relationship to liver volume and effect of adjusting for body mass Gastroenterology, 115 (1998), pp. 1552-1557

A Model Comparison

We basically focus on choices of priors.

Firstly we will test how sensitive our model is with different priors in table 9:

- Prior A choose student-t distribution for coefficients of gender variables.
- Prior B use a narrower variance for coefficients of gender variables.

Table 9: Comparison priors with original prior

Parameter	Original	Prior_A	Prior_B
Regression coefficient: male	Normal(0, 2)	Student-t(3, 0, 2)	Normal(0, 1)
Regression coefficient: female	Normal(0, 2)	Student-t(3, 0, 2)	Normal(0, 1)
Regression coefficients (others)	Normal(0, 0.5)	Normal(0, 0.5)	Normal(0, 0.01)
Residual SD (sigma)	Exponential(1)	Exponential(1)	Exponential(1)

As you can see in table 10, the LOO validation shows the model is sensitive with prior choice. Smaller variance can make the model worse.

Table 10: LOO Comparison of different priors' model

Model	elpd_diff	se_diff
fit_A	0.000	0.000
fit_single	-0.033	0.033
fit_B	-0.698	2.656

Other than this, if we plot the mean posterior β value with true β value, the results will be more clear. Since the prior variance of coefficients is seted very small, the value of β is mainly predicted by gender, which you can find clearly two groups for prior B's model.

[1] A. W. Jones, “Evidence-based survey of the elimination rates of ethanol from blood with applications in forensic casework,” *Forensic Science International*, vol. 200, pp. 1–20, 2010, doi: 10.1016/j.forsciint.2010.02.021.



Figure 12: Joint posterior distribution