Bayesian Linear Models
The **blim** Package

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```
> library(devtools)
> install_github("vankesteren/blim")
> library(blim)
```

How to blim

Anyone who can use the lm function in R can use blim! This is how to make a **blimfit** object:

```
> fit <- blim(formula = y~x1+x2,
              data = dataset)
```

It is easy to get your results:

```
> summary(fit)
```

The blimfit object

A blimfit object contains:

1. The **trace**: a matrix of all the sampled parameters
2. The **summary**: parameter estimates and credible intervals
3. The **priors**: the prior information about the parameters
4. The **data**: matrix representations of the input data

The example

Birthweight data. 189 babies were weighed. Their mothers were checked for **smoking** during pregnancy and history of **hypertension**.

	No Smoking	Smoking
No HY	μ1	μ2
HY	μ3	μ4

Informative Hypothesis

$$\mu 1 > \mu 2 > \mu 3 > \mu 4$$

The Algorithm

blim's **rmhs** method uses **Gibbs sampling** for conjugate priors and a **random-walk Metropolis** algorithm for evaluating the posterior in case of **nonconjugate priors**:

```
# bhat = current beta sample in trace
# fx = target (posterior) distribution
# var[v] is the tuning param for b[v]

# first sample candidate value:
bstar <- bhat[v] + rnorm(1, 0, var[v])

# then compute acceptance ratio
r <- min(1,fx(bstar)/fx(beta[i,v]))

# Assign to beta when accepted
if (runif(1) <= r) bhat[v] <- bstar
```

The Model

I specify an **ANOVA** model:

$$\text{bwt}_i = \mu_1 \cdot \text{no}_i + \mu_2 \cdot \text{sm}_i + \mu_3 \cdot \text{hy}_i + \mu_4 \cdot \text{smhy}_i + \varepsilon_i$$

In R, this translates to:

```
mod1 <- blim(bwt~0+no+sm+hy+smhy,
             birthwt, iter = 99999,
             mtsprior = TRUE,
             burnin = 100)
```

Model 2 with mother's weight (lwt) with nonconjugate cauchy prior:

```
mod2 <- blim(bwt~ ... + scale(lwt), ...
             prior_b = c( ...
                     ,"dcauchy(0,100)"),
             method = "rmhs", dtuning = 100)
```

Posterior Predictive Check

An important assumption of the ANOVA is the **normality of residuals**. blim can constructs a p-value for this using the kolmogorov-smirnov statistic as its **discrepancy measure**. The difference between expected and observed discrepancies is of interest. In R the observed discrepancy vector is calculated like so:

```
ObsD <- apply(trace,1,function(b){
    resid <- blimfit$y-blimfit$X%*%b
    D <- ks.test(resid,pnorm)$statistic
    return(D)
}
```

The p-value in the example is around 0.5, so no violation

Model Selection

Unlike frequentist statistics, Bayesian analysis allows for model selection with **Bayes Factors**, quantifying the amount of evidence there is for model 1 relative to model 2. blim can calculate a Bayes Factor comparing two models using the **Laplace-Metropolis estimator**:

$$f(\text{D}) \approx (2\pi)^{P/2} |\mathbf{H}^*|^{1/2} f(\theta^*) f(\text{D}|\theta^*)$$

It can also indicate the precision of this estimate using a **bootstrap**:
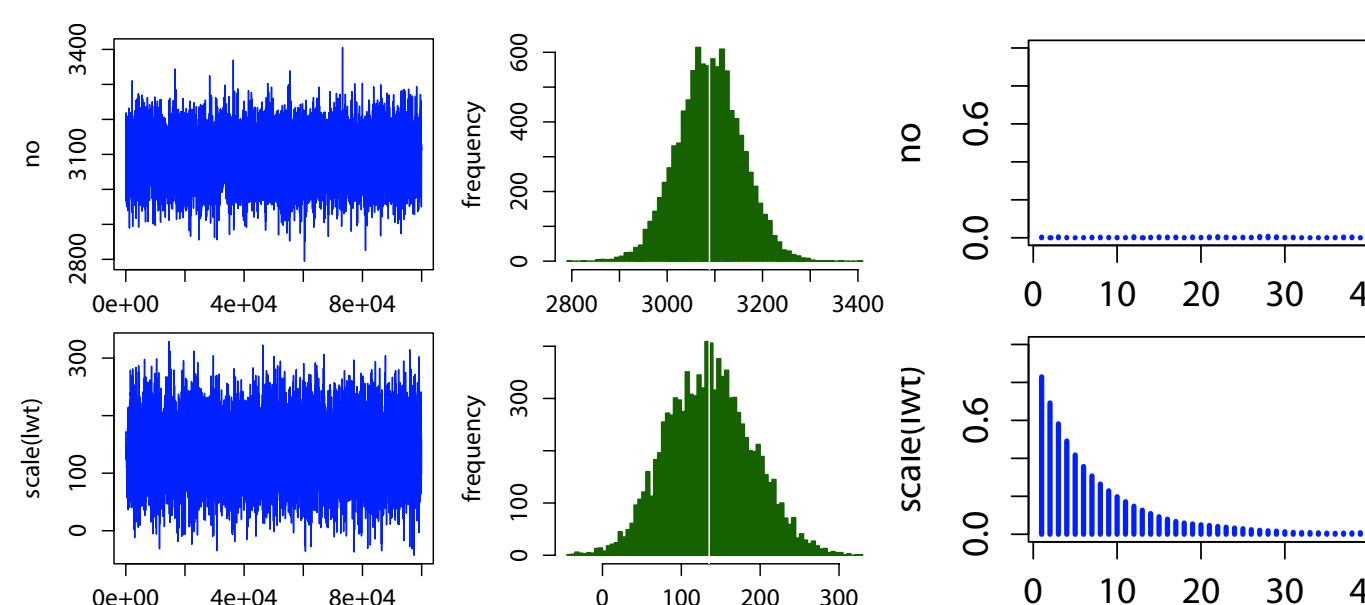
```
> BF(mod1, mod2, bootstrap = TRUE)
```
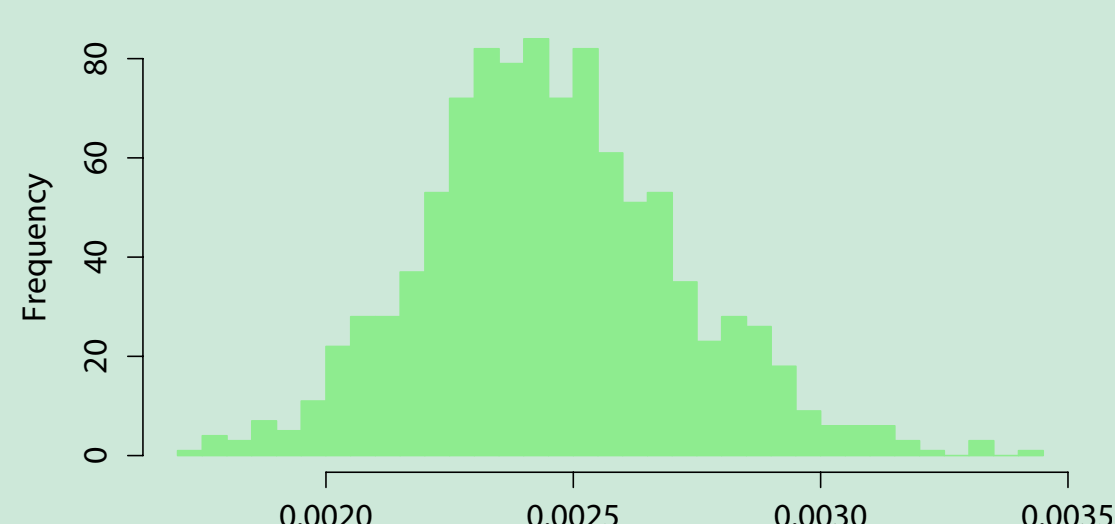

BF12 is around 0.0025. This indicates that model 2 is 400 times as likely as model 1. Δ(**DIC**) ≈ 15.7

Convergence

Convergence and autocorrelation of μ1 and the covariate are shown below.

```
> cplots(mod2)    > aplots(mod2)
```


Dynamic Tuning

blim performs tuning of the Metropolis algorithm acceptance rate by dynamically optimising the variance of the proposal distribution:

```
# pcur is current acceptrate, popt=0.45
if (pcur > 0.5 || pcur < 0.15){
var[v] <- (var[v]*(1/pnorm(popt/2)))/
          (1/pnorm(pcur/2))
}
```

Conclusion

μ1: 3089, 95% CI [2957; 3221]
μ2: 2811, 95% CI [2645; 2978]
μ3: 2469, 95% CI [1946; 2992]
μ4: 2337, 95% CI [1696; 2971]

BF is also the result of evaluating the hypothesis in the posterior (**fit**) and the prior (**complexity**):

```
# model in the form: "par[1]>par[2]"
fit <- mean(apply(trace, 1,
function(par) eval(parse(text=model))))
com <- mean(apply(prior, 1,
function(par) eval(parse(text=model))))
BF <- fit/com
```

My hypothesis has a Bayes Factor of around 12.5, which indicates **strong evidence** in favour of this hypothesis!