

Networks in Context Lab, 2024

Very Short Introduction to Bayesian Statistics

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Outline

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2. Very short introduction to benefits of Bayesian approach
3. Very short introduction to using **Stan**'s No-U-Turn sampler to obtain samples from posterior distribution

What is Bayesian Statistics?

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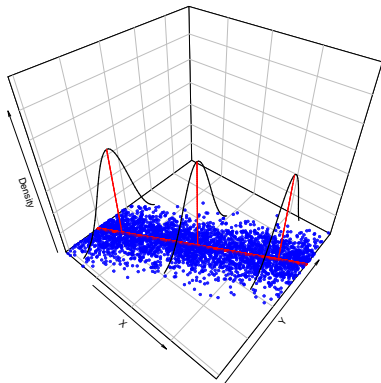
$$y \sim f(\theta, x)$$

For example, in linear regression, we assume

$$y_i \sim \text{Normal}(x_i\beta, \sigma_\epsilon)$$

where $\theta = \{\beta, \sigma_\epsilon\}$.

The objective of the analysis to estimate θ or some function of it



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The only thing that is random are the data, where randomness arises due to some sampling process.

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2. We observe some data
3. We obtain a new distribution of θ by updating our beliefs based on the data

(Of course, we might be interested in some statistic of this distribution, such as the mean or median...)

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So, let $v = \theta$ and $w = y$, which gives the updating formula

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3. $p(\theta)$ is the probability of θ *before observing the data*—i.e., the *prior distribution* of θ
4. $p(y) = \int_{\Theta} p(y | \theta)p(\theta)d\theta$ is a constant that doesn't depend on θ and is often not of theoretical interest

So, we often write

$$p(\theta | y) \propto p(y | \theta)p(\theta)$$

i.e., “the posterior is proportional to the likelihood times the prior”

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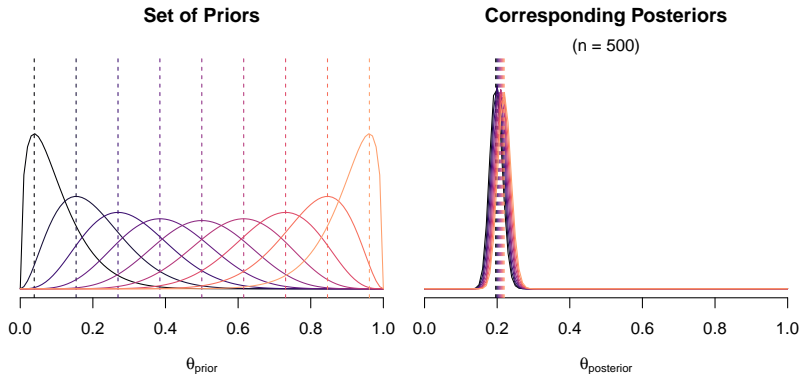
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Further, *the likelihood will dominate the prior as n grows large*. So, in large samples, the MAP will approach the MLE

A similar logic applies to other models as well:



(Notes: Beta-Binomial model with $n = 500$ observations and $\text{MLE}(\theta) = .2$)

So, why bothering to use Bayesian analysis at all?

Why You Should Be a Bayesian?

There are multiple arguments for using Bayesian statistics.
Among others:

1. It's more intuitive
(95% confidence vs credible intervals...)
2. Once you get the posterior, you can make valid inference about any function of θ
(e.g., What is $p(\beta_1/\beta_2 \leq \beta_3 | y)$?)
3. It works better for “weakly” or non-identified models
e.g., “Hessian is not positive definite” situations, perfect separation in logistic regression
4. It's a natural way to regularize inference

Let's discuss 4. a bit more in detail...

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But you get more than just a point estimate: the whole *posterior distribution*

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So, you introduce a bit of a bias with the prior in exchange for reduce variance of your inference

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- ▷ Even in large datasets, you'll often find *niches* (so to say) in covariate space with little data
- ▷ The prior will regularize inference on those niches, while not influencing much the inference in other regards
- ▷ This is why random effects models (RE) perform better in prediction tasks than fixed-effect models (FE)
(REs can be understood as FEs with a prior on the group-level intercepts; conversely, FEs can be understood as REs with infinite-variance priors)

Bayesian Inference in Practice (a.k.a. MCMC)

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In this (very) short introduction, we'll focus on **Stan**, which implements an HMC algorithm (called the No-U-turn sampler)

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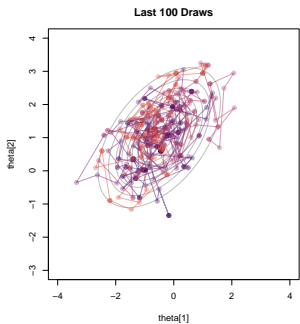
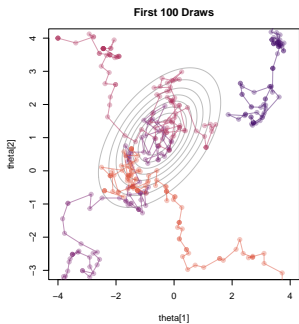
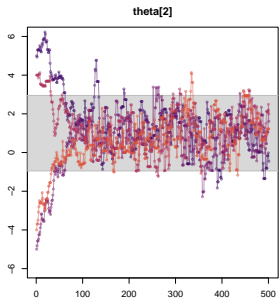
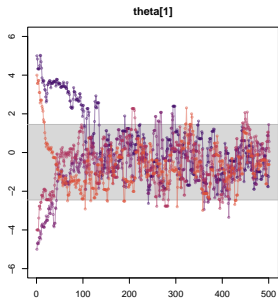
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Pause...Questions so far?

Bayesian Models in **Stan**

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Simple and Beautiful!

Here are some example data that we are going to analyze

```
> data = read.csv(here("example", "data.csv")) # data.frame object
> head(data)
      y date topic
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- ▷ **y**: A measure of ideological separability of comment threads ensuing a post
- ▷ **date**: the date of the post
- ▷ **topic**: topic of the post

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$$y_{it} = \alpha + \beta x_{it} + \epsilon_{it}, \quad \epsilon_{it} \stackrel{\text{iid}}{\sim} \text{N}(0, \sigma_\epsilon^2)$$

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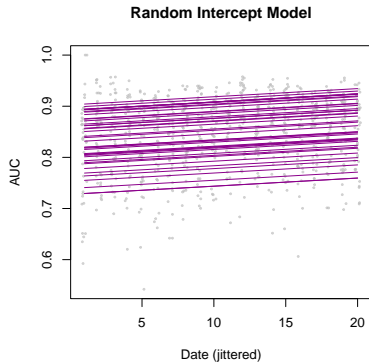
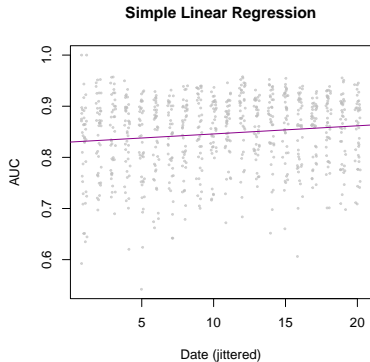
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3. Assign priors to the parameters:

$$\alpha, \beta \sim \text{N}(0, 1), \quad \sigma_\epsilon \sim \text{Exp}(1)$$

In the multilevel (random intercept) model, we assume that

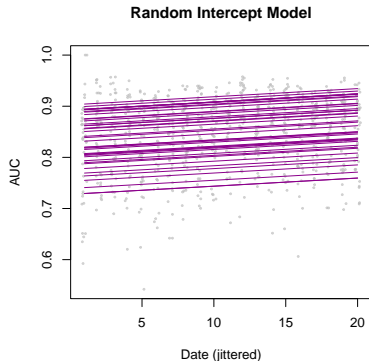
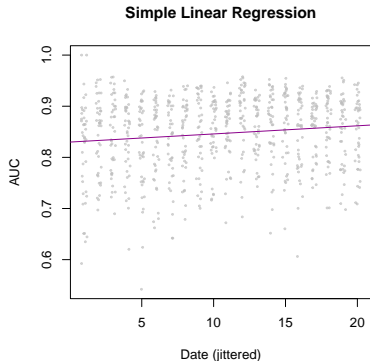
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2. The intercepts come from the same distribution (e.g., Normal distribution, but not necessarily Normal...)

Formally, we write

$$y_{it} = \alpha_i + \beta x_{it} + \epsilon_{it}, \quad \begin{aligned} \epsilon_{it} &\stackrel{\text{iid}}{\sim} \text{N}(0, \sigma_\epsilon^2) \\ \alpha_i &\stackrel{\text{iid}}{\sim} \text{N}(\mu_\alpha, \sigma_\alpha^2) \end{aligned}$$

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Model is completed by assigning priors

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Notice $\alpha_i \stackrel{\text{iid}}{\sim} \text{N}(\mu_\alpha, \sigma_\alpha^2)$ is just assigning a prior to the random intercepts

Now we have $\theta = \{\beta, \sigma_\epsilon, \alpha_1, \dots, \alpha_K, \mu_\alpha, \sigma_\alpha\}$

Model is completed by assigning priors

1. Recall α_i 's prior are already specified

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Formally, we write

$$y_{it} = \alpha_i + \beta x_{it} + \epsilon_{it}, \quad \epsilon_{it} \stackrel{\text{iid}}{\sim} \text{N}(0, \sigma_\epsilon^2)$$
$$\alpha_i \stackrel{\text{iid}}{\sim} \text{N}(\mu_\alpha, \sigma_\alpha^2)$$

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Done!

Fitting Bayesian Models in R using **brms**

Fitting Bayesian regression models is extremely easy using the `brms` (or `rstanarm`) package

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For the simple linear regression model:

```
slr_brms = brms::brm(  
  formula = y ~ date, data = data, family = gaussian(),  
  warmup = 500, iter = 1500, refresh = 1000, chains = 4,  
  cores = 4, seed = 123  
)
```

will do the job for us: creating the appropriate **Stan** code, and compile it in **C++**, and run the sampler


```
> slr_brms = brms::brm(...)
> print(slr_brms, digits = 4)
```

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	0.8300	0.0053	0.8195	0.8402	1.0010	3728	3137
date	0.0016	0.0004	0.0007	0.0025	1.0020	4686	3137

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	0.0720	0.0019	0.0683	0.0758	1.0049	861	978

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But what about the priors?

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sigma  0.0720    0.0019  0.0683  0.0758 1.0049     861     978
```

But what about the priors?

```
> prior_summary(slr_brms)
      prior      class coef group resp dpar nlpar lb ub      source
      (flat)      b
      (flat)      b date      (vectorized)
student_t(3, 0.9, 2.5) Intercept      default
student_t(3, 0, 2.5)    sigma          0      default
```

Setting custom priors is easy as well:

```
slr_brms_w_prior = brms::brm(  
  formula = y ~ date,  
  data = data,  
  family = gaussian(),  
  prior = c(  
    set_prior("normal(0, 1)", class = "Intercept"),  
    set_prior("normal(0, 1)", class = "b", coef = "date"),  
    set_prior("exponential(1)", class = "sigma")  
  ),  
  warmup = 500,  
  iter = 1500,  
  refresh = 1000,  
  chains = 4,  
  cores = 4,  
  seed = 123  
)
```

Notice that the results are almost identical:

```
> print(slr_brms_w_prior, digits = 4)
Family: gaussian
Links: mu = identity; sigma = identity
Formula: y ~ date
Data: data (Number of observations: 800)
Draws: 4 chains, each with iter = 1500; warmup = 500; thin = 1;
       total post-warmup draws = 4000

Population-Level Effects:
      Estimate Est.Error 1-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
Intercept   0.8298    0.0054   0.8196   0.8407 1.0009    3906    2517
date        0.0016    0.0005   0.0007   0.0025 1.0023    4510    2545

Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
sigma   0.0719    0.0018   0.0684   0.0756 1.0051     789     999

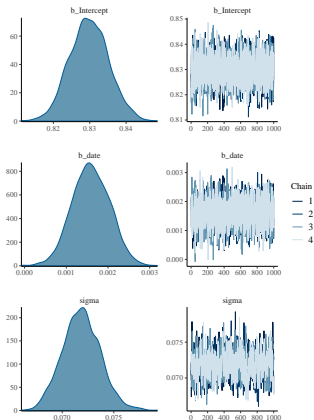
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

And we have the priors we want:

```
> prior_summary(slr_brms_w_prior)
      prior      class coef group resp dpar nlpar lb ub  source
  (flat)      b
normal(0, 1)      b date                user
normal(0, 1) Intercept                user
exponential(1)  sigma                0      user
```

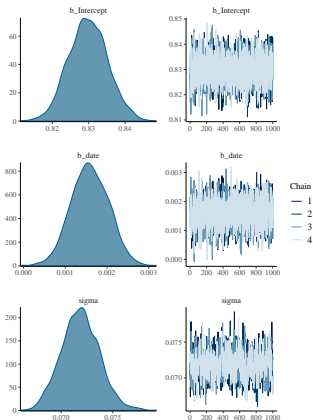
Easy to check the trace- and density-plots using the `plot` method

```
> plot(slr_brms_w_prior)
```



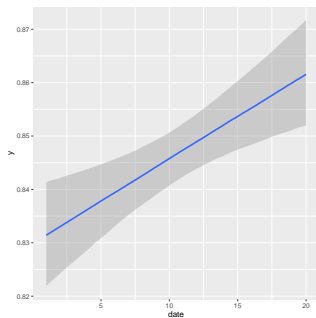
Easy to check the trace- and density-plots using the `plot` method

```
> plot(slr_brms_w_prior)
```



Or look into the conditional predictions with their credible intervals

```
> conditional_effects(  
  slr_brms_w_prior,  
  effect = "date"  
)
```



Fitting multilevel models are equally easy. We use the same formula syntax as `lme4`:

```
mlm_brms_w_prior = brms::brm(
  formula = y ~ date + (1 | topic), data = data,
  prior = c(
    set_prior("normal(0, 1)", class = "Intercept"),
    set_prior("normal(0, 1)", class = "b", coef = "date"),
    set_prior("exponential(1)", class = "sigma"),
    set_prior("exponential(1)", class = "sd")
  ),
  family = gaussian(), warmup = 1000, iter = 2000, refresh = 1000,
  chains = 4, cores = 4, seed = 123
)
```

```
> print(mlm_brms_w_prior, digits = 4)
Group-Level Effects:
~topic (Number of levels: 40)
      Estimate Est.Error 1-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
sd(Intercept)   0.0541   0.0066   0.0429   0.0690 1.0152     339     828

Population-Level Effects:
      Estimate Est.Error 1-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
Intercept   0.8297   0.0099   0.8098   0.8497 1.0135     161     417
date        0.0016   0.0003   0.0010   0.0022 1.0002    3812    2746

Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI   Rhat Bulk_ESS Tail_ESS
sigma   0.0502   0.0013   0.0479   0.0528 1.0024    3328    2852
```


It's also possible to extract the posterior draws directly:

```
> psamples = as_draws(mlm_brms_w_prior) # note: Extract draws

> class(psamples) # note: this is basically a 'list' object
[1] "draws_list" "draws"          "list"

> length(psamples) # note: length is equal to the number of chains
[1] 4

> class(psamples[[1]]) # note: each element is again a 'list'
[1] "list"

> names(psamples[[1]]) # note: which contains all the parameters
[1] "b_Intercept"          "b_date"              "sd_topic__Intercept"
[4] "sigma"                "r_topic[1,Intercept]" "r_topic[2,Intercept]"
...
[43] "r_topic[39,Intercept]" "r_topic[40,Intercept]" "lprior"
[46] "lp__"

> psamples[[1]][["b_date"]] # note: this would extract the samples
                             of the regression coefficient from
                             the first chain
      [1] 0.0017325622 0.0012639667 0.0018935499 ...
      [6] 0.0016589144 0.0020239859 0.0011239522 ...
      ...
     [991] 0.0014328793 0.0009396389 0.0021512139 ...
     [996] 0.0018722834 0.0016737117 0.0018758484 ...
```

Fitting Bayesian Models in R using `cmdstanr`

While `brms` and `rstanarm` are great packages, sometimes we need to code directly in `Stan`

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There are two packages that let you directly interact with the `Stan` language from R: `rstan` and `cmdstanr`

A Stan program consists of 7 code blocks:

1. `functions{}`
2. `data{}`
3. `transformed data{}`
4. `parameters{}`
5. `transformed parameters{}`
6. `model{}`
7. `generated quantities{}`

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So, a typical Stan program will look like:

```
functions {  
    <some user-defined functions here>  
}  
  
data {  
    <data specifications here>  
}  
...  
  
model {  
    <model definition here>  
}  
  
generated quantities {  
    <calculate some extra stuff here>  
}
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}  
  
generated quantities {  
    <calculate some extra stuff here>  
}
```

We will *not* deal with 1., 3. and 7. today

Let's return to the simple linear regression model:

$$y_i = \alpha + \beta x_i + \epsilon, \quad \epsilon \sim \text{Normal}(0, \sigma_\epsilon)$$

or equivalently

$$y_i \sim \text{Normal}(\alpha + \beta x_i, \sigma_\epsilon)$$

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The data consists of two vectors:

1. the outcome $y = [y_1, \dots, y_i, \dots, y_N]^\top$; and
2. the predictor $x = [x_1, \dots, x_i, \dots, x_N]^\top$

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We specify this in the data `data{}` block.

```
data {  
  
  int N;           // no. of obs.  
  vector[N] x;     // predictor  
  vector[N] y;     // outcome  
  
}
```

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2. $\beta \in \mathbb{R}$: the slope coefficient
3. $\sigma_\epsilon \in \mathbb{R}_+$, the residual standard deviation.

We can declare them in the `parameters{}` block:

```
parameters {  
    real alpha;  
    real beta;  
    real<lower = 0> sigma_epsilon;  
}
```

Notice that we specified `real<lower = 0>` to indicate that σ_ϵ has to be positive

Lastly, we specify the (log) posterior density (up to a constant.)

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Let us use the following weakly informative priors

$$\alpha \sim \text{Normal}(0, 2)$$

$$\beta \sim \text{Normal}(0, 1)$$

$$\sigma_{\epsilon} \sim \text{Exponential}(1)$$

As for the likelihood, notice that the model

$$y_i = \alpha + x_i\beta + \epsilon_i$$

implies that

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Hence, the likelihood is

$$\begin{aligned} p(y \mid \alpha, \beta, \sigma_\epsilon) &= \prod_{i=1}^N \text{Normal}(\alpha + \beta x_i, \sigma_\epsilon) \\ &= \prod_{i=1}^N \text{Normal}(\hat{y}_i, \sigma_\epsilon), \end{aligned}$$

where $\hat{y}_i = \alpha + \beta x_i$.

We code this up in the `model` block as follows:

```
model {  
  
  // linear predictor (local variable)  
  vector[N] yhat;  
  
  for (n in 1:N)  
    yhat[n] = alpha + beta * x[n];  
  
  // priors  
  alpha ~ normal(0, 2);  
  beta ~ normal(0, 1);  
  sigma_epsilon ~ exponential(1);  
  
  // vectorized likelihood  
  y ~ normal(yhat, sigma_epsilon);  
  
}
```


So, in sum, the **Stan** code will look like

```
data {  
  int N;           // no. of obs.  
  vector[N] x;     // predictor  
  vector[N] y;     // outcome  
}  
  
parameters {  
  real alpha;  
  real beta;  
  real<lower = 0> sigma_epsilon;  
}  
  
model {  
  // linear predictor (local variable)  
  vector[N] yhat;  
  
  ...  
  
  y ~ normal(yhat, sigma_epsilon);  
}
```

Suppose that this file is saved in a file named `slr.stan`

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> library("cmdstanr")  
> mod = cmdstan_model("slr.stan")
```

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From within `R`, we can compile the code with the `cmdstanr` package as follows:

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```
> library("cmdstanr")
> mod = cmdstan_model("slr.stan")
```

After compiling the model, we need to provide it with data to generate posterior samples. Usually, you provide the data as a `list` object:

```
> standata = list(
  N = nrow(dat),
  x = dat$date,
  y = dat$y
)
```

Sampling is then done by providing the `cmdstanr` object with the data and options:

```
fit = mod$sample(  
  data = standata,  
  chains = 4,  
  parallel_chains = 4,  
  iter_warmup = 1000,  
  iter_sampling = 1000,  
  refresh = 1000  
)
```


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  parallel_chains = 4,  
  iter_warmup = 1000,  
  iter_sampling = 1000,  
  refresh = 1000  
)
```

We can, thereafter, get summaries and extract the posterior samples with

```
> fit$summary()  
# A tibble: 4 × 10  
variable      mean median      sd      mad      q5      q95  rhat ess_bulk  
<chr>      <num> <num> <num> <num> <num> <num> <num> <num>  
1 lp__      1.70e+3 1.70e+3 1.24e+0 1.01e+0 1.70e+3 1.71e+3 1.00 1283.  
2 alpha     8.30e-1 8.30e-1 5.34e-3 5.29e-3 8.21e-1 8.39e-1 1.00 1533.  
3 beta      1.59e-3 1.59e-3 4.45e-4 4.37e-4 8.54e-4 2.32e-3 1.00 1779.  
4 sigma_epsilon 7.19e-2 7.19e-2 1.80e-3 1.77e-3 6.90e-2 7.49e-2 1.00 1377.  
> psamples2 = fit$draws()
```

which returns, as before, a `draws` object.

One nice thing about the `cmdstanr` package is that all cutting-edge **Stan** algorithms are available

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For example:

```
# Auto-diff variational Bayes
vb = mod$variational(data = standata)

# penalized MLE (L-BFGS)
pmle = mod$optimize(data = standata)

# pathfinder approximation
pfinder = mod$pathfinder(data = standata)

# laplace approximation
laplace = mod$laplace(data = standata)
```

The **Stan** program for the random intercept model is a bit more complicated

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We start with the data-structure we need to provide **Stan**

```
standat_mlm = list(  
  N      = nrow(dat), # total obs.  
  J      = length(unique(dat$topic)) # no of topics  
  topic  = dat$topic,  
  x      = dat$date,  
  y      = dat$y  
)
```

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```
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  J      = length(unique(dat$topic)) # no of topics  
  topic  = dat$topic,  
  x      = dat$date,  
  y      = dat$y  
)
```

Similarly, the `data{}` block in our **Stan** code is expanded:

```
data {  
  
  int N;           // no. of obs.  
  int J;           // no. of topics.  
  array[N] int topic; // topic indicator  
  vector[N] x;     // predictor  
  vector[N] y;     // outcome  
  
}
```

The `array[N] int` object is an array (vector) of integers (you can think of it as `std::vector<int>` and `vector[N]` as `Eigen::VectorXd`)

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Here it becomes complicated...While we can simply “sample” $\alpha_i \sim N(\mu_\alpha, \sigma_\alpha)$, **Stan** works much better when sampling from $N(0, 1)$.

So, we'll use the “Matt trick” and sample $\alpha_i^{\text{raw}} \sim N(0, 1)$, and calculate

$$\alpha_i = \mu_\alpha + \sigma_\alpha * \alpha_i^{\text{raw}},$$

which *induces*

$$\alpha_i \sim N(\mu_\alpha, \sigma_\alpha)$$

The `parameter` block would need 3 new elements:

1. The mean of the random intercepts, μ_α
2. The standard deviation of the random intercepts, σ_α
3. A length- J vector of random intercepts, $[\alpha_1, \dots, \alpha_J]^\top$

Here it becomes complicated...While we can simply “sample” $\alpha_i \sim N(\mu_\alpha, \sigma_\alpha)$, **Stan** works much better when sampling from $N(0, 1)$.

So, we'll use the “Matt trick” and sample $\alpha_i^{\text{raw}} \sim N(0, 1)$, and calculate

$$\alpha_i = \mu_\alpha + \sigma_\alpha * \alpha_i^{\text{raw}},$$

which *induces*

$$\alpha_i \sim N(\mu_\alpha, \sigma_\alpha)$$

This will make us use the `transformed parameter` block...

Hence, the Stan code looks like:

```
parameters {  
  
  // regression coef  
  real beta;  
  // resid std. dev.  
  real<lower = 0> sigma_epsilon;  
  
  // grand mean of random intercepts  
  real mu_alpha;  
  // std. dev. of random intercepts  
  real<lower = 0> sigma_alpha;  
  // aux var for efficient sampling  
  vector[J] alpha_raw;  
  
}  
  
transformed parameters {  
  
  // random intercepts  
  // note: alpha ~ Normal(mu_alpha, sigma_alpha^2)  
  vector[J] alpha = alpha_raw * sigma_alpha + mu_alpha;  
  
}
```

The model block remains almost the same:

```
model {  
  
  // linear predictor (local variable)  
  vector[N] yhat;  
  
  for (n in 1:N)  
    yhat[n] = alpha[topic[n]] + beta * x[n];  
  
  // priors  
  beta ~ normal(0, 1);  
  sigma_epsilon ~ exponential(1);  
  
  mu_alpha ~ normal(0, 2);  
  sigma_alpha ~ exponential(1);  
  alpha_raw ~ normal(0, 1);  
  
  // vectorized likelihood  
  y ~ normal(yhat, sigma_epsilon);  
  
}
```


Assuming the **Stan** code is stored in the file `re.stan`, we can compile and obtain posterior draws as before.

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This time, let's try out the Pathfinder algorithm

```
> mlm = cmdstan_model(here("example", "re.stan"))
> pf = mlm$pathfinder(data = standata_mlm)
> pf$print(digits = 5)
```

variable	mean	median	sd	mad	q5	q95
lp_approx__	21.43907	21.54090	6.61650	5.20230	4.55942	32.03380
lp__	1195.49274	1197.07000	6.14990	5.12980	1179.50000	1204.89250
beta	0.00150	0.00150	0.00042	0.00047	0.00084	0.00214
sigma_epsilon	0.04941	0.04940	0.00109	0.00087	0.04750	0.05133
mu_alpha	0.83045	0.83125	0.00349	0.00226	0.82258	0.83693
sigma_alpha	0.05272	0.04976	0.00686	0.00390	0.04561	0.06513
alpha[1]	0.89406	0.89628	0.00915	0.00861	0.87887	0.90943
alpha[2]	0.83116	0.83402	0.01069	0.01407	0.81564	0.84480
...						
alpha[39]	0.90629	0.90522	0.01037	0.01258	0.88813	0.91947
alpha[40]	0.87823	0.87935	0.00962	0.00686	0.85935	0.89172

These results are very close to the (gold-standard) HMC results!

(As before, we could analyze the results further using `mlm$draws()` to obtain the posterior draws)