

# Supplement2

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## Bayesian hierarchical model

As a sensitivity analysis, we performed a 3-level (patient/hospital) Bayesian hierarchical model. We conducted a complete case analysis. We used the following packages; rstan (version 2.21.2), code(0.19-4).

### 1-0. Data preparation

```
datalist <- list(  
  N = nrow(d_comp),  
  N_pat = length(unique(d_comp$pat_id)),  
  N_hosp = length(unique(d_comp$hosp_id)),  
  ID_pat = d_comp$pat_id,  
  ID_hosp = d_comp$hosp_id,  
  Y = d_comp$los,  
  A = d_comp$broad,  
  X1 = d_comp$adl,  
  X2 = d_comp$rr,  
  X3 = d_comp$bmi,  
  X4 = d_comp$age,  
  X5 = d_comp$count,  
  Z1 = d_comp$sams,  
  Z2 = d_comp$o2,  
  Z3 = d_comp$hr_over109,  
  Z4 = d_comp$steroid,  
  Z5 = d_comp$hot  
)
```

### 1-1. Performing a 3-level Bayesian hierarchical model using Stan

```
model <- stan_model ("model2.stan")
```

This is the Stan code for 3-level Bayesian hierarchical model. We used a 3-level random intercept model that was both patient- and hospital-specific effects were implemented as random effects. The following variables were selected as potential confounding factors: age, body mass index, home oxygen therapy use, respiratory rate, heart rate, oxygen use on admission, mental status, systemic steroid use on admission or the next day regardless of the dose, activities of daily living, and the number of recurrences. Non-informative uniform distribution was used for all parameters.

```
data{  
  int N; //total obs  
  int N_pat; //number of patients  
  int N_hosp; //number of hospitals  
  int ID_pat[N]; //patient ID  
  int ID_hosp[N]; //hospital ID  
  real Y[N]; //outcome:los
```

```

    real A[N]; //treatment:broad
    //continuous covariates
    real<lower=0> X1[N]; //adl
    real<lower=0> X2[N]; //rr
    real<lower=0> X3[N]; //bmi
    real<lower=0> X4[N]; //age
    real<lower=0> X5[N]; //count
    //dichotomous covariates
    int<lower=0> Z1[N]; //ams
    int<lower=0> Z2[N]; //o2
    int<lower=0> Z3[N]; //hr_over109
    int<lower=0> Z4[N]; //steroid
    int<lower=0> Z5[N]; //hot
}

parameters{
    real a[12];
    real b_pat_0[N_pat-1];
    real b_hosp_0[N_hosp-1];
    real<lower=0> s_pat;
    real<lower=0> s_hosp;
    real<lower=0> s;
}

transformed parameters{
    real b_pat[N_pat];
    real b_hosp[N_hosp];
    real mu[N];
    b_pat[1:(N_pat-1)] = b_pat_0;
    b_pat[N_pat] = -sum(b_pat_0);
    b_hosp[1:(N_hosp-1)] = b_hosp_0;
    b_hosp[N_hosp] = -sum(b_hosp_0);
    for(i in 1:N){
        mu[i] = a[1]+a[2]*A[i]+a[3]*X1[i]+a[4]*X2[i]+a[5]*X3[i]+a[6]*X4[i]+a[7]*X5[i]
               +a[8]*Z1[i]+a[9]*Z2[i]+a[10]*Z3[i]+a[11]*Z4[i]+a[12]*Z5[i]
               +b_pat[ID_pat[i]]+b_hosp[ID_hosp[i]];
    }
}

model{
    for(i in 1:N_pat){
        target += normal_lpdf(b_pat[i]|0,s_pat);
    }
    for(i in 1:N_hosp){
        target += normal_lpdf(b_hosp[i]|0,s_hosp);
    }
    for(i in 1:N){
        Y[i] ~ gamma(s,s/mu[i]);
    }
}

```

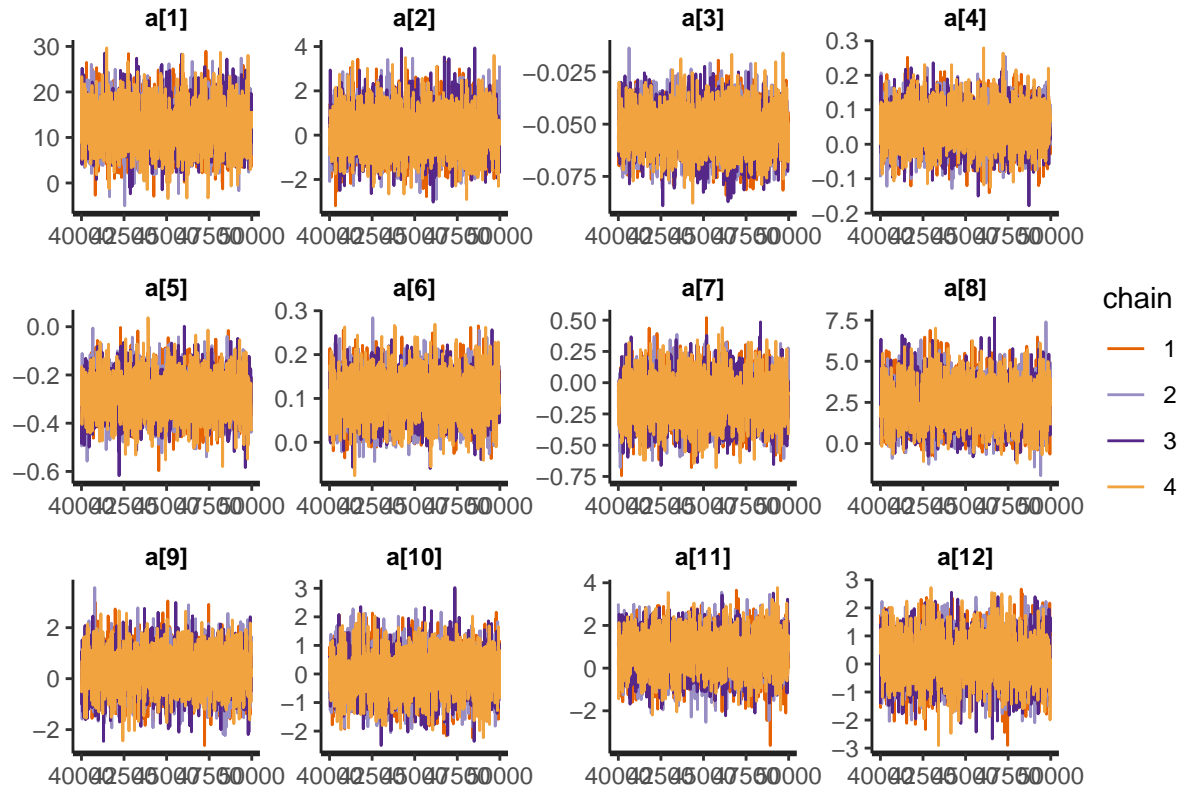
## 1-2. Checking the sampling convergence

We set four separate sampling chains, each consisting of 5000 samples (including 4000 samples discarded for convergence). We evaluated the sampling convergence by trace plots and the Gelman-Rubin Statistic

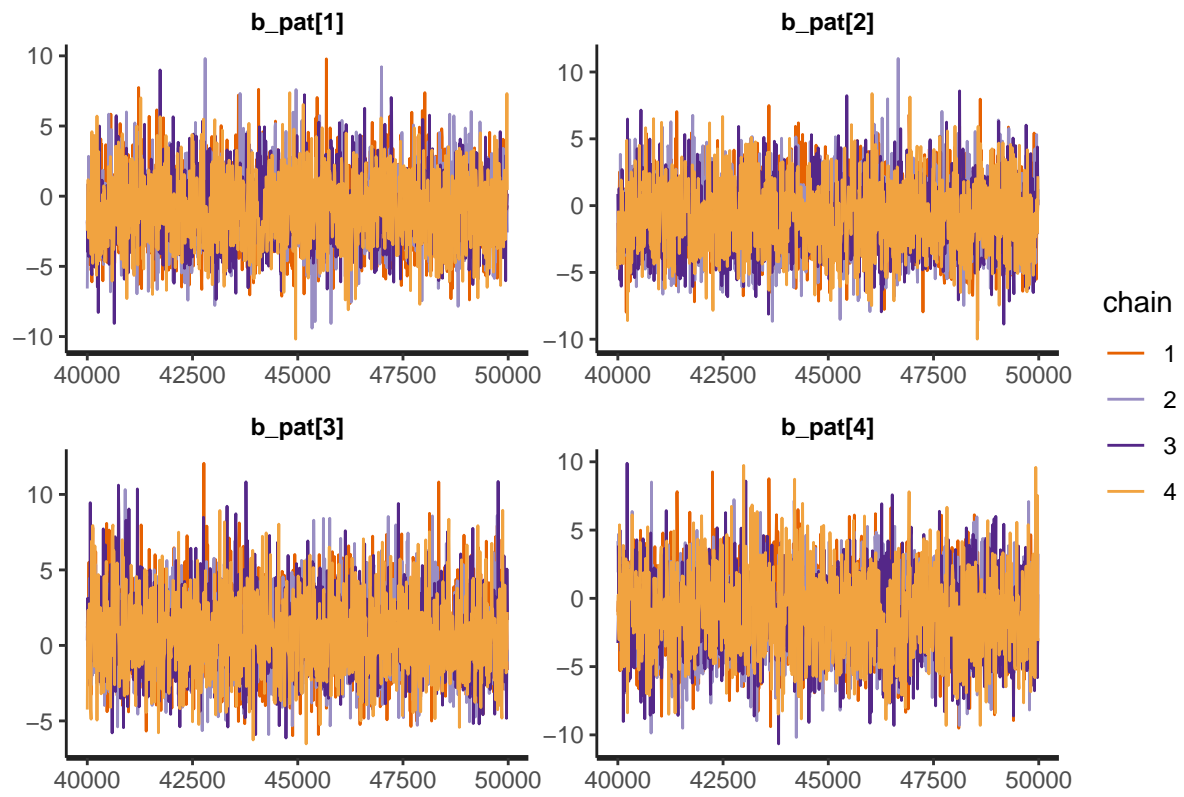
(R-hat).

```
fit <- sampling(model,
  data=datalist,
  iter=50000,
  warmup=40000,
  chains=4,
  thin=10,
  cores=4)
```

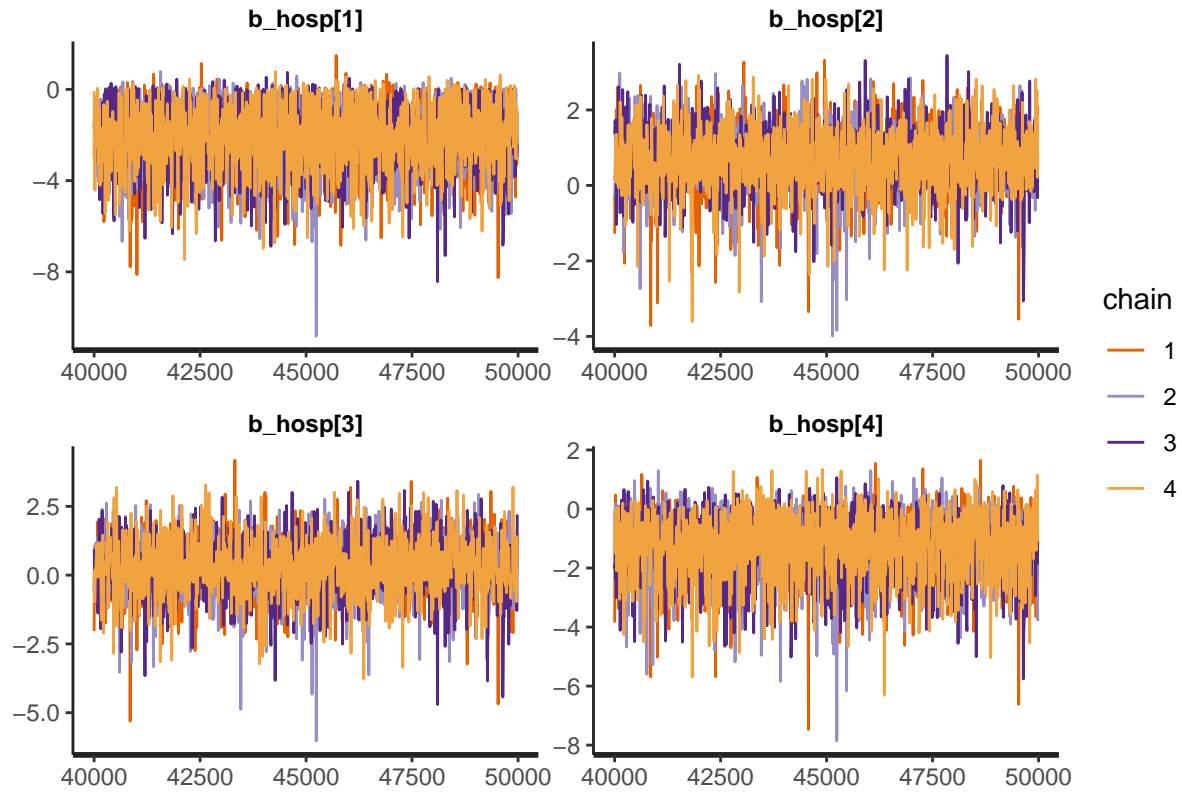
```
stan_trace(fit, pars=c("a"))
```



```
stan_trace(fit, pars=c("b_pat[1]", "b_pat[2]", "b_pat[3]", "b_pat[4]"))
```



```
stan_trace(fit, pars=c("b_hosp[1]", "b_hosp[2]", "b_hosp[3]", "b_hosp[4]"))
```



Checked all R-hats < 1.1.

```
all(summary(fit)$summary[,"Rhat"]<=1.10, na.rm=T)
```

```
## [1] TRUE
```

1-3. Calculating 95% highest density interval

```
coef_a <- c("a[1]","a[2]","a[3]","a[4]","a[5]","a[6]",  
            "a[7]","a[8]","a[9]","a[10]","a[11]","a[12]")
```

```
round(summary(fit)$summary[coef_a,c("mean","sd","2.5%","50%","97.5%")],digits=3)
```

```
##      mean    sd  2.5%  50% 97.5%  
## a[1] 12.794 4.925  3.258 12.739 22.495  
## a[2]  0.178 1.002 -1.714  0.175  2.210  
## a[3] -0.053 0.011 -0.074 -0.053 -0.032  
## a[4]  0.053 0.059 -0.064  0.052  0.169  
## a[5] -0.285 0.086 -0.452 -0.285 -0.114  
## a[6]  0.104 0.051  0.004  0.104  0.205  
## a[7] -0.141 0.180 -0.481 -0.144  0.214  
## a[8]  2.365 1.305 -0.045  2.319  4.985  
## a[9]  0.313 0.824 -1.327  0.322  1.865  
## a[10] -0.023 0.745 -1.461 -0.033  1.465  
## a[11]  0.729 0.944 -1.149  0.753  2.469  
## a[12]  0.156 0.809 -1.394  0.156  1.734
```

```
re_hosp <- c("b_hosp[1]","b_hosp[2]","b_hosp[3]","b_hosp[4]","b_hosp[5]","b_hosp[6]")
```

```
round(summary(fit)$summary[re_hosp,c("mean","sd","2.5%","50%","97.5%")],digits=3)
```

```
##           mean    sd   2.5%   50%  97.5%
## b_hosp[1] -2.136 1.477 -5.328 -2.055  0.085
## b_hosp[2]  0.671 0.825 -1.049  0.681  2.280
## b_hosp[3]  0.253 0.991 -1.842  0.234  2.187
## b_hosp[4] -1.257 1.118 -3.742 -1.109  0.432
## b_hosp[5]  0.145 1.226 -2.469  0.103  2.769
## b_hosp[6]  2.323 3.112 -0.935  1.395 10.707
```

```
fit_extract <- rstan::extract(fit)
hdi(fit_extract$a,credMass = 0.95)
```

```
##
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## lower  3.304708 -1.836179 -0.07295538 -0.06494139 -0.4571423  0.002533178
## upper 22.515473  2.060479 -0.03138897  0.16810168 -0.1222664  0.199549682
##
##           [,7]      [,8]      [,9]      [,10]     [,11]     [,12]
## lower -0.4805014 -0.08273402 -1.274527 -1.447325 -1.167150 -1.370097
## upper  0.2155662  4.92077753  1.894807  1.469075  2.442834  1.747826
## attr("credMass")
## [1] 0.95
```

```
hdi(fit_extract$b_hosp,credMass=0.95)
```

```
##
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## lower -4.9786524 -0.9294889 -1.809480 -3.4683788 -2.309832 -1.558114
## upper  0.2295804  2.3558010  2.208732  0.6273056  2.899803  8.990707
## attr("credMass")
## [1] 0.95
```

```
# "Intercept",
# "Anti-pseudomonal antibiotics",
# "Activity of daily living",
# "Respiratory rate",
# "Body mass index",
# "Age",
# "The number of recurrences",
# "Altered mental status",
# "Oxygen demand",
# "Heart rate",
# "Steroid therapy",
# "Home oxygen therapy"
```