Bayesian Methods - Ex3a - Linear Mixed-Effects Model

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Full assignment in PDF

This assignment is supposed to be solved via JAGS and `library(runjags)`. List through the manual to find what you need.

Data and model description

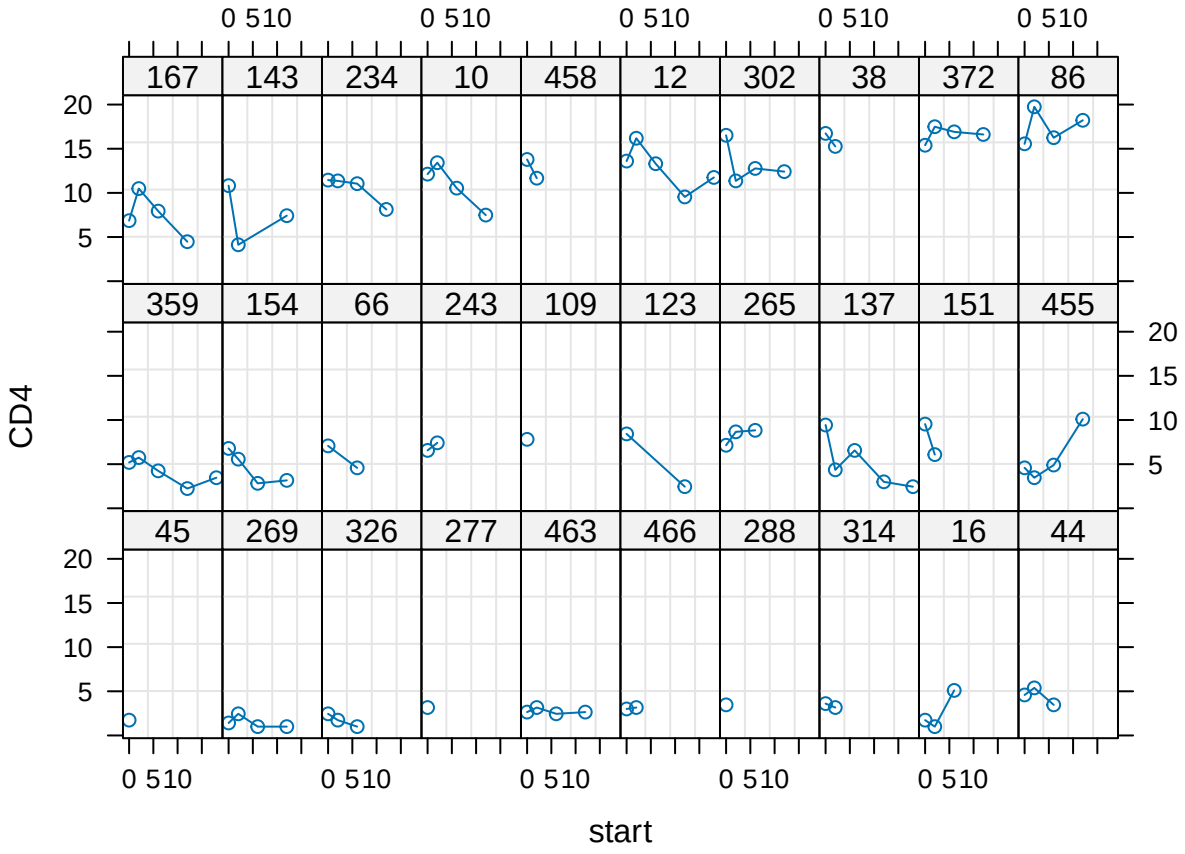
We will work with the `aids` data from `library(JM)`, see `help(aids)` for more details. It is of both longitudinal and survival data nature. In this part of the exercise, we will focus on the **longitudinal** aspect:

```
set.seed(123456789)
library(JM)
head(aids[,c("patient", "CD4", "obstime", "drug")], 15)
```

```
##    patient       CD4 obstime drug
## 1        1 10.677078       0  ddC
## 2        1  8.426150       6  ddC
## 3        1  9.433981      12  ddC
## 4        2  6.324555       0  ddI
## 5        2  8.124038       6  ddI
## 6        2  4.582576      12  ddI
## 7        2  5.000000      18  ddI
## 8        3  3.464102       0  ddI
## 9        3  3.605551       2  ddI
## 10       3  6.164414       6  ddI
## 11       4  3.872983       0  ddC
## 12       4  4.582576       2  ddC
## 13       4  2.645751       6  ddC
## 14       4  1.732051      12  ddC
## 15       5  7.280110       0  ddI
```

It consists of 467 HIV infected patients who were treated with two antiretroviral drugs (`drug`).

We will model the evolution of `CD4` cell count for each individual `patient`.
The time at which the measurement of `CD4` was taken is `obstime` in months. It is either 0, 2, 6, 12 or 18 (prescribed times of visits). Let us have a look on several random patients:



For some people the cell count decreases in time, for some increases. We will use this observation to construct linear mixed-effects (LME) model.

Task 1 - Frequentistic approach

Fit LME model (e.g. `lme` from `library(nlme)`) with random intercept and slope estimated with ML approach:

- $Y_{ij} = \beta_1 + B_{1i} + (\beta_2 + B_{2i})t_{ij} + \beta_3 D_i t_{ij} + \varepsilon_{ij}$, is the `CD4` cell count of patient i at visit j,
- $\varepsilon_{ij} \sim \mathsf{N}(0, \sigma^2)$ is the iid model error,
- t_{ij} is the time of the observation of patient i at visit j,
- D_i is the indicator of `drug` level `ddI`,
- B_{1i} and B_{2i} are the random intercept and slope for patient i,
- $\mathbf{B}_i = (B_{1i}, B_{2i})^\top \sim \mathsf{N}_2(\mathbf{0}, \Sigma)$, where Σ is general positive-definite matrix.

Notice that there is no $\beta_4 D_i$ within the formula It would have the interpretation of difference between drug when $t = 0$ (study has not started yet). It is reasonable to assume $\beta_4 = 0$ and not include it within the model.

Print the summary of the model. Look at the magnitude of the coefficients including standard errors. Use this information to choose non-informative prior in the next Task.

Task 2 - Bayesian approach - JAGS implementation

Consider the same model from Task 1. Reparametrize the variance parameters through precisions instead: $\tau = \sigma^{-2}$, $\Omega = \Sigma^{-1}$. Move the parametrization of intercept and slope for patient i into the prior mean of respective random effects to reduce the autocorrelation:

$$\mathsf{E}\, B_{1i} = \beta_1 \qquad \mathsf{E}\, B_{2i} = \beta_2 + \beta_3 D_i.$$

(You can implement other versions with $\mathsf{E}B_{1i} = 0$ or $\mathsf{E}B_{2i} = 0$ or $\mathsf{E}B_{2i} = \beta_2$ to see the difference for yourself.)

Assume the independent block structure of the prior for model parameters:

$$p(\boldsymbol{\beta}, \tau, \Omega) = \prod_{j=1}^{3} p(\beta_j)\, p(\tau)\, p(\Omega)$$

Choose weakly informative *normal* prior for β_j, *gamma* prior for τ and *Wishart* distribution (`dwish`) for Ω.

Write down (and print) the model implementation within JAGS.

Task 3 - Running JAGS

Sample two Markov chains using JAGS to approximate the posterior distribution $p(\boldsymbol{\beta}, \tau, \Omega \,|\, \mathsf{data})$. Choose appropriate `burnin` and `thin` by monitoring the trajectories and autocorrelation.

Task 4 - Monte Carlo estimates

Provide summaries including ET and HPD intervals for primary model parameters. Compare them to the outputs in Task 1.