STAT 393 Assignment 4: Solutions

A group of 50 people all wished to lose weight. Each person was assigned randomly to one of three treatment programs. They all followed the instructions given in the assigned program for 4 months. At the end of each month, a researcher measured and recorded each participant's weight. Data (in the file `loss.csv` – available on Nuku) include the weight loss since the participants started the program (`loss`), gender (`gender`, 0: female; 1: male), a personal identifier (`id`), initial weight (`weight`), month (`time`), and treatment (`trt`).

1. Use the following `R` code to read in the data, then use `summary()` to display information about all the variables:

```
lossdata<-read.table("loss.csv",sep=",",header=T,as.is=T)
lossdata$trt <- as.factor(lossdata$trt)
lossdata$gender <- as.factor(lossdata$gender)
summary(lossdata)
```

```
##      loss          gender       id           weight          time        trt
##  Min.   : 0.500   0:120   Min.   : 1.0   Min.   : 61.10   Min.   :1.00   1:60
##  1st Qu.: 6.700   1: 80   1st Qu.:13.0   1st Qu.: 75.00   1st Qu.:1.75   2:56
##  Median : 9.100           Median :25.5   Median : 90.45   Median :2.50   3:84
##  Mean   : 9.184           Mean   :25.5   Mean   : 90.93   Mean   :2.50
##  3rd Qu.:11.500           3rd Qu.:38.0   3rd Qu.:106.60   3rd Qu.:3.25
##  Max.   :17.300           Max.   :50.0   Max.   :119.60   Max.   :4.00
```

The given code (above) produces the required output.

2. Plot the weight loss against the 4 time points (months) for all subjects. Comment, briefly – what features are 'obvious'? Some suggested R code follows.

```
loss.long <- matrix(lossdata$loss,ncol=4,byrow=T)
trt.long <- matrix(lossdata$trt,ncol=4,byrow=T)
plot(range(lossdata$time), range(lossdata$loss), type="n",xlab="time",
     ylab="weight loss", xaxp = c(1, 4, 3))
for(i in 1:50){points(c(1:4),loss.long[i,],type="l") }
```

Or, use different colours in the plot for different programs/treatments, which is somewhat more informative. Again, possible R code follows – along with the resulting plot.

```
loss.long <- matrix(lossdata$loss,ncol=4,byrow=T)
trt.long <- matrix(lossdata$trt,ncol=4,byrow=T)
plot(range(lossdata$time),range(lossdata$loss),
 type="n",xlab="time",ylab="weight loss", xaxp = c(1, 4, 3))
for(i in 1:50){
  if(trt.long[i,1]==1){
    points(c(1:4),loss.long[i,],type="l",col="red")}
  else if(trt.long[i,1]==2){
    points(c(1:4),loss.long[i,],type="l",col="black")}
  else {points(c(1:4),loss.long[i,],type="l",col="green")}
}
legend("topleft",c("Trt 1","Trt 2","Trt 3"),title = "Treatment",
       lty=1, col=c("red","black","green"))
```
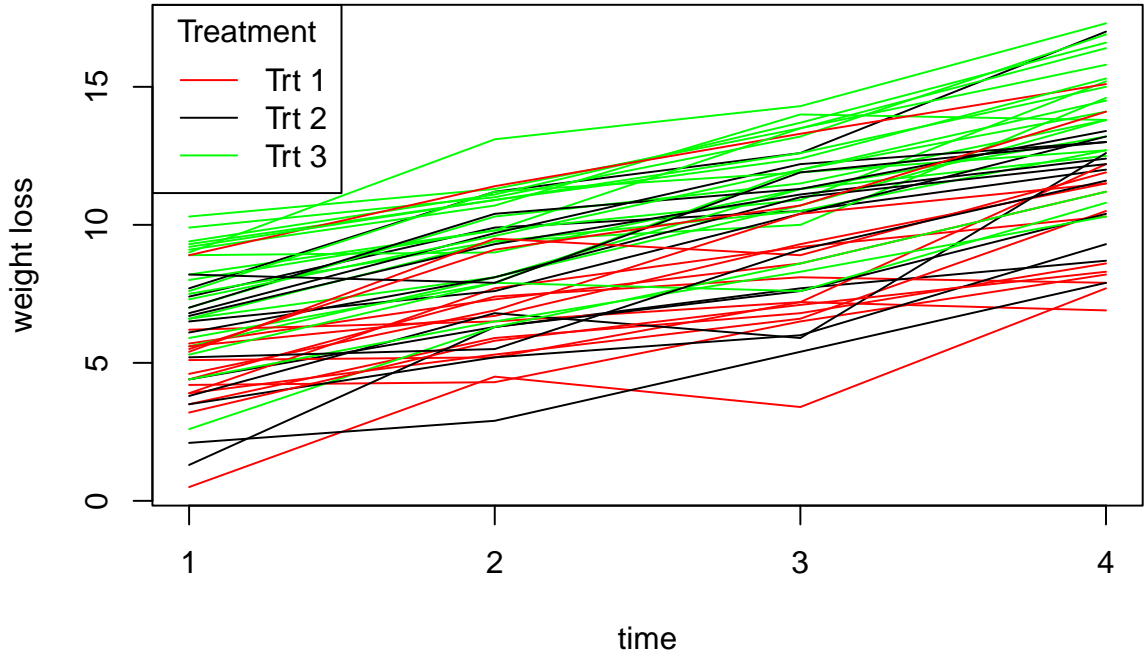
When taken along with the information from `summary()` in Q1, the 'obvious' features are that all weight losses are positive and, in general, weight losses increase over time, as people progress in the treatment programs. The minimum weight loss is 0.5 kg, recorded 1 month after the program started by someone on treatment 1, while the maximum weight loss is 17.3 kg, recorded after 4 months by someone on treatment 3. Given the aim of all 50 people was to lose weight, these results are in line with what we would expect to see – and what the participants would hope for!

3. Consider the following linear model:

$$
\begin{aligned}
y_{ij} \quad = \quad & \beta_0 + \beta_1(\text{trt2})_{ij} + \beta_2(\text{trt3})_{ij} + \beta_3(\text{gender1})_{ij} + \beta_4(\text{time})_{ij} + \beta_5(\text{weight})_{ij} \\
& + b_{i0} + b_{i1}(\text{trt2})_{ij} + b_{i2}(\text{trt3})_{ij} + b_{i3}(\text{gender1})_{ij} + b_{i4}(\text{time})_{ij} + b_{i5}(\text{weight})_{ij} + \varepsilon_{ij},
\end{aligned}
$$

where:

- $(\text{trt2})_{ij} = 1$ if the ith subject received treatment 2 at time j. Otherwise, $(\text{trt2})_{ij} = 0$,
- $(\text{trt3})_{ij} = 1$ if the ith subject received treatment 3 at time j. Otherwise, $(\text{trt3})_{ij} = 0$,
- $(\text{gender1})_{ij} = 1$ if the ith subject is male. Otherwise, $(\text{gender1})_{ij} = 0$,
- $(\text{time})_{ij}$ is the number of months, j, that the ith subject has been in the program $(j = 1, \ldots, 4)$,
- $(\text{weight})_{ij}$ is the ith subject's initial weight,
- y_{ij} is the response variable: the ith subject's overall weight loss after j months in the program.

Note: The $(\text{trt2})_{ij}$ and $(\text{trt3})_{ij}$ are dummy variables for the treatments. We use the `R` default setting for handling dummy variables, with the intercept including the first level of the treatments. Also, $(\text{gender1})_{ij}$ is a dummy variable for gender, with the intercept including the first level; i.e. females are included in the intercept.

a. Name all the time-invariant explanatory variables.

The time-invariant explanatory variables are treatment (`trt`), gender (`gender`) and initial weight (`weight`). This means that most of the random coefficients in the displayed general model equation will be identically zero, since there is no variation in the corresponding explanatory variables for different values of time j. Hence the fixed effects will estimate the relevant contribution from those time-invariant explanatory variables and only b_{i0} and b_{i4} can be estimated as random effect coefficients. Estimating those two parameters means we allow a random intercept for each subject's weight loss over time and also a random slope, which allows the (linear) changes in weight loss to differ between subjects as time increases from $j = 1$ to $j = 4$.

b. Fit the model in 6 ways, giving 6 separate model fits, by using the three correlation structures: AR1 (`corAR1`), compound symmetry (`corCompSymm`), and a general, unrestricted correlation structure (`corSymm`). Also, for each correlation structure fit the random intercept model first, followed by the random intercept plus random slope model. Use the the function `lme()` and the REML estimation method. **Which of the 6 models do you recommend is best, and why?**

Note: To fit those 6 models you need to load the `R` packages `MASS` and `nlme`. Some suggested code for the random intercept model with the `corAR1` correlation structure follows. Also note that even though REML will not return the true log-likelihood, the restricted log-likelihoods **can** be compared, since every model has the same fixed effects and they are all fitted using the same (REML) approach. So, for example, model selection using penalised log-likelihoods is valid.

```
library(MASS)
library(nlme)
loss.lme1a <- lme(fixed = loss ~ trt + gender + time + weight,
                  random = ~ 1 | id,
                  correlation = corAR1(form = ~ time| id ),
                  method = "REML",
                  data=lossdata)
summary(loss.lme1a)
```

Code follows to fit the 6 required models, along with the resulting output for each model.

```
library(MASS)
library(nlme)


##########################################
# random intercept + AR1
##########################################
loss.lme1a <- lme(fixed = loss ~ trt + gender + time + weight,
                  random = ~ 1 | id,
                  correlation = corAR1(form = ~ time| id ),
                  method = "REML",
                  data=lossdata)
summary(loss.lme1a)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC    logLik
##   678.5378 707.9486 -330.2689
##
## Random effects:
##  Formula: ~1 | id
##         (Intercept) Residual
## StdDev:    1.385239 0.965238
##
## Correlation Structure: AR(1)
##  Formula: ~time | id
##  Parameter estimate(s):
##       Phi
## 0.107256
## Fixed effects:  loss ~ trt + gender + time + weight
##                  Value Std.Error  DF  t-value p-value
## (Intercept) -1.5180285 1.2380532 149 -1.22614  0.2221
## trt2         0.3703686 0.5658313  45  0.65456  0.5161
## trt3         1.8896905 0.6128619  45  3.08339  0.0035
## gender1     -2.2261800 0.4426500  45 -5.02921  0.0000
```

3

```
## time          2.0640557 0.0623530 149 33.10276   0.0000
## weight        0.0609064 0.0151067  45  4.03175   0.0002
##  Correlation:
##         (Intr) trt2   trt3   gendr1 time
## trt2    -0.018
## trt3     0.351  0.541
## gender1  0.058  0.131  0.068
## time    -0.126  0.000  0.000  0.000
## weight  -0.932 -0.217 -0.575 -0.209  0.000
##
## Standardized Within-Group Residuals:
##          Min          Q1         Med          Q3         Max
## -2.42656701 -0.48764628 -0.01587156  0.58834354  2.37633572
##
## Number of Observations: 200
## Number of Groups: 50
```

```r
#############################################
# random intercept + slope + AR1
#############################################
loss.lme1b <- lme(fixed = loss ~ trt+gender+time+weight,
                  random = ~ time | id,
                  correlation = corAR1(form = ~ time| id ),
                  data=lossdata)
summary(loss.lme1b)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC     logLik
##   679.3491 715.2955 -328.6745
##
## Random effects:
##  Formula: ~time | id
##  Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev    Corr
## (Intercept) 1.4024163 (Intr)
## time        0.2937002 -0.224
## Residual    0.8355439
##
## Correlation Structure: AR(1)
##  Formula: ~time | id
##  Parameter estimate(s):
##        Phi
## -0.1110023
## Fixed effects:  loss ~ trt + gender + time + weight
##                  Value Std.Error  DF    t-value p-value
## (Intercept) -1.2113051 1.2149406 149 -0.997008  0.3204
## trt2         0.2220010 0.5566480  45  0.398818  0.6919
## trt3         1.7265674 0.6029153  45  2.863698  0.0063
## gender1     -2.2059564 0.4354659  45 -5.065738  0.0000
## time         2.0524171 0.0658426 149 31.171577  0.0000
## weight       0.0589061 0.0148615  45  3.963671  0.0003
##  Correlation:
##         (Intr) trt2   trt3   gendr1 time
## trt2    -0.018
## trt3     0.352  0.541
## gender1  0.058  0.131  0.068
## time    -0.105  0.000  0.000  0.000
## weight  -0.935 -0.217 -0.575 -0.209  0.000
```

```
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.88175060 -0.47465787 -0.01358368  0.56594350  2.44929676
##
## Number of Observations: 200
## Number of Groups: 50
```

```r
#############################################
# random intercept + compound symmetry
#############################################
loss.lme2a <- lme(fixed = loss ~ trt+gender+time+weight,
                  random = ~ 1 | id,
                  correlation = corCompSymm(form = ~ time| id ),
                  data=lossdata)
summary(loss.lme2a)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC    logLik
##    679.142 708.5528 -330.571
##
## Random effects:
##  Formula: ~1 | id
##         (Intercept)  Residual
## StdDev:    1.403439 0.9366059
##
## Correlation Structure: Compound symmetry
##  Formula: ~time | id
##  Parameter estimate(s):
## Rho
##    0
## Fixed effects:  loss ~ trt + gender + time + weight
##                  Value Std.Error  DF  t-value p-value
## (Intercept) -1.5215012 1.2364120 149 -1.23058  0.2204
## trt2         0.3645311 0.5655138  45  0.64460  0.5225
## trt3         1.8784803 0.6125180  45  3.06682  0.0037
## gender1     -2.2276575 0.4424016  45 -5.03537  0.0000
## time         2.0584000 0.0592362 149 34.74905  0.0000
## weight       0.0611408 0.0150982  45  4.04954  0.0002
##  Correlation:
##         (Intr) trt2   trt3   gendr1 time
## trt2    -0.018
## trt3     0.351  0.541
## gender1  0.058  0.131  0.068
## time    -0.120  0.000  0.000  0.000
## weight  -0.933 -0.217 -0.575 -0.209  0.000
##
## Standardized Within-Group Residuals:
##          Min           Q1          Med          Q3          Max
## -2.470923005 -0.502343779 -0.005612071  0.594049624  2.484843364
##
## Number of Observations: 200
## Number of Groups: 50
```

```r
#############################################
# random intercept + slope + compound symmetry
#############################################
loss.lme2b <- lme(fixed = loss ~ trt+gender+time+weight,
```

```
                  random = ~ time | id,
                  correlation = corCompSymm(form = ~ time| id ),
                  data=lossdata)
summary(loss.lme2b)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC    logLik
##   679.6607 715.6071 -328.8303
##
## Random effects:
##  Formula: ~time | id
##  Structure: General positive-definite, Log-Cholesky parametrization
##            StdDev    Corr
## (Intercept) 1.3359838 (Intr)
## time        0.2540811 -0.112
## Residual    0.8781211
##
## Correlation Structure: Compound symmetry
##  Formula: ~time | id
##  Parameter estimate(s):
##         Rho
## 2.20968e-05
## Fixed effects:  loss ~ trt + gender + time + weight
##                 Value Std.Error  DF   t-value p-value
## (Intercept) -1.2076947 1.2153529 149 -0.993699  0.3220
## trt2         0.2304582 0.5567973  45  0.413900  0.6809
## trt3         1.7429565 0.6030770  45  2.890106  0.0059
## gender1     -2.2115553 0.4355827  45 -5.077234  0.0000
## time         2.0584000 0.0661473 149 31.118439  0.0000
## weight       0.0586577 0.0148655  45  3.945901  0.0003
##  Correlation:
##         (Intr) trt2   trt3   gendr1 time
## trt2    -0.018
## trt3     0.352  0.541
## gender1  0.058  0.131  0.068
## time    -0.105  0.000  0.000  0.000
## weight  -0.935 -0.217 -0.575 -0.209  0.000
##
## Standardized Within-Group Residuals:
##         Min          Q1          Med          Q3          Max
## -2.771502690 -0.468308754 -0.008784213  0.578227559  2.320552591
##
## Number of Observations: 200
## Number of Groups: 50
```

```
#################################################
# random intercept + unstructured
#################################################
loss.lme3a <- lme(fixed = loss ~ trt+gender+time+weight,
                  random = ~ 1 | id,
                  correlation = corSymm(form = ~ time| id ),
                  data=lossdata)
summary(loss.lme3a)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC    logLik
##   686.1039 731.8539 -329.052
```

```
##
## Random effects:
##  Formula: ~1 | id
##         (Intercept) Residual
## StdDev:    1.423335 0.932219
##
## Correlation Structure: General
##  Formula: ~time | id
##  Parameter estimate(s):
##  Correlation:
##   1      2      3
## 2  0.130
## 3  0.070  0.137
## 4 -0.265 -0.031 -0.068
## Fixed effects:  loss ~ trt + gender + time + weight
##                  Value Std.Error  DF   t-value p-value
## (Intercept) -1.4545355 1.2498771 149 -1.163743  0.2464
## trt2         0.4093654 0.5706100  45  0.717417  0.4768
## trt3         1.9470633 0.6180378  45  3.150395  0.0029
## gender1     -2.2302590 0.4463884  45 -4.996230  0.0000
## time         2.0411466 0.0648759 149 31.462327  0.0000
## weight       0.0605578 0.0152343  45  3.975107  0.0003
##  Correlation:
##         (Intr) trt2   trt3   gendr1 time
## trt2    -0.018
## trt3     0.350  0.541
## gender1  0.058  0.131  0.068
## time    -0.134  0.000  0.000  0.000
## weight  -0.931 -0.217 -0.575 -0.209  0.000
##
## Standardized Within-Group Residuals:
##          Min          Q1          Med          Q3          Max
## -2.695290773 -0.555626730  0.008257611  0.606298453  2.374995952
##
## Number of Observations: 200
## Number of Groups: 50
```

```r
###############################################
# random intercept + slope + unstructured
###############################################
loss.lme3b <- lme(fixed = loss ~ trt+gender+time+weight,
                  random = ~ time | id,
                  correlation = corSymm(form = ~ time| id ),
                  data=lossdata)
summary(loss.lme3b)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC    logLik
##   687.7015 739.9873 -327.8508
##
## Random effects:
##  Formula: ~time | id
##  Structure: General positive-definite, Log-Cholesky parametrization
##              StdDev    Corr
## (Intercept) 1.4415098 (Intr)
## time        0.3715052 -0.351
## Residual    0.8248586
##
```

```
## Correlation Structure: General
##  Formula: ~time | id
##  Parameter estimate(s):
##  Correlation:
##    1      2      3
## 2  0.031
## 3  0.239  0.027
## 4  0.240  0.067 -0.334
## Fixed effects:  loss ~ trt + gender + time + weight
##                   Value Std.Error  DF   t-value p-value
## (Intercept) -1.1687706 1.2142224 149 -0.962567  0.3373
## trt2          0.2172410 0.5564072  45  0.390435  0.6981
## trt3          1.7183955 0.6026545  45  2.851377  0.0065
## gender1      -2.1921958 0.4352776  45 -5.036317  0.0000
## time          2.0366152 0.0653053 149 31.186040  0.0000
## weight        0.0588464 0.0148551  45  3.961369  0.0003
##  Correlation:
##         (Intr) trt2   trt3   gendr1 time
## trt2    -0.018
## trt3     0.352  0.541
## gender1  0.058  0.131  0.068
## time    -0.103  0.000  0.000  0.000
## weight  -0.935 -0.217 -0.575 -0.209  0.000
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.88093660 -0.49394205 -0.01117896  0.52202067  2.55195416
##
## Number of Observations: 200
## Number of Groups: 50
```

Following the suggestion given as a note within the question, it is appropriate to select a 'best' model using an information criterion (i.e. a penalised log-likelihood comparison, with either AIC or BIC). The standard summary output includes the maximised log-likelihood for each model, along with both AIC and BIC. A summary of those three statistics, for the 6 models, is given next.

```
c(logLik(loss.lme1a, REML = TRUE),logLik(loss.lme1b, REML = TRUE),
  logLik(loss.lme2a, REML = TRUE),logLik(loss.lme2b, REML = TRUE),
  logLik(loss.lme3a, REML = TRUE),logLik(loss.lme3b, REML = TRUE))
```

```
## [1] -330.2689 -328.6745 -330.5710 -328.8303 -329.0520 -327.8508
```

```
AIC(loss.lme1a,loss.lme1b,loss.lme2a,loss.lme2b,loss.lme3a,loss.lme3b)
```

```
##             df      AIC
## loss.lme1a   9 678.5378
## loss.lme1b  11 679.3491
## loss.lme2a   9 679.1420
## loss.lme2b  11 679.6607
## loss.lme3a  14 686.1039
## loss.lme3b  16 687.7015
```

```
BIC(loss.lme1a,loss.lme1b,loss.lme2a,loss.lme2b,loss.lme3a,loss.lme3b)
```

```
##             df      BIC
## loss.lme1a   9 707.9486
## loss.lme1b  11 715.2955
## loss.lme2a   9 708.5528
## loss.lme2b  11 715.6071
## loss.lme3a  14 731.8539
## loss.lme3b  16 739.9873
```

All models have the same six fixed effects parameters and an estimated variance for the error term. So the only differences between the six models are how the random effects are modelled, and how many parameters are used to model the correlation structure. With AR1 or compound symmetry correlation structures there is only a single parameter to model the correlations in the 4×4 symmetric correlation matrix (of correlations between the four treatment times), while the unrestricted correlation structure needs $0.5 \times 4 \times 3 = 6$ parameters. The random intercept model needs a further variance parameter (for the variance of the random intercepts for each subject), while the random intercept plus random slope model needs three further covariance parameters (one for the variance of the random intercepts, one for the variance of the random slopes, and one for the covariance between the intercept and the slope for each subject). Hence the simplest random intercept models have 9 parameters (6+1+1+1), while the simplest random intercept plus random slope models have 11 parameters (6+1+1+3). The unrestricted correlation structure model needs 14 parameters with a random intercept (6+1+6+1) and 16 parameters with a random intercept plus random slope (6+1+6+3).

Since the fixed effects are the same in all cases, the model with most (variance) parameters fits best: the unrestricted correlation structure, with random intercept plus random slope. That gives the maximum value across the six maximised log-likelihoods, of -327.85. The difference between the best and worst maximised log-likelihoods is quite small though (2.72), while the difference in the numbers of parameters is quite large (16-9=7). So, given the closeness in quality of fit between all the models, both information criteria select one of the simplest models as 'best' – and in both cases it is the random intercept model plus AR1 correlation structure that is selected, with minimum AIC = 678.54 and minimum BIC = 707.95. This means that the selected model allows a random intercept for each participant's weight loss but then restricts the (linear) changes in weight loss over time to be the same for each participant, once the effects of the time-invariant explanatory variables have been taken into account.

c. Give the parameter estimates for the model you recommended was best in Question 3b, including the estimated correlation parameters.

As noted above, the best model has a random intercept and AR1 correlation structure. The following `R` code extracts the relevant model parameters.

The fixed effects coefficients, $\hat{\boldsymbol{\beta}} = (\hat{\beta}_0, \hat{\beta}_1, \ldots, \hat{\beta}_5)$:

```
# The fixed effects coefficients:
beta_hat1a=loss.lme1a$coefficients$fixed
beta_hat1a
```

```
## (Intercept)        trt2        trt3     gender1        time      weight
## -1.51802852  0.37036856  1.88969051 -2.22618001  2.06405568  0.06090639
```

The standard deviation parameter for ε, $\hat{\sigma}$:

```
# The estimated error standard deviation:
sigma_hat1a=loss.lme1a$sigma
sigma_hat1a
```

```
## [1] 0.965238
```

The covariance matrix for $\mathbf{b}$, $\hat{\mathbf{D}}$, which in this model is just the variance of the normally distributed random intercept:

```
# The estimated random intercept variance:
D1a <- getVarCov(loss.lme1a)
D1a
```

```
## Random effects variance covariance matrix
##             (Intercept)
## (Intercept)      1.9189
##    Standard Deviations: 1.3852
```

The random effects coefficients: $\hat{\mathbf{b}}_i = \hat{b}_{i0}$, $i = 1, 2, \ldots, 50$. For example, the following code prints the random intercepts for participants 1 to 5, $\hat{\mathbf{b}}_1, \ldots, \hat{\mathbf{b}}_5$.

```
loss.lme1a$coefficients$random$id[1:5,]
```

```
##          1          2          3          4          5
##  1.3335323 -0.6132535 -0.7697587  0.8703211 -0.6992229
```

As an example of estimated subject-specific effects, participant $i = 12$ is a woman who initially weighed 70.8 kg and who was randomly assigned to treatment program 1. We can calculate their estimated weight losses over the four months of the program (and plot those estimates along with the realised weight loss values):

```
# Prediction of `loss` values for Participant 12.
loss12 = lossdata[lossdata$id==12,]
loss12$predict <- predict(loss.lme1a, loss12)
loss12
```

```
##     loss gender id weight time trt   predict
## 45   5.7      0 12   70.8    1   1  5.085765
## 46   7.3      0 12   70.8    2   1  7.149820
## 47   8.6      0 12   70.8    3   1  9.213876
## 48  11.2      0 12   70.8    4   1 11.277932
```
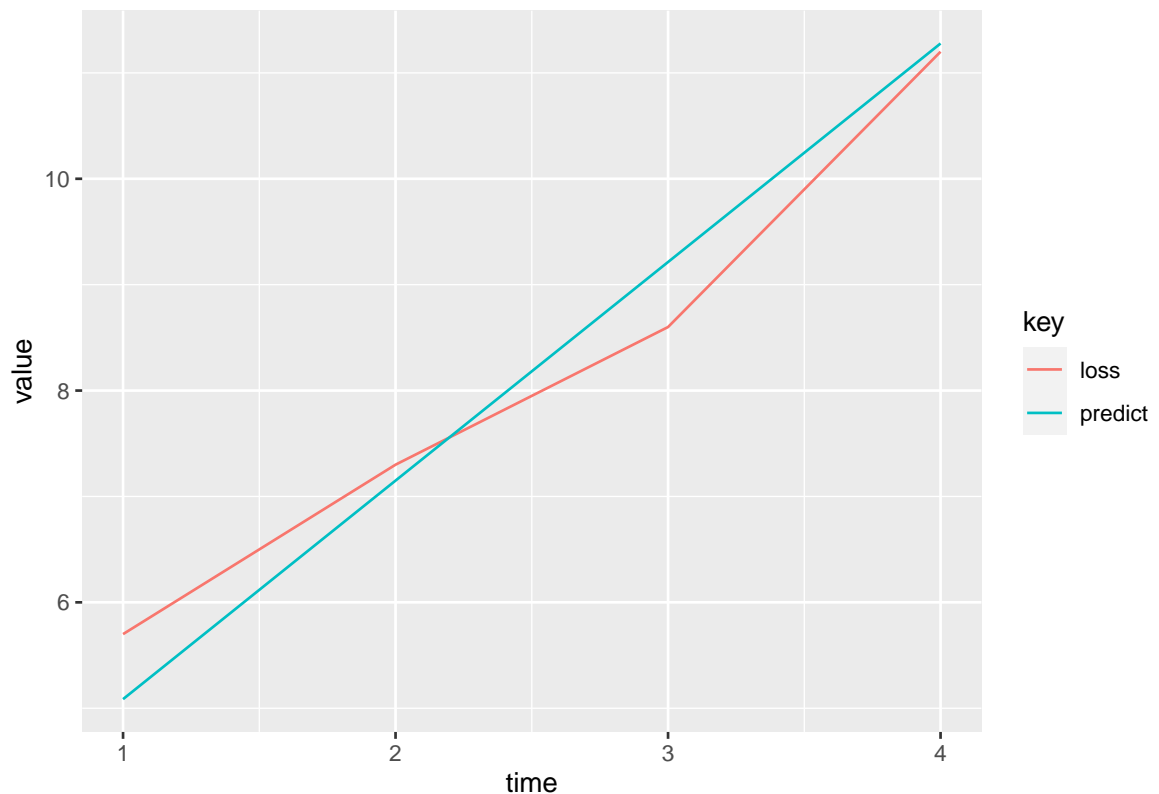
```
library(tidyverse)
library(ggplot2)
loss12 %>%
  gather(key,value, loss, predict) %>%
  ggplot(aes(x=time, y=value, colour=key)) +
  geom_line()
```


Here are the corresponding predictions for participant $i = 32$, a man who initially weighed 75.5 kg and who was randomly assigned to treatment program 2. Note that the successive predicted weight loss values differ by the same amount (2.064 kg per month). Also note the predicted weight loss per month is the same value for both participant 12 and participant 32, even though their initial weight losses in the first month are different. The behaviour of these predicted values is a consequence of

the specific 'best model' that was selected using AIC/BIC.

```
loss32 = lossdata[lossdata$id==32,]
loss32$predict <- predict(loss.lme1a, loss32)
loss32
```

```
##      loss gender id weight time trt   predict
## 125  3.8       1 32   75.5    1   2  4.114103
## 126  6.8       1 32   75.5    2   2  6.178159
## 127  5.9       1 32   75.5    3   2  8.242215
## 128 12.6       1 32   75.5    4   2 10.306270
```

Further, we can look at the estimated 4×4 covariance (and correlation) matrix for participant $i = 12$:

```
# Marginal covariance matrix for Participant 12
margCov1a <- getVarCov(loss.lme1a, individuals = 12,
                       type = "marginal")
margCov1a
```

```
## id 12
## Marginal variance covariance matrix
##        1      2      3      4
## 1 2.8506 2.0188 1.9296 1.9200
## 2 2.0188 2.8506 2.0188 1.9296
## 3 1.9296 2.0188 2.8506 2.0188
## 4 1.9200 1.9296 2.0188 2.8506
##   Standard Deviations: 1.6884 1.6884 1.6884 1.6884
```

```
cov2cor(margCov1a[[1]])
```

```
##           1         2         3         4
## 1 1.0000000 0.7082145 0.6769188 0.6735621
## 2 0.7082145 1.0000000 0.7082145 0.6769188
## 3 0.6769188 0.7082145 1.0000000 0.7082145
## 4 0.6735621 0.6769188 0.7082145 1.0000000
```

d. Interpret $\hat{\beta}_1$ and $\hat{\beta}_2$ for the model recommended in Question 3b.

From the summary output for the selected (first) model, $\hat{\beta}_1 = 0.3704$ with p-value $= 0.5161$. Given other variables (gender, time, and initial weight) at a fixed level, using treatment program 2 the average weight loss is 0.3704 kg more than using treatment program 1. Since the p-value > 0.05, however, the difference between programs 1 and 2 is not significant at a 5% level. For treatment program 3, $\hat{\beta}_2 = 1.8897$ with p-value $= 0.0035$. Given other variables (gender, time, and initial weight) at a fixed level, using treatment program 3 the average weight loss is 1.8897 kg more than using treatment program 1. The difference between programs 1 and 3 is significant at a 5% level, since the p-value is < 0.05.

4. Briefly comment on any differences among the three weight loss programs. Which program would you recommend as most effective?

From Q3d, it is clear that with the selected model, program 3 is significantly better than program 1 for average weight loss over participants. We can use `anova.lme()` to compare the terms in that model using likelihood ratio tests for significance:

```
anova.lme(loss.lme1a)
```

```
##                numDF denDF   F-value p-value
## (Intercept)        1   149 1925.8227  <.0001
## trt                2    45   21.4110  <.0001
## gender             1    45   18.3266   1e-04
## time               1   149 1095.7929  <.0001
## weight             1    45   16.2550   2e-04
```

Clearly, every term in the model is highly significant, including the factor `trt`. To directly test whether the higher average weight loss in program 3 is significantly different from that in program 2, we can reset the base level for `trt` to be program 2 rather than program 1:

```
loss.lme1a_trt2 <- lme(fixed = loss ~ relevel(trt, ref = "2")+gender+time+weight,
                       random = ~ 1 | id,
                       correlation = corAR1(form = ~ time| id ),
                       data=lossdata)
summary(loss.lme1a_trt2)
```

```
## Linear mixed-effects model fit by REML
##   Data: lossdata
##        AIC      BIC    logLik
##   678.5378 707.9486 -330.2689
##
## Random effects:
##  Formula: ~1 | id
##         (Intercept) Residual
## StdDev:    1.385239 0.965238
##
## Correlation Structure: AR(1)
##  Formula: ~time | id
##  Parameter estimate(s):
##       Phi
## 0.107256
## Fixed effects:  loss ~ relevel(trt, ref = "2") + gender + time + weight
##                             Value Std.Error  DF  t-value p-value
## (Intercept)             -1.1476600 1.3517614 149 -0.84901  0.3972
## relevel(trt, ref = "2")1 -0.3703686 0.5658313  45 -0.65456  0.5161
## relevel(trt, ref = "2")3  1.5193219 0.5659413  45  2.68459  0.0101
## gender1                 -2.2261800 0.4426500  45 -5.02921  0.0000
## time                     2.0640557 0.0623530 149 33.10276  0.0000
## weight                   0.0609064 0.0151067  45  4.03175  0.0002
##  Correlation:
##                          (Intr) r(,r="2")1 r(,r="2")3 gendr1 time
## relevel(trt, ref = "2")1 -0.402
## relevel(trt, ref = "2")3  0.192  0.414
## gender1                   0.108 -0.131      -0.058
## time                     -0.115  0.000       0.000     0.000
## weight                   -0.945  0.217      -0.405    -0.209  0.000
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.42656701 -0.48764628 -0.01587156  0.58834354  2.37633572
##
## Number of Observations: 200
## Number of Groups: 50
```

Of course the model fit is identical in terms of the maximised log-likelihood value, but the intercept now includes program 2 so the p-value of 0.0101 for $\hat{\beta}_2 = 1.5193$ confirms that the difference of just over 1.5 kg between programs 2 and 3 is also significant at a 5% level, given the other variables

(gender, time, and initial weight) remain at a fixed level. Program 3 certainly seems to be best for weight loss, on average.

5. Consider whether your recommended weight loss program should be the same for males and females. Can you perform a hypothesis test for a gender difference in the effectiveness of the different programs, using the model you recommended in Question 3b? If so, report that test result and if not, find a way to carry out that hypothesis test and then report the result.

The models considered so far have only included the main (fixed) effect of each time-invariant explanatory variable. It is possible that there could be an interaction between the two factors gender and treatment, but that can't be tested using the models fitted up to now. Since any effects due to gender or treatment are time-invariant though, we can test for an interaction between those terms using regular maximum likelihood (rather than REML) to estimate a suitable model that includes the interaction term. Here's some code that does that, still using the selected correlation structure from the 'best' model:

```
loss.lme1interML <- lme(fixed = loss ~ trt*gender+time+weight,
                        random = ~ 1 | id,
                        correlation = corAR1(form = ~ time| id ),
                        method = "ML",
                        data=lossdata)
anova.lme(loss.lme1interML)
```

```
##              numDF denDF   F-value p-value
## (Intercept)     1   149 2104.0107  <.0001
## trt             2    43   23.3884  <.0001
## gender          1    43   20.0231  0.0001
## time            1   149 1065.1072  <.0001
## weight          1    43   17.7681  0.0001
## trt:gender      2    43    0.5808  0.5638
```

So there is no significant interaction between gender and treatment program, since the p-value on that interaction term in the ANOVA output is 0.5638. Hence the best weight loss program, for both males and females, is program 3 – although females lose significantly more weight than males (an extra 2.2262 kg on average), given the other variables (program, time, and initial weight) remain at a fixed level.