

Stat 207 HW5

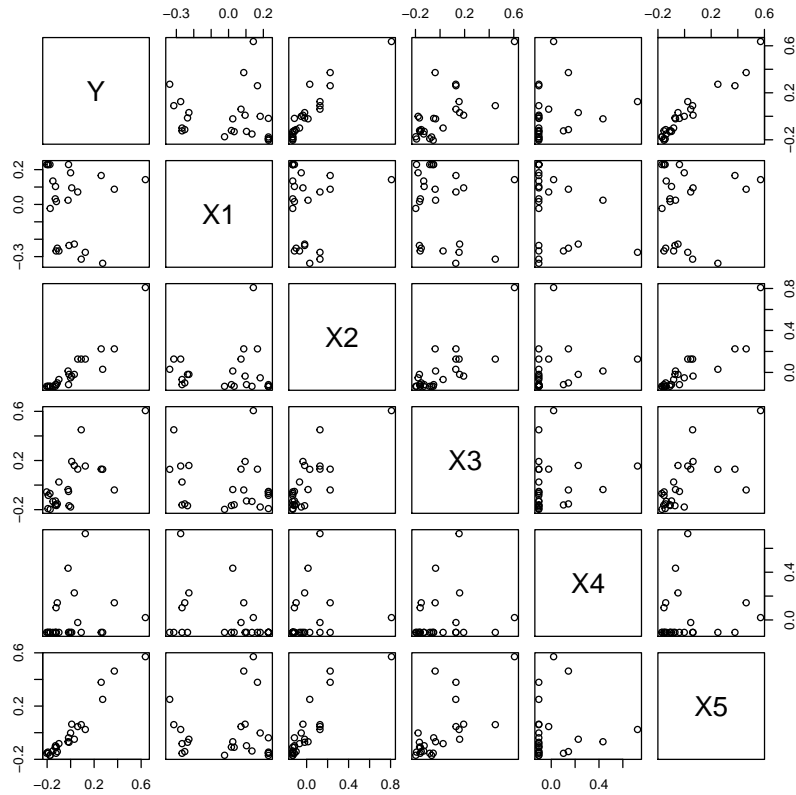
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1 1

```
(a) require(gdata)
## Loading required package: gdata
## gdata: read.xls support for 'XLS' (Excel 97-2004) files ENABLED.
##
## gdata: read.xls support for 'XLSX' (Excel 2007+) files ENABLED.
##
## Attaching package: 'gdata'
##
## The following object is masked from 'package:stats':
##
##     nobs
##
## The following object is masked from 'package:utils':
##
##     object.size

dat1 = read.xls("apartment.xlsx", header = TRUE)
dat.stan = dat1
for(j in 1:ncol(dat1))
  dat.stan[,j] = (dat1[,j] - mean(dat1[,j]))/(sd(dat1[,j])*(sqrt(25-1)))
dat = dat.stan
plot(dat)
```



```
cor(dat)
```

```
##           Y           X1           X2           X3           X4           X5
## Y      1.0000000 -0.11453460  0.92345442  0.7413715  0.22497528 0.96813120
## X1 -0.1145346  1.00000000 -0.01415504 -0.1885895 -0.36265249 0.02700832
## X2  0.9234544 -0.01415504  1.00000000  0.8000696  0.22412565 0.87786360
## X3  0.7413715 -0.18858951  0.80006959  1.0000000  0.16609137 0.67269398
## X4  0.2249753 -0.36265249  0.22412565  0.1660914  1.00000000 0.08929658
## X5  0.9681312  0.02700832  0.87786360  0.6726940  0.08929658 1.00000000
```

We find that Y is highly correlated with X2, X3 and X5. and X2, X3 and X5 are highly correlated with each other, which means the multicollinearity is present.

(b)

```
require(Matrix)
```



```
## Loading required package: Matrix
```

```
## Warning: package 'Matrix' was built under R version 3.1.2

X = dat[, 2:6]
X = as.matrix(X)
P = t(X) %*% X
eigen(P)

## $values
## [1] 2.63414515 1.33018568 0.65704211 0.29575194 0.08287513
##
## $vectors
##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] -0.1012189  0.720376426  0.63332131 -0.25097092  0.08203814
## [2,]  0.5913231  0.122265531  0.09155295  0.08619205 -0.78713218
## [3,]  0.5475583  0.004633543 -0.24983677 -0.73925733  0.30205730
## [4,]  0.1893656 -0.646792392  0.72651658 -0.06042441  0.11967806
## [5,]  0.5517357  0.218511047  0.01665599  0.61598053  0.51781389
```

Some eigenvalues are close to zero, so that it does exist multicollinearity.

```
(c) fit = lm(Y ~ 0 + ., data = dat)
summary(fit)

##
## Call:
## lm(formula = Y ~ 0 + ., data = dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.052406 -0.016609 -0.004069  0.014375  0.070701
##
## Coefficients:
##      Estimate Std. Error t value Pr(>|t|)
## X1 -0.10461    0.03556  -2.942  0.00807 **
## X2  0.24656    0.08636   2.855  0.00979 **
## X3  0.01854    0.05545   0.334  0.74159
## X4  0.06294    0.03581   1.758  0.09410 .
## X5  0.73642    0.06744  10.920 7.06e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03121 on 20 degrees of freedom
## Multiple R-squared:  0.9805, Adjusted R-squared:  0.9757
## F-statistic: 201.4 on 5 and 20 DF, p-value: < 2.2e-16
```

```
anova(fit)

## Analysis of Variance Table
##
## Response: Y
##          Df Sum Sq Mean Sq  F value    Pr(>F)
## X1         1  0.01312  0.01312   13.4704  0.001519 **
## X2         1  0.84995  0.84995  872.7651 < 2.2e-16 ***
## X3         1  0.00073  0.00073    0.7458  0.398038
## X4         1  0.00061  0.00061    0.6247  0.438588
## X5         1  0.11612  0.11612  119.2409 7.064e-10 ***
## Residuals 20  0.01948  0.00097
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In this multiple regression model, X1, X2, and X5 are more important to predict sale price.

(d)

```
require(faraway)

## Loading required package: faraway

vif(fit)

## Warning in vif.lm(fit): No intercept term detected. Results
## may surprise.

##          X1          X2          X3          X4          X5
## 1.298654 7.657888 3.157590 1.316618 4.670186
```

All VIF >1 shows that each X variable has the intercorrelation with the rest of the X variables.

(e)

```
library('MASS')

## Warning: package 'MASS' was built under R version 3.1.2

select(lm.ridge(Y ~ 0 + ., data = dat,
               lambda = seq(0, 1, .001)))

## modified HKB estimator is 0.1181183
## modified L-W estimator is 0.07448998
## smallest value of GCV at 0.321

k = .321
require('ridge')
```

```
## Loading required package: ridge
## Warning: package 'ridge' was built under R version 3.1.2

model = linearRidge(Y ~ 0 + ., data = dat,
                    lambda = k, scaling = 'none'); model

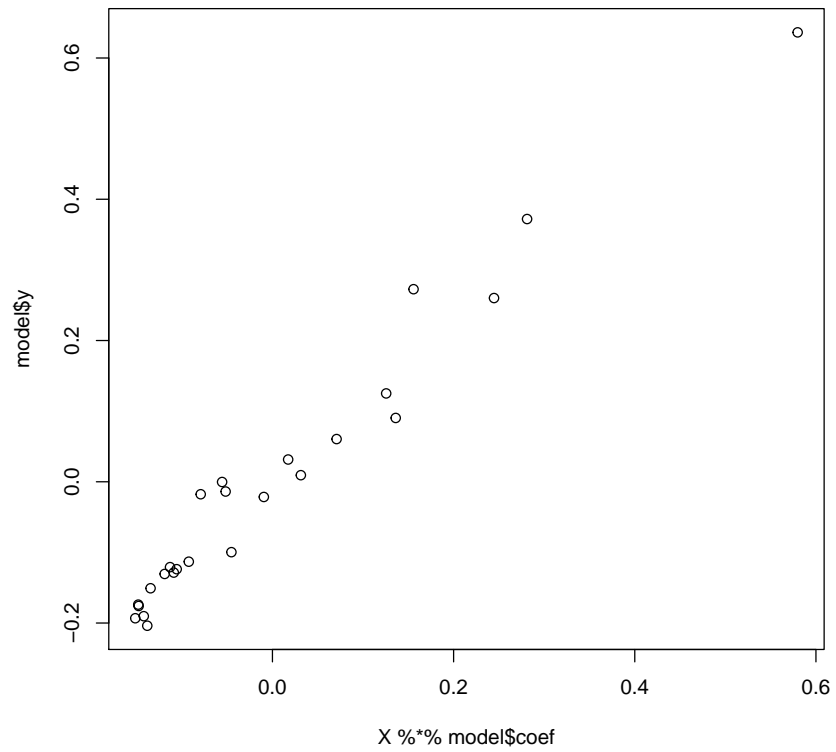
##
## Call:
## linearRidge(formula = Y ~ 0 + ., data = dat, lambda = k, scaling = "none")
##
##           X1           X2           X3           X4           X5
## -0.06004494  0.30522205  0.12451487  0.05500698  0.46414629

summary(model)

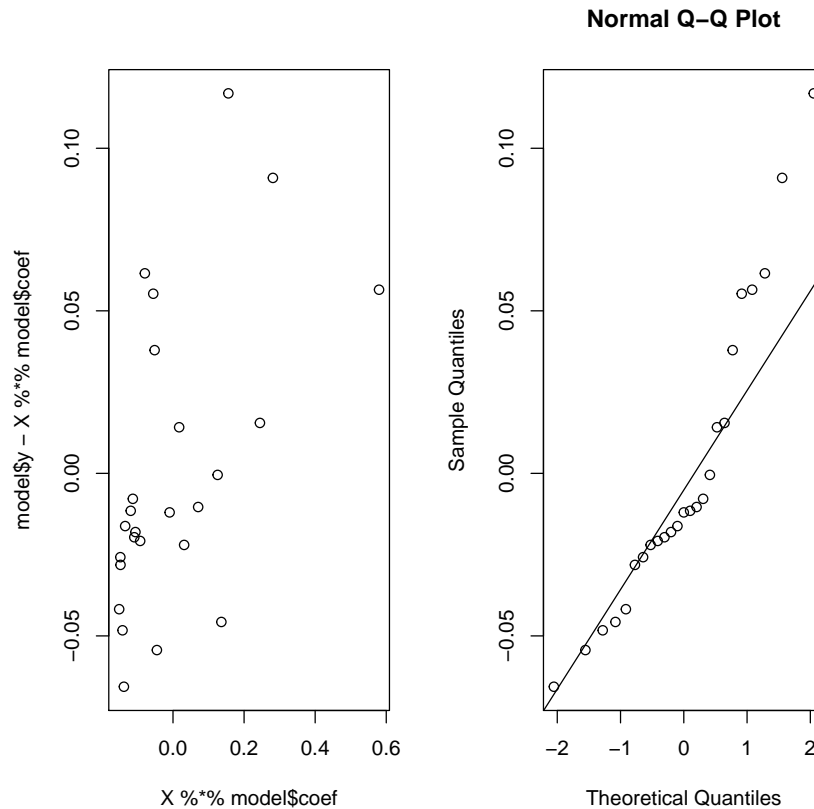
##
## Call:
## linearRidge(formula = Y ~ 0 + ., data = dat, lambda = k, scaling = "none")
##
##
## Coefficients:
##      Estimate Std. Error t value Pr(>|t|)
## X1 -0.06004    0.03763   1.596  0.11060
## X2  0.30522    0.03263   9.355 < 2e-16 ***
## X3  0.12451    0.03829   3.252  0.00114 **
## X4  0.05501    0.03774   1.457  0.14501
## X5  0.46415    0.03640  12.751 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Ridge parameter: 0.321
##
## Degrees of freedom: model 3.053 , variance 2.167 , residual 3.94
```

Parameter estimates and their standard errors are shown in the `summary(model)`.

(f) `plot(X%*%model$coef, model$y)`



```
par( mfrow = c(1, 2))  
plot(X %%% model$coef, model$y - X %%% model$coef)  
qqnorm(model$y - X %%% model$coef)  
qqline(model$y - X %%% model$coef)
```

The residuals versus fitted values plots shows no sign for unequal variance. And the QQ-plot indicates approximately normal distribution with heavy tail, so that normality assumption seems to be reasonable, we can use model here.

```
(g) ans = solve(P + diag(k,5,5)) %*% P %*% solve(P + diag(k,5,5))
      diag(ans)

##          X1          X2          X3          X4          X5
## 0.5841713 0.4390908 0.6045876 0.5875868 0.5465513
```

VIF of the estimated ridge regression are shown in the above. All VIF are smaller than 1, which means they have little intercorrelation between X variables.

2 2

(a)

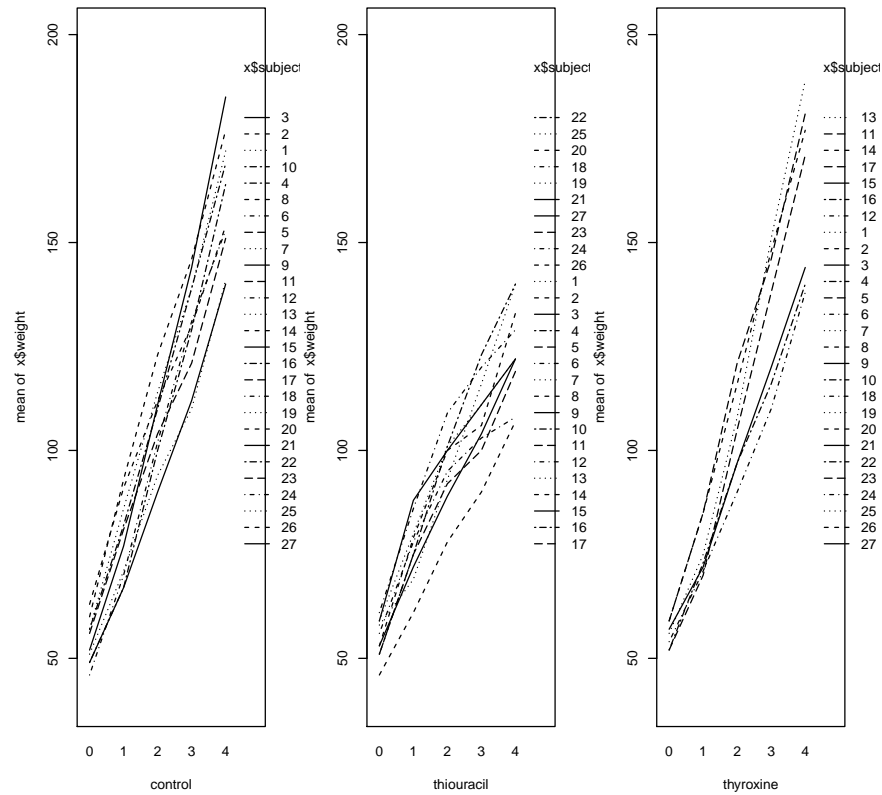
```
require(gdata)
dat = read.xls("ratdrink.xlsx")
dat = dat[, 1:4]
dat$wk = dat$weeks - mean(dat$weeks); dat$wk

##      [1] -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0
##     [24]  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2
##     [47] -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1
##     [70]  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1
##     [93]  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2
##    [116] -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2 -2 -1  0  1  2

dat$wk2 = dat$wk^2; dat$wk2

##      [1]  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4
##     [36]  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4
##     [71]  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4
##    [106]  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4  4  1  0  1  4

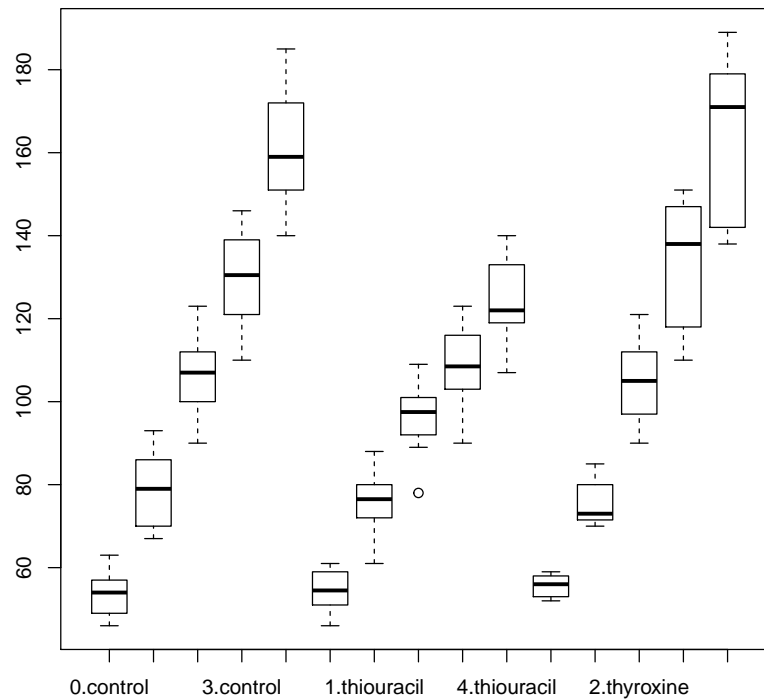
dat$weeks = as.factor(dat$weeks)
dat$subject = as.factor(dat$subject)
datt = split(dat, dat$treat)
par(mfrow = c(1, 3))
sapply(datt, function(x){interaction.plot(x$weeks, x$subject, x$weight,
                                           ylim = c(40, 200), xlab = unique(x$treat))})})
```



```
## $control
## NULL
##
## $thiouracil
## NULL
##
## $thyroxine
## NULL
```

(b)

```
par(mfrow = c(1, 1))
boxplot(weight ~ factor(weeks)*treat, data = dat)
```

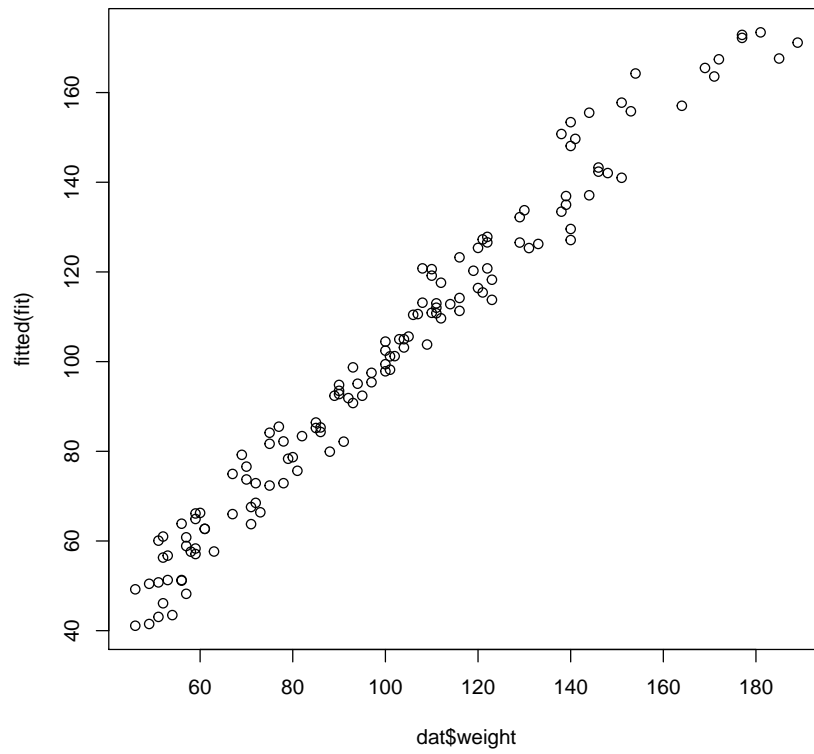


The mean weight becomes larger over time. And the variability of weight change over time gets bigger, treatment thyroxine has the biggest variability over time.

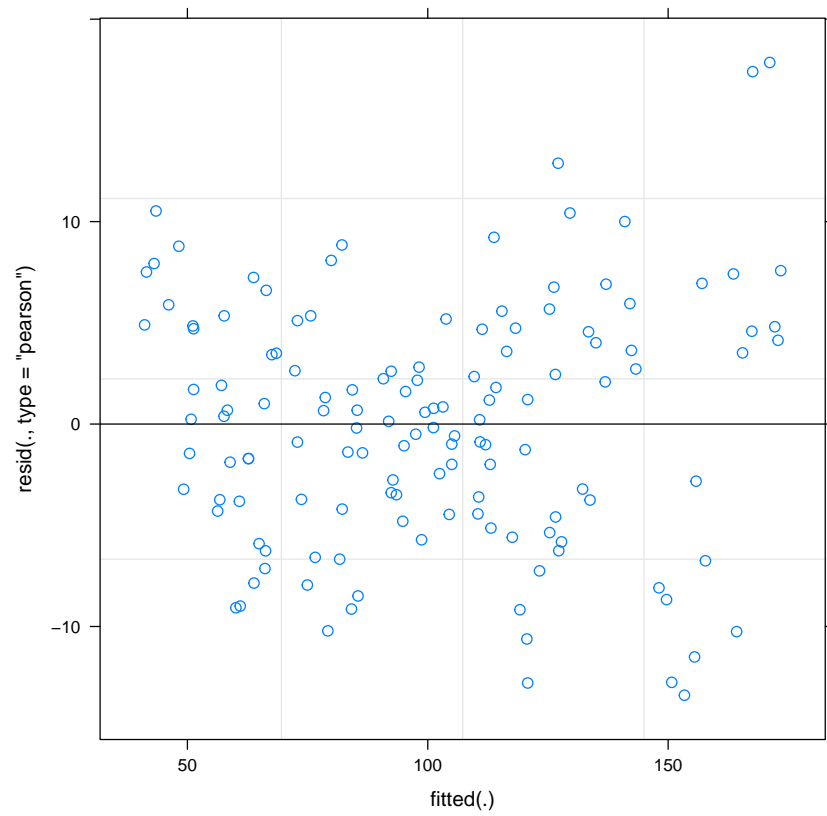
(c)

```
require(lme4)
## Loading required package: lme4
## Warning: package 'lme4' was built under R version 3.1.2
## Loading required package: Rcpp
## Warning: package 'Rcpp' was built under R version 3.1.2

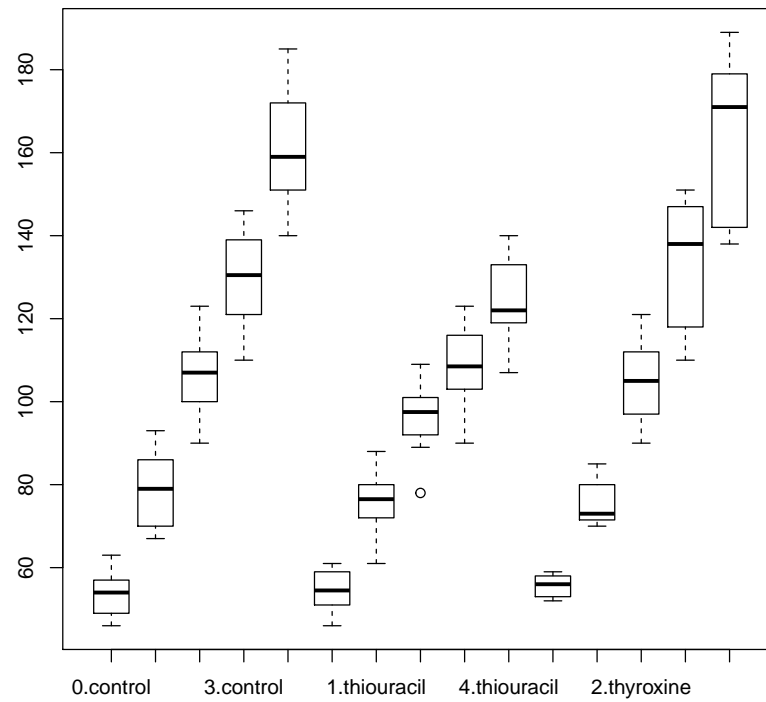
fit = lmer(weight ~ factor(weeks) + treat + factor(weeks):treat + (1|subject), data =
par(mfrow = c(1, 1))
plot(dat$weight, fitted(fit))
```



```
plot(fit, which = 1)
```



```
par(mfrow = c(1, 1))  
boxplot(weight ~ weeks*treat, data = dat)
```



The residuals versus fitted values plots shows no sign for unequal variance. And the plot seems to be normal distributed.

(d) `summary(fit)`

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## weight ~ factor(weeks) + treat + factor(weeks):treat + (1 | subject)
## Data: dat
##
## REML criterion at convergence: 892.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.90369 -0.60408  0.03345  0.64957  2.53828
##
## Random effects:
```

```

## Groups      Name      Variance Std.Dev.
## subject (Intercept) 71.55      8.459
## Residual          49.51      7.036
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      54.0000      3.4794  15.52
## factor(weeks)1      24.5000      3.1468   7.79
## factor(weeks)2      52.0000      3.1468  16.52
## factor(weeks)3      76.1000      3.1468  24.18
## factor(weeks)4     106.6000      3.1468  33.88
## treatthiouracil      0.7000      4.9206   0.14
## treatthyroxine      1.5714      5.4222   0.29
## factor(weeks)1:treatthiouracil -2.9000      4.4503  -0.65
## factor(weeks)2:treatthiouracil -10.9000      4.4503  -2.45
## factor(weeks)3:treatthiouracil -22.4000      4.4503  -5.03
## factor(weeks)4:treatthiouracil -37.1000      4.4503  -8.34
## factor(weeks)1:treatthyroxine  -4.2143      4.9039  -0.86
## factor(weeks)2:treatthyroxine  -2.7143      4.9039  -0.55
## factor(weeks)3:treatthyroxine   1.0429      4.9039   0.21
## factor(weeks)4:treatthyroxine   0.6857      4.9039   0.14
##
## Correlation of Fixed Effects:
##              (Intr) fct()1 fct()2 fct()3 fct()4 trtthr trtthy
## factr(wks)1      -0.452
## factr(wks)2      -0.452  0.500
## factr(wks)3      -0.452  0.500  0.500
## factr(wks)4      -0.452  0.500  0.500  0.500
## treatthirc1      -0.707  0.320  0.320  0.320  0.320
## treatthyrxn      -0.642  0.290  0.290  0.290  0.290  0.454
## fctr(wks)1:trtthr  0.320 -0.707 -0.354 -0.354 -0.354 -0.452 -0.205
## fctr(wks)2:trtthr  0.320 -0.354 -0.707 -0.354 -0.354 -0.452 -0.205
## fctr(wks)3:trtthr  0.320 -0.354 -0.354 -0.707 -0.354 -0.452 -0.205
## fctr(wks)4:trtthr  0.320 -0.354 -0.354 -0.354 -0.707 -0.452 -0.205
## fctr(wks)1:trtthy  0.290 -0.642 -0.321 -0.321 -0.321 -0.205 -0.452
## fctr(wks)2:trtthy  0.290 -0.321 -0.642 -0.321 -0.321 -0.205 -0.452
## fctr(wks)3:trtthy  0.290 -0.321 -0.321 -0.642 -0.321 -0.205 -0.452
## fctr(wks)4:trtthy  0.290 -0.321 -0.321 -0.321 -0.642 -0.205 -0.452
## fctr(wks)1:trtthr fctr(wks)2:trtthr fctr(wks)3:trtthr
## factr(wks)1
## factr(wks)2
## factr(wks)3
## factr(wks)4
## treatthirc1

```



```

## treatthyrxn
## fctr(wks)1:trtthr
## fctr(wks)2:trtthr 0.500
## fctr(wks)3:trtthr 0.500 0.500
## fctr(wks)4:trtthr 0.500 0.500 0.500
## fctr(wks)1:trtthy 0.454 0.227 0.227
## fctr(wks)2:trtthy 0.227 0.454 0.227
## fctr(wks)3:trtthy 0.227 0.227 0.454
## fctr(wks)4:trtthy 0.227 0.227 0.227
## fctr(wks)4:trtthr fctr(wks)1:trtthy fctr(wks)2:trtthy
## factr(wks)1
## factr(wks)2
## factr(wks)3
## factr(wks)4
## treatthirc1
## treatthyrxn
## fctr(wks)1:trtthr
## fctr(wks)2:trtthr
## fctr(wks)3:trtthr
## fctr(wks)4:trtthr
## fctr(wks)1:trtthy 0.227
## fctr(wks)2:trtthy 0.227 0.500
## fctr(wks)3:trtthy 0.227 0.500 0.500
## fctr(wks)4:trtthy 0.454 0.500 0.500
## fctr(wks)3:trtthy
## factr(wks)1
## factr(wks)2
## factr(wks)3
## factr(wks)4
## treatthirc1
## treatthyrxn
## fctr(wks)1:trtthr
## fctr(wks)2:trtthr
## fctr(wks)3:trtthr
## fctr(wks)4:trtthr
## fctr(wks)1:trtthy
## fctr(wks)2:trtthy
## fctr(wks)3:trtthy
## fctr(wks)4:trtthy 0.500

anova(fit)

## Analysis of Variance Table
## Df Sum Sq Mean Sq F value
## factor(weeks) 4 145188 36297 733.0981

```

```
## treat          2    770    385    7.7774
## factor(weeks):treat  8   6403    800   16.1641

fit1 = lm(weight ~ factor(weeks) + treat + factor(weeks):treat, data = dat )
fit2 = lmer(weight ~ treat + factor(weeks):treat + (1|subject), data = dat )
fit3 = lmer(weight ~ factor(weeks) + factor(weeks):treat + (1|subject), data = dat )
fit4 = lmer(weight ~ factor(weeks) + treat + (1|subject), data = dat )
AIC(fit)

## [1] 926.1398

AIC(fit1)

## [1] 1046.712

AIC(fit2)

## [1] 926.1398

AIC(fit3)

## [1] 926.1398

AIC(fit4)

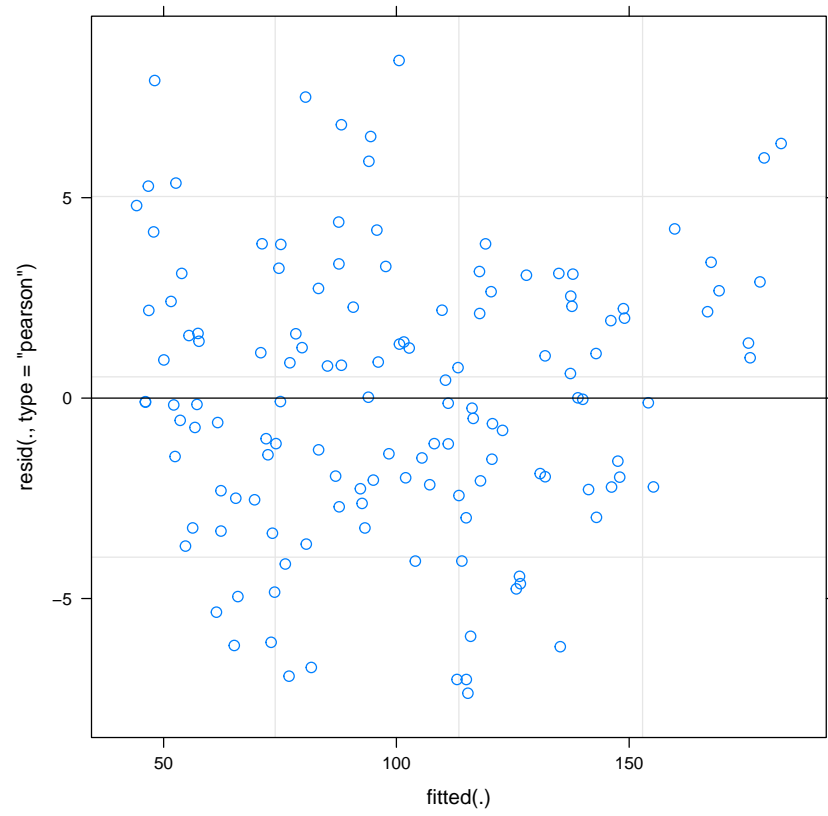
## [1] 1034.661
```

The AIC of the full model is 926.1398, which means it's the smallest AIC of all. So there's no need to drop the terms.

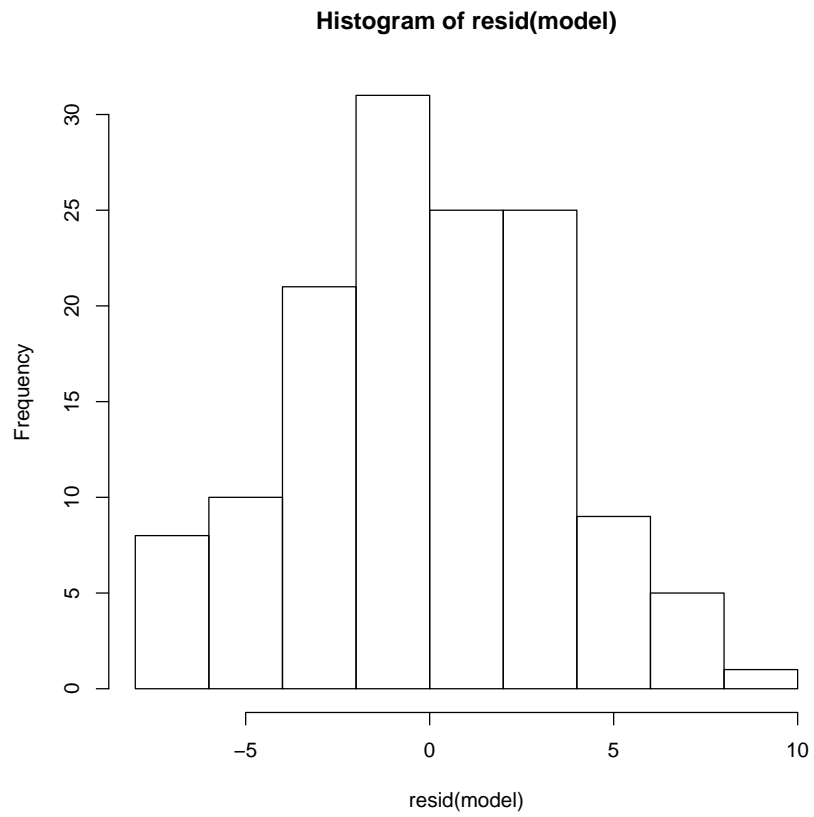
3 3

- (a)

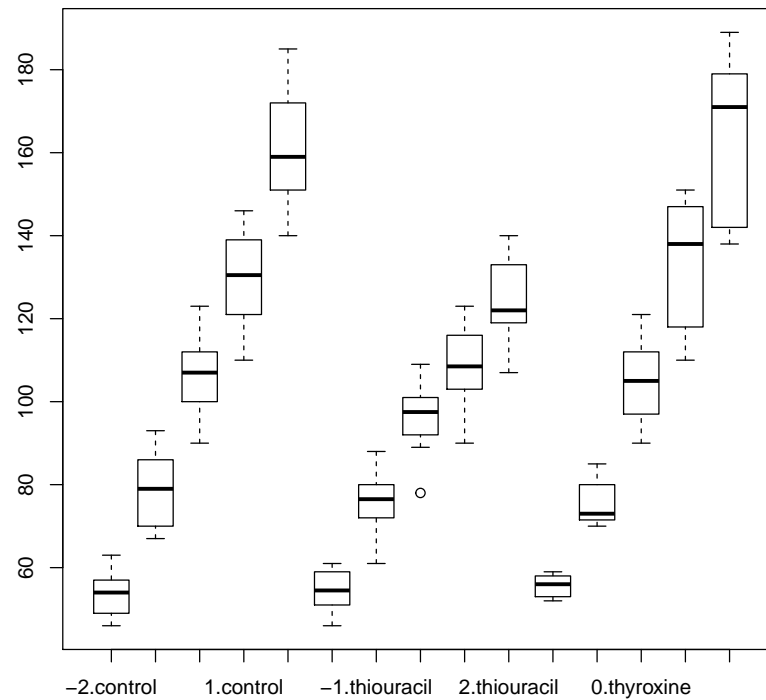
```
model = lmer(weight ~ wk + treat + (1|subject) + (0 + wk|subject), data = dat)
par( mfrow = c(1, 1))
plot(model, which = 1)
```



```
hist(resid(model))
```



```
boxplot(weight ~ wk*treat, data = dat)
```



The residuals versus fitted values plots shows no sign for unequal variance. The histogram shows the residual seems to be normal distributed. The mean weight becomes larger over time. And the variability of weight change over time gets bigger, treatment thyroxine has the biggest variability over time.

```
(b) model2 = lmer(weight ~ wk + wk2 + treat + (1|subject) + (0 + wk|subject) + (0 + wk2|subject))
      summary(model2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: weight ~ wk + wk2 + treat + (1 | subject) + (0 + wk | subject) +
##          (0 + wk2 | subject)
## Data: dat
##
## REML criterion at convergence: 908.3
##
## Scaled residuals:
```

```
##      Min      1Q  Median      3Q      Max
## -2.4904 -0.4034  0.0611  0.3895  1.7395
##
## Random effects:
## Groups      Name             Variance Std.Dev.
## subject    (Intercept)  87.138    9.335
## subject.1 wk           36.444    6.037
## subject.2 wk2           2.042    1.429
## Residual                    9.402    3.066
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   104.87487    3.02136   34.71
## wk             23.18148    1.17669   19.70
## wk2            0.08201    0.31704    0.26
## treatthiouracil -11.04663    4.26709   -2.59
## treatthyroxine  -0.54055    4.70210   -0.11
##
## Correlation of Fixed Effects:
##              (Intr) wk      wk2      trtthr
## wk              0.000
## wk2             -0.052  0.000
## treatthircl -0.706  0.000  0.000
## treatthyrxn -0.641  0.000  0.000  0.454
```

No, they seems to be different, the second model has term wk2.

```
(c)  AIC(model)

## [1] 939.0791

AIC(model2)

## [1] 926.3378
```

The AIC of the first model is 939.0791, which is bigger than 926.3378(second model). So that, we should choose the first model with wk2.

```
summary(model2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: weight ~ wk + wk2 + treat + (1 | subject) + (0 + wk | subject) +
##          (0 + wk2 | subject)
```

```
## Data: dat
##
## REML criterion at convergence: 908.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4904 -0.4034  0.0611  0.3895  1.7395
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## subject     (Intercept)    87.138     9.335
## subject.1 wk              36.444     6.037
## subject.2 wk2              2.042     1.429
## Residual                    9.402     3.066
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   104.87487    3.02136   34.71
## wk             23.18148    1.17669   19.70
## wk2            0.08201    0.31704    0.26
## treatthiouracil -11.04663    4.26709   -2.59
## treatthyroxine  -0.54055    4.70210   -0.11
##
## Correlation of Fixed Effects:
##              (Intr) wk      wk2      trtthr
## wk              0.000
## wk2             -0.052  0.000
## treatthircl    -0.706  0.000  0.000
## treatthyrxn    -0.641  0.000  0.000  0.454
```

(d) `model3 = lmer(weight ~ wk + wk2 + treat + (1|subject) + wk*treat + wk2*treat, data = summary(model3))`

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: weight ~ wk + wk2 + treat + (1 | subject) + wk * treat + wk2 *
##      treat
## Data: dat
##
## REML criterion at convergence: 936.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9910 -0.5755  0.0700  0.6061  2.5878
```

```

##
## Random effects:
##   Groups   Name                Variance Std.Dev.
## subject (Intercept) 71.83      8.475
## Residual                48.12      6.937
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)    104.6114     3.0855   33.90
## wk              26.4800     0.6937   38.17
## wk2             0.6143     0.5863    1.05
## treatthiouracil -10.0886     4.3635   -2.31
## treatthyroxine  -0.8931     4.8084   -0.19
## wk:treatthiouracil -9.3700     0.9811   -9.55
## wk:treatthyroxine  0.6629     1.0811    0.61
## wk2:treatthiouracil -1.9357     0.8291   -2.33
## wk2:treatthyroxine  0.7122     0.9137    0.78
##
## Correlation of Fixed Effects:
##           (Intr) wk      wk2      trtthr trtthy wk:trtthr wk:trtthy
## wk              0.000
## wk2            -0.380  0.000
## treatthircl   -0.707  0.000  0.269
## treatthyrxn   -0.642  0.000  0.244  0.454
## wk:trtthrc   0.000 -0.707  0.000  0.000  0.000
## wk:trtthyrc  0.000 -0.642  0.000  0.000  0.000  0.454
## wk2:trtthrc  0.269  0.000 -0.707 -0.380 -0.172  0.000  0.000
## wk2:trtthyrc 0.244  0.000 -0.642 -0.172 -0.380  0.000  0.000
##           wk2:trtthr
## wk
## wk2
## treatthircl
## treatthyrxn
## wk:trtthrc
## wk:trtthyrc
## wk2:trtthrc
## wk2:trtthyrc 0.454

```

The model for control is $Y = 104.6114 + 26.48 \cdot \text{wk} + 0.6143 \cdot \text{wk}^2$
 The model for thiouracil is $Y = 104.6114 + 26.48 \cdot \text{wk} + 0.6143 \cdot \text{wk}^2 - 10.0886 - 9.37 \cdot \text{wk} - 1.9357 \cdot \text{wk}^2 = 94.5228 + 17.11 \cdot \text{wk} - 1.3214 \cdot \text{wk}^2$
 The model for thyroxine is $Y = 104.6114 + 26.48 \cdot \text{wk} + 0.6143 \cdot \text{wk}^2 - 0.8931 + 0.6629 \cdot \text{wk} + 0.7122 \cdot \text{wk}^2 = 103.7183 + 27.1429 \cdot \text{wk} + 1.3265 \cdot \text{wk}^2$

So that the slope are dependent on treatment.

```
(e) summary(model3)

## Linear mixed model fit by REML ['lmerMod']
## Formula: weight ~ wk + wk2 + treat + (1 | subject) + wk * treat + wk2 *
##      treat
##      Data: dat
##
## REML criterion at convergence: 936.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9910 -0.5755  0.0700  0.6061  2.5878
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##  subject (Intercept) 71.83     8.475
##  Residual              48.12     6.937
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    104.6114     3.0855   33.90
## wk              26.4800     0.6937   38.17
## wk2              0.6143     0.5863    1.05
## treatthiouracil -10.0886     4.3635   -2.31
## treatthyroxine  -0.8931     4.8084   -0.19
## wk:treatthiouracil -9.3700     0.9811  -9.55
## wk:treatthyroxine  0.6629     1.0811    0.61
## wk2:treatthiouracil -1.9357     0.8291  -2.33
## wk2:treatthyroxine  0.7122     0.9137    0.78
##
## Correlation of Fixed Effects:
##              (Intr) wk      wk2      trtthr trtthy wk:trtthr wk:trtthy
## wk              0.000
## wk2            -0.380  0.000
## treatthircl -0.707  0.000  0.269
## treatthyrxn -0.642  0.000  0.244  0.454
## wk:trtthrc1  0.000 -0.707  0.000  0.000  0.000
## wk:trtthyrc  0.000 -0.642  0.000  0.000  0.000  0.454
## wk2:trtthrc  0.269  0.000 -0.707 -0.380 -0.172  0.000  0.000
## wk2:trtthyrc 0.244  0.000 -0.642 -0.172 -0.380  0.000  0.000
##              wk2:trtthr
## wk
```

```
## wk2
## treatthirc1
## treatthyrxn
## wk:trtthrc1
## wk:trtthyrx
## wk2:trtthrc
## wk2:trtthyr 0.454

drop1(model3)

## Single term deletions
##
## Model:
## weight ~ wk + wk2 + treat + (1 | subject) + wk * treat + wk2 *
##      treat
##           Df      AIC
## <none>      976.38
## wk:treat    2 1057.36
## wk2:treat   2  982.20
```

From the drop1 function, we know that when we don't drop anything, the AIC is the smallest, which is 976.38. So the model3 is the final model.

(f)

(g) The final model:

$$Y_{ij} = \mu + \rho_i + \beta_1 wk_j + \gamma_{i2} wk_j + treat_i + \beta_2 wk_j * treat_j + \gamma_{i3} wk_j * treat_j + \beta_3 wk_j^2 + \gamma_{i4} wk_j^2 + \beta_4 wk_j^2 * treat_j + \gamma_{i5} wk_j^2 * treat_j + \epsilon_{ij}$$

4 4

(a)

$$\begin{aligned}
E(Y_{ij}) &= E(\mu + \rho_i + \beta_1 x_i + \gamma_1 t_j + \epsilon_{ij}) \\
&= \mu + \beta_1 x_i + \gamma_1 t_j \\
Var(Y_{ij}) &= var(\mu + \rho_i + \beta_1 x_i + \gamma_1 t_j + \epsilon_{ij}) \\
&= var(\rho_i + \epsilon_{ij}) \\
&= \sigma_\rho^2 + \sigma^2 \text{ (since } \rho_i \text{ and } \epsilon_{ij} \text{ are independent)} \\
Cov(Y_{ij}, Y_{ij'}) &= E((Y_{ij} - E(Y_{ij}))(Y_{ij'} - E(Y_{ij'}))) \\
&= E((\rho_i + \epsilon_{ij})(\rho_i + \epsilon_{ij'})) \\
&= E(\rho_i^2) \text{ (since } \rho_i \text{ and } \epsilon_{ij} \text{ and } \epsilon_{ij'} \text{ are independent)} \\
&= Var(\rho_i) + (E(\rho_i))^2 \\
&= \sigma_\rho^2 \\
Corr(Y_{ij}, Y_{ij'}) &= \frac{Cov(Y_{ij}, Y_{ij'})}{\sqrt{Var(Y_{ij}) * Var(Y_{ij'})}} \\
&= \frac{\sigma_\rho^2}{\sigma_\rho^2 + \sigma^2}
\end{aligned}$$

(b)

$$\begin{aligned}
E(Y_{ij}) &= E(\mu + \rho_i + \beta_1 x_i + \gamma_1 t_j + \gamma_{i1} t_j + \epsilon_{ij}) \\
&= \mu + \beta_1 x_i + \gamma_1 t_j \\
Var(Y_{ij}) &= var(\mu + \rho_i + \beta_1 x_i + \gamma_1 t_j + \gamma_{i1} t_j + \epsilon_{ij}) \\
&= var(\rho_i + \gamma_{i1} t_j + \epsilon_{ij}) \\
&= \sigma_\rho^2 + t_j^2 \sigma_{\gamma_1}^2 + \sigma^2 \text{ (since } \rho_i, \gamma_{i1} \text{ and } \epsilon_{ij} \text{ are independent)} \\
Cov(Y_{ij}, Y_{ij'}) &= E((Y_{ij} - E(Y_{ij}))(Y_{ij'} - E(Y_{ij'}))) \\
&= E((\rho_i + \gamma_{i1} t_j + \epsilon_{ij})(\rho_i + \gamma_{i1} t_{j'} + \epsilon_{ij'})) \\
&= E(\rho_i^2 + \gamma_{i1}^2 t_j * t_{j'}) \text{ (since } \rho_i, \gamma_{i1}, \epsilon_{ij} \text{ and } \epsilon_{ij'} \text{ are independent)} \\
&= E(\rho_i^2) + (t_j * t_{j'}) * E(\gamma_{i1}^2) \\
&= \sigma_\rho^2 + (t_j * t_{j'}) \sigma_{\gamma_1}^2 \\
Corr(Y_{ij}, Y_{ij'}) &= \frac{Cov(Y_{ij}, Y_{ij'})}{\sqrt{Var(Y_{ij}) * Var(Y_{ij'})}} \\
&= \frac{\sigma_\rho^2 + (t_j * t_{j'}) \sigma_{\gamma_1}^2}{\sqrt{(\sigma_\rho^2 + t_j^2 \sigma_{\gamma_1}^2 + \sigma^2)(\sigma_\rho^2 + t_{j'}^2 \sigma_{\gamma_1}^2 + \sigma^2)}}
\end{aligned}$$