Homework 5

Psych 5068

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April 14, 2018

Contents

data (popularity.csv) to explore methods for examining the adequacy of hierarchical linear models. Begin with the unconditional model:
# Workspace

Packages

```
library(psych)
library(lme4)
library(knitr)
library(qqplotr)
library(influence.ME)
library(HLMdiag)
library(kableExtra)
library(plyr)
library(tidyverse)
```

Data

```
data_url <- "https://raw.githubusercontent.com/emoriebeck/homeworks/master/homework5/popularity(6).csv"
dat      <- read.csv(url(data_url)) %>% tbl_df %>%
  mutate(sex12 = sex,
         sex = factor(sex, levels = 0:1, labels = c("Male", "Female")))
```

Question 1.

Test the homogeneity of Level 1 residual variances (σ^2) assumption by comparing a model that estimates a single Level 1 variance (the default, call it Pop_Fit_1) to a model that estimates a separate variance for each classroom (call it Pop_Fit_2).

Reminder: This needs to be done with the nlme package, which allows specifying separate variances for each Level 2 unit.

Level 1:

$$popular_{ij} = \beta_{0j} + r_{ij}$$

Level 2:

$$\beta_{0j} = \gamma_{00} + u_{0j}$$

```
source("https://raw.githubusercontent.com/emoriebeck/homeworks/master/table_fun.R")
library(nlme)
Pop_Fit_1 <- lme(popular ~ 1, random = ~1 | class, data = dat)
Pop_Fit_2 <- lme(popular ~ 1, random = ~1 | class, data = dat, varIdent(form = ~ 1 | class))

Pop_Fit_1 %>% summary
```

```
## Linear mixed-effects model fit by REML
##  Data: dat
##       AIC      BIC    logLik
##   6336.51 6353.311 -3165.255
##
## Random effects:
```

```
##  Formula: ~1 | class
##         (Intercept) Residual
## StdDev:   0.8379169 1.105348
##
## Fixed effects: popular ~ 1
##                Value  Std.Error   DF  t-value p-value
## (Intercept) 5.07786 0.08739443 1900 58.10279       0
##
## Standardized Within-Group Residuals:
##          Min           Q1          Med           Q3          Max
## -3.565536840 -0.697542781  0.001956985  0.675810799  3.317504350
##
## Number of Observations: 2000
## Number of Groups: 100
```

```
Pop_Fit_2 %>% summary
```

```
## Linear mixed-effects model fit by REML
##  Data: dat
##        AIC      BIC    logLik
##   6405.673 6976.914 -3100.837
##
## Random effects:
##  Formula: ~1 | class
##         (Intercept)  Residual
## StdDev:   0.8379648 0.9521529
##
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: ~1 | class
##  Parameter estimates:
##         1         2         3         4         5         6         7
## 1.0000000 1.0499363 1.2207029 0.8541240 0.9973815 1.0157321 1.1445444
##         8         9        10        11        12        13        14
## 1.2170772 1.3346129 0.8740021 0.9586056 1.0060780 0.8900662 1.3095554
##        15        16        17        18        19        20        21
## 1.2881853 1.2804569 1.2384373 1.0313981 1.1937506 1.4532934 0.9313162
##        22        23        24        25        26        27        28
## 0.8019151 1.1213246 1.3330274 1.1738459 1.1501272 1.1511586 0.8015011
##        29        30        31        32        33        34        35
## 0.9217862 1.2674700 1.8038285 1.2396037 1.4369198 1.3081363 0.6554007
##        36        37        38        39        40        41        42
## 1.0910736 1.2617634 1.0847395 0.7528253 1.4065366 0.8272193 1.2179219
##        43        44        45        46        47        48        49
## 0.8003435 1.0748452 1.2180299 1.3702985 0.9218534 1.6334850 0.9792693
##        50        51        52        53        54        55        56
## 0.8405058 1.0975264 1.1401357 0.9160148 1.0518165 1.0291801 1.2322453
##        57        58        59        60        61        62        63
## 1.5467456 1.2170930 1.1781249 1.5876935 1.0859182 1.1135284 1.2075701
##        64        65        66        67        68        69        70
## 1.3015184 1.1231329 1.2757089 0.9583205 0.9910443 1.0042414 1.1896880
##        71        72        73        74        75        76        77
## 1.3150873 1.0775448 1.0769280 1.0474515 0.9294291 0.8908559 1.3637457
##        78        79        80        81        82        83        84
## 1.0494309 1.3123283 1.1232540 1.0290107 1.3425965 0.8867385 1.0345774
##        85        86        87        88        89        90        91
## 0.9229351 1.2415380 1.5730716 1.2662948 1.3487742 0.9957063 1.1889781
##        92        93        94        95        96        97        98
## 0.9918226 1.1231373 1.0658333 1.0113186 1.2665757 1.2133722 0.9214493
##        99       100
## 1.2959411 1.8378429
## Fixed effects: popular ~ 1
##                Value  Std.Error   DF t-value p-value
## (Intercept) 5.085095 0.08733616 1900 58.2244       0
##
## Standardized Within-Group Residuals:
##          Min           Q1          Med           Q3          Max
## -4.222647455 -0.817049909 -0.009953112  0.767681205  3.845590285
##
## Number of Observations: 2000
## Number of Groups: 100
```

```r
anova(Pop_Fit_1,Pop_Fit_2)
```

```
##           Model  df      AIC      BIC    logLik   Test  L.Ratio p-value
## Pop_Fit_1     1   3 6336.510 6353.311 -3165.255
## Pop_Fit_2     2 102 6405.673 6976.914 -3100.837 1 vs 2 128.8365  0.0236
```

Thus, we do not meet the homogeneity of variance assumption. The model that estimates separate variances is slightly better than one that does not.

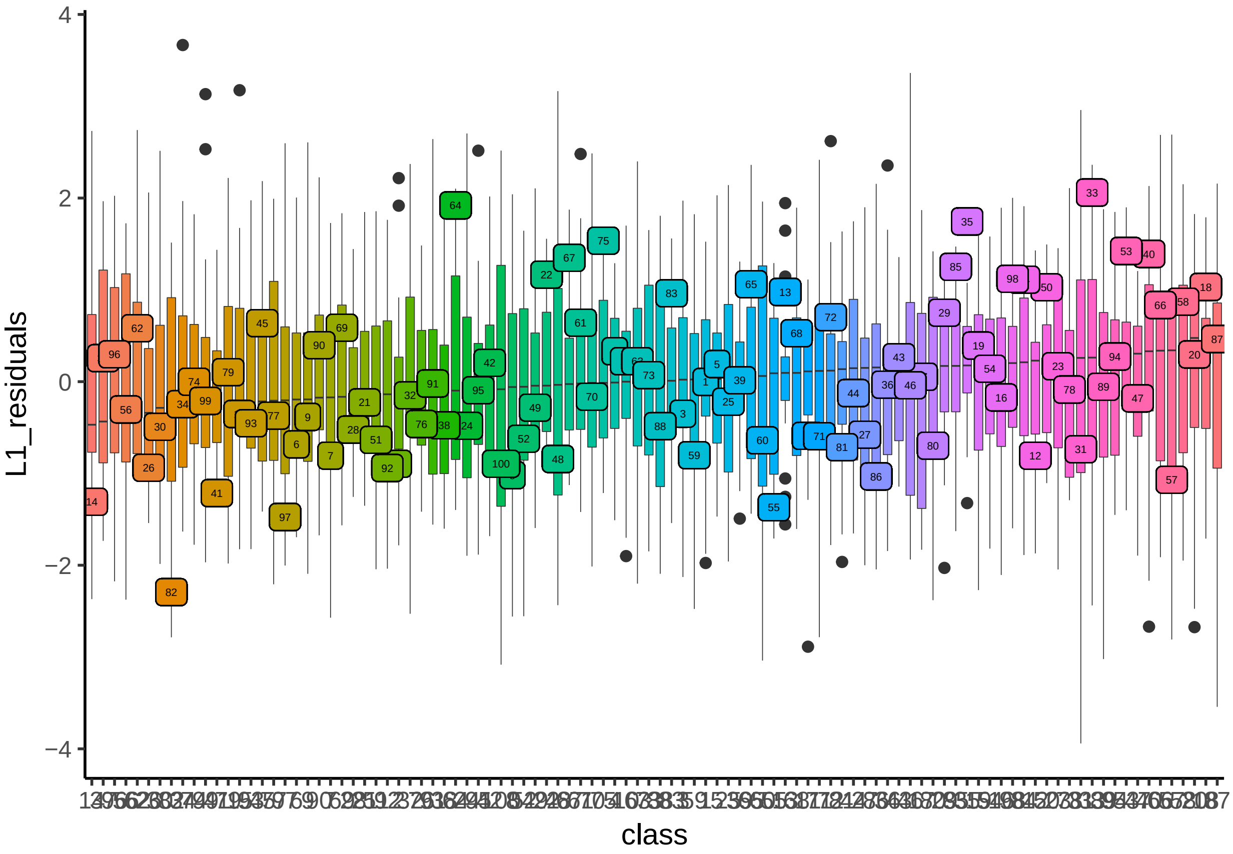
Question 2

Add the Level 1 residuals (and fitted values) from Pop_Fit_1 to the popularity data file (name them L1_residuals and L1_fitted, respectively) and produce a boxplot figure showing the residual distributions by classroom (class).

```r
dat <- broom::augment(Pop_Fit_1) %>% tbl_df %>%
  mutate(class = as.character(class)) %>%
  full_join(
    ranef(Pop_Fit_1) %>% data.frame %>% setNames("L2_residuals") %>%
      mutate(class = rownames(.)) %>% tbl_df
  ) %>% rename(L1_residuals = .resid)

orders <- dat %>%
  group_by(class) %>%
  summarize(median = median(L1_residuals, na.rm = T)) %>%
  arrange(median)

dat %>%
  mutate(class = factor(class, levels = orders$class)) %>%
  ggplot(aes(x = class, y = L1_residuals, fill = class)) +
  geom_boxplot(size = .15) +
  geom_label(data = dat, aes(y = L2_residuals,  label = class), size = 1.5) +
  theme_classic() +
  theme(legend.position = "none")
```



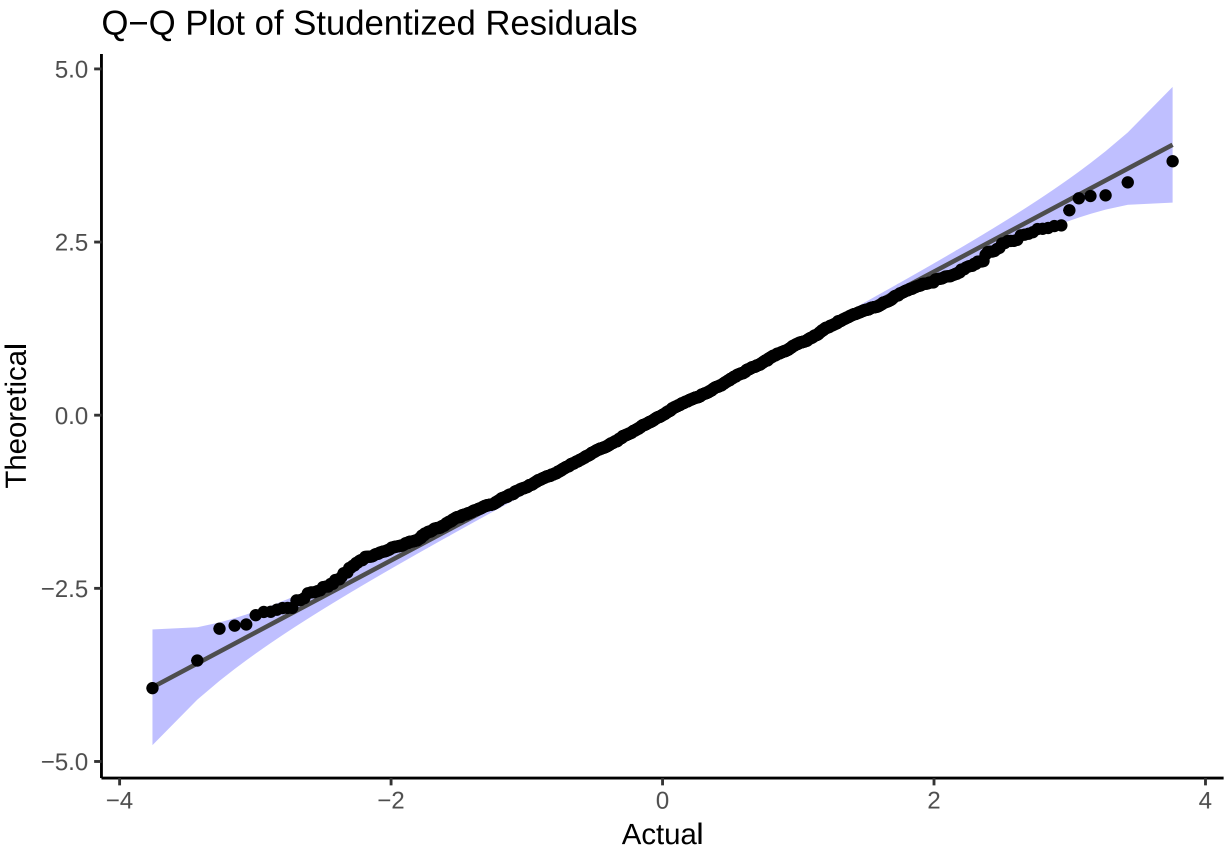
Question 3

Examine the Level 1 residuals:

Part A

Construct a Q-Q plot of the Level 1 residuals.

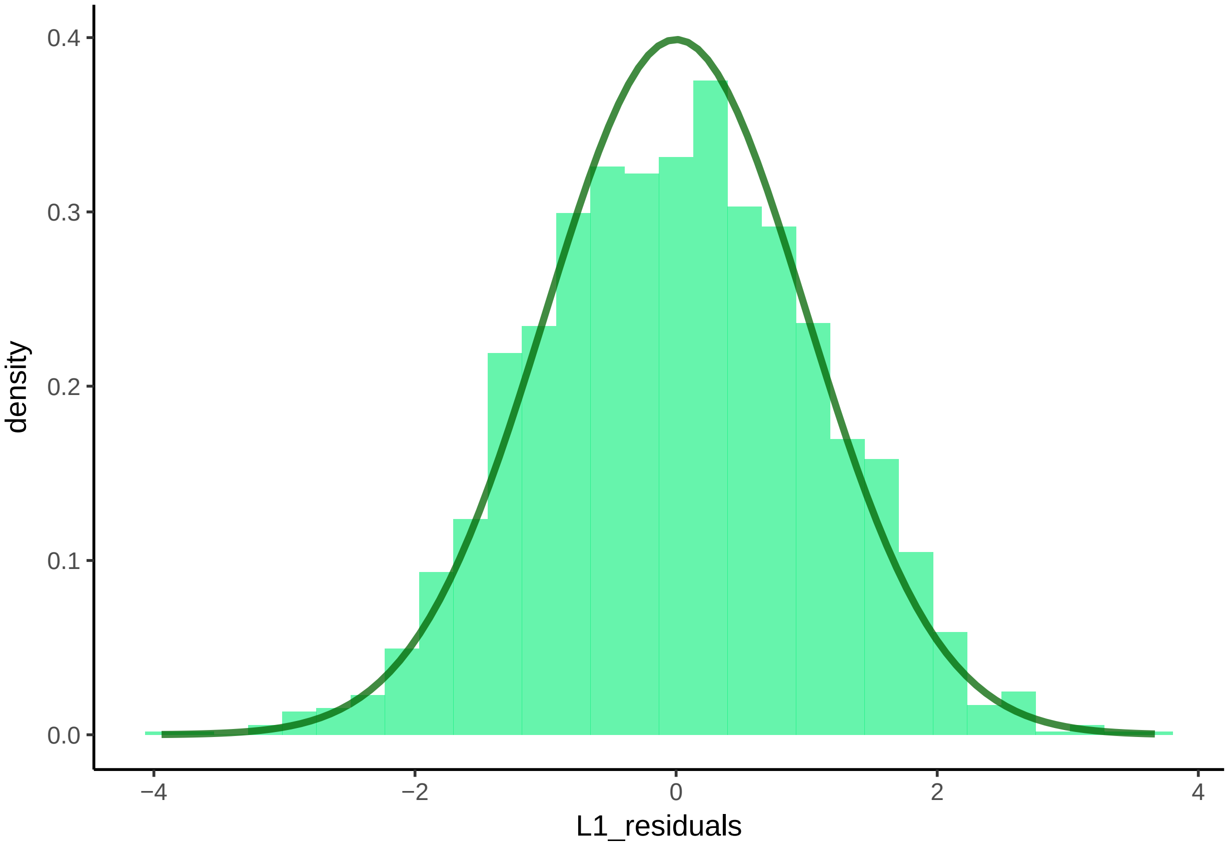
```
dat %>%
  ggplot(aes(sample=L1_residuals)) +
  stat_qq_band(fill = "blue", alpha = .25) +
  stat_qq_line() +
  stat_qq_point() +
  labs(x = "Actual", y = "Theoretical",
       title = "Q-Q Plot of Studentized Residuals") +
  theme_classic()
```



Part B

Construct a histogram of the Level 1 residuals with a normal distribution overlay.

```r
dat %>%
  ggplot(aes(x = L1_residuals)) +
  geom_histogram(aes(y = ..density..), fill = "springgreen2", alpha = .6) +
  stat_function(fun = dnorm, size = 1.25, color = "darkgreen", alpha = .75,
                args = list(mean = 0, sd =1)) +
  theme_classic()
```



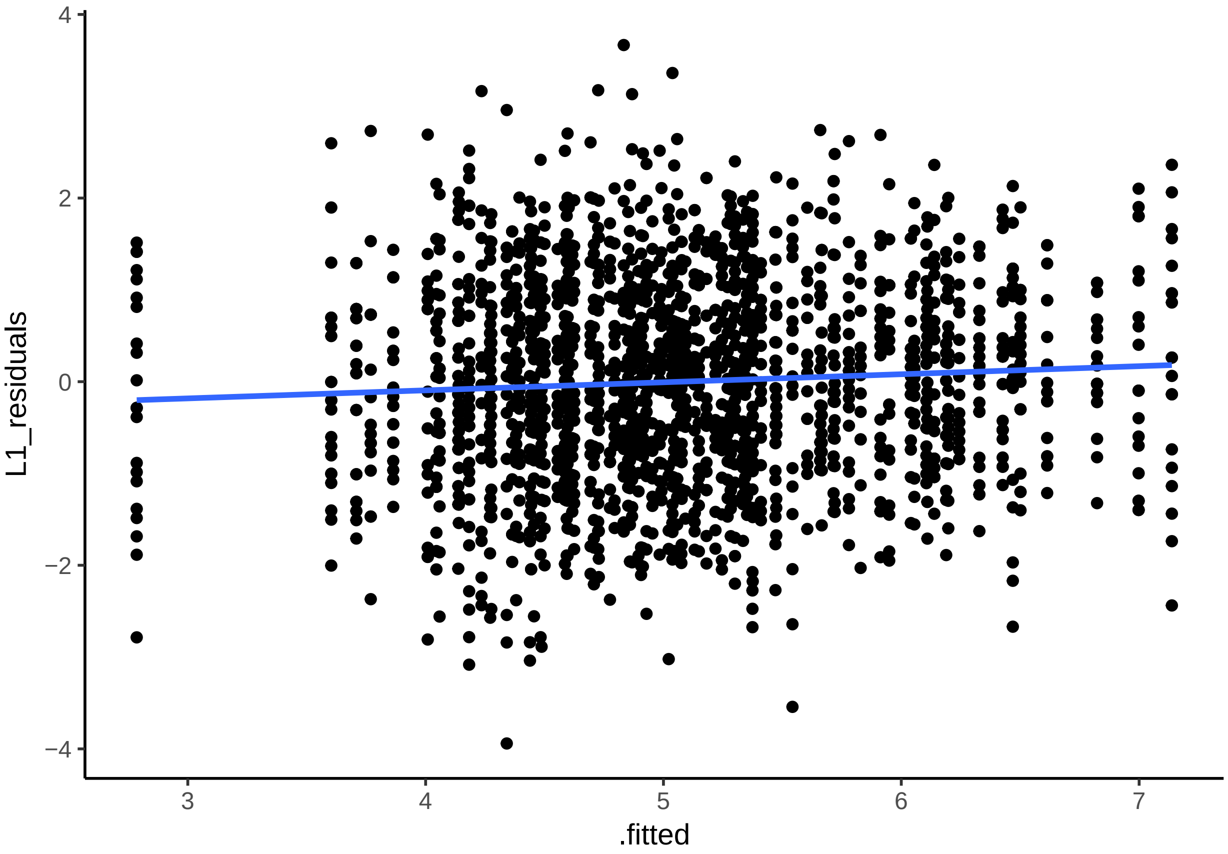
Part C

Are the Level 1 residuals normally distributed? Yes, the level 1 residuals are normally distributed.

Part D

Construct a scatterplot of the Level 1 residuals against the Level 1 fitted values. Comment on the assumption of homoscedasticity and what that means for this unconditional model.

```
dat %>%
  ggplot(aes(x = .fitted, y = L1_residuals)) +
  geom_point() +
  geom_smooth(method = "lm", se = F) +
  theme_classic()
```



The plot of Level 1 residuals v. Level 1 fitted values suggests that we meet the assumption of homoscedasticity. There is a very weak positive relationship, but not strong enough to worry.

Question 4

Now determine if Level 1 predictors should be added to the model.

Part A

Correlate the Level 1 residuals with extraversion. Is there evidence that this predictor should be included?

```
r <- dat %>% select(extrav, sex12, .fitted, L1_residuals) %>% cor

r[upper.tri(r, diag = T)] <- NA
r <- r %>% data.frame() %>% mutate(v1 = rownames(.)) %>% select(v1, everything())

options(knitr.kable.NA = '')
r %>%
  kable(., "latex", digits = 2, booktabs = T,
        col.names = c("", "extrav", "sex", "fitted", "L1 resid"))
```

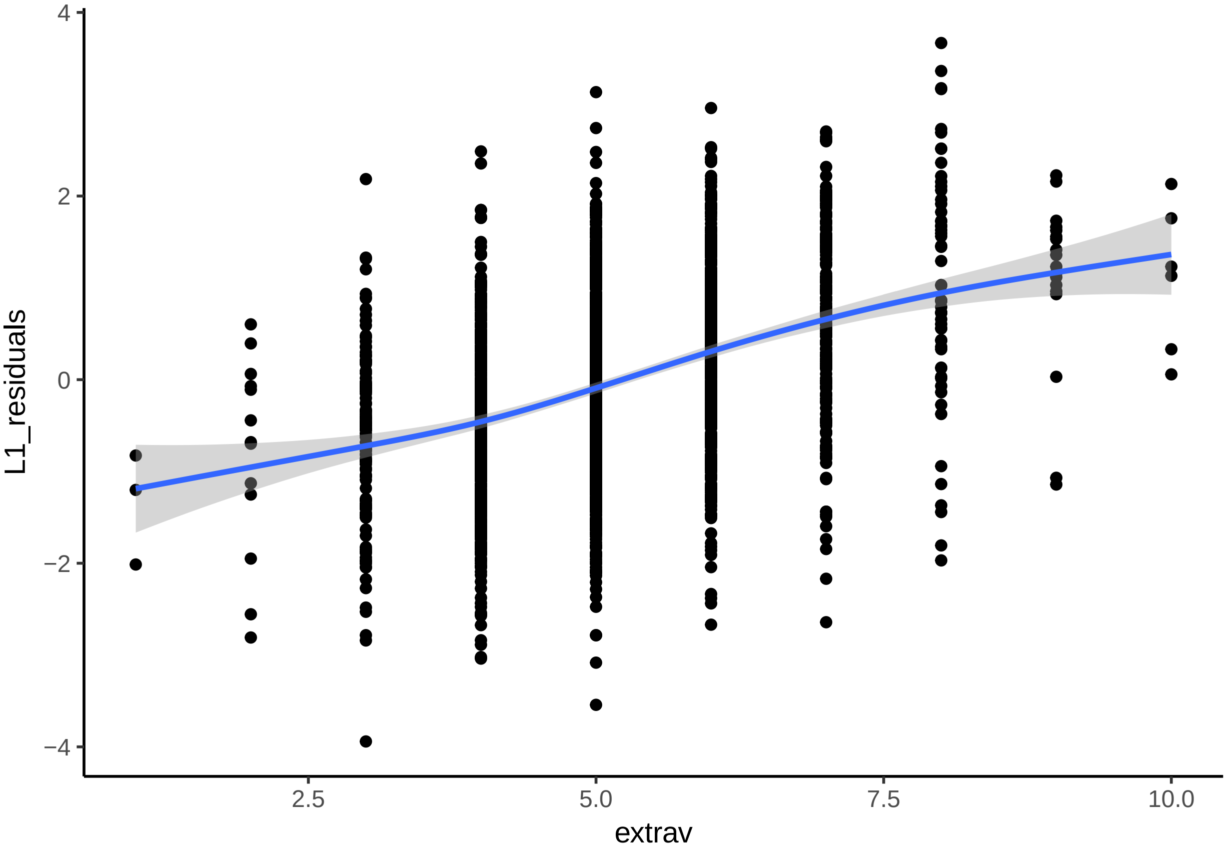
	extrav	sex	fitted	L1 resid
extrav				
sex12	0.09			
.fitted	-0.01	0.26		
L1_residuals	0.41	0.54	0.06	

Extraversion is moderately correlated with the level 1 residuals (r = 0.41), suggesting that it should be included in the model.

Part B

Create a scatterplot showing the relationship between the Level 1 residuals and extraversion. Does there appear to be any need to model nonlinearity?

```r
dat %>%
  ggplot(aes(x = extrav, y = L1_residuals)) +
  geom_point() +
  geom_smooth() +
  theme_classic()
```



No, there is possibly a very small, non-linear effect, but the degree of nonlinearity is very small.

Part C

Correlate the Level 1 residuals with student sex. Is there evidence that this predictor should be included? Sex is moderately to strongly correlated with the level 1 residuals ($r = 0.54$), suggesting that it should be included in the model.

Part D

Should both predictors be included in the model? That is, do they appear to be unique predictors?

Extraversion and sex are nearly uncorrelated (r = 0.09), suggesting that they do appear to be unique predictors.

Question 5

Examine the Level 2 residuals:

Part A

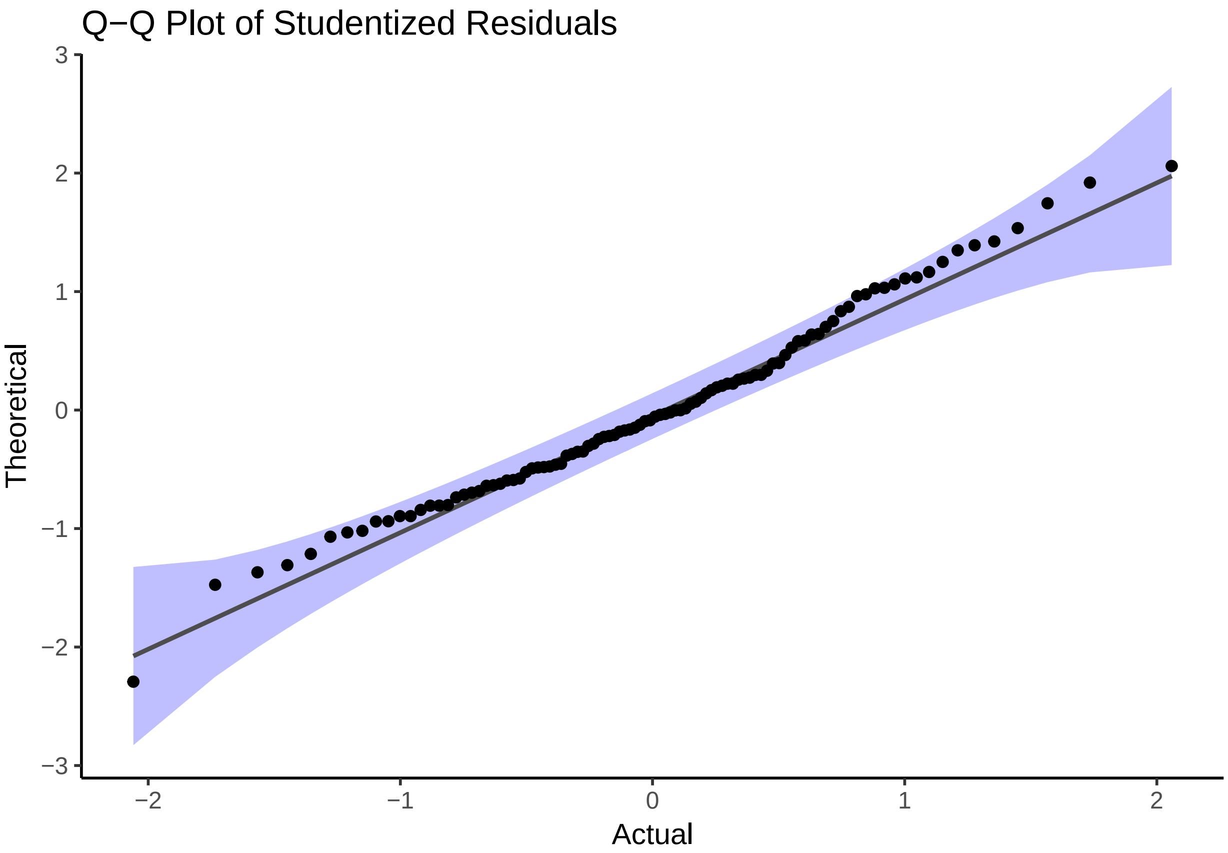
Create a classroom level data frame (call it Class_Data) that contains the Level 2 residuals (only intercept residuals are available so far; name it R_Intercept) and the grand-mean centered classroom means for extraversion (name it Mean_E_GMC).

```r
Class_Data <- dat %>%
  mutate(E_gmc = as.numeric(scale(extrav, scale = F, center = T))) %>%
  group_by(class) %>%
  summarise(Mean_E_GMC = mean(E_gmc, na.rm = T)) %>%
  full_join(unique(dat %>% select(class, L2_residuals)))
```

Part B

Construct a Q-Q plot of the Level 2 residuals

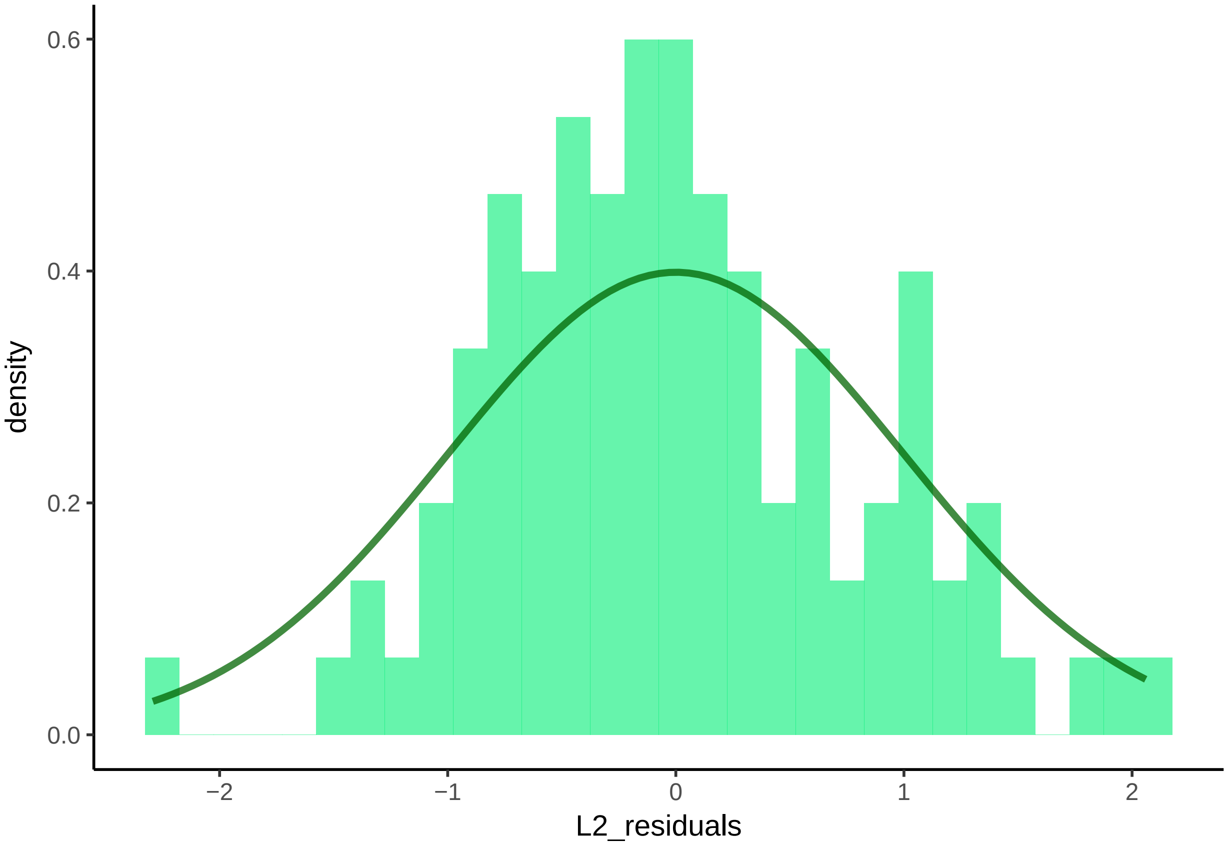
```r
Class_Data %>%
  ggplot(aes(sample=L2_residuals)) +
  stat_qq_band(fill = "blue", alpha = .25) +
  stat_qq_line() +
  stat_qq_point() +
  labs(x = "Actual", y = "Theoretical",
       title = "Q-Q Plot of Studentized Residuals") +
  theme_classic()
```



Part C

Construct a histogram of the Level 2 residuals with a normal distribution overlay.

```
Class_Data %>%
  ggplot(aes(x = L2_residuals)) +
  geom_histogram(aes(y = ..density..), fill = "springgreen2", alpha = .6) +
  stat_function(fun = dnorm, size = 1.25, color = "darkgreen", alpha = .75,
                args = list(mean = 0, sd =1)) +
  theme_classic()
```



Part D

Are the Level 2 residuals normally distributed? The Level 2 residuals do appear to be relatively normally distributed. Although there are some deviations from normality, there doesn't appears to be a clear skew in the residuals.

Part E

Correlate the Level 2 residuals with classroom mean extraversion. Is there evidence that this predictor should be included in the Level 2 model?

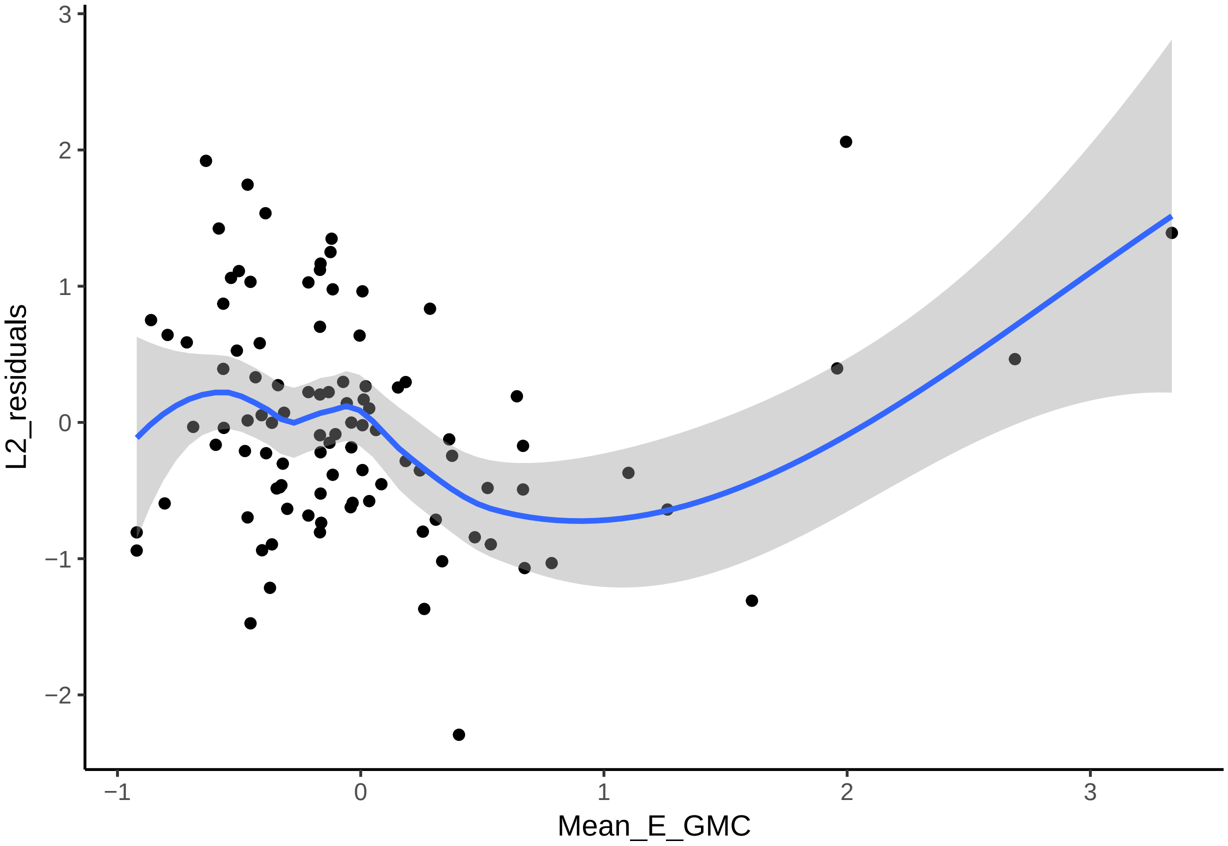
```r
r2 <- Class_Data %>% summarize(r = cor(Mean_E_GMC, L2_residuals))
```

Classroom mean extraversion is almost entirely uncorrellated ($r = -0.02$) with the Level 2 resiudals.

Part F

Create a scatterplot showing the relationship between the Level 2 residuals and classroom mean extraversion. Does there appear to be any need to model nonlinearity at Level 2?

```r
Class_Data %>%
  ggplot(aes(y = L2_residuals, x = Mean_E_GMC)) +
  geom_point() +
  geom_smooth() +
  theme_classic()
```



The relationship between classroom mean extraversion and the Level 2 residuals does appear to be slightly nonlinear.

Question 6

6. Fit a new model based on what you have discovered so far:
   To fit this model, you will need to create a new variable, Mean_E_GMC_SQ, that is the square of Mean_E_GMC. Merge both variables into the original data frame, and fit the new model (call it Pop_Fit_3). Use the lme4 package so that you don't encounter convergence problems. Is there any evidence of curvilinearity at Level 2?

```
dat <- Class_Data %>% mutate(Mean_E_GMC_SQ = Mean_E_GMC^2) %>%
  full_join(dat)

Pop_Fit_3 <- lmer(popular ~  extrav*Mean_E_GMC + extrav*Mean_E_GMC_SQ + sex*Mean_E_GMC +
                    sex*Mean_E_GMC_SQ + (extrav + sex|class), data = dat)
tab_Fit_3 <- table_fun(Pop_Fit_3)

tab_Fit_3 %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", c("b", "CI"))) %>%
  add_header_above(c(" " = 1, "Fit 3" = 2)) %>%
  group_rows("Fixed", 1,9) %>%
  group_rows("Random", 10,12) %>%
  group_rows("Fixed", 13,14)
```

	Fit 3	
Term	b	CI
Fixed		
Intercept	1.88	[1.33, 2.34]
extrav	0.46	[0.42, 0.54]
Mean E GMC	-2.07	[-2.56, -1.09]
Mean E GMC SQ	0.28	[-0.13, 0.52]
sexFemale	1.26	[1.18, 1.32]
extrav:Mean E GMC	0.21	[0.10, 0.26]
extrav:Mean E GMC SQ	-0.03	[-0.05, 0.01]
Mean E GMC:sexFemale	0.11	[-0.02, 0.20]
Mean E GMC SQ:sexFemale	-0.01	[-0.12, 0.10]
Random		
τ00	1.58	[1.04, 1.89]
τ11	0.02	[0.01, 0.03]
τ22	0.00	[0.00, 0.05]
R^2m	0.43	
R^2c	0.70	

There is evidence of nonlinearity at Level 2, $b_{Mean\_E\_GMC\_SQ} = 0.28$ 95% CI [-0.13, 0.52]

Question 7

Fit a model that eliminates the squared terms in Level 2 (call it Pop_Fit_4) and compare it to the full model. Are you justified in eliminating the squared terms?

```
Pop_Fit_4 <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (extrav + sex | class), data = dat)
tab_Fit_4 <- table_fun(Pop_Fit_4)

tab_Fit_4 %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", c("b", "CI"))) %>%
  add_header_above(c(" " = 1, "Fit 4" = 2)) %>%
  group_rows("Fixed", 1,6) %>%
  group_rows("Random", 7,9) %>%
  group_rows("Fixed", 10,11)
```

	Fit 4	
Term	b	CI
Fixed		
Intercept	2.01	[1.86, 2.24]
extrav	0.45	[0.41, 0.48]
Mean E GMC	-1.69	[-1.86, -1.54]
sexFemale	1.25	[1.17, 1.28]
extrav:Mean E GMC	0.17	[0.15, 0.21]
Mean E GMC:sexFemale	0.10	[0.03, 0.21]
Random		
τ00	1.59	[1.22, 2.10]
τ11	0.02	[0.02, 0.03]
τ22	0.00	[0.00, 0.05]
R^2m	0.41	
R^2c	0.69	

```r
anova(Pop_Fit_4, Pop_Fit_3)
```

```
Data: dat Models: Pop_Fit_4: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav +
Pop_Fit_4: sex | class) Pop_Fit_3: popular ~ extrav * Mean_E_GMC + extrav * Mean_E_GMC_SQ +
sex * Pop_Fit_3: Mean_E_GMC + sex * Mean_E_GMC_SQ + (extrav + sex | class) Df AIC BIC logLik
deviance Chisq Chi Df Pr(>Chisq) Pop_Fit_4 13 4837.8 4910.6 -2405.9 4811.8
Pop_Fit_3 16 4841.2 4930.8 -2404.6 4809.2 2.6108 3 0.4556
```

Debatably, the model that includes the squared term does not fit better than the one that doesn't. I would drop it.

Question 8

Using the simpler Pop_Fit_4 model, determine if either or both of the slope variances at Level 2 can be set to 0.

```r
Pop_Fit_4a <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (extrav | class), data = dat)
Pop_Fit_4b <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (sex | class), data = dat)
Pop_Fit_4c <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (1 | class), data = dat)

f4a.tab <- table_fun(Pop_Fit_4a)
f4b.tab <- table_fun(Pop_Fit_4b)
f4c.tab <- table_fun(Pop_Fit_4c)

f4a.tab %>% mutate(model = "Fit 4a") %>%
  full_join(f4b.tab %>% mutate(model = "Fit 4b")) %>%
  full_join(f4c.tab %>% mutate(model = "Fit 4c"))  %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  gather(key = est, value = value, b, CI) %>%
  unite(tmp, model, est, sep = ".") %>%
  mutate(type = factor(type, levels = c("Fixed Parts", "Random Parts", "Model Terms"))) %>%
  spread(key = tmp, value = value) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", rep(c("b", "CI"), times = 3))) %>%
  add_header_above(c(" " = 1, "extrav RE" = 2, "sex RE" = 2, "No RE Slopes" = 2)) %>%
  group_rows("Fixed", 1,6) %>%
  group_rows("Random", 7,8) %>%
  group_rows("Fixed", 9,10)
```

	extrav RE		sex RE		No RE Slopes	
Term	b	CI	b	CI	b	CI
Fixed						
extrav	0.45	[0.44, 0.48]	0.45	[0.43, 0.46]	0.45	[0.43, 0.47]
extrav:Mean E GMC	0.17	[0.14, 0.24]	0.17	[0.13, 0.21]	0.17	[0.14, 0.20]
Intercept	2.01	[1.77, 2.10]	2.02	[1.88, 2.17]	2.02	[1.91, 2.15]
Mean E GMC	-1.70	[-2.30, -1.46]	-1.71	[-2.04, -1.47]	-1.72	[-1.90, -1.55]
Mean E GMC:sexFemale	0.11	[-0.01, 0.24]	0.09	[-0.03, 0.18]	0.09	[-0.01, 0.17]
sexFemale	1.25	[1.20, 1.30]	1.25	[1.19, 1.32]	1.25	[1.20, 1.33]
Random						
$\tau00$	1.60	[1.50, 2.52]	0.49	[0.39, 0.67]	0.46	[0.42, 0.56]
$\tau11$	0.02	[0.01, 0.04]	0.00	[0.00, 0.05]		
R^2c	0.69		0.68		0.68	
R^2m	0.41		0.41		0.41	

```
anova(Pop_Fit_4, Pop_Fit_4a, Pop_Fit_4b, Pop_Fit_4c)
```

```
## Data: dat
## Models:
## Pop_Fit_4c: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (1 | class)
## Pop_Fit_4a: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav |
## Pop_Fit_4a:     class)
## Pop_Fit_4b: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (sex | class)
## Pop_Fit_4: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav +
## Pop_Fit_4:     sex | class)
##            Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## Pop_Fit_4c  8 4865.8 4910.6 -2424.9   4849.8
## Pop_Fit_4a 10 4833.0 4889.0 -2406.5   4813.0 36.802      2  1.020e-08 ***
## Pop_Fit_4b 10 4869.1 4925.1 -2424.6   4849.1  0.000      0          1
## Pop_Fit_4  13 4837.8 4910.6 -2405.9   4811.8 37.315      3  3.947e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Part A

Eliminate the random effect for extrav (call this model Pop_Fit_5). Is this model indistinguishable from Pop_Fit_4?

```
Pop_Fit_5 <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (sex | class), data = dat)
tab_Fit_5 <- table_fun(Pop_Fit_5)

tab_Fit_5 %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", c("b", "CI"))) %>%
  add_header_above(c(" " = 1, "Fit 5" = 2)) %>%
  group_rows("Fixed", 1,6) %>%
  group_rows("Random", 7,8) %>%
  group_rows("Fixed", 9,10)
```

	Fit 5	
Term	b	CI
Fixed		
Intercept	2.02	[1.73, 2.24]
extrav	0.45	[0.44, 0.48]
Mean E GMC	-1.71	[-1.83, -1.27]
sexFemale	1.25	[1.16, 1.38]
extrav:Mean E GMC	0.17	[0.13, 0.19]
Mean E GMC:sexFemale	0.09	[-0.02, 0.20]
Random		
$\tau 00$	0.49	[0.40, 0.57]
$\tau 11$	0.00	[0.00, 0.05]
$R^2 m$	0.41	
$R^2 c$	0.68	

```r
anova(Pop_Fit_4, Pop_Fit_5)
```

```
## Data: dat
## Models:
## Pop_Fit_5: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (sex | class)
## Pop_Fit_4: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav +
## Pop_Fit_4:     sex | class)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## Pop_Fit_5 10 4869.1 4925.1 -2424.6   4849.1
## Pop_Fit_4 13 4837.8 4910.6 -2405.9   4811.8 37.315      3  3.947e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This model is distinguishable from the model from question 4 – eliminating the extraversion random slope improves model fit.

Part B

Eliminate the random effect for sex (call this model Pop_Fit_6). Is this model indistinguishable from Pop_Fit_4?

```r
Pop_Fit_6 <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (extrav | class), data = dat)

table_fun(Pop_Fit_6)  %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", c("b", "CI"))) %>%
  add_header_above(c(" " = 1, "Fit 6")) %>%
  group_rows("Fixed", 1,6) %>%
  group_rows("Random", 7,8) %>%
  group_rows("Fixed", 9,10)
```

	Fit 6	
Term	b	CI
Fixed		
Intercept	2.01	[1.78, 2.30]
extrav	0.45	[0.42, 0.48]
Mean E GMC	-1.70	[-1.93, -1.06]
sexFemale	1.25	[1.19, 1.33]
extrav:Mean E GMC	0.17	[0.10, 0.20]
Mean E GMC:sexFemale	0.11	[0.01, 0.29]
Random		
τ00	1.60	[1.35, 1.89]
τ11	0.02	[0.02, 0.03]
R^2m	0.41	
R^2c	0.69	

```
anova(Pop_Fit_4, Pop_Fit_6)
```

```
## Data: dat
## Models:
## Pop_Fit_6: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav |
## Pop_Fit_6:     class)
## Pop_Fit_4: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav +
## Pop_Fit_4:     sex | class)
##           Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## Pop_Fit_6 10 4833.0 4889.0 -2406.5   4813.0
## Pop_Fit_4 13 4837.8 4910.6 -2405.9   4811.8 1.247      3     0.7418
```

Yes, the model that does not include the random slope for sex is indistinguishable from one that does.

Part C

Finally, eliminate them both (call this Pop_Fit_7) and compare it to Pop_Fit_4. Which simpler model is justified?

```
Pop_Fit_7 <- lmer(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC + (1 | class), data = dat)

table_fun(Pop_Fit_7) %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", c("b", "CI"))) %>%
  add_header_above(c(" " = 1, "Fit 7")) %>%
  group_rows("Fixed", 1,6) %>%
  group_rows("Random", 7,7) %>%
  group_rows("Fixed", 8,9)
```

	Fit 7	
Term	b	CI
Fixed		
Intercept	2.02	[1.76, 2.12]
extrav	0.45	[0.44, 0.47]
Mean E GMC	-1.72	[-2.02, -1.27]
sexFemale	1.25	[1.21, 1.30]
extrav:Mean E GMC	0.17	[0.12, 0.21]
Mean E GMC:sexFemale	0.09	[0.03, 0.24]
Random		
τ00	0.46	[0.37, 0.63]
R^2m	0.41	
R^2c	0.68	

```
anova(Pop_Fit_4, Pop_Fit_5, Pop_Fit_6, Pop_Fit_7)
```

```
## Data: dat
## Models:
## Pop_Fit_7: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (1 | class)
## Pop_Fit_5: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (sex | class)
## Pop_Fit_6: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav |
## Pop_Fit_6:     class)
## Pop_Fit_4: popular ~ extrav * Mean_E_GMC + sex * Mean_E_GMC + (extrav +
## Pop_Fit_4:     sex | class)
##           Df    AIC    BIC  logLik deviance   Chisq Chi Df Pr(>Chisq)
## Pop_Fit_7  8 4865.8 4910.6 -2424.9   4849.8
## Pop_Fit_5 10 4869.1 4925.1 -2424.6   4849.1  0.7339      2     0.6928
## Pop_Fit_6 10 4833.0 4889.0 -2406.5   4813.0 36.0681      0     <2e-16 ***
## Pop_Fit_4 13 4837.8 4910.6 -2405.9   4811.8  1.2470      3     0.7418
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pop_Fit_6 is the best model.

Question 9

Use the simplest model justified from the previous question.

Part A

Retest the Level 1 homogeneity assumption. Is there any improvement compared to what was found for Question 1?

```
cl1 <- lmeControl(maxIter=100000, msMaxIter=100000, niterEM=100000, msMaxEval=100000,
                  tolerance=.000001,msTol=.0000001,returnObject=TRUE,minAbsParApVar=.05,
                  opt = c("nlminb"), optimMethod="BFGS")

Pop_Fit_6.lme <- lme(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC, random = ~ 1 + extrav|class, data = 
Pop_Fit_6.a <- lme(popular ~ extrav*Mean_E_GMC + sex*Mean_E_GMC, random = ~ 1 + extrav|class,
                   data = dat, varIdent(form = ~ 1 +extrav| class), control = cl1)

anova(Pop_Fit_6.lme, Pop_Fit_6.a)
```

```
##                Model  df      AIC      BIC    logLik   Test L.Ratio p-value
## Pop_Fit_6.lme     1  10 4859.194 4915.173 -2419.597
## Pop_Fit_6.a       2 109 4939.475 5549.646 -2360.737 1 vs 2 117.719  0.0966
```

In this case, we meet the homogeneity of variance assumption. The model that fits unique variances is not better than one that does not.

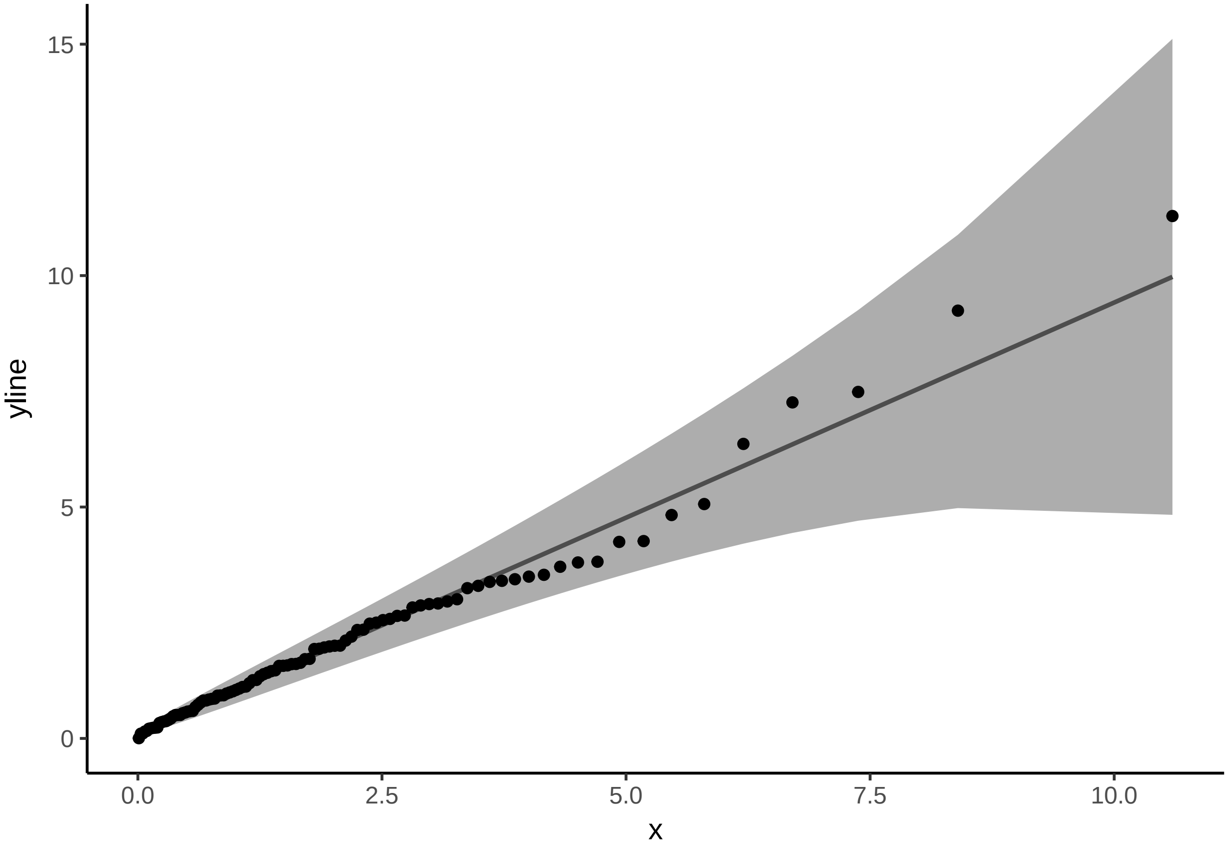
Part B

Check the multivariate normality assumption for the residuals at Level 2 using Mahalanobis distance. Are the residuals multivariate normal?

```
L2_residuals <- ranef(Pop_Fit_6)[[1]]
MD.v <- mahalanobis(L2_residuals, colMeans(L2_residuals), cov(L2_residuals))

MD.df <- MD.v %>% data.frame %>% setNames("MD") %>% mutate(class = names(MD.v))

MD.df %>%
  ggplot(aes(sample = MD)) +
  stat_qq_band(distribution = "chisq", dparams = list(df = 2)) +
  stat_qq_line(distribution = "chisq", dparams = list(df = 2)) +
  stat_qq_point(distribution = "chisq", dparams = list(df = 2)) +
  theme_classic()
```



The residuals do appear to be multivariate normal.

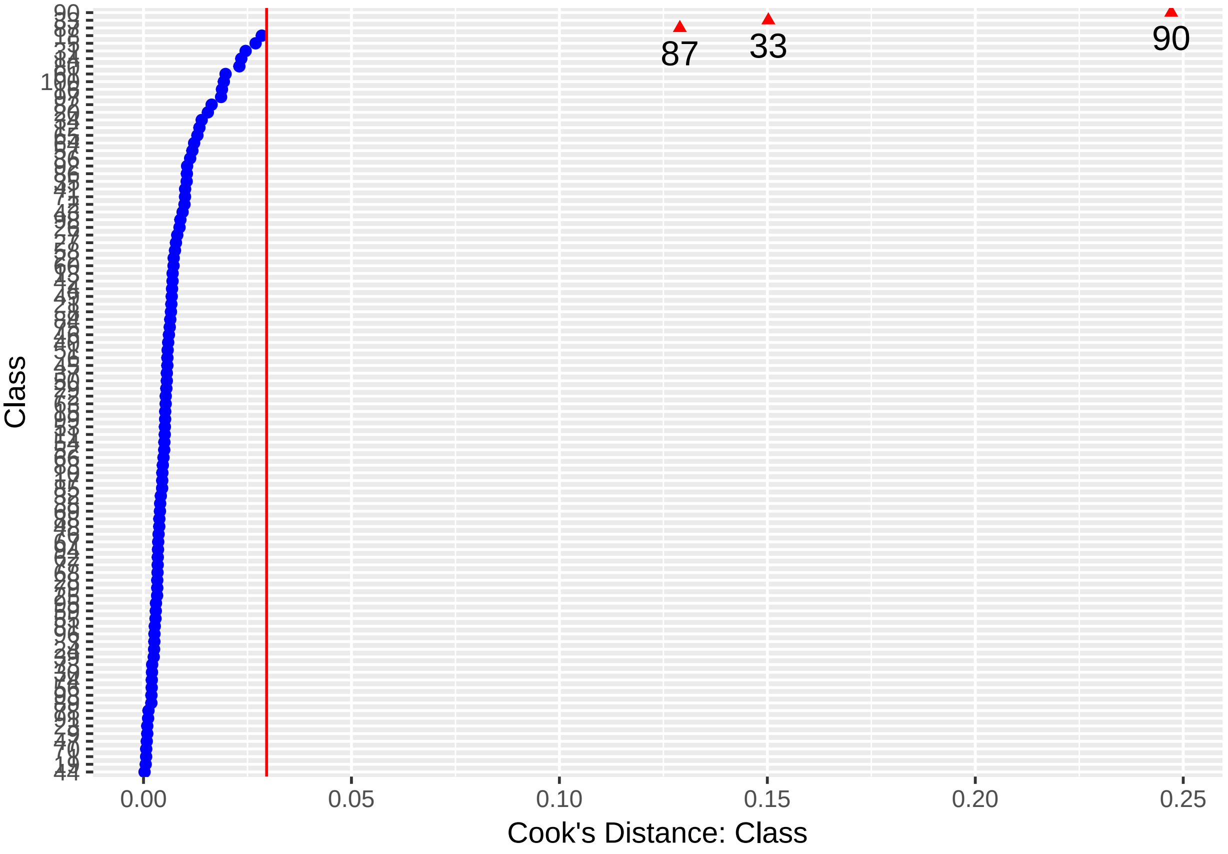
Question 10

Use Cook's distance to examine how influential the classrooms are in the model fit for Question 9.

```
Pop_Fit_6.i <- influence(Pop_Fit_6, group = "class")

Cooks_Class <- cooks.distance(Pop_Fit_6.i, group = "class")
Cooks_Class <- Cooks_Class %>% data.frame %>% setNames("cooks.distance") %>%
  mutate(class = rownames(Cooks_Class))

dotplot_diag(x = cooks.distance, index = class, data = Cooks_Class,
             cutoff = "internal", name = "cooks.distance",
             ylab = "Cook's Distance: Class", xlab = "Class")
```



Part A

How many classrooms stand out as distinctly more influential than the others? 3 classrooms: 33, 87, and 90.

Part B

If those classrooms are excluded from the analysis and the model is refit, do any conclusions change?

```
Pop_Fit_6.cd <- update(Pop_Fit_6, data = dat %>% filter(!(class %in% c(87, 33, 90))))

table_fun(Pop_Fit_6.cd) %>%
  mutate(term = str_replace_all(term, "_", " ")) %>%
  select(-type) %>%
  kable(., "latex", escape = F, booktabs = T,
        col.names = c("Term", c("b", "CI"))) %>%
  add_header_above(c(" " = 1, "Fit 7 Outliers Removed")) %>%
  group_rows("Fixed", 1,6) %>%
  group_rows("Random", 7,7) %>%
  group_rows("Fixed", 8,9)
```

	Fit 7 Outliers Removed	
Term	b	CI
Fixed		
Intercept	1.91	[1.66, 2.18]
extrav	0.46	[0.42, 0.49]
Mean E GMC	-2.16	[-2.49, -1.35]
sexFemale	1.26	[1.20, 1.31]
extrav:Mean E GMC	0.21	[0.10, 0.23]
Mean E GMC:sexFemale	0.15	[0.07, 0.28]
Random		
τ00	1.54	[0.95, 1.77]
Fixed		
τ11	0.02	[0.01, 0.02]
$R^2 m$	0.43	
$R^2 c$	0.69	

The interaction between Level 1 and Level 2 extraversion is now significant, suggesting that in those classes wtih higher mean extraversion, higher extraversion is even more predictive of popularity than in less extraverted classrooms.