

Group C Analysis_FV

```
library(lme4)      # for linear mixed-effects models
```

Loading required package: Matrix

```
library(lmerTest)  # for p-values in mixed models
```

Warning: package 'lmerTest' was built under R version 4.4.3

Attaching package: 'lmerTest'

The following object is masked from 'package:lme4':

lmer

The following object is masked from 'package:stats':

step

```
library(ggplot2)
library(here)
```

here() starts at C:/Users/april/Downloads

```
# 1. Data Loading and Preparation
nursebp <- read.csv(here("nursebp.csv"))
# Convert appropriate columns to factors
nursebp$SNUM <- factor(nursebp$SNUM)
nursebp$DAY <- factor(nursebp$DAY)      # 'W' or 'NW'
nursebp$PHASE <- factor(nursebp$PHASE)  # 'F' or 'L'
nursebp$POSTURE <- factor(nursebp$POSTURE) # 'SIT', 'STAND', 'RECLINE'
nursebp$FH123 <- factor(nursebp$FH123, levels=c("NO", "YES", "YESYES"))
nursebp$STR <- factor(nursebp$STR, levels=c(1,2,3,4,5))
nursebp$HAP <- factor(nursebp$HAP, levels=c(1,2,3,4,5))
nursebp$TIR <- factor(nursebp$TIR, levels=c(1,2,3,4,5))
```

```
nursebp_complete <- na.omit(nursebp)
# after remove NA, we still have 7896 rows, which is sufficient for analysis
```

Descriptive statistics

```
summary(nursebp_complete$SYS)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
75.0	108.0	117.0	118.2	127.0	199.0

```
# (This will output min, 1Q, median, mean, etc., as seen in the report)
table(nursebp_complete$FH123)
```

NO	YES	YESYES
4448	2895	553

```
table(nursebp_complete$DAY)
```

NW	W
3558	4338

```
# etc., to see distribution of categorical variables
```

Create time variables (center and quadratic term)

```
nursebp_complete$time_c <- scale(nursebp_complete$time, center=TRUE, scale=TRUE)
nursebp_complete$time_c2 <- (nursebp_complete$time_c)^2
```

Model 1: with DBP, random intercept and slope for time

```
model1 <- lmer(SYS ~ AGE + DIA + FH123 + HAP + HRT + MNACT5 + STR + TIR +
  DAY + PHASE + POSTURE + time_c + time_c2 +
  (1 + time_c | SNUM),
  data = nursebp_complete, REML=TRUE)
summary(model1)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]

Formula: SYS ~ AGE + DIA + FH123 + HAP + HRT + MNACT5 + STR + TIR + DAY + PHASE + POSTURE + time_c + time_c2 + (1 + time_c | SNUM)
Data: nursebp_complete

REML criterion at convergence: 61187.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.9283	-0.5513	-0.0596	0.4793	7.4456

Random effects:

```

Groups   Name             Variance Std.Dev. Corr
SNUM     (Intercept)    39.12     6.254
          time_c         3.16     1.778   0.25
Residual                126.04    11.227
Number of obs: 7896, groups: SNUM, 182

```

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.274e+01	4.196e+00	7.268e+02	17.336	< 2e-16 ***
AGE	-3.127e-02	7.390e-02	1.733e+02	-0.423	0.67276
DIA	4.920e-01	1.195e-02	7.850e+03	41.180	< 2e-16 ***
FH123YES	-7.467e-01	1.019e+00	1.727e+02	-0.733	0.46449
FH123YESYES	4.584e+00	1.928e+00	1.745e+02	2.378	0.01849 *
HAP2	2.650e-01	6.286e-01	7.541e+03	0.422	0.67340
HAP3	7.790e-02	6.426e-01	6.435e+03	0.121	0.90353
HAP4	-9.254e-02	7.102e-01	5.944e+03	-0.130	0.89633
HAP5	-5.150e-01	8.763e-01	4.760e+03	-0.588	0.55680
HRT	3.998e-02	1.446e-02	6.835e+03	2.765	0.00571 **
MNACT5	3.153e-02	2.443e-03	7.836e+03	12.905	< 2e-16 ***
STR2	2.041e-01	3.592e-01	7.679e+03	0.568	0.56995
STR3	-5.438e-01	5.797e-01	7.510e+03	-0.938	0.34817
STR4	1.249e+00	9.703e-01	7.749e+03	1.288	0.19794
STR5	4.681e-01	1.693e+00	7.753e+03	0.277	0.78216
TIR2	1.475e-01	3.963e-01	5.994e+03	0.372	0.70972
TIR3	9.876e-02	4.898e-01	5.382e+03	0.202	0.84021
TIR4	-6.731e-01	6.690e-01	4.432e+03	-1.006	0.31439
TIR5	2.938e-01	1.091e+00	3.389e+03	0.269	0.78767
DAYW	1.183e+00	9.627e-01	1.751e+02	1.229	0.22064
PHASEL	6.634e-01	9.621e-01	1.727e+02	0.690	0.49143
POSTURERECLINE	6.079e-01	2.732e+00	7.752e+03	0.223	0.82390
POSTURESIT	1.179e+00	2.670e+00	7.739e+03	0.441	0.65886
POSTURESTAND	1.205e+00	2.669e+00	7.740e+03	0.451	0.65169
time_c	1.947e-01	1.993e-01	2.094e+02	0.977	0.32978
time_c2	1.386e-01	1.501e-01	6.528e+03	0.923	0.35589

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as p = 26 > 12.

Use print(x, correlation=TRUE) or

vcov(x) if you need it

Model 2: without DBP

```

model2 <- lmer(SYS ~ AGE + FH123 + HAP + HRT + MNACT5 + STR + TIR +
  DAY + PHASE + POSTURE + time_c + time_c2 +
  (1 + time_c | SNUM),

```

```
data = nursebp_complete, REML=TRUE)
summary(model2)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
 Formula: SYS ~ AGE + FH123 + HAP + HRT + MNACT5 + STR + TIR + DAY + PHASE + POSTURE + time_c + time_c2 + (1 + time_c | SNUM)
 Data: nursebp_complete

REML criterion at convergence: 62705.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.3416	-0.5425	-0.0370	0.5118	6.5274

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
SNUM	(Intercept)	61.469	7.840	
	time_c	5.715	2.391	0.22
Residual		151.321	12.301	

Number of obs: 7896, groups: SNUM, 182

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	99.12135	4.86219	567.33828	20.386	< 2e-16 ***
AGE	0.06947	0.09192	174.67661	0.756	0.45077
FH123YES	-0.81579	1.26779	174.58924	-0.643	0.52076
FH123YESYES	7.13193	2.39679	175.63012	2.976	0.00334 **
HAP2	0.15744	0.69529	7744.15098	0.226	0.82086
HAP3	0.07469	0.71501	7041.21011	0.104	0.91681
HAP4	0.21890	0.79166	6664.81699	0.277	0.78217
HAP5	-0.38183	0.98171	5686.14551	-0.389	0.69733
HRT	0.09928	0.01597	7311.89026	6.216	5.38e-10 ***
MNACT5	0.03277	0.00269	7836.00026	12.184	< 2e-16 ***
STR2	0.49583	0.39655	7796.64154	1.250	0.21121
STR3	-0.27736	0.64059	7690.87522	-0.433	0.66504
STR4	2.06556	1.06916	7799.40965	1.932	0.05340 .
STR5	2.77618	1.86308	7780.72224	1.490	0.13624
TIR2	-0.17164	0.44070	6695.07422	-0.389	0.69694
TIR3	-0.54590	0.54606	6158.48998	-1.000	0.31749
TIR4	-1.50086	0.74754	5281.03394	-2.008	0.04472 *
TIR5	-0.31342	1.22139	4236.86114	-0.257	0.79749
DAYW	2.71693	1.19667	176.00117	2.270	0.02439 *
PHASEL	0.40430	1.19742	174.49783	0.338	0.73604
POSTURERECLINE	-3.59311	2.99891	7730.35675	-1.198	0.23090
POSTURESIT	0.16078	2.93213	7714.78556	0.055	0.95627
POSTURESTAND	0.53537	2.93160	7715.88110	0.183	0.85510
time_c	0.07149	0.24245	210.46124	0.295	0.76840
time_c2	0.34664	0.16602	6959.29514	2.088	0.03684 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as $p = 25 > 12$.

Use `print(x, correlation=TRUE)` or
`vcov(x)` if you need it

Compare Model 1 and Model 2 fit

```
AIC(model1, model2)
```

	df	AIC
model1	30	61247.55
model2	29	62763.90

We expect model1 (with DIA) to have lower AIC (better fit) but model2 to reveal more effects.

Compare with model 1 (random intercept model)

```
model0 <- lmer(SYS ~ AGE + FH123 + HAP + HRT + MNACT5 + STR + TIR +
               DAY + PHASE + POSTURE + time_c + time_c2 + (1|SNUM),
               data=nursebp_complete, REML=TRUE)
AIC(model0, model1)
```

	df	AIC
model0	27	62871.81
model1	30	61247.55

```
anova(model0, model1) # likelihood ratio test for random slope significance
```

refitting model(s) with ML (instead of REML)

Data: nursebp_complete

Models:

model0: SYS ~ AGE + FH123 + HAP + HRT + MNACT5 + STR + TIR + DAY + PHASE + POSTURE + time_c + time_c2 + (1 | SNUM)

model1: SYS ~ AGE + DIA + FH123 + HAP + HRT + MNACT5 + STR + TIR + DAY + PHASE + POSTURE + time_c + time_c2 + (1 + time_c | SNUM)

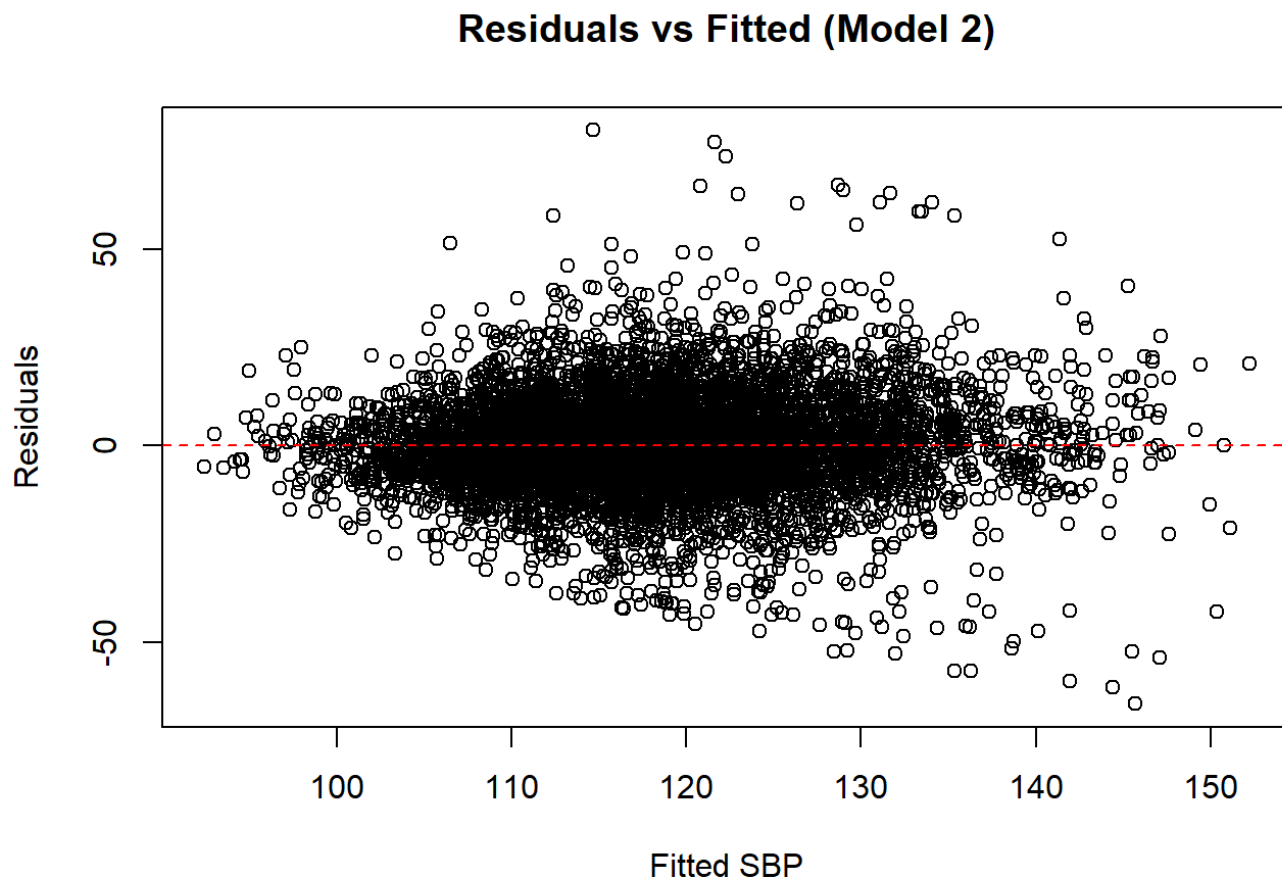
	npar	AIC	BIC	logLik	deviance	Chisq	Df	Pr(>Chisq)
model0	27	62875	63063	-31411	62821			
model1	30	61239	61448	-30589	61179	1642.5	3	< 2.2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Diagnostic plots for Model 2

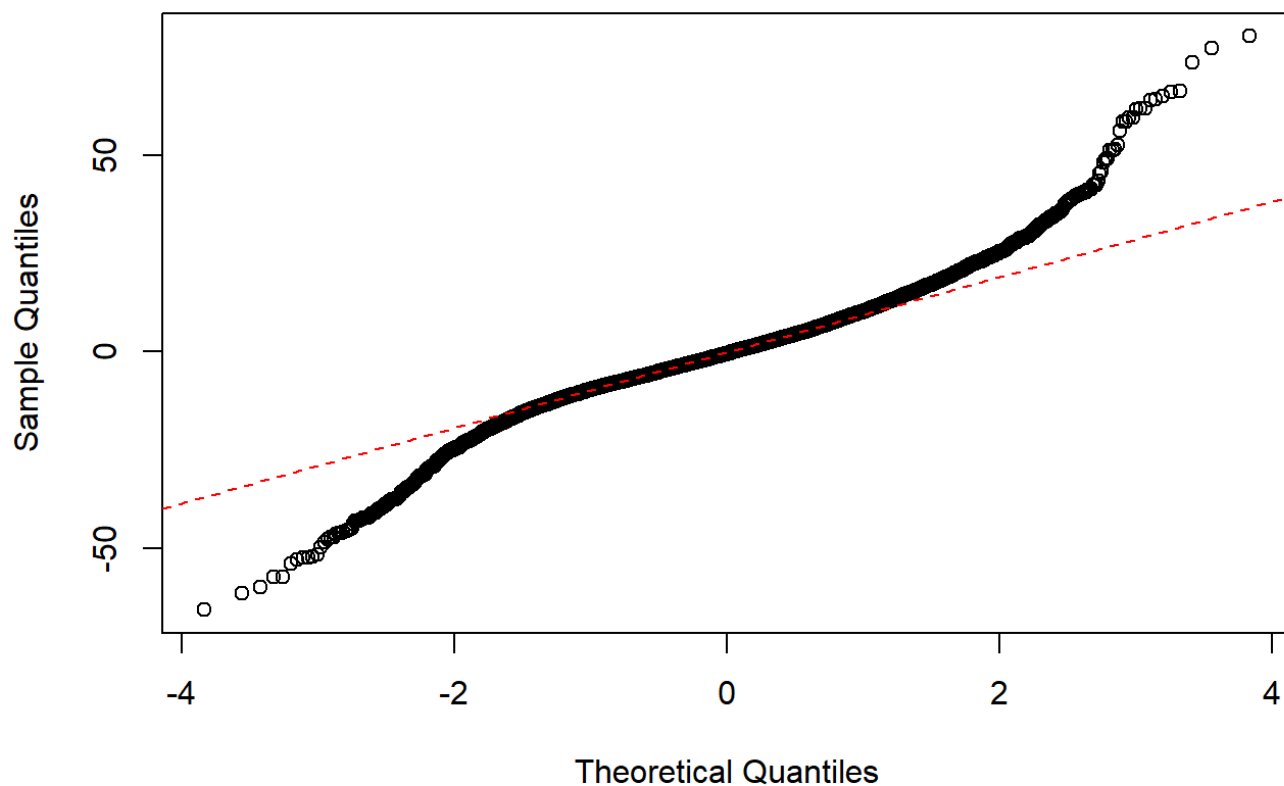
```
resid2 <- residuals(model2)
fitted2 <- fitted(model2)

# Residuals vs fitted
plot(fitted2, resid2, xlab="Fitted SBP", ylab="Residuals",
     main="Residuals vs Fitted (Model 2)",
     abline(h=0, col="red", lty=2))
```



```
# Normal Q-Q plot of residuals
qqnorm(resid2, main="Q-Q Plot of Residuals (Model 2)")
qqline(resid2, col="red", lty=2)
```

Q-Q Plot of Residuals (Model 2)

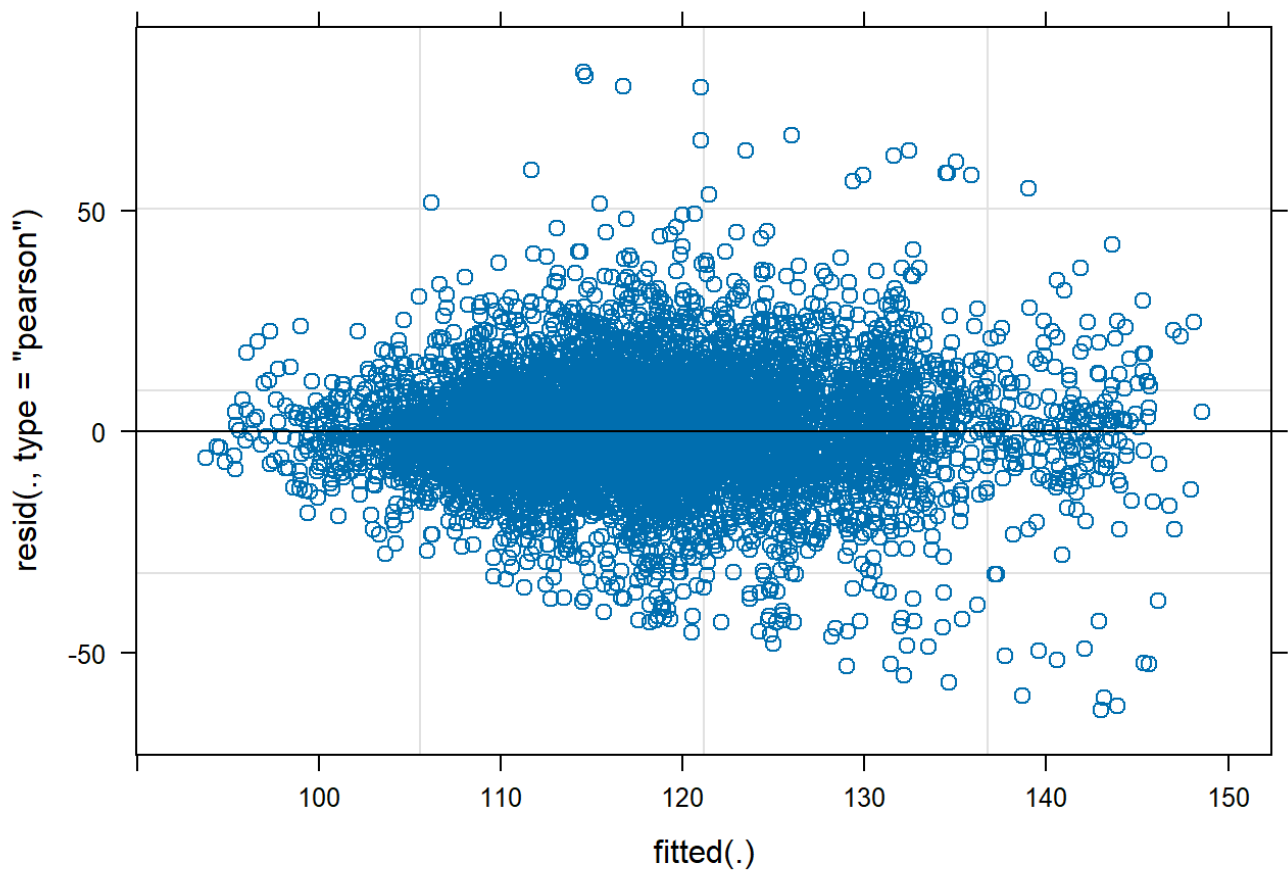


```
# We can also examine random effects
ranef(model2)$SNUM[1:5, ] # show first 5 nurses' random intercept and slope
```

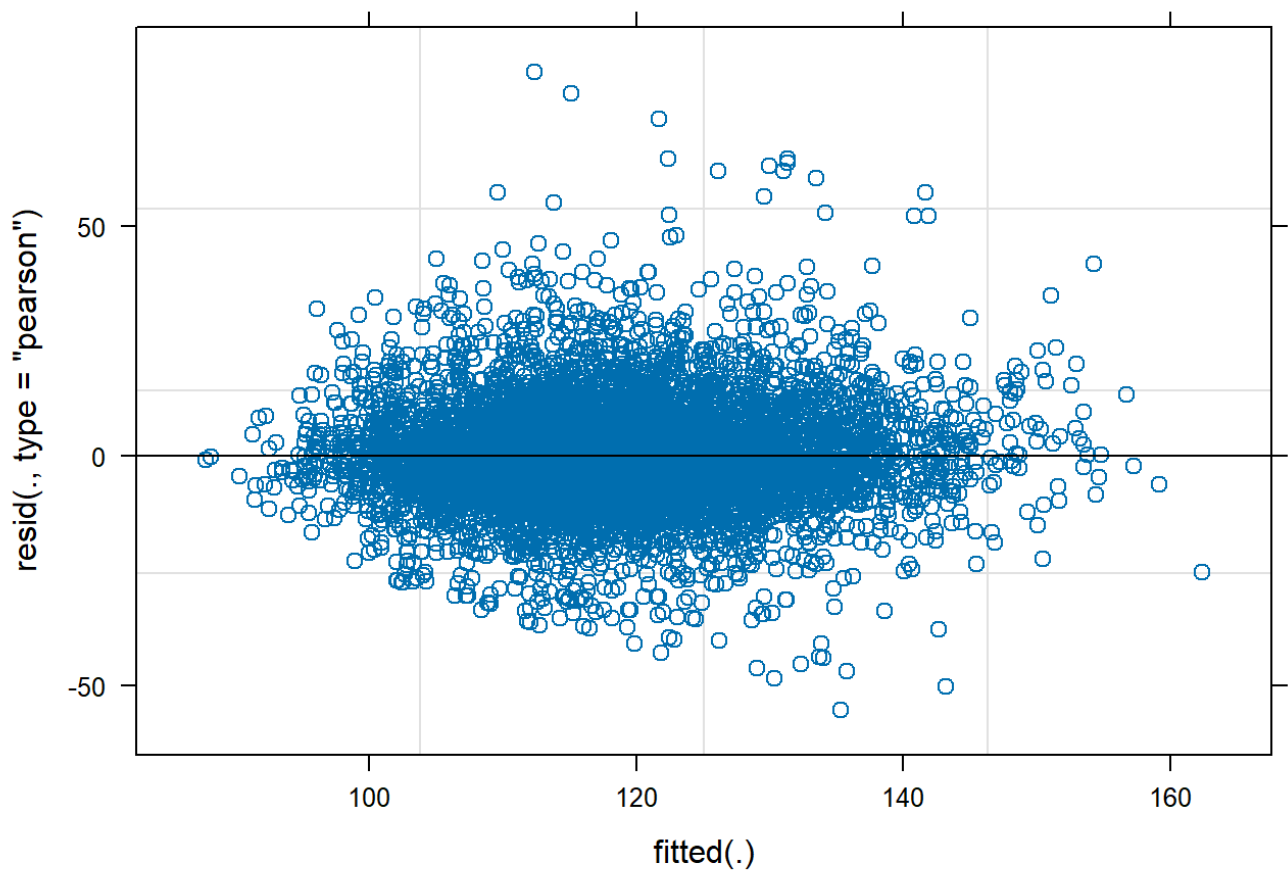
	(Intercept)	time_c
1002	4.8800701	2.14716377
1004	-3.9045516	0.08809951
1005	0.1883276	-1.02098865
1006	0.5542371	1.48528632
1010	5.7485705	1.82431868

Diagnostics for Model 0 and 1

```
plot(model0)
```



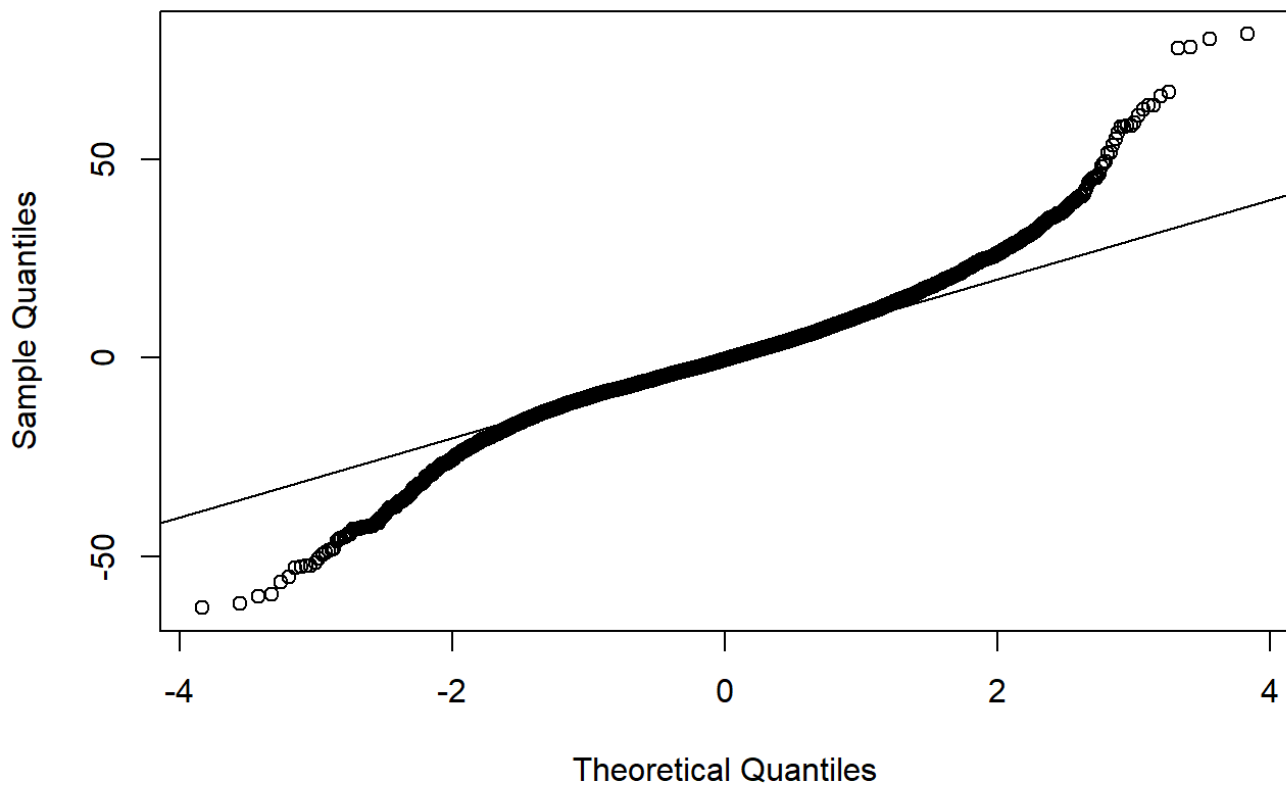
```
plot(model1)
```

```
# More detailed residual diagnostics
res0 <- residuals(model0)
res1 <- residuals(model1)

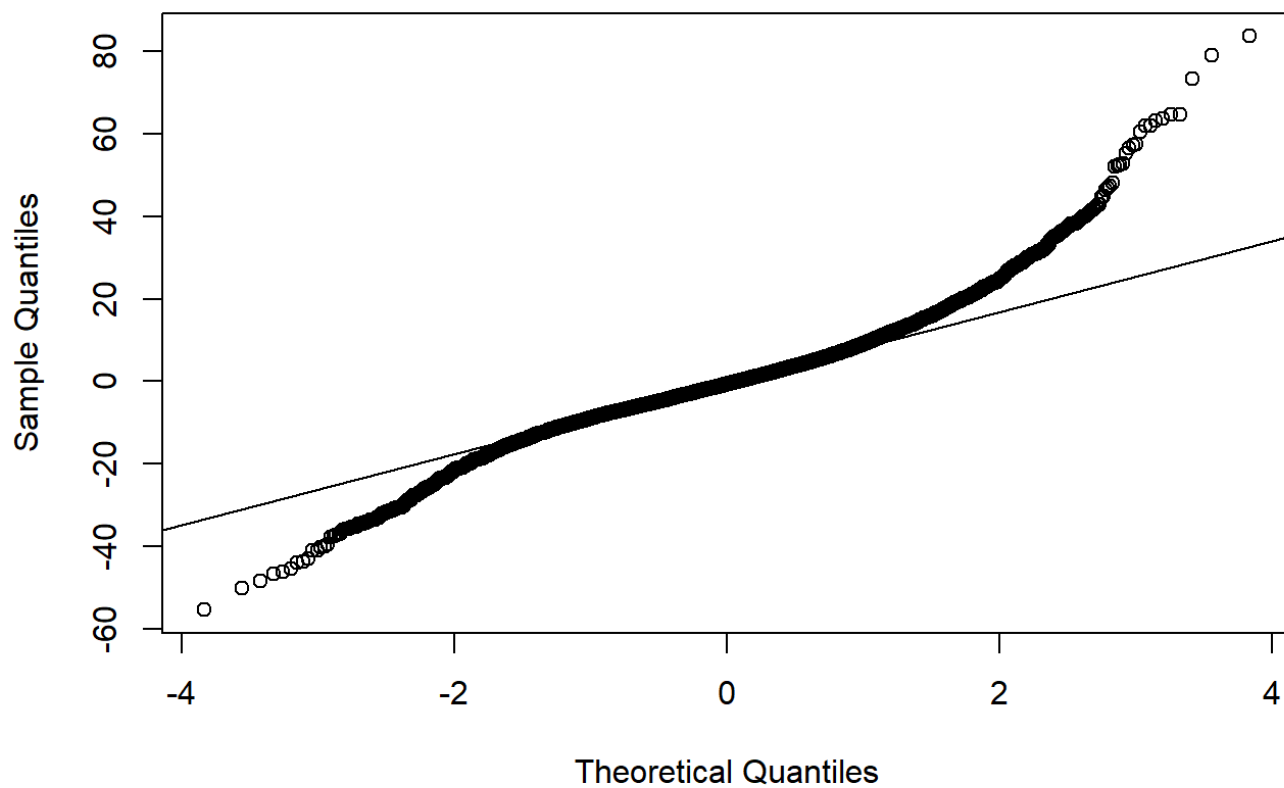
# QQ plots
qqnorm(res0); qqline(res0)
```

Normal Q-Q Plot

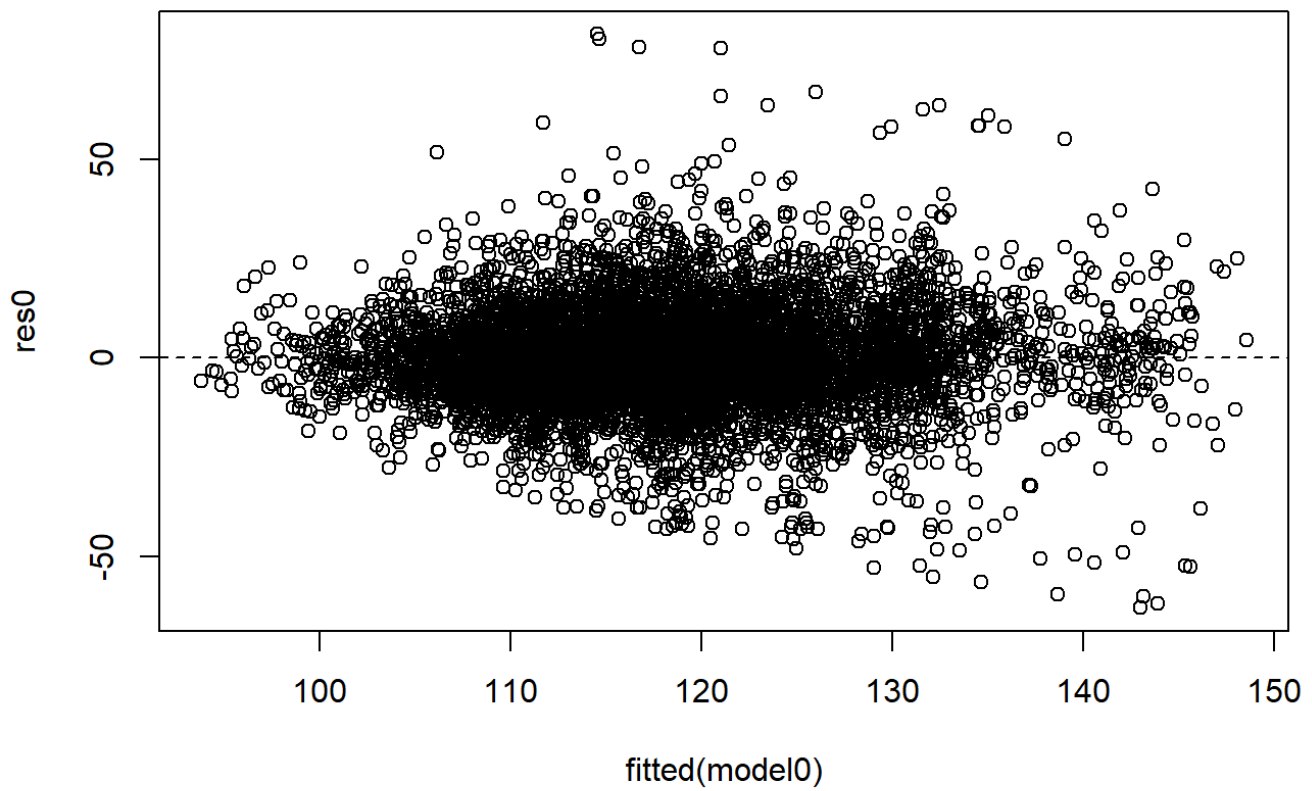


```
qqnorm(res1); qqline(res1)
```

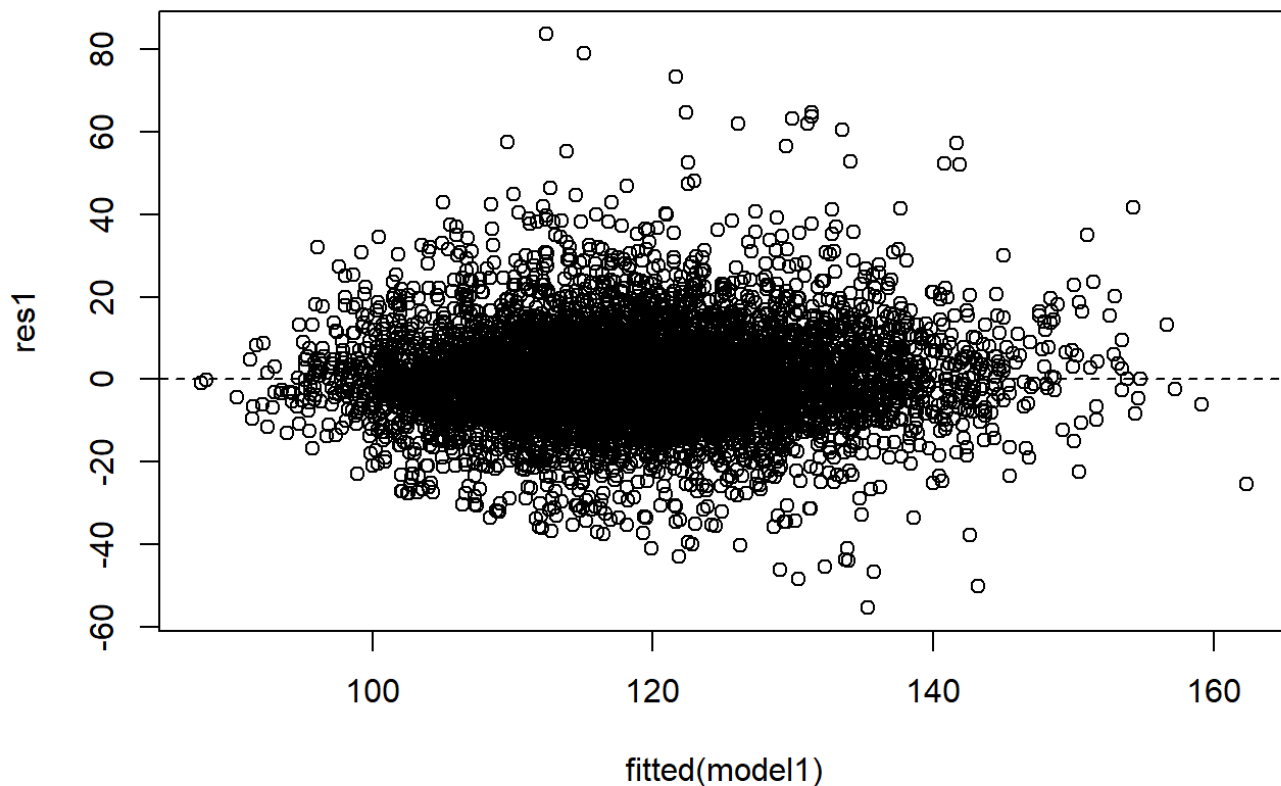
Normal Q-Q Plot



```
# Residuals vs. fitted  
plot(fitted(model0), res0)  
abline(h=0, lty=2)
```



```
plot(fitted(model1), res1)  
abline(h=0, lty=2)
```



```
#compare 2 models
anova(model0, model1)
```

refitting model(s) with ML (instead of REML)

Data: nursebp_complete

Models:

model0: SYS ~ AGE + FH123 + HAP + HRT + MNACT5 + STR + TIR + DAY + PHASE + POSTURE + time_c + time_c2 + (1 | SNUM)

model1: SYS ~ AGE + DIA + FH123 + HAP + HRT + MNACT5 + STR + TIR + DAY + PHASE + POSTURE + time_c + time_c2 + (1 + time_c | SNUM)

	npar	AIC	BIC	logLik	deviance	Chisq	Df	Pr(>Chisq)
model0	27	62875	63063	-31411	62821			
model1	30	61239	61448	-30589	61179	1642.5	3	< 2.2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
AIC(model0, model1)
```

	df	AIC
model0	27	62871.81

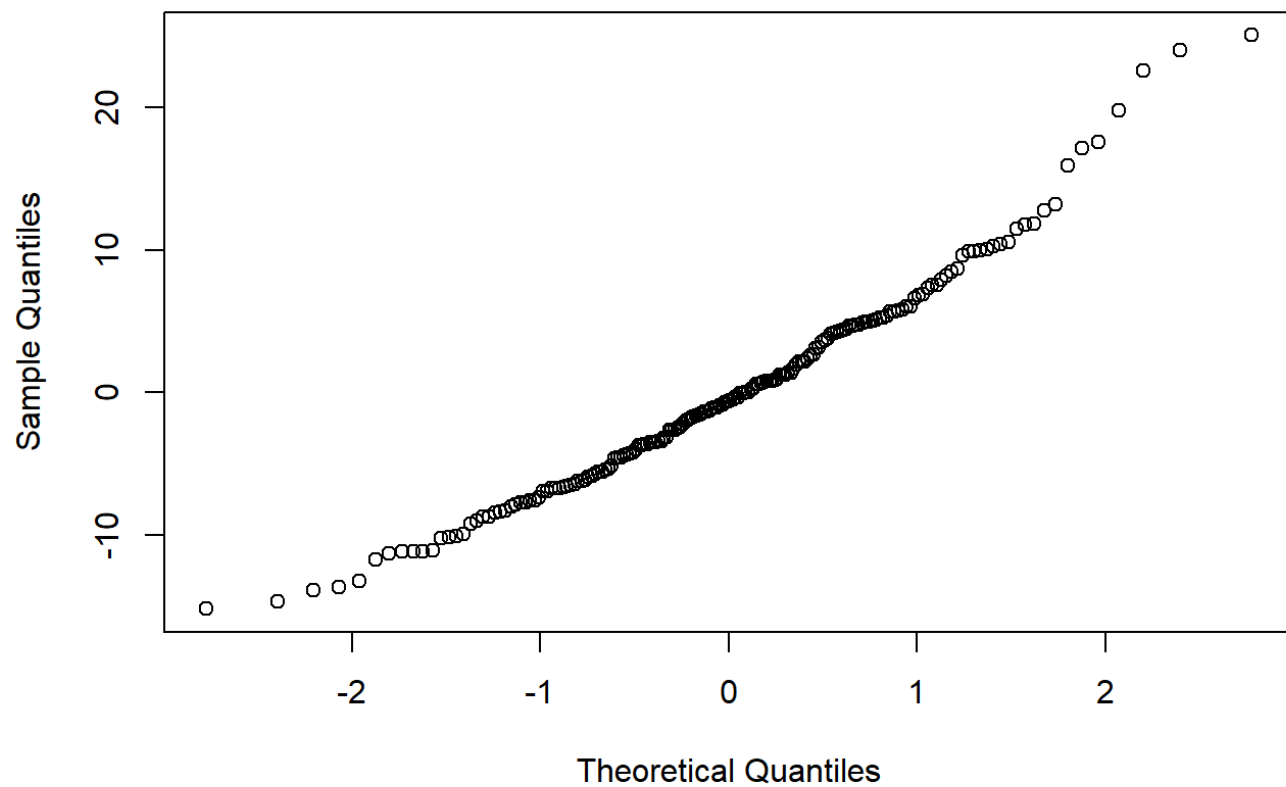
```
model1 30 61247.55
```

```
BIC(model0, model1)
```

	df	BIC
model0	27	63060.11
model1	30	61456.78

```
# Extract random effects  
re0 <- ranef(model0)  
re1 <- ranef(model1)  
  
# Plot random effects  
qqnorm(unlist(re0$SNUM))
```

Normal Q-Q Plot



```
qqnorm(unlist(re1$SNUM))
```

Normal Q-Q Plot

