Assignment 1

2024-12-09

5.

We simulate the data. We simulate 10^5 data points form the multivariate normal distribution with mean $\begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}$ and variance $\begin{pmatrix} 1 & 0.25 & 0.5 \\ 0.25 & 1 & 0.5 \\ 0.5 & 0.5 & 1 \end{pmatrix}$.

```
set.seed(7878)
n <- 10^5
sigma <- matrix(c(1, 0.25, 0.5, 0.25, 1, 0.5, 0.5, 0.5, 1), nrow = 3)
X <- mvrnorm(n, c(0,0, 0), sigma)
```

We will illustrate that the conditional distribution of $\begin{pmatrix} X_1 \\ X_2 \end{pmatrix} |X_3 = x_3$ is as expected by conditioning on $|X_3| = 0$. To approximate this (X_3 has a continuous distribution), we find the rows of X for which $|X_3| \leq 0.05$:

```
cond <- which(abs(X[,3]) < 0.05)
```

We calculate the correlation of X_1 and X_2 for those X_1 and X_2 for which $|X_3| \leq 0.05$.

```
cor(X[cond,1], X[cond,2])
```

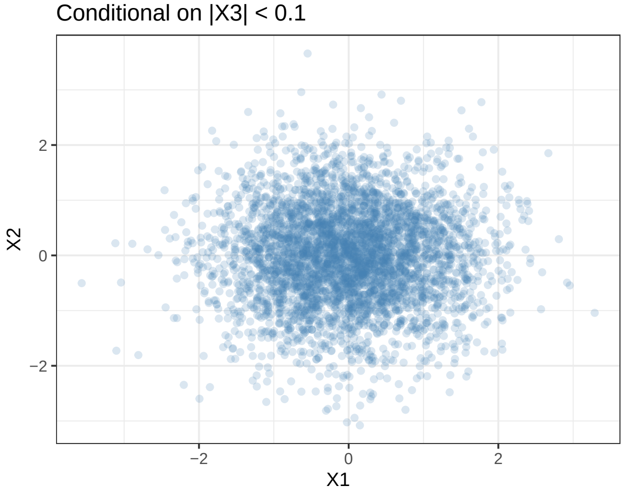
```
## [1] 0.001381612
```

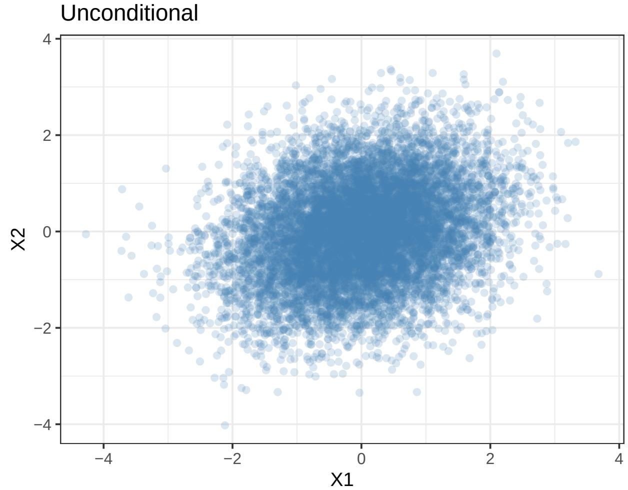
Which is as expected close to 0. This is different from the correlation of X_1 and X_2 in general, which is by construction ≈ 0.25:

```
cor(X[,1], X[,2])
```

```
## [1] 0.2495407
```

To visualize the conditional distribution of X_1 and X_2 we create the two scatterplot below. In the unconditional distribution the two variables are positively correlated, while they in the conditional distribution are uncorrelated, and thus (since they are normal) independent.

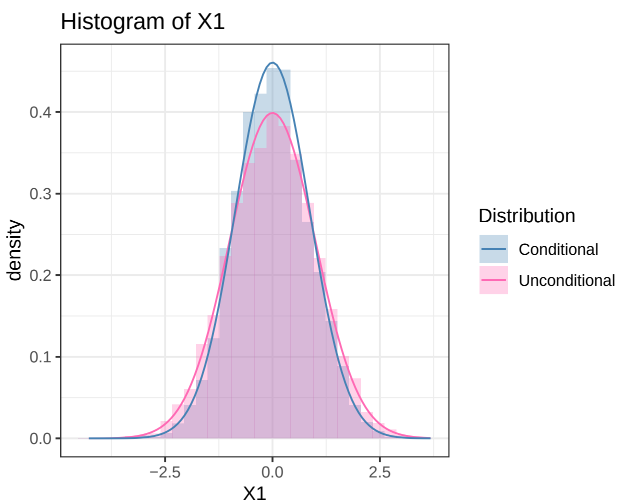


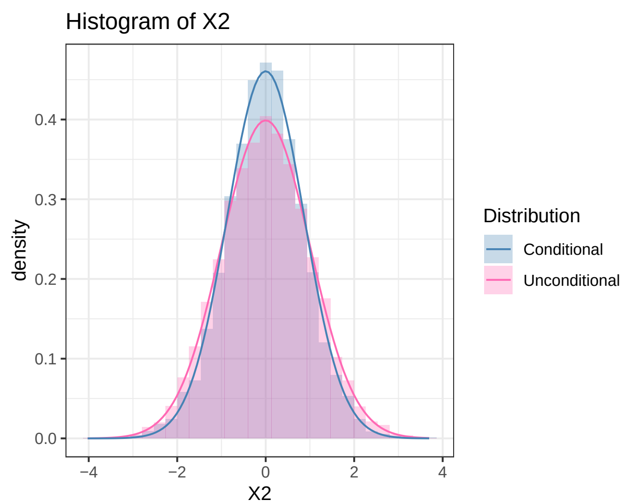


As a last illustration, we have made histograms of the marginal distributions of the two random variables, conditional on $X_3 = 0$ and unconditionally. The marginal distribution of both variables unconditionally is $\mathcal{N}(0,1)$ and conditionally on $X_3 = 0$, it is, with use of our calculations from the previous exercises, $\mathcal{N}(0, 0.75)$.

```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```





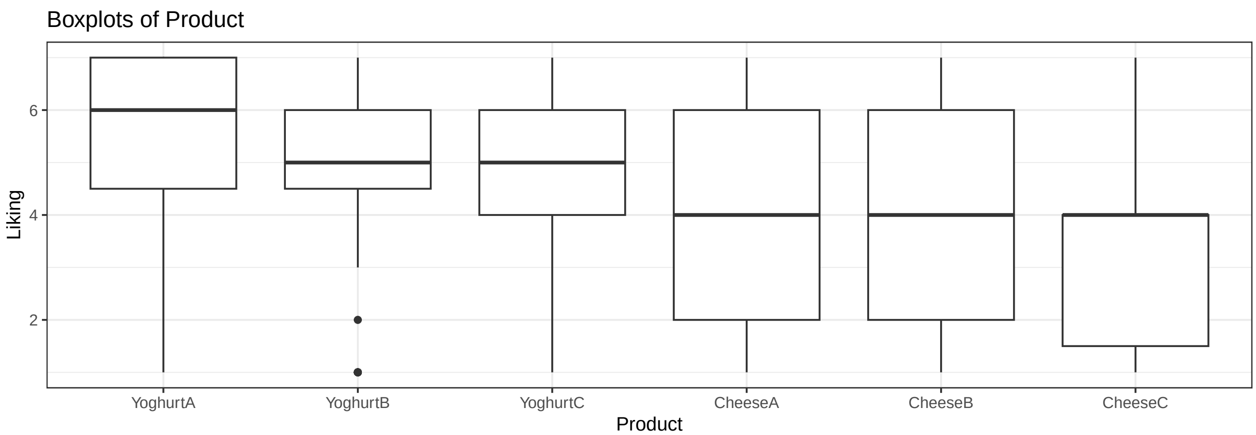
Notice also how the variance reduces as we condition, this is also to be expected as we gain further information.

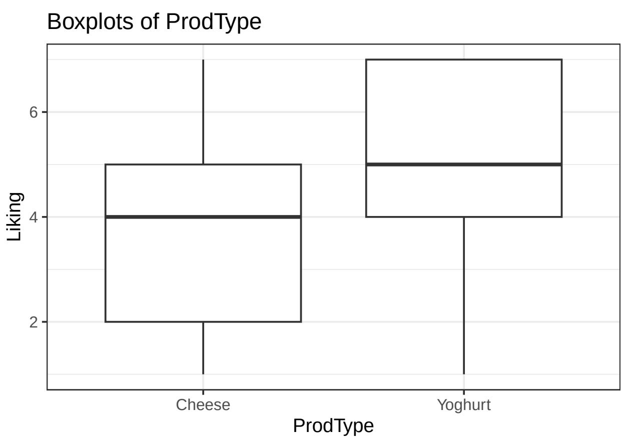
In example 2.5 we showed that the variance matrix of the conditional distribution of Gaussian random variables does not depend on the value of the conditioning variable. Having illustrated that the two random variables $X_1|X_3 = 0$ and $X_2|X_3 = 0$ are independent and with the expected variance, this will also be true for all other values of X_3.

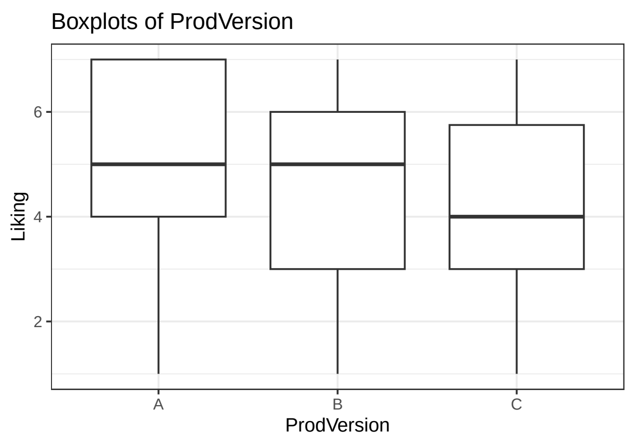
All in all the conditional distribution of $\begin{pmatrix} X_1 \\ X_2 \end{pmatrix} |X_3$ behaves very much as expected.

Part 2

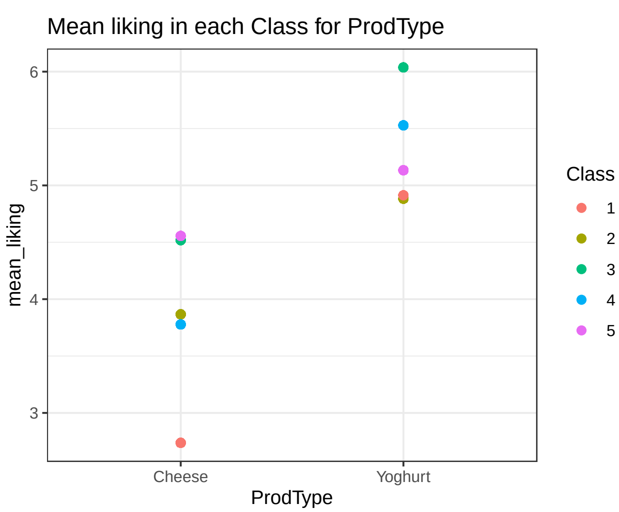
We start out by visualizing the data. We first simply plot boxplots for each of the different products.

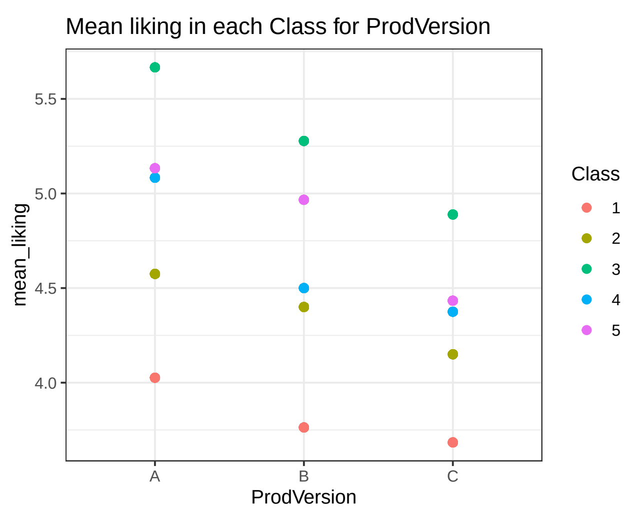




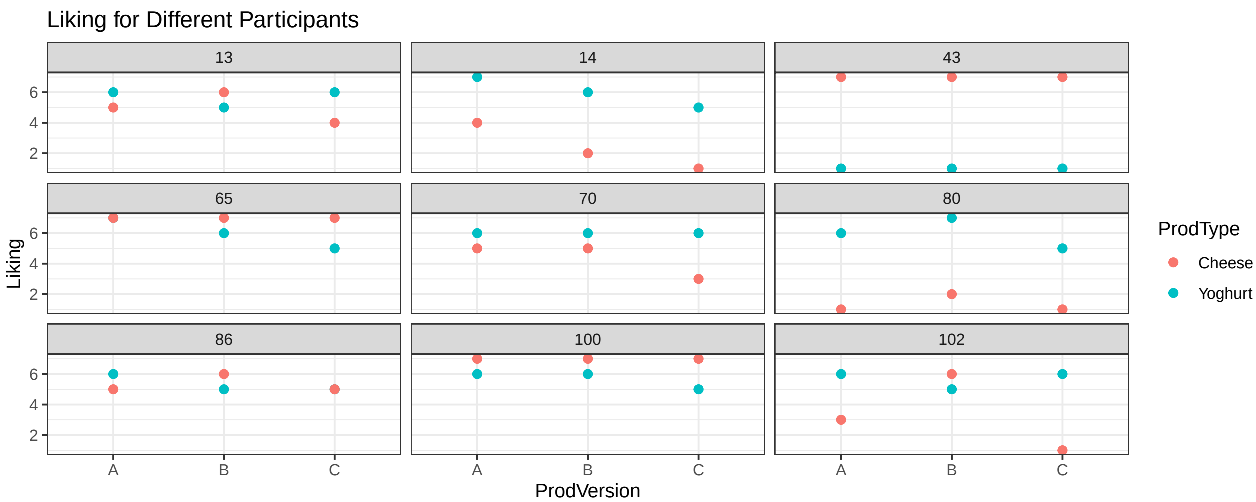


To visualize if there could possibly be a difference in overall liking based on `Class` we calculate the average liking in each Class for both `Product`, `ProdType` and `ProdVersion` and plot them.





Based on the `ProdVersion`-plot it definitely seems that there might be a difference in the overall liking of the products based on `Class`. We are also interested in visualizing any potential effect of the different students on the liking of the products. So we draw 9 random participants and plot their `Liking` of the different product versions and colored according to the type of product.



Here we can see that there indeed does seem to be variations between the overall preferences of the participants, both in terms of overall rating, but also how the liking is linked to the different product types.

1.

Let Y_{ijk} define the response of participant j in class k testing product i. The first model is then defined by

$$Y_{ijk} = \beta_0 + B_j^P + B_k^C + \beta_i + \epsilon_{ijk}$$

where β_0 is the global intercept corresponding to `ProductYoghurtA` and β_i for $i \in \{ProductYoghurtA, ProductYoghurtB, Prod$ describes the difference between the global intercept and each other product. Hence there is no $\beta_{ProductYoghurtA}$ in the model as it is included in β_0. $B_j^{participant} \overset{i.i.d}{\sim} \mathcal{N}(0, \tau_P^2 I)$ is the random parameter of participant $j = 1, ..., 75$ and $B_k^C \overset{i.i.d}{\sim} \mathcal{N}(0, \tau_C^2 I)$ is the random parameter of class $k = 1, ..., 5$. Finally, $\epsilon_{ijk} \overset{i.i.d}{\sim} \mathcal{N}(0, \sigma^2)$ is the residual for participant j in class k, testing product i.

We model participant and class as random effects because these variables are random samples from a larger population and we are as such not interested in these specific variables, only the variance they add to the model. We model `Product` as fixed effect because we want to estimate the effect of the different products the liking of the product by the children.

2.

The formula for the correlation for two random variables X and Y is $\frac{Cov(X,Y)}{\sqrt{(VY \cdot VY)}}$. By the independence of the random variables in the statistical model for `fit1` we get that $VY_{ijk} = \tau_{\text{par}}^2 + \tau_{\text{class}}^2 + \sigma^2$. for all i, j and k. We now consider the two different cases:

If we look at the correlation between two observations for the same participants Y_{ijk} and Y_{ljk}, we have independence between all random variables in the statistical model, except for B_j^{par} and B_k^{class}, which are not independent of themselves. We can use this alongside the bilinear properties of the covariance to see:

$$Cov(Y_{ijk}, Y_{ljk}) = Cov(B_j^{\text{par}}, B_j^{\text{par}}) + Cov(B_k^{\text{class}}, B_k^{\text{class}}) = V(B_j^{\text{par}}) + V(B_k^{\text{class}}) = \tau_{\text{par}}^2 + \tau_{\text{class}}^2$$

Thus we get that $cor(Y_{ijk}, Y_{ljk}) = \frac{\tau_{\text{par}}^2 + \tau_{\text{class}}^2}{\tau_{\text{par}}^2 + \tau_{\text{class}}^2 + \sigma^2}$ for observations from the same participant.

If we now look at the correlation between observations from the same class, but not the same participant, we now have independence between all random variables in the model except for B_k^{class}. So by a similar argument to that above we get:

$$cor(Y_{ijk}, Y_{lpk}) = \frac{\tau_{\text{class}}^2}{\tau_{\text{par}}^2 + \tau_{\text{class}}^2 + \sigma^2}$$

3.

The factor `Product` is the interaction of the two factors `ProdVersion` and `ProdType`, therefore the subspace spanned by `ProdVersion` and `ProdType` is included in the subspace spanned by `Product`, and fit2 is thus a submodel of fit1. In other words if we know the `Product` we also know the `ProdVersion` and `ProdType`.

In fit1 we estimate 6 different fixed effects parameters, 1 intercept parameter, and then 5 additional parameters for each additional interaction level between `ProdVersion` and `ProdType`. In fit2 we estimate 4 fixed effect parameters, 1 intercept parameter, 2 for each additional `ProdVersion` level and 1 for the last level of `ProdType`. We assume no interaction effects between the two factors `ProdVersion` and `ProdType` in fit2.

Letting L_0 denote the subspace of $\mathbb{R}^n$ spanned by the model matrix from fit2 and L_X denote the subspace of $\mathbb{R}^n$ spanned by the model matrix from fit1, we can test the hypothesis of $EY \in L_0 \subseteq L_X$ with the likelihood ratio statistic. The test relies on asymptotic results which we use without further arguments. We perform the test by use of the anova command:

```
anova(fit1,fit2)
```

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

## Data: likingdata
## Models:
## fit2: Liking ~ ProdVersion + ProdType + (1 | Participant) + (1 | Class)
## fit1: Liking ~ Product + (1 | Participant) + (1 | Class)
##      npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## fit2    7 1777.8 1806.6 -881.91   1763.8
## fit1    9 1781.1 1818.1 -881.56   1763.1 0.7031  2     0.7036
```

With a significance level of 0.05 we can most certainly not reject the null hypothesis, and we can conclude that the interaction factor `product` does not improve the model fit significantly.

4.

To test whether the children like all three versions of the product equally well, we can check that none of the fixed effects are significantly different from each other. That is, we check if `ProdVersion` or `ProdType` are significant in the model, as this would suggest, that the children do not like all three versions equally well. To sum up, we test the two hypotheses: $H_{01} : \beta_{ProdVersion} = 0$ and $H_{02} : \beta_{ProdType} = 0$. We test both of these hypotheses using the `drop1()` function with `test = "Chisq"`:

```
drop1(fit2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Liking ~ ProdVersion + ProdType + (1 | Participant) + (1 | Class)
##             npar    AIC    LRT Pr(Chi)
## <none>           1777.8
## ProdVersion    2 1782.9  9.051 0.01083 *
## ProdType       1 1856.5 80.707 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We get a p-value of `0.011` for `ProdVersion` and a p-value of `< 2e-16` for `ProdType`, so on a 5% significance level, we reject both null hypotheses. This means, that there is evidence that the children do not like all three versions equally well and that there is evidence that the children do not like cheese and yoghurt equally well. We should keep in mind, that the chisquare test is an asymptotic test, and we do not know if the asymptotics have set in, so we should be careful with the results, especially for `ProdVersion` as this is only borderline significant.

Having determined that the children's preferences differ between product versions and product types, we can also examine in what way. From the model coefficients, we see evidence that the children like yoghurt better than cheese. To check which product version the children like better, we determine the 95%-profile likelihood confidence interval for the model parameters:

```
confint(fit2, oldNames = FALSE)
```

```
## Computing profile confidence intervals ...
```

```
##                                  2.5 %      97.5 %
## sd_(Intercept)|Participant   0.6595997  1.11693070
## sd_(Intercept)|Class         0.0000000  1.00530558
## sigma                        1.4591641  1.68384627
## (Intercept)                  3.5917611  4.70819767
## ProdVersionB                -0.6417187  0.06838533
## ProdVersionC                -0.9017187 -0.19161467
## ProdTypeYoghurt              1.1101013  1.68989874
```

The children seem to like `ProdVersionA` better than `ProdVersionC` (CI for `ProdVersionC` does not include 0), but there is not strong evidence that they like `ProdVersionA` over `ProdVersionB` (CI for `ProdVersionB` includes 0). To investigate if the children like `ProdVersionB` better than `ProdVersionC`, we refit the model with `ProdVersionB` as the reference level and determine the 95%-profile likelihood confidence intervals in this parametrization:

```
relevelfit <- lmer(Liking ~ relevel(ProdVersion, ref = 2) + ProdType + (1 | Participant) + (1 | Class),
confint(relevelfit, oldNames = FALSE)
```

```
## Computing profile confidence intervals ...
```

```
##                                        2.5 %    97.5 %
## sd_(Intercept)|Participant        0.65959969 1.1169307
## sd_(Intercept)|Class              0.00000000 1.0053055
## sigma                             1.45916409 1.6838463
## (Intercept)                       3.30509444 4.4215310
## relevel(ProdVersion, ref = 2)A -0.06838533 0.6417187
## relevel(ProdVersion, ref = 2)C -0.61505200 0.0950520
## ProdTypeYoghurt                   1.11010126 1.6898987
```

From the confidence intervals we see no strong evidence that the children like `ProductVersionB` better than `ProductVersionC`. To sum up: On a 95% significance level the children seem to like `ProductVersionA` better than `ProductVersionC`, but there is not enough evidence that the children like `ProductVersionA` better than `ProductVersionB` or `ProductVersionB` better than `ProductVersionC`, according to this model.

5.

We use the code from the hint to run 2000 simulations from `fit2`. We first extract the modelmatrices X and Z and the parameterestimates for $\beta, \tau^2_{\text{par}}, \tau^2_{\text{classr}}$ and σ^2. We then create an empty 3×2000 matrix to store the simulations of $\hat{\delta}$ and the corresponding Wald confidence bands. Then we fill out the entries of the matrix with a for loop. So for each i we simulate values respectively 75, 5 and 450 values from $B^{\text{par}}, B^{\text{class}}$ and ϵ, and use those to create a new set of y-values $y = X\beta + Z(B^{\text{par}} + B^{\text{class}}) + \epsilon$. We then fit a new model specified as `fit2` and calculate corresponding confidence intervals using the Wald-method.

```
library(MASS)
M <- 10

#Extracting parameters and modelmatrices
X <- fit2 %>% model.matrix()
Z <- fit2 %>% getME(name="Z")
```

```r
beta <- fixef(fit2)
tauP <- data.frame(VarCorr(fit2))$sdcor[1]
tauC <- data.frame(VarCorr(fit2))$sdcor[2]
sigma <- data.frame(VarCorr(fit2))$sdcor[3]

#Creating matrix
deltasim <- matrix(NA, M, 3)
#Iteratively simulating delta and confidence intervals
for (i in 1:M)
{
B1 <- mvrnorm(75, 0, tauP)
B2 <- mvrnorm(5, 0, tauC)
eps <- mvrnorm(450, 0, sigma)
B <- c(B1,B2)
y <- X %*% beta + Z %*% B + eps
y <- y %>% as.numeric() # NB. This seems to be necessary
lmm2 <- lmer(y ~ ProdVersion + ProdType + (1|Participant) + (1|Class), data=likingdata)
deltasim[i,1] <- fixef(lmm2)[4]
deltasim[i,2:3] <- (lmm2 %>% confint(method="Wald"))[7,]
}

#Changing format to a dataframe and changing names
deltasim <- deltasim %>% data.frame()
names(deltasim) <- c("est","lower","upper")
```

To see if $\hat{\delta}$ is approximately an unbiased estimator of δ, we check whether the mean of $\hat{\delta}$ is approximately equal to δ.

```r
delta <- fixef(fit2)[4]
unname(mean(deltasim$est) - delta)
```

```
## [1] -0.05369987
```

This is close to 0, so $\hat{\delta}$ seems to be fairly unbiased.

To check if we obtain the desired coverage, we simply calculate what percentage of the simulated intervals cover our true δ-vaule.

```r
sum(delta < deltasim$upper & delta > deltasim$lower)/2000
```

```
## [1] 0.0045
```

As we can see, we obtain approximately the desired coverage.

6.

Simulating from the t-distribution

The mean of the t-distribution is already 0. The variance of the t-distribution with ν degrees of freedom is $\frac{\nu}{\nu-2} = \frac{3}{3-2} = 3$. In order to achieve a variance of σ^2 we would therefore need to scale $X \sim t(3)$ with

$$\sigma^2 = V(c \cdot X) = c^2 3 \Leftrightarrow c = \frac{\sigma}{\sqrt{3}}$$

We define the scaling factors

```r
c_par <- tauP / sqrt(3)
c_class <- tauC / sqrt(3)
c_eps <- sigma / sqrt(3)
```

We modify the simulation from question 5 to draw from the t-distribution. The variables drawn are scaled by the scaling factors defined above.

```
M <- 10
n_eps <- nrow(likingdata)
n_par <- unique(likingdata$Participant) |> length()
n_class <- unique(likingdata$Class) |> length()

X <- fit2 |> model.matrix()
Z <- getME(fit2, "Z")
beta <- (summary(fit2) |> coef())[,1]
tauP <- data.frame(VarCorr(fit2))[1,5]
tauC <- data.frame(VarCorr(fit2))[2,5]
sigma <- data.frame(VarCorr(fit2))[3,5]
deltasim2 <- matrix(NA,M,3)

for (i in 1:M){
  B1 <- rt(n = n_par, df = 3) * c_par
  B2 <- rt(n = n_class, df = 3) * c_class
  eps <- rt(n = n_eps, df = 3) * c_eps
  B <- c(B1,B2)
  y <- X %*% beta + Z %*% B + eps
  y <- y |> as.numeric() # NB. This seems to be necessary
  lmm2 <- lmer(y ~ ProdVersion + ProdType + (1|Participant) + (1|Class), data=likingdata)
  deltasim2[i,1] <- fixef(lmm2)[4]
  deltasim2[i,2:3] <- (lmm2 |> confint(method="Wald"))[7,]
}

deltasim2 <- deltasim2 |> data.frame()
names(deltasim2) <- c("est","lower","upper")
```

We calculate the bias:

```
mean(deltasim2$est - fixef(fit2)[4]) |> knitr::kable(col.names = " ")
```

-0.0381201

And the coverage:

```
mean(deltasim2$lower <= fixef(fit2)[4] & fixef(fit2)[4] <= deltasim2$upper) |> knitr::kable(col.names =
```

1

The estimates are still practically unbiased and the confidence intervals achieve accurate coverage.

Simulating from the exponential distribution

The mean of an exponentially distributed random variable X with rate equal to 1, is $E(X) = 1$. And the variance of an is $\frac{1}{\lambda^2} = 1$. In order to achieve a mean of 0 and a variance of σ^2 we would therefore need to shift and scale $X \sim exp(1)$ with

$$\sigma^2 = V(c \cdot X - k) = c^2 \Leftrightarrow c = \sigma$$

and

$$0 = E(\sigma X - k) = \sigma - k \Leftrightarrow k = \sigma$$

We define the shift and scaling constants

```
c_par <- tauP
c_class <- tauC
c_eps <- sigma
```

```
deltasim3 <- matrix(NA,M,3)

for (i in 1:M){
  B1 <- rexp(n = n_par, rate = 1) * c_par - c_par
  B2 <- rexp(n = n_class, rate = 1) * c_class -  c_class
  eps <- rexp(n = n_eps, rate = 1) * c_eps - c_eps
  B <- c(B1,B2)
  y <- X %*% beta + Z %*% B + eps
  y <- y |> as.numeric() # NB. This seems to be necessary
  lmm2 <- lmer(y ~ ProdVersion + ProdType + (1|Participant) + (1|Class), data=likingdata)
  deltasim3[i,1] <- fixef(lmm2)[4]
  deltasim3[i,2:3] <- (lmm2 |> confint(method="Wald"))[7,]
}

deltasim3 <- deltasim3 |> data.frame()
names(deltasim3) <- c("est","lower","upper")
```

We calculate the bias:

```
mean(deltasim3$est - fixef(fit2)[4]) |> knitr::kable(col.names = " ")
```

-0.0520435

And the coverage:

```
mean(deltasim3$lower <= fixef(fit2)[4] & fixef(fit2)[4] <= deltasim3$upper) |> knitr::kable(col.names =
```

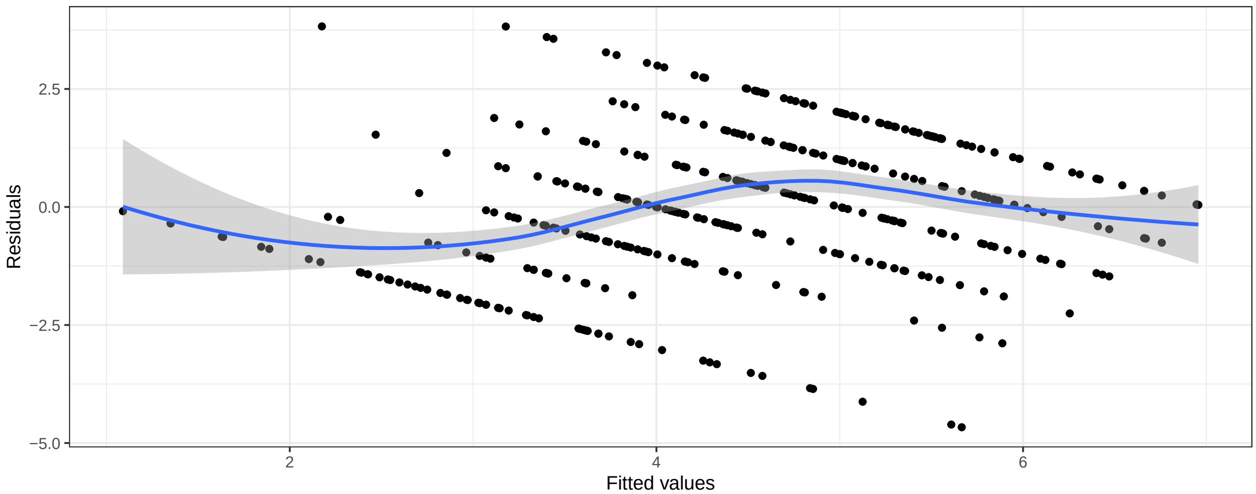
1

The estimates are still almost unbiased and the confidence achieve accurate coverage. We can conclude that the model estimates and confidence intervals are not too sensitive to the type of distribution as long as the mean and variance is correctly specified.

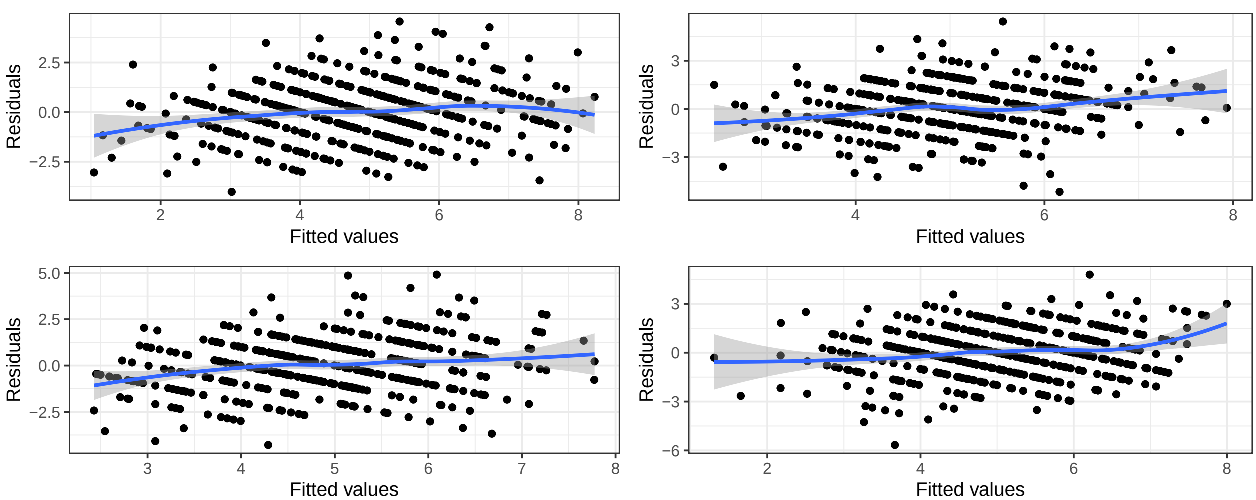
plot evt. histogrammer

7.

We proceed to carry out model validaiton for `fit2`. We follow the procedure given in chapter 5 of the lecture notes on mixed models. We start with a residual plot:

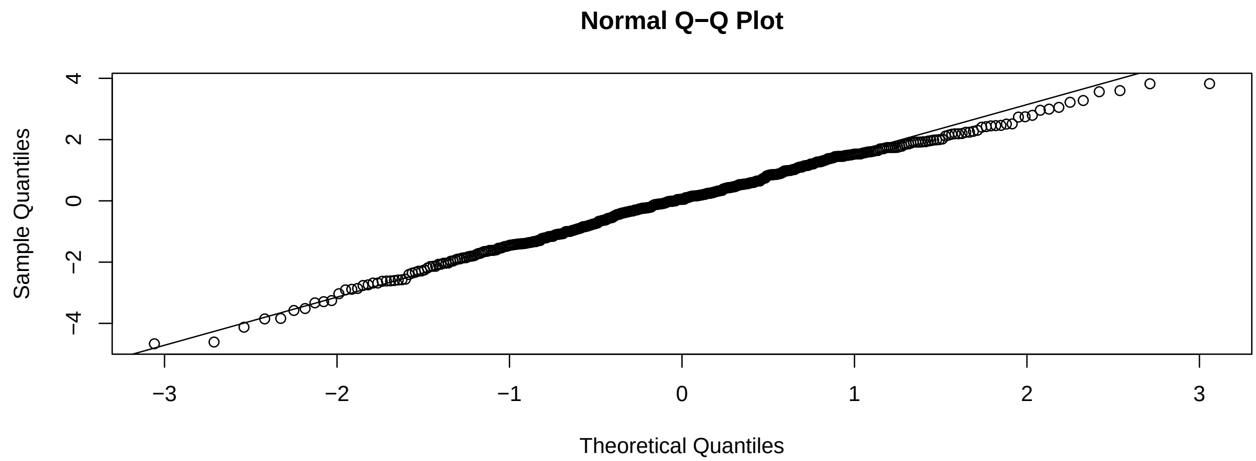


We may be tempted to conclude that the residuals display an alarming pattern. We should however keep in mind, that the response is discrete while the fitted values are not. Hence, the lines in the plot, are in fact to be expected. In particular, for each response value, $a = 1, ..., 7$, we have a linear relationship between the fitted values and the residuals $Resdiual = a - Fitted$. The line fitted with `geom_smooth` suggests, that the residuals have mean around zero, and display no concerning trend. We run a few simulations to check the residual plot:



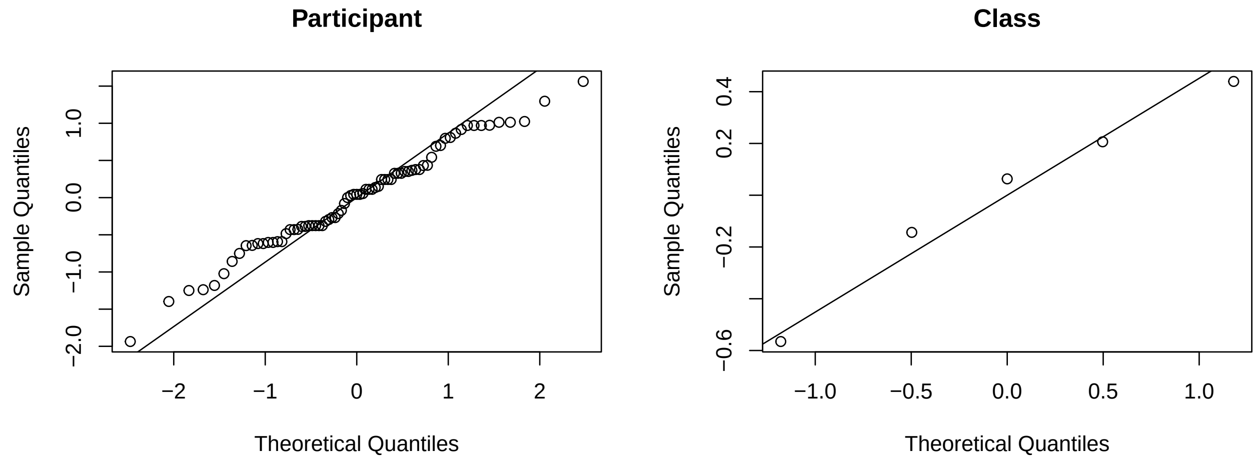
Note, we have discretized the response in the simulations to get a more fair picture of the residual. We have no other restrictions on the predictions, so the model simulates responses outside the range 1 to 7. This gives more lines that the original residual plot. But beside these facts, the residual plots for the simulations resemble the residual plot for the original model. Hence, it seems reasonable to conclude that the model captures the mean structure of the data.

We proceed to check normality of the residuals with a qq-plot:



The qq-plot shows that the residuals to a large extent are normal. There are some issues in the upper tail suggesting that the distribution of the residuals may be slightly left-skewed, so they are not perfectly normal. This is not a major concern though, as the assumption of normality is secondary for the validity of the model, as we also saw in the simulations in the previous question.

We finally inspect the predicted random effects. As we have 75 random effects for participants, it makes sense to make a qq-plot for this random effect. With only 5 classes we may argue that a qq-plot for this random effect is less informative, but for completeness we plot this as well.



The qq-plot to the left suggests that the random effects for participants are not perfectly normally distributed. Again this is not a major concern, as the assumption of normality is secondary for the validity of the model, and as we saw in the simulations in the previous question, the model is robust to deviations from normality. It is difficult to draw conclusions from the qq-plot to the right due to the few classes, but there are no immediate concerns. To sum up, we find the model does a decent job in describing the data.

8.

In order to examine how discretization of the response affects the LMM-based estimator for δ, we simulate from the fit2 model, discretize the simulations by using the `round` function, fit a model on the simulated discretized data and extract the estimates and the CI boundaries.

```
deltasim4 <- matrix(NA,M,3)

for (i in 1:M){
  y <- simulate(fit2)$sim_1 |> round() # evt. put alle forudsigelser større end 7 til 7, er det derfor
```

```r
  lmm2 <- lmer(y ~ ProdVersion + ProdType + (1|Participant) + (1|Class), data=likingdata)
  deltasim4[i,1] <- fixef(lmm2)[4]
  deltasim4[i,2:3] <- (lmm2 |> confint(method="Wald"))[7,]
}

deltasim4 <- deltasim4 |> data.frame()
names(deltasim4) <- c("est","lower","upper")
```

We calculate the bias:

```r
mean(deltasim4$est - fixef(fit2)[4]) |> knitr::kable(col.names = " ")
```

0.028

And coverage:

```r
mean(deltasim4$lower <= fixef(fit2)[4] & fixef(fit2)[4] <= deltasim4$upper) |> knitr::kable(col.names =
```

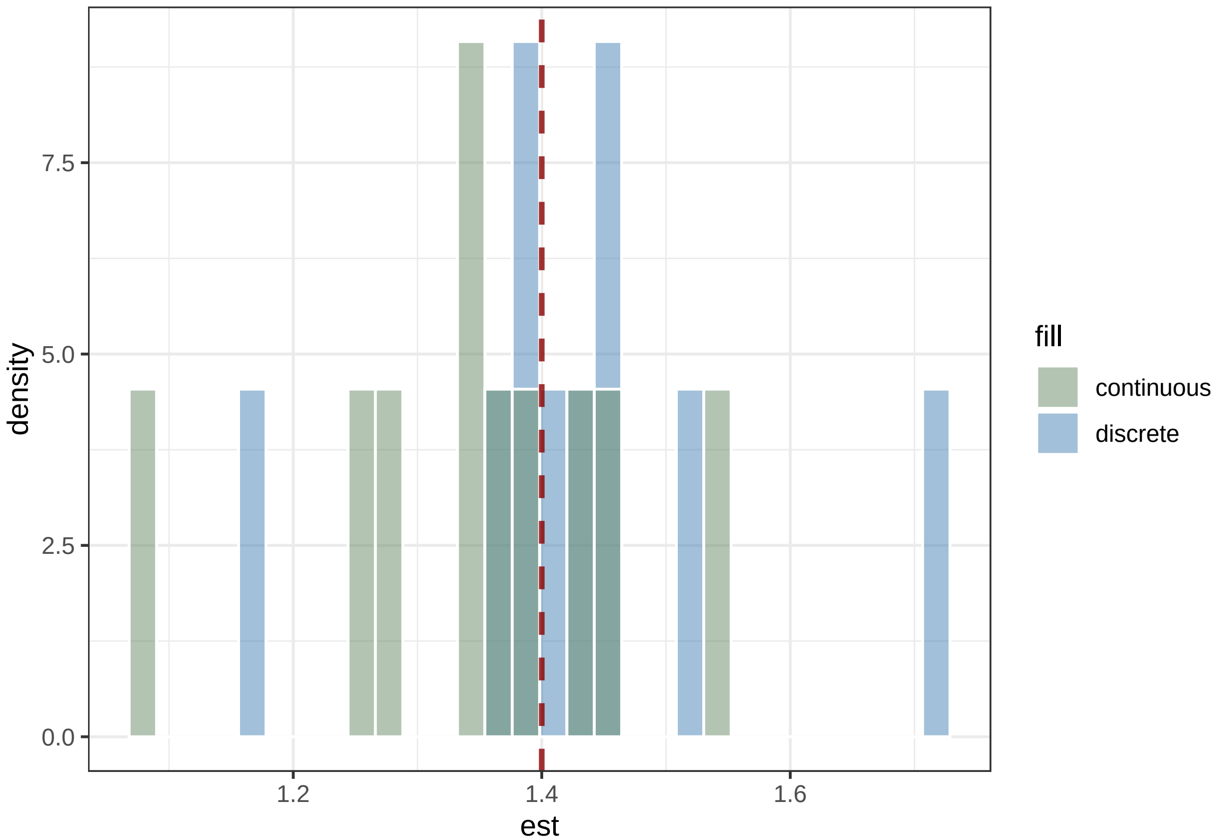
1

So we still obtain the desired coverage and it seems that $\hat{\delta}$ is still an unbiased estimator, no matter whether we discretize the predictor-variables or not.

To further investigate whether the two estimators behave the same, we plot a histogram of their distributions.

```r
data.frame(deltasim4) %>%
  ggplot() +
  geom_histogram(aes(x = est, y = ..density.., fill = "discrete"),
                 color = "white", alpha = 0.5, bins = 30) +
  geom_histogram(data = data.frame(deltasim),
                 aes(x = est, y = ..density.., fill = "continuous"),
                 color = "white", alpha = 0.5, bins = 30) +
  geom_vline(xintercept = fixef(fit2)[4],
             color = "darkred", linetype = "dashed", size = 1, alpha = 0.8) +
  scale_fill_manual(values = c("discrete" = "steelblue", "continuous" = "darkseagreen4"))
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



Their distributions seem fairly similar as well. Although the one without discretization has smaller variance and is thus slightly more peaked. But overall it seems that both methods provide descent estimators of δ.