

RMET original vs revised 5-20-2019

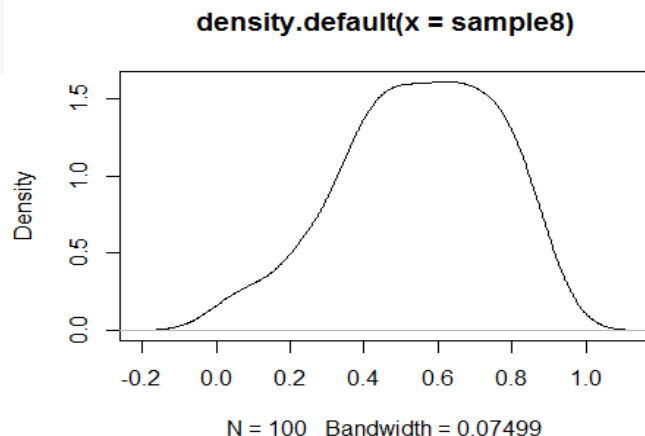
Analysis of data from original RMET:

```
library(tidyverse)
library(tibble)
library(readxl)
library(pastecs)
library(forecast)
library(car)
library(compute.es)
library(effects)
library(multcomp)
library(lsmmeans)
library(stats)
library(nlme)

RMET_orig <- read_excel("RMET_orig.xlsx",
  col_types = c("numeric", "numeric", "numeric", "numeric", "text", "numeric",
    "numeric", "numeric", "numeric", "text", "numeric", "text", "numeric", "text",
    "text", "text", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "num
    eric"), na = "NA")

RMET_1 <- RMET_orig %>%
  mutate(acc2 = acc_pall_sall^2)

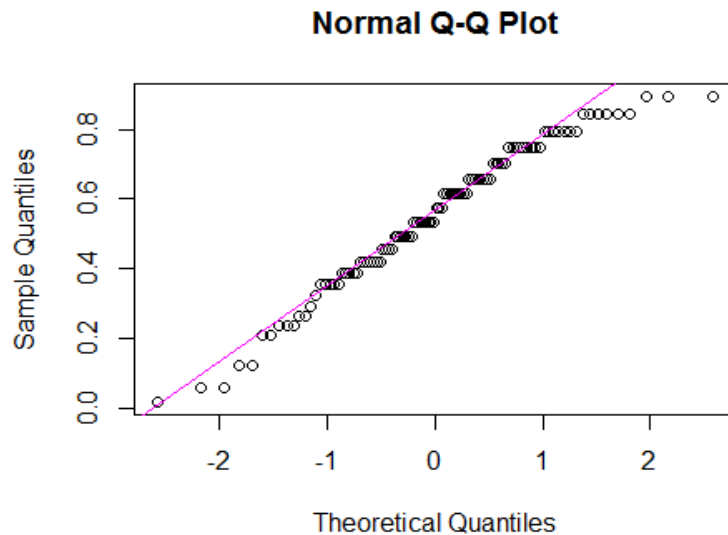
sample8 <- sample(RMET_1$acc2, 100)
plot(density(sample8))
```



```
shapiro.test(sample8)

##
##  Shapiro-Wilk normality test
##
## data:  sample8
## W = 0.96902, p-value = 0.01861

qqnorm(sample8);qqline(sample8, col = 6)
```

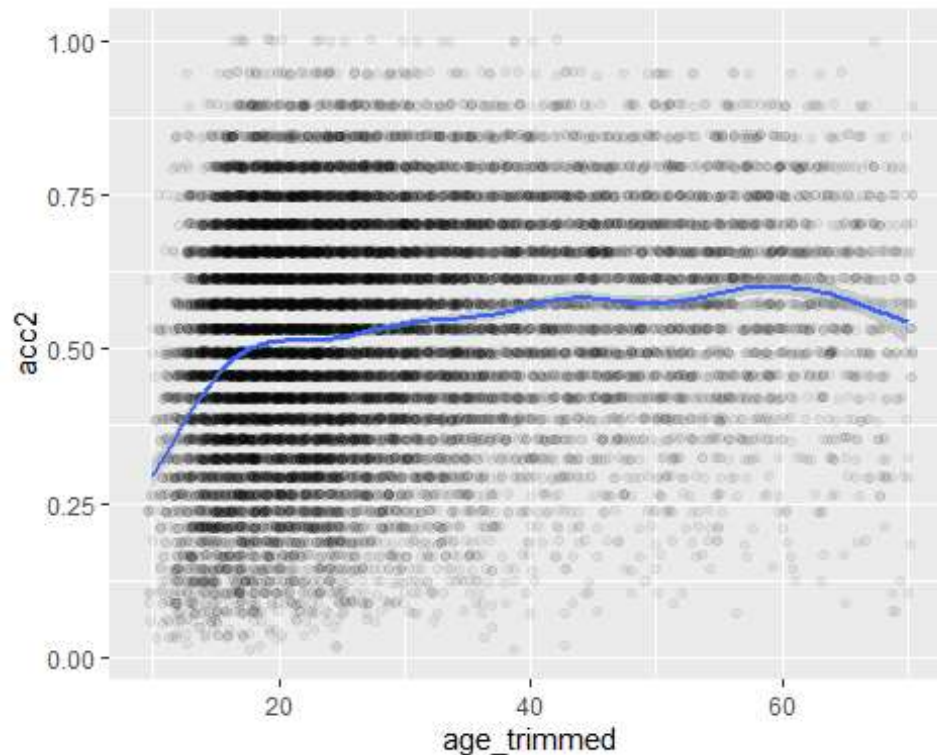


Note: tried checking the goodness-of-fit to a normal distribution by calculating the Vasicek estimator of Shannon entropy (package `vsgoftest`, function `vs.test`); this is the test recommended by Noughabi and Arghami (2011; see below for citation). However, that test requires that there not be ties (I assume this means multiple data points with the exact same value), and the test could not be performed. Noughabi and Arghami (2011) found that, for a data set bounded by (0,1), the Shapiro-Wilk test has more power than any test of normality other than Vasicek's.

Noughabi, H. A., & Arghami, N. R. (2011). Monte Carlo comparison of seven normality tests. *Journal of Statistical Computation and Simulation*, 81(8), 965-972.

```
p <- RMET_1 %>%
  ggplot (aes(x = age_trimmed, y = acc2)) +
  geom_point(na.rm = TRUE, alpha = 0.05, position = "jitter") +
  geom_smooth()

p
```



```
RMET_1 <- RMET_1 %>%
  mutate (age2 = ifelse(age_trimmed <=60 & age_trimmed >=20, age_trimmed, NA)
, gender = factor(gender), education = factor(education), Eng_primary = facto
r(Eng_primary), hispanic = factor(hispanic), eth2 = ifelse(ethnicity == 'Euro
pe' & hispanic == 1, 'Hispanic', ethnicity))

RMET_1 <- RMET_1 %>%
  mutate (eth3 = ifelse(eth2 == 'Australia' | ethnicity == 'Americas', NA, et
h2), edu2 = ifelse(education == 1, 2, education))
```

“Hispanic” was split out as an ethnicity separate from non-Hispanic European. Few participants classified themselves as being of American or Australian descent, so these categories were removed. Because of small sample sizes, the first two education classes were also combined into one.

```
library(dplyr)
temp <- RMET_1[complete.cases(RMET_1[,c(8,11,100,101,103, 104)]),] %>%
  group_by(Eng_primary, eth3, edu2, gender) %>%
  summarize (v = var(acc2))

temp2 <- as.data.frame(temp)
```

#from the above code, one of the groups has a variance that is 7.5x smaller than the variance of another group.

```

mod <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*edu2 + gender*Eng_primary + gender*age2 + gender*eth3 +
  edu2*Eng_primary + edu2*age2 + edu2*eth3 +
  Eng_primary*age2 + Eng_primary*eth3 +
  age2*eth3 +
  gender*edu2*Eng_primary + gender*edu2*age2 + gender*edu2*eth3 +
  gender*Eng_primary*age2 + gender*Eng_primary*eth3 +
  gender*age2*eth3 +
  edu2*Eng_primary*age2 + edu2*Eng_primary*eth3 + edu2*age2*eth3 +
  Eng_primary*age2*eth3, data = RMET_1[complete.cases(RMET_1[,c(8,
11,100,101,103, 104)])], weights = varIdent(form = ~1 | gender*edu2*eth3))

temp <- anova(mod)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][,3]
d_full <- tibble(rownames(temp))
temp1 <- array(round(p.adjust(p, "BH"), 3))
d_full$T1 <- temp1

temp <- Anova(mod, type = 2)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "BH"), 3))
d_full$T2 <- c(0,temp2)

mod <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*eth3 + gender*edu2 +
  edu2*age2 + edu2*eth3 +
  Eng_primary*age2 + Eng_primary*eth3 +
  age2*eth3 +
  gender*edu2*eth3 +
  edu2*age2*eth3, data = RMET_1[complete.cases(RMET_1[,c(8,11,100,
101,103, 104)])], weights = varIdent(form = ~1 | gender*edu2*eth3))

temp <- anova(mod)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][,3]
d_trimmed <- tibble(rownames(temp))
temp1 <- array(round(p.adjust(p, "BH"), 3))
d_trimmed$T1 <- temp1

temp <- Anova(mod, type = 2)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "BH"), 3))
d_trimmed$T2 <- c(0,temp2)

```

#Effects removed, in order of removal, with Type I and II p-values:

```
#gender:edu2:age2 0.657 0.759
#gender:Eng_primary:age2 0.714 0.707
#edu2:Eng_primary:age2 0.227 0.538
#Eng_primary:age2:eth3 0.462 0.449
#gender:edu2:Eng_primary 0.328 0.359
#gender:age2:eth3 0.176 0.269
#edu2:Eng_primary:eth3 0.259 0.270
#gender:Eng_primary:eth3 0.062 0.084
```

```
#edu2:Eng_primary 0.197 0.505
#gender:Eng_primary 0.378 0.300
#gender:age2 0.871 0.202
```

Applying a stricter correction for multiple comparisons:

```
mod <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*eth3 + gender*edu2 +
  edu2*age2 + edu2*eth3 +
  Eng_primary*age2 + Eng_primary*eth3 +
  age2*eth3 +
  gender*edu2*eth3 +
  edu2*age2*eth3, data = RMET_1[complete.cases(RMET_1[,c(8,11,100,
101,103, 104)]),], weights = varIdent(form = ~1 | gender*edu2*eth3))
```

```
temp <- Anova(mod, type = 2)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][3][[1]]
d_trimmed_2 <- tibble(rownames(temp))
d_trimmed_2$Bonferroni <- array(round(p.adjust(p, "bonferroni"), 3))
d_trimmed_2$Holm <- array(round(p.adjust(p, "holm"), 3))
d_trimmed_2$Hochberg <- array(round(p.adjust(p, "hochberg"), 3))
d_trimmed_2$Hommel <- array(round(p.adjust(p, "hommel"), 3))
d_trimmed_2$BH <- array(round(p.adjust(p, "BH"), 3))
d_trimmed_2$BY <- array(round(p.adjust(p, "BY"), 3))
```

```
mod <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*eth3 +
  edu2*age2 + edu2*eth3 +
  age2*eth3 + edu2*age2*eth3, data = RMET_1[complete.cases(RMET_1[
,c(8,11,100,101,103, 104)]),], weights = varIdent(form = ~1 | gender*edu2*eth
3))
```

```
temp <- Anova(mod, type = 2)
prtAnova <- tibble(temp)
```

```

p <- prtAnova[[1]][3][[1]]
d_trimmed_2 <- tibble(rownames(temp))
d_trimmed_2$Holm <- array(round(p.adjust(p, "holm"), 3))

#Eng_primary:eth3 0.120
#Eng_primary:age2 0.132
#gender:edu2:eth3 0.104
#gender:edu2 0.408

mod <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*eth3 +
  edu2*age2 + edu2*eth3 +
  age2*eth3, data = RMET_1[complete.cases(RMET_1[,c(8,11,100,101,1
03, 104)]),], weights = varIdent(form = ~1 | gender*edu2*eth3))

temp <- Anova(mod, type = 2)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][3][[1]]
d_trimmed_2 <- tibble(rownames(temp))
d_trimmed_2$Holm <- array(round(p.adjust(p, "holm"), 3))

# Analysis without accounting for different variances among groups of the ind
ependent variables:

mod3 <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*eth3 +
  edu2*age2 + edu2*eth3 +
  age2*eth3 +
  edu2*age2*eth3, data = RMET_1[complete.cases(RMET_1[,c(8,11,100,
101,103, 104)]),])

temp <- anova(mod3)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][,3]
d_temp <- tibble(rownames(temp))
temp1 <- array(round(p.adjust(p, "holm"), 3))
d_temp$T1 <- temp1

temp <- Anova(mod3, type = 2)
prtAnova <- tibble(temp)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "holm"), 3))
d_temp$T2 <- c(0,temp2)

```

I used an ANCOVA that allows different groups (in this case, each combination of the levels of gender, education, and ethnicity) to have different variances. I started with a “full”

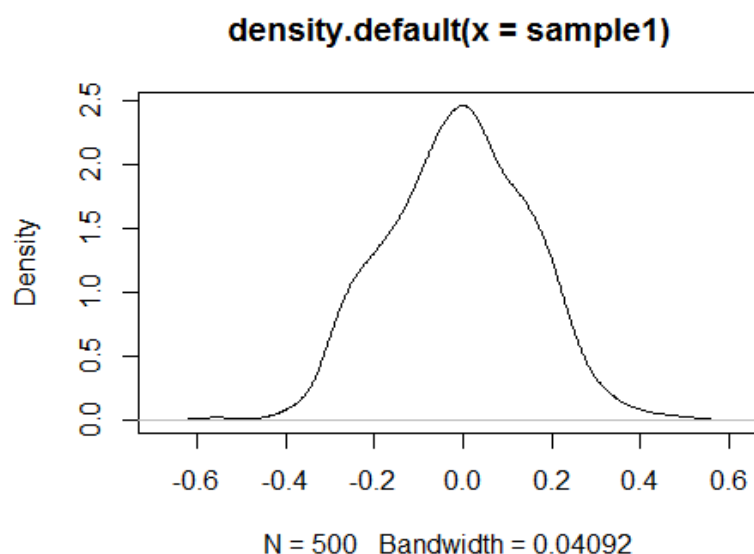
analysis that included all main effects and interactions up to three-way interactions. P-values were initially corrected with a BH correction to account for the number of statistical tests. I removed the interaction with the highest p-value and re-ran the analysis until only significant effects and interactions remained. The interactions and their associated p-values are listed here in the order of their removal.

I switched over to a more conservative Holm correction and removed a few last factors in order to arrive at the final “trimmed” model.

Extracting some of the statistics from the analysis that allows different groups to have different variances has proven to be difficult. Before trying to dig more deeply into that problem, I checked to see if the differences in variances among groups really warrant the more complex model. If groups are created for every possible interaction between gender, eth3, edu2, and Eng_primary, one of the groups has a very low variance, such that the group with the maximum variance has a variance about 7.5x the minimum variance. The rule of thumb is that ANOVA may not be robust to differences of more than 4x.

However, this four-way interaction doesn’t appear in the trimmed model, leading me to question whether these are really the groups whose variances I need to be comparing. I re-ran the analysis without allowing different groups to have different variances (last block of code above) and found that it recovered the same factors and interactions as significant. I interpret this as meaning that the different variances among groups do not compromise the analysis, and I’m going to move forward using the simpler model.

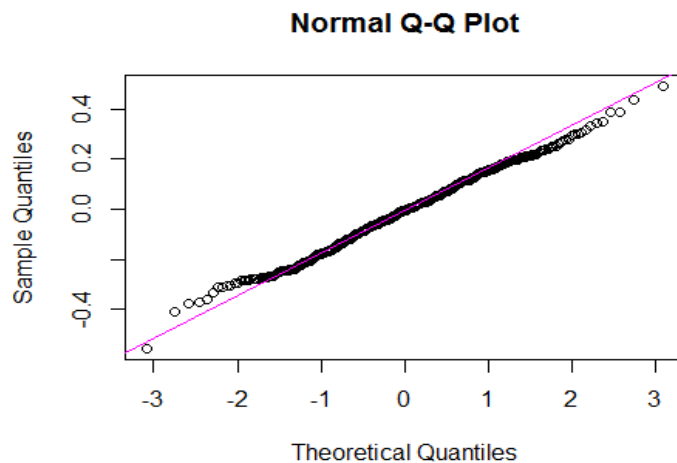
```
rsd <- tibble(resid(mod3))  
colnames(rsd) <- c("residuals")  
  
sample1 <- sample(rsd$residuals, 500)  
plot(density(sample1))
```



```
shapiro.test(sample1)

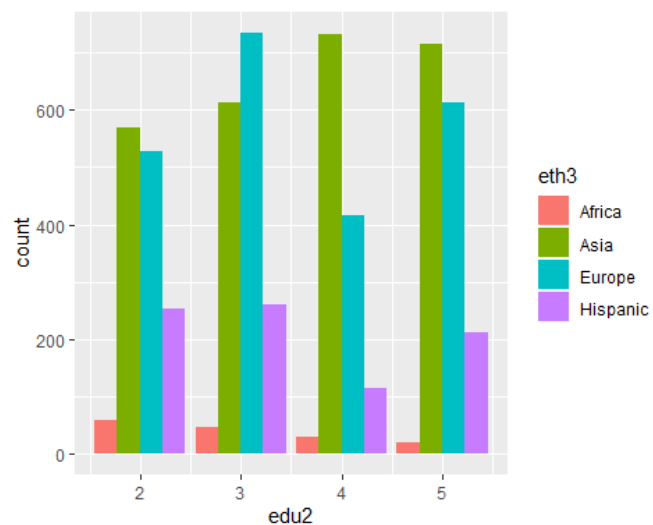
##
##  Shapiro-Wilk normality test
##
## data:  sample1
## W = 0.99599, p-value = 0.2354

qqnorm(sample1);qqline(sample1, col = 6)
```



```
# Sample sizes for ethnicity*education*Eng_primary
```

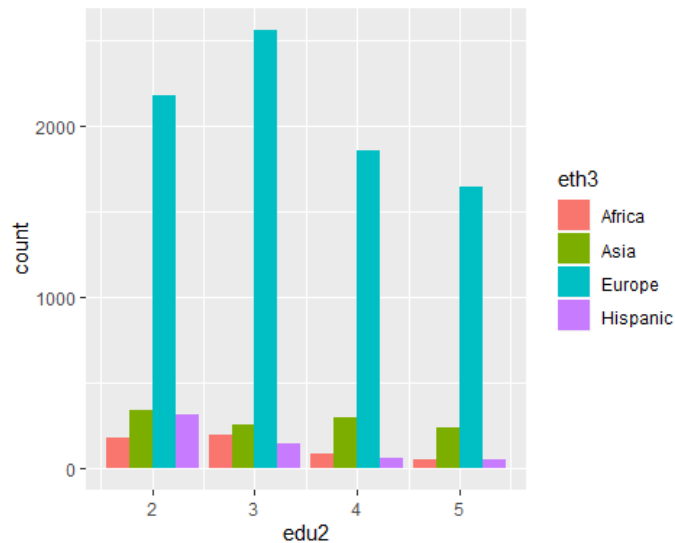
```
RMET_1 %>%
  filter(!is.na(eth3)) %>%
  filter(!is.na(edu2)) %>%
  filter(Eng_primary == '0') %>%
  ggplot() +
  geom_bar(mapping = aes(x = edu2, fill = eth3), position = "dodge")
```




```

RMET_1 %>%
  filter(!is.na(eth3)) %>%
  filter(!is.na(edu2)) %>%
  filter(Eng_primary == '1') %>%
  ggplot() +
  geom_bar(mapping = aes(x = edu2, fill = eth3), position = "dodge")

```

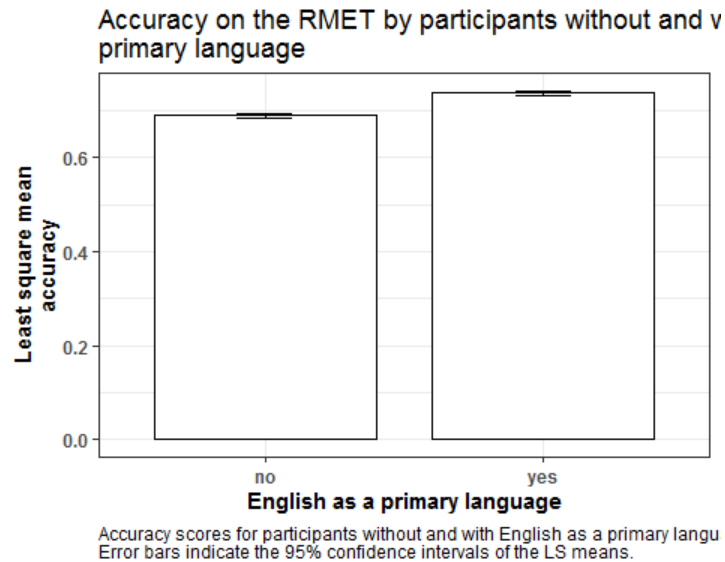


```

#Eng_primary
emm3 <- emmeans(mod3, pairwise ~ Eng_primary, data = RMET_1)

as.data.frame(summary(emm3)$emmean)[c('emmean', 'SE')] %>%
  mutate(levs=c('no', 'yes')) %>%
  ggplot(aes(x = levs, y = emmean^0.5)) +
  geom_bar(stat='identity', color = "black", fill = "white", width = 0.8) +
  geom_errorbar(aes(ymin = (emmean-(1.96*SE))^0.5, ymax = (emmean+(1.96*SE))^
0.5), width = 0.2) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "English as a primary language", y = "Least square mean\naccuracy"
,
        title = "Accuracy on the RMET by participants without and with English
as a\nprimary language",
        caption = "Accuracy scores for participants without and with English
as a primary language. Bars indicate the LS mean.\nError bars indicate the 95
% confidence intervals of the LS means.",
        hjust=0.5)

```



```
#gender*ethnicity
emm5tttest <- emmeans(mod3, pairwise ~ gender*eth3, data = RMET_1)
emm5 <- emmeans(mod3, ~ gender*eth3, data = RMET_1)

CLD5 <- cld(emm5, alpha = 0.05, Letters = letters, adjust="tukey")

temp <- as.data.frame(CLD5) %>%
  mutate(gender = c('male', 'male', 'female', 'female', 'male', 'male', 'female',
                    'female'))

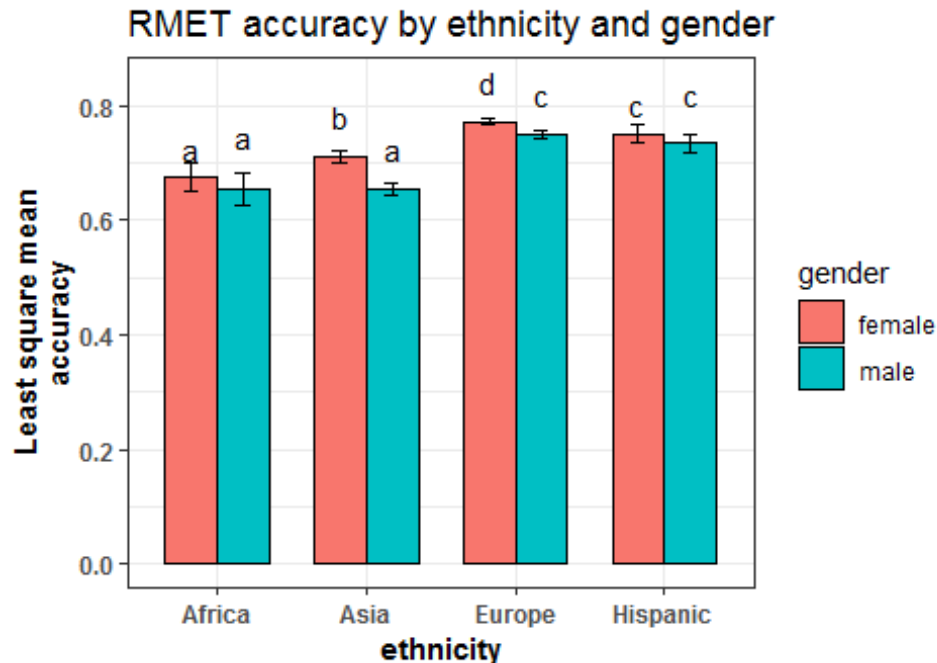
temp$.group = gsub(" ", "", temp$.group)

h <- 0.18
v <- 0.07

pd = position_dodge(0.7)    ### How much to jitter the bars on the plot

ggplot(temp, aes(x = eth3, y = emmean^0.5, fill = gender, label = .group)) +
  geom_bar(stat = "identity", width = 0.7, color = "black", position = pd) +
  geom_errorbar(aes(ymin = lower.CL^0.5, ymax = upper.CL^0.5), width = 0.2, size = 0.7, position = pd) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "ethnicity", y = "Least square mean\naccuracy",
       title = "RMET accuracy by ethnicity and gender",
       caption = "Accuracy scores (squared) for both genders across three ethnic groups. Bars indicate the LS mean.\nError bars indicate the 95% confidence intervals of the LS means. Means sharing a letter are not\nsignificantly different (Tukey-adjusted comparisons).",
       hjust = 0.5) +
```

```
geom_text(nudge_x = c(h, -h, h, -h, -h, h,h, -h),
          nudge_y = c(v,v,v,v,v,v,v,v),
          color = "black")
```

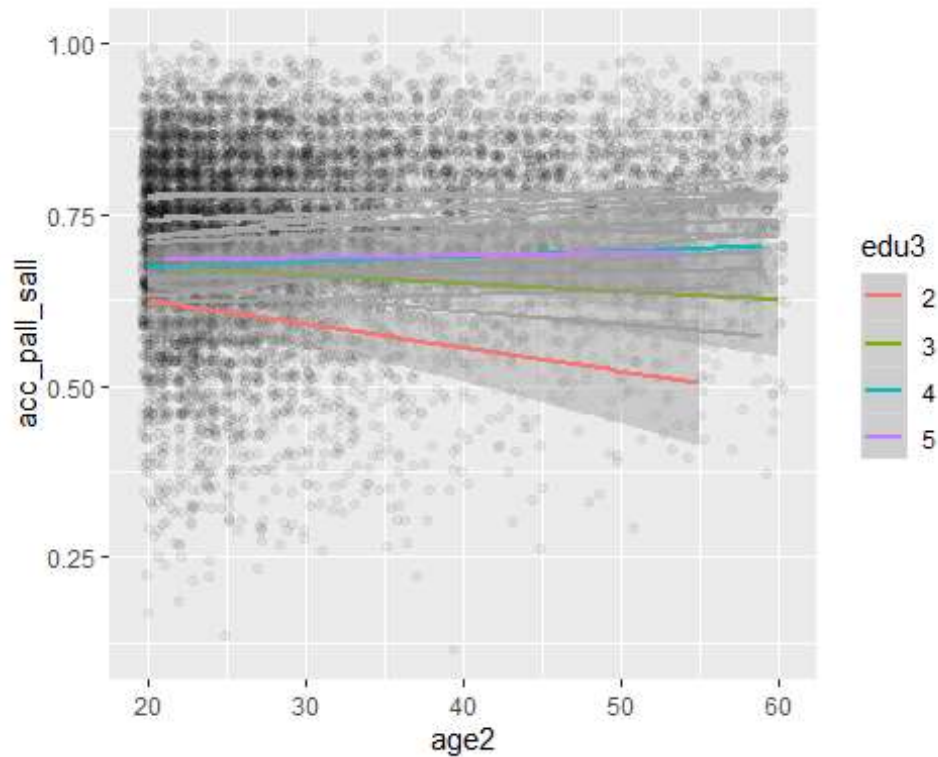


Accuracy scores (squared) for both genders across three ethnic groups. Bar Error bars indicate the 95% confidence intervals of the LS means. Means sh significantly different (Tukey-adjusted comparisons).

*#ethnicity*education*age*

```
RMET_1 <- RMET_1 %>%
  mutate(edu3 = as.factor(edu2))
```

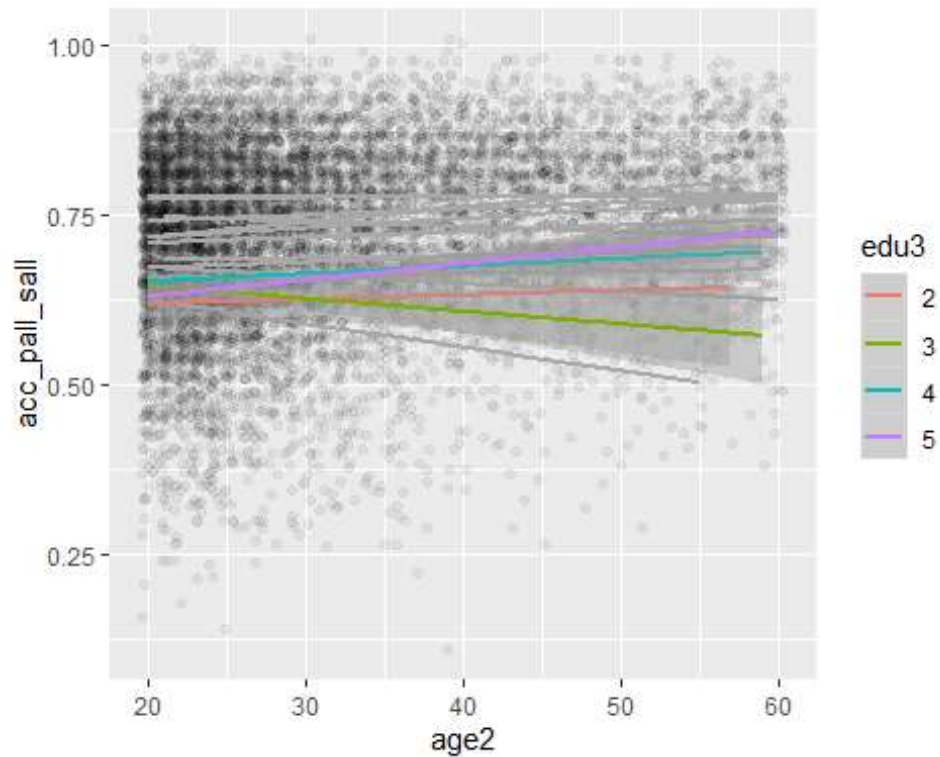
```
RMET_1 %>%
  drop_na(eth3, age2, edu3) %>%
  ggplot(aes(x = age2, y = acc_pall_sall)) +
  geom_point(mapping = aes(), alpha = 0.05, position = "jitter") +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Hispanic" & !is.na(eth3) & !is.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Europe" & !is.na(eth3) & !is.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, ethnicity == "Asia" & !is.na(eth3) & !is.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(color = edu3), method = 'lm', se = TRUE, data = filter(RMET_1, eth3 == "Africa" & !is.na(eth3) & !is.na(age2) & !is.na(edu3)))
```



```

RMET_1 %>%
  drop_na(eth3, age2, edu3) %>%
  ggplot(aes(x = age2, y = acc_pall_sall)) +
  geom_point(mapping = aes(), alpha = 0.05, position = "jitter") +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Hispanic" & !is.na(eth3) & !is.na(
age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Europe" & !is.na(eth3) & !is.na(
age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, ethnicity == "Africa" & !is.na(eth3) & !i
s.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(color = edu3), method = 'lm', se = TRUE, data = f
ilter(RMET_1, eth3 == "Asia" & !is.na(eth3) & !is.na(age2) & !is.na(edu3)))

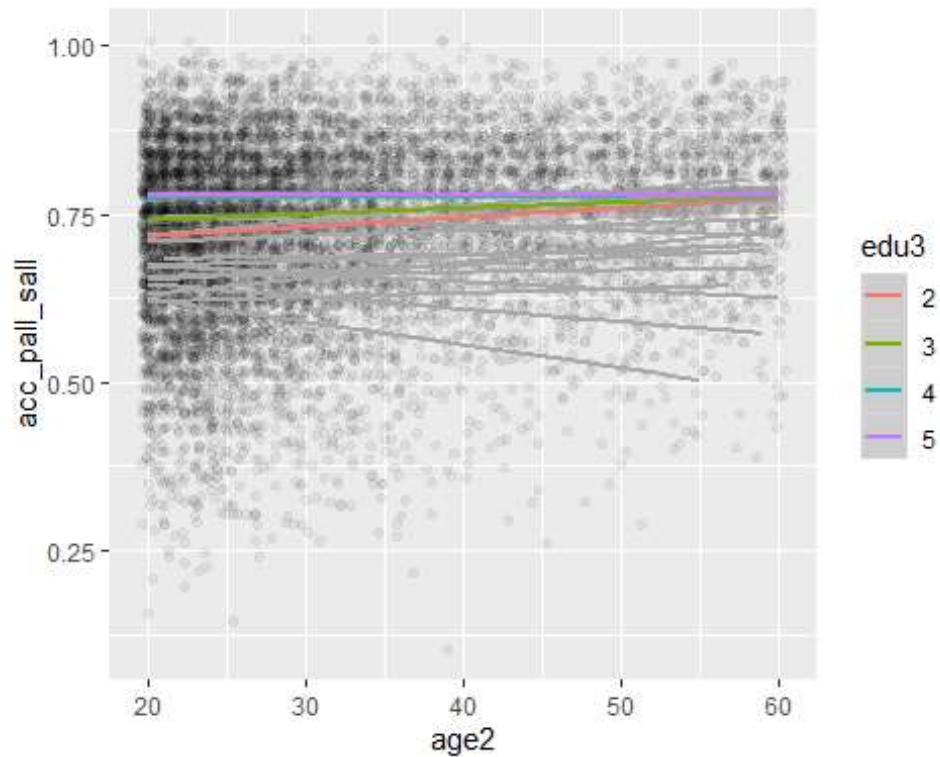
```



```

RMET_1 %>%
  drop_na(eth3, age2, edu3) %>%
  ggplot(aes(x = age2, y = acc_pall_sall)) +
  geom_point(mapping = aes(), alpha = 0.05, position = "jitter") +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Hispanic" & !is.na(eth3) & !is.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Africa" & !is.na(eth3) & !is.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, ethnicity == "Asia" & !is.na(eth3) & !is.na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(color = edu3), method = 'lm', se = TRUE, data = filter(RMET_1, eth3 == "Europe" & !is.na(eth3) & !is.na(age2) & !is.na(edu3)))

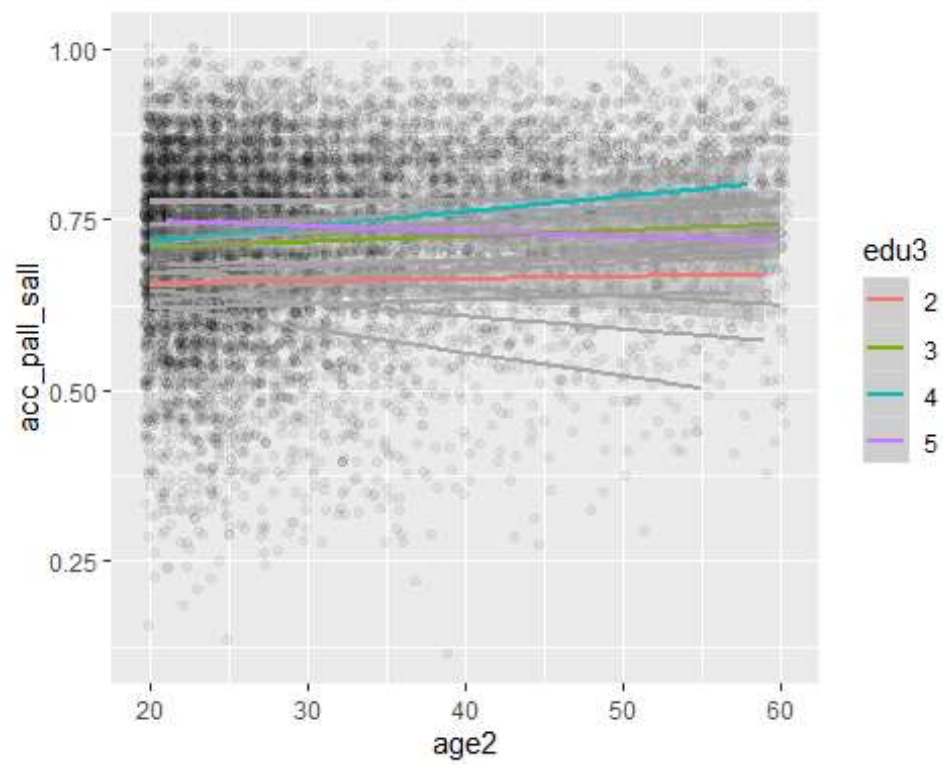
```



```

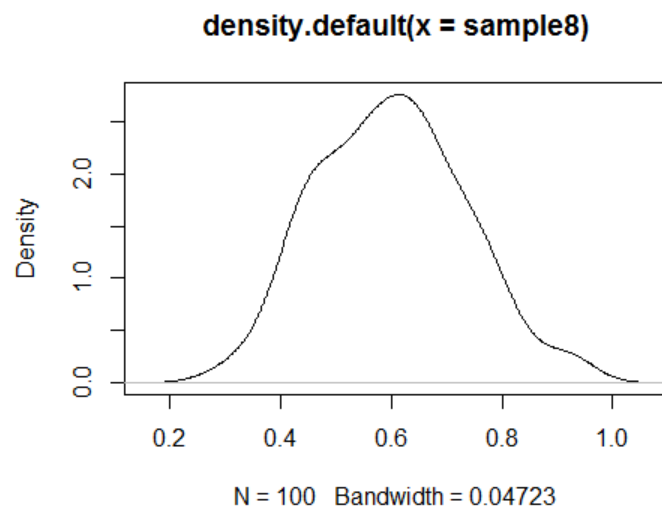
RMET_1 %>%
  drop_na(eth3, age2, edu3) %>%
  ggplot(aes(x = age2, y = acc_pall_sall)) +
  geom_point(mapping = aes(), alpha = 0.05, position = "jitter") +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Africa" & !is.na(eth3) & !is.na(
age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, eth3 == "Europe" & !is.na(eth3) & !is.na(
age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(group = edu2), color = "dark gray", method = 'lm'
, se = FALSE, data = filter(RMET_1, ethnicity == "Asia" & !is.na(eth3) & !is.
na(age2) & !is.na(edu3))) +
  geom_smooth(mapping = aes(color = edu3), method = 'lm', se = TRUE, data = f
ilter(RMET_1, eth3 == "Hispanic" & !is.na(eth3) & !is.na(age2) & !is.na(edu3)
))

```



[illegible][illegible]

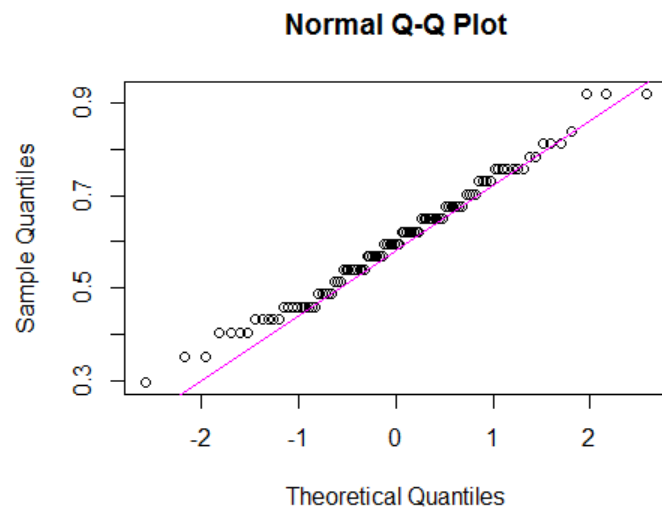
```
sample8 <- sample(RMET2_orig$accuracy, 100)
plot(density(sample8))
```

```
shapiro.test(sample8)

##
##  Shapiro-Wilk normality test
##
## data:  sample8
## W = 0.98534, p-value = 0.3357

qqnorm(sample8);qqline(sample8, col = 6)
```

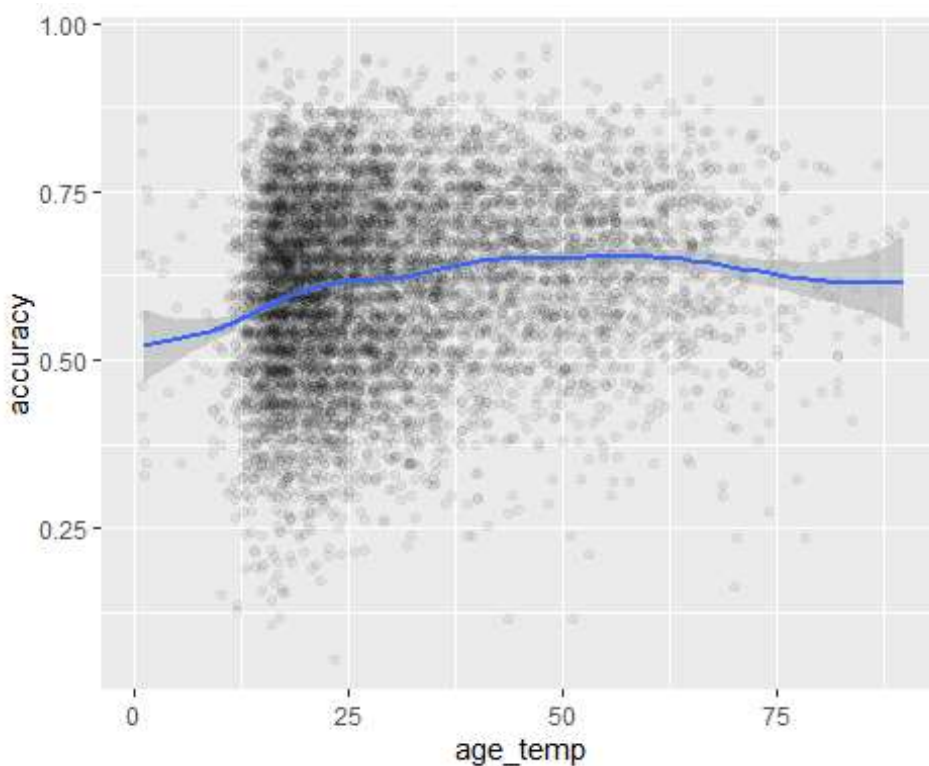


When “accuracy” is squared, as in the data for the original RMET, the Shapiro-Wilk test shows that there’s a departure from normality that borders on statistical significance. In order to keep the analysis comparable to the analysis of the original RMET, I’m going to go

with accuracy-squared as the dependent variable; I suspect that the residuals will wind up normally distributed regardless. (A lot of the problem is a lump of unusually low scores, which may be test runs or partial test attempts that may get filtered out anyway.)

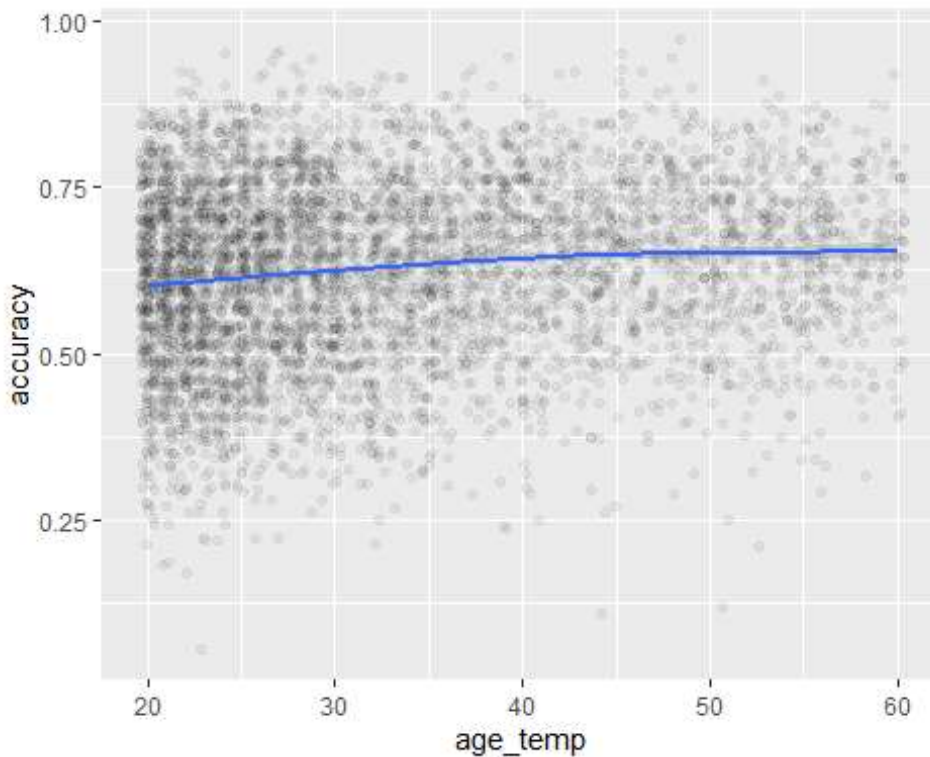
```
p <- RMET2_1 %>%  
  mutate (age_temp = ifelse(age <=90 & age >=0, age, NA)) %>%  
  #mutate (age2 = ifelse(age <=60 & age >=20, age, NA)) %>%  
  ggplot (aes(x = age_temp, y = accuracy)) +  
  geom_point(na.rm = TRUE, alpha = 0.05, position = "jitter") +  
  geom_smooth()
```

p



```
p <- RMET2_1 %>%  
  mutate (age_temp = ifelse(age <=60 & age >=20, age, NA)) %>%  
  #mutate (age2 = ifelse(age <=60 & age >=20, age, NA)) %>%  
  ggplot (aes(x = age_temp, y = accuracy)) +  
  geom_point(na.rm = TRUE, alpha = 0.05, position = "jitter") +  
  geom_smooth()
```

p



```

RMET2_1 <- RMET2_1 %>%
  mutate (age2 = ifelse(age <=60 & age >=20, age, NA), gen2 = factor(gen2), e
du2 = factor(edu2), Eng2 = factor(Eng2), eth3 = ifelse(eth2 == 'Europe' & his
panic == 1, 'Hispanic', eth2)) %>%
  mutate (eth3 = ifelse(eth3 == 'Pacific' | eth3 == 'Americas', NA, eth3))

temp <- RMET2_1[complete.cases(RMET2_1[,c(107,108,110,111,112, 113)]),] %>%
  group_by(Eng2, eth3, edu2, gen2) %>%
  summarize (v = var(acc2))

temp2 <- as.data.frame(temp)
max(temp2$v)/min(temp2$v)

## [1] 7.367078

```

Note that, as with the analysis of the original RMET, there's a group with a variance that is 7.4x that of another group. Going forward with the same process as before: run the analysis with and without allowing different groups to have different variances, and see if it alters the outcome.

```

mod <- gls(acc2 ~
  gen2 + edu2 + Eng2 + age2 + eth3 +
  gen2*edu2 + gen2*eth3 +
  edu2*Eng2 + edu2*eth3 +
  Eng2*eth3 +
  age2*eth3 +
  gen2*edu2*eth3 +

```

```

edu2*Eng2*eth3, data = RMET2_1[complete.cases(RMET2_1[,c(107,108,
110,111,112, 113)])], weights = varIdent(form = ~1 | gen2*edu2*eth3))

tempr <- anova(mod)
prtAnova <- tibble(tempr)
p <- prtAnova[[1]][,3]
d_full_r <- tibble(rownames(tempr))
temp1 <- array(round(p.adjust(p, "BH"), 3))
d_full_r$T1 <- temp1

tempr <- Anova(mod, type = 2)
prtAnova <- tibble(tempr)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "BH"), 3))
d_full_r$T2 <- c(0,temp2)

#factors removed:
#gen2:age2:eth3 0.832 0.986
#gen2:edu2:Eng2 0.908 0.658
#edu2:Eng2:age2 0.992 0.521
#gen2:Eng2:eth3 0.381 0.329
#gen2:edu2:age2 0.425 0.294
#gen2:Eng2:age2 0.284 0.263
#Eng2:age2:eth3 0.103 0.114
#edu2:age2:eth3 0.038 0.051
#edu2:age2 0.517 0.981
#gen2:Eng2 0.180 0.253
#gen2:age2 0.618 0.138
#Eng2:age2 0.010 0.171

mod <- gls(acc2 ~
  gen2 + edu2 + Eng2 + age2 + eth3 +
  edu2*eth3 +
  age2*eth3, data = RMET2_1[complete.cases(RMET2_1[,c(107,108,110,
111,112, 113)])], weights = varIdent(form = ~1 | gen2*edu2*eth3))

tempr <- anova(mod)
prtAnova <- tibble(tempr)
p <- prtAnova[[1]][,3]
d_full_r <- tibble(rownames(tempr))
temp1 <- array(round(p.adjust(p, "holm"), 3))
d_full_r$T1 <- temp1

tempr <- Anova(mod, type = 2)
prtAnova <- tibble(tempr)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "holm"), 3))
d_full_r$T2 <- c(0,temp2)

```

```

#edu2:Eng2:eth3 0.049 0.054
#edu2:Eng2 0.409 1.000
#gen2:edu2:eth3 0.043 0.051
#Eng2:eth3 0.166 0.479
#gen2:edu2 0.086 0.334
#gen2:eth3 0.033 0.077

#Model without allowing different variances for different groups:

mod <- gls(acc2 ~
            gen2 + edu2 + Eng2 + age2 + eth3 +
            gen2*edu2 + gen2*eth3 +
            edu2*eth3 +
            age2*eth3 + gen2*edu2*eth3, data = RMET2_1[complete.cases(RMET2_
1[,c(107,108,110,111,112, 113)])],))

tempr2 <- anova(mod)
prtAnova <- tibble(tempr2)
p <- prtAnova[[1]][,3]
d_full_r2 <- tibble(rownames(tempr2))
temp1 <- array(round(p.adjust(p, "BH"), 3))
d_full_r2$T1 <- temp1

tempr2 <- Anova(mod, type = 2)
prtAnova <- tibble(tempr2)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "BH"), 3))
d_full_r2$T2 <- c(0,temp2)

#factors removed:
#1 gen2:age2:eth3 0.832 0.986 gen2:age2:eth3 0.984 0.979
#2 gen2:edu2:Eng2 0.908 0.658 gen2:edu2:Eng2 0.879 0.668
#3 edu2:Eng2:age2 0.992 0.521 edu2:Eng2:age2 0.994 0.662
#4 gen2:Eng2:eth3 0.381 0.329
#4 gen2:edu2:age2 0.474 0.349
#5 gen2:edu2:age2 0.425 0.294
#5 gen2:Eng2:eth3 0.326 0.282
#6 gen2:Eng2:age2 0.284 0.263 gen2:Eng2:age2 0.298 0.241
#7 Eng2:age2:eth3 0.103 0.114 Eng2:age2:eth3 0.120 0.122
#8 edu2:age2:eth3 0.038 0.051 edu2:age2:eth3 0.061 0.080
#9 edu2:age2 0.517 0.981
#9 edu2:Eng2:eth3 0.052 0.061
#10 gen2:Eng2 0.180 0.253
#10 edu2:age2 0.496 0.966
#11 gen2:age2 0.618 0.138
#11 edu2:Eng2 0.302 0.423
#12 Eng2:age2 0.010 0.171
#12 gen2:Eng2 0.168 0.273
#13 Eng2:eth3 0.150 0.183

```

```
#14          gen2:age2 0.566 0.129
#15          Eng2:age2 0.009 0.060
```

```
mod <- gls(acc2 ~
            gen2 + edu2 + Eng2 + age2 + eth3 +
            edu2*eth3 +
            age2*eth3, data = RMET2_1[complete.cases(RMET2_1[,c(107,108,110,
111,112, 113)])],))
```

```
tempr2 <- anova(mod)
prtAnova <- tibble(tempr2)
p <- prtAnova[[1]][,3]
d_full_r2 <- tibble(rownames(tempr2))
temp1 <- array(round(p.adjust(p, "holm"), 3))
d_full_r2$T1 <- temp1
```

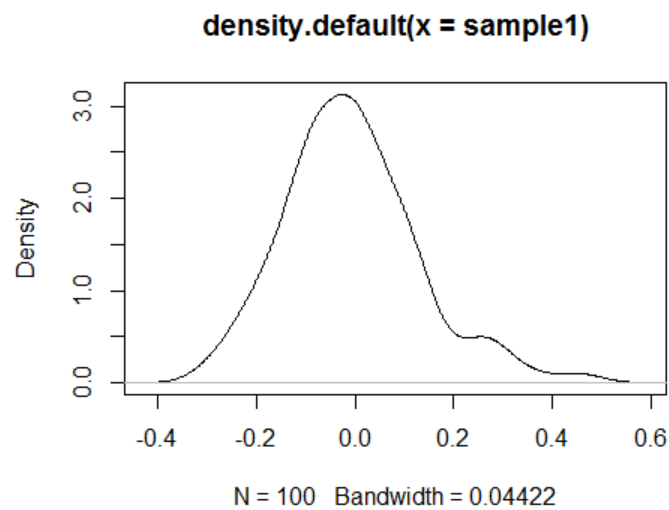
```
tempr2 <- Anova(mod, type = 2)
prtAnova <- tibble(tempr2)
p <- prtAnova[[1]][3][[1]]
temp2 <- array(round(p.adjust(p, "holm"), 3))
d_full_r2$T2 <- c(0,temp2)
```

```
#16          gen2:edu2:eth3 0.052 0.069
#17          gen2:edu2 0.149 0.312
#18          gen2:eth3 0.042 0.091
```

#The outcome, in terms of statistical significance, is the same as the outcome of the model that allows different groups to have different variances. As before, I think it's reasonable to calculate the LS means from the second, simpler model.

```
rsd <- tibble(resid(mod))
colnames(rsd) <- c("residuals")

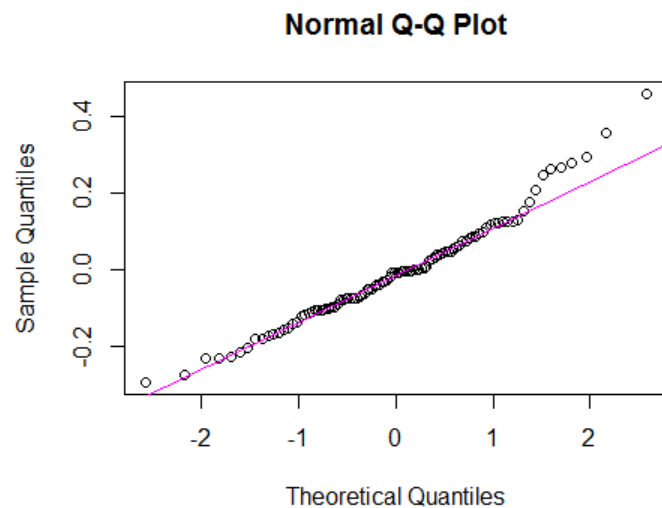
sample1 <- sample(rsd$residuals, 100)
plot(density(sample1))
```



```
shapiro.test(sample1)

##
##  Shapiro-Wilk normality test
##
## data:  sample1
## W = 0.97193, p-value = 0.03113

qqnorm(sample1);qqline(sample1, col = 6)
```



The residuals sometimes do some strange things at the tails, and some samples are significantly different from normal at a sample size of 500, but I don't see any egregious violation of ANOVA assumptions.

```

orig_complete <- RMET_1[complete.cases(RMET_1[,c(8,11,100,101,103, 104)]),]
rev_complete <- RMET2_1[complete.cases(RMET2_1[,c(107,108,110,111,112, 113)]),]

mod_orig <- gls(acc2 ~
  gender + edu2 + Eng_primary + age2 + eth3 +
  gender*eth3 +
  edu2*age2 + edu2*eth3 +
  age2*eth3 +
  edu2*age2*eth3, data = RMET_1[complete.cases(RMET_1[,c(8,11,100,
101,103, 104)]),])

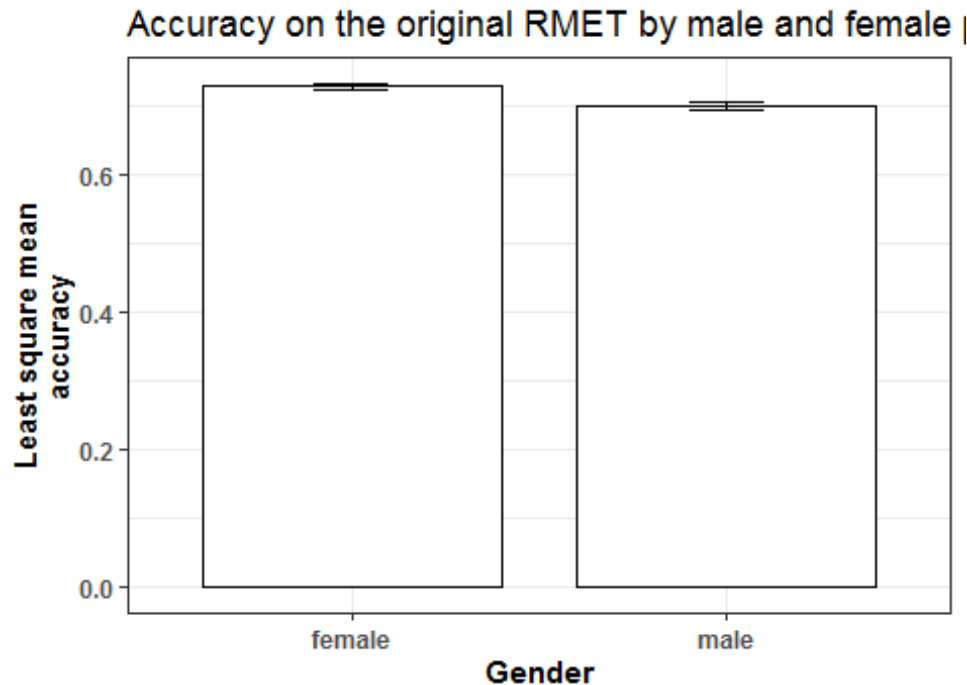
mod_rev <- gls(acc2 ~
  gen2 + edu2 + Eng2 + age2 + eth3 +
  edu2*eth3 +
  age2*eth3, data = RMET2_1[complete.cases(RMET2_1[,c(107,108,110,
111,112, 113)]),])

#main effects:
# 1) gender (significant in both tests; part of gen*eth in original RMET)
emm_orig <- emmeans(mod_orig, pairwise ~ gender, data = orig_complete)

## NOTE: Results may be misleading due to involvement in interactions

as.data.frame(summary(emm_orig)$emmean)[c('emmean', 'SE')] %>%
  mutate(levs=c('male', 'female')) %>%
  ggplot(aes(x = levs, y = emmean^0.5)) +
  geom_bar(stat='identity', color = "black", fill = "white", width = 0.8) +
  geom_errorbar(aes(ymin = (emmean-(1.96*SE))^0.5, ymax = (emmean+(1.96*SE))^
0.5), width = 0.2) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "Gender", y = "Least square mean\naccuracy",
        title = "Accuracy on the original RMET by male and female participants
",
        caption = "Accuracy on the original RMET for male and female particip
ants. Bars indicate the LS mean.\nError bars indicate the 95% confidence inte
rvals of the LS means.", hjust=0.5)

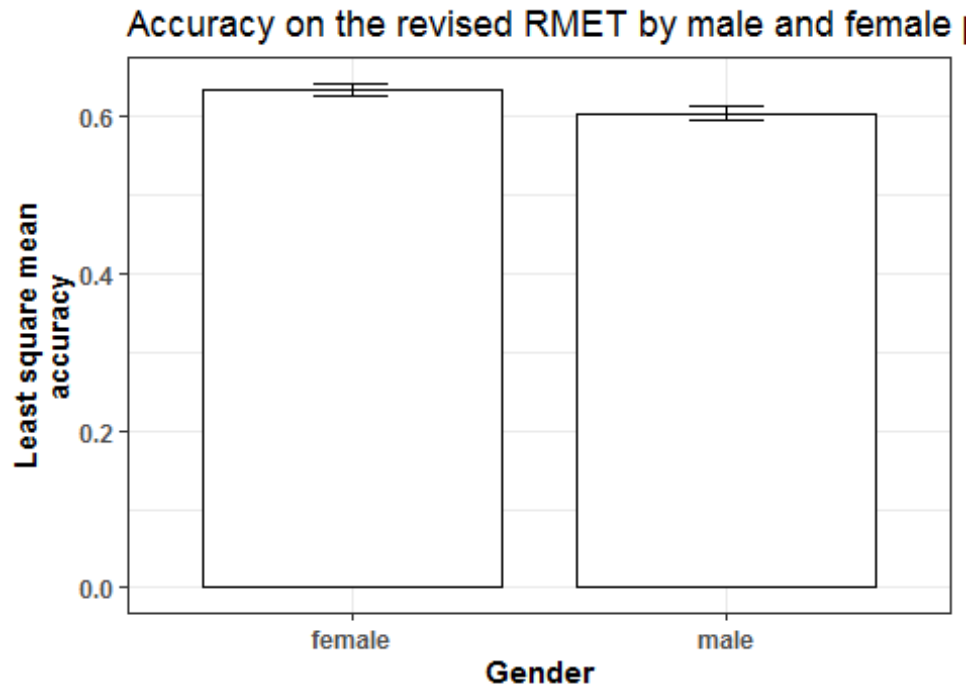
```

Accuracy on the original RMET for male and female participants. Bars indicate the LS mean. Error bars indicate the 95% confidence intervals of the LS means.

```
emm_rev <- emmeans(mod_rev, pairwise ~ gen2, data = rev_complete)

as.data.frame(summary(emm_rev)$emmean)[c('emmean', 'SE')] %>%
  mutate(levs=c('male', 'female')) %>%
  ggplot(aes(x = levs, y = emmean^0.5)) +
  geom_bar(stat='identity', color = "black", fill = "white", width = 0.8) +
  geom_errorbar(aes(ymin = (emmean-(1.96*SE))^0.5, ymax = (emmean+(1.96*SE))^
0.5), width = 0.2) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "Gender", y = "Least square mean\naccuracy",
        title = "Accuracy on the revised RMET by male and female participants"
,
        caption = "Accuracy on the revised RMET for male and female participants. Bars indicate the LS mean.\nError bars indicate the 95% confidence intervals of the LS means.", hjust=0.5)
```

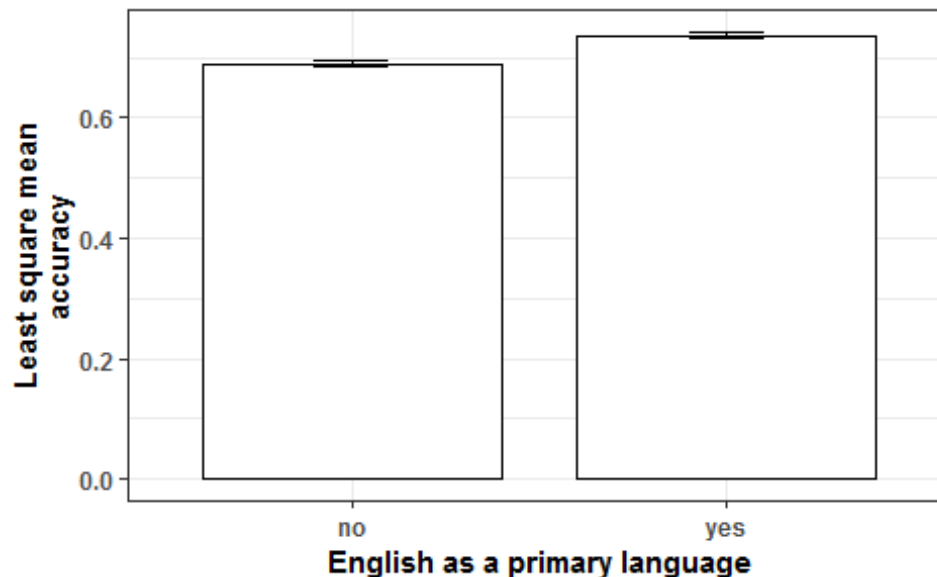


Accuracy on the revised RMET for male and female participants. Bars indicate Error bars indicate the 95% confidence intervals of the LS means.

```
# 3) English_primary (significant in both tests)
emm_orig <- emmeans(mod_orig, pairwise ~ Eng_primary, data = orig_complete)

as.data.frame(summary(emm_orig)$emmean)[c('emmean', 'SE')] %>%
  mutate(levs=c('no', 'yes')) %>%
  ggplot(aes(x = lev, y = emmean^0.5)) +
  geom_bar(stat='identity', color = "black", fill = "white", width = 0.8) +
  geom_errorbar(aes(ymin = (emmean-(1.96*SE))^0.5, ymax = (emmean+(1.96*SE))^
0.5), width = 0.2) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "English as a primary language", y = "Least square mean\naccuracy"
,
        title = "Accuracy on the original RMET by participants without and with\nEnglish as a primary language",
        caption = "Accuracy on the original RMET for participants for whom English is not a primary\nlanguage, and participants for whom English is a primary language. Bars indicate the LS mean.\nError bars indicate the 95% confidence intervals of the LS means.", hjust=0.5)
```

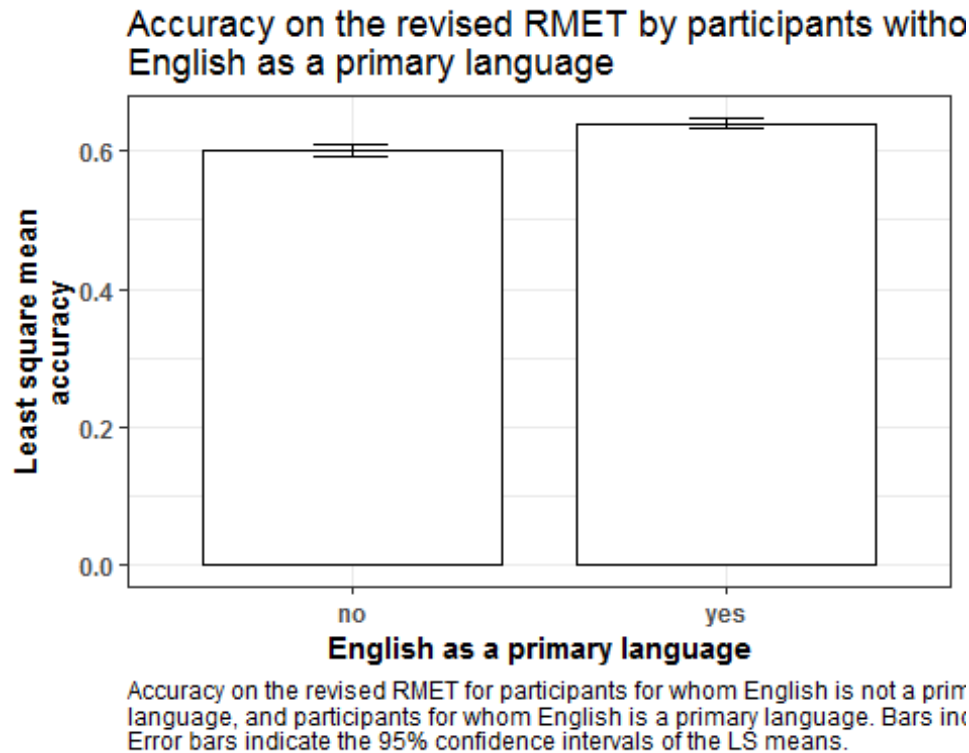
Accuracy on the original RMET by participants with English as a primary language



Accuracy on the original RMET for participants for whom English is not a primary language, and participants for whom English is a primary language. Bars indicate the LS mean. Error bars indicate the 95% confidence intervals of the LS means.

```
emm_rev <- emmeans(mod_rev, pairwise ~ Eng2, data = rev_complete)

as.data.frame(summary(emm_rev)$emmean)[c('emmean', 'SE')] %>%
  mutate(levs=c('no', 'yes')) %>%
  ggplot(aes(x = levs, y = emmean^0.5)) +
  geom_bar(stat='identity', color = "black", fill = "white", width = 0.8) +
  geom_errorbar(aes(ymin = (emmean-(1.96*SE))^0.5, ymax = (emmean+(1.96*SE))^
0.5), width = 0.2) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "English as a primary language", y = "Least square mean\naccuracy"
,
        title = "Accuracy on the revised RMET by participants without and with\nEnglish as a primary language",
        caption = "Accuracy on the revised RMET for participants for whom Eng
lish is not a primary\nlanguage, and participants for whom English is a prima
ry language. Bars indicate the LS mean.\nError bars indicate the 95% confiden
ce intervals of the LS means.", hjust=0.5)
```



4) ethnicity (significant in both tests; part of $edu*eth*age$ in original RMET, and part of $edu*eth$ in revised RMET)

```
emm_orig <- emmeans(mod_orig, ~ eth3, data = orig_complete)
```

NOTE: Results may be misleading due to involvement in interactions

```
CLD_orig <- cld(emm_orig, alpha = 0.05, Letters = letters, adjust="tukey")
```

```
temp <- arrange(as.data.frame(CLD_orig), by_group = eth3)
```

```
temp$eth3 <- c('African', 'Asian', 'European non-Hispanic', 'European Hispanic')
```

```
temp$eth3 <- factor(temp$eth3, levels = c('African', 'Asian', 'European non-Hispanic', 'European Hispanic'))
```

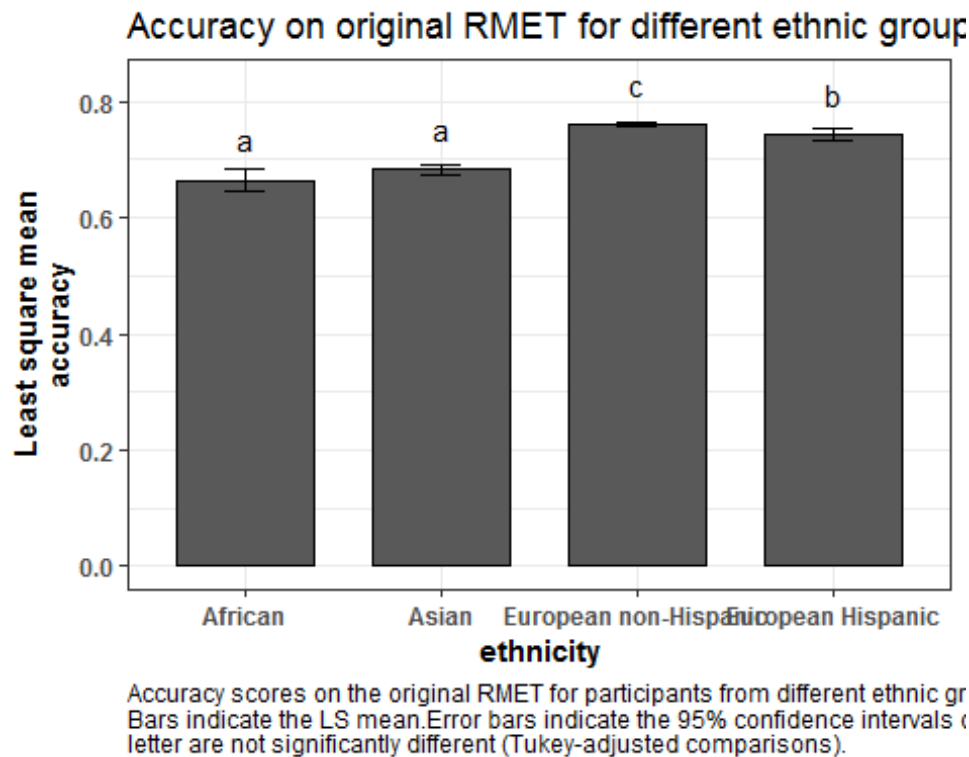
```
temp$.group = gsub(" ", "", temp$.group)
```

```
h <- 0.18
```

```
v <- 0.07
```

```
ggplot(temp, aes(x = eth3, y = emmean^0.5, label = .group)) + geom_bar(stat = "identity", width = 0.7, color = "black") +
  geom_errorbar(aes(ymin = lower.CL^0.5, ymax = upper.CL^0.5), width = 0.2, size = 0.7, position = pd) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "ethnicity", y = "Least square mean\naccuracy",
        title = "Accuracy on original RMET for different ethnic groups",
```

```
caption = "Accuracy scores on the original RMET for participants from
different ethnic groups.\nBars indicate the LS mean.Error bars indicate the 9
5% confidence intervals of the LS means. Means sharing a\nletter are not sign
ificantly different (Tukey-adjusted comparisons).", hjust=0.5) +
  geom_text(nudge_y = c(v,v,v,v),
            color = "black")
```



```
emm_rev <- emmeans(mod_rev, ~ eth3, data = rev_complete)

## NOTE: Results may be misleading due to involvement in interactions

CLD_rev <- cld(emm_rev, alpha = 0.05, Letters = letters, adjust="tukey")
temp <- arrange(as.data.frame(CLD_rev), by_group = eth3)

temp$eth3 <- c('African','Asian','European non-Hispanic','European Hispanic')
temp$eth3 <- factor(temp$eth3, levels = c('African','Asian','European non-Hispanic','European Hispanic'))
temp$.group=gsub(" ", "", temp$.group)

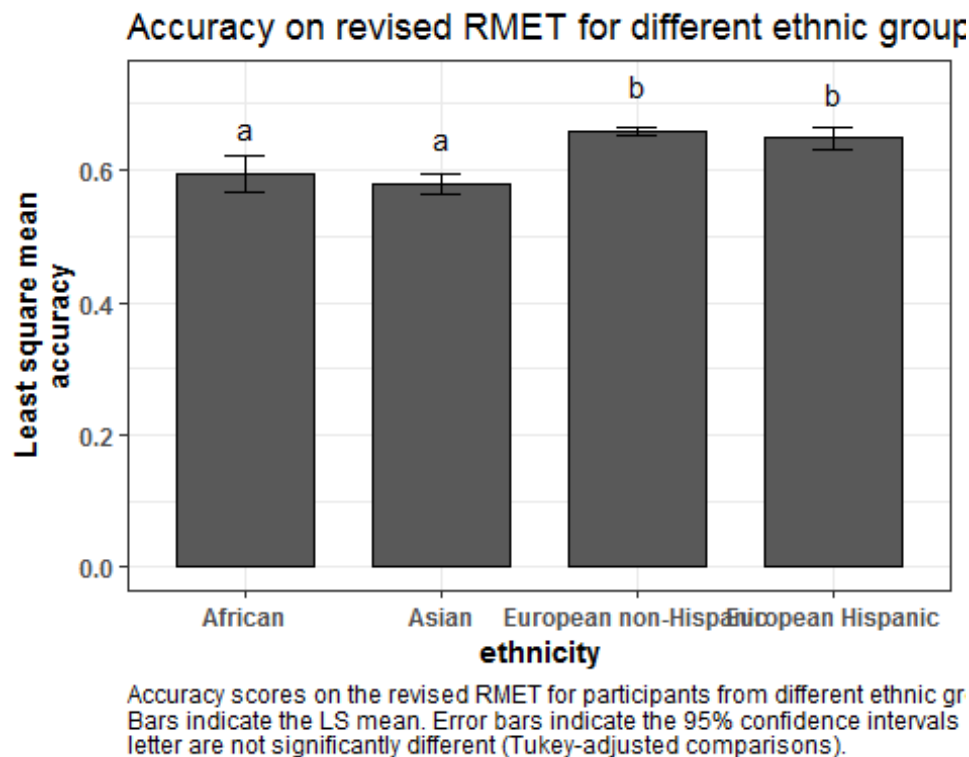
h <- 0.18
v <- 0.07

ggplot(temp,aes(x = eth3,y = emmean^0.5, label = .group)) + geom_bar(stat = "identity", width = 0.7, color = "black") +
  geom_errorbar(aes(ymin = lower.CL^0.5, ymax = upper.CL^0.5),width = 0.2,size = 0.7, position = pd) +
  theme_bw() +
```

```

theme(axis.title = element_text(face = "bold"),
      axis.text = element_text(face = "bold"),
      plot.caption = element_text(hjust = 0)) +
labs(x = "ethnicity", y = "Least square mean\naccuracy",
     title = "Accuracy on revised RMET for different ethnic groups",
     caption = "Accuracy scores on the revised RMET for participants from
different ethnic groups.\nBars indicate the LS mean. Error bars indicate the
95% confidence intervals of the LS means. Means sharing a\nletter are not sig
nificantly different (Tukey-adjusted comparisons).", hjust=0.5) +
geom_text(nudge_y = c(v,v,v,v),
         color = "black")

```



```

#interactions:
# 5) gender * ethnicity (significant in original RMET only)
emm_orig <- emmeans(mod_orig, ~ gender*eth3, data = orig_complete)
CLD_orig <- cld(emm_orig, alpha = 0.05, Letters = letters, adjust="tukey")
temp <- as.data.frame(CLD_orig)
temp <- temp[order(as.numeric(row.names(temp))),] %>%
  mutate(gender = c('male', 'female', 'male', 'female', 'male', 'female', 'male',
, 'female'),
         ethnicity = c('African', 'African', 'Asian', 'Asian', 'European non-Hisp
anic', 'European non-Hispanic', 'European Hispanic', 'European Hispanic'))

temp$.group=gsub(" ", "", temp$.group)

h <- 0.18
v <- 0.07

```

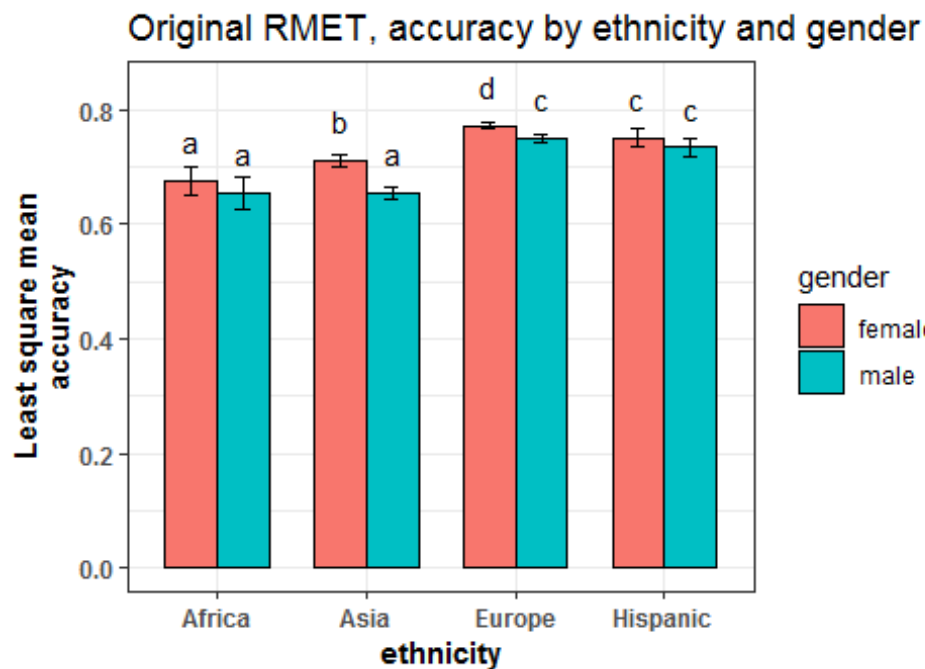
```

pd = position_dodge(0.7)    ### How much to jitter the points on the plot

ggplot(temp,aes(x = eth3,y = emmean^0.5, fill = gender, label = .group)) +
  geom_bar(stat = "identity", width = 0.7, color = "black", position = pd) +
  geom_errorbar(aes(ymin = lower.CL^0.5, ymax = upper.CL^0.5),width = 0.2,si
ze = 0.7, position = pd) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "ethnicity", y = "Least square mean\naccuracy",
       title = "Original RMET, accuracy by ethnicity and gender",
       caption = "Accuracy scores for both genders across four ethnic groups
. Bars indicate the LS mean.\nError bars indicate the 95% confidence interval
s of the LS means. Means sharing a letter are not\nsignificantly different (T
ukey-adjusted comparisons).",
       hjust=0.5) +

  geom_text(nudge_x = c(h, -h, h, -h, h, -h, h, -h),
           nudge_y = c(v,v,v,v,v,v,v,v),
           color = "black")

```



Accuracy scores for both genders across four ethnic groups. Bars indicate the LS mean. Error bars indicate the 95% confidence intervals of the LS means. Means sharing a letter are not significantly different (Tukey-adjusted comparisons).

```

emm_rev <- emmeans(mod_rev, ~ gen2*eth3, data = rev_complete)
CLD_rev <- cld(emm_rev, alpha = 0.05, Letters = letters, adjust="tukey")
temp <- as.data.frame(CLD_rev)

```

```

temp <- temp[order(as.numeric(row.names(temp))),] %>%
  mutate(gen2 = c('male','female','male', 'female','male', 'female','male', '
female'),
          ethnicity = c('African','African','Asian','Asian','European non-Hisp
anic','European non-Hispanic', 'European Hispanic','European Hispanic'))

temp$.group=gsub(" ", "", temp$.group)

h <- 0.18
v <- 0.07

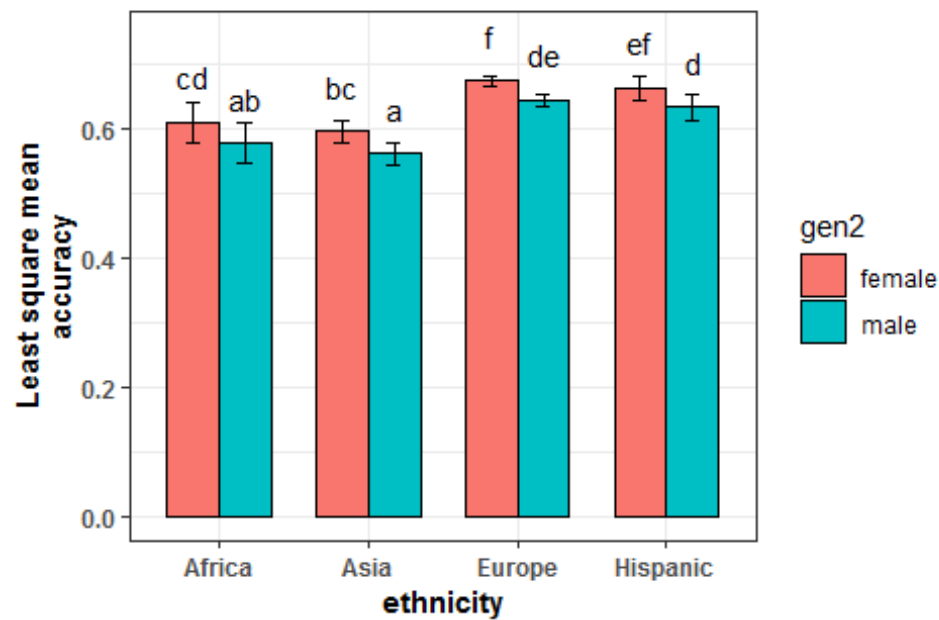
pd = position_dodge(0.7)    ### How much to jitter the points on the plot

ggplot(temp,aes(x = eth3,y = emmean^0.5, fill = gen2, label = .group)) +
  geom_bar(stat = "identity", width = 0.7, color = "black", position = pd) +
  geom_errorbar(aes(ymin = lower.CL^0.5, ymax = upper.CL^0.5),width = 0.2,si
ze = 0.7, position = pd) +
  theme_bw() +
  theme(axis.title = element_text(face = "bold"),
        axis.text = element_text(face = "bold"),
        plot.caption = element_text(hjust = 0)) +
  labs(x = "ethnicity", y = "Least square mean\naccuracy",
        title = "Revised RMET, accuracy by ethnicity and gender",
        caption = "Accuracy scores for both genders across four ethnic groups
. Bars indicate the LS mean.\nError bars indicate the 95% confidence interval
s of the LS means. Means sharing a letter are not\nsignificantly different (T
ukey-adjusted comparisons).",
        hjust=0.5) +

  geom_text(nudge_x = c(h, -h, h, -h, h, -h, h, -h),
            nudge_y = c(v,v,v,v,v,v,v,v),
            color = "black")

```


Revised RMET, accuracy by ethnicity and gender



Accuracy scores for both genders across four ethnic groups. Bars indicate the least square means. Error bars indicate the 95% confidence intervals of the LS means. Means significantly different (Tukey-adjusted comparisons).