

Sample characteristics by treatment

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```
map <- read.table("data/maps/UserName_map.txt", sep = "\t", header = TRUE)

#drop subjects who didn't complete
map_drop <- map %>%
  filter(Supplement == "EVOO" | Supplement == "MCT") %>%
  droplevels()

# make a long version of the map
map_long <- read.table("data/maps/UserName_map_long.txt", sep = "\t", header = TRUE)

map_long_drop <- map_long %>% filter(Supplement == "EVOO" | Supplement == "MCT") %>% droplevels()

mean(map_drop$Age)

## [1] 30.82353
sd(map_drop$Age)

## [1] 10.26326
mean(map_drop$Weight)

## [1] 68.51765
sd(map_drop$Weight)

## [1] 14.64872
mean(map_drop$Height)

## [1] 171.5118
sd(map_drop$Height)

## [1] 9.443669
mean(map_drop$Waist.Circumference, na.rm = TRUE)

## [1] 86.75
sd(map_drop$Waist.Circumference, na.rm = T)

## [1] 7.872369
mean(map_drop$Cholesterol.Baseline, na.rm=T)

## [1] 163.75
sd(map_drop$Cholesterol.Baseline, na.rm=T)

## [1] 32.32297
mean(map_drop$Trigs.Baseline, na.rm = T)

## [1] 66.125
```

```

sd(map_drop$Trigs.Baseline, na.rm = T)

## [1] 20.13623
mean(map_drop$HDL.Baseline, na.rm = T)

## [1] 56.8125
sd(map_drop$HDL.Baseline, na.rm = T)

## [1] 11.0174
mean(map_drop$LDL.Baseline, na.rm = T)

## [1] 93.65625
sd(map_drop$LDL.Baseline, na.rm = T)

## [1] 29.01013
mean(map_drop$Glu.Baseline, na.rm = T)

## [1] 86.0625
sd(map_drop$Glu.Baseline, na.rm = T)

## [1] 7.224231
mean(map_drop$Ins.Baseline, na.rm = T)

## [1] 8.634375
sd(map_drop$Ins.Baseline, na.rm = T)

## [1] 3.478655
smry_gender <- ddply(map_drop, .(Gender), summarise,
  Age_mean=mean(Age),
  Age_sd = sd(Age),
  Gender_count=length(Gender),
  Weight_mean = mean(Weight),
  Weight_sd = sd(Weight),
  Height_mean = mean(Height),
  Height_sd = sd(Height),
  Waist_cir_mean = mean(Waist.Circumference, na.rm = TRUE),
  Waist_cir_sd = sd(Waist.Circumference, na.rm = TRUE),
  Base_Chole_mean = mean(Cholesterol.Baseline, na.rm = TRUE),
  Base_Chole_sd = sd(Cholesterol.Baseline, na.rm = TRUE),
  Base_Trig_mean = mean(Trigs.Baseline, na.rm = TRUE),
  Base_Trig_sd = sd(Trigs.Baseline, na.rm = TRUE),
  Base_HDL_mean = mean(HDL.Baseline, na.rm = TRUE),
  Base_HDL_sd = sd(HDL.Baseline, na.rm = TRUE),
  Base_LDL_mean = mean(LDL.Baseline, na.rm = TRUE),
  Base_LDL_sd = sd(LDL.Baseline, na.rm = TRUE),
  Base_Glu_mean = mean(Glu.Baseline, na.rm = TRUE),
  Base_Glu_sd = sd(Glu.Baseline, na.rm = TRUE),
  Base_Ins_mean = mean(Ins.Baseline, na.rm = TRUE),
  Base_Ins_sd = sd(Ins.Baseline, na.rm = TRUE),
  Base_HOMA_IR_mean = mean(Homa.IR.Baseline, na.rm = TRUE),
  Base_HOMA_IR_sd = sd(Homa.IR.Baseline, na.rm = TRUE))

```

```
t(column_to_rownames(smry_gender, "Gender"))
```

```
##              F              M
## Age_mean      28.8150000  33.692857
## Age_sd         9.6788579  10.742329
## Gender_count   20.0000000  14.000000
## Weight_mean    59.8050000  80.964286
## Weight_sd       8.2303338  12.731584
## Height_mean    165.6050000 179.950000
## Height_sd       4.5129609   8.140190
## Waist_cir_mean  83.3111111  91.171429
## Waist_cir_sd    5.5213904   8.395917
## Base_Chole_mean 166.9444444 159.642857
## Base_Chole_sd   27.7625906  38.094230
## Base_Trig_mean  61.1111111  72.571429
## Base_Trig_sd    13.7921072  25.269971
## Base_HDL_mean   60.6666667  51.857143
## Base_HDL_sd     11.0080185   9.163952
## Base_LDL_mean   93.9444444  93.285714
## Base_LDL_sd     23.2997658  36.009462
## Base_Glu_mean   85.0555556  87.357143
## Base_Glu_sd     5.5780265   8.975241
## Base_Ins_mean   9.0611111   8.085714
## Base_Ins_sd     2.5718245   4.430638
## Base_HOMA_IR_mean 1.9011111  1.785000
## Base_HOMA_IR_sd 0.5506669   1.127617
```

```
t.test(Age ~ Gender, data = map_drop)
```

```
##
## Welch Two Sample t-test
##
## data: Age by Gender
## t = -1.3567, df = 26.187, p-value = 0.1865
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -12.26568  2.50997
## sample estimates:
## mean in group F mean in group M
##      28.81500      33.69286
```

```
t.test(Weight ~ Gender, data = map_drop)
```

```
##
## Welch Two Sample t-test
##
## data: Weight by Gender
## t = -5.4697, df = 20.517, p-value = 2.16e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -29.21574 -13.10283
## sample estimates:
## mean in group F mean in group M
##      59.80500      80.96429
```

```
t.test(Height ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Height by Gender  
## t = -5.9816, df = 18.607, p-value = 1.019e-05  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -19.371697 -9.318303  
## sample estimates:  
## mean in group F mean in group M  
## 165.605 179.950
```

```
t.test(Waist.Circumference ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Waist.Circumference by Gender  
## t = -3.0302, df = 21.368, p-value = 0.006283  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -13.249157 -2.471478  
## sample estimates:  
## mean in group F mean in group M  
## 83.31111 91.17143
```

```
t.test(Cholesterol.Baseline ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Cholesterol.Baseline by Gender  
## t = 0.6033, df = 22.963, p-value = 0.5522  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -17.73699 32.34017  
## sample estimates:  
## mean in group F mean in group M  
## 166.9444 159.6429
```

```
t.test(Trigs.Baseline ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Trigs.Baseline by Gender  
## t = -1.529, df = 18.944, p-value = 0.1428  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -27.151380 4.230745  
## sample estimates:  
## mean in group F mean in group M  
## 61.11111 72.57143
```

```
t.test(HDL.Baseline ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: HDL.Baseline by Gender  
## t = 2.4691, df = 29.826, p-value = 0.0195  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 1.52096 16.09809  
## sample estimates:  
## mean in group F mean in group M  
## 60.66667 51.85714
```

```
t.test(LDL.Baseline ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: LDL.Baseline by Gender  
## t = 0.059449, df = 21.131, p-value = 0.9532  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -22.37595 23.69341  
## sample estimates:  
## mean in group F mean in group M  
## 93.94444 93.28571
```

```
t.test(Glu.Baseline ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Glu.Baseline by Gender  
## t = -0.8414, df = 20.565, p-value = 0.4098  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -7.997535 3.394361  
## sample estimates:  
## mean in group F mean in group M  
## 85.05556 87.35714
```

```
t.test(Ins.Baseline ~ Gender, data = map_drop)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Ins.Baseline by Gender  
## t = 0.73323, df = 19.673, p-value = 0.4721  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -1.802474 3.753268  
## sample estimates:  
## mean in group F mean in group M  
## 9.061111 8.085714
```

```

smry_supp <- ddply(map_drop, .(Supplement), summarise,
  Age_mean=mean(Age),
  Age_sd = sd(Age),
  Subject_no=length(Gender),
  Weight_mean = mean(Weight),
  Weight_sd = sd(Weight),
  Height_mean = mean(Height),
  Height_sd = sd(Height),
  Waist_cir_mean = mean(Waist.Circumference, na.rm = TRUE),
  Waist_cir_sd = sd(Waist.Circumference, na.rm = TRUE),
  Base_Chole_mean = mean(Cholesterol.Baseline, na.rm = TRUE),
  Base_Chole_sd = sd(Cholesterol.Baseline, na.rm = TRUE),
  Base_Trig_mean = mean(Trigs.Baseline, na.rm = TRUE),
  Base_Trig_sd = sd(Trigs.Baseline, na.rm = TRUE),
  Base_HDL_mean = mean(HDL.Baseline, na.rm = TRUE),
  Base_HDL_sd = sd(HDL.Baseline, na.rm = TRUE),
  Base_LDL_mean = mean(LDL.Baseline, na.rm = TRUE),
  Base_LDL_sd = sd(LDL.Baseline, na.rm = TRUE),
  Base_Glu_mean = mean(Glu.Baseline, na.rm = TRUE),
  Base_Glu_sd = sd(Glu.Baseline, na.rm = TRUE),
  Base_Ins_mean = mean(Ins.Baseline, na.rm = TRUE),
  Base_Ins_sd = sd(Ins.Baseline, na.rm = TRUE),
  Base_HOMA_IR_mean = mean(Homa.IR.Baseline, na.rm = TRUE),
  Base_HOMA_IR_sd = sd(Homa.IR.Baseline, na.rm = TRUE))

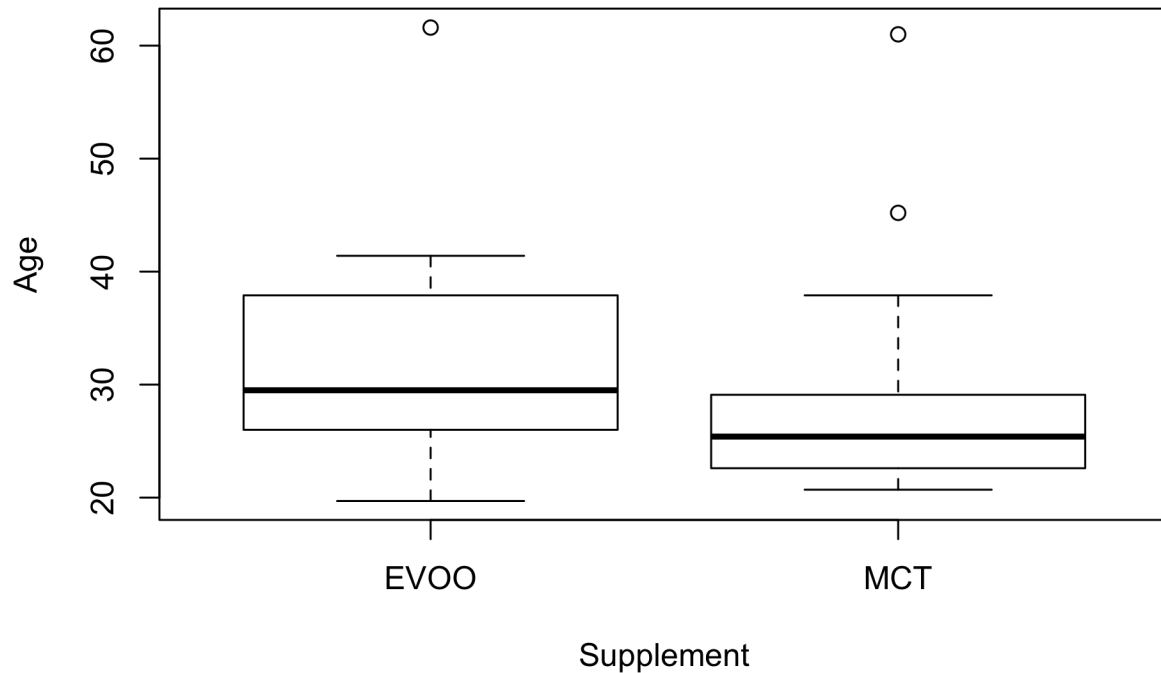
t(column_to_rownames(smry_supp, "Supplement"))

```

##	EV00	MCT
## Age_mean	32.535294	29.111765
## Age_sd	10.093559	10.447301
## Subject_no	17.000000	17.000000
## Weight_mean	69.176471	67.858824
## Weight_sd	12.802223	16.666211
## Height_mean	171.258824	171.764706
## Height_sd	10.688256	8.340559
## Waist_cir_mean	87.700000	85.800000
## Waist_cir_sd	6.814494	8.928456
## Base_Chole_mean	169.250000	158.250000
## Base_Chole_sd	34.609247	29.947732
## Base_Trig_mean	67.062500	65.187500
## Base_Trig_sd	18.727765	22.030944
## Base_HDL_mean	58.625000	55.000000
## Base_HDL_sd	12.462611	9.409215
## Base_LDL_mean	97.250000	90.062500
## Base_LDL_sd	30.788526	27.636856
## Base_Glu_mean	84.750000	87.375000
## Base_Glu_sd	7.995832	6.344289
## Base_Ins_mean	8.237500	9.031250
## Base_Ins_sd	2.447822	4.322147
## Base_HOMA_IR_mean	1.728750	1.971875
## Base_HOMA_IR_sd	0.560962	1.051914

At baseline, there are no differences in characteristics between supplementation groups

```
# view the categories and see if there are any differences between groups at baseline
plot(Age ~ Supplement, data = map_drop)
```



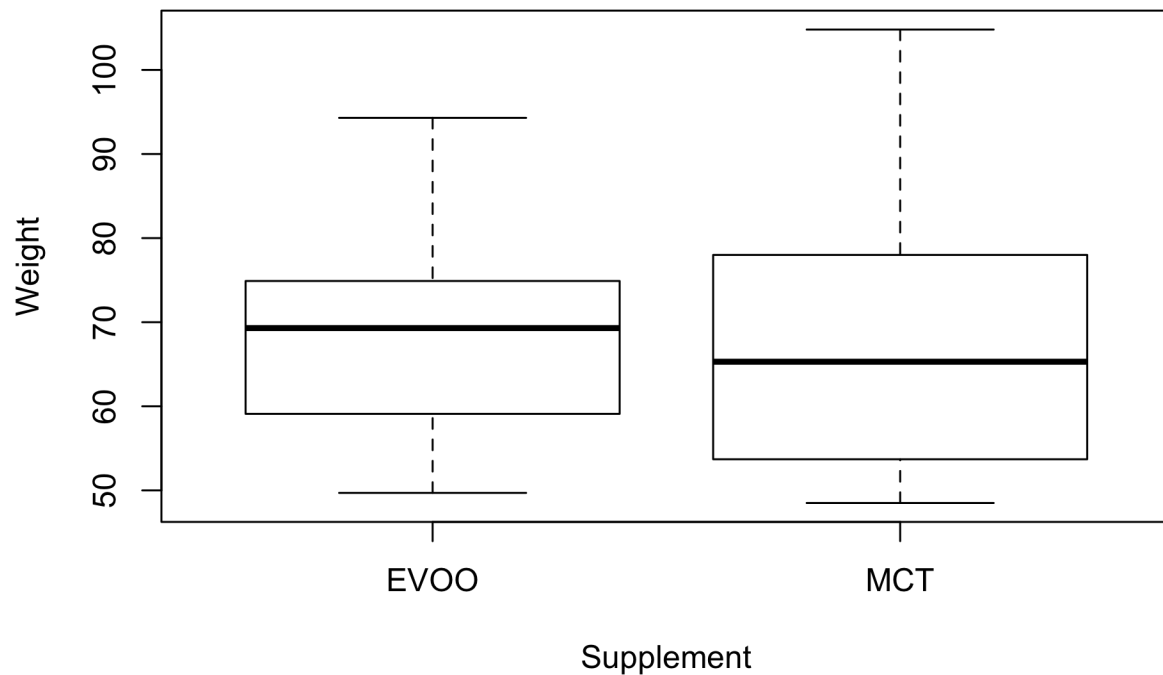
```
t.test(Age ~ Supplement, data = map_drop) # p-val = 0.34
```

```
##
## Welch Two Sample t-test
##
## data: Age by Supplement
## t = 0.9717, df = 31.962, p-value = 0.3385
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.753431 10.600490
## sample estimates:
## mean in group EVOO mean in group MCT
## 32.53529 29.11176
```

```
# view Gender
# plot(Gender ~ Supplement, data = map_drop)
# table(map_drop$Gender)
```

```
# what is the easiest way to test frequency? Chi-sq?
# TODO, figure this out??!
```

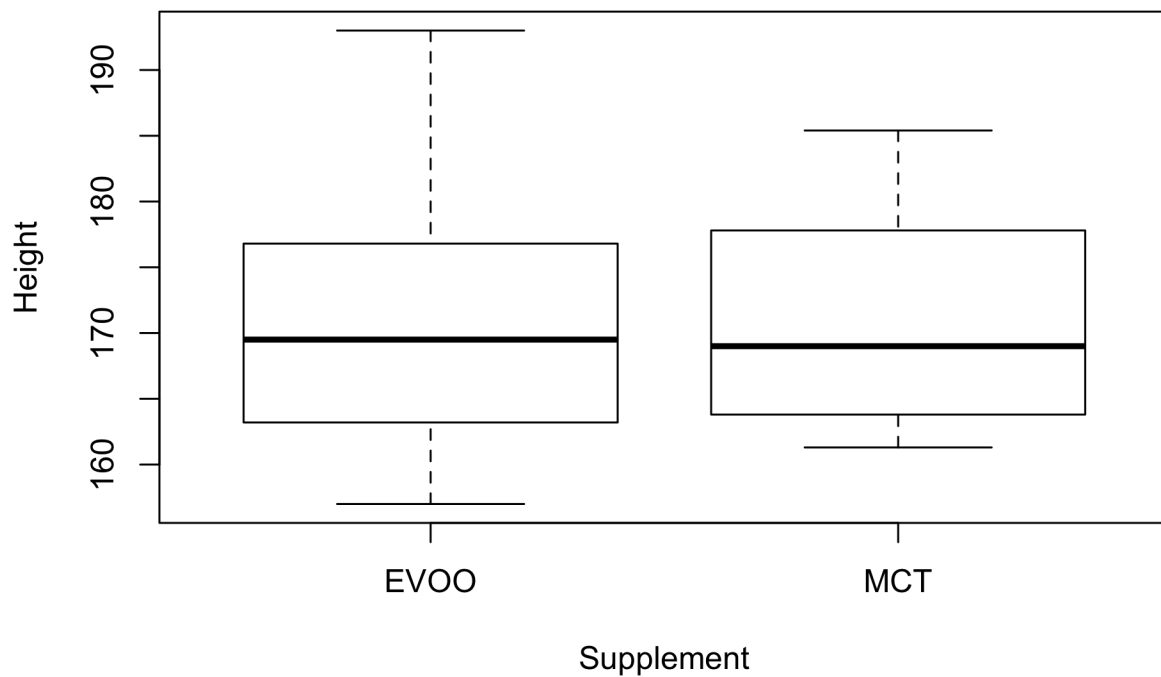
```
# view weight
plot(Weight ~ Supplement, data = map_drop)
```



```
t.test(Weight ~ Supplement, data = map_drop) # p-val = 0.82

##
## Welch Two Sample t-test
##
## data: Weight by Supplement
## t = 0.25851, df = 30.006, p-value = 0.7978
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -9.091847 11.727141
## sample estimates:
## mean in group EV00 mean in group MCT
## 69.17647 67.85882

# view height
plot(Height ~ Supplement, data = map_drop)
```

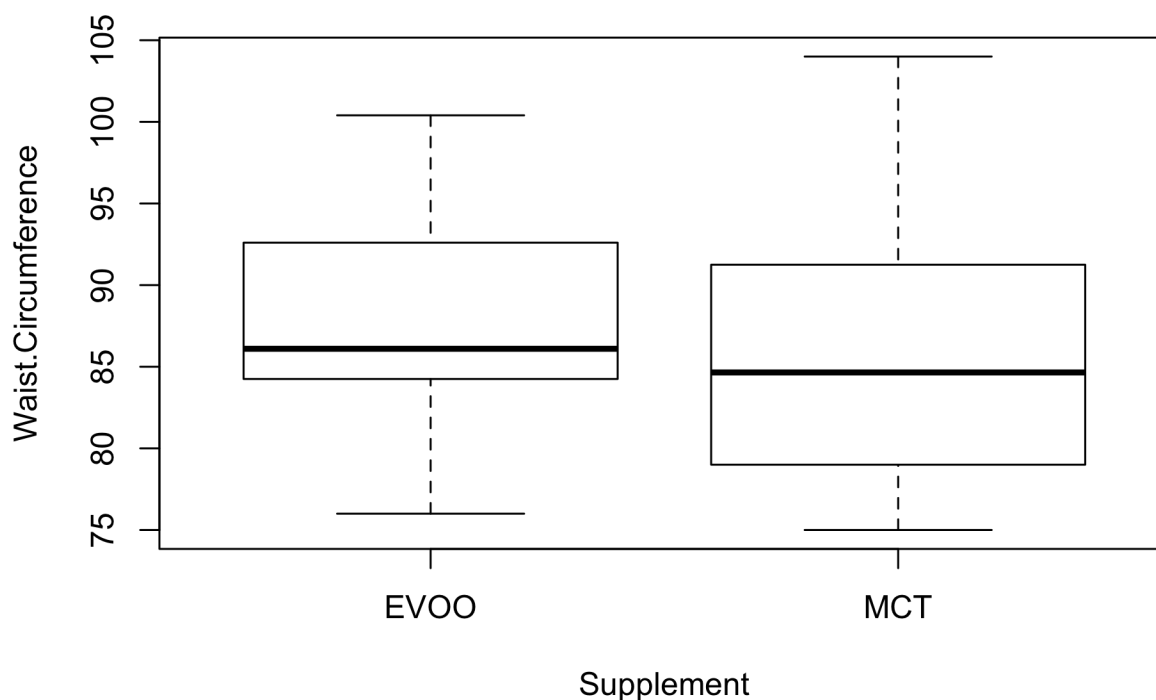



```
t.test(Height ~ Supplement, data = map_drop) # p-val = 0.89
```

```
##
##  Welch Two Sample t-test
##
## data:  Height by Supplement
## t = -0.15385, df = 30.215, p-value = 0.8788
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -7.219194  6.207429
## sample estimates:
## mean in group EVOO  mean in group MCT
##      171.2588      171.7647
```

```
# view waist circumference
```

```
plot(Waist.Circumference ~ Supplement, data = map_drop)
```

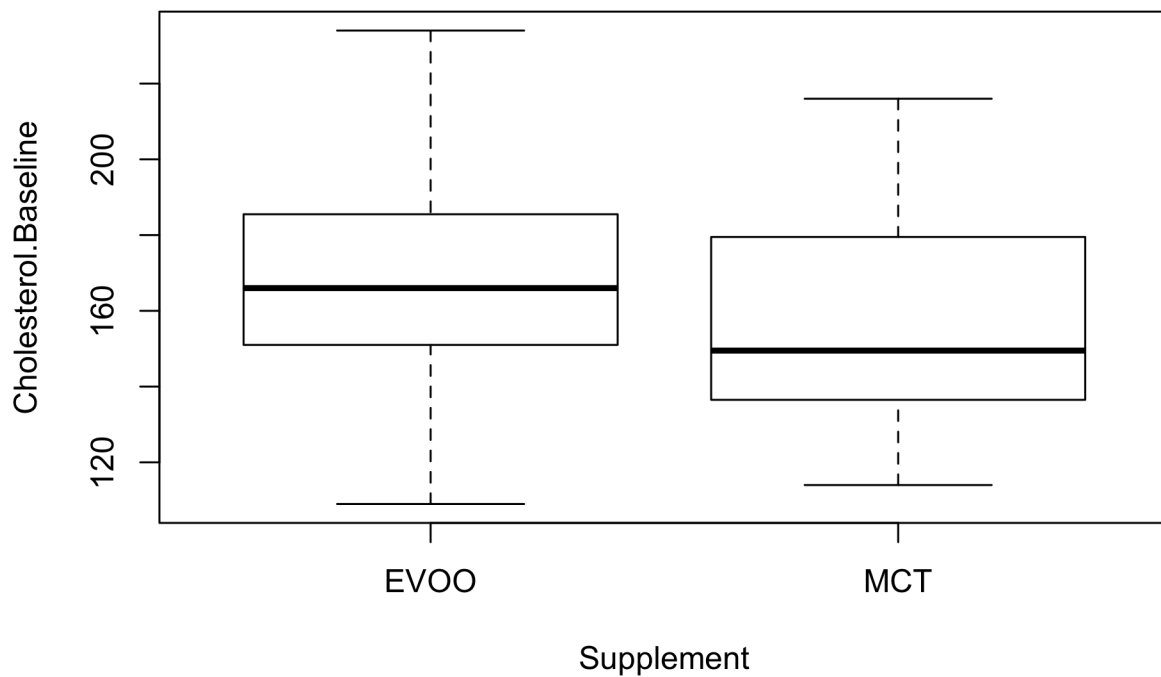


```
t.test(Waist.Circumference ~ Supplement, data = map_drop) # p-val = 0.51
```

```
##
## Welch Two Sample t-test
##
## data: Waist.Circumference by Supplement
## t = 0.67665, df = 28.048, p-value = 0.5042
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.851411 7.651411
## sample estimates:
## mean in group EVOO mean in group MCT
## 87.7 85.8
```

```
# view baseline cholesterol
```

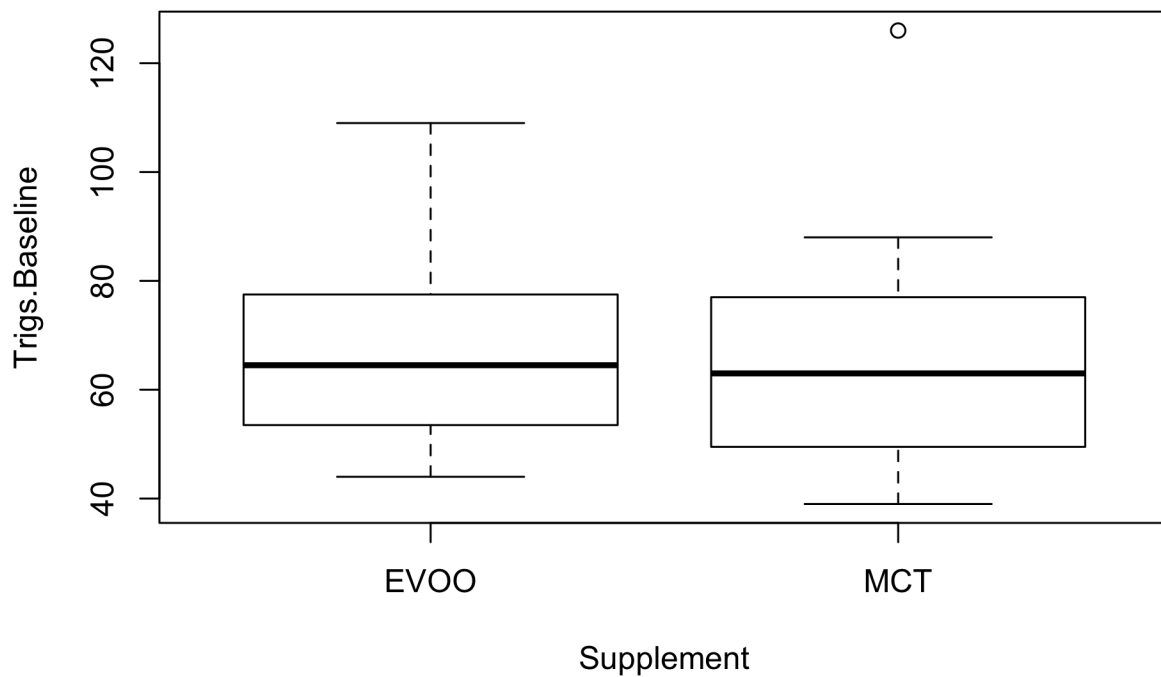
```
plot(Cholesterol.Baseline ~ Supplement, data = map_drop)
```



```
t.test(Cholesterol.Baseline ~ Supplement, data = map_drop) # p-val = 0.34
```

```
##
## Welch Two Sample t-test
##
## data: Cholesterol.Baseline by Supplement
## t = 0.96138, df = 29.393, p-value = 0.3442
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -12.38768 34.38768
## sample estimates:
## mean in group EVOO mean in group MCT
## 169.25 158.25
```

```
# view baseline Trigs
plot(Trigs.Baseline ~ Supplement, data = map_drop)
```

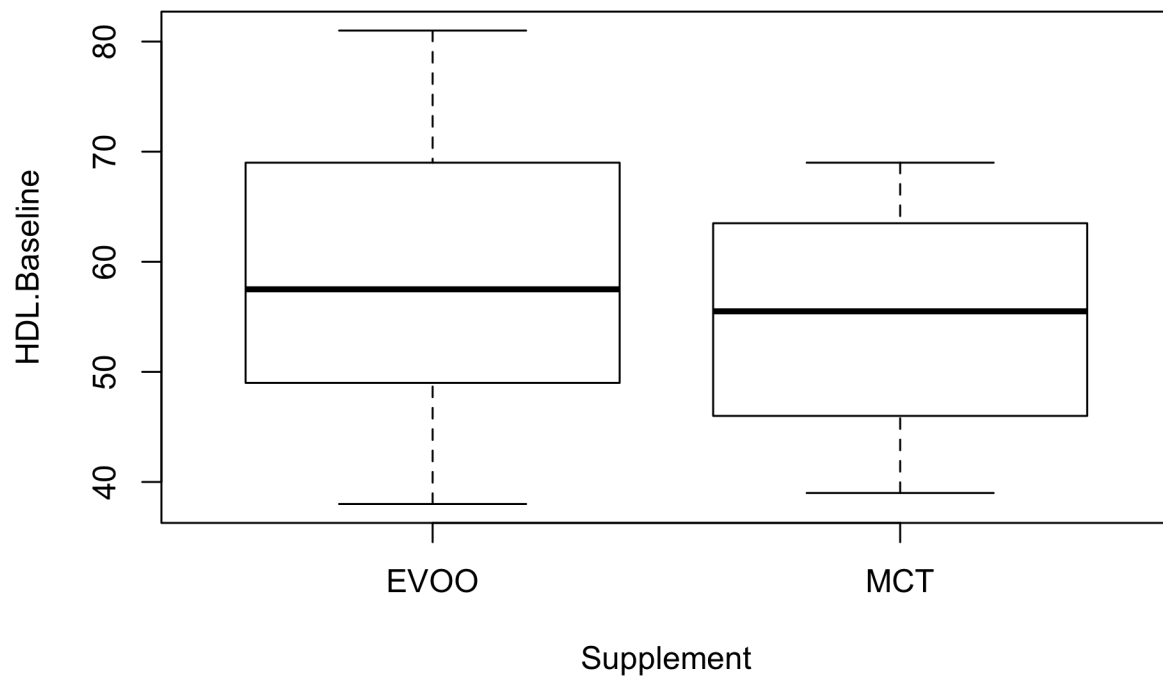


```
t.test(Trigs.Baseline ~ Supplement, data = map_drop) # p-val = 0.79
```

```
##
## Welch Two Sample t-test
##
## data: Trigs.Baseline by Supplement
## t = 0.25938, df = 29.242, p-value = 0.7972
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -12.90427 16.65427
## sample estimates:
## mean in group EVOO mean in group MCT
## 67.0625 65.1875
```

```
# view hdl baseline
```

```
plot(HDL.Baseline ~ Supplement, data = map_drop)
```

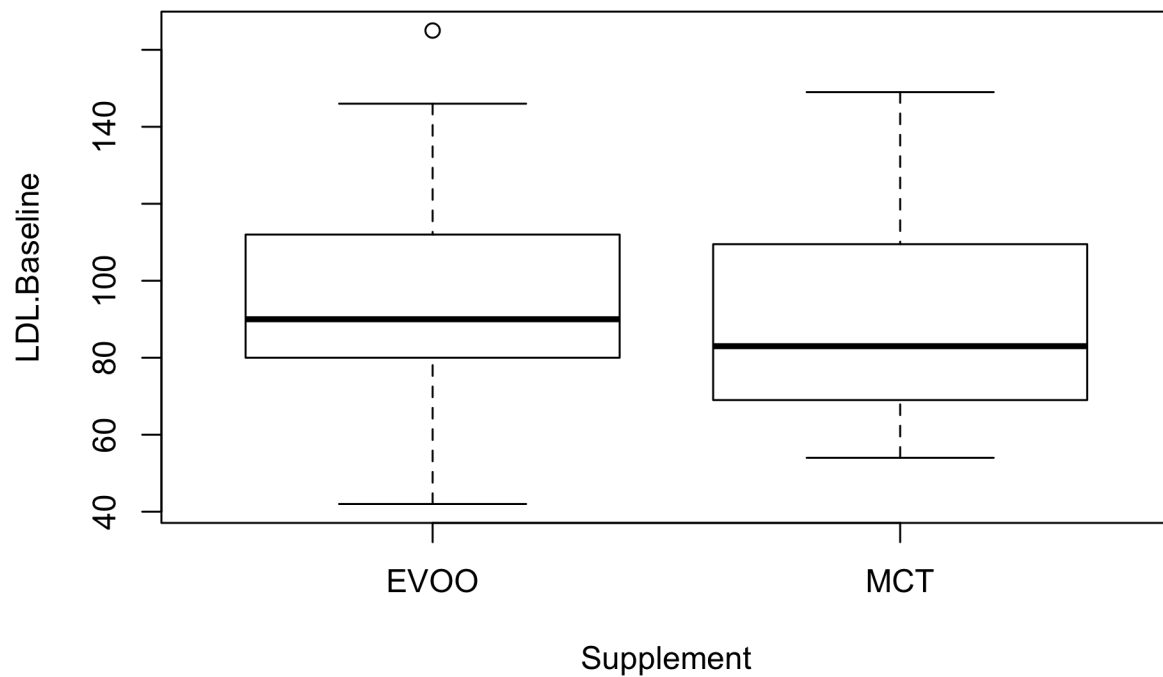


```
t.test(HDL.Baseline ~ Supplement, data = map_drop) # p-val = 0.36
```

```
##
## Welch Two Sample t-test
##
## data: HDL.Baseline by Supplement
## t = 0.92855, df = 27.907, p-value = 0.3611
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -4.373029 11.623029
## sample estimates:
## mean in group EVOO mean in group MCT
## 58.625 55.000
```

```
# view ldl baseline
```

```
plot(LDL.Baseline ~ Supplement, data = map_drop)
```

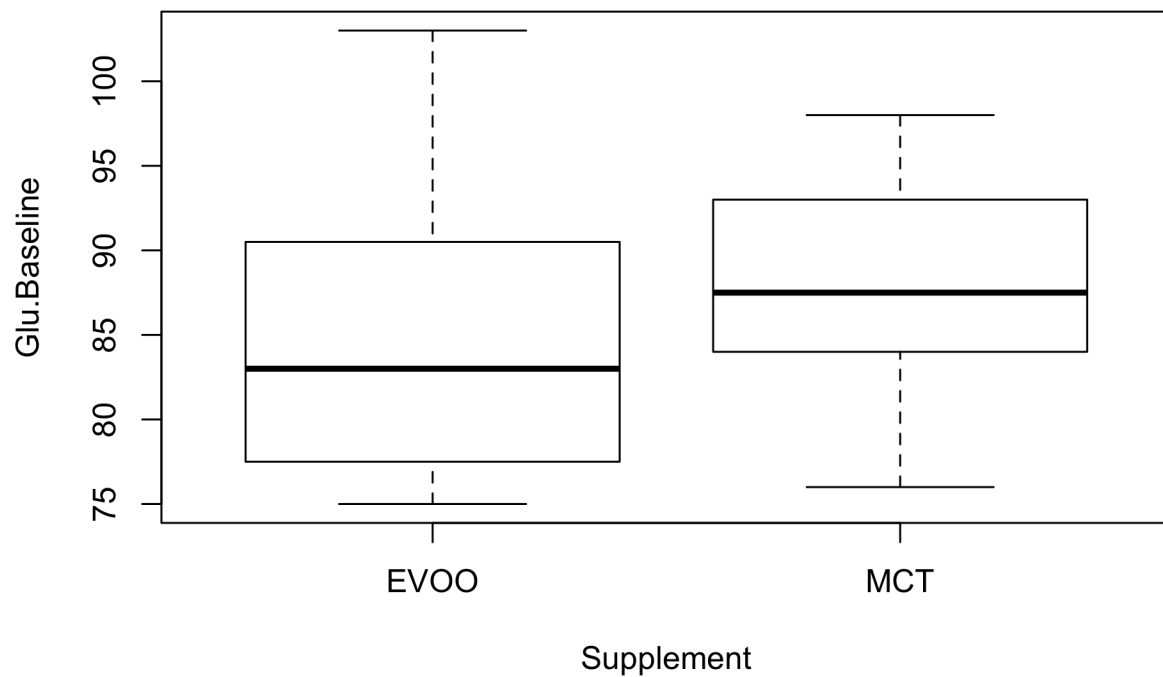


```
t.test(LDL.Baseline ~ Supplement, data = map_drop) # p-val = 0.49
```

```
##
## Welch Two Sample t-test
##
## data: LDL.Baseline by Supplement
## t = 0.6949, df = 29.657, p-value = 0.4925
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -13.94651 28.32151
## sample estimates:
## mean in group EVOO mean in group MCT
## 97.2500 90.0625
```

```
# view glucose
```

```
plot(Glu.Baseline ~ Supplement, data = map_drop)
```

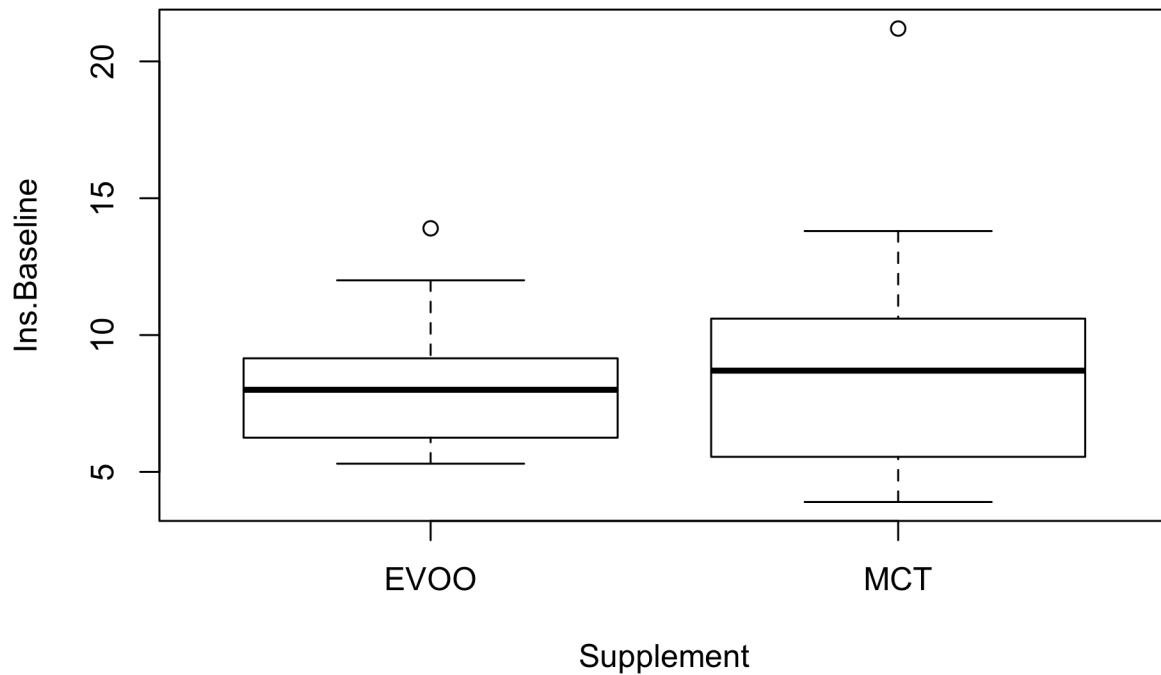


```
t.test(Glu.Baseline ~ Supplement, data = map_drop) # p-val = 0.31
```

```
##
##  Welch Two Sample t-test
##
## data:  Glu.Baseline by Supplement
## t = -1.0287, df = 28.526, p-value = 0.3123
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -7.847697  2.597697
## sample estimates:
## mean in group EVOO mean in group MCT
##           84.750           87.375
```

```
# view insulin
```

```
plot(Ins.Baseline ~ Supplement, data = map_drop) # p-val = 0.52
```



```
t.test(Ins.Baseline ~ Supplement, data = map_drop)
```

```
##
##  Welch Two Sample t-test
##
## data:  Ins.Baseline by Supplement
## t = -0.6392, df = 23.725, p-value = 0.5288
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -3.358259  1.770759
## sample estimates:
## mean in group EVOO mean in group MCT
##           8.23750           9.03125
```

```
# get p-value for each blood results for plotting (Welch two sample t-test)
```

```
myvals <- NULL
```

```
myvals[1] <- t.test((Cholesterol.Final - Cholesterol.Baseline) ~ Supplement, data = map_drop)$p.value
myvals[2] <- t.test((map_drop$Trigs.Final - map_drop$Trigs.Baseline) ~ map_drop$Supplement)$p.value
myvals[3] <- t.test((map_drop$HDL.Final - map_drop$HDL.Baseline) ~ map_drop$Supplement)$p.value
myvals[4] <- t.test((map_drop$LDL.Final - map_drop$LDL.Baseline) ~ map_drop$Supplement)$p.value
myvals[5] <- t.test((map_drop$NonHDL.Final - map_drop$NonHDL.Chol.Baseline) ~ map_drop$Supplement)$p.value
myvals[6] <- t.test((map_drop$Glu.Final - map_drop$Glu.Baseline) ~ map_drop$Supplement)$p.value
myvals[7] <- t.test((map_drop$Ins.Final - map_drop$Ins.Baseline) ~ map_drop$Supplement)$p.value
myvals[8] <- t.test((map_drop$HOMA.IR.Final - map_drop$Homa.IR.Baseline) ~ map_drop$Supplement)$p.value
```

```
myvals <- p.adjust(myvals, method = "fdr")
```

```
myvals # after adjustment for multiple comparisons
```



```
## [1] 0.2120705 0.9269963 0.8979897 0.1135247 0.1135247 1.0000000 0.8979897
## [8] 0.8979897
```

```
# Cholesterol
```

```
Chole <- ggplot(map_long_drop, aes(x = Blood.draw, y = Cholesterol)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")
```

```
# Triglycerides
```

```
Trigs <- ggplot(map_long_drop, aes(x = Blood.draw, y = Trigs)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")
```

```
# HDL
```

```
HDL <- ggplot(map_long_drop, aes(x = Blood.draw, y = HDL)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")
```

```
# LDL
```

```
LDL <- ggplot(map_long_drop, aes(x = Blood.draw, y = LDL)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")
```

```
# Non-HDL Chol
```

```
nonHDL.Chol <- ggplot(map_long_drop, aes(x = Blood.draw, y = NonHDL.Chol)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")
```

```
# Glu
```

```

Glu <- ggplot(map_long_drop, aes(x = Blood.draw, y = Glu)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")

#Insulin
Ins <- ggplot(map_long_drop, aes(x = Blood.draw, y = Ins)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")

# Homa.ir
Homa.IR <- ggplot(map_long_drop, aes(x = Blood.draw, y = Homa.IR)) +
  geom_point(aes(group = UserName, color = Supplement)) +
  geom_line(aes(group = UserName, color = Supplement)) +
  facet_grid(~Supplement) +
  geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE, color = "grey") +
  scale_color_manual(values = c("#e66101", "#5e3c99"))+
  theme(legend.position = "none")

```

```

plot_grid(Chole, Trigs , HDL, LDL, nonHDL.Chol, Glu, Ins, Homa.IR, ncol = 2)

```

```

## Warning: Removed 4 rows containing non-finite values (stat_smooth).
## Warning: Removed 4 rows containing missing values (geom_point).
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```

Warning: Removed 4 rows containing missing values (geom_point).

