Woods\_Defense\_Stats\_10-22-22.R

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library(tidyverse)  
library(readxl)  
library(lmerTest)  
library(multcomp)  
library(emmeans)  
  
setwd("C:/Users/Phil/Dropbox/Thesis- Stretch Activation/Data/Woods - Master's Thesis/Project/Tension + AaBbCc")  
  
my\_data <- read\_excel("SA-Fatigue\_Tension+Step+Kinetics\_PW\_10-28-22.xlsx",   
 sheet = "Included",  
 skip = 5,  
 na="") %>%   
 filter(Exp\_Con\_Num %in% c(3,5,6)) %>%   
 filter(fiber\_type\_num %in% c(1:4)) %>%   
 filter(Ran\_Num == 1)  
  
### Within Group Differences (changes within a fiber type) ----------------------------------------------------  
  
### MHC I......  
  
fiberI <- my\_data %>%   
 filter(fiber\_type == "I")  
  
fiberI.p3 <- fiberI %>%   
 filter(P3\_num == 1)  
  
## Repeated measured linear mixed model  
fiberI.f0.fit <- lmer(Po\_Post\_Step ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
anova(fiberI.f0.fit)  
  
## Getting estimated marginal means  
(I\_F0\_emm <- emmeans(fiberI.f0.fit, specs = "Exp\_Con"))  
  
# Post-hoc tests (two types)  
(I\_F0\_posthoc <- summary(glht(fiberI.f0.fit,  
 linfct = mcp(Exp\_Con = "Tukey")))  
)  
# this from example I found online that also used linear model  
# I\_F0\_posthoc <- summary(glht(fiberI.f0.fit,   
# linfct = mcp(Exp\_Con = "Tukey")),  
# test = adjusted(type = "bonferroni"))  
  
# # this from youtube video I found that used emmeans on model (did not show creation of model)  
# I\_tukey <- contrast(I\_F0\_emm,  
# method = "pairwise")  
# summary(I\_tukey)  
# #   
# # I\_tukey.2 <- contrast(I\_eff,   
# # method = "pairwise",  
# # adjust = "bonferroni")  
  
  
fiberI.fsa.fit <- lmer(Fsa ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.fsa.fit)  
(I\_Fsa\_emm <- emmeans(fiberI.fsa.fit, specs = "Exp\_Con"))  
# (I\_Fsa\_posthoc <- summary(glht(fiberI.fsa.fit,   
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
fiberI.ratio.fit <- lmer(FsaF0 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.ratio.fit)  
(I\_ratio\_emm <- emmeans(fiberI.ratio.fit, specs = "Exp\_Con"))  
# (I\_ratio\_posthoc <- summary(glht(fiberI.ratio.fit,   
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
fiberI.a2.fit <- lmer(a2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.a2.fit)  
(I\_a2\_emm <- emmeans(fiberI.a2.fit, specs = "Exp\_Con"))  
# (I\_a2\_posthoc <- summary(glht(fiberI.a2.fit,   
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberI.a3.fit <- lmer(a3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.a3.fit)  
(I\_a3\_emm <- emmeans(fiberI.a3.fit, specs = "Exp\_Con"))  
# (I\_a3\_posthoc <- summary(glht(fiberI.a3.fit,   
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberI.a4.fit <- lmer(a4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.a4.fit)  
(I\_a4\_emm <- emmeans(fiberI.a4.fit, specs = "Exp\_Con"))  
# (I\_a4\_posthoc <- summary(glht(fiberI.a4.fit,  
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberI.r2.fit <- lmer(r2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.r2.fit)  
(I\_r2\_emm <- emmeans(fiberI.r2.fit, specs = "Exp\_Con"))  
# (I\_r2\_posthoc <- summary(glht(fiberI.r2.fit,   
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberI.r3.fit <- lmer(r3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.r3.fit)  
(I\_r3\_emm <- emmeans(fiberI.r3.fit, specs = "Exp\_Con"))  
# (I\_r3\_posthoc <- summary(glht(fiberI.r3.fit,   
# linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberI.t3.fit <- lmer(t3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
anova(fiberI.t3.fit)  
(I\_t3\_emm <- emmeans(fiberI.t3.fit, specs = "Exp\_Con"))  
# (I\_r3\_posthoc <- summary(glht(fiberI.r3.fit,   
#   
  
fiberI.r4.fit <- lmer(r4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberI)  
# anova(fiberI.r4.fit)  
(I\_r4\_emm <- emmeans(fiberI.r4.fit, specs = "Exp\_Con"))  
# I\_r4\_posthoc <- summary(glht(fiberI.r4.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
### MHC IIA .......  
  
fiberIIA <- my\_data %>%   
 filter(fiber\_type == "IIA")  
  
fiberIIA.p3 <- fiberIIA %>%   
 filter(P3\_num == 1)  
  
fiberIIA.f0.fit <- lmer(Po\_Post\_Step ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA)  
anova(fiberIIA.f0.fit)  
(IIA\_F0\_emm <- emmeans(fiberIIA.f0.fit, specs = "Exp\_Con"))  
(IIA\_F0\_posthoc <- summary(glht(fiberIIA.f0.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.fsa.fit <- lmer(Fsa ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.fsa.fit)  
(IIA\_Fsa\_emm <- emmeans(fiberIIA.fsa.fit, specs = "Exp\_Con"))  
(IIA\_Fsa\_posthoc <- summary(glht(fiberIIA.fsa.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.ratio.fit <- lmer(FsaF0 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.ratio.fit)  
(IIA\_ratio\_emm <- emmeans(fiberIIA.ratio.fit, specs = "Exp\_Con"))  
(IIA\_ratio\_posthoc <- summary(glht(fiberIIA.ratio.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.a2.fit <- lmer(a2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.a2.fit)  
(IIA\_a2\_emm <- emmeans(fiberIIA.a2.fit, specs = "Exp\_Con"))  
(IIA\_a2\_posthoc <- summary(glht(fiberIIA.a2.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.a3.fit <- lmer(a3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.a3.fit)  
(IIA\_a3\_emm <- emmeans(fiberIIA.a3.fit, specs = "Exp\_Con"))  
(IIA\_a3\_posthoc <- summary(glht(fiberIIA.a3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.a4.fit <- lmer(a4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.a4.fit)  
(IIA\_a4\_emm <- emmeans(fiberIIA.a4.fit, specs = "Exp\_Con"))  
(IIA\_a4\_posthoc <- summary(glht(fiberIIA.a4.fit,  
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.r2.fit <- lmer(r2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.r2.fit)  
(IIA\_r2\_emm <- emmeans(fiberIIA.r2.fit, specs = "Exp\_Con"))  
(IIA\_r2\_posthoc <- summary(glht(fiberIIA.r2.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.r3.fit <- lmer(r3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.r3.fit)  
(IIA\_r3\_emm <- emmeans(fiberIIA.r3.fit, specs = "Exp\_Con"))  
(IIA\_r3\_posthoc <- summary(glht(fiberIIA.r3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.r3.fit <- lmer(r3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3,  
 control = lmerControl(optimizer = "Nelder\_Mead"))  
anova(fiberIIA.r3.fit)  
(IIA\_r3\_emm <- emmeans(fiberIIA.r3.fit, specs = "Exp\_Con"))  
(IIA\_r3\_posthoc <- summary(glht(fiberIIA.r3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIA.t3.fit <- lmer(t3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
anova(fiberIIA.t3.fit)  
(IIA\_t3\_emm <- emmeans(fiberIIA.t3.fit, specs = "Exp\_Con"))  
(IIA\_t3\_posthoc <- summary(glht(fiberIIA.t3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
fiberIIA.t3.fit <- lmer(t3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3,  
 control = lmerControl(optimizer = "Nelder\_Mead"))  
anova(fiberIIA.t3.fit)  
(IIA\_t3\_emm <- emmeans(fiberIIA.t3.fit, specs = "Exp\_Con"))  
(IIA\_t3\_posthoc <- summary(glht(fiberIIA.t3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
  
fiberIIA.r4.fit <- lmer(r4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3)  
  
fiberIIA.r4.fit <- lmer(r4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIA.p3,  
 control = lmerControl(optimizer = "Nelder\_Mead"))  
anova(fiberIIA.r4.fit)  
(IIA\_r4\_emm <- emmeans(fiberIIA.r4.fit, specs = "Exp\_Con"))  
(IIA\_r4\_posthoc <- summary(glht(fiberIIA.r4.fit,  
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
### MHC IIX .......  
  
fiberIIX <- my\_data %>%   
 filter(fiber\_type == "IIX")  
fiberIIX.p3 <- fiberIIX %>%   
 filter(P3\_num ==1)  
  
fiberIIX.f0.fit <- lmer(Po\_Post\_Step ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX)  
anova(fiberIIX.f0.fit)  
(IIX\_F0\_emm <- emmeans(fiberIIX.f0.fit, specs = "Exp\_Con"))  
(IIX\_F0\_posthoc <- summary(glht(fiberIIX.f0.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIX.fsa.fit <- lmer(Fsa ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.fsa.fit)  
(IIX\_Fsa\_emm <- emmeans(fiberIIX.fsa.fit, specs = "Exp\_Con"))  
(IIX\_Fsa\_posthoc <- summary(glht(fiberIIX.fsa.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIX.ratio.fit <- lmer(FsaF0 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.ratio.fit)  
(IIX\_ratio\_emm <- emmeans(fiberIIX.ratio.fit, specs = "Exp\_Con"))  
(IIX\_ratio\_posthoc <- summary(glht(fiberIIX.ratio.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIX.a2.fit <- lmer(a2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.a2.fit)  
(IIX\_a2\_emm <- emmeans(fiberIIX.a2.fit, specs = "Exp\_Con"))  
# IIX\_a2\_posthoc <- summary(glht(fiberIIX.a2.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
fiberIIX.a3.fit <- lmer(a3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.a3.fit)  
(IIX\_a3\_emm <- emmeans(fiberIIX.a3.fit, specs = "Exp\_Con"))  
# IIX\_a3\_posthoc <- summary(glht(fiberIIX.a3.fit,  
# linfct = mcp(Exp\_Con = "Tukey")))  
  
fiberIIX.a4.fit <- lmer(a4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.a4.fit)  
(IIX\_a4\_emm <- emmeans(fiberIIX.a4.fit, specs = "Exp\_Con"))  
# IIX\_a4\_posthoc <- summary(glht(fiberIIX.a4.fit,  
# linfct = mcp(Exp\_Con = "Tukey")))  
  
fiberIIX.r2.fit <- lmer(r2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.r2.fit)  
(IIX\_r2\_emm <- emmeans(fiberIIX.r2.fit, specs = "Exp\_Con"))  
# IIX\_r2\_posthoc <- summary(glht(fiberIIX.r2.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
fiberIIX.r3.fit <- lmer(r3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.r3.fit)  
(IIX\_r3\_emm <- emmeans(fiberIIX.r3.fit, specs = "Exp\_Con"))  
(IIX\_r3\_posthoc <- summary(glht(fiberIIX.r3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIX.t3.fit <- lmer(t3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.t3.fit)  
(IIX\_t3\_emm <- emmeans(fiberIIX.t3.fit, specs = "Exp\_Con"))  
(IIX\_t3\_posthoc <- summary(glht(fiberIIX.t3.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIX.r4.fit <- lmer(r4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIX.p3)  
anova(fiberIIX.r4.fit)  
(IIX\_r4\_emm <- emmeans(fiberIIX.r4.fit, specs = "Exp\_Con"))  
(IIX\_r4\_posthoc <- summary(glht(fiberIIX.r4.fit,  
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
### MHC IIB .......  
  
fiberIIB <- my\_data %>%   
 filter(fiber\_type == "IIB")  
  
fiberIIB.f0.fit <- lmer(Po\_Post\_Step ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.f0.fit)  
(IIB\_F0\_emm <- emmeans(fiberIIB.f0.fit, specs = "Exp\_Con"))  
(IIB\_F0\_posthoc <- summary(glht(fiberIIB.f0.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
fiberIIB.Fsa.fit <- lmer(Fsa ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.Fsa.fit)  
(IIB\_Fsa\_emm <- emmeans(fiberIIB.Fsa.fit, specs = "Exp\_Con"))  
(IIB\_Fsa\_posthoc <- summary(glht(fiberIIB.Fsa.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
fiberIIB.ratio.fit <- lmer(FsaF0 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.ratio.fit)  
(IIB\_ratio\_emm <- emmeans(fiberIIB.ratio.fit, specs = "Exp\_Con"))  
(IIB\_ratio\_posthoc <- summary(glht(fiberIIB.ratio.fit,   
 linfct = mcp(Exp\_Con = "Tukey"))))  
  
  
fiberIIB.a2.fit <- lmer(a2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.a2.fit)  
(IIB\_a2\_emm <- emmeans(fiberIIB.a2.fit, specs = "Exp\_Con"))  
# IIB\_a2\_posthoc <- summary(glht(fiberIIB.a2.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
fiberIIB.a3.fit <- lmer(a3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.a3.fit)  
(IIB\_a3\_emm <- emmeans(fiberIIB.a3.fit, specs = "Exp\_Con"))  
# IIB\_a3\_posthoc <- summary(glht(fiberIIB.a3.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
fiberIIB.a4.fit <- lmer(a4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.a4.fit)  
(IIB\_a4\_emm <- emmeans(fiberIIB.a4.fit, specs = "Exp\_Con"))  
# IIB\_a4\_posthoc <- summary(glht(fiberIIB.a4.fit,  
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
fiberIIB.r2.fit <- lmer(r2 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.r2.fit)  
(IIB\_r2\_emm <- emmeans(fiberIIB.r2.fit, specs = "Exp\_Con"))  
# IIB\_r2\_posthoc <- summary(glht(fiberIIB.r2.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
fiberIIB.r3.fit <- lmer(r3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.r3.fit)  
(IIB\_r3\_emm <- emmeans(fiberIIB.r3.fit, specs = "Exp\_Con"))  
# IIB\_r3\_posthoc <- summary(glht(fiberIIB.r3.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
fiberIIB.t3.fit <- lmer(t3 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.t3.fit)  
(IIB\_t3\_emm <- emmeans(fiberIIB.t3.fit, specs = "Exp\_Con"))  
# IIB\_r3\_posthoc <- summary(glht(fiberIIB.r3.fit,   
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
fiberIIB.r4.fit <- lmer(r4 ~ Exp\_Con + (1 + as.factor(Exp\_Con) |Mouse), data = fiberIIB)  
anova(fiberIIB.r4.fit)  
(IIB\_r4\_emm <- emmeans(fiberIIB.r4.fit, specs = "Exp\_Con"))  
# IIB\_r4\_posthoc <- summary(glht(fiberIIB.r4.fit,  
# linfct = mcp(Exp\_Con = "Tukey")))  
  
  
  
### Between Group Differences (changes within experimental group) ---------------------------------------------------------------------  
  
## Fatigue pCa 5.2.........................................  
  
# fat\_pca\_5.2 <- my\_data %>%   
# filter(Exp\_Con\_Num == 2)  
#   
# fat\_pca\_5.2.p3 <- fat\_pca\_5.2 %>%   
# filter(P3\_num == 1)  
#   
# f5.2\_f0\_model <- lmer(Po\_Post\_Step ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.2)  
# anova(f5.2\_f0\_model)  
# # f5.2\_f0\_emm <- emmeans(f5.2\_f0\_model, specs = "fiber\_type")  
# # f5.2\_f0\_posthoc <- summary(glht(f5.2\_f0\_model,   
# # linfct = mcp(fiber\_type = "Tukey")))  
#   
# f5.2\_fsa\_model <- lmer(Fsa ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.2.p3)  
# anova(f5.2\_fsa\_model)  
# # f5.2\_fsa\_emm <- emmeans(f5.2\_fsa\_model, specs = "fiber\_type")  
# # f5.2\_fsa\_posthoc <- summary(glht(f5.2\_fsa\_model,  
# # linfct = mcp(fiber\_type = "Tukey")))  
#   
# f5.2\_ratio\_model <- lmer(FsaF0~ fiber\_type + (1|Mouse), data = fat\_pca\_5.2.p3)  
# anova(f5.2\_ratio\_model)  
# f5.2\_ratio\_emm <- emmeans(f5.2\_ratio\_model, specs = "fiber\_type")  
# # f5.2\_ratio\_posthoc <- summary(glht(f5.2\_ratio\_model,  
# # linfct = mcp(fiber\_type = "Tukey")))  
  
  
## Fatigue pCa 5.1............................................  
fat\_pca\_5.1 <- my\_data %>%   
 filter(Exp\_Con\_Num == 3)  
  
fat\_pca\_5.1.p3 <- fat\_pca\_5.1 %>%   
 filter(P3\_num == 1 )  
  
f5.1\_f0\_model <- lmer(Po\_Post\_Step ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.1)  
anova(f5.1\_f0\_model)  
f5.1\_f0\_emm <- emmeans(f5.1\_f0\_model, specs = "fiber\_type")  
f5.1\_f0\_posthoc <- summary(glht(f5.1\_f0\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f5.1\_fsa\_model <- lmer(Fsa ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.1.p3)  
anova(f5.1\_fsa\_model)  
f5.1\_fsa\_emm <- emmeans(f5.1\_fsa\_model, specs = "fiber\_type")  
f5.1\_fsa\_posthoc <- summary(glht(f5.1\_fsa\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f5.1\_ratio\_model <- lmer(FsaF0~ fiber\_type + (1|Mouse), data = fat\_pca\_5.1.p3)  
anova(f5.1\_ratio\_model)  
f5.1\_ratio\_emm <- emmeans(f5.1\_ratio\_model, specs = "fiber\_type")  
f5.1\_ratio\_posthoc <- summary(glht(f5.1\_ratio\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f5.1\_r2\_model <- lmer(r2 ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.1.p3)  
anova(f5.1\_r2\_model)  
f5.1\_r2\_emm <- emmeans(f5.1\_r2\_model, specs = "fiber\_type")  
f5.1\_r2\_posthoc <- summary(glht(f5.1\_r2\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
### How am I getting a negative number??  
f5.1\_r3\_model <- lmer(r3 ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.1.p3)  
anova(f5.1\_r3\_model)  
f5.1\_r3\_emm <- emmeans(f5.1\_r3\_model, specs = "fiber\_type")  
f5.1\_r3\_posthoc <- summary(glht(f5.1\_r3\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f5.1\_r4\_model <- lmer(r4 ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.1.p3)  
anova(f5.1\_r4\_model)  
f5.1\_r4\_emm <- emmeans(f5.1\_r4\_model, specs = "fiber\_type")  
f5.1\_r4\_posthoc <- summary(glht(f5.1\_r4\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
## Fatigue pCa 5.0..........................................  
# fat\_pca\_5.0 <- my\_data %>%   
# filter(Exp\_Con\_Num == 4)  
#   
# fat\_pca\_5.0.p3 <- fat\_pca\_5.0 %>%   
# filter(P3\_num == 1 )  
#   
# f5.0\_f0\_model <- lmer(Po\_Post\_Step ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.0)  
# anova(f5.0\_f0\_model)  
# f5.0\_f0\_emm <- emmeans(f5.0\_f0\_model, specs = "fiber\_type")  
# # f5.0\_f0\_posthoc <- summary(glht(f5.0\_f0\_model,  
# # linfct = mcp(fiber\_type = "Tukey")))  
#   
# f5.0\_fsa\_model <- lmer(Fsa ~ fiber\_type + (1|Mouse), data = fat\_pca\_5.0.p3)  
# anova(f5.0\_fsa\_model)  
# f5.0\_fsa\_emm <- emmeans(f5.0\_fsa\_model, specs = "fiber\_type")  
# # f5.0\_fsa\_posthoc <- summary(glht(f5.0\_fsa\_model,  
# # linfct = mcp(fiber\_type = "Tukey")))  
#   
# f5.0\_ratio\_model <- lmer(FsaF0~ fiber\_type + (1|Mouse), data = fat\_pca\_5.0.p3)  
# anova(f5.0\_ratio\_model)  
# f5.0\_ratio\_emm <- emmeans(f5.0\_ratio\_model, specs = "fiber\_type")  
# f5.0\_ratio\_posthoc <- summary(glht(f5.0\_ratio\_model,  
# linfct = mcp(fiber\_type = "Tukey")))  
#   
  
## Fatigue pCa 4.5...........................................  
fat\_pca\_4.5 <- my\_data %>%   
 filter(Exp\_Con\_Num == 5)  
  
fat\_pca\_4.5.p3 <- fat\_pca\_4.5 %>%   
 filter(P3\_num==1)  
  
f4.5\_f0\_model <- lmer(Po\_Post\_Step ~ fiber\_type + (1|Mouse), data = fat\_pca\_4.5)  
anova(f4.5\_f0\_model)  
f4.5\_f0\_emm <- emmeans(f4.5\_f0\_model, specs = "fiber\_type")  
# f4.5\_f0\_posthoc <- summary(glht(f4.5\_f0\_model,  
# linfct = mcp(fiber\_type = "Tukey")))  
  
f4.5\_fsa\_model <- lmer(Fsa ~ fiber\_type + (1|Mouse), data = fat\_pca\_4.5.p3)  
anova(f4.5\_fsa\_model)  
f4.5\_fsa\_emm <- emmeans(f4.5\_fsa\_model, specs = "fiber\_type")  
f4.5\_fsa\_posthoc <- summary(glht(f4.5\_fsa\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f4.5\_ratio\_model <- lmer(FsaF0~ fiber\_type + (1|Mouse), data = fat\_pca\_4.5.p3)  
anova(f4.5\_ratio\_model)  
f4.5\_ratio\_emm <- emmeans(f4.5\_ratio\_model, specs = "fiber\_type")  
f4.5\_ratio\_posthoc <- summary(glht(f4.5\_ratio\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f4.5\_r2\_model <- lmer(r2 ~ fiber\_type + (1|Mouse), data = fat\_pca\_4.5.p3)  
anova(f4.5\_r2\_model)  
f4.5\_r2\_emm <- emmeans(f4.5\_r2\_model, specs = "fiber\_type")  
f4.5\_r2\_posthoc <- summary(glht(f4.5\_r2\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f4.5\_r3\_model <- lmer(r3 ~ fiber\_type + (1|Mouse), data = fat\_pca\_4.5.p3)  
anova(f4.5\_r3\_model)  
f4.5\_r3\_emm <- emmeans(f4.5\_r3\_model, specs = "fiber\_type")  
f4.5\_r3\_posthoc <- summary(glht(f4.5\_r3\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
f4.5\_r4\_model <- lmer(r4 ~ fiber\_type + (1|Mouse), data = fat\_pca\_4.5.p3)  
anova(f4.5\_r4\_model)  
f4.5\_r4\_emm <- emmeans(f4.5\_r3\_model, specs = "fiber\_type")  
f4.5\_r4\_posthoc <- summary(glht(f4.5\_r4\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
  
## Active............................................  
act <- my\_data %>%   
 filter(Exp\_Con\_Num==6)  
  
act\_f0\_model <- lmer(Po\_Post\_Step ~ fiber\_type + (1|Mouse), data = act)  
anova(act\_f0\_model)  
act\_f0\_emm <- emmeans(act\_f0\_model, specs = "fiber\_type")  
# act\_f0\_posthoc <- summary(glht(act\_f0\_model,  
# linfct = mcp(fiber\_type = "Tukey")))  
  
act\_fsa\_model <- lmer(Fsa ~ fiber\_type + (1|Mouse), data = act)  
anova(act\_fsa\_model)  
act\_fsa\_emm <- emmeans(act\_fsa\_model, specs = "fiber\_type")  
act\_fsa\_posthoc <- summary(glht(act\_fsa\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
act\_ratio\_model <- lmer(FsaF0~ fiber\_type + (1|Mouse), data = act)  
anova(act\_ratio\_model)  
act\_ratio\_emm <- emmeans(act\_ratio\_model, specs = "fiber\_type")  
act\_ratio\_posthoc <- summary(glht(act\_ratio\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
act\_r2\_model <- lmer(r2 ~ fiber\_type + (1|Mouse), data = act)  
anova(act\_r2\_model)  
act\_r2\_emm <- emmeans(act\_f0\_model, specs = "fiber\_type")  
act\_r2\_posthoc <- summary(glht(act\_r2\_model,  
 linfct = mcp(fiber\_type = "Tukey")))  
  
act\_r3\_model <- lmer(r3 ~ fiber\_type + (1|Mouse), data = act)  
anova(act\_r3\_model)  
(act\_r3\_emm <- emmeans(act\_r3\_model, specs = "fiber\_type"))  
(act\_r3\_posthoc <- summary(glht(act\_r3\_model,  
 linfct = mcp(fiber\_type = "Tukey"))))  
  
act\_r4\_model <- lmer(r4 ~ fiber\_type + (1|Mouse), data = act)  
anova(act\_r4\_model)  
act\_r4\_emm <- emmeans(act\_f0\_model, specs = "fiber\_type")  
act\_r4\_posthoc <- summary(glht(act\_r4\_model,  
 linfct = mcp(fiber\_type = "Tukey")))