

# Fecal matter transplant in Huntington's disease (Male)

Data Analysis

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## Executive Summary

- For repeated measures, Linear Mixed Models (LMM) were fitted with time as a covariate.
- For one time point measures, Linear Mixed Models (LMM) were fitted with all two way interactions except for ATB\*FMT (No observations for FMT and no ATB). However, only main effects were considered for variables that had few samples when covariates are considered together. For example IL17A-w14 had only 3 samples in HD-FMT group but when considered separately HD had 15 samples and FMT had 8 samples. Thus, IL17A-w14 was modeled without interactions.
- Claspings score was modeled using a cumulative link mixed model.
- For all models with significant effects on categorical variables (i.e, genotype, FMT, ATB), pairwise comparisons were performed using emmeans package.

## 1 Data Input

```
# load data from the csv file first. (the csv file is from your xlsx file)
data <- read_excel("Data/CarolGubert_FMT_male_data_July2021_final.xlsx")
data <- as.data.frame(data)
# extract group information
data$genotype <- factor(data$genotype, levels = c("WT", "HD"))
data$ATB <- factor(data$ATB, levels = c("NO", "YES"))
data$FMT <- factor(data$FMT, levels = c("NO", "YES"))
data$BOX <- factor(data$BOX)

Treatment <- ifelse((data$ATB=="YES"&data$FMT=="YES"), "ATB_FMT",
```

```

      ifelse((data$ATB=="YES"&data$FMT=="NO"),"Only ATB","No treatment"))%>%
      factor(levels = c("No treatment","Only ATB","ATB_FMT"))
data.new<-add_column(data, Treatment = Treatment, .after = 5)

```

## 2 Linear Mixed Models - Repeated measures analysis

```

data.repeated.1<-data.new[,c(1:6,8:37,61:75,91:116)]
long_data.repeated.1<-data.repeated.1 %>%
  gather(v, value, BodyWeight_W6:FecalWaterContent_W20) %>%
  separate(v, c("col", "Time"),sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)
long_data.repeated.1$Time <-as.numeric(long_data.repeated.1$Time)
#filter out Time 6 and 7
long_data.repeated.1<-long_data.repeated.1%>%filter(Time!=6 &Time!=7)
long_data.repeated.1$Time<-long_data.repeated.1$Time-7

```

### 2.1 LMM for Body Weight, Weight Gain, Rotarod, Fecal Output and Fecal water content

```

#subset(long_data.repeated.1, !is.na(BodyWeight)) %>%
#group_by(genotype, FMT, ATB) %>%
#tally()

#subset(long_data.repeated.1, !is.na(BodyWeight)) %>%
#group_by(genotype, Treatment, Time) %>%
#tally()%>% summary()

#Interaction between ATB & FMT not considered as all no ATB had no FMT
BodyWeight.lmm <- lme(BodyWeight ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time,random = (~1|BOX),
  data = subset(long_data.repeated.1, !is.na(BodyWeight)))

WeightGain.lmm <- lme(WeightGain ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time,random = (~1|BOX),
  data = subset(long_data.repeated.1, !is.na(WeightGain)))

Rotarod.lmm <- lme(Rotarod ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time,random = (~1|BOX),
  data = subset(long_data.repeated.1, !is.na(Rotarod)))

FecalOutput.lmm <- lme(FecalOutput ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time,random = (~1|BOX),

```

```

data = subset(long_data.repeated.1, !is.na(FecalOutput)))

FecalWaterContent.lmm <- lme(FecalWaterContent ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time, random = (~1|BOX),
  data = subset(long_data.repeated.1, !is.na(FecalWaterContent)))

stargazer(BodyWeight.lmm, WeightGain.lmm, Rotarod.lmm,
  FecalWaterContent.lmm, FecalOutput.lmm, type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"), notes.append = FALSE)

```

Dependent variable:					
	BodyWeight (1)	WeightGain (2)	Rotarod (3)	FecalWaterContent (4)	FecalOutput (5)
genotypeHD	-0.7785 p = 0.4161	2.5896 p = 0.4955	-8.1307 p = 0.6406	-14.1599 p = 0.1225	1.9431 p = 0.2412
TreatmentOnly ATB	-3.0662** p = 0.0041	-7.8967+ p = 0.0662	21.1478 p = 0.2676	4.8862 p = 0.6306	-0.7293 p = 0.6924
TreatmentATB_FMT	-1.1681 p = 0.2681	-3.8837 p = 0.3519	15.7874 p = 0.4028	1.3579 p = 0.8897	0.2536 p = 0.8867
Time	0.6337*** p = 0.0000	2.5328*** p = 0.0000	3.3567** p = 0.0012	1.6068*** p = 0.000005	0.0298 p = 0.7119
genotypeHD:TreatmentOnly ATB	4.4431*** p = 0.0002	11.5724** p = 0.0100	-35.9295+ p = 0.0955	26.0433* p = 0.0140	3.6911+ p = 0.0569
genotypeHD:TreatmentATB_FMT	1.0657 p = 0.4370	-1.2411 p = 0.8108	-30.1095 p = 0.2137	21.4059+ p = 0.0926	2.2866 p = 0.3023
genotypeHD:Time	-0.6817*** p = 0.0000	-2.8962*** p = 0.0000	-9.1999*** p = 0.0000	-0.2176 p = 0.5202	-0.6899*** p = 0.0000
TreatmentOnly ATB:Time	0.0365 p = 0.4596	0.0886 p = 0.6414	-1.3462 p = 0.2768	-0.7961+ p = 0.0548	0.0506 p = 0.5991
TreatmentATB_FMT:Time	0.0951+ p = 0.0528	0.2528 p = 0.1792	-3.1172* p = 0.0116	-0.8635* p = 0.0361	0.0780 p = 0.4151
Constant	26.9199*** p = 0.0000	108.6238*** p = 0.0000	164.2514*** p = 0.0000	42.5601*** p = 0.0000	12.4161*** p = 0.0000

```
## -----
## Observations          1378          715          1346          710          713
## Log Likelihood        -3198.6550 -2497.1390 -7412.5200 -3028.3720 -2007.4000
## Akaike Inf. Crit.      6421.3090  5018.2780 14849.0400  6080.7430  4038.8000
## Bayesian Inf. Crit.    6483.9620  5072.9760 14911.4100  6135.3560  4093.4640
## =====
## Note:                  + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

## 2.2 LMM for Food and Water intake

```
FoodIntake.data<-data.new[,c(1:6,38:49)]
long_FoodIntake.data<-FoodIntake.data %>%
  gather(v, value, FoodIntake_W9:FoodIntake_W20) %>%
  separate(v, c("col", "Time"),sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)
long_FoodIntake.data$Time <-as.numeric(long_FoodIntake.data$Time)
long_FoodIntake.data$Time<-long_FoodIntake.data$Time-8

WaterIntake.data<-data.new[,c(1:6,50:60)]
long_WaterIntake.data<-WaterIntake.data %>%
  gather(v, value, WaterIntake_W10:WaterIntake_W20) %>%
  separate(v, c("col", "Time"),sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)
long_WaterIntake.data$Time <-as.numeric(long_WaterIntake.data$Time)
long_WaterIntake.data$Time<-long_WaterIntake.data$Time-9

FoodIntake.lmm <- lme(FoodIntake ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time,random = (~1|BOX),
  data = subset(long_FoodIntake.data, !is.na(FoodIntake)))
WaterIntake.lmm <- lme(WaterIntake ~ genotype+Treatment+Time+
  genotype:Treatment+genotype:Time+
  Treatment:Time,random = (~1|BOX),
  data = subset(long_WaterIntake.data, !is.na(WaterIntake)))
stargazer(FoodIntake.lmm,WaterIntake.lmm, type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"), notes.append = FALSE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               FoodIntake      WaterIntake
##                               (1)             (2)
## -----
```

```
## genotypeHD          0.1195*          0.2391
##                    p = 0.0135          p = 0.1308
##
## TreatmentOnly ATB    0.2039***        0.5717***
##                    p = 0.0001          p = 0.0010
##
## TreatmentATB_FMT     0.2070***        0.3296+
##                    p = 0.0004          p = 0.0578
##
## Time                 -0.0290***       -0.0469***
##                    p = 0.0000          p = 0.00005
##
## genotypeHD:TreatmentOnly ATB -0.2220*** -0.1428
##                    p = 0.000005        p = 0.4277
##
## genotypeHD:TreatmentATB_FMT -0.2221***  0.0375
##                    p = 0.0002          p = 0.8518
##
## genotypeHD:Time      -0.0034         0.0569***
##                    p = 0.4308          p = 0.000001
##
## TreatmentOnly ATB:Time -0.0020       -0.0333*
##                    p = 0.6974          p = 0.0146
##
## TreatmentATB_FMT:Time -0.0047       -0.0093
##                    p = 0.3776          p = 0.4904
##
## Constant             0.9929***        1.2985***
##                    p = 0.0000          p = 0.0000
##
## -----
## Observations          324             296
## Log Likelihood        154.5813        -103.4265
## Akaike Inf. Crit.     -285.1626        230.8530
## Bayesian Inf. Crit.   -240.1699        274.7249
## =====
## Note:                  + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

## 2.3 LMM for CFC Conditioning and Extinction

```
CFC.data<-data.new[,c(1:6,165:171)]
long_CFC.data<-CFC.data %>%
  gather(v, value, CONDT_1:CONDT_6) %>%
  separate(v, c("col", "Time"),sep="_") %>%
  arrange(ID) %>%
  spread(col, value)
long_CFC.data$Time <-as.numeric(long_CFC.data$Time)

CFC.ex.data<-data.new[,c(1:6,172:181)]
long_CFC.ex.data<-CFC.ex.data %>%
  gather(v, value, `EXT_1-5`:`EXT_41-45`) %>%
  separate(v, c("col", "Time"),sep="_") %>%
```

```

arrange(ID) %>%
spread(col, value)
long_CFC.ex.data$Time <- factor(long_CFC.ex.data$Time,ordered = TRUE,
                                levels = c('1-5', '6-10',
                                             '11-15', '16-20',
                                             '21-25', '26-30',
                                             '31-35', '36-40',
                                             '41-45'))
long_CFC.ex.data$Time = as.numeric(long_CFC.ex.data$Time)

```

```

CFC_Conditioning.lmm <- lme(CONDT ~ genotype+Treatment+Time+CONDT_Base+
                             genotype:Treatment+genotype:Time+genotype:CONDT_Base+
                             Treatment:Time+Treatment:CONDT_Base+Time:CONDT_Base,
                             random=(~1|BOX),data =subset(long_CFC.data,!is.na(CONDT )))

CFC_Extinction.lmm <- lme(EXT ~ genotype+Treatment+Time+EXT_Base+
                             genotype:Treatment+genotype:Time+genotype:EXT_Base+
                             Treatment:Time+Treatment:EXT_Base+Time:EXT_Base,
                             random=(~1|BOX),data =subset(long_CFC.ex.data,!is.na(EXT )))

stargazer(CFC_Conditioning.lmm,CFC_Extinction.lmm, type = "text",
           digits = 4,
           report = ('vc*p'),
           star.char = c("+", "*", "**", "***"),
           star.cutoffs = c(.1, .05, .01, .001),
           digit.separator = "",
           notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
           notes.append = FALSE)

```

```

##
## =====
##                               Dependent variable:
##                               -----
##                               CONDT          EXT
##                               (1)           (2)
##                               -----
## genotypeHD                    -0.9536      -15.7142**
##                               p = 0.9120      p = 0.0025
##
## TreatmentOnly ATB             3.1574        2.2257
##                               p = 0.7355      p = 0.6633
##
## TreatmentATB_FMT              3.2605        8.1952
##                               p = 0.7353      p = 0.1311
##
## Time                          15.7786***    -1.9155***
##                               p = 0.0000      p = 0.0002
##
## CONDT_Base                    4.4344***
##                               p = 0.0002
##
## EXT_Base                      1.0142***
##                               p = 0.0000

```

```
##
## genotypeHD:TreatmentOnly ATB      -1.3767      -0.7753
##                                   p = 0.8802      p = 0.8935
##
## genotypeHD:TreatmentATB_FMT        2.5462      -9.6438
##                                   p = 0.7870      p = 0.1087
##
## genotypeHD:Time                     1.0692      2.6709***
##                                   p = 0.4813      p = 0.000000
##
## genotypeHD:CONDT_Base              0.2661
##                                   p = 0.7985
##
## genotypeHD:EXT_Base                0.1023
##                                   p = 0.1881
##
## TreatmentOnly ATB:Time              -0.4149      -0.2114
##                                   p = 0.8200      p = 0.7130
##
## TreatmentATB_FMT:Time               -0.1887      -0.6628
##                                   p = 0.9198      p = 0.2583
##
## TreatmentOnly ATB:CONDT_Base        0.2672
##                                   p = 0.8551
##
## TreatmentATB_FMT:CONDT_Base        -2.6367*
##                                   p = 0.0133
##
## Time:CONDT_Base                    -0.2468+
##                                   p = 0.0835
##
## TreatmentOnly ATB:EXT_Base          -0.3969***
##                                   p = 0.000001
##
## TreatmentATB_FMT:EXT_Base           0.1283
##                                   p = 0.2153
##
## Time:EXT_Base                      -0.0703***
##                                   p = 0.0000
##
## Constant                          -19.9046**      19.2334***
##                                   p = 0.0064      p = 0.000003
##
## -----
## Observations                        522      783
## Log Likelihood                     -2491.0010      -3354.7000
## Akaike Inf. Crit.                   5016.0030      6743.4000
## Bayesian Inf. Crit.                 5087.8880      6822.3440
## =====
## Note:                               + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```



## 3 Linear Mixed Models - One Time point analysis

### 3.1 Y-maze

```
Ymaze.data<-data.new[,c(1:6,120:121)]
long_Ymaze.data<-Ymaze.data %>%
  gather(v, value, Ymaze_novelArm:Ymaze_familiarArm) %>%
  separate(v, c("col", "Arm"),sep="_") %>%
  arrange(ID) %>%
  spread(col, value)

long_Ymaze.data$Arm = factor(long_Ymaze.data$Arm,
                             levels = c("novelArm","familiarArm"),
                             labels = c("Novel","Familiar"))

Ymaze.lmm <- lme(Ymaze ~ genotype+Treatment+Arm+
                 genotype:Treatment+genotype:Arm+
                 Treatment:Arm,random=list(BOX=~1, ID=~1),
                 data =subset(long_Ymaze.data,!is.na(Ymaze)))

stargazer(Ymaze.lmm, type = "text",
           digits = 4,
           report = ('vc*p'),
           star.char = c("+", "*", "**", "***"),
           star.cutoffs = c(.1, .05, .01, .001),
           digit.separator = "",
           notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
           notes.append = FALSE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               Ymaze
## -----
## genotypeHD                    -17.1598*
##                               p = 0.0431
##
## TreatmentOnly ATB             -4.0338
##                               p = 0.6500
##
## TreatmentATB_FMT              8.2060
##                               p = 0.3454
##
## ArmFamiliar                   -2.8522
##                               p = 0.7350
##
## genotypeHD:TreatmentOnly ATB  14.2992
##                               p = 0.1543
##
## genotypeHD:TreatmentATB_FMT   2.7253
##                               p = 0.7797
```

```
##
## genotypeHD:ArmFamiliar          0.8503
##                                p = 0.9136
##
## TreatmentOnly ATB:ArmFamiliar    -10.6377
##                                p = 0.2800
##
## TreatmentATB_FMT:ArmFamiliar     -15.3970
##                                p = 0.1141
##
## Constant                        73.8479***
##                                p = 0.0000
##
## -----
## Observations                     170
## Log Likelihood                   -759.3475
## Akaike Inf. Crit.                1544.6950
## Bayesian Inf. Crit.              1584.6720
## =====
## Note:                            + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

### 3.2 Phenotypic Variables (Gut Transit Time, Gut permeability, Cecum Weight, Cecum Length, ColonLength, Y-maze difference, Y-maze index, Y-maze Dist trial1, NOR, Brain Weight, Brake Ratio)

```
dep_vars <-c("Ymaze_index", "Ymaze_Dist_trial1", "NOR_RI_5min",
             "BrainWeight", "Digigait_PropelBrakeRatio_W14",
             "GutTransitTime_W14", "GutTransitTime_W20", "FITC_w14",
             "FITC_w20", "CecumWeight_w14", "CecumWeight_w20",
             "CecumLength_w14", "CecumLength_w20",
             "ColonLength_w14", "ColonLength_w20")

p_val<-lapply(dep_vars, function(r) {
  m <- lme(formula(paste(r, "genotype+Treatment+genotype:Treatment", sep = "~")),
           random=~1|BOX, data = subset(data.new, !is.na(eval(parse(text = r))))
  assign(paste0(r, ".lmm_"), m, envir = .GlobalEnv)
  summary(m)$tTable[,5]})

stargazer(Ymaze_index.lmm_, Ymaze_Dist_trial1.lmm_,
           NOR_RI_5min.lmm_, BrainWeight.lmm_, Digigait_PropelBrakeRatio_W14.lmm_,
           type = "text",
           digits = 4,
           report = ('vc*p'),
           star.char = c("+", "*", "**", "***"),
           star.cutoffs = c(.1, .05, .01, .001),
           digit.separator = "",
           notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
           notes.append = FALSE,
           dep.var.labels.include = FALSE,
           column.labels=c("YmazeIndex", "YmazeDist", "NOR",
```

```
align=TRUE)      "BrainWeight","PropelBrakeRatio"),
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               YmazeIndex  YmazeDist  NOR      BrainWeight  PropelBrakeRatio
##                               (1)         (2)         (3)         (4)           (5)
## -----
## genotypeHD                   -0.2238    -3097.5080    -0.9825    -0.0700**    1.4822**
##                               p = 0.1310    p = 0.4623    p = 0.8634    p = 0.0033    p = 0.0044
##
## TreatmentOnly ATB            0.0526     -501.3699     0.7903     -0.0075      0.5922
##                               p = 0.7190    p = 0.9005    p = 0.8882    p = 0.7280    p = 0.2368
##
## TreatmentATB_FMT             0.0870     1392.4650     4.5609      0.0336      0.2232
##                               p = 0.5483    p = 0.7601    p = 0.4261    p = 0.1181    p = 0.6388
##
## genotypeHD:TreatmentOnly ATB 0.1328      929.3390     -7.6252      0.0190     -1.8307*
##                               p = 0.5218    p = 0.8743    p = 0.3359    p = 0.5240    p = 0.0110
##
## genotypeHD:TreatmentATB_FMT  0.2237     2227.8640     -8.0220      0.0056     -0.4834
##                               p = 0.2801    p = 0.7183    p = 0.3154    p = 0.8512    p = 0.4914
##
## Constant                     1.1261***   27415.8500***  59.8142***   0.4275***   3.4404***
##                               p = 0.0000    p = 0.0000    p = 0.0000    p = 0.0000    p = 0.0000
## -----
## Observations                  94         84         92         52         93
## Log Likelihood                -36.8822    -830.9299   -364.6142    73.4326   -157.8347
## Akaike Inf. Crit.             89.7644    1677.8600   745.2284   -130.8652   331.6694
## Bayesian Inf. Crit.           109.5831   1696.7140   764.8632   -116.2361   351.3967
## =====
## Note:                          + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```
stargazer(GutTransitTime_W14.lmm_,
  GutTransitTime_W20.lmm_,FITC_w14.lmm_,FITC_w20.lmm_,
  type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
  notes.append = FALSE,
  dep.var.labels.include = FALSE,
  column.labels=c("GutTransitTime-W14",
    "GutTransitTime-W20","FITC-W14","FITC-W20"),
  align=TRUE)
```

```
##
```

```
## =====
##                                     Dependent variable:
##                                     -----
##                                     GutTransitTime-W14 GutTransitTime-W20 FITC-W14 FITC-W20
##                                     (1) (2) (3) (4)
## -----
## genotypeHD                      36.0361      -12.2482      0.0751      0.5967*
##                                p = 0.2631      p = 0.8391      p = 0.8132 p = 0.0250
##
## TreatmentOnly ATB                11.7028      -60.2482      -0.3718      -0.0200
##                                p = 0.7143      p = 0.3242      p = 0.2326 p = 0.9293
##
## TreatmentATB_FMT                 9.2306       31.7518      -0.5159      -0.0348
##                                p = 0.7487      p = 0.5997      p = 0.1303 p = 0.8775
##
## genotypeHD:TreatmentOnly ATB    -52.6194      92.7482      0.2728      -0.3062
##                                p = 0.2533      p = 0.2775      p = 0.5377 p = 0.3657
##
## genotypeHD:TreatmentATB_FMT    -46.6216       2.1232      -0.0355      0.2578
##                                p = 0.2771      p = 0.9799      p = 0.9399 p = 0.4377
##
## Constant                       154.3806***    271.7482***    0.9959***    0.4059*
##                                p = 0.0000      p = 0.000003    p = 0.0002 p = 0.0262
##
## -----
## Observations                     87          47          41          30
## Log Likelihood                  -461.5515    -256.1310    -28.6413    -8.7940
## Akaike Inf. Crit.               939.1031     528.2621     73.2826     33.5880
## Bayesian Inf. Crit.             958.2587     541.9707     85.7254     43.0124
## =====
## Note:                          + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```
stargazer(CecumWeight_w14.lmm_,CecumWeight_w20.lmm_,CecumLength_w14.lmm_,
  CecumLength_w20.lmm_,
  type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
  notes.append = FALSE,
  dep.var.labels.include = FALSE,
  column.labels=c("CecumWeight-W14", "CecumWeight-W20",
    "CecumLength-W14", "CecumLength-W20"),
  align=TRUE)
```

```
##
## =====
##                                     Dependent variable:
##                                     -----
##                                     CecumWeight-W14 CecumWeight-W20 CecumLength-W14 CecumLength-W20
##                                     (1) (2) (3) (4)
## -----
```

```
## genotypeHD          -0.0593      0.0061      -0.0697      -0.1464
##                    p = 0.1218      p = 0.9154      p = 0.7425      p = 0.5702
##
## TreatmentOnly ATB    -0.0300      0.0893      0.0250      -0.3250
##                    p = 0.4047      p = 0.1339      p = 0.9042      p = 0.1993
##
## TreatmentATB_FMT     -0.0850*     0.0102     -0.0208      0.3583
##                    p = 0.0393      p = 0.8559      p = 0.9260      p = 0.1469
##
## genotypeHD:TreatmentOnly ATB  0.0493      -0.0649     -0.2178      0.1464
##                    p = 0.3431      p = 0.4092      p = 0.4667      p = 0.6752
##
## genotypeHD:TreatmentATB_FMT  0.0373      0.0921     -0.1770     -0.2869
##                    p = 0.5138      p = 0.2456      p = 0.5878      p = 0.4127
##
## Constant             0.4250***     0.4857***     2.7375***     2.9750***
##                    p = 0.0000      p = 0.0000      p = 0.0000      p = 0.0000
##
## -----
## Observations          42           51           42           51
## Log Likelihood        38.8129       30.4576      -16.4150     -38.2558
## Akaike Inf. Crit.    -61.6257     -44.9151      48.8300      92.5117
## Bayesian Inf. Crit.  -48.9576     -30.4618      61.4982     106.9650
## =====
## Note:                  + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```
stargazer(ColonLength_w14.lmm_,ColonLength_w20.lmm_,
  type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
  notes.append = FALSE,
  dep.var.labels.include = FALSE,
  column.labels=c("ColonLength-W14","ColonLength-W20"),
  align=TRUE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               ColonLength-W14      ColonLength-W20
##                               (1)                  (2)
##                               -----
## genotypeHD                  -0.3969              -1.2244**
##                               p = 0.3566              p = 0.0085
##
## TreatmentOnly ATB          -0.0750              -0.7750+
##                               p = 0.8561              p = 0.0740
##
## TreatmentATB_FMT            -0.3458              -0.3600
##                               p = 0.4427              p = 0.3785
```

```
##
## genotypeHD:TreatmentOnly ATB      0.1469      0.7761
##                                p = 0.8044      p = 0.1917
##
## genotypeHD:TreatmentATB_FMT      0.2493      0.3441
##                                p = 0.7031      p = 0.5558
##
## Constant      8.9625***      8.6250***
##                                p = 0.0000      p = 0.0000
##
## -----
## Observations      42      51
## Log Likelihood      -45.5742      -60.2668
## Akaike Inf. Crit.      107.1483      136.5335
## Bayesian Inf. Crit.      119.8165      150.9868
## =====
## Note:      + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

### 3.3 Metabolic Variables (Acetate, Propionate, Isobutyrate, 2-Methylbutyrate)

#### 3.3.1 LMM with only main effects as the number of samples were less than four for HD-FMT group

```
#subset(data.new, !is.na(Acetate_w14)) %>%
#group_by(genotype, Treatment) %>%
#tally()
dep_vars <-c("Acetate_w14", "Propionate_w14",
             "Isobutyrate_w14", "Methylbutyrate_w14")

p_val<-lapply(dep_vars, function(r) {
  m <- lme(formula(paste(r, "genotype+Treatment", sep = "~")),
           random=~1|BOX, data = subset(data.new, !is.na(eval(parse(text = r)))))
  assign(paste0(r, ".lmm"), m, envir = .GlobalEnv)
  summary(m)$tTable[,5]})

stargazer(Acetate_w14.lmm, Propionate_w14.lmm,
          Isobutyrate_w14.lmm, Methylbutyrate_w14.lmm,
          type = "text",
          digits = 4,
          report = ('vc*p'),
          star.char = c("+", "*", "**", "***"),
          star.cutoffs = c(.1, .05, .01, .001),
          digit.separator = "",
          notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
          notes.append = FALSE,
          dep.var.labels.include = FALSE,
          column.labels=c("Acetate-14", "Propionate-14",
                          "Isobutyrate-14", "Methylbutyrate-14"),
          align=TRUE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               Acetate-14 Propionate-14 Isobutyrate-14 Methylbutyrate-14
##                               (1)         (2)         (3)         (4)
##                               -----
## genotypeHD                29.5120*    0.9088      0.5904      0.1806
##                               p = 0.0425  p = 0.5602    p = 0.2188    p = 0.2247
##
## TreatmentOnly ATB         4.7346      1.7019      0.3049     -0.1399
##                               p = 0.7555  p = 0.3241    p = 0.5616    p = 0.3874
##
## TreatmentATB_FMT          11.0272     -1.5247     -0.3897     -0.2389
##                               p = 0.5474  p = 0.4770    p = 0.5441    p = 0.2377
##
## Constant                   64.8784***   2.9463*     2.5912***   0.7841***
##                               p = 0.0001  p = 0.0469    p = 0.00002   p = 0.00002
##
## -----
## Observations                36          36          35          36
## Log Likelihood              -161.9543   -97.9223    -55.1535    -20.7752
## Akaike Inf. Crit.           335.9086   207.8446   122.3070    53.5503
## Bayesian Inf. Crit.         344.7030   216.6390   130.9109    62.3447
## =====
## Note:                        + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

### 3.3.2 With all two way interactions (except FMT\*ATB)

```
dep_vars <-c("Acetate_w20","Propionate_w20","Isobutyrate_w20",
             "Methylbutyrate_w20")

p_val<-lapply(dep_vars, function(r) {
  m <- lme(formula(paste(r, "genotype+Treatment+genotype:Treatment", sep = "~")),
            random=~1|BOX,data = subset(data.new,!is.na(eval(parse(text = r))))
  assign(paste0(r,".lmm"),m, envir = .GlobalEnv)
  summary(m)$tTable[,5]})

stargazer(Acetate_w20.lmm,Propionate_w20.lmm,
           Isobutyrate_w20.lmm,Methylbutyrate_w20.lmm,
           type = "text",
           digits = 4,
           report = ('vc*p'),
           star.char = c("+", "*", "**", "***"),
           star.cutoffs = c(.1, .05, .01, .001),
           digit.separator = "",
           notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
           notes.append = FALSE,
           dep.var.labels.include = FALSE,
           column.labels=c("Acetate-20","Propionate-20",
                           "Isobutyrate-20","Methylbutyrate-20"),
```

align=TRUE)

```
##
## =====
##                               Dependent variable:
##                               -----
##                               Acetate-20  Propionate-20  Isobutyrate-20  Methylbutyrate-20
##                               (1)         (2)         (3)         (4)
##                               -----
## genotypeHD                    -9.5017      -0.0525       0.0254       0.2137
##                               p = 0.6195    p = 0.9900     p = 0.9763    p = 0.7970
##
## TreatmentOnly ATB             -10.3542      0.2268       0.7819       1.4797+
##                               p = 0.5463    p = 0.9496     p = 0.3360    p = 0.0644
##
## TreatmentATB_FMT              -20.1300     -7.4825+      1.1532       -0.1066
##                               p = 0.2506    p = 0.0945     p = 0.1651    p = 0.8859
##
## genotypeHD:TreatmentOnly ATB  57.6720*      6.7326       1.4744       -0.9962
##                               p = 0.0435    p = 0.2574     p = 0.2282    p = 0.3887
##
## genotypeHD:TreatmentATB_FMT   39.6838     10.5947+      0.6947       0.3270
##                               p = 0.1465    p = 0.0990     p = 0.5607    p = 0.7741
##
## Constant                      70.8392***    10.4182**     2.6521***     0.6934
##                               p = 0.00004   p = 0.0011     p = 0.0003    p = 0.1986
##
## -----
## Observations                   32          26          32          32
## Log Likelihood                 -129.3232    -67.7728     -44.8358     -47.8591
## Akaike Inf. Crit.              274.6464    151.5456     105.6716     111.7182
## Bayesian Inf. Crit.            284.7112    159.5114     115.7364     121.7829
## =====
## Note:                          + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

### 3.4 Cytokines Variables

#### 3.4.1 LMM with only main effects due to low samples

```
#subset(data, !is.na(IFNg_w14)) %>%
#  group_by(genotype, FMT, ATB) %>%
#  tally()

dep_vars <-c("IL17A_w14", "IL17E_w14", "IL21_w14", "IL7R_w14" )

p_val<-lapply(dep_vars, function(r) {
  m <- lme(formula(paste(r, "genotype+Treatment", sep = "~")),
    random=(-1|BOX),data = subset(data.new,!is.na(eval(parse(text = r))))
  assign(paste0(r,".lmm"),m, envir = .GlobalEnv)
  summary(m)$tTable[,5]})
```



```
stargazer(IL17A_w14.lmm, IL17E_w14.lmm, IL21_w14.lmm, IL7R_w14.lmm,
  type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
  notes.append = FALSE,
  dep.var.labels.include = FALSE,
  column.labels=c( "IL17A-14", "IL17E-14", "IL21-14", "IL7R-14"),
  align=TRUE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               IL17A-14   IL17E-14   IL21-14   IL7R-14
##                               (1)        (2)        (3)        (4)
## -----
## genotypeHD                   0.0589      0.4301     -0.0558     1.0230*
##                               p = 0.6692   p = 0.1134   p = 0.4973   p = 0.0162
##
## TreatmentOnly ATB            -0.1186      0.1212     -0.0518     -0.5898
##                               p = 0.4588   p = 0.6958   p = 0.5905   p = 0.2102
##
## TreatmentATB_FMT             -0.0928      0.3462      0.1637     -0.2757
##                               p = 0.5949   p = 0.2649   p = 0.1212   p = 0.5620
##
## Constant                     0.2550+      0.5904*     0.3083***    0.7143+
##                               p = 0.0615   p = 0.0206   p = 0.0009   p = 0.0565
##
## -----
## Observations                  31           26           31           25
## Log Likelihood                -12.6930     -21.9144      3.9388     -28.7985
## Akaike Inf. Crit.             37.3860     55.8288      4.1224     69.5970
## Bayesian Inf. Crit.          45.1610     62.3750     11.8975     75.8642
## =====
## Note:                        + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

### 3.4.2 With all two way interactions (except FMT\*ATB)

```
dep_vars <-c("IFNg_w14", "IL1b_w14", "IL22_w14", "IL6_w14", "TNFa_w14",
  "IFNg_w20", "IL17A_w20", "IL17E_w20", "IL1b_w20",
  "IL21_w20", "IL22_w20", "IL6_w20", "TNFa_w20")

p_val<-lapply(dep_vars, function(r) {
  m <- lme(formula(paste(r, "genotype+Treatment+genotype:Treatment", sep = "~")),
    random=(-1|BOX), data = subset(data.new, !is.na(eval(parse(text = r))))
  assign(paste0(r, ".lmm"), m, envir = .GlobalEnv)
  summary(m)$tTable[,5]})
```

```
stargazer(IFNg_w14.lmm,IL1b_w14.lmm,IL22_w14.lmm,IL6_w14.lmm,TNFa_w14.lmm,
          IFNg_w20.lmm,
          type = "text",
          digits = 4,
          report = ('vc*p'),
          star.char = c("+", "*", "**", "***"),
          star.cutoffs = c(.1, .05, .01, .001),
          digit.separator = "",
          notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
          notes.append = FALSE,
          dep.var.labels.include = FALSE,
          column.labels=c("IFNg-14","IL1b-14","IL22-14","IL6-14","TNFa-14",
                          "IFNg-20"),
          align=TRUE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               IFNg-14   IL1b-14   IL22-14   IL6-14   TNFa-14   IFNg-20
##                               (1)       (2)       (3)       (4)       (5)       (6)
## -----
## genotypeHD                    -0.0100   -0.0718   -0.0097   -0.2248   0.3622   -0.0247+
##                               p = 0.4778 p = 0.7599 p = 0.9651 p = 0.3504 p = 0.9964 p = 0.0591
##
## TreatmentOnly ATB             -0.0015    0.2181   -0.0400    0.0233   -0.0461   -0.0107
##                               p = 0.9147 p = 0.3593 p = 0.8577 p = 0.9219 p = 0.9996 p = 0.4101
##
## TreatmentATB_FMT              -0.0030    0.1976    0.1203   -0.0779    0.3905    0.0191
##                               p = 0.8382 p = 0.4268 p = 0.6081 p = 0.7546 p = 0.9964 p = 0.1501
##
## genotypeHD:TreatmentOnly ATB  0.0175   -0.1764   -0.1169    0.1759    0.2442    0.0247
##                               p = 0.3724 p = 0.5900 p = 0.7061 p = 0.5949 p = 0.9983 p = 0.1869
##
## genotypeHD:TreatmentATB_FMT  0.0245    0.0438   -0.0483    0.6705+  150.3674   -0.0180
##                               p = 0.2475 p = 0.8999 p = 0.8875 p = 0.0803 p = 0.2201 p = 0.3410
##
## Constant                      0.0362**   0.3428+   0.5447**   0.8044***   0.8442    0.0405***
##                               p = 0.0021 p = 0.0529 p = 0.0032 p = 0.0003 p = 0.9876 p = 0.0003
##
## -----
## Observations                   35         35         34         34         33         37
## Log Likelihood                 61.9874   -19.8067  -17.7358  -19.5024  -174.8050   67.8828
## Akaike Inf. Crit.             -107.9749   55.6134   51.4717   55.0047   365.6099  -119.7656
## Bayesian Inf. Crit.           -97.0365   66.5518   62.1293   65.6624   375.9766  -108.2937
## =====
## Note:                          + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```
stargazer(IL17A_w20.lmm,IL17E_w20.lmm,IL1b_w20.lmm,IL21_w20.lmm,
          IL22_w20.lmm,
          type = "text",
```

```

digits = 4,
report = ('vc*p'),
star.char = c("+", "*", "**", "***"),
star.cutoffs = c(.1, .05, .01, .001),
digit.separator = "",
notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),
notes.append = FALSE,
dep.var.labels.include = FALSE,
column.labels=c("IL17A-20", "IL17E-20", "IL1b-20",
  "IL21-20", "IL22-20"),
align=TRUE)

```

```

##
## =====
##                                     Dependent variable:
##                                     -----
##                                     IL17A-20  IL17E-20  IL1b-20  IL21-20  IL22-20
##                                     (1)       (2)       (3)       (4)       (5)
## -----
## genotypeHD                      -0.0107    0.1313    0.1719    -0.2490    -0.0978
##                                p = 0.8701 p = 0.5654 p = 0.7236 p = 0.1524 p = 0.7838
##
## TreatmentOnly ATB                -0.0146   -0.0321    0.3688    -0.1318     0.1930
##                                p = 0.8388 p = 0.8612 p = 0.4511 p = 0.3863 p = 0.5895
##
## TreatmentATB_FMT                 0.0685    0.4044*   -0.1591    0.0579    -0.1003
##                                p = 0.3454 p = 0.0432 p = 0.7535 p = 0.7138 p = 0.7868
##
## genotypeHD:TreatmentOnly ATB     0.0787   -0.1703    0.3263    0.1306     0.5237
##                                p = 0.4319 p = 0.5683 p = 0.6426 p = 0.5842 p = 0.3159
##
## genotypeHD:TreatmentATB_FMT      0.0824   -0.5396+   0.1651    0.1002     0.3911
##                                p = 0.4164 p = 0.0900 p = 0.8172 p = 0.6710 p = 0.4593
##
## Constant                        0.1448**   0.6645***  0.6860+   0.7783***  1.1129***
##                                p = 0.0062 p = 0.0001 p = 0.0581 p = 0.000003 p = 0.0004
## -----
## Observations                     35         33         39         30         39
## Log Likelihood                   17.3611   -11.4072  -47.8369   -6.1180   -38.4919
## Akaike Inf. Crit.                -18.7222   38.8143  111.6737   28.2359   92.9839
## Bayesian Inf. Crit.              -7.7838   49.1810  123.6458   37.6604  104.9559
## =====
## Note:                             + p<0.1; * p<0.05; ** p<0.01; *** p<0.001

```

```

stargazer(IL6_w20.lmm, TNFa_w20.lmm,
  type = "text",
  digits = 4,
  report = ('vc*p'),
  star.char = c("+", "*", "**", "***"),
  star.cutoffs = c(.1, .05, .01, .001),
  digit.separator = "",
  notes = c("+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001"),

```

```
notes.append = FALSE,
dep.var.labels.include = FALSE,
column.labels=c("IL6-20", "TNFa-20"),
align=TRUE)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               IL6-20          TNFa-20
##                               (1)           (2)
## -----
## genotypeHD                  -0.2050        -0.9973
##                               p = 0.7827      p = 0.5521
##
## TreatmentOnly ATB           0.0898         -0.7883
##                               p = 0.9038      p = 0.6377
##
## TreatmentATB_FMT            1.0858         -0.8374
##                               p = 0.1762      p = 0.6308
##
## genotypeHD:TreatmentOnly ATB 0.3921         0.6315
##                               p = 0.7163      p = 0.7933
##
## genotypeHD:TreatmentATB_FMT -0.3485         4.3945+
##                               p = 0.7500      p = 0.0956
##
## Constant                     0.8100         1.7749
##                               p = 0.1356      p = 0.1458
##
## -----
## Observations                 39              38
## Log Likelihood               -59.1479        -86.8274
## Akaike Inf. Crit.            134.2957        189.6548
## Bayesian Inf. Crit.          146.2678        201.3807
## =====
## Note:                        + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

## 4 Claspig score

```
data_claspig <- data.new[,c(1:6,78:90)] # extract the columns of data that will become Y
long_claspig<-data_claspig %>%
  gather(v, value, Claspig_W8:Claspig_W20) %>%
  separate(v, c("col", "Time"), sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)
long_claspig$Time <-as.numeric(long_claspig$Time)-7
long_claspig$Claspig<-factor(long_claspig$Claspig, ordered = TRUE , levels = c(0:4))
t<-table(long_claspig$Time,long_claspig$Claspig)
t1<-table(long_claspig$Time,long_claspig$Claspig)%>%prop.table(margin = 1)
```

```
#subset(long_clasping, !is.na(Clasping)) %>%
#group_by(genotype, Treatment, Time) %>%
#tally() %>% summary()
```

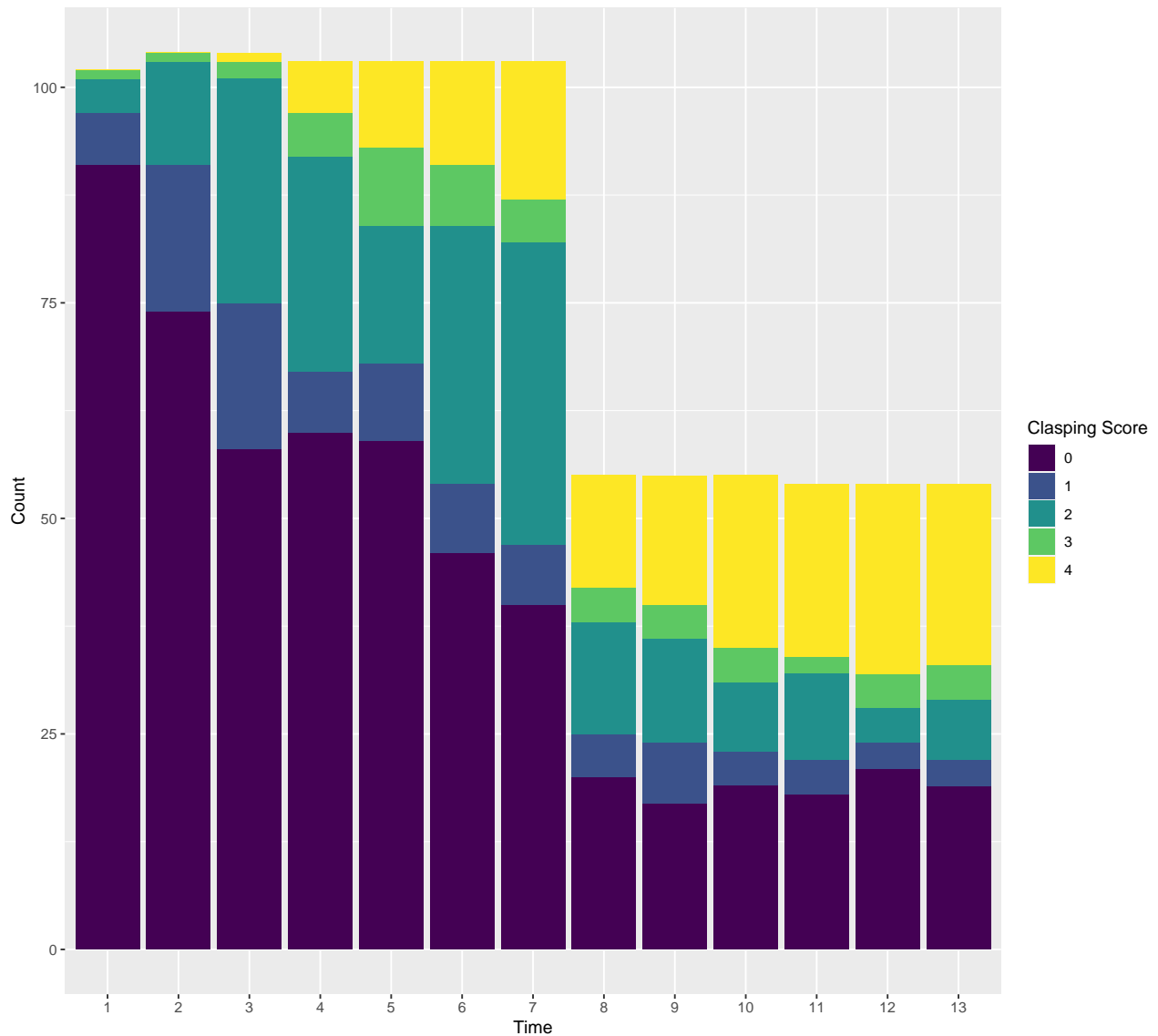


Figure 1: Bar plot for clasping over the 12 weeks

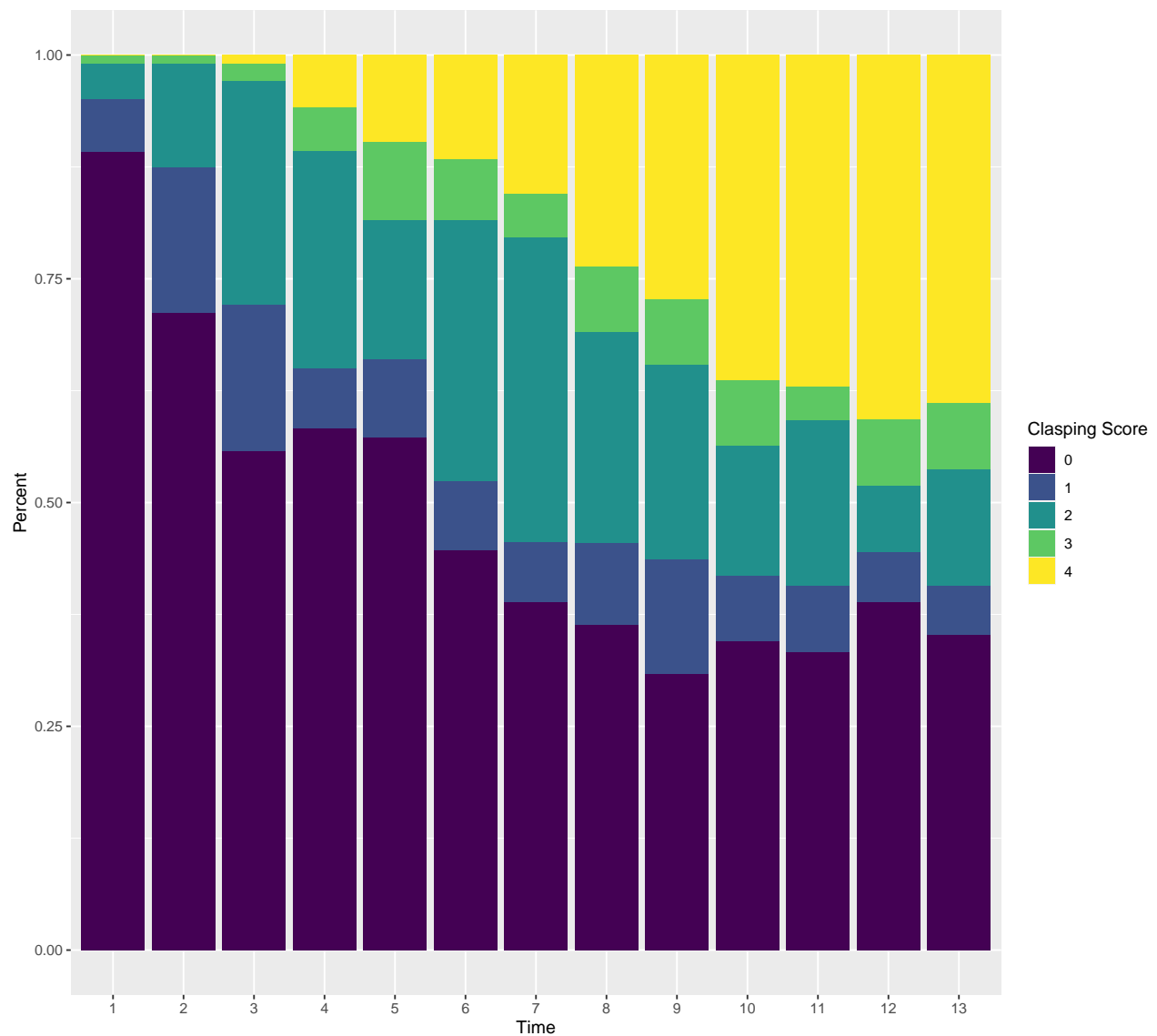


Figure 2: Bar plot for clasping over the 12 weeks

```
# HD mice clasping score
long_clasping_hd<-data_clasping %>%
  gather(v, value, Clasping_W8:Clasping_W20) %>%
  separate(v, c("col", "Time"),sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)%>%filter(genotype=="HD")
long_clasping_hd$Time <-as.numeric(long_clasping_hd$Time)-7
long_clasping_hd$Clasping<-factor(long_clasping_hd$Clasping, ordered = TRUE , levels = c(0:4))
t1<-table(long_clasping_hd$Time,long_clasping_hd$Clasping)%>%prop.table(margin = 1)
```

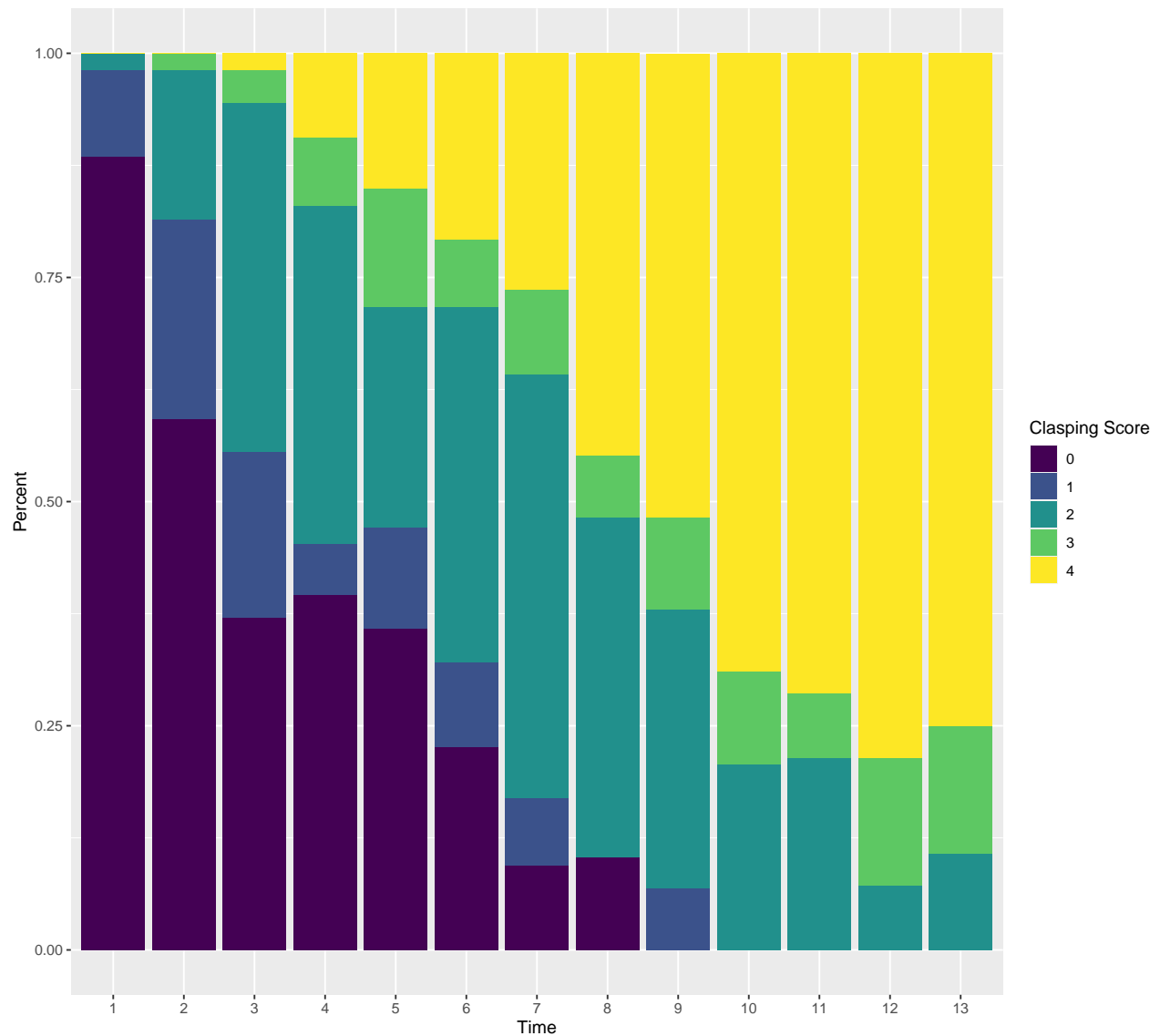


Figure 3: Bar plot for clasping over the 12 weeks for HD mice

```
# WT mice clasping score
long_clasping_wt<-data_clasping %>%
  gather(v, value, Clasping_W8:Clasping_W20) %>%
  separate(v, c("col", "Time"),sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)%>%filter(genotype=="WT")
long_clasping_wt$Time <-as.numeric(long_clasping_wt$Time)-7
long_clasping_wt$Clasping<-factor(long_clasping_wt$Clasping, ordered = TRUE , levels = c(0:4))
t1<-table(long_clasping_wt$Time,long_clasping_wt$Clasping)%>%prop.table(margin = 1)
```

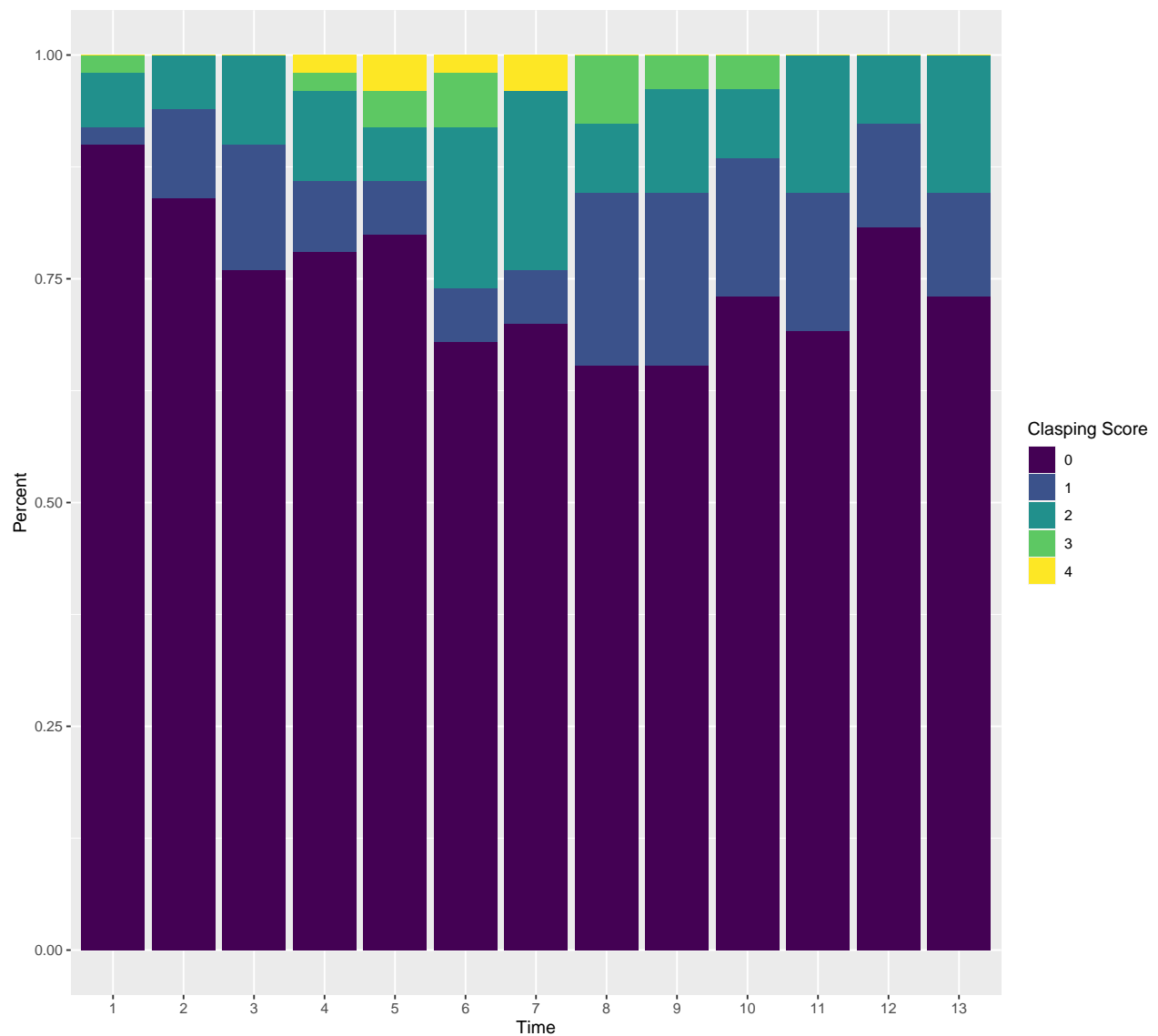


Figure 4: Bar plot for clasping over the 12 weeks for WT mice

## 4.1 Ordinal regression

```
Clasping.clm = clm(Clasping~genotype + Treatment + Time,
                   data=long_clasping, Hess=TRUE)
summary(Clasping.clm)
```

```
## formula: Clasping ~ genotype + Treatment + Time
## data:    long_clasping
##
## link threshold nobs logLik   AIC      niter max.grad cond.H
## logit flexible 1049 -1092.97 2201.95 8(0)  4.02e-08 3.4e+03
##
## Coefficients:
```



```
##               Estimate Std. Error z value Pr(>|z|)
## genotypeHD      2.75256    0.15712  17.519   <2e-16 ***
## TreatmentOnly ATB 0.34900    0.15791   2.210   0.0271 *
## TreatmentATB_FMT 0.06226    0.15916   0.391   0.6957
## Time            0.30508    0.02033  15.009   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##      Estimate Std. Error z value
## 0|1    3.4581    0.2182  15.85
## 1|2    4.0397    0.2278  17.73
## 2|3    5.5397    0.2630  21.07
## 3|4    6.0657    0.2761  21.96
## (927 observations deleted due to missingness)
```

## 4.2 Ordinal regression with random effect

```
Clasping.clmm = clmm(Clasping~genotype + Treatment + Time+(1|BOX),
                      data=long_clasping, Hess=TRUE)
summary(Clasping.clmm)
```

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: Clasping ~ genotype + Treatment + Time + (1 | BOX)
## data:    long_clasping
##
## link threshold nobs logLik AIC      niter      max.grad cond.H
## logit flexible 1049 -996.58 2011.17 523(3468) 6.98e-05 3.6e+03
##
## Random effects:
## Groups Name      Variance Std.Dev.
## BOX      (Intercept) 2.6      1.613
## Number of groups:  BOX 51
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## genotypeHD      3.87110    0.51567   7.507 6.05e-14 ***
## TreatmentOnly ATB 0.32919    0.40377   0.815   0.415
## TreatmentATB_FMT 0.33935    0.55081   0.616   0.538
## Time            0.44920    0.02752  16.325 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##      Estimate Std. Error z value
## 0|1    5.1074    0.5320   9.601
## 1|2    5.8632    0.5418  10.822
## 2|3    7.7182    0.5720  13.494
## 3|4    8.3527    0.5824  14.341
## (927 observations deleted due to missingness)
```

### 4.3 Comparison between Cumulative Link Model and Cumulative Link Mixed Model

```
anova( Claspings.clmm,Claspings.clm)

## Likelihood ratio tests of cumulative link models:
##
##               formula:                      link:
## Claspings.clm  Claspings ~ genotype + Treatment + Time      logit
## Claspings.clmm Claspings ~ genotype + Treatment + Time + (1 | BOX) logit
##               threshold:
## Claspings.clm  flexible
## Claspings.clmm flexible
##
##               no.par    AIC    logLik LR.stat df Pr(>Chisq)
## Claspings.clm      8 2201.9 -1092.97
## Claspings.clmm     9 2011.2 -996.58  192.78  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cumulative link mixed model is better than the cumulative link model with a lower AIC value.

## 5 Post-Hoc test

### 5.1 Body Weight

```
x<-emmeans(BodyWeight.lmm, pairwise ~ genotype*Treatment,
            at = list(Time = c(1:13)))
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype *Treatment in body weight") %>%
  kable_styling(latex_options = c("repeat_header")) %>%
  column_spec(6,bold = that_cell,
              color = ifelse(that_cell,"red","black")) %>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 1: Post-hoc results for genotype \*Treatment in body weight

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	5.5503	0.9342	71	5.9415	<b>0.0000</b>
WT No treatment - WT Only ATB	2.8106	1.0413	1297	2.6992	0.0760
WT No treatment - HD Only ATB	3.9178	0.9354	71	4.1886	<b>0.0011</b>
WT No treatment - WT ATB_FMT	0.5025	1.0205	71	0.4924	0.9963
WT No treatment - HD ATB_FMT	4.9871	1.0245	71	4.8679	<b>0.0001</b>
HD No treatment - WT Only ATB	-2.7396	0.9361	71	-2.9266	0.0503
HD No treatment - HD Only ATB	-1.6325	0.5282	1297	-3.0908	<b>0.0249</b>

Table 1: Post-hoc results for genotype \*Treatment in body weight (*continued*)

contrast	estimate	SE	df	t.ratio	p.value
HD No treatment - WT ATB_FMT	-5.0478	0.9141	71	-5.5224	<b>0.0000</b>
HD No treatment - HD ATB_FMT	-0.5632	0.9119	71	-0.6176	0.9894
WT Only ATB - HD Only ATB	1.1072	0.9336	71	1.1859	0.8421
WT Only ATB - WT ATB_FMT	-2.3082	1.0205	71	-2.2617	0.2236
WT Only ATB - HD ATB_FMT	2.1765	1.0245	71	2.1244	0.2869
HD Only ATB - WT ATB_FMT	-3.4153	0.9129	71	-3.7411	<b>0.0048</b>
HD Only ATB - HD ATB_FMT	1.0693	0.9113	71	1.1734	0.8480
WT ATB_FMT - HD ATB_FMT	4.4846	0.9988	71	4.4900	<b>0.0004</b>

## 5.2 Weight Gain

```
x<-emmeans(WeightGain.lmm, pairwise ~ genotype*Treatment,
            at = list(Time = c(1:13)))
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype * Treatment in Weight Gain") %>%
  kable_styling(latex_options = c("repeat_header")) %>%
  column_spec(6,bold = that_cell,
              color = ifelse(that_cell,"red","black")) %>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 2: Post-hoc results for genotype \* Treatment in Weight Gain

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	17.6839	3.5853	23	4.9324	<b>0.0007</b>
WT No treatment - WT Only ATB	7.2766	4.0791	682	1.7839	0.4769
WT No treatment - HD Only ATB	13.3880	3.5875	23	3.7319	<b>0.0123</b>
WT No treatment - WT ATB_FMT	2.1142	3.8698	23	0.5463	0.9935
WT No treatment - HD ATB_FMT	21.0392	3.8809	23	5.4212	<b>0.0002</b>
HD No treatment - WT Only ATB	-10.4073	3.5853	23	-2.9028	0.0759
HD No treatment - HD Only ATB	-4.2958	1.8509	682	-2.3209	0.1870
HD No treatment - WT ATB_FMT	-15.5697	3.3452	23	-4.6544	<b>0.0014</b>
HD No treatment - HD ATB_FMT	3.3553	3.3580	23	0.9992	0.9135
WT Only ATB - HD Only ATB	6.1114	3.5875	23	1.7035	0.5432
WT Only ATB - WT ATB_FMT	-5.1624	3.8698	23	-1.3340	0.7637
WT Only ATB - HD ATB_FMT	13.7626	3.8809	23	3.5463	<b>0.0188</b>
HD Only ATB - WT ATB_FMT	-11.2738	3.3476	23	-3.3678	<b>0.0281</b>
HD Only ATB - HD ATB_FMT	7.6512	3.3604	23	2.2769	0.2434
WT ATB_FMT - HD ATB_FMT	18.9250	3.6602	23	5.1704	<b>0.0004</b>

## 5.3 Fecal Water Content

```
x<-emmeans(FecalWaterContent.lmm, pairwise ~ genotype*Treatment,
            at = list(Time = c(1:13)))
```

```
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype * Treatment in Fecal Water Content") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(6,bold = that_cell,
    color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 3: Post-hoc results for genotype \* Treatment in Fecal Water Content

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	15.6830	8.5175	23	1.8413	0.4608
WT No treatment - WT Only ATB	0.6866	9.7349	677	0.0705	1.0000
WT No treatment - HD Only ATB	-9.6736	8.5237	23	-1.1349	0.8618
WT No treatment - WT ATB_FMT	4.6863	9.2371	23	0.5073	0.9954
WT No treatment - HD ATB_FMT	-1.0366	9.2566	23	-0.1120	1.0000
HD No treatment - WT Only ATB	-14.9964	8.5175	23	-1.7607	0.5086
<b>HD No treatment - HD Only ATB</b>	<b>-25.3566</b>	<b>4.1105</b>	<b>677</b>	<b>-6.1687</b>	<b>0.0000</b>
HD No treatment - WT ATB_FMT	-10.9967	7.9437	23	-1.3843	0.7356
HD No treatment - HD ATB_FMT	-16.7196	7.9664	23	-2.0988	0.3224
WT Only ATB - HD Only ATB	-10.3603	8.5237	23	-1.2155	0.8249
WT Only ATB - WT ATB_FMT	3.9997	9.2371	23	0.4330	0.9978
WT Only ATB - HD ATB_FMT	-1.7233	9.2566	23	-0.1862	1.0000
HD Only ATB - WT ATB_FMT	14.3599	7.9504	23	1.8062	0.4814
HD Only ATB - HD ATB_FMT	8.6370	7.9730	23	1.0833	0.8830
WT ATB_FMT - HD ATB_FMT	-5.7229	8.7315	23	-0.6554	0.9851

## 5.4 Food Intake

```
x<-emmeans(FoodIntake.lmm, pairwise ~ genotype*Treatment,
    at = list(Time = c(1:12)))
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype * Treatment in Food Intake") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(6,bold = that_cell,
    color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 4: Post-hoc results for genotype \* Treatment in Food Intake

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	-0.0973	0.0345	22	-2.8239	0.0906
<b>WT No treatment - WT Only ATB</b>	<b>-0.1906</b>	<b>0.0366</b>	<b>292</b>	<b>-5.2061</b>	<b>0.0000</b>
WT No treatment - HD Only ATB	-0.0659	0.0345	22	-1.9130	0.4208
<b>WT No treatment - WT ATB_FMT</b>	<b>-0.1767</b>	<b>0.0347</b>	<b>22</b>	<b>-5.0869</b>	<b>0.0005</b>

Table 4: Post-hoc results for genotype \* Treatment in Food Intake (*continued*)

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD ATB_FMT	-0.0519	0.0366	22	-1.4181	0.7162
HD No treatment - WT Only ATB	-0.0933	0.0345	22	-2.7089	0.1134
HD No treatment - HD Only ATB	0.0314	0.0304	292	1.0328	0.9066
HD No treatment - WT ATB_FMT	-0.0794	0.0324	22	-2.4472	0.1835
HD No treatment - HD ATB_FMT	0.0454	0.0345	22	1.3168	0.7729
<b>WT Only ATB - HD Only ATB</b>	0.1247	0.0345	22	3.6199	<b>0.0166</b>
WT Only ATB - WT ATB_FMT	0.0139	0.0347	22	0.4008	0.9985
<b>WT Only ATB - HD ATB_FMT</b>	0.1387	0.0366	22	3.7879	<b>0.0113</b>
<b>HD Only ATB - WT ATB_FMT</b>	-0.1108	0.0324	22	-3.4144	<b>0.0262</b>
HD Only ATB - HD ATB_FMT	0.0140	0.0345	22	0.4058	0.9984
<b>WT ATB_FMT - HD ATB_FMT</b>	0.1248	0.0347	22	3.5921	<b>0.0177</b>

## 5.5 Water Intake

```
x<-emmeans(WaterIntake.lmm, pairwise ~ Treatment|genotype,
            at = list(Time = c(1:11)))
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for Treatment given genotype in Water Intake") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
              color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 5: Post-hoc results for Treatment given genotype in Water Intake

contrast	genotype	estimate	SE	df	t.ratio	p.value
<b>No treatment - Only ATB</b>	WT	-0.3721	0.1511	264	-2.4622	<b>0.0383</b>
No treatment - ATB_FMT	WT	-0.2737	0.1434	22	-1.9092	0.1598
Only ATB - ATB_FMT	WT	0.0984	0.1434	22	0.6862	0.7739
No treatment - Only ATB	HD	-0.2293	0.0974	264	-2.3526	0.0505
No treatment - ATB_FMT	HD	-0.3113	0.1372	22	-2.2691	0.0817
Only ATB - ATB_FMT	HD	-0.0820	0.1372	22	-0.5974	0.8229

## 5.6 CFC Extinction

```
x<-emmeans(CFC_Extinction.lmm, pairwise ~ genotype|Treatment)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype given Treatment in CFC Extinction") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
```

```
color = ifelse(that_cell,"red","black"))%>%
column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 6: Post-hoc results for genotype given Treatment in CFC Extinction

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	0.8993	4.0707	41	0.2209	0.8263
WT - HD	Only ATB	1.6746	4.0536	41	0.4131	0.6817
<b>WT - HD</b>	<b>ATB_FMT</b>	10.5431	4.2334	41	2.4905	<b>0.0169</b>

## 5.7 Ymaze

```
x<-emmeans(Ymaze.lmm, pairwise ~ genotype|Treatment*Arm)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype given Treatment*Arm in Ymaze") %>%
    kable_styling(latex_options = c("repeat_header"))%>%
    column_spec(8,bold = that_cell,
        color = ifelse(that_cell,"red","black"))%>%
    column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 7: Post-hoc results for genotype given Treatment\*Arm in Ymaze

contrast	Treatment	Arm	estimate	SE	df	t.ratio	p.value
<b>WT - HD</b>	No treatment	Novel	17.1598	8.2060	39	2.0911	<b>0.0431</b>
WT - HD	Only ATB	Novel	2.8606	7.7449	39	0.3694	0.7139
WT - HD	ATB_FMT	Novel	14.4345	7.5293	39	1.9171	0.0626
WT - HD	No treatment	Familiar	16.3095	8.2060	39	1.9875	0.0539
WT - HD	Only ATB	Familiar	2.0103	7.7449	39	0.2596	0.7966
WT - HD	ATB_FMT	Familiar	13.5842	7.5293	39	1.8042	0.0789

## 5.8 Brain Weight

```
x<-emmeans(BrainWeight.lmm_, pairwise ~ genotype|Treatment)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for for genotype given Treatment in Brain weight") %>%
    kable_styling(latex_options = c("repeat_header"))%>%
    column_spec(7,bold = that_cell,
        color = ifelse(that_cell,"red","black"))%>%
    column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 8: Post-hoc results for for genotype given Treatment in Brain weight

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	0.0700	0.0213	23	3.2864	<b>0.0032</b>
WT - HD	Only ATB	0.0510	0.0202	23	2.5239	<b>0.0190</b>
WT - HD	ATB_FMT	0.0644	0.0201	23	3.2091	<b>0.0039</b>

## 5.9 Propel Brake Ratio- Week 14

```
x<-emmeans(Digigait_PropelBrakeRatio_W14.lmm_, pairwise ~ genotype|Treatment)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype given Treatment in Propel Brake Ratio") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
    color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 9: Post-hoc results for genotype given Treatment in Propel Brake Ratio

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	-1.4822	0.4934	45	-3.0043	<b>0.0043</b>
WT - HD	Only ATB	0.3485	0.4786	42	0.7281	0.4706
WT - HD	ATB_FMT	-0.9988	0.4918	45	-2.0310	<b>0.0482</b>

## 5.10 FITC- Week 20

```
x<-emmeans(FITC_w20.lmm_, pairwise ~ genotype|Treatment)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype given Treatment in FITC") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
    color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 10: Post-hoc results for genotype given Treatment in FITC

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	-0.5967	0.2329	12	-2.5616	<b>0.0249</b>
WT - HD	Only ATB	-0.2904	0.2277	12	-1.2756	0.2262
WT - HD	ATB_FMT	-0.8545	0.2211	12	-3.8653	<b>0.0022</b>

### 5.11 CecumWeight- Week 14

```
x<-emmeans(CecumWeight_w14.lmm_, pairwise ~ Treatment|genotype)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for Treatment given genotype in Cecum Weight") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
    color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 11: Post-hoc results for Treatment given genotype in Cecum Weight

contrast	genotype	estimate	SE	df	t.ratio	p.value
No treatment - Only ATB	WT	0.0300	0.0350	16	0.8560	0.6747
No treatment - ATB_FMT	WT	0.0850	0.0379	16	2.2455	0.0936
Only ATB - ATB_FMT	WT	0.0550	0.0379	16	1.4530	0.3388
No treatment - Only ATB	HD	-0.0193	0.0363	16	-0.5317	0.8571
No treatment - ATB_FMT	HD	0.0477	0.0410	16	1.1626	0.4914
Only ATB - ATB_FMT	HD	0.0670	0.0400	16	1.6768	0.2442

### 5.12 Colon Length- Week 20

```
x<-emmeans(ColonLength_w20.lmm_, pairwise ~ genotype|Treatment)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype given Treatment in Colon length") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
    color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 12: Post-hoc results for genotype given Treatment in Colon length

contrast	Treatment	estimate	SE	df	t.ratio	p.value
<b>WT - HD</b>	No treatment	1.2244	0.4248	23	2.8821	<b>0.0084</b>
WT - HD	Only ATB	0.4483	0.3918	22	1.1443	0.2648
<b>WT - HD</b>	ATB_FMT	0.8804	0.3882	23	2.2675	<b>0.0331</b>

### 5.13 Acetate- Week 20

```
x<-emmeans(Acetate_w20.lmm, pairwise ~ genotype*Treatment)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
```



```
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for genotype Treatment in Acetate") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(6,bold = that_cell,
              color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 13: Post-hoc results for genotype Treatment in Acetate

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	9.5017	18.6410	12	0.5097	0.9948
WT No treatment - WT Only ATB	10.3542	16.6730	12	0.6210	0.9872
WT No treatment - HD Only ATB	-37.8161	17.4868	12	-2.1625	0.3206
WT No treatment - WT ATB_FMT	20.1300	16.6730	12	1.2073	0.8254
WT No treatment - HD ATB_FMT	-10.0521	17.4868	12	-0.5748	0.9909
HD No treatment - WT Only ATB	0.8525	18.6410	12	0.0457	1.0000
HD No treatment - HD Only ATB	-47.3178	19.3723	12	-2.4425	0.2161
HD No treatment - WT ATB_FMT	10.6283	18.6410	12	0.5702	0.9913
HD No treatment - HD ATB_FMT	-19.5538	19.3723	12	-1.0094	0.9061
WT Only ATB - HD Only ATB	-48.1703	17.4868	12	-2.7547	0.1342
WT Only ATB - WT ATB_FMT	9.7758	16.6730	12	0.5863	0.9901
WT Only ATB - HD ATB_FMT	-20.4063	17.4868	12	-1.1670	0.8439
HD Only ATB - WT ATB_FMT	57.9461	17.4868	12	3.3137	0.0539
HD Only ATB - HD ATB_FMT	27.7640	18.2644	12	1.5201	0.6593
WT ATB_FMT - HD ATB_FMT	-30.1821	17.4868	12	-1.7260	0.5414

## 5.14 IL17E- Week 20

```
x<-emmeans(IL17E_w20.lmm, pairwise ~ Treatment|genotype)
df<-data.frame(x$contrasts)
that_cell<-df$p.value<0.05
kbl(x$contrasts, longtable=T, linesep = "", booktabs = T, digits = c(4,4,4,4,4,4),
    format = "latex",caption = "Post-hoc results for Treatment given genotype in IL17E") %>%
  kable_styling(latex_options = c("repeat_header"))%>%
  column_spec(7,bold = that_cell,
              color = ifelse(that_cell,"red","black"))%>%
  column_spec(1,color = ifelse(that_cell,"red","black"))
```

Table 14: Post-hoc results for Treatment given genotype in IL17E

contrast	genotype	estimate	SE	df	t.ratio	p.value
No treatment - Only ATB	WT	0.0321	0.1801	14	0.1782	0.9827
No treatment - ATB_FMT	WT	-0.4044	0.1819	14	-2.2229	0.1018
Only ATB - ATB_FMT	WT	-0.4365	0.1877	14	-2.3252	0.0850
No treatment - Only ATB	HD	0.2024	0.2292	14	0.8833	0.6592
No treatment - ATB_FMT	HD	0.1352	0.2339	14	0.5783	0.8337
Only ATB - ATB_FMT	HD	-0.0672	0.1952	14	-0.3442	0.9371

## 6 Information about the used R session

```
sessionInfo()
```

```
## R version 4.1.0 (2021-05-18)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_AU.UTF-8/en_AU.UTF-8/en_AU.UTF-8/C/en_AU.UTF-8/en_AU.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] tidble_3.1.6      MASS_7.3-54      kableExtra_1.3.4  patchwork_1.1.1
## [5] rstatix_0.7.0     lmerTest_3.1-3   lme4_1.1-27.1     Matrix_1.3-4
## [9] viridis_0.6.1     viridisLite_0.4.0 ordinal_2019.12-10 tidyr_1.1.4
## [13] emmeans_1.7.0     jtools_2.1.4     TSA_1.3           xtable_1.8-4
## [17] sjPlot_2.8.9      dotwhisker_0.7.4 stargazer_5.2.2    nlme_3.1-153
## [21] car_3.0-11        carData_3.0-4    ggpubr_0.4.0      ggplot2_3.3.5
## [25] magrittr_2.0.1    readxl_1.3.1     dplyr_1.0.7       knitr_1.36
##
## loaded via a namespace (and not attached):
## [1] TH.data_1.1-0      minqa_1.2.4      colorspace_2.0-2
## [4] ggsignif_0.6.3     ellipsis_0.3.2   rio_0.5.27
## [7] sjlabelled_1.1.8    estimability_1.3 ggstance_0.3.5
## [10] parameters_0.14.0  rstudioapi_0.13  farver_2.1.0
## [13] fansi_0.5.0        mvtnorm_1.1-2    xml2_1.3.2
## [16] codetools_0.2-18   splines_4.1.0    leaps_3.1
## [19] sjmisc_2.8.7       nloptr_1.2.2.2   ggeffects_1.1.1
## [22] broom_0.7.9        effectsize_0.5   compiler_4.1.0
## [25] httr_1.4.2         sjstats_0.18.1   backports_1.2.1
## [28] assertthat_0.2.1   fastmap_1.1.0    htmltools_0.5.2
## [31] tools_4.1.0        coda_0.19-4      gtable_0.3.0
## [34] glue_1.5.0         Rcpp_1.0.7       cellranger_1.1.0
## [37] vctr_0.3.8         svglite_2.0.0    insight_0.14.4
## [40] xfun_0.26          stringr_1.4.0    openxlsx_4.2.4
## [43] rvest_1.0.1        lifecycle_1.0.1  zoo_1.8-9
## [46] scales_1.1.1       hms_1.1.1        sandwich_3.0-1
## [49] yaml_2.2.1         curl_4.3.2       gridExtra_2.3
## [52] pandoc_0.6.4       stringi_1.7.5    ucminf_1.1-4
## [55] bayestestR_0.11.0  boot_1.3-28      zip_2.2.0
## [58] rlang_0.4.12       pkgconfig_2.0.3  systemfonts_1.0.2
## [61] evaluate_0.14      lattice_0.20-45  purrr_0.3.4
## [64] labeling_0.4.2     tidyselect_1.1.1 R6_2.5.1
## [67] generics_0.1.0     multcomp_1.4-17  DBI_1.1.1
## [70] pillar_1.6.4       haven_2.4.3      foreign_0.8-81
```

```
## [73] withr_2.4.2          mgcv_1.8-37          survival_3.2-13
## [76] datawizard_0.2.1     abind_1.4-5          performance_0.8.0
## [79] modelr_0.1.8         crayon_1.4.2         utf8_1.2.2
## [82] rmarkdown_2.11       locfit_1.5-9.4       grid_4.1.0
## [85] data.table_1.14.2    forcats_0.5.1        digest_0.6.28
## [88] webshot_0.5.2        numDeriv_2016.8-1.1 munsell_0.5.0
```