Fecal matter transplant in Huntington's disease (Female)
Data Analysis

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Contents

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.
- Clasping score was modelled 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_HD-FMT_female_data-5.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(1:6,8:37,66:80,96:123)]
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)
long_data.repeated.1<-long_data.repeated.1[order(long_data.repeated.1$ID,
                                          long_data.repeated.1$BOX,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   WeightGain    Rotarod   FecalWaterContent FecalOutput
##                              (1)          (2)          (3)          (4)             (5)
## -------------------------------------------------------------------------------------------
## genotypeHD                  1.1755       4.8237      -51.9162**    -5.8761*        4.6744**
##                           p = 0.2412   p = 0.2606   p = 0.0093   p = 0.0452      p = 0.0040
##
## TreatmentOnly ATB          -0.0552       2.0178       5.1384       3.5819         3.7614*
##                           p = 0.9577   p = 0.6370   p = 0.7984   p = 0.2385      p = 0.0192
##
## TreatmentATB_FMT           -1.7310      -5.1443      -18.9256      6.8879*        0.4479
##                           p = 0.1196   p = 0.2683   p = 0.3731   p = 0.0423      p = 0.7734
##
## Time                        0.6396***    2.6739***   -0.6704      -0.1747        0.2152*
##                           p = 0.0000   p = 0.0000   p = 0.6009   p = 0.5021      p = 0.0228
##
## genotypeHD:TreatmentOnly ATB  -0.4385   -5.6549      20.2853      -0.2541        -1.3646
##                           p = 0.7479   p = 0.3130   p = 0.4141   p = 0.9285      p = 0.4246
##
## genotypeHD:TreatmentATB_FMT  -0.5350     0.7530      49.2853+     -1.3893        0.0192
##                           p = 0.7030   p = 0.8986   p = 0.0602   p = 0.6454      p = 0.9916
##
## genotypeHD:Time            -0.1802***   -0.8039***  -9.6906***    0.2450        -0.5881***
##                           p = 0.00002  p = 0.000001 p = 0.0000   p = 0.3356      p = 0.0000
##
## TreatmentOnly ATB:Time      0.0818+      0.2788      -0.8217      -0.0895        -0.1074
##                           p = 0.0984   p = 0.1460   p = 0.5831   p = 0.7665      p = 0.3257
##
## TreatmentATB_FMT:Time       0.1462**     0.5953**    -2.7319+     -0.7601*       0.1009
##                           p = 0.0051   p = 0.0036   p = 0.0826   p = 0.0180      p = 0.3822
##
## Constant                   18.8680***  104.4897***  215.8280***  45.8208***     9.5707***
##                           p = 0.0000   p = 0.0000   p = 0.0000   p = 0.0000      p = 0.0000
##
## -------------------------------------------------------------------------------------------
## Observations                 765          535          762          531            533
## Log Likelihood            -1634.5660   -1812.4550   -4182.6570   -2015.3560     -1499.7590
## Akaike Inf. Crit.          3293.1320    3648.9100    8389.3140    4054.7130      3023.5180
## Bayesian Inf. Crit.        3348.6530    3700.0700    8444.7870    4105.7820      3074.6330
## ===========================================================================================
## 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(1:6,40:51)]
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)
```

```r
long_FoodIntake.data$Time<-long_FoodIntake.data$Time-8

WaterIntake.data<-data.new[,c(1:6,55:65)]
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
```

```r
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                     -0.0797                -0.1168
##                              p = 0.6337             p = 0.6193
## 
## TreatmentOnly ATB              -0.0347                -0.0153
##                              p = 0.8414             p = 0.9501
## 
## TreatmentATB_FMT               0.1567                 0.0651
##                              p = 0.3922             p = 0.7990
## 
## Time                          -0.0294***             -0.0384***
##                              p = 0.0000             p = 0.0000
## 
## genotypeHD:TreatmentOnly ATB   0.1415                 0.2056
##                              p = 0.5470             p = 0.5358
## 
## genotypeHD:TreatmentATB_FMT    0.1379                 0.3450
##                              p = 0.5674             p = 0.3139
## 
## genotypeHD:Time                0.0109**               0.0156***
```

```
##                                    p = 0.0032             p = 0.000001
##
## TreatmentOnly ATB:Time              0.0022                -0.0029
##                                    p = 0.6158             p = 0.3900
##
## TreatmentATB_FMT:Time             -0.0063                -0.0067+
##                                    p = 0.1745             p = 0.0648
##
## Constant                           1.2568***              1.7348***
##                                    p = 0.0000             p = 0.0000
##
## -----------------------------------------------------------------------
## Observations                          316                   219
## Log Likelihood                     172.1180               201.5562
## Akaike Inf. Crit.                 -320.2361              -379.1123
## Bayesian Inf. Crit.               -275.5531              -339.0043
## =======================================================================
## 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(1:6,164:170)]
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(1:6,171:180)]
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                 5.0471              -14.4999**
##                          p = 0.5677            p = 0.0065
##
## TreatmentOnly ATB          -0.7073              -1.3935
##                          p = 0.9428            p = 0.8000
##
## TreatmentATB_FMT           1.0556               -1.8747
##                          p = 0.9215            p = 0.7514
##
## Time                      18.6442***            -2.1146***
##                          p = 0.0000            p = 0.00003
##
## CONDT_Base                 6.4268
##                          p = 0.3435
##
## EXT_Base                                        2.2963***
##                                               p = 0.0000
##
## genotypeHD:TreatmentOnly ATB   -0.7958          -4.9231
##                          p = 0.9303            p = 0.4283
##
## genotypeHD:TreatmentATB_FMT    16.5852           3.4605
##                          p = 0.1022            p = 0.5979
##
## genotypeHD:Time            -1.7397               1.6931***
##                          p = 0.2959            p = 0.0005
##
## genotypeHD:CONDT_Base      -6.8865
##                          p = 0.2676
##
## genotypeHD:EXT_Base                             -0.7483**
##                                               p = 0.0025
##
## TreatmentOnly ATB:Time     -0.6602               1.3433*
##                          p = 0.7428            p = 0.0193
##
## TreatmentATB_FMT:Time      -3.0163               0.4503
```

```
##                                      p = 0.1386              p = 0.4398
##
## TreatmentOnly ATB:CONDT_Base          4.1776
##                                      p = 0.4671
##
## TreatmentATB_FMT:CONDT_Base          -2.2604
##                                      p = 0.7432
##
## Time:CONDT_Base                      -0.3199
##                                      p = 0.7187
##
## TreatmentOnly ATB:EXT_Base                                   -0.0503
##                                                             p = 0.8638
##
## TreatmentATB_FMT:EXT_Base                                    -0.6967**
##                                                             p = 0.0094
##
## Time:EXT_Base                                                -0.1928***
##                                                             p = 0.0000
##
## Constant                            -23.6141**              21.9989***
##                                      p = 0.0024             p = 0.000001
##
## -----------------------------------------------------------------------
## Observations                           414                    621
## Log Likelihood                      -1949.0900             -2578.3110
## Akaike Inf. Crit.                    3932.1800              5190.6220
## Bayesian Inf. Crit.                  3999.9920              5265.5390
## =======================================================================
## 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(1:6,128:129)]
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                              -18.6328**
##                                         p = 0.0049
## 
## TreatmentOnly ATB                        -6.3639
##                                         p = 0.3458
## 
## TreatmentATB_FMT                         -2.0624
##                                         p = 0.7684
## 
## ArmFamiliar                             -22.3397***
##                                         p = 0.0007
## 
## genotypeHD:TreatmentOnly ATB             6.4673
##                                         p = 0.3973
## 
## genotypeHD:TreatmentATB_FMT             10.9862
##                                         p = 0.1691
## 
## genotypeHD:ArmFamiliar                   8.7165
##                                         p = 0.1712
## 
## TreatmentOnly ATB:ArmFamiliar           10.8711
##                                         p = 0.1531
## 
## TreatmentATB_FMT:ArmFamiliar             -2.1384
##                                         p = 0.7843
## 
## Constant                                78.8515***
##                                         p = 0.0000
## 
## --------------------------------------------------------------
## Observations                               146
## Log Likelihood                          -607.7721
## Akaike Inf. Crit.                       1241.5440
## Bayesian Inf. Crit.                     1279.4090
## ==============================================================
## 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)

```r
dep_vars <-c("Ymaze_index","Ymaze_Dist_trial1","NOR_RI_5min",
          "BrainWeight_W14","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_W14.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",
                    "BrainWeight","PropelBrakeRatio"),
        align=TRUE)
```

```
##
## =================================================================================
##                                       Dependent variable:
##                     -------------------------------------------------------------
##                      YmazeIndex   YmazeDist      NOR     BrainWeight PropelBrakeRatio
##                         (1)          (2)         (3)        (4)           (5)
## -------------------------------------------------------------------------------
## genotypeHD              -0.0712    -2915.5500    4.1861     -0.0450        0.6744
##                      p = 0.7977   p = 0.3825  p = 0.4550 p = 0.3131    p = 0.1464
##
## TreatmentOnly ATB       -0.1040    -3159.4810   -9.7778+    -0.0058        0.1673
##                      p = 0.7183   p = 0.3620  p = 0.0984 p = 0.9047    p = 0.7243
##
## TreatmentATB_FMT         0.3836    -4316.4450  -10.8267+    -0.0308       -0.2662
##                      p = 0.2099   p = 0.2372  p = 0.0817 p = 0.5304    p = 0.6038
##
## genotypeHD:TreatmentOnly ATB  -0.0359   -815.7683    1.9508     0.0125       -0.5201
##                      p = 0.9275   p = 0.8629  p = 0.8059 p = 0.8484    p = 0.4270
```

```
## 
## genotypeHD:TreatmentATB_FMT      -0.2877        886.5785      12.0022      0.0358         0.0097
##                                 p = 0.4809    p = 0.8559    p = 0.1472  p = 0.5771      p = 0.9886
## 
## Constant                         1.2684***    30221.2400*** 62.6416***  0.4233***      2.6890***
##                                 p = 0.000001  p = 0.0000    p = 0.0000  p = 0.0000      p = 0.0000
## 
## ----------------------------------------------------------------------------------------------------
## Observations                         73            73            74          33             73
## Log Likelihood                    -60.2326      -698.1030     -271.4605   37.7967       -111.9956
## Akaike Inf. Crit.                  136.4651      1412.2060     558.9210   -59.5933       239.9911
## Bayesian Inf. Crit.                154.1027      1429.8430     576.6771   -49.2266       257.6287
## ====================================================================================================
## 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                       -44.3333            26.1667        -0.1611      0.4804*
##                                 p = 0.1054         p = 0.1532     p = 0.3441  p = 0.0375
## 
## TreatmentOnly ATB                 -0.3333            -23.3333       -0.1137      -0.1040
##                                 p = 0.9908         p = 0.1997     p = 0.5258  p = 0.6127
## 
## TreatmentATB_FMT                 -60.5833+           -10.0000        0.1477      0.0279
##                                 p = 0.0540         p = 0.5986     p = 0.4131  p = 0.8914
## 
## genotypeHD:TreatmentOnly ATB      8.1667             4.3352         0.1014      -0.1824
##                                 p = 0.8324         p = 0.8591     p = 0.6781  p = 0.5349
## 
## genotypeHD:TreatmentATB_FMT      68.7283+           -10.1667        -0.1096     -0.1030
##                                 p = 0.0900         p = 0.6953     p = 0.6539  p = 0.7394
## 
## Constant                         148.3333***         122.3333***    0.5493***   0.6108***
##                                 p = 0.000001       p = 0.0000     p = 0.0002  p = 0.0006
```

```
## 
## --------------------------------------------------------------------------------
## Observations                    33              41              31              33
## Log Likelihood             -141.4386       -172.3472         -7.4224         -3.7280
## Akaike Inf. Crit.           298.8771        360.6943         30.8448         23.4560
## Bayesian Inf. Crit.         309.2438        373.1371         40.5958         33.8227
## ================================================================================
## Note:                                      + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```r
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                   0.0733          0.0433         -0.1333         -0.1500
##                            p = 0.1705      p = 0.2966      p = 0.5866      p = 0.6834
## 
## TreatmentOnly ATB            0.0150          0.0533         -0.5167+         0.4167
##                            p = 0.7935      p = 0.2041      p = 0.0783      p = 0.2683
## 
## TreatmentATB_FMT             0.0450         -0.0483         -0.4917+         0.5833
##                            p = 0.4379      p = 0.2470      p = 0.0917      p = 0.1301
## 
## genotypeHD:TreatmentOnly ATB -0.0467         -0.0917          0.1167         -0.1667
##                            p = 0.5465      p = 0.1286      p = 0.7500      p = 0.7483
## 
## genotypeHD:TreatmentATB_FMT  -0.1182         -0.0050          0.2808         -0.5333
##                            p = 0.1357      p = 0.9306      p = 0.4396      p = 0.3141
## 
## Constant                     0.3500***       0.3083***       3.2167***       2.7000***
##                            p = 0.000000    p = 0.0000      p = 0.0000      p = 0.0000
## 
## ------------------------------------------------------------------------------------
## Observations                    33              36              33              36
## Log Likelihood               30.1053         37.5024        -15.1882        -28.5994
## Akaike Inf. Crit.           -44.2107        -59.0049         46.3764         73.1989
## Bayesian Inf. Crit.         -33.8440        -47.7953         56.7431         84.4085
```

```
## =====================================================================================
## Note:                                                    + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```r
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                        0.9500+                0.4667
##                                  p = 0.0606            p = 0.4375
##
## TreatmentOnly ATB                 0.6667                 1.2000+
##                                  p = 0.2162            p = 0.0612
##
## TreatmentATB_FMT                  0.3167                 0.4500
##                                  p = 0.5458            p = 0.4536
##
## genotypeHD:TreatmentOnly ATB     -0.5333                -0.5000
##                                  p = 0.4505            p = 0.5542
##
## genotypeHD:TreatmentATB_FMT      -0.1318                 0.2500
##                                  p = 0.8475            p = 0.7662
##
## Constant                          7.8833***              8.0333***
##                                  p = 0.0000            p = 0.0000
##
## ------------------------------------------------------------------------------
## Observations                        33                     36
## Log Likelihood                   -34.3428               -45.8489
## Akaike Inf. Crit.                 84.6855                107.6977
## Bayesian Inf. Crit.               95.0522                118.9073
## ==============================================================================
## Note:                          + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

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

```r
#subset(data, !is.na(Acetate_w14)) %>%
    #group_by(genotype, FMT, ATB) %>%
    #tally()
dep_vars <-c("Acetate_w14","Propionate_w14",
            "Isobutyrate_w14","Methylbutyrate_w14",
            "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_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                   38.7357+    -0.7309       -0.7858          0.4986
##                            p = 0.0706  p = 0.9007    p = 0.3314      p = 0.1249
## 
## TreatmentOnly ATB            14.5745     0.1275        -0.0158          0.0564
##                            p = 0.4488  p = 0.9821    p = 0.9834      p = 0.8497
## 
## TreatmentATB_FMT             17.5657    -2.0237        -0.3104         -0.0682
##                            p = 0.3859  p = 0.7257    p = 0.6963      p = 0.8252
## 
## genotypeHD:TreatmentOnly ATB -17.0560    0.2815        0.4770          -0.5904
##                            p = 0.5482  p = 0.9730    p = 0.6717      p = 0.1924
## 
## genotypeHD:TreatmentATB_FMT  17.3568    -2.1452        1.5722          -0.4113
##                            p = 0.5501  p = 0.7942    p = 0.1866      p = 0.3633
## 
## Constant                     52.2931**   9.6166*       2.9692***        0.9686***
##                            p = 0.0014  p = 0.0327    p = 0.0001      p = 0.0004
```

```
## 
## --------------------------------------------------------------------------------
## Observations                     32             28             32             32
## Log Likelihood              -132.2004       -76.5134       -48.3574       -21.2659
## Akaike Inf. Crit.            280.4009       169.0268       112.7149        58.5317
## Bayesian Inf. Crit.          290.4657       177.7551       122.7796        68.5965
## ================================================================================
## Note:                                      + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```r
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                  26.8063      -1.1543       0.3708       0.1820
##                            p = 0.2066   p = 0.8074   p = 0.6891   p = 0.5637
## 
## TreatmentOnly ATB           24.7463      -0.0569       0.4860       0.4082
##                            p = 0.2810   p = 0.9912   p = 0.6316   p = 0.2414
## 
## TreatmentATB_FMT            33.0547      10.8384*      1.0963       0.4162
##                            p = 0.1276   p = 0.0428   p = 0.2528   p = 0.2038
## 
## genotypeHD:TreatmentOnly ATB  -29.2282    7.0222       0.3220      -0.0468
##                            p = 0.3432   p = 0.3287   p = 0.8139   p = 0.9187
## 
## genotypeHD:TreatmentATB_FMT  -37.2222    -6.1014       0.0403      -0.1764
##                            p = 0.2143   p = 0.3726   p = 0.9754   p = 0.6909
## 
## Constant                    71.5411***    7.0118*      2.3977***    0.7544**
##                            p = 0.0001   p = 0.0302   p = 0.0009   p = 0.0016
## 
## -------------------------------------------------------------------------------
## Observations                   29           29           29           29
## Log Likelihood             -115.8745     -81.6858      -44.3597      -16.9530
## Akaike Inf. Crit.           247.7490      179.3717      104.7194       49.9061
## Bayesian Inf. Crit.         256.8330      188.4556      113.8034       58.9900
```

```
## ================================================================================
## 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

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

dep_vars <-c("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(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( "IL21-14","IL7R-14"),
          align=TRUE)
```

```
##
## ================================================================
##                              Dependent variable:
##                      ----------------------------------------
##                          IL21-14                IL7R-14
##                            (1)                    (2)
## ----------------------------------------------------------------
## genotypeHD                -0.1450+               0.1326
##                          p = 0.0850            p = 0.4143
##
## TreatmentOnly ATB         -0.0533               0.1881
##                          p = 0.5576            p = 0.3270
##
## TreatmentATB_FMT          -0.0493               -0.0156
##                          p = 0.6213            p = 0.9374
##
## Constant                  0.5979***             0.4767**
##                          p = 0.000003          p = 0.0093
##
## ----------------------------------------------------------------
```

```
## Observations                    26                 24
## Log Likelihood                1.0641            -12.7426
## Akaike Inf. Crit.             9.8717             37.4851
## Bayesian Inf. Crit.          16.4180             43.4595
## =================================================================
## Note:                   + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

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

```r
dep_vars <-c("IL17A_w14", "IL17E_w14", "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)))),
         control = lmeControl(opt = 'optim'))
  assign(paste0(r,".lmm"),m, envir = .GlobalEnv)
  summary(m)$tTable[,5]})

stargazer(IL17A_w14.lmm,IL17E_w14.lmm,
        IFNg_w14.lmm,IL1b_w14.lmm,IL22_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","IFNg-14","IL1b-14","IL22-14"),
        align=TRUE)
```

```
##
## =====================================================================================
##                                          Dependent variable:
##                          -----------------------------------------------------------
##                            IL17A-14   IL17E-14    IFNg-14      IL1b-14     IL22-14
##                              (1)        (2)         (3)          (4)         (5)
## -----------------------------------------------------------------------------------
## genotypeHD                 -0.0103     0.2609    -0.0200*      0.8150      0.4568
##                          p = 0.8914 p = 0.3931  p = 0.0225  p = 0.1036 p = 0.3588
##
## TreatmentOnly ATB           0.0665     0.3395     0.0130      -0.0696     -0.0976
##                          p = 0.3849 p = 0.2725  p = 0.1153  p = 0.8830 p = 0.8419
##
## TreatmentATB_FMT            0.0182     0.5259     0.0010       0.0325      0.7720
##                          p = 0.8094 p = 0.1023  p = 0.9027  p = 0.9451 p = 0.1327
##
## genotypeHD:TreatmentOnly ATB  -0.0337   0.0339    -0.0015      -0.6118     -0.2245
##                          p = 0.7521 p = 0.9413  p = 0.8935  p = 0.3681 p = 0.7459
```

```
## 
## genotypeHD:TreatmentATB_FMT    -0.0763     -0.7119       0.0042      -0.1118     -1.1779
##                               p = 0.4781 p = 0.1278  p = 0.7045  p = 0.8672 p = 0.1074
## 
## Constant                        0.1702**   0.6938**   0.0382***    0.6141+     0.6753+
##                               p = 0.0044 p = 0.0061 p = 0.000002 p = 0.0768 p = 0.0614
## 
## -------------------------------------------------------------------------------------
## Observations                       36         30          36          36          36
## Log Likelihood                  14.1085    -19.8117    82.1098     -39.1337    -42.3066
## Akaike Inf. Crit.              -12.2171    55.6234    -148.2197    94.2674     100.6132
## Bayesian Inf. Crit.             -1.0075    65.0479    -137.0101   105.4769     111.8228
## =====================================================================================
## Note:                                     + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```r
stargazer(IL6_w14.lmm,TNFa_w14.lmm,
        IFNg_w20.lmm,IL17A_w20.lmm,IL17E_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("IL6-14","TNFa-14",
                        "IFNg-20","IL17A-20","IL17E-20"),
        align=TRUE)
```

```
## 
## =====================================================================================
##                                               Dependent variable:
##                               -------------------------------------------------------
##                                  IL6-14     TNFa-14     IFNg-20     IL17A-20    IL17E-20
##                                   (1)         (2)         (3)         (4)         (5)
## -------------------------------------------------------------------------------------
## genotypeHD                       -0.2108     0.0258     -0.0157     -0.1527+    -0.4371
##                               p = 0.2667 p = 0.9825 p = 0.3309  p = 0.0744 p = 0.2364
## 
## TreatmentOnly ATB                0.3772+    -0.0080      0.0156     -0.0509     -0.3544
##                               p = 0.0591 p = 0.9944 p = 0.3862  p = 0.5686 p = 0.3716
## 
## TreatmentATB_FMT                 -0.0017     1.6155     -0.0012     -0.1382     -0.5879
##                               p = 0.9928 p = 0.1686 p = 0.9448  p = 0.1389 p = 0.1506
## 
## genotypeHD:TreatmentOnly ATB     -0.1689     0.3394     -0.0142      0.0785      0.3963
##                               p = 0.5216 p = 0.8378 p = 0.5533  p = 0.5134 p = 0.4547
## 
## genotypeHD:TreatmentATB_FMT      0.0676     -1.5066      0.0138      0.2035+     0.6322
##                               p = 0.7962 p = 0.3624 p = 0.5522  p = 0.0990 p = 0.2301
## 
## Constant                         0.7274***   0.8728     0.0403**   0.2588***   1.0919***
##                               p = 0.00003 p = 0.2794 p = 0.0019  p = 0.0002 p = 0.0005
```

```
## 
## ----------------------------------------------------------------------------
## Observations               36        34        34        34        32
## Log Likelihood         -13.1248   -60.4890   74.4579   20.6591   -18.8717
## Akaike Inf. Crit.       42.2495   136.9779  -132.9158  -25.3181   53.7434
## Bayesian Inf. Crit.     53.4591   147.6356  -122.2582  -14.6605   63.8081
## ============================================================================
## Note:                                  + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

```r
stargazer(IL1b_w20.lmm,IL21_w20.lmm,
         IL22_w20.lmm,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("IL1b-20",
             "IL21-20","IL22-20","IL6-20","TNFa-20"),
         align=TRUE)
```

```
## 
## =================================================================================
##                                       Dependent variable:
##                           -------------------------------------------------------
##                            IL1b-20    IL21-20    IL22-20    IL6-20     TNFa-20
##                              (1)        (2)        (3)        (4)        (5)
## -------------------------------------------------------------------------------
## genotypeHD                  0.4596    -0.0047     0.4040    -0.4964    -0.4820
##                           p = 0.1730  p = 0.9510  p = 0.6271  p = 0.1477  p = 0.1298
## 
## TreatmentOnly ATB           0.2706     0.1423     0.1274     0.1559    -0.3684
##                           p = 0.4590  p = 0.1190  p = 0.8905  p = 0.6703  p = 0.2855
## 
## TreatmentATB_FMT            0.2454    -0.0622    -0.0860    -0.2278    -0.3580
##                           p = 0.5009  p = 0.4752  p = 0.9259  p = 0.5358  p = 0.2988
## 
## genotypeHD:TreatmentOnly ATB  -0.3485    -0.2108+    -0.6839    -0.0815     0.4548
##                           p = 0.4767  p = 0.0888  p = 0.5841  p = 0.8679  p = 0.3216
## 
## genotypeHD:TreatmentATB_FMT   -0.1846     0.2091+     0.6249     0.6418     0.7472
##                           p = 0.6958  p = 0.0833  p = 0.6065  p = 0.1947  p = 0.1072
## 
## Constant                    0.4852*    0.3807***   0.8332    1.1527***   1.1667***
##                           p = 0.0440  p = 0.000002  p = 0.1632  p = 0.0001  p = 0.00005
## 
## -------------------------------------------------------------------------------
## Observations               34        34        34        34        33
## Log Likelihood         -27.8835    12.2008   -52.5298   -21.1180   -11.3178
## Akaike Inf. Crit.       71.7670    -8.4017   121.0595    58.2361    38.6356
## Bayesian Inf. Crit.     82.4246     2.2559   131.7172    68.8937    49.0023
```

```
## ================================================================================
## Note:                                        + p<0.1; * p<0.05; ** p<0.01; *** p<0.001
```

4 Clasping score

```r
data_clasping <- data.new[,c(1:6,83:95)] # extract the columns of data that will become Y
long_clasping<-data_clasping %>%
  gather(v, value, Clasping_W8:Clasping_W20) %>%
  separate(v, c("col", "Time"),sep="_W") %>%
  arrange(ID) %>%
  spread(col, value)
long_clasping$Time <-as.numeric(long_clasping$Time)-7
long_clasping$Clasping<-factor(long_clasping$Clasping, ordered = TRUE , levels = c(0:4))
t<-table(long_clasping$Time,long_clasping$Clasping)
t1<-table(long_clasping$Time,long_clasping$Clasping)%>%prop.table(margin = 1)
#subset(long_clasping, !is.na(Clasping)) %>%
#group_by(genotype, Treatment, Time) %>%
#tally() %>% summary()
```
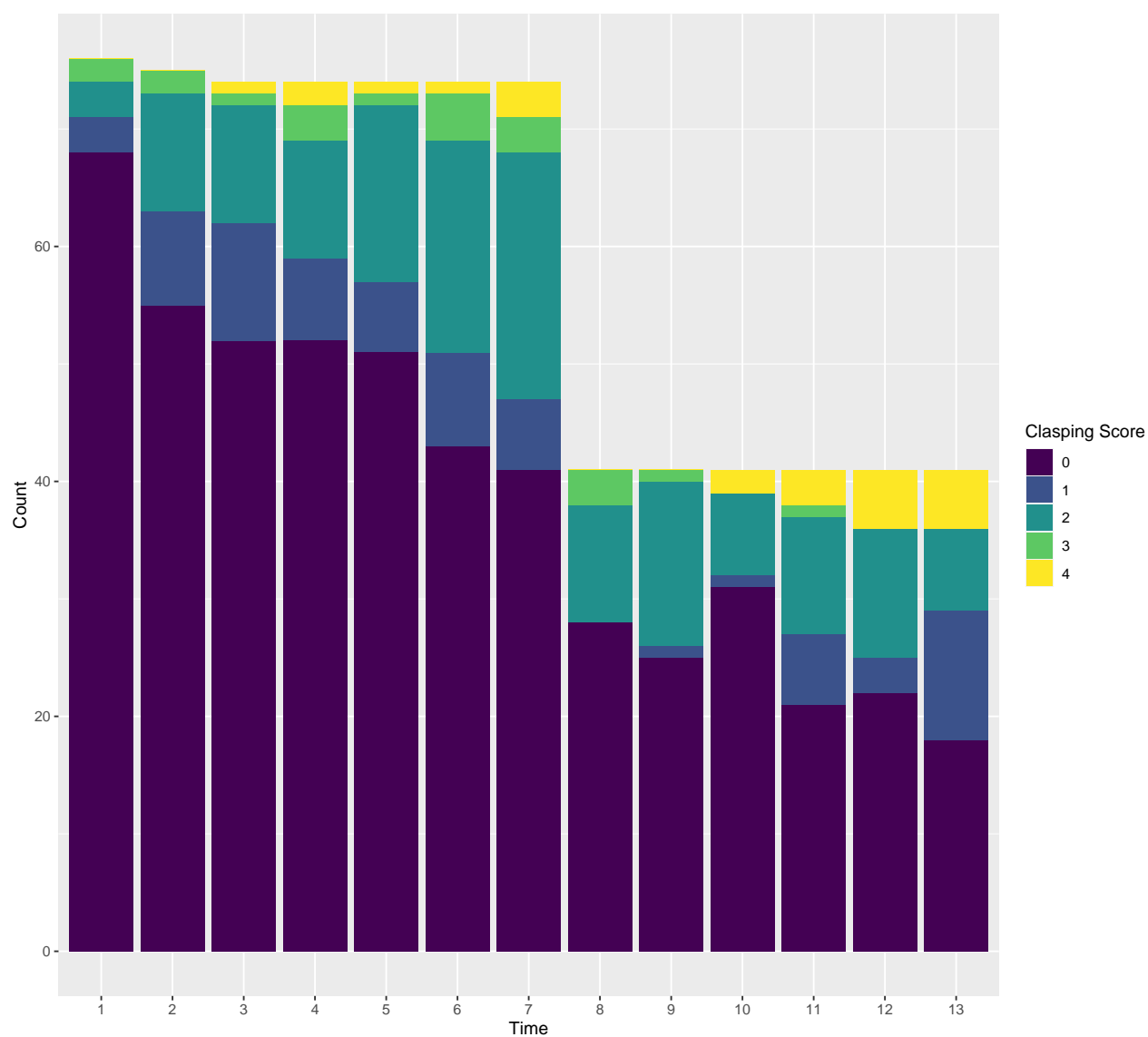
Figure 1: Bar plot for clasping over the 12 weeks
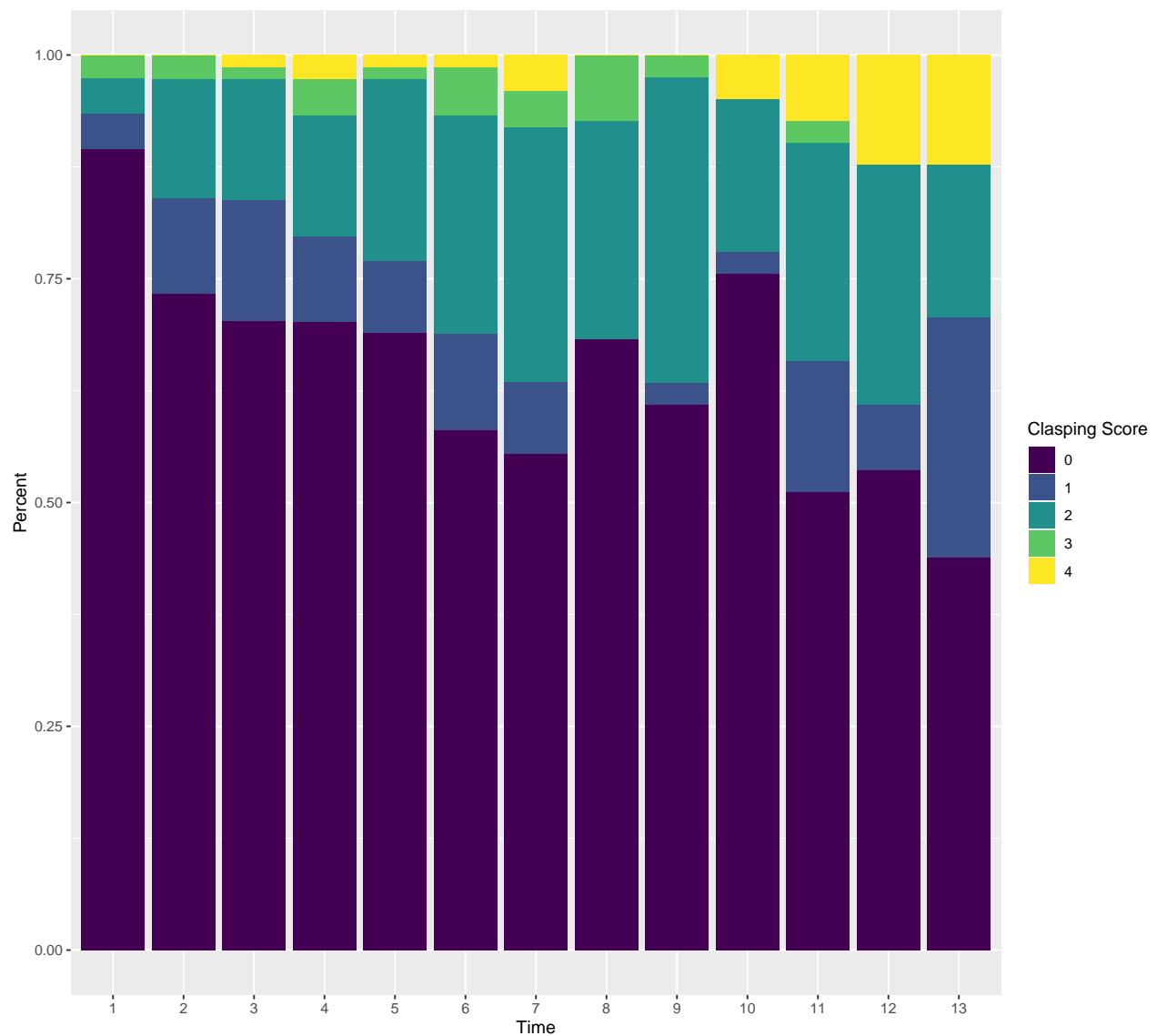
Figure 2: Bar plot for clasping over the 12 weeks

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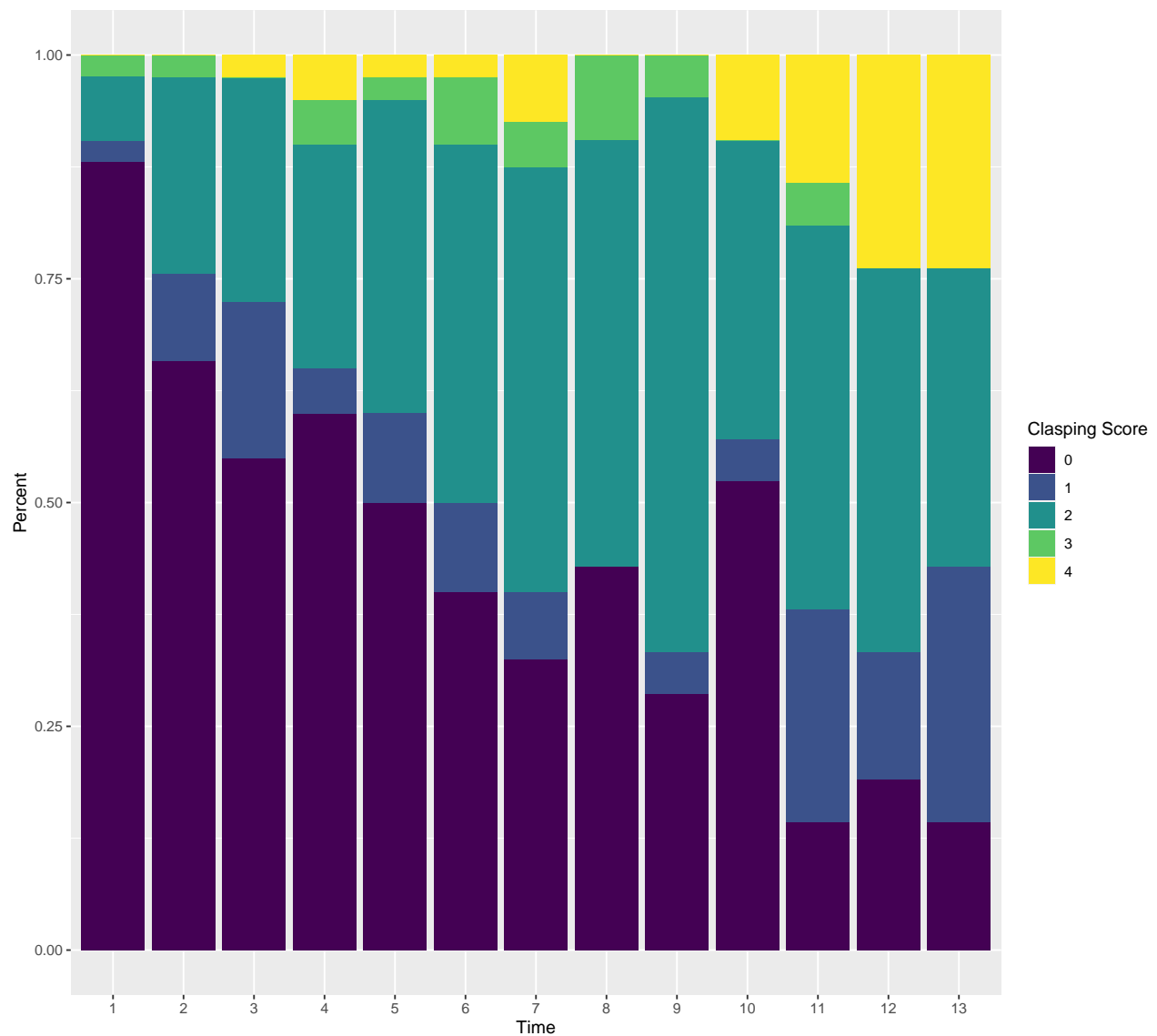
Figure 3: Bar plot for clasping over the 12 weeks for HD mice

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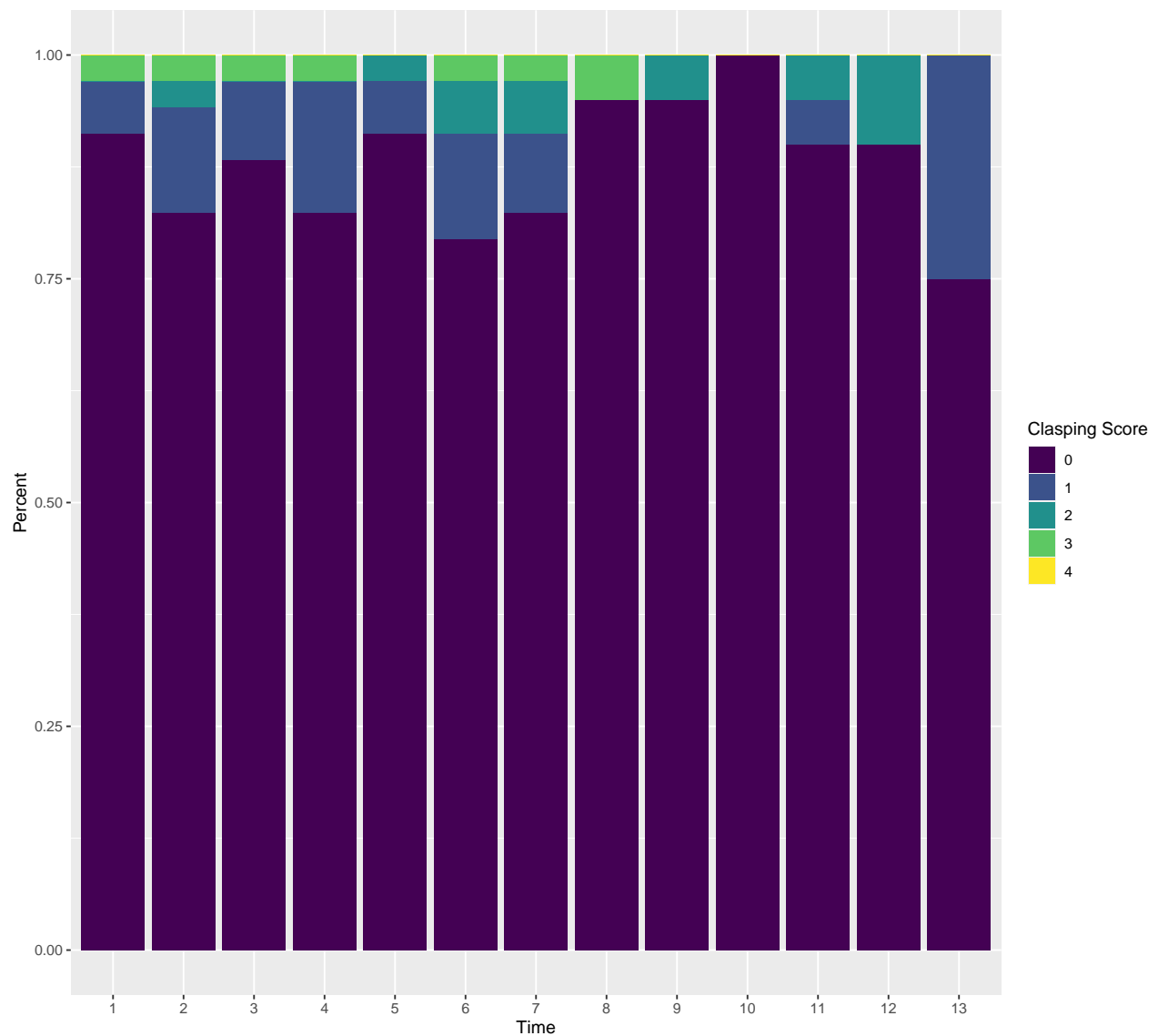
Figure 4: Bar plot for clasping over the 12 weeks for WT mice

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  767  -661.83 1339.67 8(0)  6.26e-08 3.8e+03
##
## Coefficients:
```

```
##                    Estimate Std. Error z value Pr(>|z|)
## genotypeHD          2.3070      0.1973  11.691  < 2e-16 ***
## TreatmentOnly ATB   0.2065      0.2038   1.013    0.311
## TreatmentATB_FMT    1.0321      0.2053   5.028 4.97e-07 ***
## Time                0.1587      0.0232   6.840 7.95e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##     Estimate Std. Error z value
## 0|1   3.4826     0.2855   12.20
## 1|2   4.0775     0.2987   13.65
## 2|3   6.0678     0.3511   17.28
## 3|4   6.7937     0.3845   17.67
## (221 observations deleted due to missingness)
```

4.2   Ordinal regression with random effect

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

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: Clasping ~ genotype + ATB + FMT + Time + (1 | BOX)
## data:    long_clasping
##
##  link  threshold nobs logLik  AIC     niter      max.grad cond.H
##  logit flexible  767  -595.23 1208.46 527(3284) 4.13e-05 3.5e+03
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  BOX    (Intercept) 2.263    1.504
## Number of groups:  BOX 38
##
## Coefficients:
##            Estimate Std. Error z value Pr(>|z|)
## genotypeHD  3.15276    0.55615   5.669 1.44e-08 ***
## ATBYES      0.06121    0.65293   0.094    0.925
## FMTYES      0.93591    0.65882   1.421    0.155
## Time        0.30660    0.03155   9.718  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##     Estimate Std. Error z value
## 0|1   4.8931     0.6234   7.849
## 1|2   5.6723     0.6347   8.937
## 2|3   8.1575     0.6824  11.955
## 3|4   9.0109     0.7076  12.734
## (221 observations deleted due to missingness)
```

4.3 Comparison between Cumulative Link Model and Cumulative Link Mixed Model

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

```
## Likelihood ratio tests of cumulative link models:
##
##               formula:                                         link:
## Clasping.clm  Clasping ~ genotype + Treatment + Time            logit
## Clasping.clmm Clasping ~ genotype + ATB + FMT + Time + (1 | BOX) logit
##               threshold:
## Clasping.clm  flexible
## Clasping.clmm flexible
##
##               no.par   AIC  logLik LR.stat df Pr(>Chisq)
## Clasping.clm       8 1339.7 -661.83
## Clasping.clmm      9 1208.5 -595.23   133.2  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 Rotarod

```
x<-emmeans(Rotarod.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 given Treatment in Rotarod") %>%
  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 1: Post-hoc results for genotype given Treatment in Rotarod

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	119.7505	17.4210	32	6.8739	0e+00
WT - HD	Only ATB	99.4652	17.3779	32	5.7237	0e+00
WT - HD	ATB_FMT	70.4652	18.4903	32	3.8109	6e-04

5.2 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 2: Post-hoc results for genotype * Treatment in Fecal Water Content

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	4.1612	2.0162	15	2.0639	0.3548
WT No treatment - WT Only ATB	-2.9555	2.0162	15	-1.4659	0.6892
WT No treatment - HD Only ATB	1.4598	2.0630	15	0.7076	0.9781
WT No treatment - WT ATB_FMT	-1.5672	2.1601	15	-0.7255	0.9756
WT No treatment - HD ATB_FMT	3.9833	2.1600	15	1.8441	0.4693
HD No treatment - WT Only ATB	-7.1167	1.8666	15	-3.8126	**0.0173**
HD No treatment - HD Only ATB	-2.7014	1.9171	15	-1.4091	0.7215
HD No treatment - WT ATB_FMT	-5.7284	2.0212	15	-2.8341	0.1055
HD No treatment - HD ATB_FMT	-0.1779	2.0211	15	-0.0880	1.0000
WT Only ATB - HD Only ATB	4.4153	1.9171	15	2.3031	0.2518
WT Only ATB - WT ATB_FMT	1.3883	2.0212	15	0.6869	0.9807
WT Only ATB - HD ATB_FMT	6.9388	2.0211	15	3.4331	**0.0355**
HD Only ATB - WT ATB_FMT	-3.0270	2.0680	15	-1.4637	0.6904
HD Only ATB - HD ATB_FMT	2.5235	2.0679	15	1.2203	0.8206
WT ATB_FMT - HD ATB_FMT	5.5505	2.1647	15	2.5641	0.1668

5.3   Fecal Output

```
x<-emmeans(FecalOutput.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 Post-hoc results for genotype*Treatment in Fecal Output
  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 Post-hoc results for genotype*Treatment in Fecal Output

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	-0.5577	1.2129	15	-0.4598	0.9969
WT No treatment - WT Only ATB	-3.0096	1.2129	15	-2.4813	0.1908

Table 3: Post-hoc results Post-hoc results for genotype*Treatment in Fecal Output *(continued)*

contrast	estimate	SE	df	t.ratio	p.value
WT No treatment - HD Only ATB	-2.2027	1.2259	15	-1.7967	0.4959
WT No treatment - WT ATB_FMT	-1.1538	1.2966	15	-0.8899	0.9432
WT No treatment - HD ATB_FMT	-1.7308	1.2966	15	-1.3348	0.7623
HD No treatment - WT Only ATB	-2.4519	1.1229	15	-2.1835	0.3002
HD No treatment - HD Only ATB	-1.6450	1.1370	15	-1.4468	0.7002
HD No treatment - WT ATB_FMT	-0.5962	1.2129	15	-0.4915	0.9958
HD No treatment - HD ATB_FMT	-1.1731	1.2129	15	-0.9672	0.9214
WT Only ATB - HD Only ATB	0.8069	1.1370	15	0.7097	0.9778
WT Only ATB - WT ATB_FMT	1.8558	1.2129	15	1.5300	0.6519
WT Only ATB - HD ATB_FMT	1.2788	1.2129	15	1.0544	0.8916
HD Only ATB - WT ATB_FMT	1.0488	1.2259	15	0.8555	0.9515
HD Only ATB - HD ATB_FMT	0.4719	1.2259	15	0.3849	0.9987
WT ATB_FMT - HD ATB_FMT	-0.5769	1.2966	15	-0.4449	0.9973

```
x<-emmeans(FecalOutput.lmm, pairwise ~ genotype*Treatment|Time,
        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 Post-hoc results for genotype*Treatment given Time in
  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 4: Post-hoc results Post-hoc results for genotype*Treatment given Time in Fecal Output

contrast	Time	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	1	-4.0863	1.3321	15	-3.0675	0.0697
WT No treatment - WT Only ATB	1	-3.6540	1.3785	15	-2.6508	0.1445
WT No treatment - HD Only ATB	1	-6.3756	1.5162	15	-4.2050	**0.0081**
WT No treatment - WT ATB_FMT	1	-0.5487	1.4697	15	-0.3734	0.9988
WT No treatment - HD ATB_FMT	1	-4.6543	1.5832	15	-2.9397	0.0876
HD No treatment - WT Only ATB	1	0.4323	1.3892	15	0.3112	0.9995
HD No treatment - HD Only ATB	1	-2.2894	1.3122	15	-1.7447	0.5258
HD No treatment - WT ATB_FMT	1	3.5375	1.4865	15	2.3797	0.2239
HD No treatment - HD ATB_FMT	1	-0.5680	1.3963	15	-0.4068	0.9983
WT Only ATB - HD Only ATB	1	-2.7216	1.2634	15	-2.1543	0.3130
WT Only ATB - WT ATB_FMT	1	3.1053	1.3906	15	2.2330	0.2794
WT Only ATB - HD ATB_FMT	1	-1.0003	1.4890	15	-0.6718	0.9825
HD Only ATB - WT ATB_FMT	1	5.8269	1.5130	15	3.8511	**0.0160**
HD Only ATB - HD ATB_FMT	1	1.7214	1.4020	15	1.2278	0.8170
WT ATB_FMT - HD ATB_FMT	1	-4.1055	1.4088	15	-2.9142	0.0917
WT No treatment - HD No treatment	2	-3.4982	1.2968	15	-2.6975	0.1335
WT No treatment - WT Only ATB	2	-3.5466	1.3301	15	-2.6665	0.1407
WT No treatment - HD Only ATB	2	-5.6801	1.4338	15	-3.9617	**0.0130**
WT No treatment - WT ATB_FMT	2	-0.6496	1.4190	15	-0.4578	0.9970
WT No treatment - HD ATB_FMT	2	-4.1670	1.5015	15	-2.7753	0.1169

Table 4: Post-hoc results Post-hoc results for genotype*Treatment given Time in Fecal Output *(continued)*

contrast	Time	estimate	SE	df	t.ratio	p.value
HD No treatment - WT Only ATB	2	-0.0484	1.3136	15	-0.0369	1.0000
HD No treatment - HD Only ATB	2	-2.1820	1.2612	15	-1.7300	0.5343
HD No treatment - WT ATB_FMT	2	2.8486	1.4086	15	2.0223	0.3751
HD No treatment - HD ATB_FMT	2	-0.6688	1.3430	15	-0.4980	0.9955
WT Only ATB - HD Only ATB	2	-2.1335	1.2261	15	-1.7400	0.5285
WT Only ATB - WT ATB_FMT	2	2.8970	1.3388	15	2.1638	0.3088
WT Only ATB - HD ATB_FMT	2	-0.6204	1.4104	15	-0.4399	0.9975
HD Only ATB - WT ATB_FMT	2	5.0305	1.4314	15	3.5143	**0.0304**
HD Only ATB - HD ATB_FMT	2	1.5131	1.3507	15	1.1203	0.8656
WT ATB_FMT - HD ATB_FMT	2	-3.5174	1.3755	15	-2.5572	0.1687
WT No treatment - HD No treatment	3	-2.9101	1.2673	15	-2.2963	0.2543
WT No treatment - WT Only ATB	3	-3.4392	1.2891	15	-2.6679	0.1404
WT No treatment - HD Only ATB	3	-4.9846	1.3626	15	-3.6582	**0.0232**
WT No treatment - WT ATB_FMT	3	-0.7504	1.3762	15	-0.5453	0.9931
WT No treatment - HD ATB_FMT	3	-3.6798	1.4311	15	-2.5712	0.1648
HD No treatment - WT Only ATB	3	-0.5291	1.2483	15	-0.4239	0.9979
HD No treatment - HD Only ATB	3	-2.0746	1.2180	15	-1.7033	0.5499
HD No treatment - WT ATB_FMT	3	2.1596	1.3414	15	1.6100	0.6048
HD No treatment - HD ATB_FMT	3	-0.7697	1.2976	15	-0.5931	0.9900
WT Only ATB - HD Only ATB	3	-1.5454	1.1948	15	-1.2935	0.7841
WT Only ATB - WT ATB_FMT	3	2.6888	1.2949	15	2.0764	0.3488
WT Only ATB - HD ATB_FMT	3	-0.2406	1.3426	15	-0.1792	1.0000
HD Only ATB - WT ATB_FMT	3	4.2342	1.3610	15	3.1110	0.0644
HD Only ATB - HD ATB_FMT	3	1.3049	1.3071	15	0.9983	0.9114
WT ATB_FMT - HD ATB_FMT	3	-2.9293	1.3476	15	-2.1737	0.3045
WT No treatment - HD No treatment	4	-2.3220	1.2438	15	-1.8669	0.4567
WT No treatment - WT Only ATB	4	-3.3318	1.2563	15	-2.6520	0.1442
WT No treatment - HD Only ATB	4	-4.2892	1.3046	15	-3.2878	**0.0465**
WT No treatment - WT ATB_FMT	4	-0.8513	1.3420	15	-0.6343	0.9864
WT No treatment - HD ATB_FMT	4	-3.1925	1.3739	15	-2.3237	0.2440
HD No treatment - WT Only ATB	4	-1.0098	1.1951	15	-0.8450	0.9539
HD No treatment - HD Only ATB	4	-1.9672	1.1832	15	-1.6625	0.5738
HD No treatment - WT ATB_FMT	4	1.4707	1.2868	15	1.1429	0.8559
HD No treatment - HD ATB_FMT	4	-0.8705	1.2613	15	-0.6902	0.9803
WT Only ATB - HD Only ATB	4	-0.9573	1.1699	15	-0.8183	0.9595
WT Only ATB - WT ATB_FMT	4	2.4805	1.2597	15	1.9691	0.4021
WT Only ATB - HD ATB_FMT	4	0.1393	1.2875	15	0.1082	1.0000
HD Only ATB - WT ATB_FMT	4	3.4379	1.3037	15	2.6371	0.1478
HD Only ATB - HD ATB_FMT	4	1.0966	1.2722	15	0.8620	0.9500
WT ATB_FMT - HD ATB_FMT	4	-2.3412	1.3256	15	-1.7662	0.5134
WT No treatment - HD No treatment	5	-1.7339	1.2267	15	-1.4134	0.7191
WT No treatment - WT Only ATB	5	-3.2244	1.2324	15	-2.6164	0.1530
WT No treatment - HD Only ATB	5	-3.5937	1.2615	15	-2.8487	0.1029
WT No treatment - WT ATB_FMT	5	-0.9521	1.3170	15	-0.7230	0.9760
WT No treatment - HD ATB_FMT	5	-2.7053	1.3315	15	-2.0317	0.3705
HD No treatment - WT Only ATB	5	-1.4905	1.1555	15	-1.2899	0.7860
HD No treatment - HD Only ATB	5	-1.8598	1.1578	15	-1.6063	0.6069
HD No treatment - WT ATB_FMT	5	0.7817	1.2463	15	0.6273	0.9871
HD No treatment - HD ATB_FMT	5	-0.9714	1.2346	15	-0.7868	0.9656
WT Only ATB - HD Only ATB	5	-0.3692	1.1517	15	-0.3206	0.9994

Table 4: Post-hoc results Post-hoc results for genotype*Treatment given Time in Fecal Output *(continued)*

contrast	Time	estimate	SE	df	t.ratio	p.value
WT Only ATB - WT ATB_FMT	5	2.2723	1.2339	15	1.8415	0.4707
WT Only ATB - HD ATB_FMT	5	0.5191	1.2466	15	0.4165	0.9981
HD Only ATB - WT ATB_FMT	5	2.6415	1.2611	15	2.0947	0.3402
HD Only ATB - HD ATB_FMT	5	0.8884	1.2467	15	0.7126	0.9774
WT ATB_FMT - HD ATB_FMT	5	-1.7531	1.3096	15	-1.3387	0.7603
WT No treatment - HD No treatment	6	-1.1458	1.2164	15	-0.9420	0.9290
WT No treatment - WT Only ATB	6	-3.1170	1.2178	15	-2.5595	0.1680
WT No treatment - HD Only ATB	6	-2.8982	1.2349	15	-2.3468	0.2355
WT No treatment - WT ATB_FMT	6	-1.0530	1.3018	15	-0.8089	0.9614
WT No treatment - HD ATB_FMT	6	-2.2180	1.3055	15	-1.6990	0.5524
HD No treatment - WT Only ATB	6	-1.9712	1.1312	15	-1.7426	0.5270
HD No treatment - HD Only ATB	6	-1.7524	1.1422	15	-1.5342	0.6495
HD No treatment - WT ATB_FMT	6	0.0928	1.2213	15	0.0760	1.0000
HD No treatment - HD ATB_FMT	6	-1.0722	1.2184	15	-0.8800	0.9456
WT Only ATB - HD Only ATB	6	0.2188	1.1407	15	0.1919	1.0000
WT Only ATB - WT ATB_FMT	6	2.0640	1.2182	15	1.6943	0.5551
WT Only ATB - HD ATB_FMT	6	0.8990	1.2214	15	0.7360	0.9740
HD Only ATB - WT ATB_FMT	6	1.8452	1.2348	15	1.4943	0.6728
HD Only ATB - HD ATB_FMT	6	0.6801	1.2312	15	0.5524	0.9927
WT ATB_FMT - HD ATB_FMT	6	-1.1650	1.2999	15	-0.8962	0.9416
WT No treatment - HD No treatment	7	-0.5577	1.2129	15	-0.4598	0.9969
WT No treatment - WT Only ATB	7	-3.0096	1.2129	15	-2.4813	0.1908
WT No treatment - HD Only ATB	7	-2.2027	1.2259	15	-1.7967	0.4959
WT No treatment - WT ATB_FMT	7	-1.1538	1.2966	15	-0.8899	0.9432
WT No treatment - HD ATB_FMT	7	-1.7308	1.2966	15	-1.3348	0.7623
HD No treatment - WT Only ATB	7	-2.4519	1.1229	15	-2.1835	0.3002
HD No treatment - HD Only ATB	7	-1.6450	1.1370	15	-1.4468	0.7002
HD No treatment - WT ATB_FMT	7	-0.5962	1.2129	15	-0.4915	0.9958
HD No treatment - HD ATB_FMT	7	-1.1731	1.2129	15	-0.9672	0.9214
WT Only ATB - HD Only ATB	7	0.8069	1.1370	15	0.7097	0.9778
WT Only ATB - WT ATB_FMT	7	1.8558	1.2129	15	1.5300	0.6519
WT Only ATB - HD ATB_FMT	7	1.2788	1.2129	15	1.0544	0.8916
HD Only ATB - WT ATB_FMT	7	1.0488	1.2259	15	0.8555	0.9515
HD Only ATB - HD ATB_FMT	7	0.4719	1.2259	15	0.3849	0.9987
WT ATB_FMT - HD ATB_FMT	7	-0.5769	1.2966	15	-0.4449	0.9973
WT No treatment - HD No treatment	8	0.0304	1.2164	15	0.0250	1.0000
WT No treatment - WT Only ATB	8	-2.9022	1.2178	15	-2.3832	0.2227
WT No treatment - HD Only ATB	8	-1.5072	1.2349	15	-1.2205	0.8205
WT No treatment - WT ATB_FMT	8	-1.2547	1.3018	15	-0.9638	0.9224
WT No treatment - HD ATB_FMT	8	-1.2435	1.3055	15	-0.9526	0.9259
HD No treatment - WT Only ATB	8	-2.9326	1.1312	15	-2.5925	0.1592
HD No treatment - HD Only ATB	8	-1.5376	1.1422	15	-1.3461	0.7563
HD No treatment - WT ATB_FMT	8	-1.2851	1.2213	15	-1.0522	0.8925
HD No treatment - HD ATB_FMT	8	-1.2739	1.2184	15	-1.0456	0.8949
WT Only ATB - HD Only ATB	8	1.3950	1.1407	15	1.2230	0.8193
WT Only ATB - WT ATB_FMT	8	1.6475	1.2182	15	1.3524	0.7528
WT Only ATB - HD ATB_FMT	8	1.6587	1.2214	15	1.3580	0.7498
HD Only ATB - WT ATB_FMT	8	0.2525	1.2348	15	0.2045	0.9999
HD Only ATB - HD ATB_FMT	8	0.2637	1.2312	15	0.2141	0.9999
WT ATB_FMT - HD ATB_FMT	8	0.0112	1.2999	15	0.0086	1.0000

Table 4: Post-hoc results Post-hoc results for genotype*Treatment given Time in Fecal Output *(continued)*

contrast	Time	estimate	SE	df	t.ratio	p.value
WT No treatment - HD No treatment	9	0.6185	1.2267	15	0.5042	0.9952
WT No treatment - WT Only ATB	9	-2.7948	1.2324	15	-2.2678	0.2654
WT No treatment - HD Only ATB	9	-0.8117	1.2615	15	-0.6434	0.9855
WT No treatment - WT ATB_FMT	9	-1.3555	1.3170	15	-1.0293	0.9008
WT No treatment - HD ATB_FMT	9	-0.7563	1.3315	15	-0.5680	0.9917
HD No treatment - WT Only ATB	9	-3.4133	1.1555	15	-2.9539	0.0855
HD No treatment - HD Only ATB	9	-1.4302	1.1578	15	-1.2353	0.8134
HD No treatment - WT ATB_FMT	9	-1.9740	1.2463	15	-1.5840	0.6202
HD No treatment - HD ATB_FMT	9	-1.3748	1.2346	15	-1.1135	0.8684
WT Only ATB - HD Only ATB	9	1.9831	1.1517	15	1.7219	0.5390
WT Only ATB - WT ATB_FMT	9	1.4393	1.2339	15	1.1664	0.8456
WT Only ATB - HD ATB_FMT	9	2.0385	1.2466	15	1.6353	0.5898
HD Only ATB - WT ATB_FMT	9	-0.5439	1.2611	15	-0.4313	0.9977
HD Only ATB - HD ATB_FMT	9	0.0554	1.2467	15	0.0444	1.0000
WT ATB_FMT - HD ATB_FMT	9	0.5993	1.3096	15	0.4576	0.9970
WT No treatment - HD No treatment	10	1.2066	1.2438	15	0.9701	0.9205
WT No treatment - WT Only ATB	10	-2.6874	1.2563	15	-2.1391	0.3198
WT No treatment - HD Only ATB	10	-0.1162	1.3046	15	-0.0891	1.0000
WT No treatment - WT ATB_FMT	10	-1.4564	1.3420	15	-1.0852	0.8798
WT No treatment - HD ATB_FMT	10	-0.2690	1.3739	15	-0.1958	1.0000
HD No treatment - WT Only ATB	10	-3.8940	1.1951	15	-3.2584	**0.0491**
HD No treatment - HD Only ATB	10	-1.3228	1.1832	15	-1.1179	0.8665
HD No treatment - WT ATB_FMT	10	-2.6630	1.2868	15	-2.0695	0.3521
HD No treatment - HD ATB_FMT	10	-1.4756	1.2613	15	-1.1700	0.8440
WT Only ATB - HD Only ATB	10	2.5712	1.1699	15	2.1979	0.2941
WT Only ATB - WT ATB_FMT	10	1.2310	1.2597	15	0.9772	0.9183
WT Only ATB - HD ATB_FMT	10	2.4184	1.2875	15	1.8784	0.4504
HD Only ATB - WT ATB_FMT	10	-1.3402	1.3037	15	-1.0280	0.9012
HD Only ATB - HD ATB_FMT	10	-0.1528	1.2722	15	-0.1201	1.0000
WT ATB_FMT - HD ATB_FMT	10	1.1874	1.3256	15	0.8957	0.9417
WT No treatment - HD No treatment	11	1.7947	1.2673	15	1.4162	0.7175
WT No treatment - WT Only ATB	11	-2.5800	1.2891	15	-2.0014	0.3856
WT No treatment - HD Only ATB	11	0.5793	1.3626	15	0.4252	0.9979
WT No treatment - WT ATB_FMT	11	-1.5572	1.3762	15	-1.1315	0.8608
WT No treatment - HD ATB_FMT	11	0.2182	1.4311	15	0.1525	1.0000
HD No treatment - WT Only ATB	11	-4.3747	1.2483	15	-3.5046	**0.0310**
HD No treatment - HD Only ATB	11	-1.2154	1.2180	15	-0.9979	0.9116
HD No treatment - WT ATB_FMT	11	-3.3519	1.3414	15	-2.4988	0.1855
HD No treatment - HD ATB_FMT	11	-1.5765	1.2976	15	-1.2149	0.8232
WT Only ATB - HD Only ATB	11	3.1593	1.1948	15	2.6442	0.1461
WT Only ATB - WT ATB_FMT	11	1.0228	1.2949	15	0.7898	0.9650
WT Only ATB - HD ATB_FMT	11	2.7982	1.3426	15	2.0842	0.3451
HD Only ATB - WT ATB_FMT	11	-2.1366	1.3610	15	-1.5698	0.6285
HD Only ATB - HD ATB_FMT	11	-0.3611	1.3071	15	-0.2762	0.9997
WT ATB_FMT - HD ATB_FMT	11	1.7755	1.3476	15	1.3175	0.7716
WT No treatment - HD No treatment	12	2.3828	1.2968	15	1.8374	0.4730
WT No treatment - WT Only ATB	12	-2.4726	1.3301	15	-1.8590	0.4610
WT No treatment - HD Only ATB	12	1.2748	1.4338	15	0.8891	0.9434
WT No treatment - WT ATB_FMT	12	-1.6581	1.4190	15	-1.1685	0.8447
WT No treatment - HD ATB_FMT	12	0.7055	1.5015	15	0.4698	0.9966

Table 4: Post-hoc results Post-hoc results for genotype*Treatment given Time in Fecal Output *(continued)*

contrast	Time	estimate	SE	df	t.ratio	p.value
HD No treatment - WT Only ATB	12	-4.8554	1.3136	15	-3.6964	**0.0216**
HD No treatment - HD Only ATB	12	-1.1080	1.2612	15	-0.8785	0.9460
HD No treatment - WT ATB_FMT	12	-4.0409	1.4086	15	-2.8688	0.0993
HD No treatment - HD ATB_FMT	12	-1.6773	1.3430	15	-1.2490	0.8066
WT Only ATB - HD Only ATB	12	3.7474	1.2261	15	3.0563	0.0711
WT Only ATB - WT ATB_FMT	12	0.8145	1.3388	15	0.6084	0.9887
WT Only ATB - HD ATB_FMT	12	3.1781	1.4104	15	2.2534	0.2711
HD Only ATB - WT ATB_FMT	12	-2.9329	1.4314	15	-2.0489	0.3620
HD Only ATB - HD ATB_FMT	12	-0.5693	1.3507	15	-0.4215	0.9979
WT ATB_FMT - HD ATB_FMT	12	2.3636	1.3755	15	1.7183	0.5411
WT No treatment - HD No treatment	13	2.9709	1.3321	15	2.2302	0.2805
WT No treatment - WT Only ATB	13	-2.3652	1.3785	15	-1.7158	0.5425
WT No treatment - HD Only ATB	13	1.9703	1.5162	15	1.2995	0.7810
WT No treatment - WT ATB_FMT	13	-1.7589	1.4697	15	-1.1968	0.8317
WT No treatment - HD ATB_FMT	13	1.1927	1.5832	15	0.7533	0.9713
HD No treatment - WT Only ATB	13	-5.3361	1.3892	15	-3.8412	**0.0164**
HD No treatment - HD Only ATB	13	-1.0006	1.3122	15	-0.7625	0.9698
HD No treatment - WT ATB_FMT	13	-4.7298	1.4865	15	-3.1818	0.0566
HD No treatment - HD ATB_FMT	13	-1.7782	1.3963	15	-1.2735	0.7944
WT Only ATB - HD Only ATB	13	4.3355	1.2634	15	3.4317	**0.0356**
WT Only ATB - WT ATB_FMT	13	0.6063	1.3906	15	0.4360	0.9976
WT Only ATB - HD ATB_FMT	13	3.5579	1.4890	15	2.3895	0.2205
HD Only ATB - WT ATB_FMT	13	-3.7293	1.5130	15	-2.4648	0.1959
HD Only ATB - HD ATB_FMT	13	-0.7776	1.4020	15	-0.5546	0.9926
WT ATB_FMT - HD ATB_FMT	13	2.9517	1.4088	15	2.0952	0.3399

5.4 CFC Extinction

```r
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 5: Post-hoc results for genotype given Treatment in CFC Extinction

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	9.8921	4.3878	31	2.2544	**0.0314**
WT - HD	Only ATB	14.8152	4.2791	31	3.4622	**0.0016**
WT - HD	ATB_FMT	6.4316	4.8933	31	1.3144	0.1984

5.5 Ymaze

```
x<-emmeans(Ymaze.lmm, pairwise ~ genotype*Arm|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 and arm given Treatment in Ymaze") %>%
  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 and arm given Treatment in Ymaze

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT Novel - HD Novel	No treatment	18.6328	6.1519	32	3.0288	**0.0237**
WT Novel - WT Familiar	No treatment	22.3397	6.2664	69	3.5650	**0.0036**
WT Novel - HD Familiar	No treatment	32.2559	7.4644	32	4.3213	**0.0008**
HD Novel - WT Familiar	No treatment	3.7069	7.4644	32	0.4966	0.9593
HD Novel - HD Familiar	No treatment	13.6231	6.0176	69	2.2639	0.1167
WT Familiar - HD Familiar	No treatment	9.9163	6.1519	32	1.6119	0.3865
WT Novel - HD Novel	Only ATB	12.1654	6.2319	32	1.9521	0.2273
WT Novel - WT Familiar	Only ATB	11.4686	6.2929	69	1.8225	0.2717
WT Novel - HD Familiar	Only ATB	14.9175	7.6010	32	1.9626	0.2232
HD Novel - WT Familiar	Only ATB	-0.6968	7.6010	32	-0.0917	0.9997
HD Novel - HD Familiar	Only ATB	2.7521	6.1654	69	0.4464	0.9701
WT Familiar - HD Familiar	Only ATB	3.4489	6.2319	32	0.5534	0.9449
WT Novel - HD Novel	ATB_FMT	7.6466	6.5573	32	1.1661	0.6521
WT Novel - WT Familiar	ATB_FMT	24.4781	6.6793	69	3.6647	**0.0027**
WT Novel - HD Familiar	ATB_FMT	23.4082	8.1203	32	2.8827	**0.0336**
HD Novel - WT Familiar	ATB_FMT	16.8315	8.1203	32	2.0728	0.1837
HD Novel - HD Familiar	ATB_FMT	15.7616	6.4032	69	2.4615	0.0752
WT Familiar - HD Familiar	ATB_FMT	-1.0699	6.5573	32	-0.1632	0.9984

5.6 FITC-W20

```
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 7: Post-hoc results for genotype given Treatment in FITC

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	-0.4804	0.2031	11	-2.3648	**0.0375**
WT - HD	Only ATB	-0.2980	0.1995	11	-1.4936	0.1634
WT - HD	ATB_FMT	-0.3774	0.2230	11	-1.6921	0.1187

5.7 Propionate- Week20

```
x<-emmeans(Propionate_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 Propionate") %>%
  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 Treatment given genotype in Propionate

contrast	genotype	estimate	SE	df	t.ratio	p.value
No treatment - Only ATB	WT	0.0569	5.0083	9	0.0114	0.9999
No treatment - ATB_FMT	WT	-10.8384	4.5975	9	-2.3575	0.0980
Only ATB - ATB_FMT	WT	-10.8953	5.4139	9	-2.0125	0.1648
No treatment - Only ATB	HD	-6.9653	4.5975	9	-1.5150	0.3293
No treatment - ATB_FMT	HD	-4.7370	4.5975	9	-1.0303	0.5775
Only ATB - ATB_FMT	HD	2.2283	4.1121	9	0.5419	0.8530

5.8 IFNg- Week14

```
x<-emmeans(IFNg_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 IFNg") %>%
  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 IFNg

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	No treatment	0.0200	0.0076	12	2.6187	**0.0224**
WT - HD	Only ATB	0.0215	0.0076	12	2.8123	**0.0157**

Table 9: Post-hoc results for genotype given Treatment in IFNg *(continued)*

contrast	Treatment	estimate	SE	df	t.ratio	p.value
WT - HD	ATB_FMT	0.0158	0.0076	12	2.0694	0.0608

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] tibble_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] vctrs_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] pander_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
```