

# Cardiac\_CT Basic: both diets

Alex Badea

01/17/23

## Contents

Data Summary	1
Plots for all cardiac metrics	2

---

## Data Summary

#We use microCT in mice on a HFD to compare cardiac metric for the following genotypes: APOE2, APOE3, APOE4, APOE-/-

```
## [1] "All data set"
```

```
## # A tibble: 15 x 4
## # Groups:   Diet, Genotype [8]
##   Diet Genotype Sex    count
##   <chr> <chr>    <chr> <int>
## 1 CTRL E22      Male     6
## 2 CTRL E33      Female   5
## 3 CTRL E33      Male     3
## 4 CTRL E44      Female   3
## 5 CTRL E44      Male     3
## 6 CTRL K0       Female   4
## 7 CTRL K0       Male     2
## 8 HFD  E22      Female   4
## 9 HFD  E22      Male     5
## 10 HFD E33      Female   6
## 11 HFD E33      Male    10
## 12 HFD E44      Female   2
## 13 HFD E44      Male     4
## 14 HFD K0       Female   5
## 15 HFD K0       Male     4
```

```
## [1] "Age <17"
```

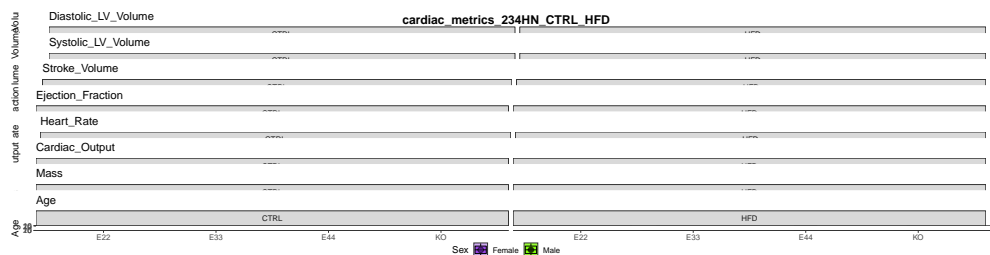
```
## # A tibble: 15 x 4
## # Groups:   Diet, Genotype [8]
##   Diet Genotype Sex    count
##   <chr> <chr>   <chr> <int>
## 1 CTRL E22     Male     6
## 2 CTRL E33     Female   5
## 3 CTRL E33     Male     3
## 4 CTRL E44     Female     1
## 5 CTRL E44     Male     3
## 6 CTRL K0      Female     4
## 7 CTRL K0      Male     1
## 8 HFD  E22     Female     4
## 9 HFD  E22     Male     5
## 10 HFD E33     Female     6
## 11 HFD E33     Male    10
## 12 HFD E44     Female     1
## 13 HFD E44     Male     1
## 14 HFD K0      Female     5
## 15 HFD K0      Male     4
```

```
## # A tibble: 15 x 4
## # Groups:   Diet, Genotype [8]
##   Diet Genotype Sex    count
##   <chr> <chr>   <chr> <int>
## 1 CTRL E22     Male     6
## 2 CTRL E33     Female     5
## 3 CTRL E33     Male     3
## 4 CTRL E44     Female     3
## 5 CTRL E44     Male     3
## 6 CTRL K0      Female     4
## 7 CTRL K0      Male     2
## 8 HFD  E22     Female     4
## 9 HFD  E22     Male     5
## 10 HFD E33     Female     6
## 11 HFD E33     Male    10
## 12 HFD E44     Female     2
## 13 HFD E44     Male     4
## 14 HFD K0      Female     5
## 15 HFD K0      Male     4
```

## Plots for all cardiac metrics

```
## 'summarise()' has grouped output by 'Diet', 'Genotype'. You can override using
## the '.groups' argument.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
```



```
lm8 <- lm(Ejection_Fraction ~ factor(Genotype)*factor(Sex)*factor(Diet), data)
anova(lm8)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Ejection_Fraction
```

```
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## factor(Genotype)	3	4293.8	1431.26	5.9470	0.001474
## factor(Sex)	1	602.0	602.01	2.5014	0.119928
## factor(Diet)	1	19.4	19.39	0.0806	0.777660
## factor(Genotype):factor(Sex)	3	890.7	296.90	1.2336	0.307110
## factor(Genotype):factor(Diet)	3	2402.5	800.84	3.3275	0.026695
## factor(Sex):factor(Diet)	1	153.2	153.23	0.6367	0.428607
## factor(Genotype):factor(Sex):factor(Diet)	2	258.7	129.37	0.5376	0.587444
## Residuals	51	12274.2	240.67		
##					
## factor(Genotype)	**				
## factor(Sex)					

```

## factor(Diet)
## factor(Genotype):factor(Sex)
## factor(Genotype):factor(Diet)          *
## factor(Sex):factor(Diet)
## factor(Genotype):factor(Sex):factor(Diet)
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

em4 <- emmeans(lm8, list(pairwise ~ factor(Genotype)*factor(Sex)*factor(Diet)), adjust="tukey")
emmeans(lm8, list(pairwise ~ facor(Diet)|factor(Genotype)), adjust="tukey")

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

## $'emmeans of Diet | Genotype'
## Genotype = E22:
##   Diet emmean   SE df lower.CL upper.CL
##   CTRL nonEst   NA NA      NA      NA
##   HFD    27.9 5.20 51    17.4    38.3
##
## Genotype = E33:
##   Diet emmean   SE df lower.CL upper.CL
##   CTRL  29.9 5.66 51    18.5    41.3
##   HFD   44.2 4.01 51    36.1    52.2
##
## Genotype = E44:
##   Diet emmean   SE df lower.CL upper.CL
##   CTRL  33.4 6.33 51    20.7    46.1
##   HFD   40.1 6.72 51    26.6    53.6
##
## Genotype = K0:
##   Diet emmean   SE df lower.CL upper.CL
##   CTRL  64.5 6.72 51    51.0    78.0
##   HFD   53.8 5.20 51    43.3    64.2
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $'pairwise differences of Diet | Genotype'
## Genotype = E22:
##   2          estimate    SE df t.ratio p.value
##   CTRL - HFD   nonEst   NA NA      NA      NA
##
## Genotype = E33:
##   2          estimate    SE df t.ratio p.value
##   CTRL - HFD  -14.25 6.94 51  -2.053  0.0452
##
## Genotype = E44:
##   2          estimate    SE df t.ratio p.value
##   CTRL - HFD   -6.69 9.23 51  -0.724  0.4723
##
## Genotype = K0:

```

```
## 2          estimate    SE df t.ratio p.value
## CTRL - HFD    10.75 8.50 51   1.265  0.2117
##
## Results are averaged over the levels of: Sex
```

```
emmeans(lm8, list(pairwise ~ facor(Genotype)|factor(Diet)), adjust="tukey")
```

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

```
## $'emmeans of Genotype | Diet'
## Diet = CTRL:
##   Genotype emmean    SE df lower.CL upper.CL
## E22      nonEst    NA NA      NA      NA
## E33      29.9 5.66 51    18.5    41.3
## E44      33.4 6.33 51    20.7    46.1
## K0       64.5 6.72 51    51.0    78.0
##
## Diet = HFD:
##   Genotype emmean    SE df lower.CL upper.CL
## E22      27.9 5.20 51    17.4    38.3
## E33      44.2 4.01 51    36.1    52.2
## E44      40.1 6.72 51    26.6    53.6
## K0       53.8 5.20 51    43.3    64.2
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $'pairwise differences of Genotype | Diet'
## Diet = CTRL:
## 2          estimate    SE df t.ratio p.value
## E22 - E33  nonEst    NA NA      NA      NA
## E22 - E44  nonEst    NA NA      NA      NA
## E22 - K0   nonEst    NA NA      NA      NA
## E33 - E44   -3.49 8.50 51   -0.411  0.9764
## E33 - K0   -34.60 8.79 51   -3.937  0.0014
## E44 - K0   -31.11 9.23 51   -3.370  0.0076
##
## Diet = HFD:
## 2          estimate    SE df t.ratio p.value
## E22 - E33  -16.29 6.57 51   -2.480  0.0752
## E22 - E44  -12.21 8.50 51   -1.437  0.4825
## E22 - K0   -25.89 7.36 51   -3.518  0.0050
## E33 - E44    4.07 7.82 51    0.521  0.9537
## E33 - K0   -9.60 6.57 51   -1.463  0.4672
## E44 - K0   -13.68 8.50 51   -1.610  0.3824
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
#em4 <- na.omit(as.data.frame(em4$`pairwise differences of Genotype, Sex, Diet`)) %>%
#   arrange(p.value) %>%
#   filter(p.value < 0.05)
```

```

#colnames(em4) <- c('comparison','estimate','SE', 'df', 't.ratio', 'p.value')
# # em4 <- em4 %>% filter(group_similarity(comparison) == 2)
# print('Significant pairwise differences of genotype, sex, and diet in Systolic_LV_Volume')
# print(em4)

```

```

#
# sink(paste(outpath, "cardiac_SimpleModels.txt"))
# lm_EF <- lm(Ejection_Fraction~ Genotype*Sex, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype , adjust = "sidak")
# contrast(EF.emm, simple = c("Genotype")) #FDR
#
# lm_EF <- lm(Diastolic_LV_Volume~ Genotype*Sex*Diet, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype|Diet )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype , adjust = "sidak")
# contrast(EF.emm, simple = c("Genotype")) #FDR
#
# lm_EF <- lm(Systolic_LV_Volume~ Genotype*Sex, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype , adjust = "sidak")
# contrast(EF.emm, simple = c("Genotype")) #FDR
#
# lm_EF <- lm(Stroke_Volume~ Genotype*Sex, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype , adjust = "sidak")
# contrast(EF.emm, simple = c("Genotype")) #FDR
#
# lm_EF <- lm(Ejection_Fraction~ Genotype*Sex, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype , adjust = "sidak")
# contrast(EF.emm, simple = c("Genotype")) #FDR
#
# lm_EF <- lm(Heart_Rate~ Genotype*Sex, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype , adjust = "sidak")

```

```

# contrast(EF.emm, simple = c("Genotype")) #FDR
#
# lm_EF <- lm(Cardiac_Output~ Genotype*Sex, data=geno_combined)
# summary(lm_EF)
# anova(lm_EF)
# summary(glht((lm_EF), emm(pairwise ~ Genotype )))
#
# EF.emm <- emmeans(lm_EF , ~ Genotype*Sex , adjust = "sidak")
# contrast(EF.emm, simple = c("Genotype", "Sex")) #FDR
#
#
#
#
#
# #33333
# #sink(paste(outpath, "cardiac_SimpleModels.txt"))
# #mydata.lm <- lm(Diastolic_LV_Volume ~ Genotype*Sex*Diet*Age, data = geno_combined)
# #anova(mydata.lm)
# #summary(glht(mydata.lm, emm(pairwise ~ Genotype|Sex, adjust="sidak"))) #consider save to file
# #summary(glht(mydata.lm, emm(pairwise ~ Sex| Genotype)))
#
# #3333
#
#
# mypairs<-pairs(EF.emm) #_consider save to file
# pairs(EF.emm, by="Genotype")
# pairs(EF.emm, by="Sex")
#
#
# print('EF')
# emmip(lm_EF, ~ Genotype | Sex )
# emmip(lm_EF, ~ Sex | Genotype )
# emmip(lm_EF, Genotype~ Sex )
#
#
#
# plot(EF.emm, by = NULL, comparisons = TRUE, adjust = "mvt",
# horizontal = FALSE, colors = "darkgreen", main ="fx VOL")
# ggsave(paste(outpath,'EF_emmeans.pdf',sep=''), plot = last_plot(), device='pdf', scale=1, width=16, h
# sink()

```