Evaluation of Energy Expenditure from BXD Datasets

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Contents

The goal is to identify genetic determinants of energy expenditure and of adaptive thermogenesis from BXD mice. To start we searched gene network for energy expenditure data, ignoring those involved in exercise physiology.

- **BXD_17621** Oxygen intake over 24h on NCD at 16 w age. Also included light/dark. Not adjusted for lean mass. Has mean +/- SE in mL/kg/h. From Prinen 2014 (https://doi.org/10.1016/j.cmet.2014.04.002)
- **BXD_17622** Oxygen intake over 24h at 16 w age on HFD?, males. Not adjusted for lean mass. Has mean +/- SE in mL/kg/h. From Williams (2016). Body weight in BXD_17560, lean mass in BXD_17574

```r
library(readr)
williams.ncd.ee <- read_csv("BXD_17621.csv", skip=9)%>%
  mutate(Diet="NCD",Age=16,Dataset="Williams")
williams.ncd.bw <- read_csv("BXD_17559.csv" , skip=9)%>%
  mutate(Diet="NCD",Age=16,Dataset="Williams")
williams.ncd.lm <- read_csv("BXD_17573.csv" , skip=9)%>%
  mutate(Diet="NCD",Age=16,Dataset="Williams")

williams.ncd <- full_join(williams.ncd.ee,williams.ncd.bw, suffix=c('_ee','_bw'), by=c("Name","Dataset"
  full_join(williams.ncd.lm) %>%
  mutate(Value_lm = Value,
         SE_lm = SE)

williams.hfd.ee <- read_csv("BXD_17622.csv" , skip=9)%>% #may be mislabelled on genenetwork
  mutate(Diet="HFD",Age=16,Dataset="Williams")
williams.hfd.bw <- read_csv("BXD_17560.csv", skip=9)%>%
  mutate(Diet="HFD",Age=16,Dataset="Williams")
williams.hfd.lm <- read_csv("BXD_17574.csv", skip=9)%>%
  mutate(Diet="HFD",Age=16,Dataset="Williams")

williams.hfd <- full_join(williams.hfd.ee,williams.hfd.bw, suffix=c('_ee','_bw'), by=c("Name","Dataset"
```

```
  full_join(williams.hfd.lm) %>%
  mutate(Value_lm = Value,
         SE_lm = SE)

data <- bind_rows(#ncd.pirinen,
                  williams.ncd,
                  williams.hfd) %>% # in mL/kg/h
  mutate(VO2_g_min = Value_ee/1000) %>% #in mL/g/h
  mutate(VO2_min = VO2_g_min*Value_bw/60) %>% # in mL/min #this seems reasonable
  mutate(MR_KJ_d = VO2_min * 60 * 24 / 1000 * 4.84 * 4.184,
         MR_KJ_d_SE = SE_ee/1000*Value_bw/60* 60 * 24 / 1000 * 4.84 * 4.184) %>% # 60min/h x 24h/day /
  mutate(MR_W = MR_KJ_d * 0.0115740741,
         MR_W_SE = MR_KJ_d_SE* 0.0115740741) %>% # in Watts
  mutate(Diet = relevel(factor(Diet), ref="NCD"))
```

These data can be found in /Users/davebrid/Documents/GitHub/PrecisionNutrition/Mouse Genetics/Energy Expenditure. This script was most recently updated on Wed Apr 13 16:37:04 2022.
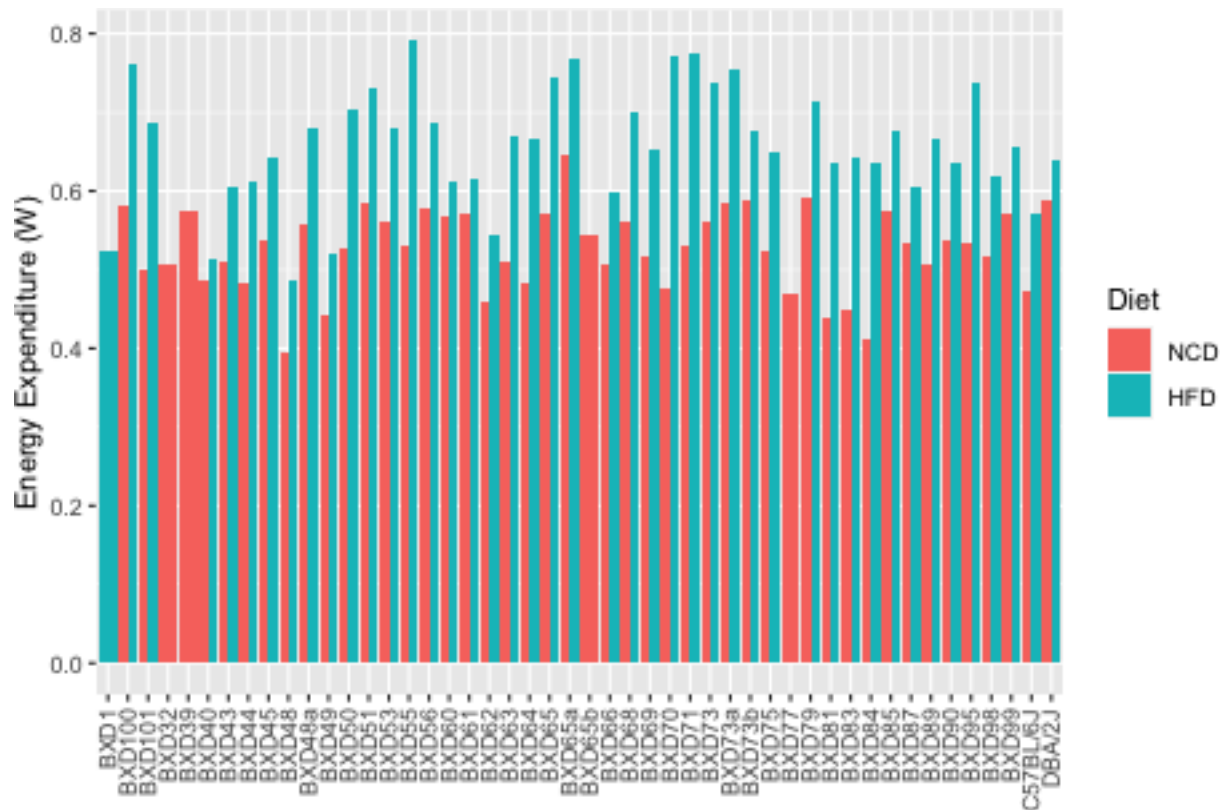
Analysis

Comparason of Datasets

```
library(ggplot2)
data %>%
  filter(!(is.na(MR_W))) %>% # complete cases only
  ggplot(aes(y=MR_W,
             x=Name,
             ymin=MR_W-MR_W_SE,
             ymax=MR_W-MR_W_SE,
             fill=Diet)) +
  geom_bar(stat='identity',position='dodge') +
  labs(y="Energy Expenditure (W)",
       x="") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```

```r
#lm(Value~Name+Diet,data=data) %>% summary

mr.order <-
  data %>%
  filter(Diet == "NCD") %>%
  arrange(desc(MR_W)) %>%
  mutate(Name = factor(Name))


data %>%
  filter(!is.na(MR_W)) %>% # complete cases only
  mutate(Name = factor(Name, levels = mr.order$Name, ordered = TRUE)) %>%
  ggplot(aes(y=MR_W,
        x=Name,
        ymin=MR_W-MR_W_SE,
        ymax=MR_W+MR_W_SE,
        fill=Diet)) +
  geom_bar(stat='identity',position='dodge', width=0.75) +
  geom_errorbar(position=position_dodge(width=0.75), width=0.5) +
  labs(y="Energy Expenditure (W)",x="") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```
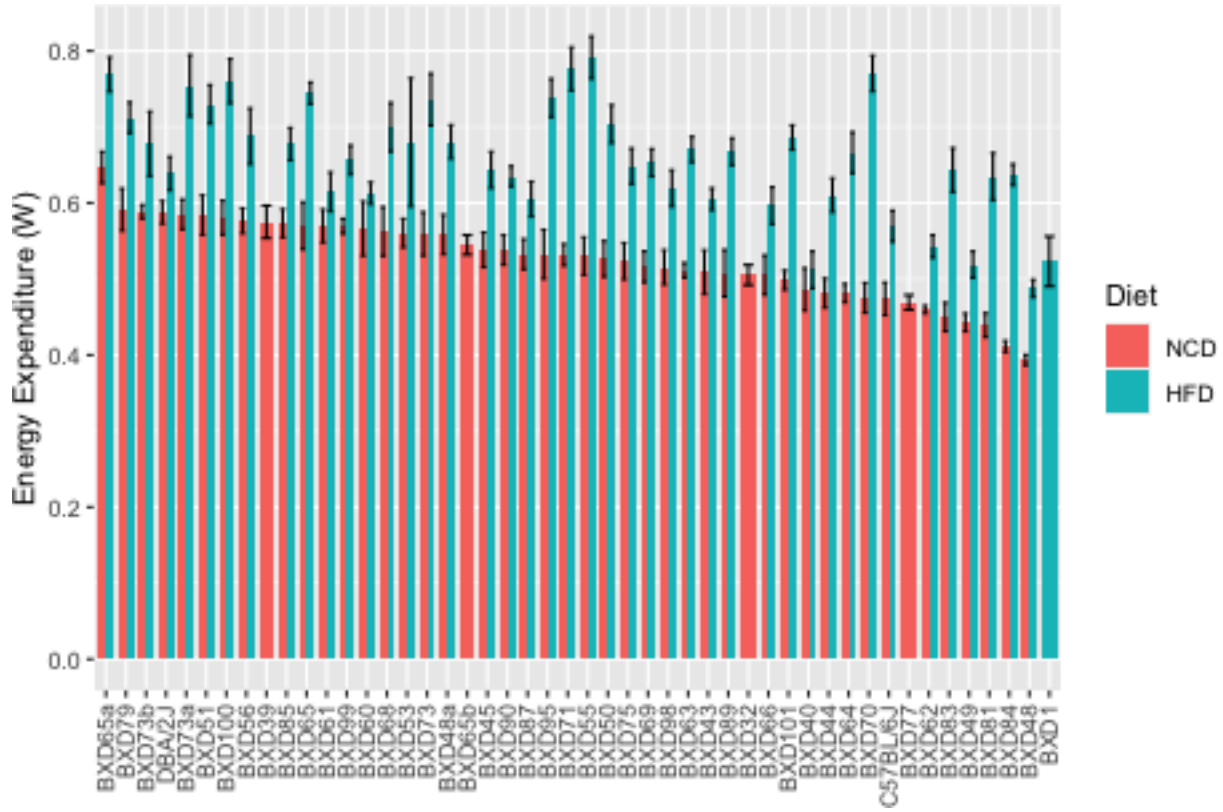
Estimating Effect Sizes

```
data %>%
  group_by(Diet) %>%
  summarize(Max = max(MR_W, na.rm=T),
            Min = min(MR_W,na.rm=T),
            Mean = mean(MR_W, na.rm=T),
            SE = mean(MR_W_SE,na.rm=T),
            N = mean(N,na.rm=T)) %>%
  mutate(SD = SE*sqrt(mean(N,na.rm=T))) %>%
  mutate(Rel.SD = SD/Mean*100) %>%
  kable(caption="Summary statistics for thermogenesis from BXD mice")
```

Table 1: Summary statistics for thermogenesis from BXD mice

Diet	Max	Min	Mean	SE	N	SD	Rel.SD
NCD	0.647	0.393	0.526	0.020	4.44	0.042	7.96
HFD	0.791	0.488	0.659	0.025	4.47	0.052	7.96

```
data %>%
  group_by(Diet) %>%
  summarize(Max = max(Value_lm, na.rm=T),
            Min = min(Value_lm,na.rm=T),
            Mean = mean(Value_lm, na.rm=T),
            SE = mean(SE_lm,na.rm=T),
```

```
          N = mean(N,na.rm=T)) %>%
  mutate(SD = SE*sqrt(mean(N,na.rm=T))) %>%
  mutate(Rel.SD = SD/Mean*100) %>%
  kable(caption="Summary statistics for lean mass from BXD mice")
```

Table 2: Summary statistics for lean mass from BXD mice

Diet	Max	Min	Mean	SE	N	SD	Rel.SD
NCD	30.7	19.7	25.4	0.623	4.44	1.31	5.19
HFD	30.2	20.0	26.0	0.612	4.47	1.29	4.97

Adjusting for Lean Mass

```
library(ggrepel)
ggplot(data, aes(y=MR_W,
          x=Value_lm)) +
  geom_point(aes(col=Diet)) +
  geom_smooth(method="lm") +
  #geom_label_repel(data = subset(data, (MR_W < 0.45&Value_lm>25.5)|MR_W>0.65&Value_lm<27), aes(label=N
  labs(y="Energy Expenditure (W)",
       x="Lean Mass (g)")
```
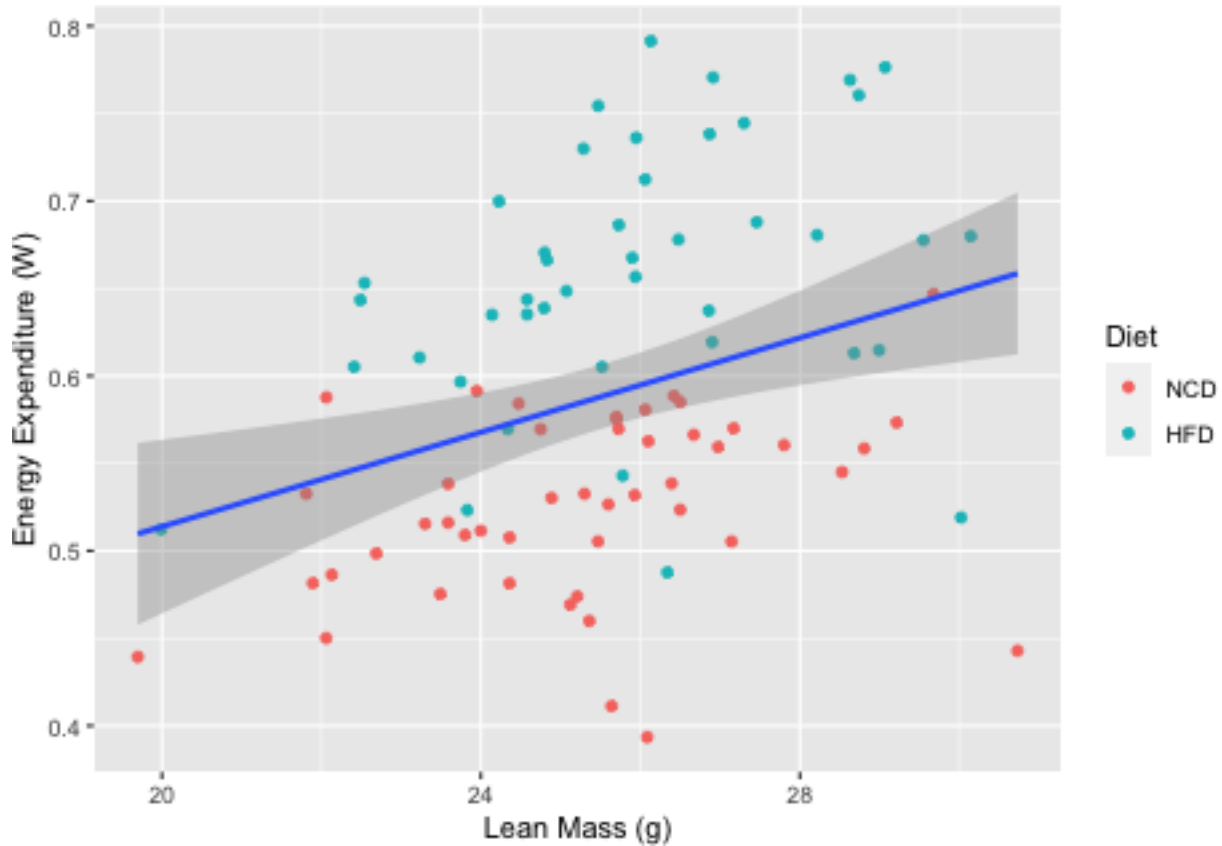


```
ggplot(data, aes(y=MR_W,
          x=Value_lm,
```

```
            col=Diet)) +
geom_point() +
geom_smooth(method="lm") +
geom_errorbar(aes(ymin=MR_W-MR_W_SE,
             ymax=MR_W+MR_W_SE)) +
geom_errorbarh(aes(xmin=Value_lm-SE_lm,
             xmax=Value_lm+SE_lm))+
#geom_label_repel(data = subset(data, (MR_W < 0.45&Value_lm>25.5)|MR_W>0.65&Value_lm<27),aes(label=Na
labs(y="Energy Expenditure (W)",
     x="Lean Mass (g)") +
theme_classic() +
theme(legend.position = c(0.1,0.85),
      text=element_text(size=18))
```
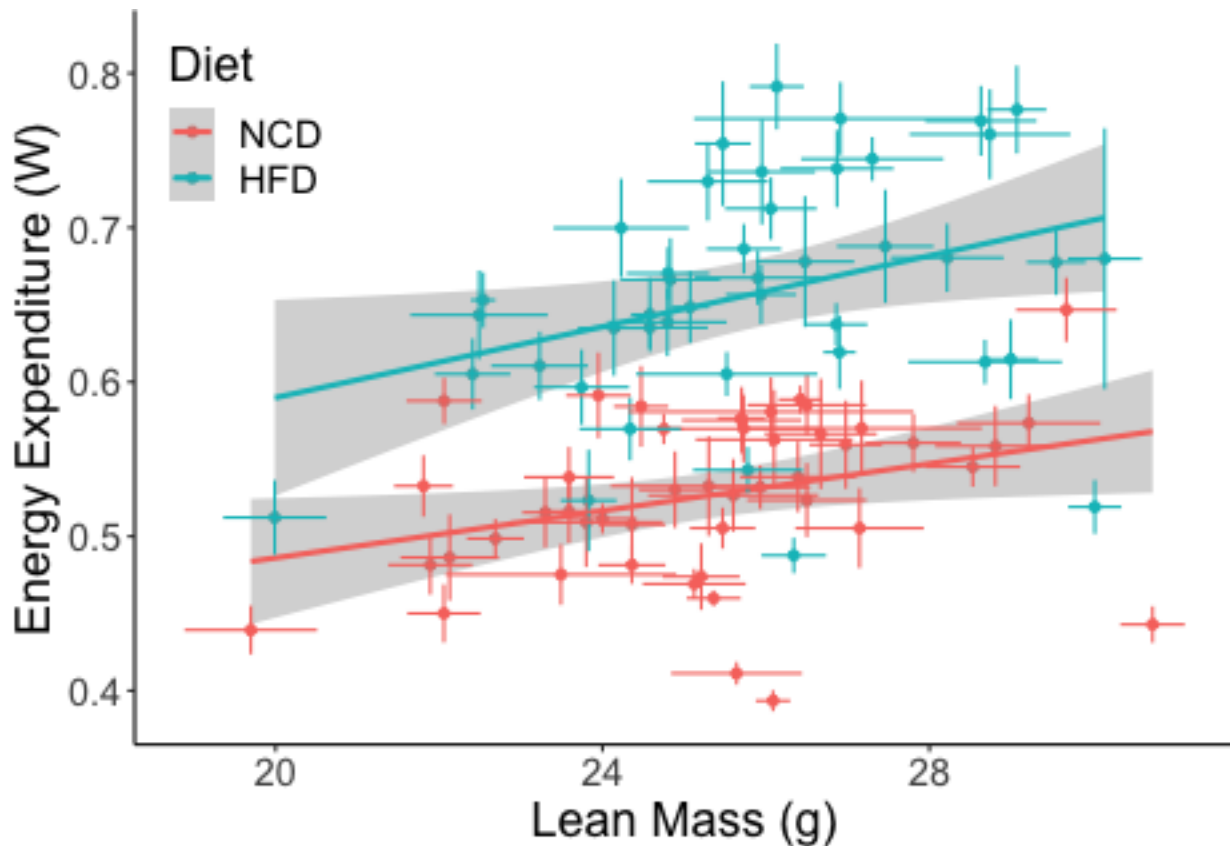


```
#chow only
ggplot(data %>% filter(Diet=="NCD"), aes(y=MR_W,
          x=Value_lm)) +
  geom_point() +
  geom_smooth(method="lm") +
  geom_label_repel(data = subset(data %>% filter(Diet=="NCD"),
                        (MR_W < 0.43&Value_lm>24.5)|MR_W>0.60&Value_lm<27),
                   aes(label=Name)) +
  guides(fill = guide_legend(override.aes = aes(color = NA))) +
  labs(y="Energy Expenditure (W)",
       x="Lean Mass (g)")
```
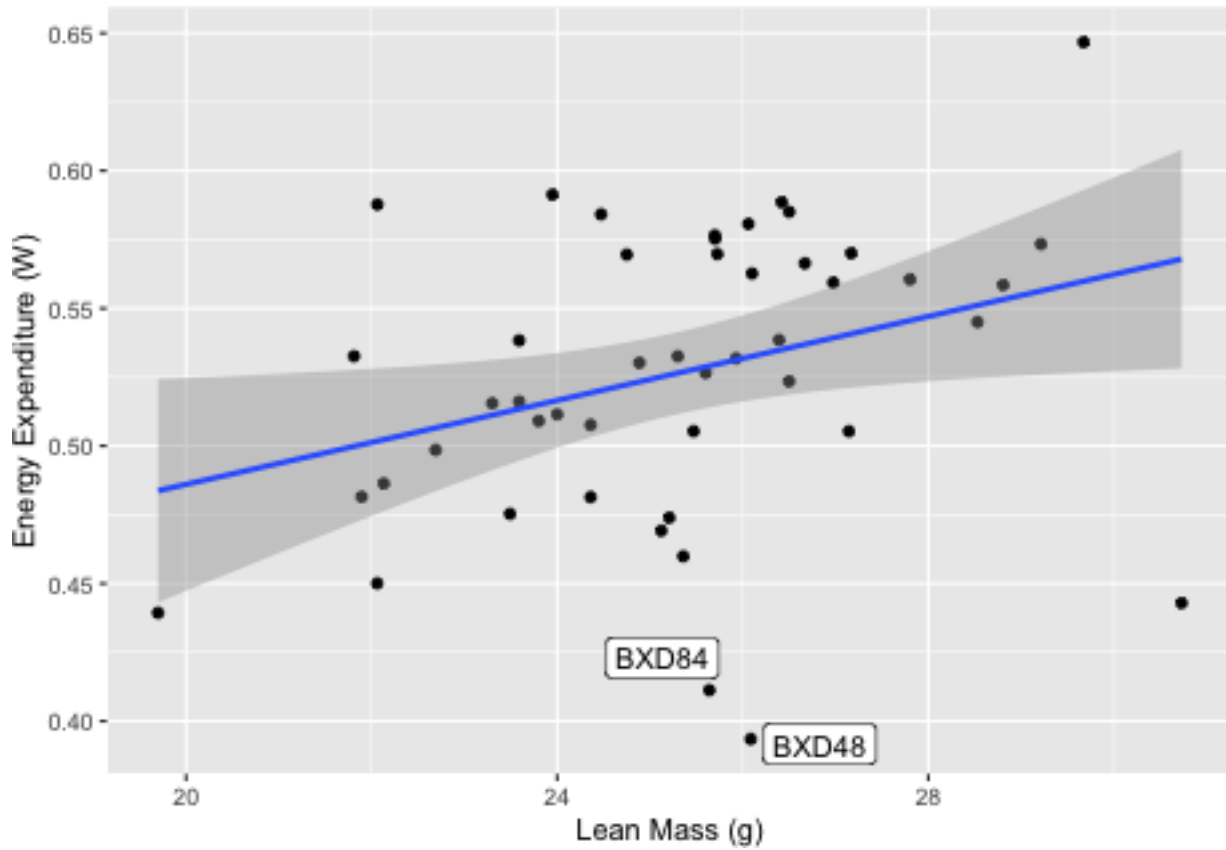
```
lm.model.1 <- lm(MR_W~Value_lm,data=data %>% filter(Diet=="NCD")) #model built on only NCD
lm.model.2 <- lm(MR_W~Value_lm+Diet,data=data) #model built on NCD and AT
library(broom)
aov(lm.model.1) %>% tidy %>% kable(caption="Model 1 summary for adjusting for lean mass")
```

Table 3: Model 1 summary for adjusting for lean mass

term	df	sumsq	meansq	statistic	p.value
Value_lm	1	0.013	0.013	5.17	0.028
Residuals	45	0.115	0.003	NA	NA

```
summary(lm.model.1) %>% tidy %>% kable(caption="Model 1 coefficients for adjusting for lean mass")
```

Table 4: Model 1 coefficients for adjusting for lean mass

term	estimate	std.error	statistic	p.value
(Intercept)	0.333	0.085	3.92	0.000
Value_lm	0.008	0.003	2.27	0.028

```
aov(lm.model.2) %>% tidy %>% kable(caption="Model 2 summary for adjusting for lean mass")
```

Table 5: Model 2 summary for adjusting for lean mass

| term	df	sumsq	meansq	statistic	p.value
Value_lm	1	0.081	0.081	21.5	0
Diet	1	0.347	0.347	92.0	0
Residuals	87	0.328	0.004	NA	NA

```
summary(lm.model.2) %>% tidy %>% kable(caption="Model 2 coefficients for adjusting for lean mass")
```

Table 6: Model 2 coefficients for adjusting for lean mass

term	estimate	std.error	statistic	p.value
(Intercept)	0.287	0.075	3.83	0.000
Value_lm	0.009	0.003	3.22	0.002
DietHFD	0.126	0.013	9.59	0.000

```
data <- data %>%
  mutate(MR_predicted = predict(lm.model.1, newdata = list(Value_lm=Value_lm))) %>%
  mutate(MR_resid = MR_W-MR_predicted) %>%
  mutate(MR_adj = MR_resid + coef(lm.model.1)['(Intercept)'] + coef(lm.model.2)['Value_lm']*mean(data$Va

data %>%
  filter(!is.na(MR_W)) %>% # complete cases only
  ggplot(aes(y=MR_resid,
        x=reorder(Name,-MR_W),
        ymin=MR_resid-MR_W_SE,
        ymax=MR_resid-MR_W_SE,
        fill=Diet)) +
  #geom_label_repel(label=Name) +
  geom_bar(stat='identity',position='dodge') +
  labs(y="EE Observed - EE Predicted (W)") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```
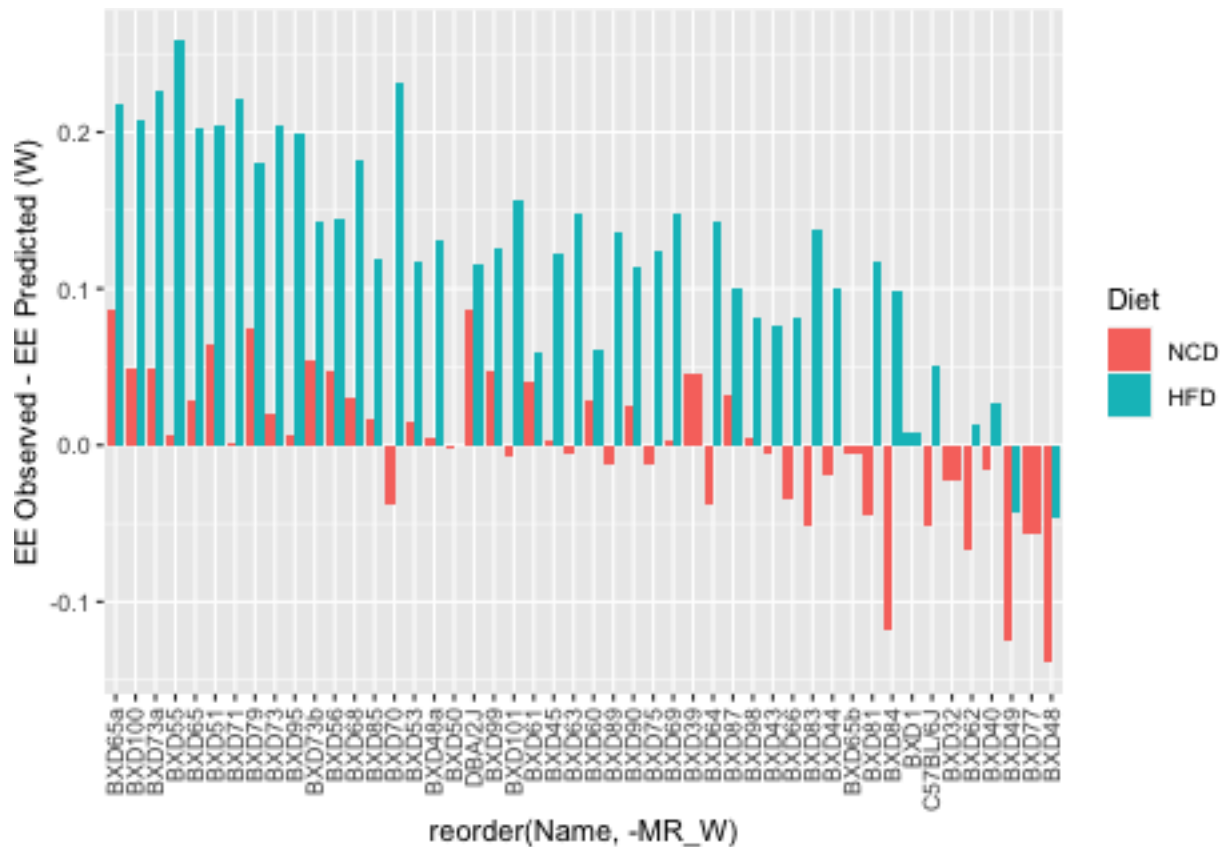
```
mr.adj.order <-
  data %>%
  filter(Diet == "NCD") %>%
  arrange(desc(MR_adj)) %>%
  mutate(Name = factor(Name))


data %>%
  filter(!is.na(MR_W)) %>% # complete cases only
  mutate(Name = factor(Name, levels = mr.adj.order$Name, ordered = TRUE)) %>%
  ggplot(aes(y=MR_adj,
        x=Name,
        ymin=MR_adj-MR_W_SE,
        ymax=MR_adj+MR_W_SE,
        fill=Diet)) +
  geom_bar(stat='identity',position='dodge', width=0.75) +
  geom_errorbar(position=position_dodge(width=0.75), width=0.5) +
  labs(y="Lean Mass Adjusted Energy Expenditure (W)",x="") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```

based on this modelling after adjusting for lean mass, HFD increases thermogenesis by `(coef(lm.model.2)["(Intercept)"]-c`

Adaptive Thermogenesis

Defined as lean mass adjusted VO2 from HFD - NCD

```r
data.wide <-
  data %>%
  select(Value_lm,SE,Value_bw, MR_W, MR_W_SE, MR_adj,Name,Diet) %>%
  pivot_wider(names_from=Diet,id_cols=Name,values_from=c(Value_lm,Value_bw, MR_W,MR_W_SE,MR_adj,SE)) %>%
  mutate(AT = MR_W_HFD - MR_W_NCD,
         AT_SE = sqrt((MR_W_SE_NCD/MR_W_NCD)^2+(MR_W_SE_HFD/MR_W_HFD)^2)*AT,
         Wt_SE = sqrt((SE_NCD/Value_bw_NCD)^2+(SE_HFD/Value_bw_NCD)^2)*Value_bw_NCD,
         Wt.Gain = Value_bw_HFD-Value_bw_NCD)

data.wide %>%
  filter(!is.na(AT)) %>% # complete cases only
  ggplot(aes(y=AT,
         x=reorder(Name,-AT),
         ymin=AT-AT_SE,
         ymax=AT+AT_SE)) +
  geom_bar(stat='identity',position='dodge') +
    geom_errorbar() +
  labs(y="HFD-Induced Adaptive Thermogenesis (W)",
       x="") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```

Thermogenesis on NCD as a Predictor of Weight Gain

```
data.wide %>%
  ggplot(aes(y=Wt.Gain,
             x=MR_W_NCD)) +
  labs(y="Weight Gained on HFD (g)",
       x="Energy Expenditure on NCD (W)") +
  geom_point() +
  geom_smooth(method="lm") +
  theme_classic() +
  theme(text=element_text(size=18))
```
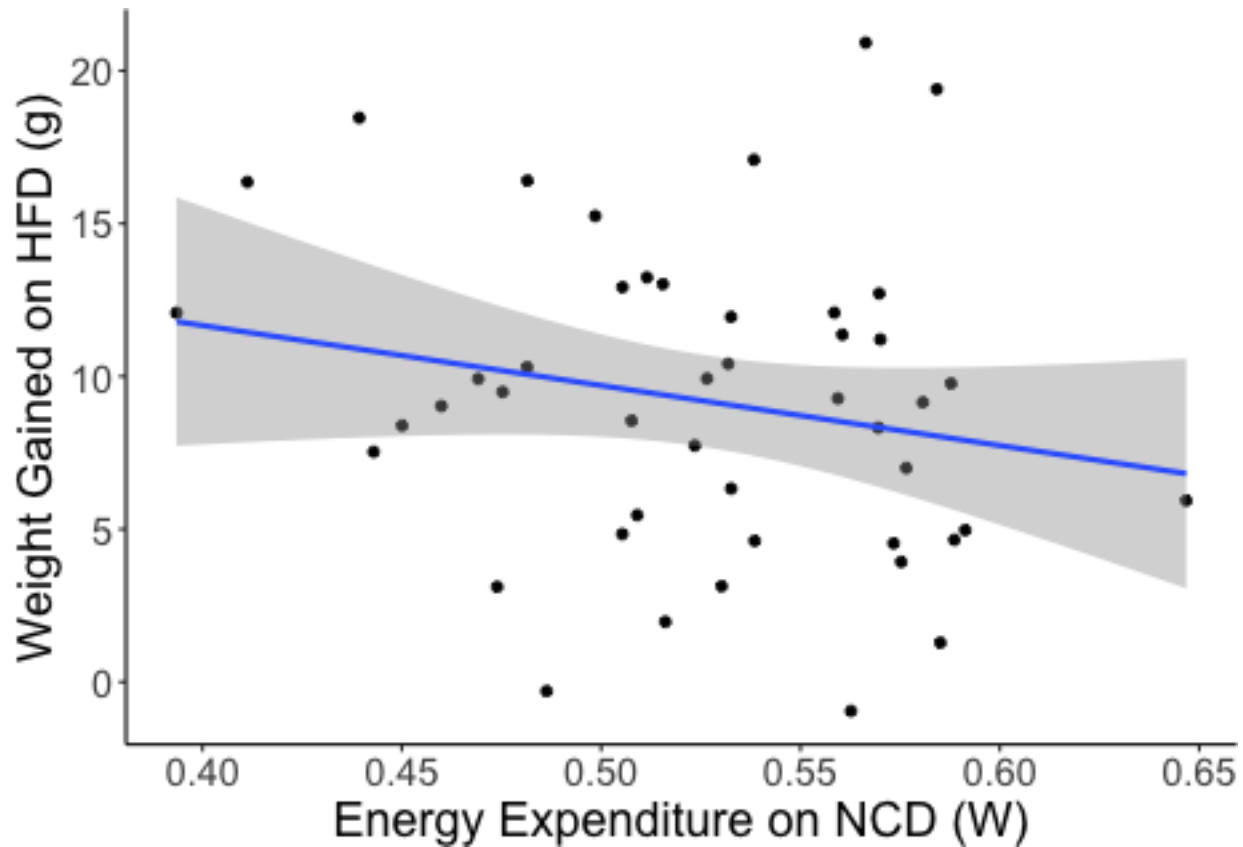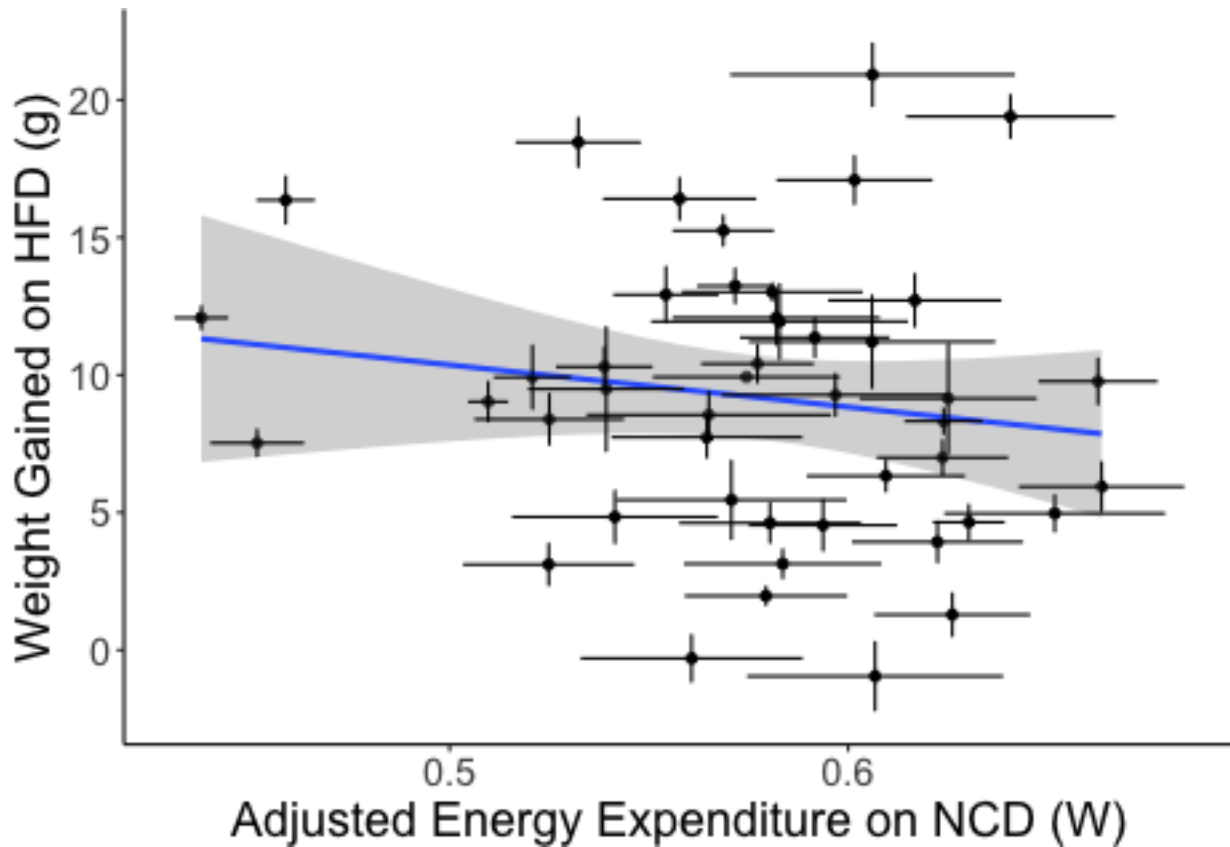
```r
lm(Wt.Gain~MR_W_NCD, data=data.wide) %>% glance %>% kable(caption="Summary of relationship between energ
```

Table 7: Summary of relationship between energy expenditure and
diet-induced weight gain

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs
0.042	0.02	5.06	1.9	0.172	1	-139	284	289	1128	44	46

```r
data.wide %>%
  ggplot(aes(y=Wt.Gain,
             x=MR_adj_NCD)) +
  labs(y="Weight Gained on HFD (g)",
       x="Adjusted Energy Expenditure on NCD (W)") +
  geom_point() +
  geom_smooth(method="lm") +
  geom_errorbarh(aes(xmin=MR_adj_NCD-MR_W_SE_NCD,
                     xmax=MR_adj_NCD+MR_W_SE_NCD))+
  geom_errorbar(aes(ymin=Wt.Gain-Wt_SE,
                    ymax=Wt.Gain+Wt_SE)) +
  theme_classic() +
  theme(text=element_text(size=18))
```

```r
lm(Wt.Gain~MR_adj_NCD, data=data.wide) %>% glance %>% kable(caption="Summary of relationship between lea
```

Table 8: Summary of relationship between lean mass adjusted
energy expenditure and diet-induced weight gain

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs
0.023	0.001	5.11	1	0.315	1	-139	285	290	1151	44	46

```r
gemma.phenotype.export <- 'Strain Level Energy Expenditure Data.csv'
data %>%
  filter(Diet=="NCD") %>%
  select(Name, MR_W, MR_adj) %>%
  write_csv(gemma.phenotype.export)
```

The data on lean mass adjusted thermogenesis was exported to Strain Level Energy Expenditure Data.csv

Heritability of NCD Thermogenesis

Since we dont have individual mouse data we will make fake data based on the mean and se of MR

```r
new.sim.data <- data.frame(Name=NA, Diet=NA,EE=NA)

for (row in 1:dim(data)[1]) {
  strain.data <- data[row,]
  if(!(is.na(strain.data$MR_W))){
  sim.data <- with(strain.data,
```

```
                    rnorm(mean=MR_W,
                          sd=MR_W_SE * sqrt(N),
                          n=N_ee
                    ))
  sim.lean.data <- with(strain.data,
                    rnorm(mean=Value_lm,
                          sd=SE_lm * sqrt(N),
                          n=N_ee
                    ))
  sim.dataset <- data.frame(Name=strain.data$Name,
                            Diet=strain.data$Diet,
                            EE=sim.data,
                            Lean=sim.lean.data)
  new.sim.data <- bind_rows(new.sim.data,sim.dataset)
  }
else{
    sim.dataset <- data.frame(Name=strain.data$Name,
                            Diet=strain.data$Diet,
                            EE=NA,
                            Lean=NA)
    new.sim.data <- bind_rows(new.sim.data,sim.dataset)
}


  }


aov(EE ~  Name, data=new.sim.data %>% filter(Diet=='NCD')) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq),
         Pct.Var = meansq/Total.Var*100) %>%
  kable(caption="Overall heritability of energy expenditure on NCD mice")
```

Table 9: Overall heritability of energy expenditure on NCD mice

term	df	sumsq	meansq	statistic	p.value	Total.Var	Pct.Var
Name	46	0.704	0.015	6.56	0	0.018	86.8
Residuals	159	0.371	0.002	NA	NA	0.018	13.2

```
aov(EE ~ Lean + Name, data=new.sim.data %>% filter(Diet=='NCD')) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq),
         Pct.Var = meansq/Total.Var*100) %>%
  kable(caption="Overall heritability of energy expenditure on NCD including lean mass")
```

Table 10: Overall heritability of energy expenditure on NCD including lean mass

term	df	sumsq	meansq	statistic	p.value	Total.Var	Pct.Var
Lean	1	0.036	0.036	15.47	0	0.053	68.25
Name	46	0.668	0.015	6.19	0	0.053	27.33
Residuals	158	0.371	0.002	NA	NA	0.053	4.41

```
aov(EE ~ Lean + Name, data=new.sim.data %>% filter(Diet=='NCD')) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq[2:3]),
         Pct.Var = meansq/Total.Var*100) -> lean.adj.ee.lean

aov(EE ~ Lean + Name, data=new.sim.data %>% filter(Diet=='NCD')) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq),
         Pct.Var = meansq/Total.Var*100) -> lean.adj.ee.all
```

```
lean.adj.ee.lean %>% kable(caption="Overall heritability of energy expenditure on NCD adjusting for lea
```

Table 11: Overall heritability of energy expenditure on NCD adjusting for lean mass

term	df	sumsq	meansq	statistic	p.value	Total.Var	Pct.Var
Lean	1	0.036	0.036	15.47	0	0.017	215.0
Name	46	0.668	0.015	6.19	0	0.017	86.1
Residuals	158	0.371	0.002	NA	NA	0.017	13.9

```
aov(EE ~ Lean + Name + Diet + Name:Diet, data=new.sim.data) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq),
         Pct.Var = meansq/Total.Var*100) -> hfd.incl.ee
```

```
hfd.incl.ee  %>% kable(caption="Overall heritability of energy expenditure including diet and lean mass
```

Table 12: Overall heritability of energy expenditure including diet and lean mass

term	df	sumsq	meansq	statistic	p.value	Total.Var	Pct.Var
Lean	1	0.190	0.190	55.90	0	1.87	10.156
Name	47	1.445	0.031	9.05	0	1.87	1.645
Diet	1	1.636	1.636	481.61	0	1.87	87.495
Name:Diet	41	0.401	0.010	2.88	0	1.87	0.523
Residuals	302	1.026	0.003	NA	NA	1.87	0.182

```
aov(EE ~ Lean + Name + Diet + Name:Diet, data=new.sim.data) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq[c(2,4,5)]),
         Pct.Var = meansq/Total.Var*100) -> hfd.adj.ee.adj

aov(EE ~ Lean + Name + Diet + Name:Diet, data=new.sim.data) %>%
  tidy %>%
  mutate(Total.Var=sum(meansq[c(2,3,4,5)]),
         Pct.Var = meansq/Total.Var*100) -> hfd.adj.ee.all
```

```
hfd.adj.ee.adj %>% kable(caption="Overall heritability of energy expenditure adjusted for diet and lean
```

Table 13: Overall heritability of energy expenditure adjusted for diet and lean mass

term	df	sumsq	meansq	statistic	p.value	Total.Var	Pct.Var
Lean	1	0.190	0.190	55.90	0	0.044	432.24
Name	47	1.445	0.031	9.05	0	0.044	70.02
Diet	1	1.636	1.636	481.61	0	0.044	3723.90
Name:Diet	41	0.401	0.010	2.88	0	0.044	22.25
Residuals	302	1.026	0.003	NA	NA	0.044	7.73

```
ee.var.data <- bind_rows(lean.adj.ee.lean %>% mutate(Diet="NCD"),hfd.adj.ee.adj %>% mutate(Diet="HFD"))

ggplot(ee.var.data %>% filter(term %in% c('Name','Name:Diet','Residuals')),
       aes(x=reorder(Diet,-Pct.Var),
           y=Pct.Var,
           fill=term)) +
  geom_bar(position="stack",stat='identity') +
  scale_fill_manual(labels = c("Strain", "Strain x Diet", "Other"), values = c("red", "pink","blue"),
                    name="Factor") +
  labs(y="Percent of Variance",
       x="") +
  theme_classic() +
  theme(legend.position="top")+
  theme(text=element_text(size=18))
```
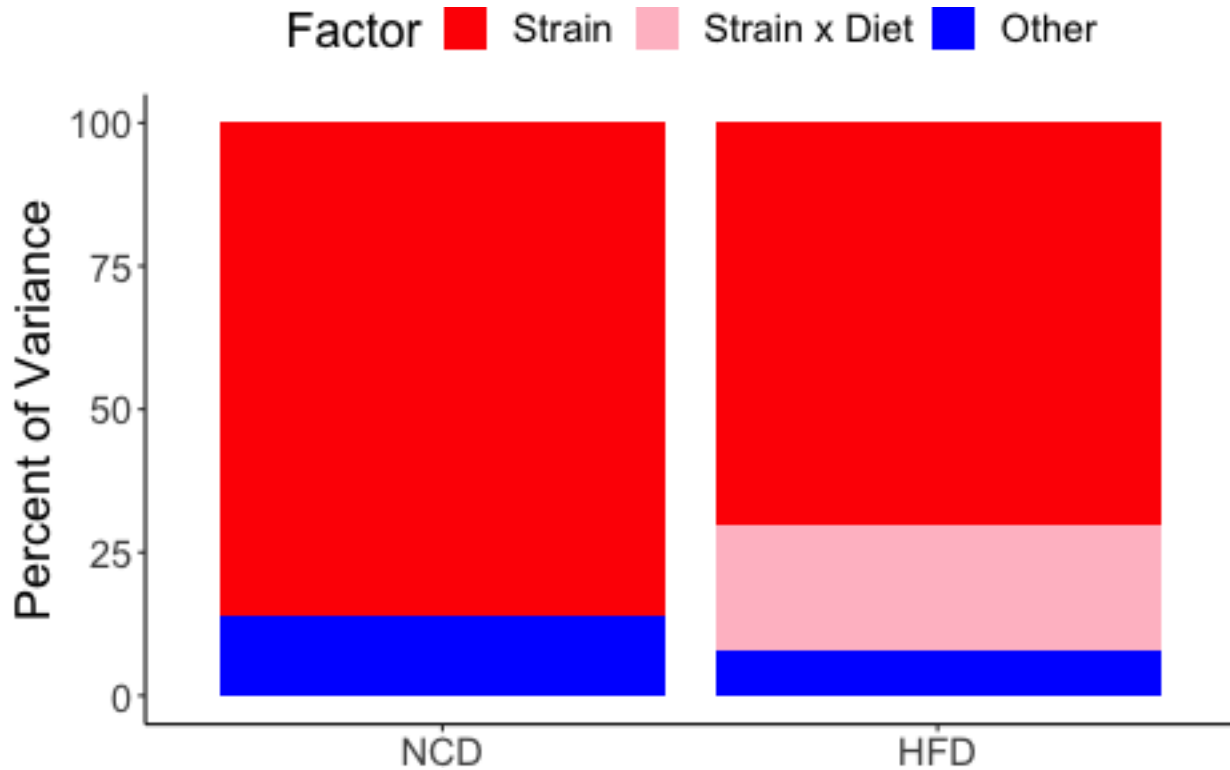


```
ee.var.all.data <- bind_rows(lean.adj.ee.all %>% mutate(Diet="NCD",Corr="None"),
                             lean.adj.ee.lean %>% mutate(Diet="NCD", Corr="Lean Mass"),
                             hfd.adj.ee.all %>% mutate(Diet="HFD", Corr="Lean Mass"),
                             hfd.adj.ee.adj %>% mutate(Diet="HFD", Corr="Lean Mass,Diet")) %>%
```

```
  mutate(Group=paste(Diet,Corr,sep="-"))

library(RColorBrewer)
ee.var.all.data %>%
        filter(term %in% c('Lean','Name','Name:Diet','Diet','Residuals')) %>%
        filter(!(term=='Lean'&Corr=='Lean Mass')) %>%
        filter(!(term=='Lean'&Corr=="Lean Mass,Diet")) %>%
        filter(!(term=='Diet'&Corr=="Lean Mass,Diet")) %>%
ggplot(aes(x=ordered(Group, levels=c("NCD-None","NCD-Lean Mass", "HFD-Lean Mass", "HFD-Lean Mass,Diet"))
            y=Pct.Var,
            fill=term)) +
  geom_bar(position="stack",stat='identity') +
  scale_fill_manual(name="Factor",
                    labels = c("Diet", "Lean Mass", "Strain", "Strain x Diet", "Residuals"),
                    values=brewer.pal(5, "Set1")) +
  labs(y="Variance Contribution (%)",
       x="Diet and Adjustments") +
  theme_classic() +
  theme(text=element_text(size=18),
        axis.text=element_text(size=8))
```
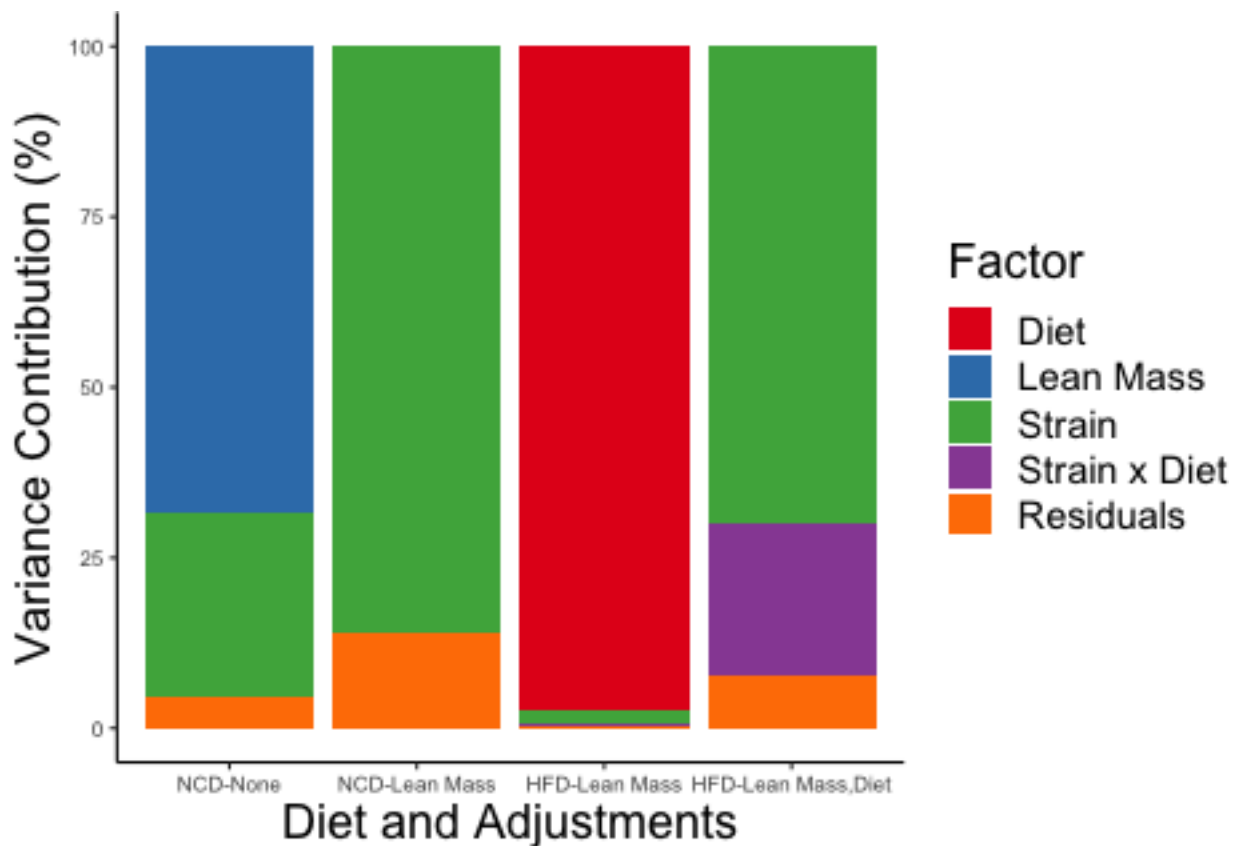

Adaptive Thermogenesis vs Weight Gain
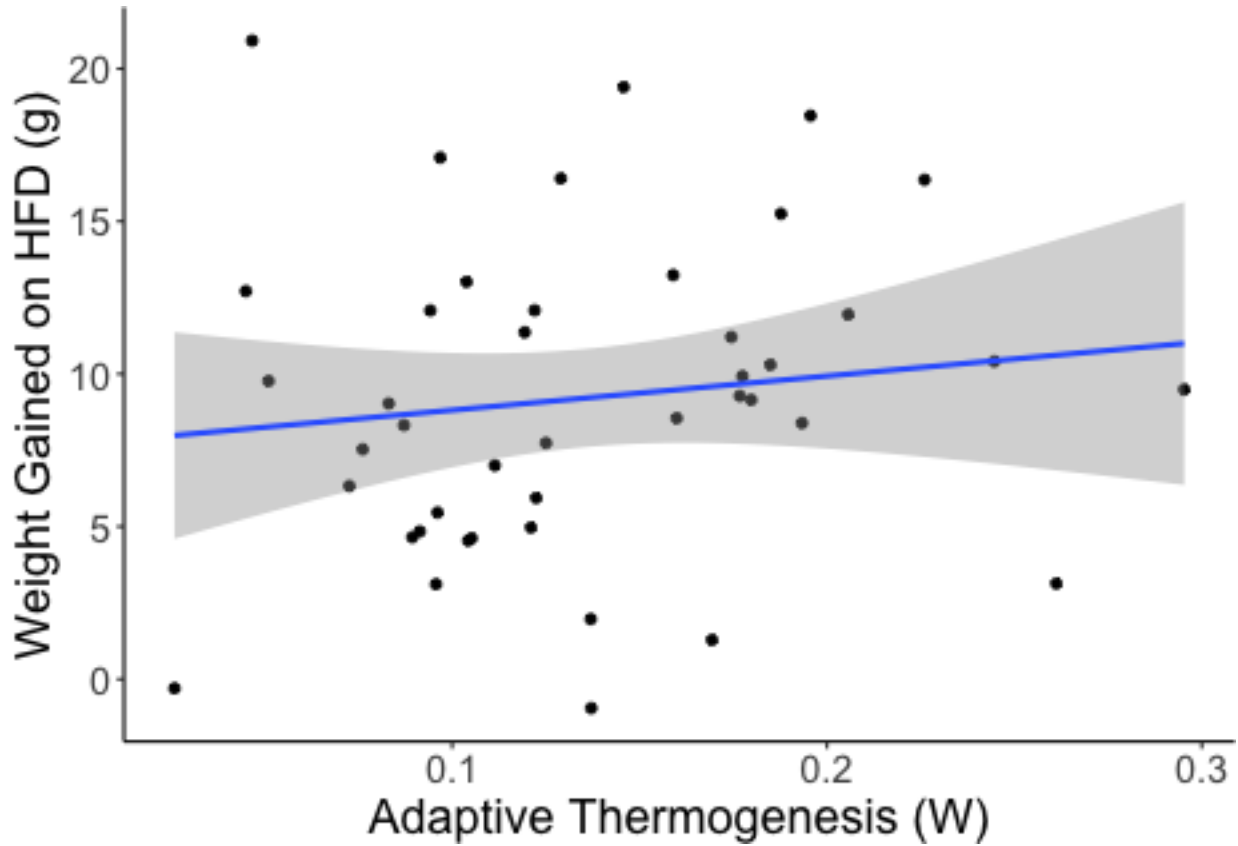
```
data.wide %>%
  ggplot(aes(y=Wt.Gain,
```

```
            x=AT)) +
  labs(y="Weight Gained on HFD (g)",
       x="Adaptive Thermogenesis (W)") +
  geom_point() +
  geom_smooth(method="lm") +  theme_classic() +
  theme(text=element_text(size=18))
```



```
lm(Wt.Gain~AT, data=data.wide) %>% glance %>% kable(caption="Summary of relationship between energy expe
```

Table 14: Summary of relationship between energy expenditure and
diet-induced weight gain

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs
0.017	-0.007	5.22	0.691	0.411	1	-131	268	273	1117	41	43

Integration with Lifespan

To ask whether BMR is related to experimental livespan we used the data from Roy et al 2021. This
determined lifespan of **female** mice in days

```
aging.datafile <- 'BXD_18441.csv'

aging.data <- read_csv(aging.datafile, skip=8) %>%
  rename(Age = Value,
         Age.SE = SE,
```
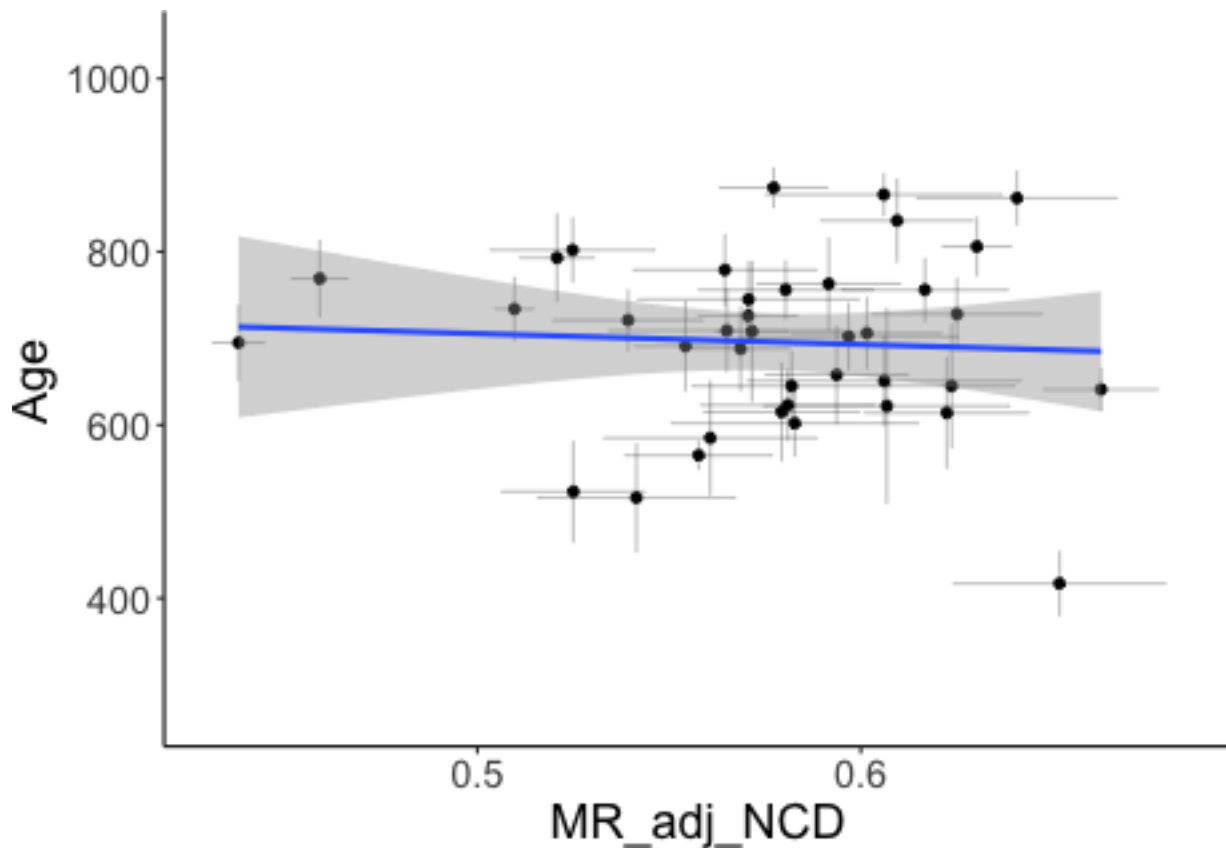
```
        Age.N = N)

combined.age.mr.data <-
  full_join(aging.data, data.wide)

combined.age.mr.data %>%
  ggplot(aes(y=Age,
             x=MR_adj_NCD)) +
  geom_point() +
  geom_errorbar(aes(ymin=Age-Age.SE,
                    ymax=Age+Age.SE),
                alpha=0.25) +
  geom_errorbarh(aes(xmin=MR_adj_NCD-MR_W_SE_NCD,
                     xmax=MR_adj_NCD+MR_W_SE_NCD),
                 alpha=0.25) +
  geom_smooth(method="lm") +
  theme_classic() +
  theme(text=element_text(size=18))
```



```
combined.age.mr.data %>%
  mutate_at(vars(Age,MR_adj_NCD), .funs=as.numeric) %>%
  summarize_at(vars(Age,MR_adj_NCD), .funs=function(x) shapiro.test(x)$p.value) %>%
  kable(caption="Shapiro-Wilk tests for normality")
```

Table 15: Shapiro-Wilk tests for normality

Age	MR_adj_NCD
0.98	0.043

```r
with(combined.age.mr.data, cor.test(Age, MR_adj_NCD)) %>%
  tidy %>%
  kable(caption="Relationship between age (of female BXD mice) and adjusted metabolic rate")
```

Table 16: Relationship between age (of female BXD mice) and adjusted metabolic rate

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.058	-0.356	0.724	37	-0.367	0.262	Pearson's product-moment correlation	two.sided

Session Information

```r
sessionInfo()
```

```
## R version 4.0.2 (2020-06-22)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS  10.16
##
## Matrix products: default
## BLAS:    /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] RColorBrewer_1.1-2 broom_0.7.11       ggrepel_0.9.1      ggplot2_3.3.5
## [5] readr_2.1.1        dplyr_1.0.7        tidyr_1.1.4        knitr_1.37
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_1.1.1 xfun_0.29         purrr_0.3.4       splines_4.0.2
##  [5] lattice_0.20-45  colorspace_2.0-2 vctrs_0.3.8       generics_0.1.1
##  [9] htmltools_0.5.2  yaml_2.2.1       mgcv_1.8-38       utf8_1.2.2
## [13] rlang_0.4.12     pillar_1.6.4     glue_1.6.0        withr_2.4.3
## [17] DBI_1.1.2        bit64_4.0.5      lifecycle_1.0.1   stringr_1.4.0
## [21] munsell_0.5.0    gtable_0.3.0     evaluate_0.14     labeling_0.4.2
## [25] tzdb_0.2.0       fastmap_1.1.0    parallel_4.0.2    fansi_1.0.0
## [29] highr_0.9        Rcpp_1.0.7       backports_1.4.1   scales_1.1.1
## [33] vroom_1.5.7      magick_2.7.3     farver_2.1.0      bit_4.0.4
## [37] hms_1.1.1        digest_0.6.29    stringi_1.7.6     grid_4.0.2
## [41] cli_3.1.0        tools_4.0.2      magrittr_2.0.1    tibble_3.1.6
```

```
## [45] crayon_1.4.2      pkgconfig_2.0.3  ellipsis_0.3.2   Matrix_1.4-0
## [49] assertthat_0.2.1 rmarkdown_2.11   rstudioapi_0.13  R6_2.5.1
## [53] nlme_3.1-153      compiler_4.0.2
```