DGRP Genetic Arch

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* aggregate plots to figures by section

#Pre-processing of data - n<10 groups removed - remove block effect when calculating SSD and SSP

# Data preparation

importing file and checking for column names

#dataset was manually relabeled and control lines removed  
df <- read.csv("~/Dropbox/\_Github\_reps/DGRP\_SSDSSP/Data/DGRPfinal\_clean\_first\_ctrl\_only.csv")  
  
#column names  
names(df)

## [1] "id" "line" "block" "day" "sex" "wing" "leg" "pupa"

add a letter in front of factorial columns

#add character in front of line, day and block  
df$line <- sprintf('L%i', df$line)  
df$day<-sprintf('D%i', df$day)  
df$block<-sprintf('B%i', df$block)  
#summary of data  
summary(df) #21410 rows

## id line block day   
## Length:21410 Length:21410 Length:21410 Length:21410   
## Class :character Class :character Class :character Class :character   
## Mode :character Mode :character Mode :character Mode :character   
##   
##   
##   
##   
## sex wing leg pupa   
## Length:21410 Min. :11.29 Min. :12.95 Min. :13.82   
## Class :character 1st Qu.:13.79 1st Qu.:13.52 1st Qu.:14.28   
## Mode :character Median :13.93 Median :13.66 Median :14.42   
## Mean :13.93 Mean :13.65 Mean :14.41   
## 3rd Qu.:14.07 3rd Qu.:13.79 3rd Qu.:14.55   
## Max. :14.55 Max. :14.38 Max. :15.14   
## NA's :638 NA's :828 NA's :2136

## Create group column for filtering

#first, create a column to indicate group by line\_sex\_day. This will be easier to filter out or subset by group later  
df$group<- paste(df$line, df$sex, df$day, sep = "\_")  
head(df,2)

## id line block day sex wing leg pupa group  
## 1 021-A-0-F-085 L21 B6 D0 F 14.23040 13.93253 14.70779 L21\_F\_D0  
## 2 021-A-0-F-086 L21 B6 D0 F 13.99867 13.65442 14.43095 L21\_F\_D0

### KEEP THIS HERE BUT RUN BEFORE ANALYSES

#filtering out groups (line x sex x day) that have less than 10 flies  
#NB: check if I run that filter after na omit before each analysis might not be better?  
#df\_sub<-df%>%  
#group\_by(group) %>%  
#filter(n() >=10)

## Is there variation among blocks = OK

Flies of lineages were collected in different blocks, periods of time. Control lineages were selected and collected repeatedly for each block so that if there is variation, we can account for that factor.

Look at the control lineages to see whether there is variation among blocks Adjusting pupa size, removing block effect

#filtering out all groups with less than 10 flies  
df\_sub<-df%>%  
group\_by(group) %>%  
filter(n() >=10)   
  
#how many Na in pupae  
sum(is.na(df\_sub$pupa)) #1970 Nas

## [1] 1970

#remove NA in wing column  
df\_sub<-df\_sub[!is.na(df\_sub$pupa), ]  
  
#subset fed and 1day starved flies  
df\_sub01<-subset(df\_sub, day=="D0"|day=="D1")  
  
#lm with block fixed effect  
blocktest01<-lm(pupa~block, data=df\_sub01)  
summary(blocktest01)

##   
## Call:  
## lm(formula = pupa ~ block, data = df\_sub01)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -0.64395 -0.12171 0.00728 0.12808 0.65787   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 14.480592 0.004798 3018.031 < 2e-16 \*\*\*  
## blockB11 -0.019641 0.007123 -2.757 0.00584 \*\*   
## blockB12 0.014971 0.006733 2.223 0.02620 \*   
## blockB13 -0.009908 0.007227 -1.371 0.17038   
## blockB4 -0.031259 0.006391 -4.892 1.01e-06 \*\*\*  
## blockB5 -0.029399 0.005959 -4.933 8.17e-07 \*\*\*  
## blockB6 -0.083454 0.006264 -13.322 < 2e-16 \*\*\*  
## blockB7 -0.092453 0.006147 -15.039 < 2e-16 \*\*\*  
## blockB8 -0.052912 0.006674 -7.928 2.38e-15 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.1809 on 15385 degrees of freedom  
## Multiple R-squared: 0.03598, Adjusted R-squared: 0.03547   
## F-statistic: 71.77 on 8 and 15385 DF, p-value: < 2.2e-16

Anova(blocktest01)

## Anova Table (Type II tests)  
##   
## Response: pupa  
## Sum Sq Df F value Pr(>F)   
## block 18.78 8 71.768 < 2.2e-16 \*\*\*  
## Residuals 503.29 15385   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#move residuals to dataframe  
df\_sub01$pupa\_noblock <- blocktest01$resid  
head(df\_sub01,2)

## # A tibble: 2 x 10  
## # Groups: group [1]  
## id line block day sex wing leg pupa group pupa\_noblock  
## <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> <dbl>  
## 1 021-A-0-F-085 L21 B6 D0 F 14.2 13.9 14.7 L21\_F\_D0 0.311   
## 2 021-A-0-F-086 L21 B6 D0 F 14.0 13.7 14.4 L21\_F\_D0 0.0338

write.csv(df\_sub01,"/Users/isabelle/Dropbox/\_Github\_reps/DGRP\_SSDSSP/Data/df\_sub01.csv")  
#df\_sub01$pupanoblock is the column I will use when I want to calculate summary and indexes for correlation analyses  
  
#rerun lm on pupa\_noblock  
blocktest01\_2<-lm(pupa\_noblock~block, data=df\_sub01)  
summary(blocktest01\_2)

##   
## Call:  
## lm(formula = pupa\_noblock ~ block, data = df\_sub01)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -0.64395 -0.12171 0.00728 0.12808 0.65787   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) -2.199e-16 4.798e-03 0 1  
## blockB11 1.190e-17 7.123e-03 0 1  
## blockB12 -8.512e-18 6.733e-03 0 1  
## blockB13 2.734e-16 7.227e-03 0 1  
## blockB4 -3.380e-16 6.391e-03 0 1  
## blockB5 1.069e-15 5.959e-03 0 1  
## blockB6 2.592e-16 6.264e-03 0 1  
## blockB7 1.940e-17 6.147e-03 0 1  
## blockB8 5.121e-19 6.674e-03 0 1  
##   
## Residual standard error: 0.1809 on 15385 degrees of freedom  
## Multiple R-squared: 5.867e-30, Adjusted R-squared: -0.00052   
## F-statistic: 1.128e-26 on 8 and 15385 DF, p-value: 1

Anova(blocktest01\_2) #block effect is gone!

## Anova Table (Type II tests)  
##   
## Response: pupa\_noblock  
## Sum Sq Df F value Pr(>F)  
## block 0.00 8 0 1  
## Residuals 503.29 15385

There is a difference between collecting blocks so we have to account for block as a random factor when using lmer, or use the adjusted values to calculate SSD and SSP values.

# Section 1: SSD in fed flies

* Question 1.1: Is there Sexual Size Dimorphism in the DGRP lines. A1.1: YES
* Question 1.2: Do we see a genetic variation of SSD in the DGRP lines. A1.2: YES
* Question 1.3: Is the SSD genetic variation due to a genetic variation in male or in female size? FEMALE

## Question 1.1: Is there Sexual Size Dimorphism in the DGRP flies that are normally fed?

To test if we have sexual size dimorphism, we want to test the effect of size with line and block as random factor. If there is a variation due to sex, that means SSD is present.

df<-df\_sub01 #do not forget to reload original csv data if I want to filter out things differently  
  
#subsetting day 0, fed flies  
df0<-subset(df, day=="D0") #8500  
head(df0,2)

## # A tibble: 2 x 10  
## # Groups: group [1]  
## id line block day sex wing leg pupa group pupa\_noblock  
## <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> <dbl>  
## 1 021-A-0-F-085 L21 B6 D0 F 14.2 13.9 14.7 L21\_F\_D0 0.311   
## 2 021-A-0-F-086 L21 B6 D0 F 14.0 13.7 14.4 L21\_F\_D0 0.0338

#na.omit only if pupa has NA if not done before  
#df0<-na.omit(df0, cols="pupa")

### Linear Mixed Model on fed flies

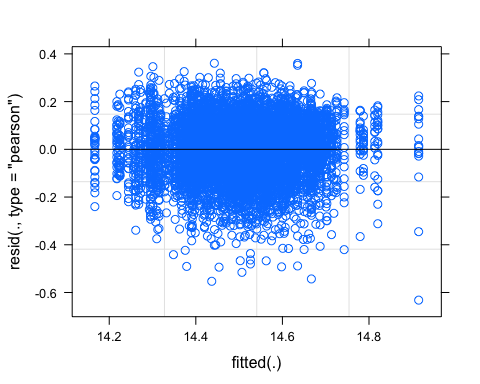
# Testing effect of sex in pupa size, with random effect for line and block.  
SSDtest<-lmer(pupa~sex+(1|line) +(1|block), REML=TRUE, data=df0)  
summary(SSDtest) #Number of obs: 8065, groups: line, 187; block, 9

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: pupa ~ sex + (1 | line) + (1 | block)  
## Data: df0  
##   
## REML criterion at convergence: -11807  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -5.4453 -0.6081 0.0870 0.6708 3.1077   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## line (Intercept) 0.010007 0.10003   
## block (Intercept) 0.002205 0.04696   
## Residual 0.013471 0.11607   
## Number of obs: 8500, groups: line, 187; block, 9  
##   
## Fixed effects:  
## Estimate Std. Error df t value Pr(>|t|)   
## (Intercept) 1.456e+01 1.758e-02 1.003e+01 828.3 <2e-16 \*\*\*  
## sexM -9.443e-02 2.559e-03 8.326e+03 -36.9 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## sexM -0.076

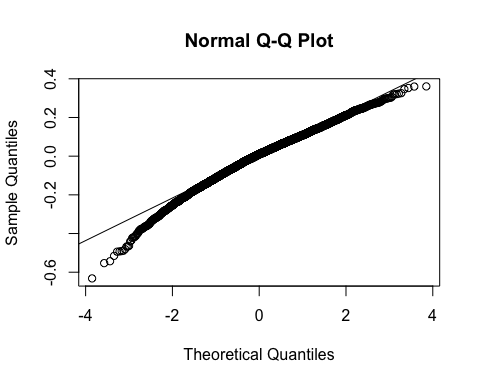
Anova(SSDtest)

## Analysis of Deviance Table (Type II Wald chisquare tests)  
##   
## Response: pupa  
## Chisq Df Pr(>Chisq)   
## sex 1361.9 1 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

plot(SSDtest)



qqnorm(resid(SSDtest))  
qqline(resid(SSDtest))



Outputting model fit results to a Table

class(SSDtest) <- "lmerMod"  
stargazer(SSDtest, style="ajps", type="text", title="Sexual Size Dimorphism in fed flies")

##   
## Sexual Size Dimorphism in fed flies  
## -------------------------------  
## pupa   
## -------------------------------  
## sexM -0.094\*\*\*   
## (0.003)   
## Constant 14.563\*\*\*   
## (0.018)   
## N 8500   
## Log Likelihood 5903.525   
## AIC -11797.050   
## BIC -11761.810   
## -------------------------------  
## \*\*\*p < .01; \*\*p < .05; \*p < .1

Answer 1.1: Yes, there is sexual size dimorphism in the DGRP flies, and females are larger than males on average.

## Question 1.2: Do we see a genetic variation of SSD in the DGRP lines?

### Comparing two models using ANOVA

#comparing two models  
model2<-lmer(pupa~sex+(1|line)+(1|block), data=df0) #model to test for SSD presence as we did above  
model1<-lmer(pupa~sex+(sex|line)+(1|block), data=df0)   
anova(model1)

## Type III Analysis of Variance Table with Satterthwaite's method  
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)   
## sex 9.8828 9.8828 1 155.3 745.76 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

anova(model1,model2)

## Data: df0  
## Models:  
## model2: pupa ~ sex + (1 | line) + (1 | block)  
## model1: pupa ~ sex + (sex | line) + (1 | block)  
## npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)   
## model2 5 -11813 -11778 5911.7 -11823   
## model1 7 -11851 -11801 5932.3 -11865 41.191 2 1.136e-09 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Stargazer output

class(model1) <- "lmerMod"  
class(model2) <- "lmerMod"  
stargazer(model1,model2, style="ajps", type="text", title="Sexual Size Dimorphism Genetic Variation")

##   
## Sexual Size Dimorphism Genetic Variation  
## ------------------------------------  
## pupa   
## Model 1 Model 2   
## ------------------------------------  
## sexM -0.095\*\*\* -0.094\*\*\*   
## (0.003) (0.003)   
## Constant 14.563\*\*\* 14.563\*\*\*   
## (0.018) (0.018)   
## N 8500 8500   
## Log Likelihood 5924.405 5903.525   
## AIC -11834.810 -11797.050  
## BIC -11785.480 -11761.810  
## ------------------------------------  
## \*\*\*p < .01; \*\*p < .05; \*p < .1

Model 1 is better, as AIC and BIC is smaller and log likelihood is higher. The difference of fit between these two models is significant.

#### Do a LRT

How many parameters for each models

(AIC(model1) - REMLcrit(model1))/2 # # of parameters the model "thinks" are being estimated

## [1] 7

(AIC(model2) - REMLcrit(model2))/2 # # of parameters the model "thinks" are being estimated

## [1] 5

So lme4/lmer is treating model 1 as having two more parameters than model2.

LR.model <- -as.numeric(REMLcrit(model1) - REMLcrit(model2))  
LR.model

## [1] 41.76099

nlevels(df$line)

## [1] 0

pchisq(q = LR.model, df=2, lower=F)

## [1] 8.545078e-10

pchisq(q = LR.model, df=nlevels(df$line), lower=F)

## [1] 0

#### Parametric boostrap

Finally, we can conduct a parametric bootstrap to compare the two models.

#### Finally using Bayesian Analysis

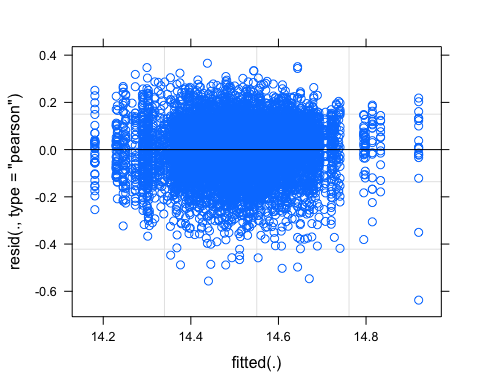
#prior.2 <-list(R=list(V=0.01, nu=0.002),   
 # G=list(G1=list(V=0.01\*diag(1), nu=0.002),  
 # G2=list(V=0.01\*diag(2), nu=0.002)))  
  
#model1M.MCMC <- MCMCglmm(pupa ~ 1 + sex,   
 # random=~block + us(1 + sex):line,  
 #prior = prior.2, burnin = 5000, nitt = 20000, thin = 10,  
 #verbose = F, pr = T,  
 #data=df0)  
#summary(model1M.MCMC)

#### Post model 1 fitting check

##### Residual distribution

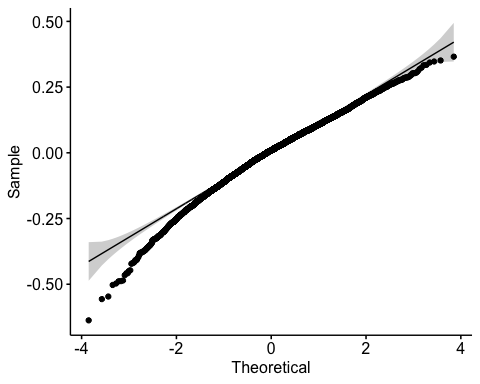
##### Model 1 residual distribution

plot(model1)



##### QQ plot

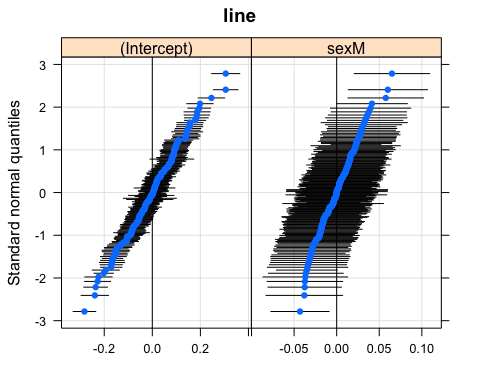
res\_model1=residuals(model1)  
ggqqplot(res\_model1)



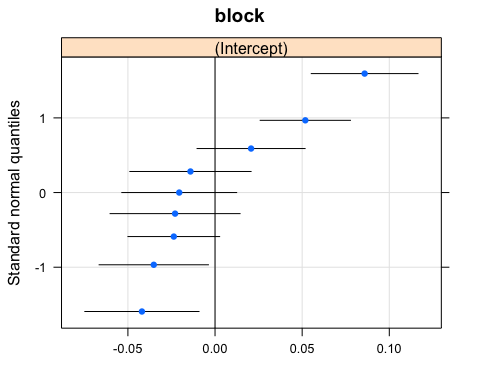
##### Random effect plot

qqmath(ranef(model1))

## $line



##   
## $block



### Plot mean size female and male per line + SSD per line

Calculate mean size per line

#calculate means for each group using pupa\_noblock  
head(df0,2)

## # A tibble: 2 x 10  
## # Groups: group [1]  
## id line block day sex wing leg pupa group pupa\_noblock  
## <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> <dbl>  
## 1 021-A-0-F-085 L21 B6 D0 F 14.2 13.9 14.7 L21\_F\_D0 0.311   
## 2 021-A-0-F-086 L21 B6 D0 F 14.0 13.7 14.4 L21\_F\_D0 0.0338

df0\_mean<-aggregate(df0[, 10], list(df0$group), mean)  
head(df0\_mean,2)

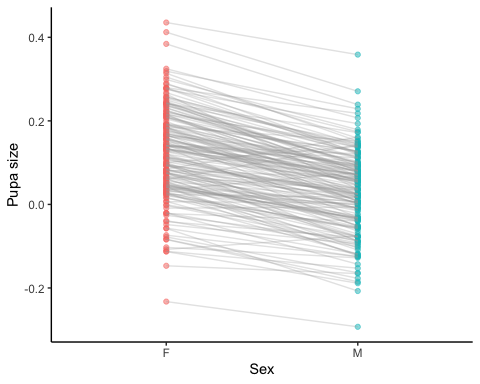
## Group.1 pupa\_noblock  
## 1 L100\_F\_D0 0.23636559  
## 2 L100\_M\_D0 0.09779092

#re-add line, day and sex columns  
df0\_mean<-df0\_mean %>%  
 separate(Group.1, c("line", "sex","day"), "\_")  
head(df0\_mean,2)

## line sex day pupa\_noblock  
## 1 L100 F D0 0.23636559  
## 2 L100 M D0 0.09779092

#### Plot mean size per line

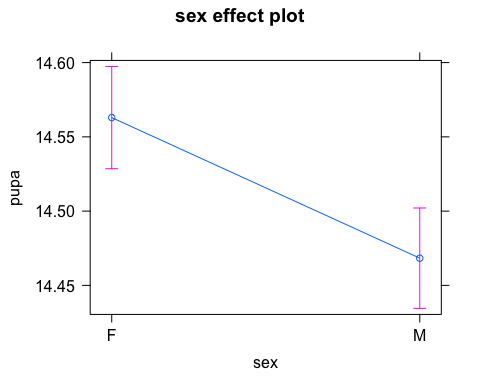
plot1<-ggplot(df0\_mean, aes(x = sex, y = pupa\_noblock, color=sex)) +  
 geom\_point(aes(fill = sex), alpha = 0.5) +  
 geom\_line(aes(group = interaction(line)),  
 alpha = 0.3, colour = "darkgrey") + theme\_classic()+labs(y="Pupa size",x="Sex")+theme(legend.position = "none")  
  
plot1



#add predicted means

### Box plot showing average difference in pupal size between male and female => ok

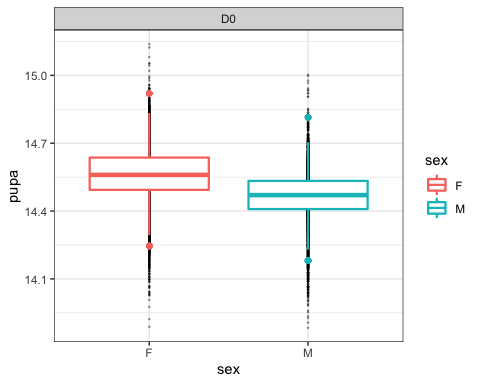
library(effects)  
plot(Effect(c("sex"),model1))



df0\_fit<-df0  
df0\_fit$fit <- predict(model1)  
head(df0\_fit,2)

## # A tibble: 2 x 11  
## # Groups: group [1]  
## id line block day sex wing leg pupa group pupa\_noblock fit  
## <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> <dbl> <dbl>  
## 1 021-A-0-F… L21 B6 D0 F 14.2 13.9 14.7 L21\_F… 0.311 14.5  
## 2 021-A-0-F… L21 B6 D0 F 14.0 13.7 14.4 L21\_F… 0.0338 14.5

plot1A<-ggplot(df0\_fit,aes(sex, pupa, group=interaction(sex, day))) +   
 facet\_grid(~day) +  
 geom\_point(alpha = 0.3, size=0.2) +   
 theme\_bw()+  
 geom\_boxplot(aes(y=fit, group=interaction(sex,day), col=sex), size=0.8 )  
plot1A



Calculate SSD index

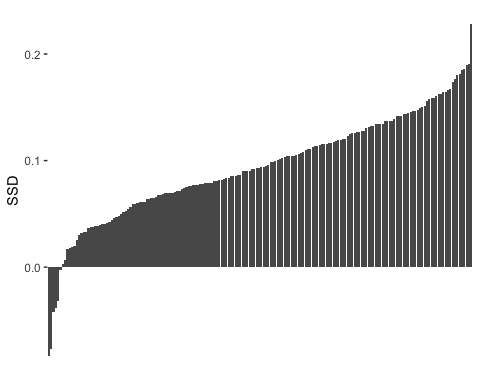
#calculate SSD0  
#separating males and females to put the values in columns  
df0\_mean\_F<-subset(df0\_mean, sex=="F")  
df0\_mean\_M<-subset(df0\_mean, sex=="M")  
  
df0\_mean\_2<-merge(x=df0\_mean\_F, y=df0\_mean\_M, by.x="line", by.y="line")  
head(df0\_mean\_2,2)

## line sex.x day.x pupa\_noblock.x sex.y day.y pupa\_noblock.y  
## 1 L100 F D0 0.23636559 M D0 0.09779092  
## 2 L101 F D0 0.08156526 M D0 0.06470751

#remove extra columns  
df0\_mean\_2<-df0\_mean\_2[,c(1,4,7)] #line, pupa\_noblockF and pupa\_noblockM  
colnames(df0\_mean\_2) <- c("line", "pupaF", "pupaM") #rename col  
  
SSD0<-df0\_mean\_2 #move back to df0\_mean  
SSD0$SSD<- SSD0$pupaF - SSD0$pupaM #since we established that females are larger than males in general, SSD is female-male sizes  
head(SSD0,2)#182 lines

## line pupaF pupaM SSD  
## 1 L100 0.23636559 0.09779092 0.13857467  
## 2 L101 0.08156526 0.06470751 0.01685776

plot2<-ggplot(SSD0, aes(x=reorder(line,SSD), y=SSD)) +  
 geom\_col() +  
 theme(axis.text.x=element\_blank(),  
 axis.ticks.x=element\_blank(),axis.title.x=element\_blank(), plot.background = element\_rect(fill = "white"),panel.background = element\_rect(fill = "white", colour="white"))   
  
plot2 +  
 labs(x = "DGRP line")

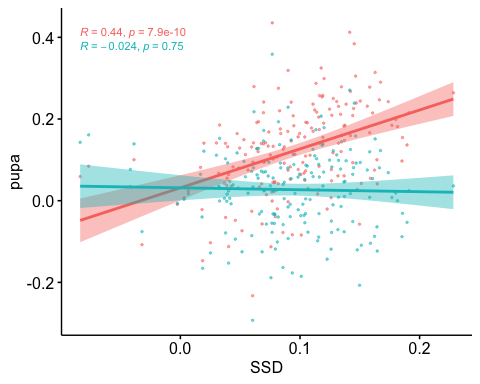


## Question 1.3: Is SSD genetic variation due to the genetic variation in male or in female size?

Correlation test and plot

#reshape data  
SSD0\_gather<-gather(SSD0,key="sex",value="pupa",pupaF:pupaM)  
#plot  
plot3 <- ggscatter(SSD0\_gather, x = "SSD", y = "pupa",  
 color = "sex",  
 add = "reg.line", conf.int = TRUE, alpha=0.5, size=0.5) +theme(legend.position="none") +ggpubr::stat\_cor(aes(color = sex), size=3)   
plot3 #stat\_cor uses the Pearson correlation

## `geom\_smooth()` using formula 'y ~ x'

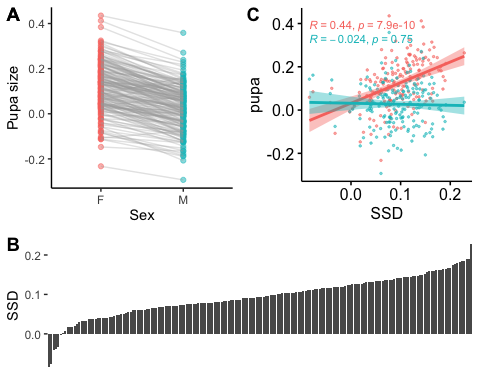


In fed flies, SSD covaries with female size.

#### Arrange plots together Figure 1

ggarrange(ggarrange(plot1,plot3,ncol=2, labels=c("A","C")),plot2,nrow=2, heights = c(1.5,1),labels=c("A","B"))

## `geom\_smooth()` using formula 'y ~ x'



# Section 2: SSD in starved flies

We found that in fed flies, SSD is female biased and it varies genetically. We finally found out that SSD covaries with female size.

How is SSD in starved conditions?

* Section 2: SSD in starved flies - use D1
  + Question 2.1: Is SSD in starved flies the same as in fed flies? (do a lmer sex\*day on D0 and D1)
    - Does SSD increase or decrease when the flies are starved? Our hypothesis is that overall SSD should decrease
  + Question 2.2: Does the SSD in starved conditions vary the same way as in fed flies?
    - use a correlation and variance analysis

## Question 2.1: Do we have the same SSD when we change environment?

### 1 day starvation data preparation = OK

#fisrt subset Day1 data from df\_sub  
df1<-subset(df\_sub01, day=="D1")   
#na.omit only if pupa has NA  
df1<-df1[!is.na(df1$pupa), ] #just in case, but already removed previously  
df1<-df1%>%  
group\_by(group) %>%  
filter(n() >=10)   
length(unique(df1$line)) #174 lines left

## [1] 174

### Model fit for SSD

# Testing effect of sex in pupa size, with random effect for line and block.  
SSD1test<-lmer(pupa~sex+(1|line) +(1|block), REML=TRUE, data=df1)  
summary(SSD1test)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: pupa ~ sex + (1 | line) + (1 | block)  
## Data: df1  
##   
## REML criterion at convergence: -7497.8  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -4.6775 -0.6418 0.0128 0.6666 3.3590   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## line (Intercept) 0.011182 0.10575   
## block (Intercept) 0.001546 0.03932   
## Residual 0.017728 0.13315   
## Number of obs: 6754, groups: line, 174; block, 9  
##   
## Fixed effects:  
## Estimate Std. Error df t value Pr(>|t|)   
## (Intercept) 1.439e+01 1.581e-02 8.509e+00 910.70 <2e-16 \*\*\*  
## sexM -6.419e-02 3.403e-03 6.658e+03 -18.86 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## sexM -0.118

Anova(SSD1test)

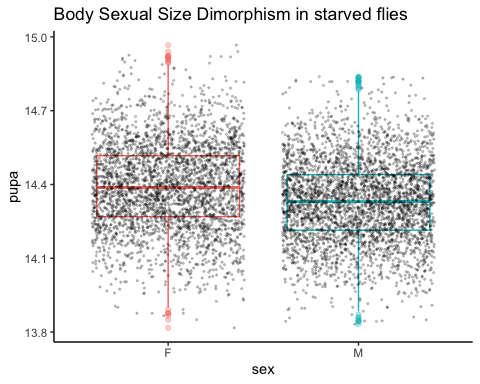
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##   
## Response: pupa  
## Chisq Df Pr(>Chisq)   
## sex 355.75 1 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

SSD still exists at 1 day starvation

### Plots

Plot with block effect

# original pupa size  
all\_pupa\_plot\_1<-SSDtest\_plot <- ggplot(df1, aes(x = sex, y = pupa, colour = sex)) +  
 geom\_boxplot(alpha=0.3) +  
 theme\_classic() +  
 geom\_jitter(color="black", size=0.4, alpha=0.2)+  
 theme(legend.position = "none",  
 panel.spacing = unit(1, "lines")) # adding space between panels  
   
all\_pupa\_plot\_1 +ggtitle("Body Sexual Size Dimorphism in starved flies")

 Plot adjusted no block effect

#removed block effect pupal size  
(SSDtest\_plot\_noblock <- ggplot(df1, aes(x = sex, y = pupa\_noblock, colour = sex)) +  
 geom\_boxplot(alpha=0.3) +  
 theme\_classic() +  
 geom\_jitter(color="black", size=0.4, alpha=0.2)+  
   
 theme(legend.position = "none",  
 panel.spacing = unit(1, "lines")) + # adding space between panels  
 ggtitle("Body Sexual Size Dimorphism in starved flies no block effect")  
 )



HERE plot of mean size male and female for starved flies

#calculate means for each group using pupa\_noblock  
df1\_mean<-aggregate(df1[, 10], list(df1$group), mean)  
head(df1\_mean,2)

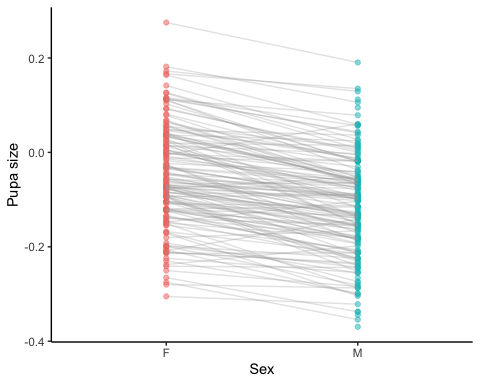
## Group.1 pupa\_noblock  
## 1 L100\_F\_D1 0.04734688  
## 2 L100\_M\_D1 0.03662500

#re-add line, day and sex columns  
df1\_mean<-df1\_mean %>%  
 separate(Group.1, c("line", "sex","day"), "\_")  
head(df1\_mean,2)

## line sex day pupa\_noblock  
## 1 L100 F D1 0.04734688  
## 2 L100 M D1 0.03662500

PLOT 4: mean female and male size connected

plot4<-ggplot(df1\_mean, aes(x = sex, y = pupa\_noblock, color=sex)) +  
 geom\_point(aes(fill = sex), alpha = 0.5) +  
 geom\_line(aes(group = interaction(line)),  
 alpha = 0.3, colour = "darkgrey") + theme\_classic()+labs(y="Pupa size",x="Sex")+theme(legend.position = "none")  
  
plot4



#add predicted means

##Question 2.2: Does overall SSD increase or decrease when the flies are starved? Our hypothesis is that overall SSD should decrease

Use df\_sub01

model2<-lmer(pupa~sex\*day+(sex+day|line)+(1|block), data=df\_sub01)  
model1<-lmer(pupa~sex\*day+(sex\*day|line)+(1|block), data=df\_sub01)  
anova(model1,model2)

## refitting model(s) with ML (instead of REML)

## Data: df\_sub01  
## Models:  
## model2: pupa ~ sex \* day + (sex + day | line) + (1 | block)  
## model1: pupa ~ sex \* day + (sex \* day | line) + (1 | block)  
## npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)   
## model2 12 -19489 -19397 9756.3 -19513   
## model1 16 -19494 -19372 9763.3 -19526 13.923 4 0.007544 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

summary(model1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: pupa ~ sex \* day + (sex \* day | line) + (1 | block)  
## Data: df\_sub01  
##   
## REML criterion at convergence: -19492.7  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -5.2044 -0.6176 0.0517 0.6581 3.5543   
##   
## Random effects:  
## Groups Name Variance Std.Dev. Corr   
## line (Intercept) 0.0112675 0.10615   
## sexM 0.0007463 0.02732 -0.49   
## dayD1 0.0061539 0.07845 -0.28 0.32   
## sexM:dayD1 0.0009538 0.03088 0.32 -0.46 -0.52  
## block (Intercept) 0.0015922 0.03990   
## Residual 0.0151956 0.12327   
## Number of obs: 15394, groups: line, 195; block, 9  
##   
## Fixed effects:  
## Estimate Std. Error df t value Pr(>|t|)   
## (Intercept) 14.566230 0.015663 10.940499 929.966 < 2e-16 \*\*\*  
## sexM -0.094440 0.003440 152.019321 -27.451 < 2e-16 \*\*\*  
## dayD1 -0.179327 0.006792 178.941747 -26.404 < 2e-16 \*\*\*  
## sexM:dayD1 0.030618 0.004900 170.094684 6.248 3.22e-09 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) sexM dayD1   
## sexM -0.218   
## dayD1 -0.167 0.339   
## sexM:dayD1 0.129 -0.593 -0.515

Using summary model 1, I can calculate the means for Female 0, Male 0, Female 1 and Male 1.

# figure out how to extract intercept values  
F0 = 14.566230  
M0 = 14.566230 -0.094440   
F1 = 14.566230 -0.179327  
M1 = 14.566230 -0.094440 -0.179327 + 0.030618   
print("SSD0")

## [1] "SSD0"

F0-M0

## [1] 0.09444

print("SSD1")

## [1] "SSD1"

F1-M1

## [1] 0.063822

SSD1<SSD0 and it is significantly different

##### Calculating SSD in both conditions

#separating males and females to put the values in columns  
df1\_mean\_F<-subset(df1\_mean, sex=="F")  
df1\_mean\_M<-subset(df1\_mean, sex=="M")  
  
df1\_mean\_2<-merge(x=df1\_mean\_F, y=df1\_mean\_M, by.x="line", by.y="line")  
head(df1\_mean\_2,2)

## line sex.x day.x pupa\_noblock.x sex.y day.y pupa\_noblock.y  
## 1 L100 F D1 0.04734688 M D1 0.0366250  
## 2 L101 F D1 -0.07406721 M D1 -0.1467936

#remove extra columns  
df1\_mean\_2<-df1\_mean\_2[,c(1,4,7)] #using pupa\_noblock  
colnames(df1\_mean\_2) <- c("line", "pupaF1", "pupaM1")  
  
df1\_mean<-df1\_mean\_2  
df1\_mean$SSD1<- df1\_mean$pupaF1 - df1\_mean$pupaM1 #since we established that females are larger than males in general  
head(df1\_mean,2)

## line pupaF1 pupaM1 SSD1  
## 1 L100 0.04734688 0.0366250 0.01072188  
## 2 L101 -0.07406721 -0.1467936 0.07272640

length(unique(df1\_mean$line)) #157 lines left after calculating SSD1

## [1] 143

#combining SSDs values without discarding rows, which would happen if I merged the dataframes (we would end up with 59 lines for all SSD2)  
head(SSD0,2)

## line pupaF pupaM SSD  
## 1 L100 0.23636559 0.09779092 0.13857467  
## 2 L101 0.08156526 0.06470751 0.01685776

SSD0<-SSD0[,c(1,4)]  
SSD0$day<-"D0"  
head(SSD0,2)

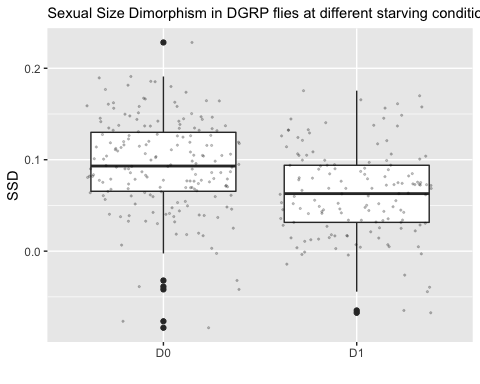
## line SSD day  
## 1 L100 0.13857467 D0  
## 2 L101 0.01685776 D0

SSD1<-df1\_mean[,c(1,4)]  
SSD1$day<-"D1"  
names(SSD1)[names(SSD1) == "SSD1"] <- "SSD"  
  
SSD\_all<-rbind(SSD0,SSD1)  
head(SSD\_all,2)

## line SSD day  
## 1 L100 0.13857467 D0  
## 2 L101 0.01685776 D0

SSD boxplot, the overall SSD decreases when flies are starved

# plotting male and female size mean  
SSD\_all %>%  
 ggplot( aes(x=day, y=SSD)) +  
 geom\_boxplot() +  
 scale\_fill\_viridis(discrete = TRUE, alpha=0.6) +  
 geom\_jitter(color="black", size=0.4, alpha=0.2) +  
 #theme\_ipsum() +  
 theme(  
 legend.position="none",  
 plot.title = element\_text(size=11)  
 ) +  
 ggtitle("Sexual Size Dimorphism in DGRP flies at different starving conditions") +  
 xlab("")

 SSD decreases at Day1 starvation

## Question 2.3: Does SSD in starved conditions vary, and does it covary with SSD0?

First, we want to see if there is genetic variation in SSD1 ### Model fit

#Comparing two model fit for SSD1 to see if there is genetic variation  
  
model2<-lmer(pupa~sex+(1|line)+(1|block), data=df1) #model to test for SSD presence as we did above  
model1<-lmer(pupa~sex+(sex|line)+(1|block), data=df1)   
anova(model1)

## Type III Analysis of Variance Table with Satterthwaite's method  
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)   
## sex 4.1056 4.1056 1 156.37 233.98 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

anova(model1,model2)

## refitting model(s) with ML (instead of REML)

## Data: df1  
## Models:  
## model2: pupa ~ sex + (1 | line) + (1 | block)  
## model1: pupa ~ sex + (sex | line) + (1 | block)  
## npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)   
## model2 5 -7503.9 -7469.8 3756.9 -7513.9   
## model1 7 -7517.2 -7469.5 3765.6 -7531.2 17.289 2 0.0001761 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Model 1 is better, as AIC and BIC is smaller and log likelihood is higher. The difference of fit between these two models is significant.

#### Do a LRT

How many parameters for each models

(AIC(model1) - REMLcrit(model1))/2 # # of parameters the model "thinks" are being estimated

## [1] 7

(AIC(model2) - REMLcrit(model2))/2 # # of parameters the model "thinks" are being estimated

## [1] 5

So lme4/lmer is treating model 1 as having two more parameters than model2.

LR.model <- -as.numeric(REMLcrit(model1) - REMLcrit(model2))  
LR.model

## [1] 17.63734

nlevels(df1$line)

## [1] 0

pchisq(q = LR.model, df=2, lower=F)

## [1] 0.0001479447

pchisq(q = LR.model, df=nlevels(df1$line), lower=F)

## [1] 0

#### Parametric boostrap

Finally, we can conduct a parametric bootstrap to compare the two models.

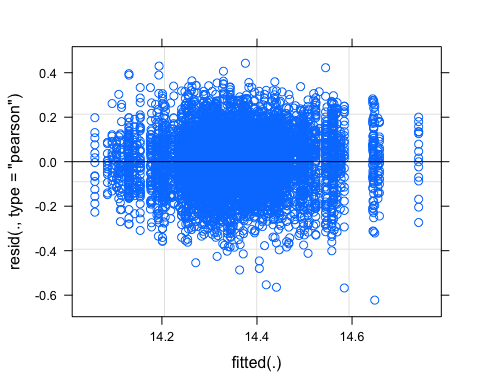
#### Finally using Bayesian Analysis

#prior.2 <-list(R=list(V=0.01, nu=0.002),   
# G=list(G1=list(V=0.01\*diag(1), nu=0.002),  
 # G2=list(V=0.01\*diag(2), nu=0.002)))  
  
#model1M.MCMC <- MCMCglmm(pupa ~ 1 + sex,   
# random=~block + us(1 + sex):line,  
 # prior = prior.2, burnin = 5000, nitt = 20000, thin = 10,  
# verbose = F, pr = T,  
 # data=df1)  
#summary(model1M.MCMC)

#### Post model 1 fitting check

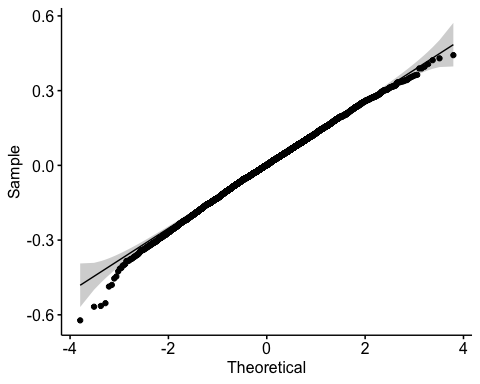
##### Model 1 residual distribution

plot(model1)



##### QQ plot

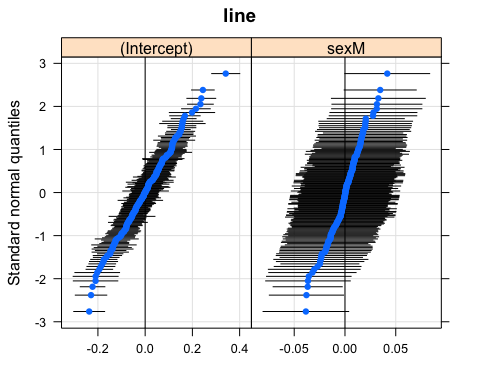
res\_model1=residuals(model1)  
ggqqplot(res\_model1)



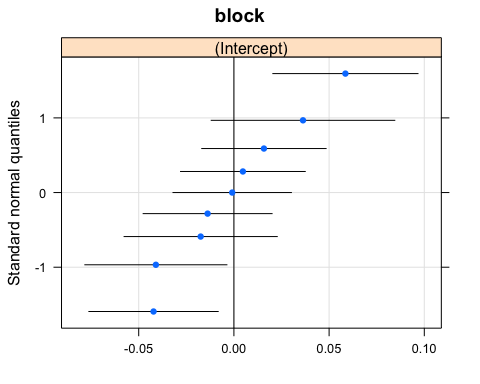
##### Random effect plot

qqmath(ranef(model1))

## $line



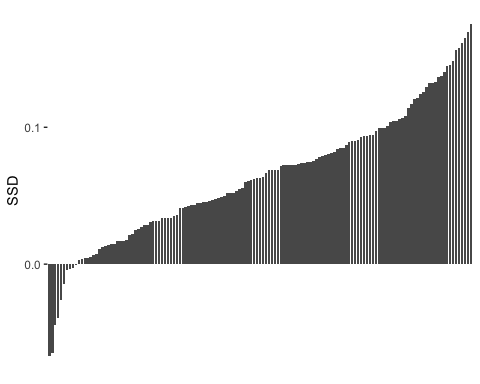
##   
## $block



SSD in starved flies varies genetically.

### Plot SSD in starved flies by line

plot5<-ggplot(SSD1, aes(x=reorder(line,SSD), y=SSD)) +  
 geom\_col() +  
 theme(axis.text.x=element\_blank(),  
 axis.ticks.x=element\_blank(),axis.title.x=element\_blank(), plot.background = element\_rect(fill = "white"),panel.background = element\_rect(fill = "white", colour="white"))   
  
plot5 +labs(x = "DGRP line")



### Covaration with which sex?

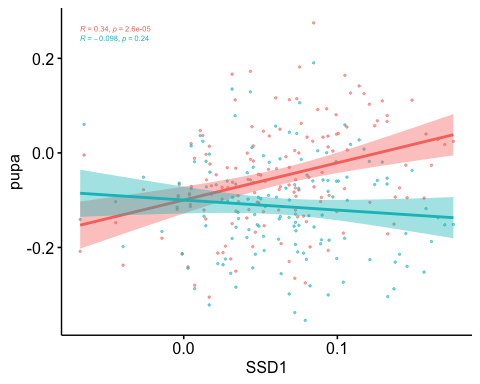
Correlation test and plot

head(df1\_mean,2)

## line pupaF1 pupaM1 SSD1  
## 1 L100 0.04734688 0.0366250 0.01072188  
## 2 L101 -0.07406721 -0.1467936 0.07272640

#reshape data  
SSD1\_gather<-gather(df1\_mean,key="sex",value="pupa",pupaF1:pupaM1)  
#plot  
plot6 <- ggscatter(SSD1\_gather, x = "SSD1", y = "pupa",  
 color = "sex",  
 add = "reg.line", conf.int = TRUE, alpha=0.5, size=0.5) +theme(legend.position="none") +ggpubr::stat\_cor(aes(color = sex), size=2)   
plot6 #stat\_cor uses the Pearson correlation

## `geom\_smooth()` using formula 'y ~ x'



### Covariation with SSD in fed flies?

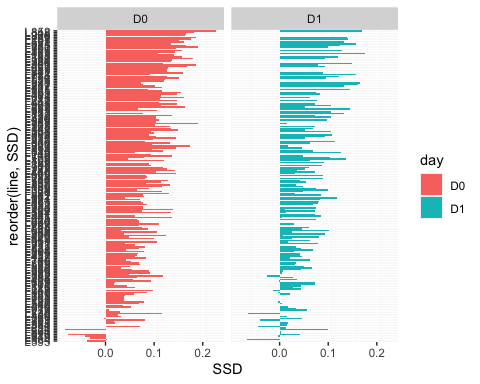
Does SSD in fed flies covary with SSD in old flies?

To know, this I am looking a the correlation between SSD values in the two food conditions, across lines. Plot of SSD values between two food conditions

head(SSD\_all,2)

## line SSD day  
## 1 L100 0.13857467 D0  
## 2 L101 0.01685776 D0

ggplot(SSD\_all, aes(x=reorder(line,SSD), y=SSD)) +  
 geom\_col(aes(fill = day)) +  
 facet\_wrap(~ day) +  
 coord\_flip()

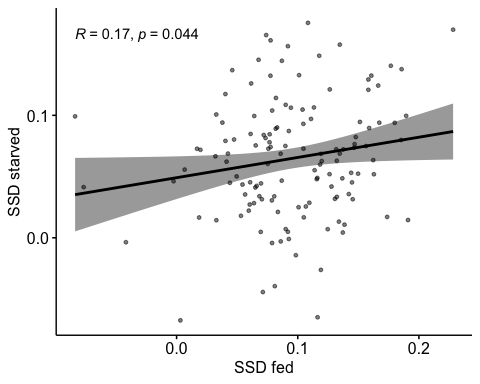
 Correlation between SSDs. Hypothesis: if SSD changes with environment, which is what we expect, we will not see a correlation between SSD0 and SSD1 and/or SSD2

#reshape data  
head(SSD\_all,2)

## line SSD day  
## 1 L100 0.13857467 D0  
## 2 L101 0.01685776 D0

x= SSD\_all[SSD\_all$day =="D0", ]  
y= SSD\_all[SSD\_all$day =="D1", ]  
  
SSD\_merged<-merge(x=SSD\_all[SSD\_all$day =="D0", ], y=SSD\_all[SSD\_all$day =="D1", ], by.x="line", by.y="line")   
#plot  
plot7 <- ggscatter(SSD\_merged, x="SSD.x" ,y="SSD.y",  
 add = "reg.line", conf.int = TRUE, alpha=0.5, size=1)+ labs(x="SSD fed", y="SSD starved") + ggpubr::stat\_cor(aes())#stat\_cor uses the Pearson correlation  
plot7

## `geom\_smooth()` using formula 'y ~ x'

 Correlation between SSD1 and SSD0, baarely significant and rsquare very low.

It seems that SSD1 may vary differently, does female covariation with SSD0 changes in starved conditions?

SSD1 also covaries with female size in starved conditions

Will still check SSD1, even though it does not correlate with SSD0, we can see if SSD1 variation covaries with either female or male variation

We have shown that SSD changes in different condition, that in starved conditions, we have a decrease in overall SSD, and that the variation of SSD partly covaries with female size. But the degree of correlation varies? (how to test that?)

SSD changes in different food conditions, that means that there is a specific plasticity between sexes, or Sex Specific Plasticity. How does it look like and which sex is responsible for this difference in plasticity that is linked to SSD?

# Section 3: SSP and Male, Female Plasticity

* Question 3.1: confirming that SSP exists - same test as SSD0 and SSD1 comparison
* Question 3.2: Does SSP vary genetically?
* Question 3.3: Is there a covariation between SSP and SSD fed flies?
* Question 3.4: Which sex plasticity contributes to SSD?

##Question 3.1: Confirming that SSP exists ### SSP: between fed and 1 day starved flies We showed in Question 2.X that SSD changed when changing food conditions. Let’s view again the summary of the Model.

model1<-lmer(pupa~sex\*day+(sex+day|line)+(1|block), data=df\_sub01)  
summary(model1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: pupa ~ sex \* day + (sex + day | line) + (1 | block)  
## Data: df\_sub01  
##   
## REML criterion at convergence: -19478.5  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -5.1820 -0.6206 0.0527 0.6592 3.6054   
##   
## Random effects:  
## Groups Name Variance Std.Dev. Corr   
## line (Intercept) 0.0109088 0.10445   
## sexM 0.0006247 0.02499 -0.39   
## dayD1 0.0051219 0.07157 -0.21 0.07  
## block (Intercept) 0.0015797 0.03974   
## Residual 0.0152436 0.12347   
## Number of obs: 15394, groups: line, 195; block, 9  
##   
## Fixed effects:  
## Estimate Std. Error df t value Pr(>|t|)   
## (Intercept) 1.457e+01 1.555e-02 1.081e+01 936.52 < 2e-16 \*\*\*  
## sexM -9.407e-02 3.327e-03 3.528e+02 -28.27 < 2e-16 \*\*\*  
## dayD1 -1.791e-01 6.330e-03 2.325e+02 -28.29 < 2e-16 \*\*\*  
## sexM:dayD1 3.016e-02 4.260e-03 9.178e+03 7.08 1.55e-12 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) sexM dayD1   
## sexM -0.184   
## dayD1 -0.136 0.229   
## sexM:dayD1 0.064 -0.553 -0.362

## Question 3.2: Does SSP vary in the DGRP flies?

### Model fit comparison - previously done to compare SSD0 and SSD1

# we want to compare effect of sex and day of starvation on pupal size. I am using df01, subset off data day 0 and day1  
  
model2<-lmer(pupa~sex\*day+(sex+day|line)+(1|block), data=df\_sub01)   
model1<-lmer(pupa~sex\*day+(sex\*day|line)+(1|block), data=df\_sub01)   
anova(model1,model2)

## Data: df\_sub01  
## Models:  
## model2: pupa ~ sex \* day + (sex + day | line) + (1 | block)  
## model1: pupa ~ sex \* day + (sex \* day | line) + (1 | block)  
## npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)   
## model2 12 -19489 -19397 9756.3 -19513   
## model1 16 -19494 -19372 9763.3 -19526 13.923 4 0.007544 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Anova(model1) #there is SSP

## Analysis of Deviance Table (Type II Wald chisquare tests)  
##   
## Response: pupa  
## Chisq Df Pr(>Chisq)   
## sex 869.840 1 < 2.2e-16 \*\*\*  
## day 731.895 1 < 2.2e-16 \*\*\*  
## sex:day 39.044 1 4.145e-10 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

class(model1) <- "lmerMod"  
class(model2) <- "lmerMod"  
stargazer(model1,model2, style="ajps", type="text", title="Table Sex Specific Plasticity Genetic Variation")

##   
## Table Sex Specific Plasticity Genetic Variation  
## ------------------------------------  
## pupa   
## Model 1 Model 2   
## ------------------------------------  
## sexM -0.094\*\*\* -0.094\*\*\*   
## (0.003) (0.003)   
## dayD1 -0.179\*\*\* -0.179\*\*\*   
## (0.007) (0.006)   
## sexM:dayD1 0.031\*\*\* 0.030\*\*\*   
## (0.005) (0.004)   
## Constant 14.566\*\*\* 14.566\*\*\*   
## (0.016) (0.016)   
## N 15394 15394   
## Log Likelihood 9746.361 9739.275   
## AIC -19460.720 -19454.550  
## BIC -19338.450 -19362.850  
## ------------------------------------  
## \*\*\*p < .01; \*\*p < .05; \*p < .1

#### Do a LRT

How many parameters for each models

(AIC(model1) - REMLcrit(model1))/2 # # of parameters the model "thinks" are being estimated

## [1] 16

(AIC(model2) - REMLcrit(model2))/2 # # of parameters the model "thinks" are being estimated

## [1] 12

So lme4/lmer is treating model 1 as having five more parameters than model2.

LR.model <- -as.numeric(REMLcrit(model1) - REMLcrit(model2))  
LR.model

## [1] 14.1722

nlevels(df\_sub01$line)

## [1] 0

pchisq(q = LR.model, df=5, lower=F)

## [1] 0.01455181

pchisq(q = LR.model, df=nlevels(df\_sub01$line), lower=F)

## [1] 0

#### Parametric boostrap

Finally, we can conduct a parametric bootstrap to compare the two models.

#### Finally using Bayesian Analysis

#### NB: did not run before need to change the model

#prior.2 <-list(R=list(V=0.01, nu=0.002),   
 # G=list(G1=list(V=0.01\*diag(1), nu=0.002),  
 # G2=list(V=0.01\*diag(2), nu=0.002)))  
  
#model1M.MCMC <- MCMCglmm(pupa ~ 1 + sex, #is this right for SSP?  
 #random=~block + us(1 + sex):line,  
 #prior = prior.2, burnin = 5000, nitt = 20000, thin = 10,  
 #verbose = F, pr = T,  
 #data=df01)  
#summary(model1M.MCMC)

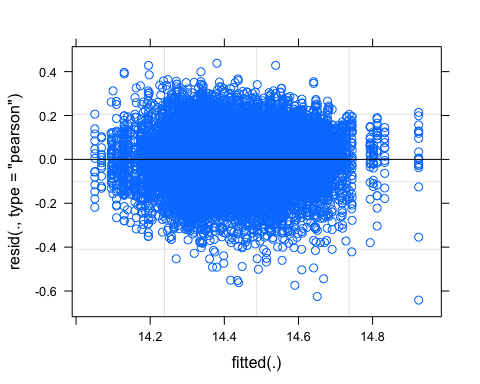
#### Post model 1 fitting check

#### Residual distribution

res\_model1=residuals(model1)

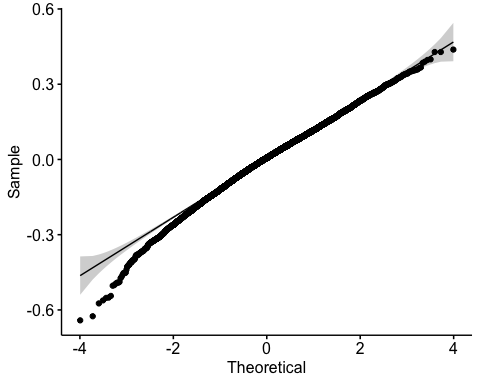
#### Model 1 residual distribution

plot(model1)



#### QQ plot

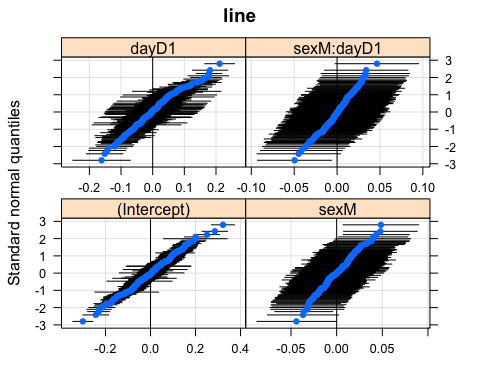
require(ggpubr)  
ggqqplot(res\_model1)



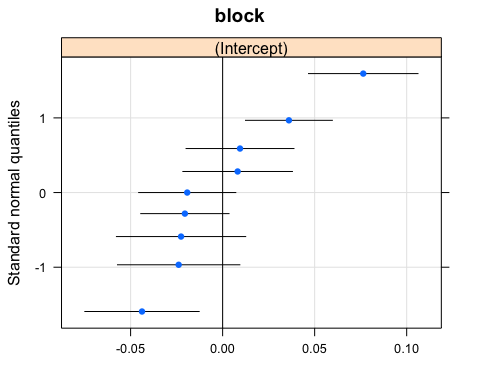
#### Random effect plot

qqmath(ranef(model1))

## $line

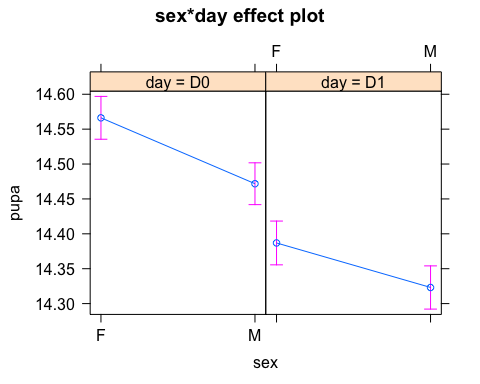


##   
## $block



### Plot of predicted values

plot(Effect(c("sex","day"),model1))

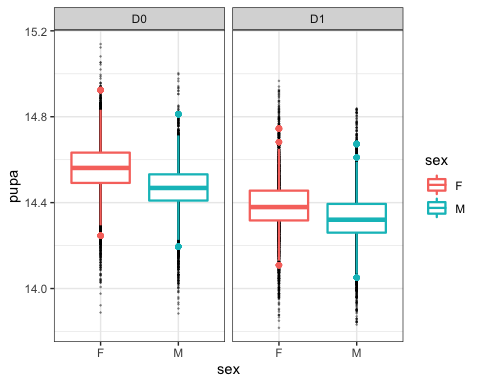


Another plot with fitted values (in color) on raw data in black

df\_sub01\_fit<-df\_sub01  
df\_sub01\_fit$fit <- predict(model1)  
head(df\_sub01\_fit,2)

## # A tibble: 2 x 11  
## # Groups: group [1]  
## id line block day sex wing leg pupa group pupa\_noblock fit  
## <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> <dbl> <dbl>  
## 1 021-A-0-F… L21 B6 D0 F 14.2 13.9 14.7 L21\_F… 0.311 14.5  
## 2 021-A-0-F… L21 B6 D0 F 14.0 13.7 14.4 L21\_F… 0.0338 14.5

plot4A<- ggplot(df\_sub01\_fit,aes(sex, pupa, group=interaction(sex, day))) +   
 facet\_grid(~day) +  
 geom\_point(alpha = 0.3, size=0.2) +   
 theme\_bw()+  
 geom\_boxplot(aes(y=fit, group=interaction(sex,day), col=sex), size=0.8 )  
  
plot4A



Answer 3.2: There is genetic variation in SSP if we compare fed flies and starved flies.

### Plot of SSP per line

#### Calculate SSP

To calculate SSP, I first calculate the plasticity of female and male and subtract the plasticity female-male

#calculate plasticity female  
  
df1F<-subset(df1, sex=="F")  
df1F\_mean<-aggregate(df1F[, 10], list(df1F$line), mean) #using pupa\_noblock  
colnames(df1F\_mean)<-c("line","pupaFmean\_1")  
  
df0F<-subset(df0, sex=="F")  
df0F\_mean<-aggregate(df0F[, 10], list(df0F$line), mean)  
colnames(df0F\_mean)<-c("line","pupaFmean\_0")  
  
pupa\_mean\_F01<-merge(x=df0F\_mean, y=df1F\_mean, by.x="line", by.y="line")   
head(pupa\_mean\_F01,2) #140 lines

## line pupaFmean\_0 pupaFmean\_1  
## 1 L100 0.23636559 0.04734688  
## 2 L101 0.08156526 -0.07406721

pupa\_mean\_F01$PF01<-pupa\_mean\_F01$pupaFmean\_0-pupa\_mean\_F01$pupaFmean\_1 #calculating plast female 01  
plastF01<-pupa\_mean\_F01

#calculate plasticity male  
head(df1,2)

## # A tibble: 2 x 10  
## # Groups: group [1]  
## id line block day sex wing leg pupa group pupa\_noblock  
## <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr> <dbl>  
## 1 021-A-1-F-024 L21 B6 D1 F 14.1 13.8 14.6 L21\_F\_D1 0.219  
## 2 021-A-1-F-026 L21 B6 D1 F 14.3 14.0 14.8 L21\_F\_D1 0.371

df1M<-subset(df1, sex=="M")  
df1M\_mean<-aggregate(df1M[, 10], list(df1M$line), mean)  
colnames(df1M\_mean)<-c("line","pupaMmean\_1")  
head(df1M\_mean,2)

## line pupaMmean\_1  
## 1 L100 0.0366250  
## 2 L101 -0.1467936

df0M<-subset(df0, sex=="M")  
df0M\_mean<-aggregate(df0M[, 10], list(df0M$line), mean)  
colnames(df0M\_mean)<-c("line","pupaMmean\_0")  
head(df0M\_mean,2)

## line pupaMmean\_0  
## 1 L100 0.09779092  
## 2 L101 0.06470751

pupa\_mean\_M01<-merge(x=df0M\_mean, y=df1M\_mean, by.x="line", by.y="line")  
head(pupa\_mean\_F01,2) #151

## line pupaFmean\_0 pupaFmean\_1 PF01  
## 1 L100 0.23636559 0.04734688 0.1890187  
## 2 L101 0.08156526 -0.07406721 0.1556325

pupa\_mean\_M01$PM01<-pupa\_mean\_M01$pupaMmean\_0-pupa\_mean\_M01$pupaMmean\_1 #calculating SSP01  
plastM01<-pupa\_mean\_M01

#SSP  
pupa\_SSP01<-merge(x=plastF01, y= plastM01, by.x="line", by.y="line") #merging male and female datasets  
head(pupa\_SSP01,2)

## line pupaFmean\_0 pupaFmean\_1 PF01 pupaMmean\_0 pupaMmean\_1 PM01  
## 1 L100 0.23636559 0.04734688 0.1890187 0.09779092 0.0366250 0.06116592  
## 2 L101 0.08156526 -0.07406721 0.1556325 0.06470751 -0.1467936 0.21150112

length(unique(pupa\_SSP01$line)) #133 lines left

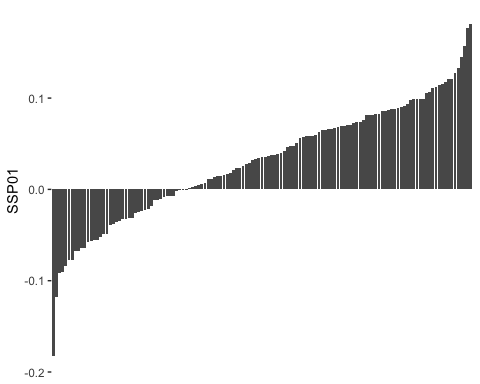
## [1] 133

#calculate SSP from the plasticity.  
pupa\_SSP01$SSP01<-pupa\_SSP01$PF01-pupa\_SSP01$PM01  
  
#calculating SSDs again to add them to the dataframe  
pupa\_SSP01$SSD0<-pupa\_SSP01$pupaFmean\_0-pupa\_SSP01$pupaMmean\_0  
pupa\_SSP01$SSD1<-pupa\_SSP01$pupaFmean\_1-pupa\_SSP01$pupaMmean\_1  
head(pupa\_SSP01,2)

## line pupaFmean\_0 pupaFmean\_1 PF01 pupaMmean\_0 pupaMmean\_1 PM01  
## 1 L100 0.23636559 0.04734688 0.1890187 0.09779092 0.0366250 0.06116592  
## 2 L101 0.08156526 -0.07406721 0.1556325 0.06470751 -0.1467936 0.21150112  
## SSP01 SSD0 SSD1  
## 1 0.12785279 0.13857467 0.01072188  
## 2 -0.05586865 0.01685776 0.07272640

#### Plot

plot8 <-ggplot(pupa\_SSP01, aes(x=reorder(line,SSP01), y=SSP01)) +  
 geom\_col() +  
 theme(axis.text.x=element\_blank(),  
 axis.ticks.x=element\_blank(),axis.title.x=element\_blank(), plot.background = element\_rect(fill = "white"),panel.background = element\_rect(fill = "white", colour="white"))   
plot8



We saw that SSD variation in both food conditions is correlated with female size variation. Do we then have SSP variation due to female size variation or possibly plasticity in one of the two sexes?

## Question 3.3: Does SSP covary with SSD?

#data SSP, pupa F, SSD0  
head(pupa\_SSP01,2)

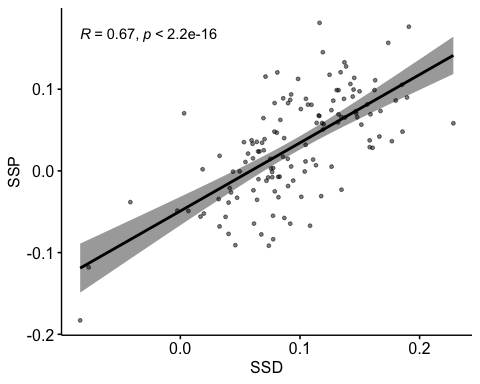
## line pupaFmean\_0 pupaFmean\_1 PF01 pupaMmean\_0 pupaMmean\_1 PM01  
## 1 L100 0.23636559 0.04734688 0.1890187 0.09779092 0.0366250 0.06116592  
## 2 L101 0.08156526 -0.07406721 0.1556325 0.06470751 -0.1467936 0.21150112  
## SSP01 SSD0 SSD1  
## 1 0.12785279 0.13857467 0.01072188  
## 2 -0.05586865 0.01685776 0.07272640

SSD0\_SSP01<-pupa\_SSP01[,c(1,8,9)]  
  
head(SSD0\_SSP01,2)

## line SSP01 SSD0  
## 1 L100 0.12785279 0.13857467  
## 2 L101 -0.05586865 0.01685776

plot9<- ggscatter(SSD0\_SSP01, x="SSD0" ,y="SSP01",  
 add = "reg.line", conf.int = TRUE, alpha=0.5, size=1) +labs(x="SSD",y="SSP")+ ggpubr::stat\_cor()#stat\_cor uses the Pearson correlation  
plot9

## `geom\_smooth()` using formula 'y ~ x'



## Question 3.4: which sex is more plastic?

model1<-lmer(pupa~sex\*day+(sex\*day|line)+(1|block), data=df\_sub01) #basic model  
summary(model1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: pupa ~ sex \* day + (sex \* day | line) + (1 | block)  
## Data: df\_sub01  
##   
## REML criterion at convergence: -19492.7  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -5.2044 -0.6176 0.0517 0.6581 3.5543   
##   
## Random effects:  
## Groups Name Variance Std.Dev. Corr   
## line (Intercept) 0.0112675 0.10615   
## sexM 0.0007463 0.02732 -0.49   
## dayD1 0.0061539 0.07845 -0.28 0.32   
## sexM:dayD1 0.0009538 0.03088 0.32 -0.46 -0.52  
## block (Intercept) 0.0015922 0.03990   
## Residual 0.0151956 0.12327   
## Number of obs: 15394, groups: line, 195; block, 9  
##   
## Fixed effects:  
## Estimate Std. Error df t value Pr(>|t|)   
## (Intercept) 14.566230 0.015663 10.940499 929.966 < 2e-16 \*\*\*  
## sexM -0.094440 0.003440 152.019321 -27.451 < 2e-16 \*\*\*  
## dayD1 -0.179327 0.006792 178.941747 -26.404 < 2e-16 \*\*\*  
## sexM:dayD1 0.030618 0.004900 170.094684 6.248 3.22e-09 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) sexM dayD1   
## sexM -0.218   
## dayD1 -0.167 0.339   
## sexM:dayD1 0.129 -0.593 -0.515

Look at the intercept values

plasticityF = (14.566230) - (14.566230-0.179327)  
print(c("plasticity female", plasticityF))

## [1] "plasticity female" "0.179327000000001"

plasticityM = (14.566230 -0.094440 )- (14.566230-0.094440-0.179327+0.030618)  
print(c("plasticity male", plasticityM))

## [1] "plasticity male" "0.148709"

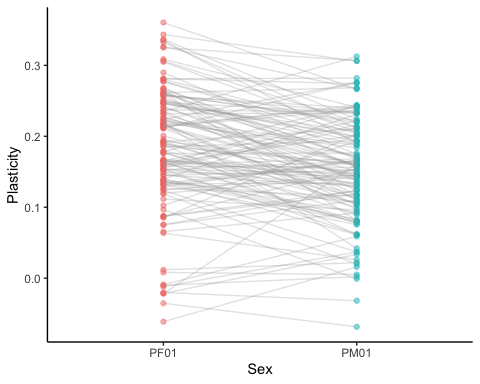
Females are more plastic than males

Plot of female and male plasticity

SSD\_plast<-pupa\_SSP01[,c(1,4,7,8,9)]  
head(SSD\_plast,2)

## line PF01 PM01 SSP01 SSD0  
## 1 L100 0.1890187 0.06116592 0.12785279 0.13857467  
## 2 L101 0.1556325 0.21150112 -0.05586865 0.01685776

pupa\_SSP01\_gather<-gather(SSD\_plast,key="sex",value="plasticity",PF01:PM01)  
  
plot10<-ggplot(pupa\_SSP01\_gather, aes(x = sex, y = plasticity, color=sex)) +  
 geom\_point(aes(fill = sex), alpha = 0.5) +  
 geom\_line(aes(group = interaction(line)),  
 alpha = 0.3, colour = "darkgrey") + theme\_classic()+labs(y="Plasticity",x="Sex")+theme(legend.position = "none")  
  
plot10



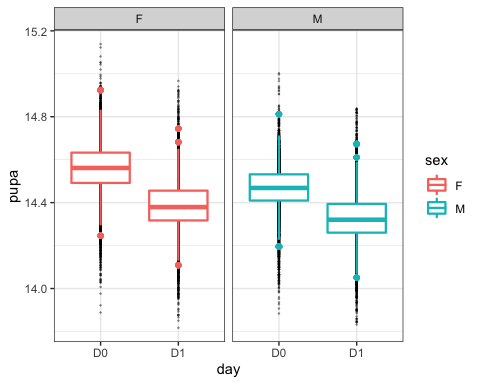
#add predicted values

plot10A<- ggplot(df\_sub01\_fit,aes(day, pupa, group=interaction(sex, day))) +   
 facet\_grid(~sex) +  
 geom\_point(alpha = 0.3, size=0.2) +   
 theme\_bw()+  
 geom\_boxplot(aes(y=fit, group=interaction(sex,day), col=sex), size=0.8 )+  
 stat\_summary(fun.y = mean, geom = 'line', aes(group = day))

## Warning: `fun.y` is deprecated. Use `fun` instead.

plot10A

## geom\_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom\_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?



CAN WE test if plasticity female varies more than plasticity male without using summary stat?

## Question 3.3: Is SSD genetic variation correlated with female or male plasticity?

#### Correlation between SSD and plasticity by sex

head(pupa\_SSP01,2)

## line pupaFmean\_0 pupaFmean\_1 PF01 pupaMmean\_0 pupaMmean\_1 PM01  
## 1 L100 0.23636559 0.04734688 0.1890187 0.09779092 0.0366250 0.06116592  
## 2 L101 0.08156526 -0.07406721 0.1556325 0.06470751 -0.1467936 0.21150112  
## SSP01 SSD0 SSD1  
## 1 0.12785279 0.13857467 0.01072188  
## 2 -0.05586865 0.01685776 0.07272640

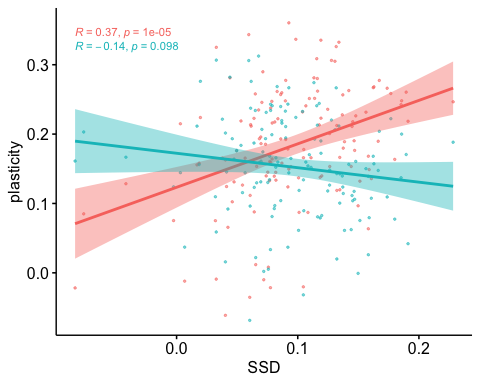
SSD\_plast<-pupa\_SSP01[,c(1,4,7,8,9)]  
head(SSD\_plast,2)

## line PF01 PM01 SSP01 SSD0  
## 1 L100 0.1890187 0.06116592 0.12785279 0.13857467  
## 2 L101 0.1556325 0.21150112 -0.05586865 0.01685776

##### Plot

#reshape data  
SSD\_plast\_gather<-gather(SSD\_plast,key="sex",value="plasticity",PF01:PM01)  
#plot  
plot11 <- ggscatter(SSD\_plast\_gather, x = "SSD0", y = "plasticity",  
 color = "sex", size=0.5,   
 add = "reg.line", conf.int = TRUE, alpha=0.5) + stat\_cor(aes(color = sex), show.legend=FALSE, size=3)+theme(legend.position = "none")+labs(x="SSD") #stat\_cor uses the Pearson correlation  
#removing legend not working  
plot11

## `geom\_smooth()` using formula 'y ~ x'



## Final figures

Figure 1

figure1 <-ggarrange(ggarrange(plot1,plot3,ncol=2, labels=c("A","C")),plot2,nrow=2, heights = c(1.5,1),labels=c("A","B"))

## `geom\_smooth()` using formula 'y ~ x'

annotate\_figure(figure1,  
 top = text\_grob(" ", color = "black", face = "bold", size = 15),  
 fig.lab = "Figure 1", fig.lab.face = "bold"  
)

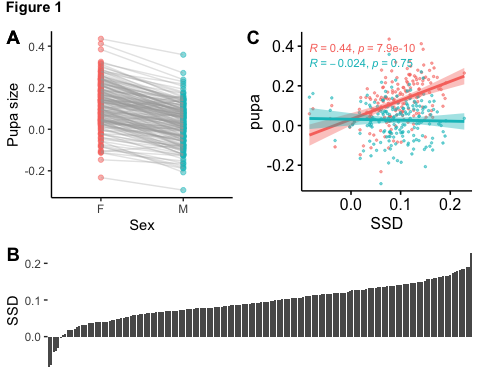


Figure S1: fitted values for SSD model and SSP model

figureS1<-ggarrange(plot1A, plot4A, nrow=1,ncol=2)  
annotate\_figure(figureS1,  
 top = text\_grob(" Fitted values for the Linear Mixed Models ", color = "black", face = "bold", size = 15),  
 fig.lab = "Figure S1", fig.lab.face = "bold"  
)

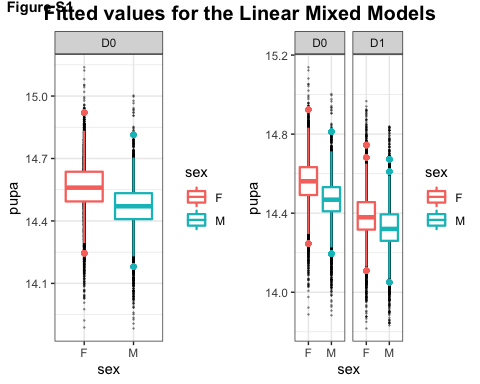


Figure S2: same as SSD in fed flies

figureS2 <-ggarrange(ggarrange(plot4,plot6,ncol=2, labels=c("A","C")),plot5,nrow=2, heights = c(1.5,1),labels=c("A","B"))

## `geom\_smooth()` using formula 'y ~ x'

annotate\_figure(figureS2,  
 top = text\_grob(" ", color = "black", face = "bold", size = 15),  
 fig.lab = "Figure S2", fig.lab.face = "bold"  
)

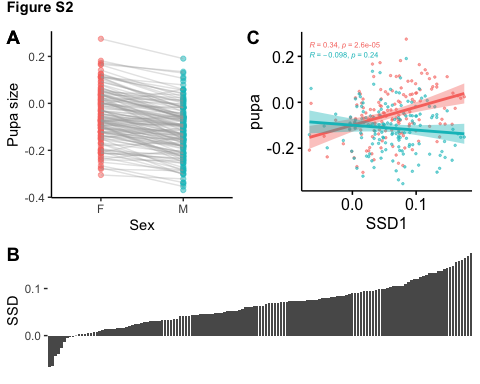


Figure S3

figureS3 <-ggarrange(plot7)

## `geom\_smooth()` using formula 'y ~ x'

annotate\_figure(figureS3,  
 top = text\_grob(" ", color = "black", face = "bold", size = 15),  
 fig.lab = "Figure S3", fig.lab.face = "bold"  
)

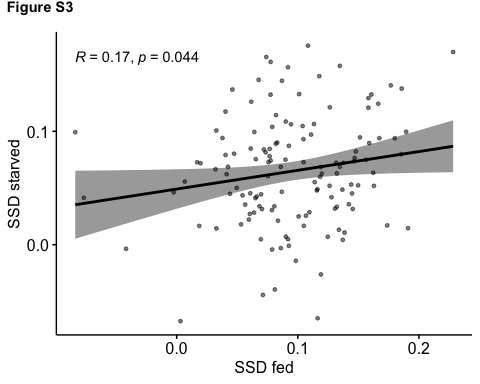


Figure 2

figure2 <-ggarrange(plot8,nrow=2, heights = c(1,1.5),labels=c("A","B"),ggarrange(plot9,ncol=2))

## `geom\_smooth()` using formula 'y ~ x'

annotate\_figure(figure2,  
 top = text\_grob(" ", color = "black", face = "bold", size = 15),  
 fig.lab = "Figure 2", fig.lab.face = "bold"  
)

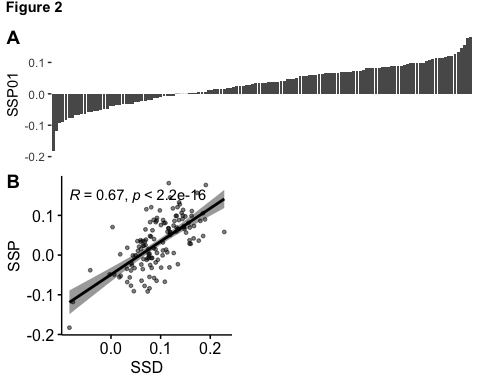


Figure 3

figure3 <-ggarrange(plot10,plot11,nrow=1,ncol=2,labels=c("A","B"))

## `geom\_smooth()` using formula 'y ~ x'

annotate\_figure(figure3,  
 top = text\_grob(" ", color = "black", face = "bold", size = 15),  
 fig.lab = "Figure 3", fig.lab.face = "bold"  
)

