

Figure 1

Figure 2A, B & C

Figure 3A & B

# Wandering Albatross Intrinsic Project: Code for Graphs and Figures

## Wandering Albatross Intrinsic Project: Code for Graphs and Figures

This R Markdown document details the code used to generate the figures and graphs for a study on the impact of intrinsic variables on parental care coordination in wandering albatrosses. It covers the creation of the models used to extract regression lines and the creation of the figures themselves. It is strongly recommended that this R markdown document be viewed alongside the R markdown document for the main study results for added context.

The setup code is featured below. This includes importing the required raw data for the graphs.

```
library(MASS)
library(knitr)
library(lme4)
library(sjPlot)
library(ggplot2)
library(optimx)
library(MuMIn)
library(dplyr)
library(here)

total_df4<-read.csv("total_df4.csv")
incu_new2<-subset(total_df4, breed_stage == "incu") # incubation subset, 260 observations
brood_new2<-subset(total_df4, breed_stage=="brood") # brooding subset, 611 observations
```

## Model Creation

Different versions of the models used in the papers main body must be created in order to extract the regression lines used in the graphs. This model examines the effects of intrinsic variables on the individual foraging trip duration and coordination strength exhibited by breeding wandering albatrosses. As some variables are presented scaled while other are

presented in their original units, two versions of each model must be computed: incubation (scaled and unscaled) and brooding (scaled and unscaled). Thus four models (plus their associated model averaging steps) are outlined below.

Altogether, these models and their model averaging steps will take between 12 and 24 hours to run.

## Incubation models

Below is the code for the model and model averaging using unscaled variables for the incubation subset. The model averaged object produced at the end will be used in the graphs.

```

# run the incubation model without scaled variables to get p_age regression line
co_ml_incu_r<- lmer(no_hours_sqrt ~
                    sex +
                    pers +
                    p_pers+
                    age+
                    age_sq +
                    p_age+
                    p_age_sq+
                    NumDays+
                    new_part+
                    ppb_ave_diff+
                    age:pers+
                    age_sq:pers+
                    age:ppb_ave_diff+
                    age_sq:ppb_ave_diff+
                    pers:ppb_ave_diff+
                    new_part:ppb_ave_diff+
                    p_age:p_pers+
                    p_age_sq:p_pers+
                    p_age:ppb_ave_diff+
                    p_age_sq:ppb_ave_diff+
                    p_pers:ppb_ave_diff+
                    p_pers:sex+
                    pers:sex+
                    (1|cycle) + (1+ppb_ave_diff|cycle_pair),
                    data = incu_new2, na.action=na.fail, REML=FALSE,
                    control=lmerControl (optimizer="optimx",optCtrl=list(method=
'nlminb'))))

summary(co_ml_incu_r)

# dredging to create model set
# linking age variables with their quadratic counterpart so either both or neither
# are retained
dr_cmin_r<-dredge(co_ml_incu_r, subset = (dc(age, age_sq) &&
                                         dc(p_age, p_age_sq) &&
                                         dc(age_sq, age) &&
                                         dc(p_age_sq, p_age)))

dr_cmin_r # view full model list

# confidence set creation
sub_m1_incu_r<-subset(dr_cmin_r, delta<2) ##subsets models delta >2

# remove nested models
nest_m1_incur <- subset(sub_m1_incu_r, !nested(.)) # removes nested models

#model averaging this object is used to get the regression line
modavm1_incur<-model.avg(nest_m1_incur, delta<2, fit = TRUE, revised.var = TRUE)

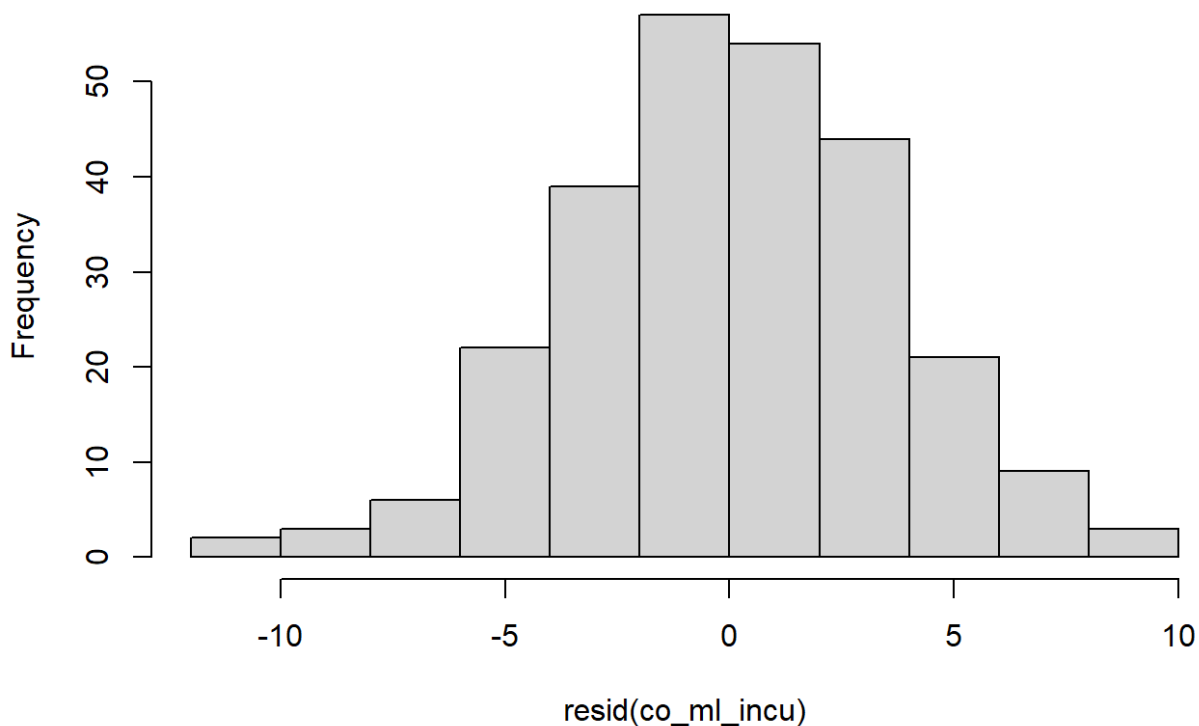
```

Below is the code for the model and model averaging using scaled variables for the incubation subset. This is the same model used in the paper's main body. The model averaged object produced at the end will be used in the graphs.

```
# run original, scaled incu model
co_ml_incu<- lmer(no_hours_sqrt ~
  sex +
  pers_sc +
  p_pers_sc+
  age_sc +
  age_sq_sc +
  p_age_sc+
  p_age_sq_sc+
  num_days_sc+
  new_part+
  ppb_ave_diff_sc+
  age_sc:pers_sc+
  age_sq_sc:pers_sc+
  age_sc:ppb_ave_diff_sc+
  age_sq_sc:ppb_ave_diff_sc+
  pers_sc:ppb_ave_diff_sc+
  new_part:ppb_ave_diff_sc+
  p_age_sc:p_pers_sc+
  p_age_sq_sc:p_pers_sc+
  p_age_sc:ppb_ave_diff_sc+
  p_age_sq_sc:ppb_ave_diff_sc+
  p_pers_sc:ppb_ave_diff_sc+
  p_pers_sc:sex+
  pers_sc:sex +
  (1|cycle) + (1+ppb_ave_diff_sc|cycle_pair),
data = incu_new2, na.action=na.fail, REML=FALSE,
control=lmerControl (optimizer="optimx",optCtrl=list(method='nl
minb'))))

summary(co_ml_incu)
hist(resid(co_ml_incu))
```

**Histogram of resid(co\_ml\_incu)**



```
# dredging to create model set
# linking age variables with their quadratic counterpart so either both or neither
# are retained
dr_cmin<-dredge(co_ml_incu, subset = (dc(age_sc, age_sq_sc) &&
                                     dc(p_age_sc, p_age_sq_sc) &&
                                     dc(age_sq_sc, age_sc) &&
                                     dc(p_age_sq_sc, p_age_sc)))

dr_cmin # view full model list

sub_m1_incu<-subset(dr_cmin, delta<2) ##subsets models delta <2

nest_m1_incu <- subset(sub_m1_incu, !nested(.)) # removes nested models

# model averaging, this object will be used in graph creation
modavm1_incu<-model.avg(nest_m1_incu, delta<2, fit = TRUE)
```

## Brooding models

Below is the code for the model and model averaging using unscaled variables for the brooding subset. The model averaged object produced at the end will be used in the graphs.

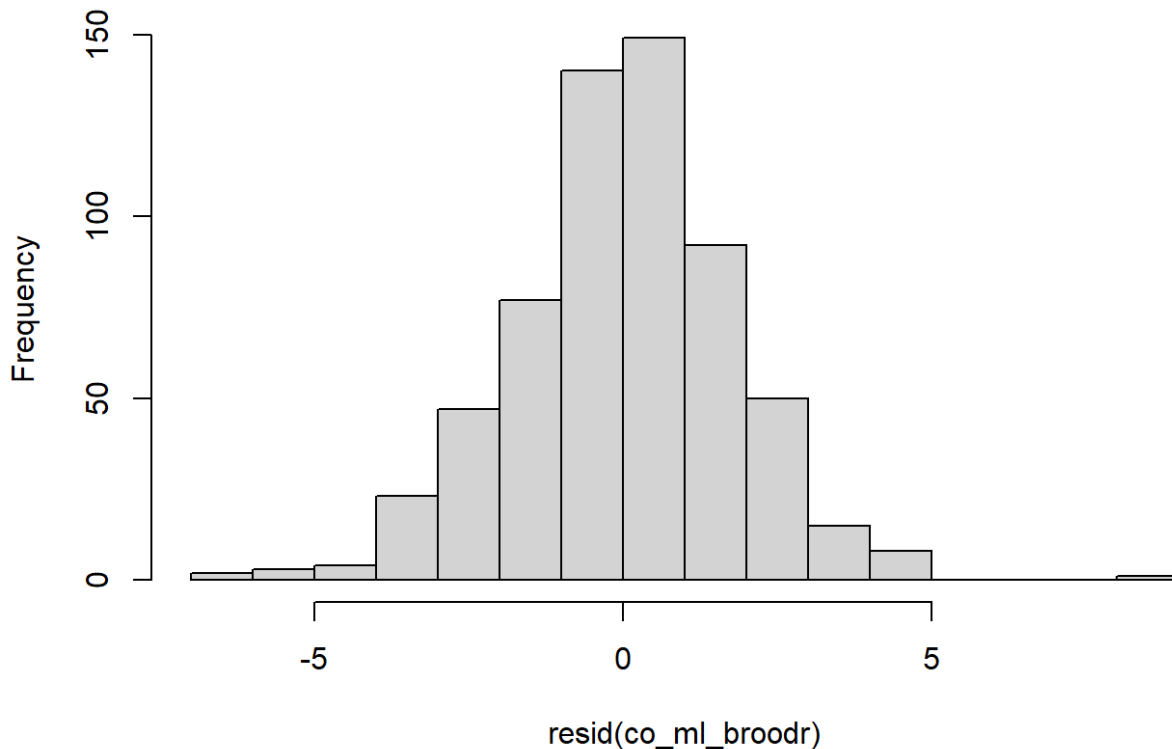
```

# run unscaled brooding model
co_ml_broodr<- lmer(no_hours_sqrt ~
                    sex +
                    pers +
                    p_pers+
                    age_sq+
                    age +
                    p_age+
                    p_age_sq+
                    NumDays+
                    new_part+
                    ppb_ave_diff+
                    age:pers+
                    age_sq:pers+
                    age:ppb_ave_diff+
                    age_sq:ppb_ave_diff+
                    pers:ppb_ave_diff+
                    new_part:ppb_ave_diff+
                    p_age:p_pers_sc+
                    p_age_sq:p_pers+
                    p_age:ppb_ave_diff+
                    p_age_sq:ppb_ave_diff+
                    p_pers:ppb_ave_diff+
                    p_pers:sex +
                    pers:sex +
                    (1|cycle) + (1+ppb_ave_diff_sc|cycle_pair),
data = brood_new2, na.action=na.fail, REML=FALSE,
control=lmerControl (optimizer="optimx",optCtrl=list(method='n
lminb'))))

summary(co_ml_broodr)
hist(resid(co_ml_broodr))

```

**Histogram of resid(co\_ml\_broodr)**



```
#dredge creating model set
# linking age variables to their equivalent quadratic version so they can only be
  discarded or retained together
dr_cmbr_r<-dredge(co_ml_broodr, subset = (dc(age, age_sq) &&
                                         dc(p_age, p_age_sq) &&
                                         dc(age_sq, age) &&
                                         dc(p_age_sq, p_age)))

dr_cmbr_r # view full model list

sub_m1_broodr<-subset(dr_cmbr_r, delta<2) ##subsets models delta <2

nest_m1_broodr <- subset(sub_m1_broodr, !nested(.))# remove nested models

## model averaging, this object will provide the graph's regression lines
modavm1_broodr<-model.avg(nest_m1_broodr, fit = TRUE)
```

Below is the code for the model and model averaging using scaled variables for the brooding subset. This is the same model used in the paper's main body. The model averaged object produced at the end will be used in the graphs.

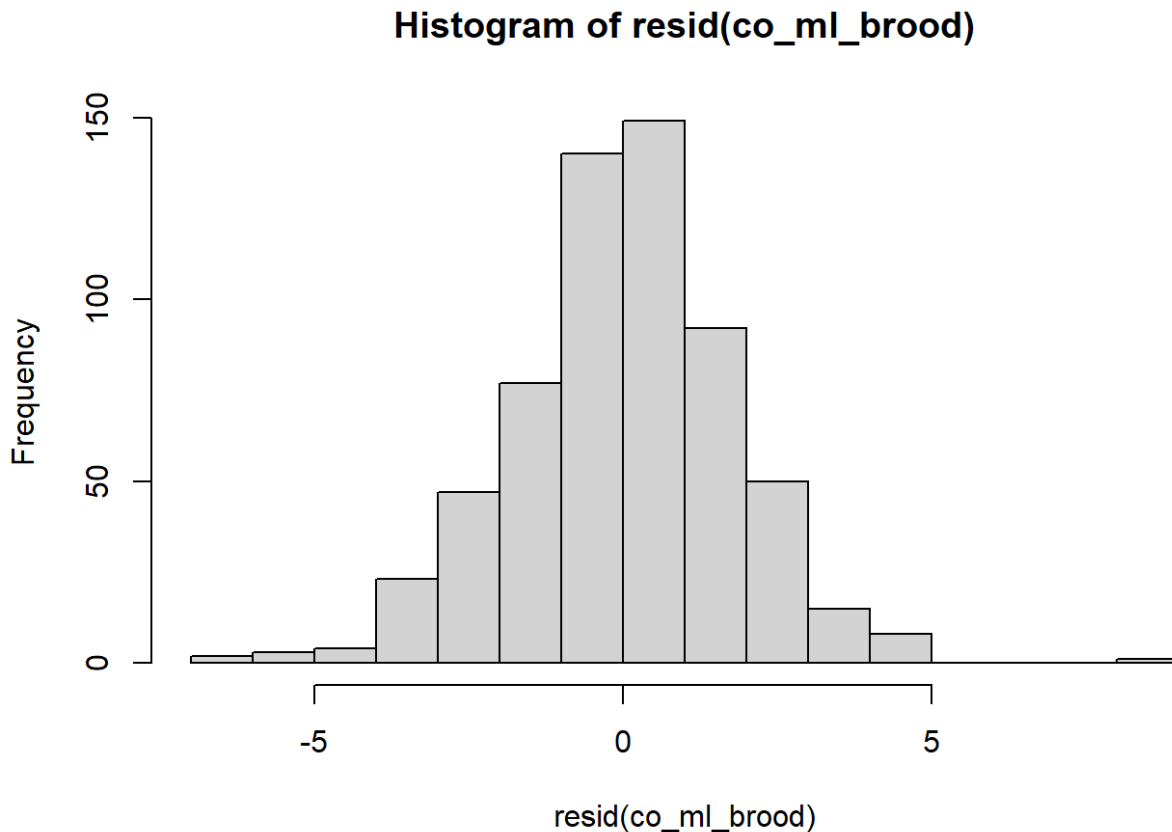
```

# run original brooding model
co_ml_brood<- lmer(no_hours_sqrt ~
                    sex +
                    pers_sc +
                    p_pers_sc+
                    age_sc +
                    age_sq_sc +
                    p_age_sc+
                    p_age_sq_sc+
                    num_days_sc+
                    new_part+
                    ppb_ave_diff_sc+
                    age_sc:pers_sc+
                    age_sq_sc:pers_sc+
                    age_sc:ppb_ave_diff_sc+
                    age_sq_sc:ppb_ave_diff_sc+
                    pers_sc:ppb_ave_diff_sc+
                    new_part:ppb_ave_diff_sc+
                    p_age_sc:p_pers_sc+
                    p_age_sq_sc:p_pers_sc+
                    p_age_sc:ppb_ave_diff_sc+
                    p_age_sq_sc:ppb_ave_diff_sc+
                    p_pers_sc:ppb_ave_diff_sc+
                    p_pers_sc:sex +
                    pers_sc:sex +
                    (1|cycle) + (1+ppb_ave_diff_sc|cycle_pair),
data = brood_new2, na.action=na.fail, REML=FALSE,
control=lmerControl (optimizer="optimx",optCtrl=list(method='n
lminb'))))

summary(co_ml_brood)
hist(resid(co_ml_brood))

```





```
#dredge creating model set
# linking age variables to their equivalent quadratic version so they can only be
  discarded or retained together
dr_cmbr<-dredge(co_ml_brood, subset = (dc(age_sc, age_sq_sc) &&
                                         dc(p_age_sc, p_age_sq_sc) &&
                                         dc(age_sq_sc, age_sc) &&
                                         dc(p_age_sq_sc, p_age_sc)))

dr_cmbr # view full model list

sub_m1_brood<-subset(dr_cmbr, delta<2) ##subsets models delta <2

nest_m1_brood <- subset(sub_m1_brood, !nested(.))# remove nested models

# model averaging, this object will be used in graph creation
modavm1_brood<-model.avg(nest_m1_brood, fit = TRUE)
```

## Figure 1

### Figure 1A: Partner boldness and trip duration

This graph illustrates the impact of partner boldness on individual trip duration.

First the regression line for partner boldness from the SCALED incubation model is extracted. Boldness score is always presented scaled.

```
#y axis = individual trip duration / no hours, x axis = scaled pers score
#(to match other pers graphs), regression line taken from scaled model
```

```
# extract regression line
mA_in<-summary(modavm1_incu)
ppers_dat <- plot_model(mA_in, type = "pred", terms = c("p_pers_sc"))
```

```
## Error: Confidence intervals could not be computed.
```

```
ppers_dat<- data.frame(ppers_dat$data)

## knitr 1a-sqrt
# non-square root data for plotting
ppers_dat_unsqr<- data.frame(x=ppers_dat$x, predicted=ppers_dat$predicted^2)
```

Then the regression line data is squared so it matches the raw data

Finally Figure 1A is produced using ggplot2 and the raw data.

```
p_pers_graph_incu<-ggplot(aes(x = x, y = predicted), data = ppers_dat_unsqr) + # r
  egression line for pers variable
  geom_line(size = 1.5, colour = "black")+
  geom_point(aes(x = p_pers_sc, y = no_hours), data = incu_new2) +
  theme_bw(base_size =15) +
  xlab("Scaled Partner Boldness Score")+
  ylab("Individual trip duration (hrs)")+
  ylim (0, 500)+
  theme_classic()+
  theme(axis.text = element_text(size = 15))+
  theme(axis.title= element_text(size=18))

p_pers_graph_incu
```

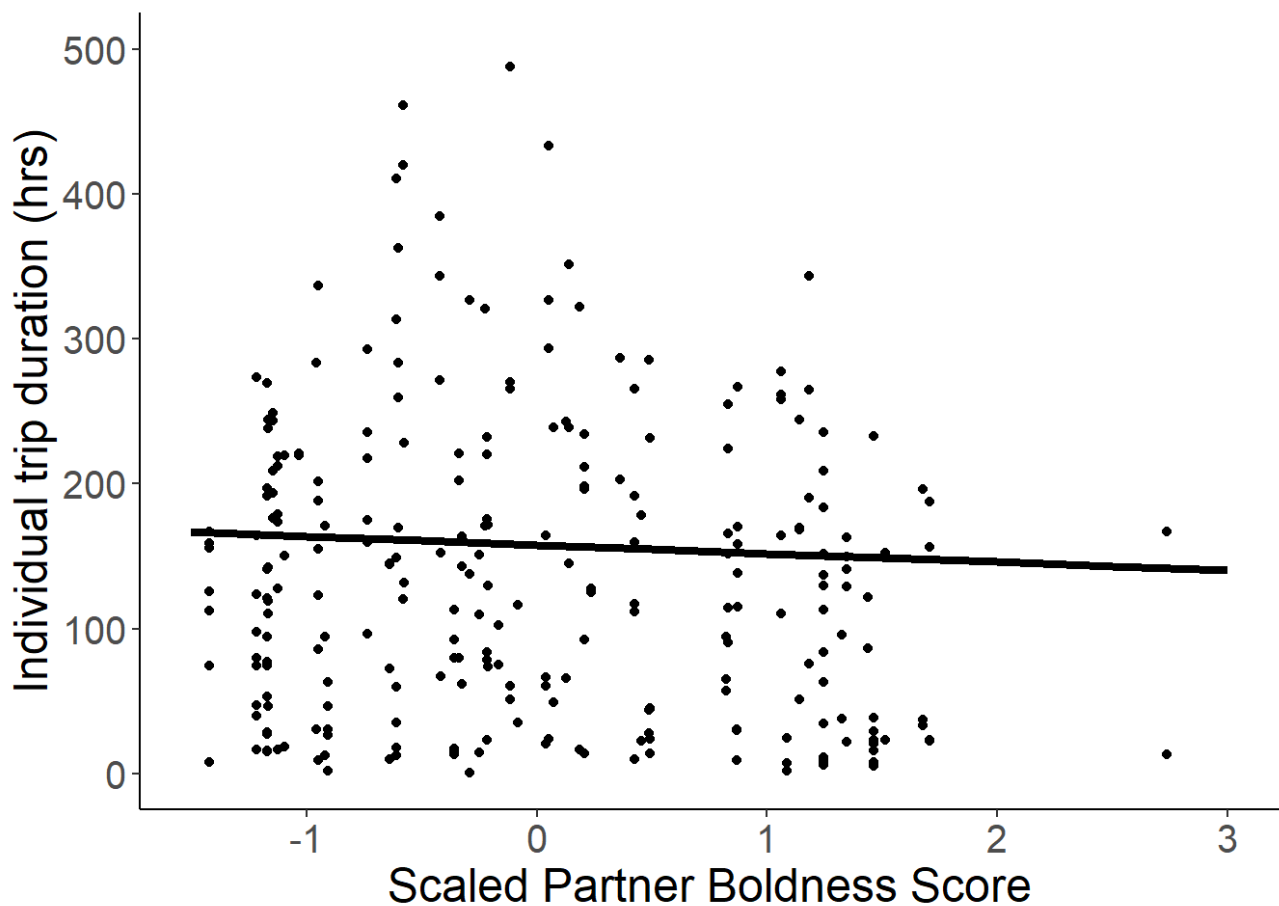


Figure 1 B: Partner age and trip duration

This graph illustrates the impact of partner age on individual trip duration.

First the regression line for partner age from the UNSCALED incubation model is extracted. Age is presented unscaled for clarity.

```
# x axis = partner age, y axis = individual trip duration, incubation only,  
# regression line taken from unscaled model to match x axis
```

```
# extract regression line  
mA_inr<-summary(modavm1_incur)  
age_dat <- plot_model(mA_inr, type = "pred", terms = c("p_age_sq"))
```

```
## Error: Confidence intervals could not be computed.
```

```
age_dat<- data.frame(age_dat$data)
```

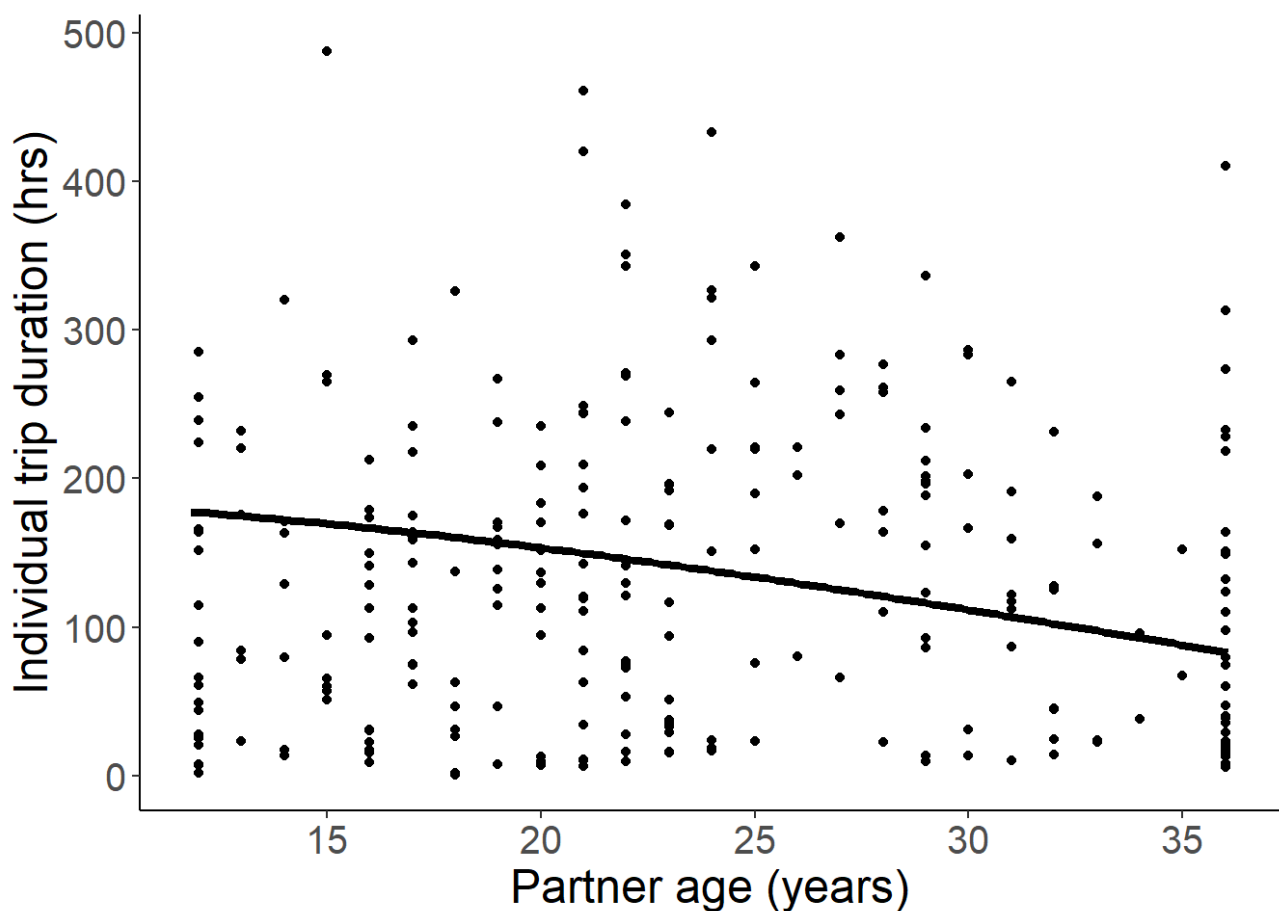
As before, the regression line is squared to account for the transformed response variable in the original model.

```
# non-square root data for plotting
age_dat<- age_dat%>% mutate(age_new = (sqrt(x))) # calculate square root of age
age_dat.unsqr<- data.frame(x=age_dat$x, age_dat$age_new, predicted=age_dat$predicted^2) # untransform response variable
```

The graph is produced using ggplot and the raw data.

```
p_ageincu_graph<-ggplot( aes(x = age_dat.age_new, y = predicted), data = age_dat.
  unsqr)+# regression line
  geom_line(size = 1.5)+
  geom_point(aes(x = p_age, y = no_hours), data = incu_new2)+ # hides data points
  theme_bw(base_size =15) +
  xlab("Partner age (years)")+
  ylab("Individual trip duration (hrs)")+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())+
  scale_x_continuous(breaks=c(10, 15, 20, 25, 30, 35, 40))+
  theme_classic()+
  theme(axis.text = element_text(size = 15))+
  theme(axis.title= element_text(size=18))

p_ageincu_graph
```



Figures 1A and 1 B are combined outside R and labeled as they appear in the paper's main body.

# Figure 2A, B & C

This graph compares the effects of female, male and partner boldness on trip duration during brooding. The three regression lines are extracted individually and used to produce three graphs which are combined together outside R. All these graph used the scaled brooding model.

The regression lines are extracted. Initially the male and female regression lines are extracted together

```
# personality graphs set up

# X axis = boldness score focal female, focal male and partner, Y axis =individual trip duration/ no hours, brooding only
# regression line taken from scaled model

mA_brsq<-summary(modavm1_brood) #summary brooding model

# extract regression line for pers:sex, pers:sex model averaged coefficients not used
brDatpers <- plot_model(mA_brsq, type = "pred", terms = c("pers_sc", "sex"))
brDatpers <- data.frame(brDatpers$data)

#extract regression line for p_pers
brDatp_pers <- plot_model(mA_brsq, type = "pred", terms = c("p_pers_sc"))
brDatp_pers <- data.frame(brDatp_pers$data)
```

The data are squared.

```
# Compute the non-square-rooted pers data for plotting
brpers_unsqr<- data.frame(x=brDatpers$x, predicted=brDatpers$predicted^2,se=brDatpers$std.error, cih = brDatpers$conf.high^2, cil =brDatpers$conf.low^2, group = brDatpers$group, group_col =brDatpers$group_col)
brp_pers_unsqr<- data.frame(x=brDatp_pers$x, predicted=brDatp_pers$predicted^2, se=brDatp_pers$std.error, cih = brDatp_pers$conf.high^2, cil =brDatp_pers$conf.low^2)
```

The male and female regression lines are separated.

```
# male and female data are subsetting
brpers_unsqr$group<- as.factor(brpers_unsqr$group)
brpers_unsqr_males<-subset(brpers_unsqr, group == "Male")
brpers_unsqr_females<-subset(brpers_unsqr, group == "Female")
```

Three graphs are produced. As per the figure heading in the paper's body, the axes are limited to exclude one outlier for clarity. This results in a warning message. The graphs are combined and labeled outside of R for inclusion in the paper.

```

#separate graphs for three lines
#p-pers
pers_graph_p_pers<-ggplot(aes(x = x, y = predicted), data = brp_pers_unsqr) + # regression line for pers variable
  geom_line(size = 1.5, colour = "black")+
  geom_ribbon (fill= "grey", alpha=0.3,aes(ymin=cil,ymax=cih))+
  geom_point(aes(x = p_pers_sc, y = no_hours), data = brood_new2) +
  theme_bw(base_size =15) +
  xlab("Scaled Boldness Score")+
  ylab("Individual trip duration (hrs)")+
  ylim (0, 200)+
  theme_classic()+
  theme(axis.text = element_text(size = 15))+
  theme(axis.title= element_text(size=18))

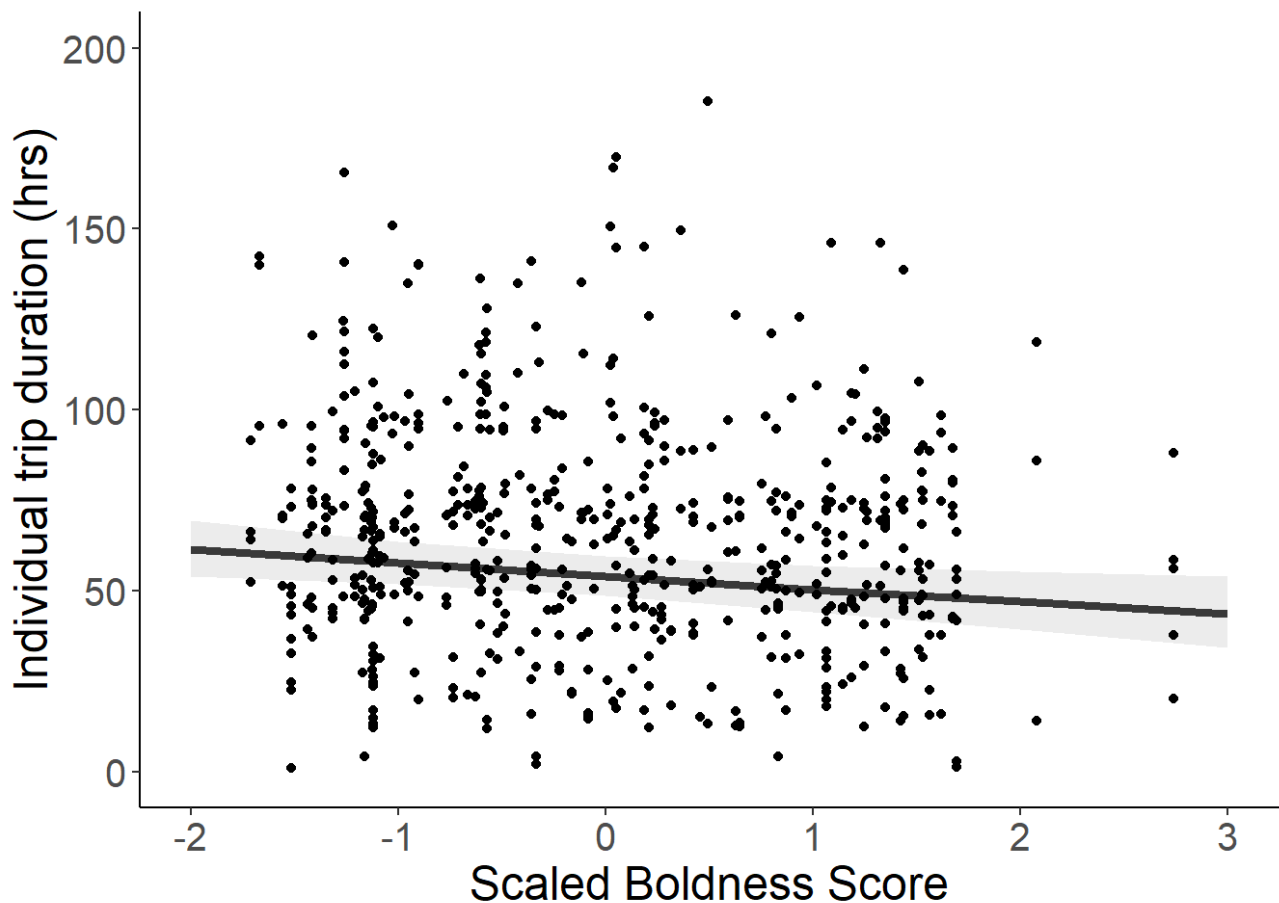
pers_graph_p_pers

```

```

## Warning: Removed 1 rows containing missing values (geom_point).

```



```

#females
pers_graph_f<-ggplot(aes(x = x, y = predicted), data = brpers_unsqr) + # regression
  line for pers variable
  geom_line(aes(x = x, y = predicted), data = brpers_unsqr_females, size =1.5, co
    lour = "black") + # regression line for female variable
  geom_ribbon (fill= "grey", alpha=0.25,data = brpers_unsqr_females, aes(ymin=cil,ymax=cih))+
  geom_point(aes(x = pers_sc, y = no_hours), data = brood_new2) +
  theme_bw(base_size =15) +
  xlab("Scaled Boldness Score")+
  ylab("Individual trip duration (hrs)")+
  ylim (0, 200)+
  theme_classic()+
  theme(axis.text = element_text(size = 15))+
  theme(axis.title= element_text(size=18))

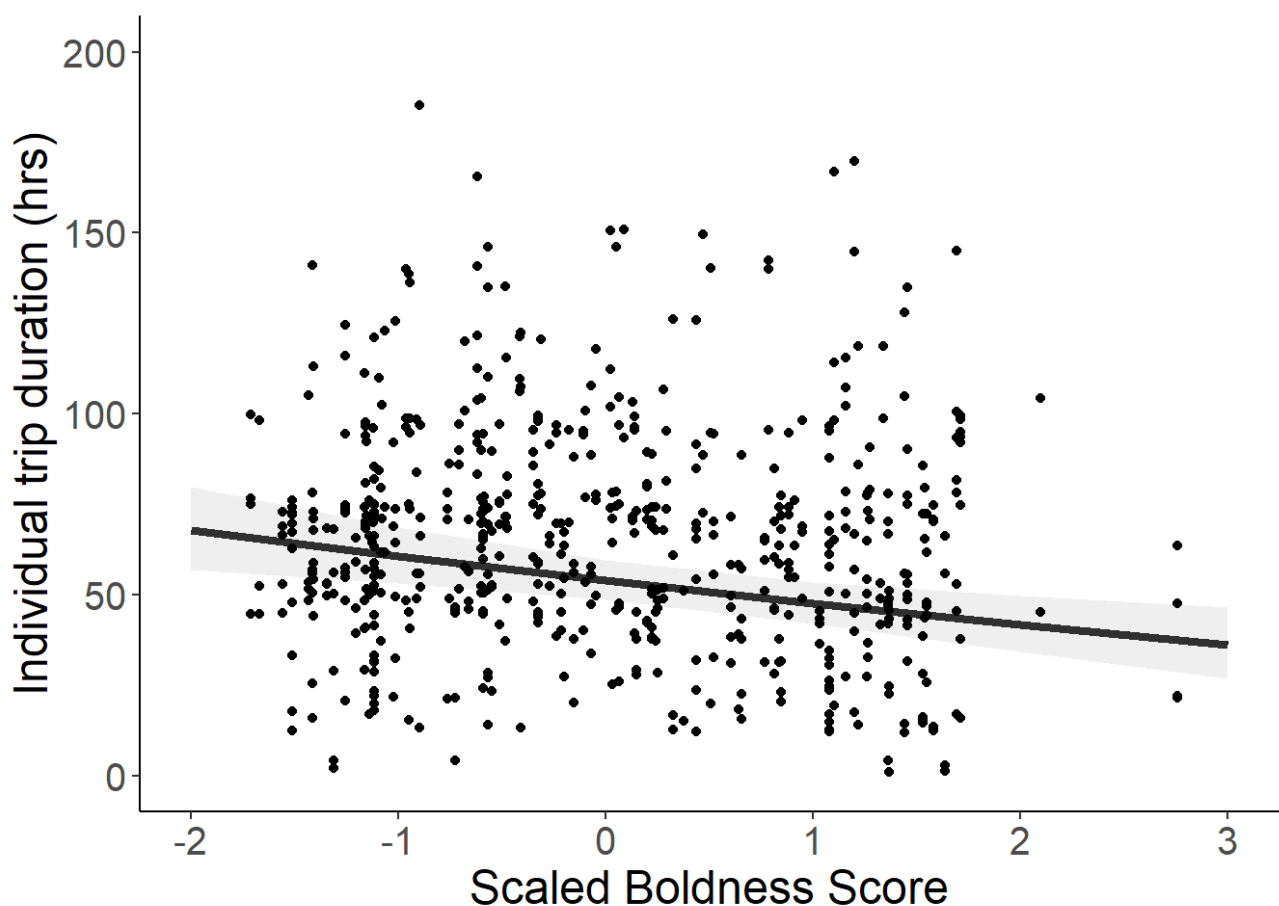
pers_graph_f

```

```

## Warning: Removed 1 rows containing missing values (geom_point).

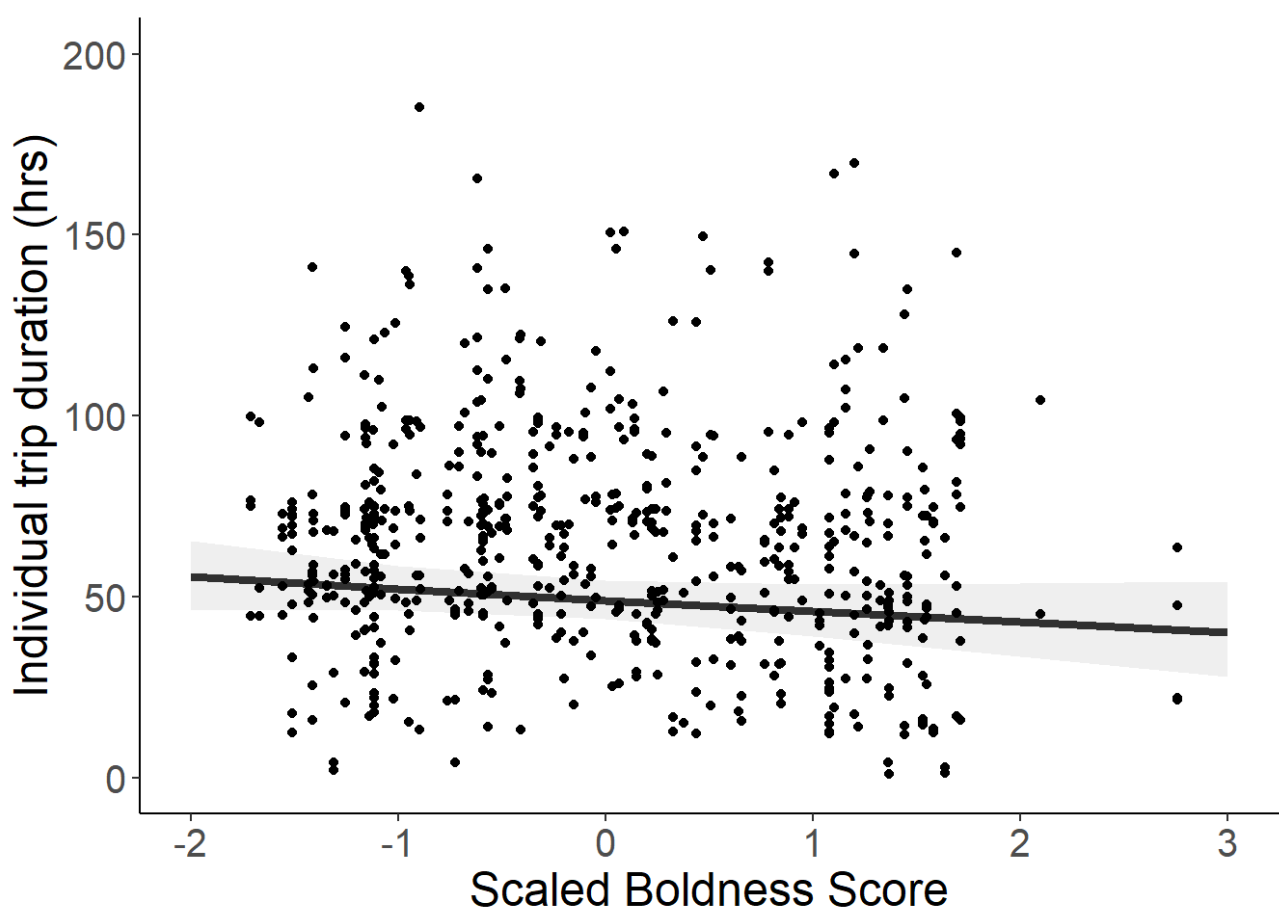
```



```
#males
pers_graph_m<-ggplot(aes(x = x, y = predicted), data = brpers_unsqr) + # regression
  line for pers variable
  geom_line(aes(x = x, y = predicted), data = brpers_unsqr_males, size =1.5, color = "black") +
  geom_ribbon (fill= "grey", alpha=0.25,data = brpers_unsqr_males, aes(ymin=cil,y
    max=cih))+
  geom_point(aes(x = pers_sc, y = no_hours), data = brood_new2) +
  theme_bw(base_size =15) +
  xlab("Scaled Boldness Score")+
  ylab("Individual trip duration (hrs)")+
  ylim (0, 200)+
  theme_classic()+
  theme(axis.text = element_text(size = 15))+
  theme(axis.title= element_text(size=18))

pers_graph_m
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



## Figure 3A & B

This graph demonstrates the relationship between individual trip duration and partner's previous trip duration, which is indicative of coordination strength within the population. This code uses the unscaled version of both the incubation and brooding models.



The regression lines for partners previous trip duration are extracted individually from the incubation and brooding models.

```
# x axis = partner previous trip duration (deviation from average trip duration), y axis = individual trip duration/ no hours
# regression lines taken from unscaled models to match x axis

# getting regression lines from models

mA_inr<-summary(modavm1_incur) # summary incu model
mA_brsq<-summary(modavm1_broodr) #summary brooding model

inDat <- plot_model(mA_inr, type = "pred", terms = c("ppb_ave_diff")) # extract regression line for incubation, identify predictor variable of interest
```

```
## Error: Confidence intervals could not be computed.
```

```
inDat <- data.frame(inDat$data)

brDatsq <- plot_model(mA_brsq, type = "pred", terms = c("ppb_ave_diff")) # extract regression line for brooding, identify predictor variable of interest
brDatsq <- data.frame(brDatsq$data)
```

This code starts the process of making incubation and brooding appear in a logical order in the graph (with incubation on the left). if this portion of the code is run multiple times the graph will appear with all data points under 'brooding'.

```
# start process of making incubation and brooding appear on the graph in a logical order
total_df4$breed_stage<- as.character(total_df4$breed_stage)

for (a in 1:(nrow(total_df4))) {
  if (total_df4$breed_stage[a] == "incu")
  {total_df4$breed_stage[a] <- "Incubation"}
  else {total_df4$breed_stage[a] <- "Brooding"}
}

total_df4<-total_df4%>% arrange(total_df4) %>%
  mutate(breed_stage = factor(breed_stage, levels=c("Incubation", "Brooding")))
```

As before, the dependent variable is squared to account for its previous transformation.

```
# Compute the non-square-rooted data for plotting
inDatr.unsqr<- data.frame(x=inDat$x, predicted=inDat$predicted^2)
brDatsq.unsqr<- data.frame(x=brDatsq$x, predicted=brDatsq$predicted^2)
```

This code finishes the process of labeling the data so they appear in a logical order.

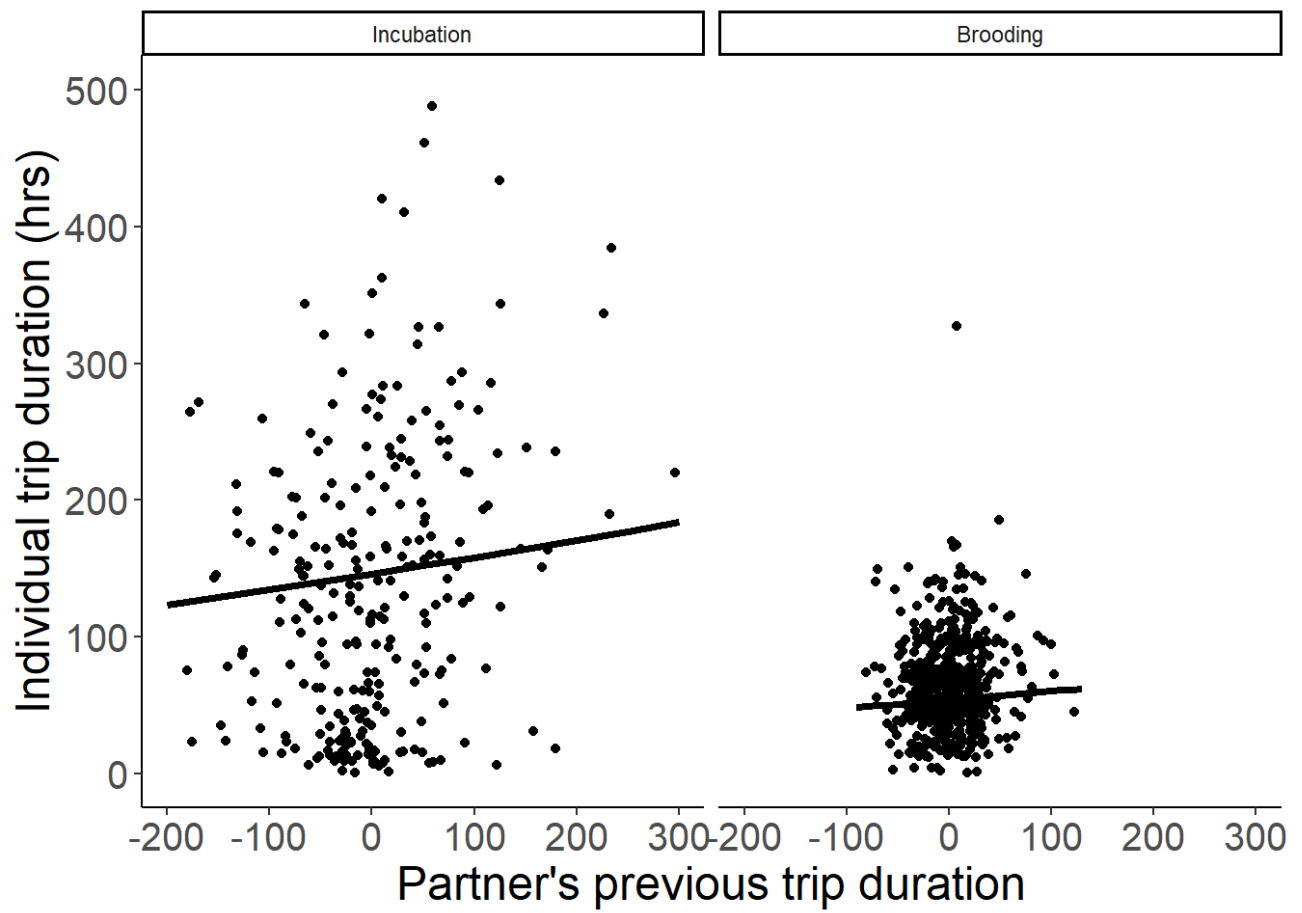
```
# Create a single data frame with both predictions, labeled by the "breed_stage"
  factor
brDatsq.unsqr $ breed_stage<- "Brooding"
inDatr.unsqr $breed_stage <- "Incubation"
all_preds<- rbind(inDatr.unsqr, brDatsq.unsqr)

#finish process of making incubation and brooding appear in a logical order
all_preds$breed_stage <- factor(all_preds$breed_stage, levels=c("Incubation", "Brooding"), ordered=TRUE) # ordered so that "incu" panel appears on left
```

The final graph is produced using the raw data and ggplot. Some aesthetic edits (e.g. adding A & B) are added outside R.

```
ppb_graph_all<-ggplot( aes(x = x, y = predicted), data = all_preds) + # regression
  line
  geom_line(size = 1.25)+
  geom_point(aes(x = ppb_ave_diff, y = no_hours), data = total_df4) + # raw data,
    not using square root
  theme_bw(base_size =15) +
  xlab("Partner's previous trip duration")+
  ylab("Individual trip duration (hrs)")+
  facet_wrap(~breed_stage)+
  ylim (0, 500)+
  theme_classic()+
  theme(axis.text = element_text(size = 15))+
  theme(axis.title= element_text(size=18))

ppb_graph_all
```



All aspects of the three graphs have now been created.