Supplemental Figure 1

Larsen & Shirey

Updated 7-Dec-2020; separated from reanalysis 25-Nov-2020

*

Create panels for Supplemental Figure 1

In this code chunk, we previously used lm.model$call references in geom_smooth, which created a string of outputs showing the calls. The current simple lm still includes geom_smooth output text, which would be nice to suppress if we can figure that out.

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.3     v dplyr   1.0.1
## v tidyr   1.1.1     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(ggplot2)
library(ggExtra)
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
library(ggpubr)
load("data/occurrences_FricAnalysis.RData")
load("data/phenometrics.RData")
reanalysis<-read_csv("outputs/LarsenShirey_SuppTable2.csv")
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

```
## Parsed with column specification:
## cols(
##   X1 = col_double(),
##   name_resultsfile = col_character(),
##   region = col_character(),
##   phenometric = col_character(),
##   indep.variable = col_character(),
##   Reanalysis_sign = col_double(),
##   Reanalysis_p = col_double(),
##   Reanalysis_coef = col_double(),
##   Fric_SR_sign = col_double(),
##   Fric_SR_p = col_double(),
##   Fric_SR_coef = col_double(),
##   Fric_RR_sign = col_double(),
##   Fric_RR_p = col_double(),
##   Fric_RR_coef = col_double()
## )
```

```
datasets<-pheno.data %>% group_by(name, region) %>% tally()
datasets<-datasets %>% mutate(set=paste(name,region,sep="-"))
```

*

Create Supplemental Figure 1

```
#################### SUPPLEMENTAL FIGURE 1


## PLOT PARAMETERS
m0 <- 0.5 #plot margins
negslope <- "blue"
posslope <- "darkgreen"
flatslope <- "black"
singles <- "red"


#Filter data to reanalyzed datasets and use Fric et al. method of defining Onset & Termination
#Keep all data but label records used as onset and offset
fric.data<-fricdata %>%
  filter(paste(name, region,sep="-")%in%datasets$set) %>%
  group_by(name,region, rndLat) %>%
  mutate(onset=min(SuccDay), term=max(SuccDay)) %>%
  add_tally() %>%
  mutate(Group=ifelse(n==1,1,0)) #, onsetobs=ifelse(onset==SuccDay,1,0), termobs=ifelse(term==SuccDay,1,0))

#################### SUPPLEMENTAL FIGURE 2 COL 1-2:
##Col 1 - Fric analysis: DOY ~ latitude
##Col 2 - Fric analysis: residuals(residuals(DOY~year)~altitude) ~ latitude

sup1a<-list()
sup1b<-list()
for(rowi in 1:nrow(datasets)) {
    #Filter Fric data
    speciesdata<-  filter(fric.data, name==datasets$name[rowi], region==datasets$region[rowi])
    onsetdata<-  filter(speciesdata, onset==SuccDay)
    termdata<-  filter(speciesdata, term==SuccDay)
    #Column 1
    #Fric onset parameters
    fric.onset.lm<-lm(onset~rndLat, data=onsetdata)
    fric.term.lm<-lm(term~rndLat, data=termdata)
    fric.onset.coef<-summary(fric.onset.lm)$coefficients
    fric.term.coef<-summary(fric.term.lm)$coefficients

    #Column 2
    #regression of residuals for onset
```

```
    fric.onset.alt<-lm(onset~alt, data=onsetdata)
    onsetdata$alt.resid<-summary(fric.onset.alt)$residuals
    fric.onset.yralt<-lm(alt.resid~year, data=onsetdata)
    onsetdata$yralt.resid<-summary(fric.onset.yralt)$residuals
    fric.onset.resid<-lm(yralt.resid~rndLat, data=onsetdata)
    fric.onset.resid.coef<-summary(fric.onset.resid)$coefficients

    #regression of residuals for termination
    fric.term.alt<-lm(term~alt, data=termdata)
    termdata$alt.resid<-summary(fric.term.alt)$residuals
    fric.term.yralt<-lm(alt.resid~year, data=termdata)
    #We add 200 here because its the easiest way *FOR US* to space out the onset & termination lines in column 2
    termdata$yralt.resid<-summary(fric.term.yralt)$residuals+ 200
    fric.term.resid<-lm(yralt.resid~rndLat, data=termdata)
    fric.term.resid.coef<-summary(fric.term.resid)$coefficients

    #set parameters for Column 1 based on LM results
    onsetline<-ifelse(fric.onset.coef[2,4]<0.05,"dashed","dotted")
    onsetcolor<-ifelse(fric.onset.coef[2,4]<0.05,ifelse(fric.onset.coef[2,1]>0,posslope,negslope),flatslope)

    termline<-ifelse(fric.term.coef[2,4]<0.05,"dashed","dotted")
    termcolor<-ifelse(fric.term.coef[2,4]<0.05,ifelse(fric.term.coef[2,1]>0,posslope,negslope),flatslope)

    # For 2 species, our LM here does not produce results consistent with Fric et al. so we manually change the line paramet
ers. there is probably ba more elegant way we could incorporate this into code by comparing lm results to fric results table
    if(rowi==16) {onsetcolor <- negslope; onsetline <- "dashed"}
    if(rowi==20) {termcolor <- posslope; termline <- "dashed"}

    mytitle<-paste(datasets$name[rowi])
    #set xmin to 35, unless there are data south of that latitude
    xmin<-ifelse(min(speciesdata$rndLat)<35,min(speciesdata$rndLat),35)
    #Set top and bottom margins for odd (top of page) and even (bottom of page) rows
    t1<-ifelse((rowi %% 2) == 0,0.5,2.8)
    b1<-ifelse((rowi %% 2) == 0,2.8,0.5)
    #Create column 1 plot
    sup1a[[rowi]] <- ggplot(speciesdata, aes(x=rndLat, y=SuccDay, color=as.factor(Group))) +
      geom_point(aes(color=as.factor(Group)), shape=3) +
      geom_point(data=onsetdata, aes(x=rndLat, y=SuccDay, color=as.factor(Group))) +
      geom_point(data=termdata, aes(x=rndLat, y=SuccDay, color=as.factor(Group))) +
      geom_segment(data=filter(speciesdata, onset==SuccDay | term==SuccDay), aes(x=rndLat, y=onset, xend=rndLat, yend=term))
+
```

```
      geom_smooth(data=onsetdata, aes(x=rndLat,y=SuccDay),  method="lm", linetype=onsetline, color=onsetcolor, fill=onsetcol
or) +
      geom_smooth(data=termdata, aes(x=rndLat,y=SuccDay), method="lm", linetype=termline, color=termcolor, fill=termcolor) +
      scale_color_manual(values=c("black","red")) +
      xlim(xmin,max(fric.data$rndLat)) + ylim(min(fric.data$SuccDay),max(fric.data$SuccDay)) +
      theme_light() +   theme(legend.position="none") +
      theme(plot.title = element_text(size=11,face = "italic"), axis.title=element_text(size=10), plot.margin = margin(t1, m
0, b1, 2, "cm")) +
      labs(x="Latitudinal Band", y="Day of Year (DOY)", title=mytitle)
    rm(onsetline,onsetcolor,termline,termcolor)

    #Supplemental Figure 1 Column 2
    #set parameters for Column 2 based on LM results
    onsetline<-ifelse(fric.onset.resid.coef[2,4]<0.05,"dashed","dotted")
    onsetcolor<-ifelse(fric.onset.resid.coef[2,4]<0.05,ifelse(fric.onset.resid.coef[2,1]>0,posslope,negslope),flatslope)

    termline<-ifelse(fric.term.resid.coef[2,4]<0.05,"dashed","dotted")
    termcolor<-ifelse(fric.term.resid.coef[2,4]<0.05,ifelse(fric.term.resid.coef[2,1]>0,posslope,negslope),flatslope)
    #Set top and bottom margins for odd (top of page) and even (bottom of page) rows
    t2<-ifelse((rowi %% 2) == 0,0.5,2.8)
    b2<-ifelse((rowi %% 2) == 0,2.8,0.5)
    #Create column 2 plot
    #sanity check: onset alone
     test<-ggplot(onsetdata, aes(x=rndLat, y=yralt.resid)) +
      geom_point(data=onsetdata,aes(x=rndLat, y=yralt.resid, color=as.factor(Group)), shape=24) +
      geom_point(data=filter(onsetdata, Group==1),aes(x=rndLat, y=yralt.resid, color=as.factor(Group)), fill="red",shape=24)
+
      #geom_point(data=termdata,aes(x=rndLat, y=yralt.resid, color=as.factor(Group), fill=as.factor(Group)), shape=25) +
      scale_color_manual(values=c("black","red")) +
      geom_smooth(data=onsetdata, aes(x=rndLat,y=yralt.resid),  method="lm", linetype=onsetline, color=onsetcolor, fill=onse
tcolor) +
      #geom_smooth(data=termdata, formula = str(fric.term.resid$call), method="lm", linetype=termline, color=termcolor, fill
=termcolor) +
      theme_light() +   theme(legend.position="none") +
      theme(axis.title=element_text(size=10), plot.margin = margin(t2, m0, b2,m0, "cm")) +
      labs(x="Latitudinal Band", y="Residuals from Onset regressions",title="")
     #The full plot
    sup1b[[rowi]] <- ggplot(onsetdata, aes(x=rndLat, y=yralt.resid)) +
      geom_point(data=onsetdata,aes(x=rndLat, y=yralt.resid, color=as.factor(Group)), shape=24) +
      geom_point(data=filter(onsetdata, Group==1),aes(x=rndLat, y=yralt.resid, color=as.factor(Group)), fill="red",shape=24)
+             geom_point(data=termdata,aes(x=rndLat, y=yralt.resid, color=as.factor(Group)), shape=25) +
```

```
      geom_point(data=filter(termdata, Group==1),aes(x=rndLat, y=yralt.resid, color=as.factor(Group)), fill="red",shape=25)
 +
      scale_color_manual(values=c("black","red")) +
      geom_smooth(data=onsetdata, aes(x=rndLat,y=yralt.resid),  method="lm", linetype=onsetline, color=onsetcolor, fill=onse
tcolor) +
      geom_smooth(data=termdata, aes(x=rndLat,y=yralt.resid), method="lm", linetype=termline, color=termcolor, fill=termcolo
r) +
      theme_light() +   theme(legend.position="none") +
      theme(axis.title=element_text(size=10), plot.margin = margin(t2, m0, b2,m0, "cm")) +
      ylim(-100,300) +
      labs(x="Latitudinal Band", title="") +
        # Custom the Y scales & Add a second axis and specify its features
  scale_y_continuous(name = "Onset Phenology Shift",
    sec.axis = sec_axis( trans=~.-200, name="Termination Phenology Shift"))

}


##################### SUPPLEMENTAL FIGURE 2 COL 3:
##Col 3: Reanalysis: DOY ~ latitude + year, displaying latitude results

sup1c<-list()

for(rowi in 1:nrow(datasets)) {
    #Filter reanalysis data
  pheno.rowi<-pheno.data %>%
    filter(name==datasets$name[rowi], region==datasets$region[rowi])
  #model  for onset
  onset.model<-lm(onset~rndLat+year, data=pheno.rowi)
  #model for termination
  term.model<-lm(term~rndLat+year, data=pheno.rowi)

  onset.params<-filter(reanalysis,name_resultsfile==datasets$name[rowi], region==datasets$region[rowi],indep.variable=="lati
tude",phenometric=="onset")
  term.params<-filter(reanalysis,name_resultsfile==datasets$name[rowi], region==datasets$region[rowi],indep.variable=="latit
ude",phenometric=="termination")


    #set parameters based on LM results
    onsetline<-ifelse(onset.params$Reanalysis_p<0.05,"dashed","dotted")
    onsetcolor<-ifelse(onset.params$Reanalysis_p<0.05,ifelse(onset.params$Reanalysis_coef>0,posslope,negslope),flatslope)
```

```
    termline<-ifelse(term.params$Reanalysis_p<0.05,"dashed","dotted")
    termcolor<-ifelse(term.params$Reanalysis_p<0.05,ifelse(term.params$Reanalysis_coef>0,posslope,negslope),flatslope)

    #Set top and bottom margins for odd (top of page) and even (bottom of page) rows
    t3<-ifelse((rowi %% 2) == 0,0.5,2.8)
    b3<-ifelse((rowi %% 2) == 0,2.8,0.5)

    #Create plot

    sup1c[[rowi]] <- ggplot(pheno.rowi, aes(x=rndLat, y=onset)) +
      geom_point(data=pheno.rowi,aes(x=rndLat, y=onset),shape=24) +             geom_point(data=pheno.rowi,aes(x=rndLat, y=
term),shape=25) +
      geom_smooth(data=pheno.rowi, aes(x=rndLat, y=onset),  method="lm", linetype=onsetline, color=onsetcolor, fill=onsetcol
or) +
      geom_smooth(data=pheno.rowi, aes(x=rndLat, y=term), method="lm", linetype=termline, color=termcolor, fill=termcolor) +
      theme_light() +   theme(legend.position="none") +
      ylim(30,330) + xlim(50,70) +
      theme(plot.title = element_text(size=11,face = "italic"), axis.title=element_text(size=10), plot.margin = margin(t3, 2
, b3, m0, "cm")) +
      labs(x="Latitudinal Band", y="Day of Year (DOY)", title="")
      #For the published figure, we used these geom_smooths. Here they have been commented out because they cause many messa
ges such as:  language lm(formula = onset ~ rndLat, data = onsetdata); language lm(formula = term ~ rndLat, data = termdata)
      #This change does not affect the final figure.
      #geom_smooth(data=pheno.rowi, formula = str(onset.model$call), aes(x=rndLat, y=onset),  method="lm", linetype=onsetlin
e, color=onsetcolor, fill=onsetcolor) +
      #geom_smooth(data=pheno.rowi, formula = str(term.model$call),  aes(x=rndLat, y=term), method="lm", linetype=termline,
 color=termcolor, fill=termcolor) +
}
```

*

A small break between creating the panels and assmembling Supplemental Figure 1. The chunk below combines the panels into Supplemental Figure 1.

```
#### COMBINE PANELS FOR SUPPLEMENTAL FIGURE 1
(p1<-grid.arrange(sup1a[[1]],sup1b[[1]],sup1c[[1]],sup1a[[2]],sup1b[[2]],sup1c[[2]],nrow = 2))
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
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## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```

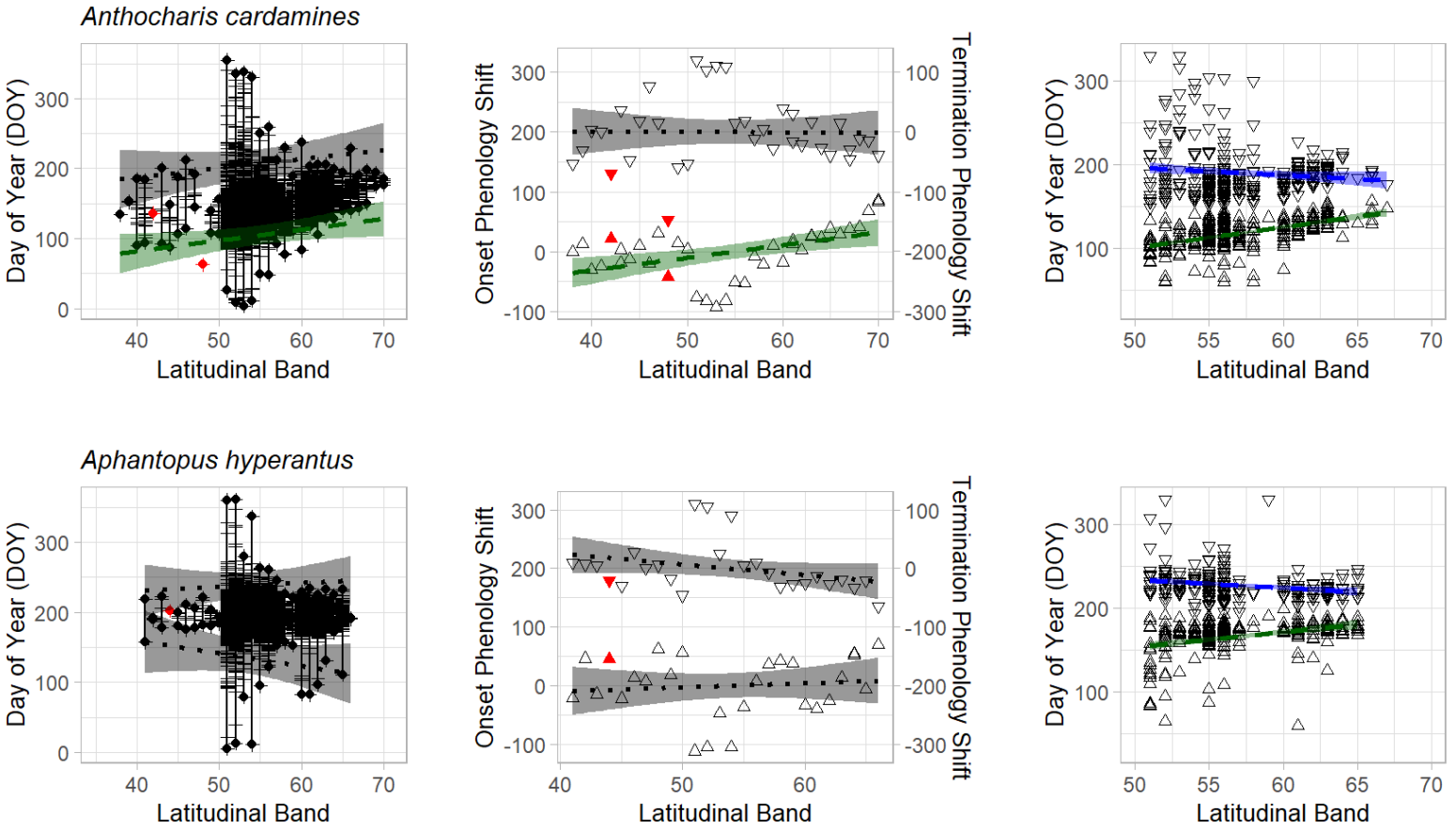
Anthocharis cardamines
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Aphantopus hyperantus

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p2<-grid.arrange(sup1a[[3]],sup1b[[3]],sup1c[[3]],sup1a[[4]],sup1b[[4]],sup1c[[4]],nrow = 2))
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
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## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```
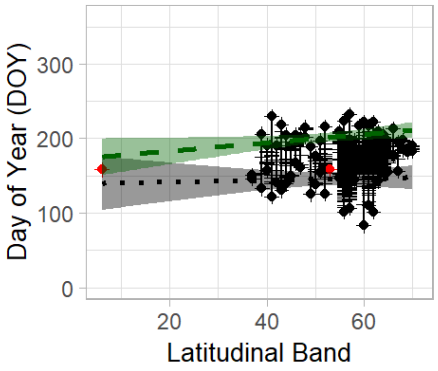
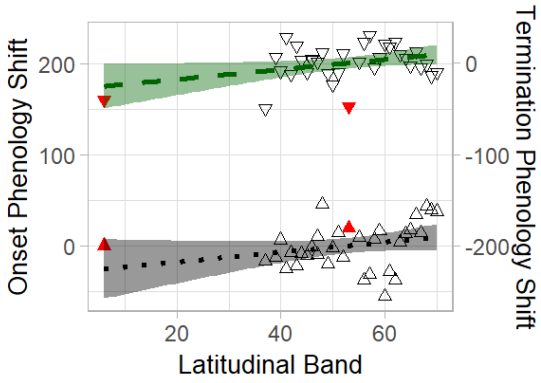
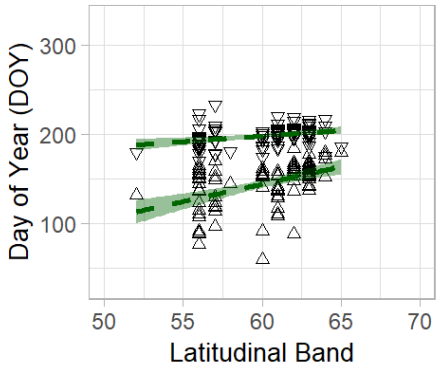
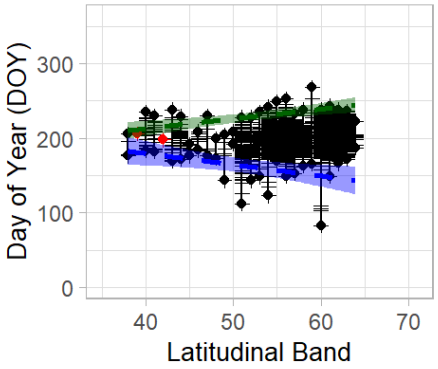

Aporia crataegi

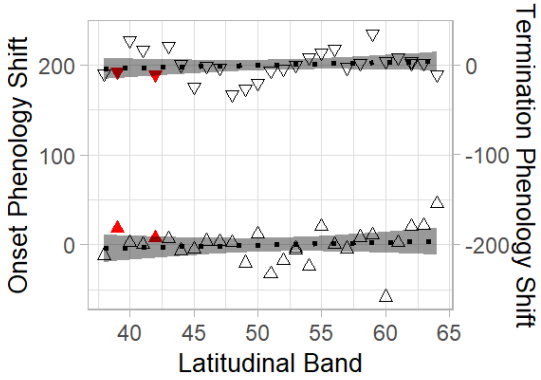


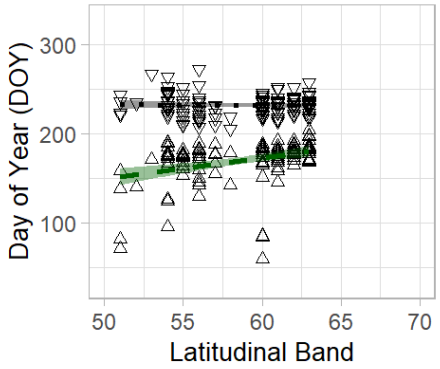




Argynnis adippe





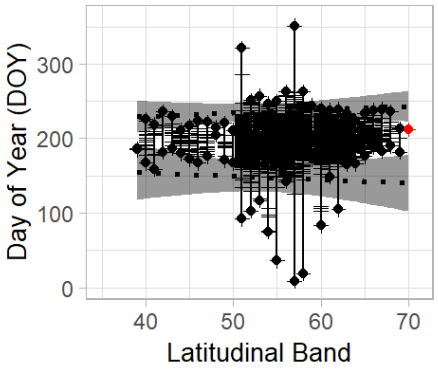


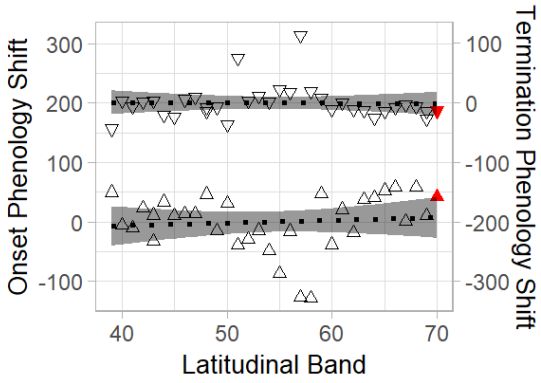
```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

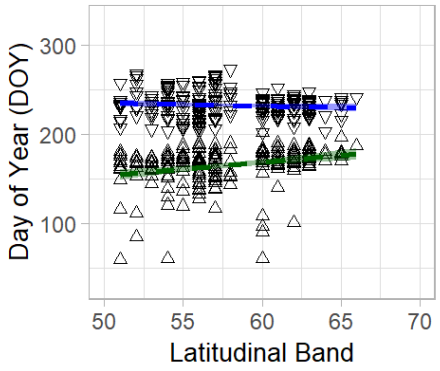
```
(p3<-grid.arrange(sup1a[[5]],sup1b[[5]],sup1c[[5]],sup1a[[6]],sup1b[[6]],sup1c[[6]],nrow = 2))
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```

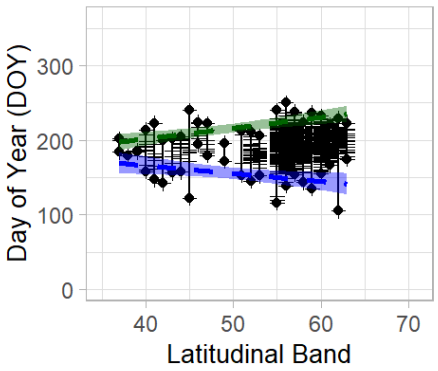
Argynnis aglaja

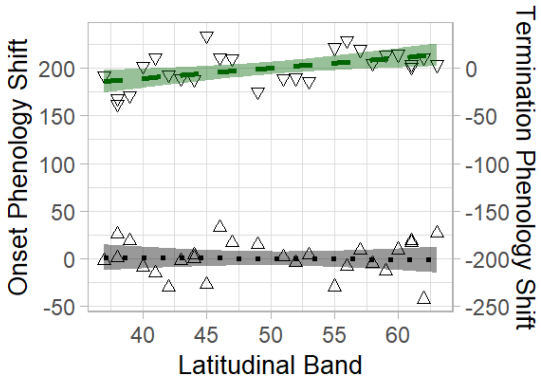


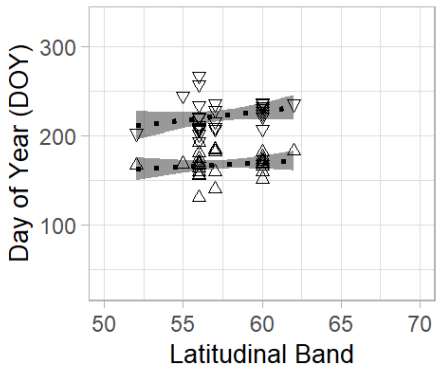




Argynnis niobe



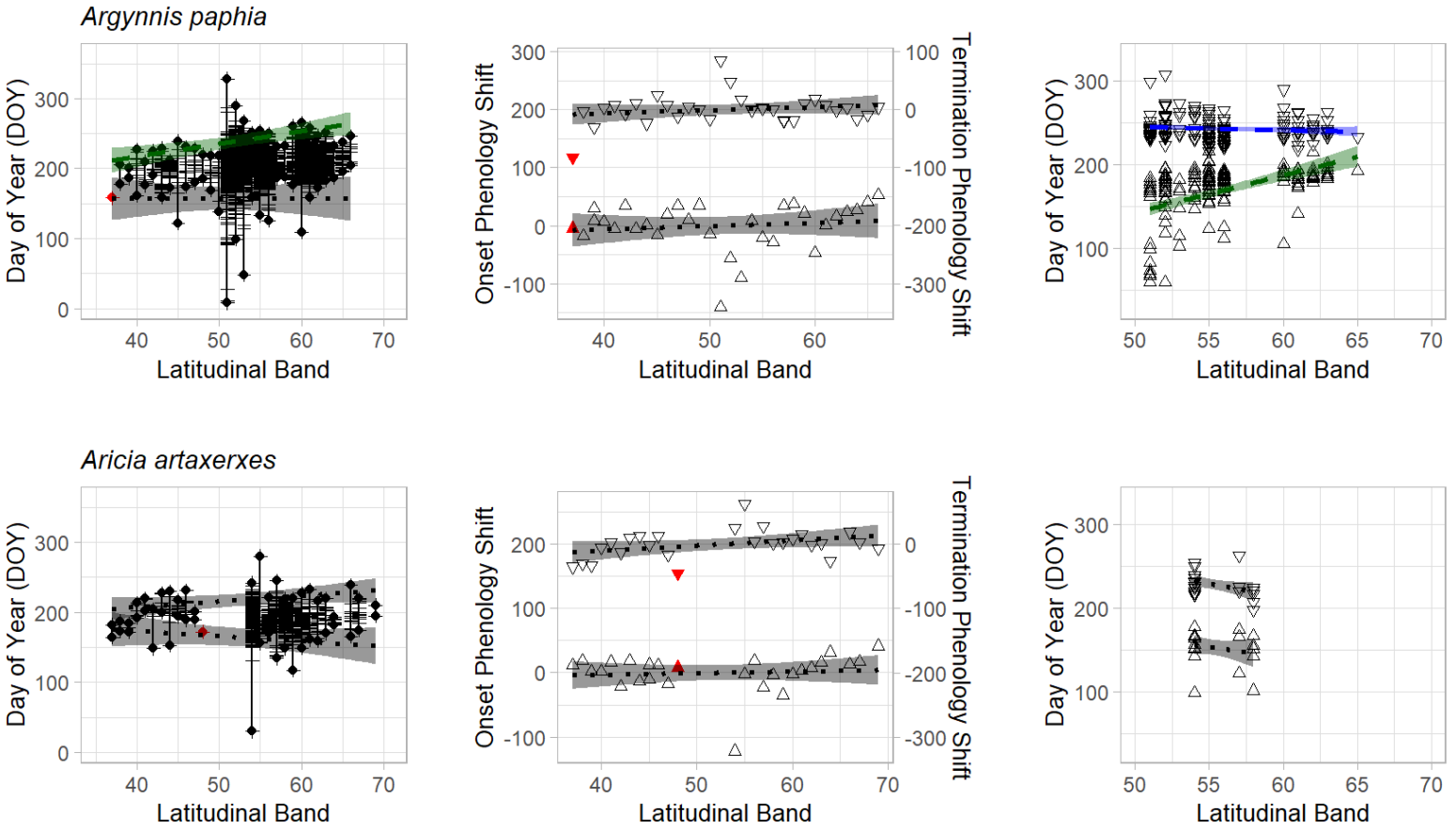




```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p4<-grid.arrange(sup1a[[7]],sup1b[[7]],sup1c[[7]],sup1a[[8]],sup1b[[8]],sup1c[[8]],nrow = 2))
```

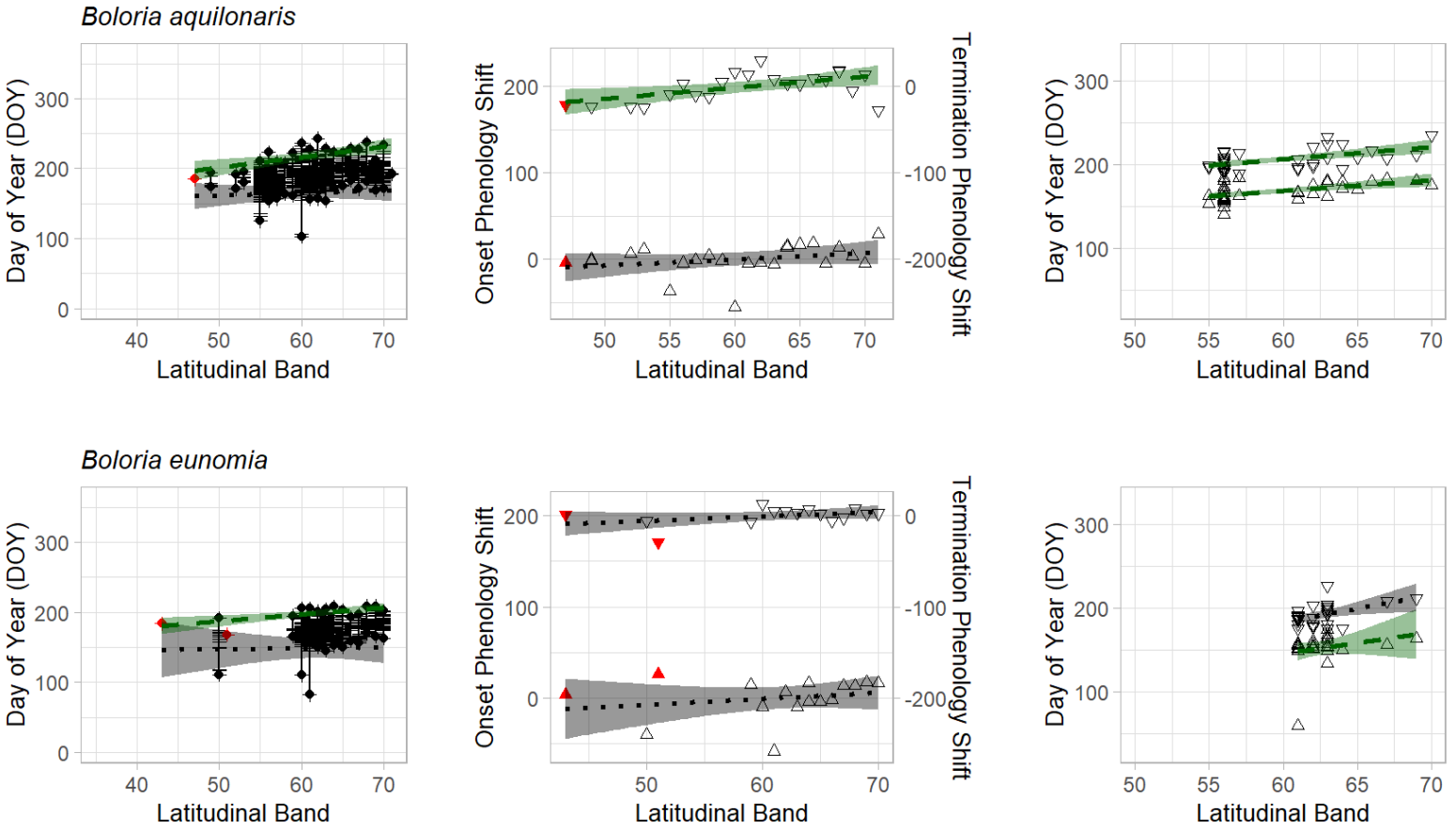
```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```


Argynnis paphia
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Aricia artaxerxes

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p5<-grid.arrange(sup1a[[9]],sup1b[[9]],sup1c[[9]],sup1a[[10]],sup1b[[10]],sup1c[[10]],nrow = 2))
```

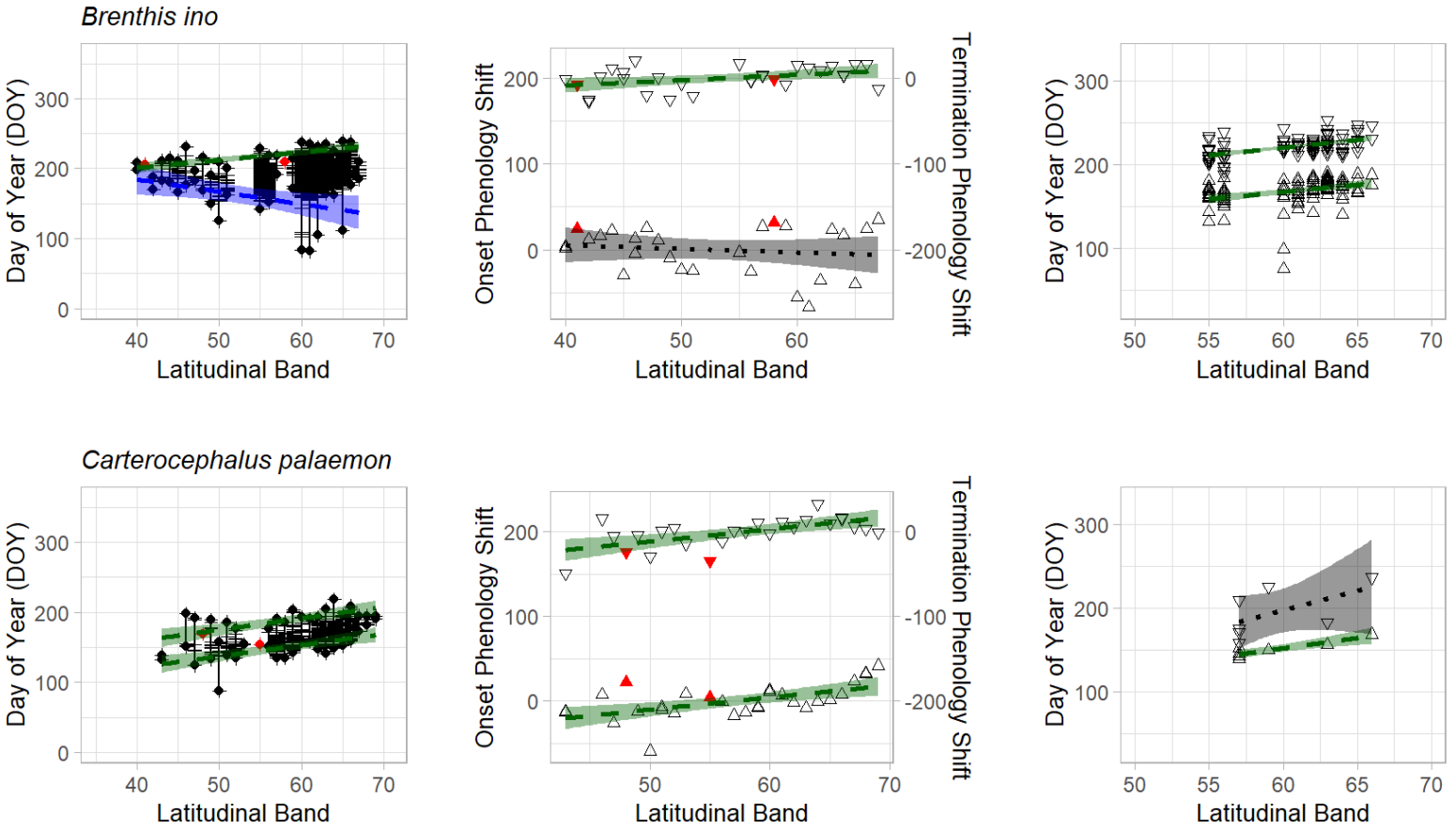
```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```


Boloria aquilonaris
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Boloria eunomia

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p6<-grid.arrange(sup1a[[11]],sup1b[[11]],sup1c[[11]],sup1a[[12]],sup1b[[12]],sup1c[[12]],nrow = 2))
```

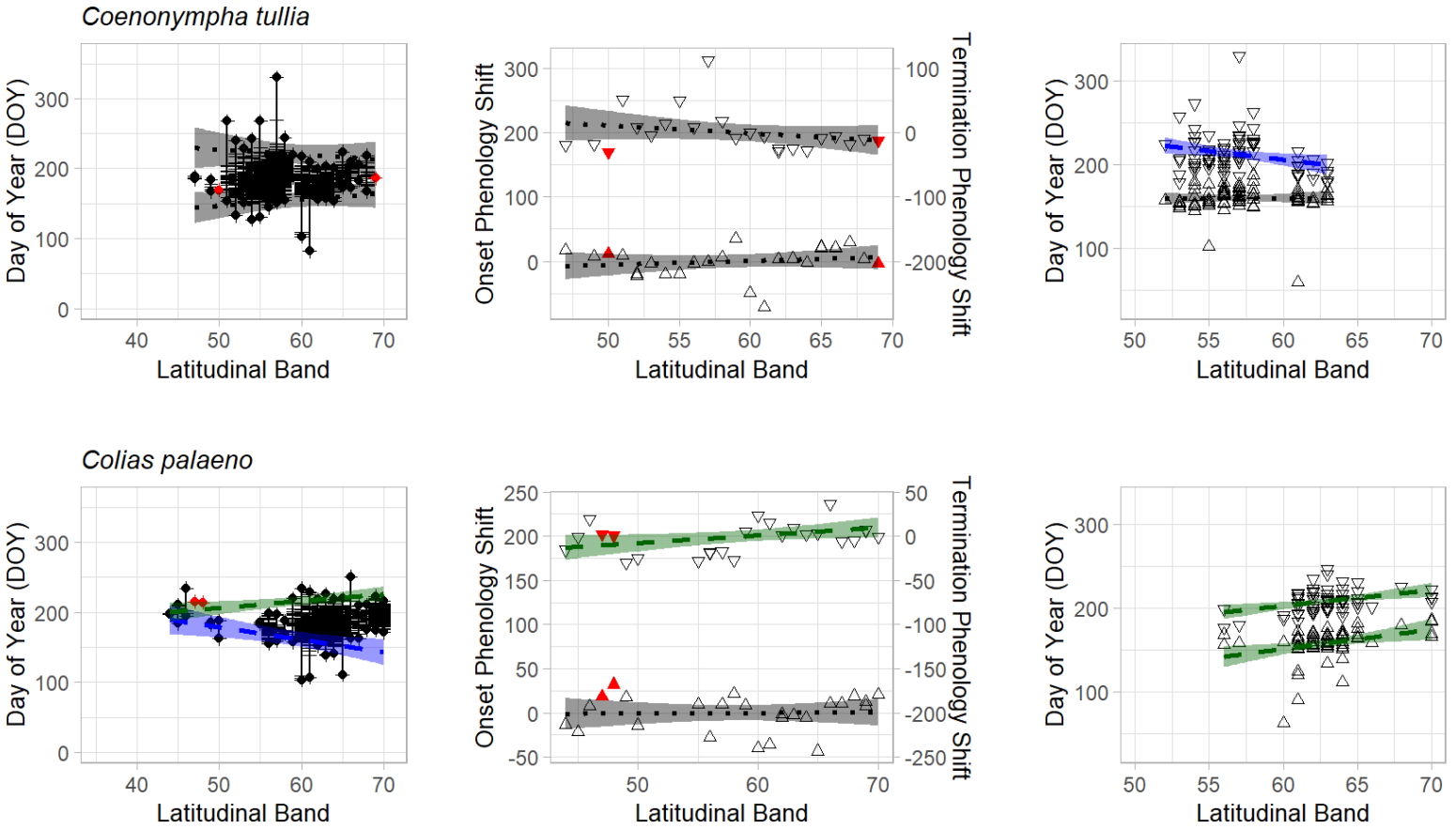
```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```


Brenthis ino
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Carterocephalus palaemon

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p7<-grid.arrange(sup1a[[13]],sup1b[[13]],sup1c[[13]],sup1a[[14]],sup1b[[14]],sup1c[[14]],nrow = 2))
```

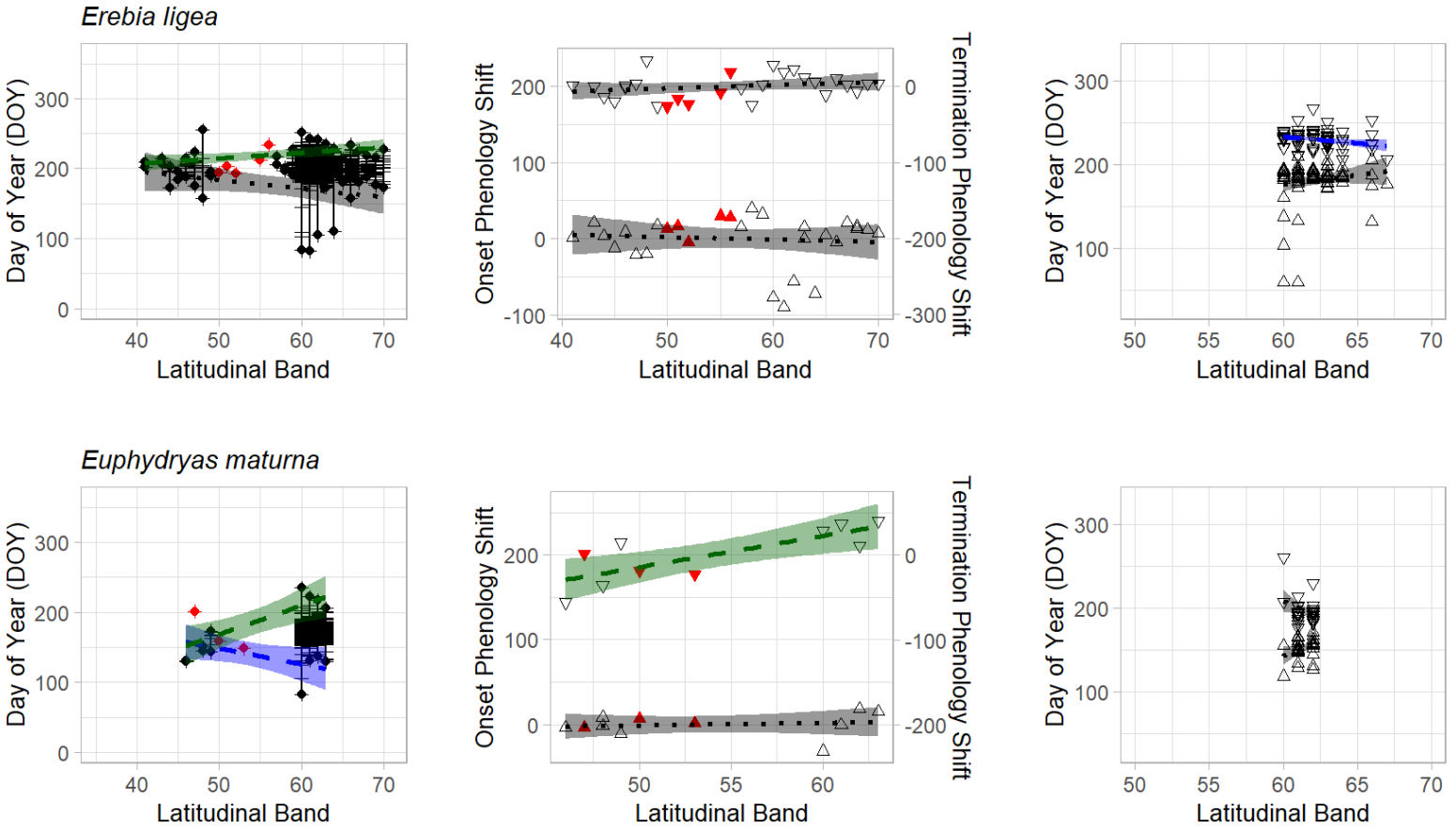
```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```


Coenonympha tullia
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Colias palaeno

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p8<-grid.arrange(sup1a[[15]],sup1b[[15]],sup1c[[15]],sup1a[[16]],sup1b[[16]],sup1c[[16]],nrow = 2))
```

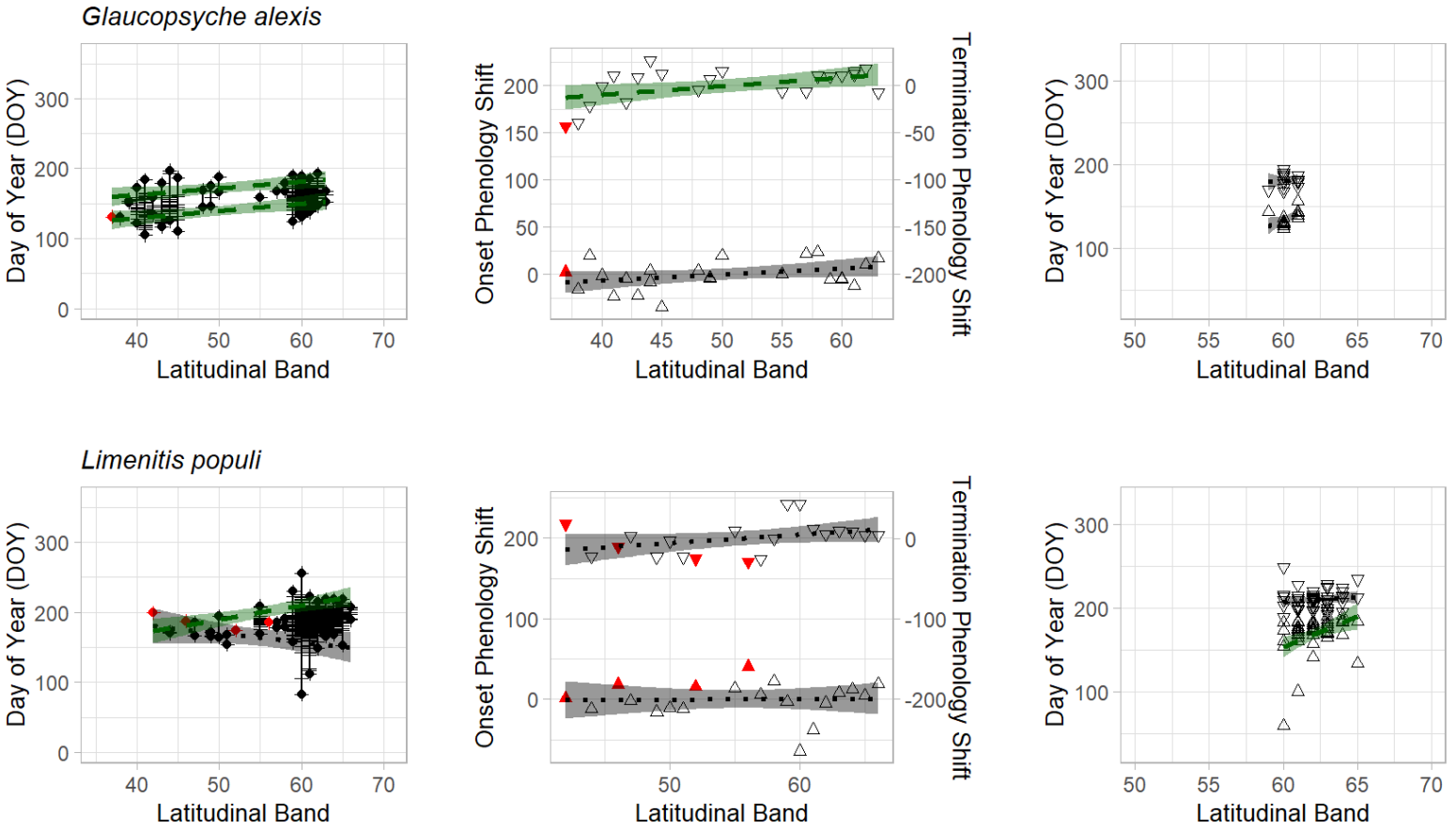
```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```


Erebia ligea
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Euphydryas maturna

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p9<-grid.arrange(sup1a[[17]],sup1b[[17]],sup1c[[17]],sup1a[[18]],sup1b[[18]],sup1c[[18]],nrow = 2))
```

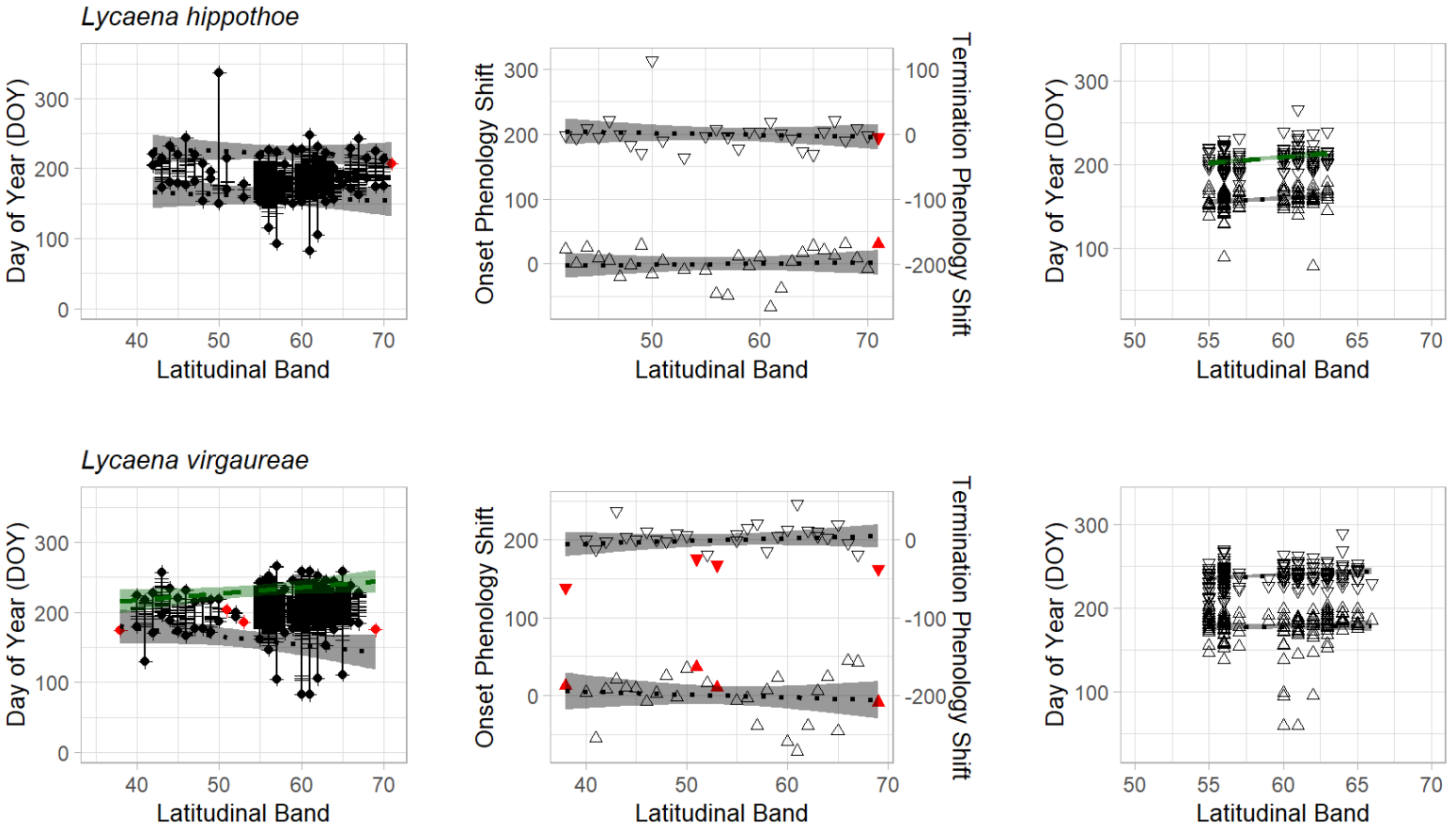
```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```


Glaucopsyche alexis
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Limenitis populi

```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
(p10<-grid.arrange(sup1a[[19]],sup1b[[19]],sup1c[[19]],sup1a[[20]],sup1b[[20]],sup1c[[20]],nrow = 2))
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```

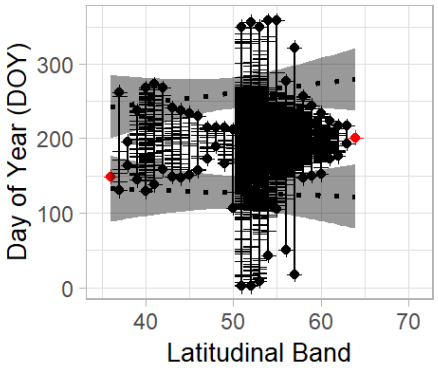

Lycaena hippothoe
Day of Year (DOY)
Latitudinal Band
Onset Phenology Shift
Termination Phenology Shift
Lycaena virgaureae

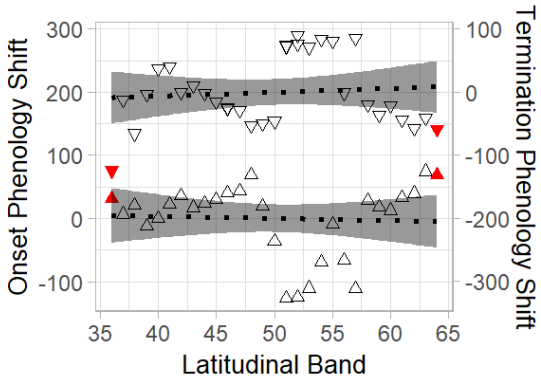
```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

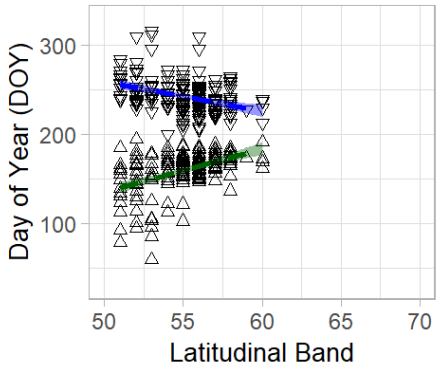
```
(p11<-grid.arrange(sup1a[[21]],sup1b[[21]],sup1c[[21]],sup1a[[22]],sup1b[[22]],sup1c[[22]],nrow = 2))
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```

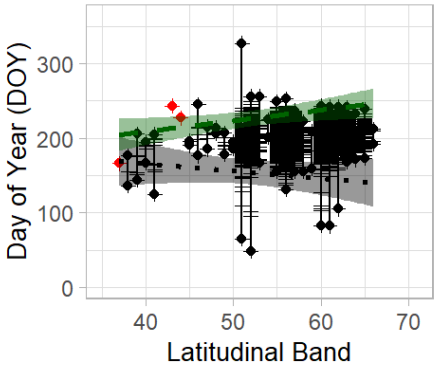
Maniola jurtina

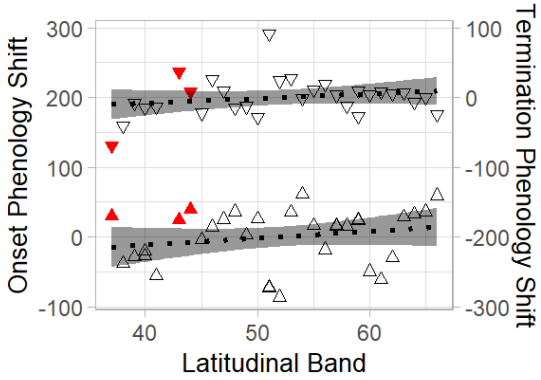


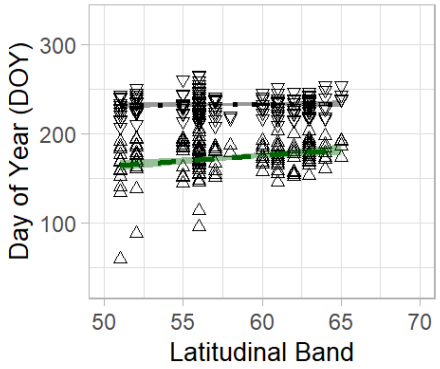




Thymelicus lineolus







```
## TableGrob (2 x 3) "arrange": 6 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (2-2,1-1) arrange gtable[layout]
## 5 5 (2-2,2-2) arrange gtable[layout]
## 6 6 (2-2,3-3) arrange gtable[layout]
```

```
##### END SUP FIG 1
```

*

Below is the code used to create Supplemental Figure 1 in R, for documentation.

We hope to add a live link to View Supplemental Figure 1 pdf.

```
#library(ggpubr)
#This code chunk adds the caption information for Supplemental Figure 1 and creates PDF output.

### ADD TITLE & CAPTION TEXT to SF1
text1<-paste("Larsen and Shirey 2020 Supplemental Figure 1")
text2<-paste("These panels display the data and regression results for onset and termination across models. Each row of 3 pa
nels represents a",
             "species in the re-analysis. In the left column, all raw occurrence data are shown as plus symbols' while onset
 and termination  ",
             "are shown as diamonds; red points indicate individual observations used as both onset and termination. Fric et
 al.’s single     ",
             "regression results of DOY ~ latitude for onset and termination are overlaid on the data. In the middle column,
 the residuals    ",
             "used in the Fric et al. (2020) regression of residuals are shown for onset (upward triangle) and termination (d
ownward triangle)",
             "respectively, with red indicating records of observations used as both onset and termination. Because each data
set is residuals,",
             "the 'phenology shift' data are centered around 0 and the termination axis is shifted for easier interpretation.
The slopes      ",
             "display the regression of residuals results from Fric et al. (2020). The right column shows the calculated onse
t  (upward       ",
             "triangle) and termination (downward triangle) phenometrics calculated using the phest package in R. (Multiple o
bservations for  ",
             "a latitudinal band represent different years), with the results from the multiple regression reanalysis. For al
l panels, the    ",
             "line format demonstrates positive (green, dashed), non-significant (black, dotted), or negative (blue, dashed)
 correlations with",
             "latitude in the corresponding models. While the Fric et al. analyses were generally reproducible, significance
 coding matches   ",
             "that reported in Fric et al. ST2, rather than our reproduction. We were unable to reproduce p values < 0.05 for
the following   ",
             "single regression analyses: E. maturna onset and L. virgaureae termination.",sep=" \n ")

spaces<-paste(" ")
tg <- text_grob(text1, just="centre",size=18)
th <- text_grob(text2, just="left",size=10)
ts <- text_grob(spaces, size=40)
lay <- rbind(c(1,1,1),c(2,NA,NA),c(3,4,5))
```

```
###  SUPP FIG 1
p0<-grid.arrange(tg,th,ts,nrow = 3,layout_matrix = lay, heights=c(1,2,3))
```

Larsen and Shirey 2020 Supplemental Figure 1

These panels display the data and regression results for onset and termination across model species in the re-analysis. In the left column, all raw occurrence data are shown as plus sym are shown as diamonds; red points indicate individual observations used as both onset and t regression results of DOY ~ latitude for onset and termination are overlaid on the data. In the used in the Fric et al. (2020) regression of residuals are shown for onset (upward triangle) ar respectively, with red indicating records of observations used as both onset and termination. the 'phenology shift' data are centered around 0 and the termination axis is shifted for easier display the regression of residuals results from Fric et al. (2020). The right column shows the triangle) and termination (downward triangle) phenometrics calculated using the phest packa a latitudinal band represent different years), with the results from the multiple regression rear line format demonstrates positive (green, dashed), non-significant (black, dotted), or negative latitude in the corresponding models. While the Fric et al. analyses were generally reproduci that reported in Fric et al. ST2, rather than our reproduction. We were unable to reproduce p single regression analyses: E. maturna onset and L. virgaureae termination.

```
l<-list(p0,p1,p2,p3,p4,p5,p6,p7,p8,p9,p10,p11)

sf1_filename<-"outputs/LarsenShirey_SuppFig1.pdf"
ggsave(sf1_filename, marrangeGrob(grobs = l, nrow=1, ncol=1), width=11, height=8.5)
```

End of file.

Author notes - Future updates should: Remove variables when we're done with them See if we can suppress geom_smooth() messages