translocation analysis - orientation

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load packages, read in processed dataset, normalize variables

```r
library(tidyverse)
library(NatParksPalettes)
library(viridis)
library(ggpubr)
library(readxl)
library(lme4)
library(car)

theme_set(theme_classic())

#edit to quantNorm function - remove NAs from estimation
quantNorm =function(x){
  x1<-x[!is.na(x)]
  x[!is.na(x)]<-qnorm(rank(x1,ties.method = "average")/(length(x1)+1))
  x
}
```

```r
birds<-read_xlsx("C:/Users/Steph/TAMU_OneDrive/Thrushes/translocation/data_archiving/translocation_data
pembertonBirds<-read_xlsx("C:/Users/Steph/TAMU_OneDrive/Thrushes/translocation/data_archiving/transloca


birds2<-rbind(pembertonBirds,birds)%>%
  mutate(fall_releaseSite_bearing_tier1=as.numeric(fall_releaseSite_bearing_tier1))%>%
  mutate(norm_releaseSite_bearing_1=quantNorm(fall_releaseSite_bearing_tier1))%>%
  mutate(ancestry=aims_ancestry*(-1)+1)

birds<-birds%>%
  mutate(fall_releaseSite_bearing_tier1=as.numeric(fall_releaseSite_bearing_tier1))%>%
  mutate(norm_releaseSite_bearing_1=quantNorm(fall_releaseSite_bearing_tier1))%>%
  mutate(ancestry=aims_ancestry*(-1)+1)
```

Orientations from Lilloet and Squamish

- expect effects of release site (environment), ancestry (genetics), and interaction between release site and environment (genetics x environment)
- orientation estimated in two ways: relative to the hybrid zone (i.e. Pemberton) and relative to each bird's release location

```
ggplot(birds,aes(x=ancestry,y=norm_releaseSite_bearing_1,
                 group=release_site,
                 colour=release_site))+
  geom_smooth(method="lm",alpha=0.18)+
  geom_point(size=4,shape=19,alpha=0.5)+
  scale_color_manual(values=natparks.pals("Banff")[c(4,1)],name="Release site")+
  xlab("Ancestry")+
  ylab("Orientation to\nrelease site")
```
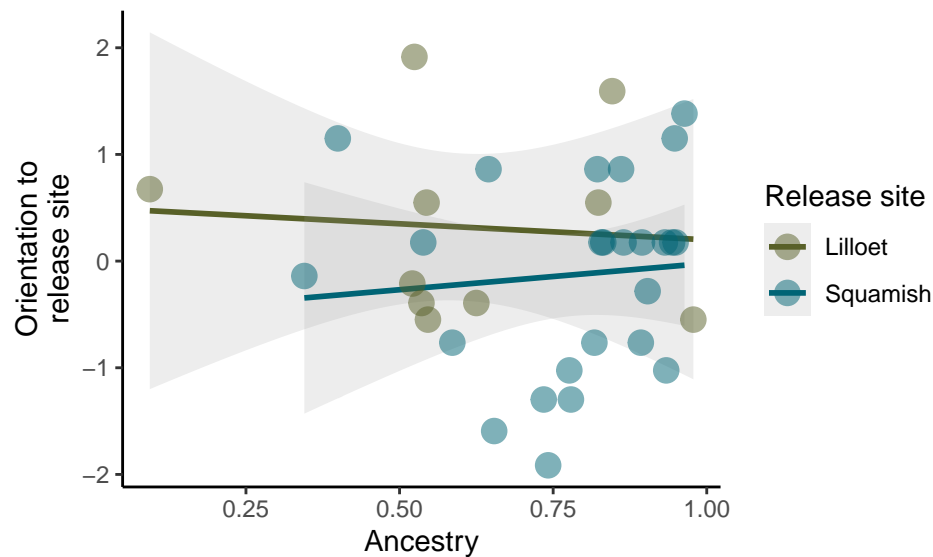


```
lm2<-lm(norm_releaseSite_bearing_1~release_site*ancestry,data=birds,
        na.action=na.exclude)
anova(lm2)
```

```
## Analysis of Variance Table
##
## Response: norm_releaseSite_bearing_1
##                      Df  Sum Sq Mean Sq F value Pr(>F)
## release_site          1  1.4247 1.42468  1.6281 0.2114
## ancestry              1  0.0275 0.02753  0.0315 0.8604
## release_site:ancestry 1  0.1913 0.19128  0.2186 0.6434
## Residuals            31 27.1270 0.87506
```

```
summary(lm2)
```

```
##
## Call:
## lm(formula = norm_releaseSite_bearing_1 ~ release_site * ancestry,
##     data = birds, na.action = na.exclude)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.7659 -0.7185  0.2119  0.3602  1.5720
##
```

```
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  0.5003     0.8283   0.604    0.550
## release_siteSquamish        -1.0165     1.2225  -0.832    0.412
## ancestry                    -0.3009     1.2815  -0.235    0.816
## release_siteSquamish:ancestry  0.7965   1.7036   0.468    0.643
##
## Residual standard error: 0.9354 on 31 degrees of freedom
##   (15 observations deleted due to missingness)
## Multiple R-squared:  0.05712,    Adjusted R-squared:  -0.03412
## F-statistic: 0.626 on 3 and 31 DF,  p-value: 0.6036
```

```
emmeans::emmeans(lm2, ~release_site)
```

```
##  release_site emmean    SE df lower.CL upper.CL
##  Lilloet       0.280 0.338 31   -0.410    0.970
##  Squamish     -0.153 0.196 31   -0.553    0.246
##
## Confidence level used: 0.95
```

```
p=visreg::visreg(lm2,"release_site",by="ancestry",overlay=T,breaks=c(0.25,0.5,0.75))
```
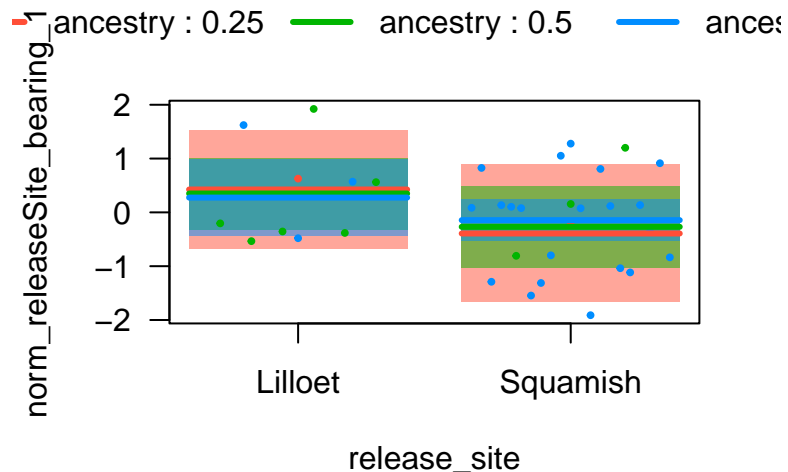


```
gg1<-ggplot(p$fit, aes(release_site, visregFit,
                colour=factor(ancestry),group=as.factor(ancestry))) +
  geom_errorbar(aes(ymin=visregLwr, ymax=visregUpr), alpha=0.5,
            linetype=1, size=0.2,width=0.1,position=position_dodge(width=0.2)) +
  geom_point(position=position_dodge(width=0.2),size=2) +
  geom_line(position=position_dodge(width=0.2),size=0.8)+
  scale_color_manual(values=natparks.pals("Banff")[c(1,6,4)],name="migratory\ngenotype")+
  labs(fill="Weight")+
  ylab("orientation")+xlab("release site")
gg1
```
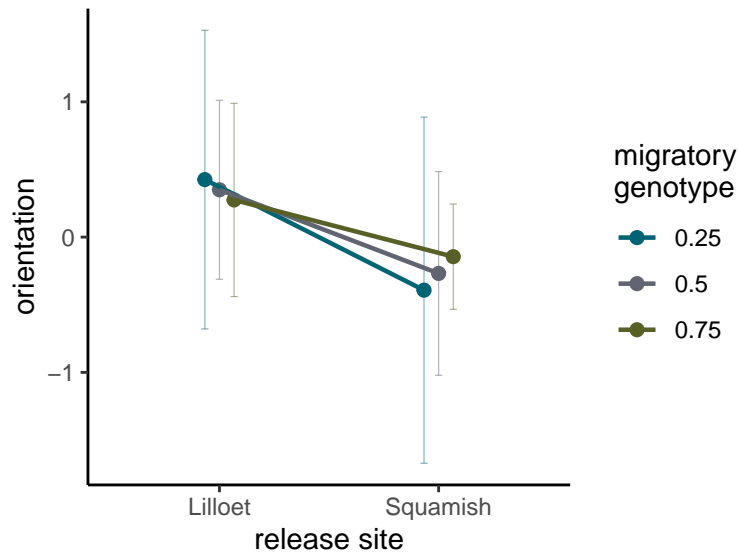
Comparison to Pemberton birds

- selected birds released in Pemberton in 2020 & 2023
- bearing shows a negative relationship to ancestry - inland birds fly east, coastal birds fly west

```
p1<-ggplot(birds,aes(x=ancestry,y=norm_releaseSite_bearing_1,
                group=release_site,
                colour=release_site))+
  geom_smooth(method="lm",alpha=0.18)+
  geom_point(size=4,shape=19,alpha=0.5)+
  scale_color_manual(values=natparks.pals("Banff")[c(4,1)],name="Release site")+
  xlab("Ancestry")+
  ylab("Orientation")

p2<-ggplot(birds2,aes(x=ancestry,y=norm_releaseSite_bearing_1,
                group=release_site,
                colour=release_site))+
  geom_smooth(method="lm",alpha=0.18)+
  geom_point(size=4,shape=19,alpha=0.5)+
  scale_color_manual(values=natparks.pals("Banff")[c(4,7,1)],name="Release site")+
  xlab("Ancestry")+
  ylab("Orientation")

ggarrange(p1,p2,labels=LETTERS)
```
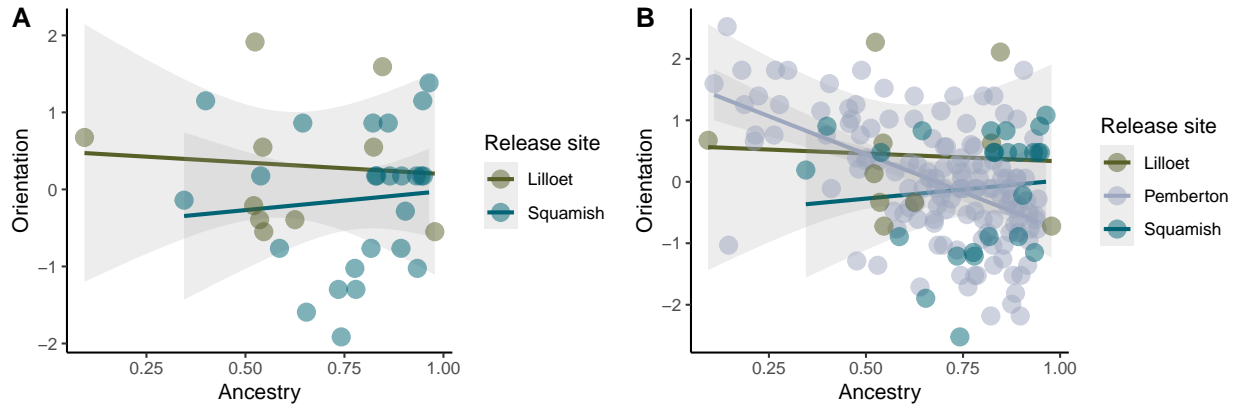
```
#ggsave("C:/Users/Steph/TAMU_OneDrive//Thrushes/translocation/FigS1.png",
#        width=9,height=3)
```

- include year as a random effect, to control for similarities among 2020 vs 2023 birds
- here, release site is unimportant, but ancestry is significant and there is an interaction between release site and ancestry
- again, more positive slopes between release site and ancestry in Lilloet and Squamish than Pemberton

```
birds2<-birds2%>%mutate(f_release_year=as.factor(release_year))%>%
  mutate(f_release_site=factor(release_site,levels=c("Squamish","Pemberton","Lilloet")))

lmer2<-lmer(norm_releaseSite_bearing_1~f_release_site*ancestry+(1|f_release_year),
          data=birds2,na.action=na.exclude)
Anova(lmer2)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: norm_releaseSite_bearing_1
##                          Chisq Df Pr(>Chisq)
## f_release_site          1.4491  2   0.484543
## ancestry               37.3270  1  9.989e-10 ***
## f_release_site:ancestry 10.2391  2   0.005979 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
coef(lmer2)
```

```
## $f_release_year
##      (Intercept) f_release_sitePemberton f_release_siteLilloet  ancestry
## 2020  -0.7110234                2.337305              1.298683 0.5924252
## 2023  -0.5703144                2.337305              1.298683 0.5924252
##      f_release_sitePemberton:ancestry f_release_siteLilloet:ancestry
## 2020                        -3.082215                     -0.8479558
## 2023                        -3.082215                     -0.8479558
##
## attr(,"class")
## [1] "coef.mer"
```

```
summary(lmer2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: norm_releaseSite_bearing_1 ~ f_release_site * ancestry + (1 |
##     f_release_year)
##    Data: birds2
##
## REML criterion at convergence: 432.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.7672 -0.6620  0.1153  0.6081  2.6633
##
## Random effects:
##  Groups         Name        Variance Std.Dev.
##  f_release_year (Intercept) 0.01651  0.1285
##  Residual                   0.74747  0.8646
## Number of obs: 171, groups:  f_release_year, 2
##
## Fixed effects:
##                                Estimate Std. Error t value
## (Intercept)                     -0.6407     0.8379  -0.765
## f_release_sitePemberton          2.3373     0.8732   2.677
## f_release_siteLilloet            1.2987     1.1357   1.144
## ancestry                         0.5924     1.0375   0.571
## f_release_sitePemberton:ancestry -3.0822     1.0989  -2.805
## f_release_siteLilloet:ancestry   -0.8480     1.5745  -0.539
##
## Correlation of Fixed Effects:
##            (Intr) f_rl_P f_rl_L ancstr f_r_P:
## f_rls_stPmb -0.949
## f_rls_stLll -0.733  0.704
## ancestry    -0.970  0.931  0.716
## f_rls_stPm:  0.917 -0.974 -0.677 -0.944
## f_rls_stLl:  0.639 -0.613 -0.945 -0.659  0.622
```

```
data.frame(Anova(lmer2))%>%
  mutate()
```

```
##                            Chisq Df   Pr..Chisq.
## f_release_site          1.449098  2 4.845430e-01
## ancestry               37.326992  1 9.989241e-10
## f_release_site:ancestry 10.239122  2 5.978647e-03
```

```
p=visreg::visreg(lmer2,"f_release_site",by="ancestry",overlay=T,breaks=c(0.25,0.5,0.75))
```
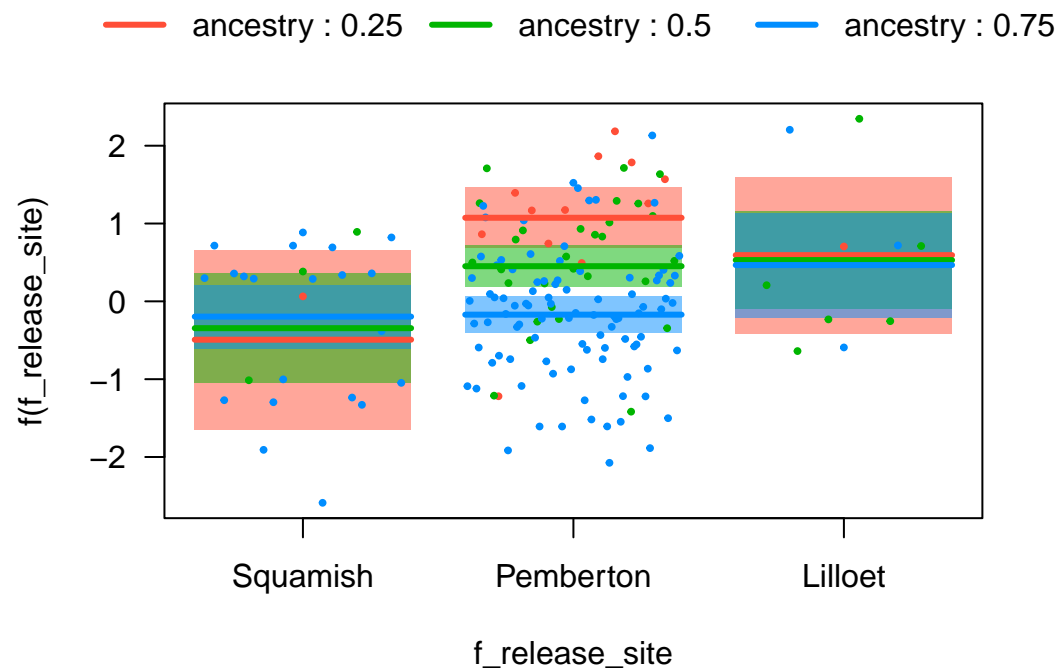
```
gg1<-ggplot(p$fit, aes(f_release_site,
                    visregFit,
                    colour=factor(ancestry),group=as.factor(ancestry))) +
  geom_errorbar(aes(ymin=visregLwr, ymax=visregUpr),
                linetype=1, size=0.6,width=0.1,position=position_dodge(width=0.2)) +
  geom_point(position=position_dodge(width=0.2),size=3) +
  geom_line(position=position_dodge(width=0.2),size=1)+
  scale_color_manual(values=natparks.pals("Banff")[c(1,7,5)],name="Ancestry",
                    labels=c("Coastal backcross","Hybrid","Inland backcross"))+
  labs(fill="Weight")+
  ylab("Orientation")+xlab("Release site")

gg1
```
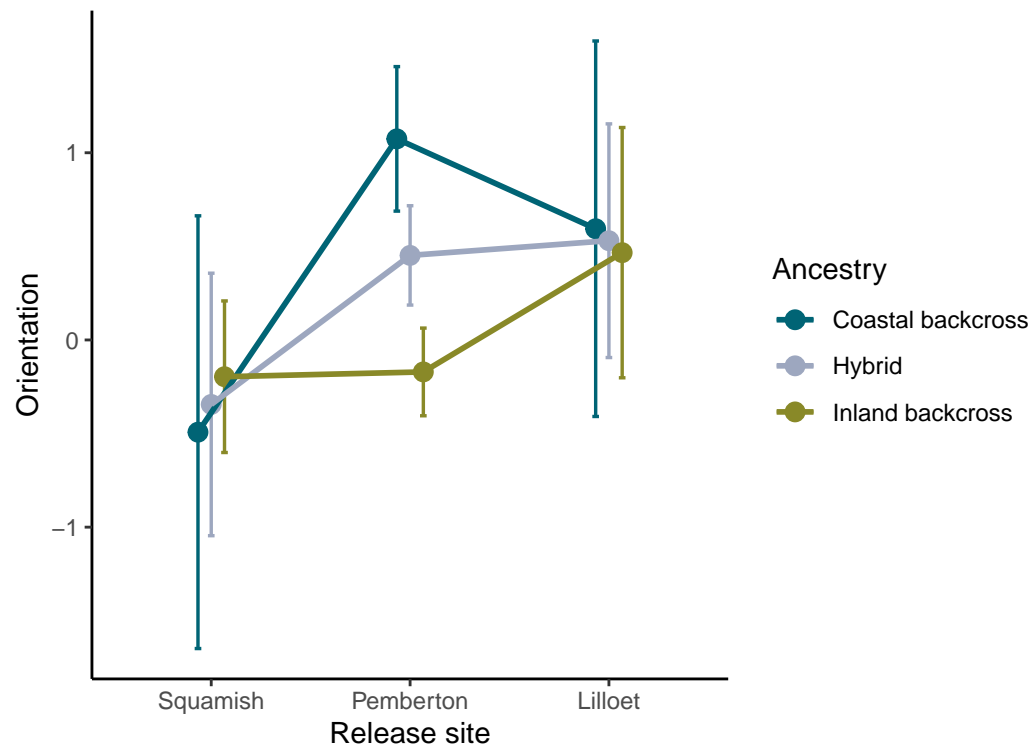
```
#ggsave(plot=gg1,
#       file="C:/Users/Steph/TAMU_OneDrive/Thrushes/translocation/Fig3B.png",
#       width=5.5,height=4)
```