

translocation analysis survival

steph

2024-09-19

- load packages & read in processed dataset
- adjust ancestry so that *coastal* = 0 and *inland* = 1

```
library(tidyverse)
library(NatParksPalettes)
library(viridis)
library(ggpubr)
library(readxl)

theme_set(theme_classic())

#manual change made to CJS output - deleted header lines to allow output to be read into R
cjs_out<-read.table("C:/Users/Steph/GitHub_data/translocation/CJS.beta.translocation.20250410.edit.txt"
  header=T)
cjs_out_pemberton<-read.table("C:/Users/Steph/GitHub_data/translocation/CJS.beta.translocation_Pemberton.20250410.edit.txt"
  header=T)

phi<-read.csv("C:/Users/Steph/GitHub_data/translocation/CJS.fit.phi.translocation.20250410.csv")
phi_pemberton<-read.csv("C:/Users/Steph/GitHub_data/translocation/CJS.fit.phi.translocation_Pemberton.20250410.csv")

birds<-read_xlsx("C:/Users/Steph/TAMU_OneDrive/Thrushes/translocation/data_archiving/translocation_data.xlsx")
pembertonBirds<-read_xlsx("C:/Users/Steph/TAMU_OneDrive/Thrushes/translocation/data_archiving/translocation_data_Pemberton.xlsx")

birds2<-rbind(pembertonBirds,birds)%>%
  mutate(ancestry=aims_ancestry*(-1)+1)

birds<-birds%>%
  mutate(ancestry=aims_ancestry*(-1)+1)
```

- Sample sizes for survival analysis

```
knitr::kable(birds2%>%
  group_by(release_site,release_year)%>%
  summarise(count=n()))
```

release_site	release_year	count
Lilloet	2020	20
Pemberton	2020	98
Pemberton	2023	90

release_site	release_year	count
Squamish	2023	30

CJS (mark recapture) models

- Fit a CJS model with detections binned into 10 day chunks to create 30 time points (data were too sparse with each day as a time point)
- Model: Survival \sim release_site + ancestry + release_site x ancestry; Detection \sim time + release_site + ancestry
- No evidence for the predicted interaction between release site and ancestry
- None of release site, ancestry, or the interaction between release site and ancestry had a significant effect on survival
- The direction of the interaction effect was not in the predicted direction - the release site x ancestry interaction is positive, meaning that the relationship between ancestry and survival is more positive for birds released in Squamish relative to those released in Lilloet
- probability of detection varied among time points, with the higher probabilities of detection occurring during fall and spring migration
- birds released in Squamish had a higher probability of detection than those released in Lilloet, but detection probability did not vary with ancestry
- Once you control for difference in detection probability - no difference in survival between release sites

Survival analysis results:

```
knitr::kable(cjs_out%>%filter(startsWith(Factor, "Phi"))%>%
  mutate_if(is.numeric, round, digits=2)%>%
  select(-se)%>%
  rename(Lower_CL=lcl, Upper_CL=ucl))
```

Factor	Estimate	Lower_CL	Upper_CL
Phi.(Intercept)	3.89	1.81	5.98
Phi.release_siteSquamish	-2.11	-5.28	1.07
Phi.ancestry	-1.94	-4.97	1.09
Phi.release_siteSquamish:ancestry	3.68	-0.61	7.98

Detection probability analysis results:

(minus variation among time points)

```
knitr::kable(cjs_out%>%filter(startsWith(Factor, "p."))%>%
  filter(!startsWith(Factor, "p.time"))%>%
  mutate_if(is.numeric, round, digits=2)%>%
  select(-se)%>%
  rename(Lower_CL=lcl, Upper_CL=ucl))
```

Factor	Estimate	Lower_CL	Upper_CL
p.(Intercept)	-1.38	-2.94	0.18
p.release_siteSquamish	2.83	1.92	3.74
p.ancestry	0.35	-1.64	2.35

CJS - with Pemberton

- Here, I would expect a flat relationship between ancestry and survival in Pemberton (ie at the centre of the hybrid zone), a positive relationship in Lilloet (better survival of inland birds) and a negative relationship in Squamish (better survival of coastal birds)
- Model: Survival ~ release_site + ancestry + release_site x ancestry; Detection ~ time + release_site + release_year + ancestry
- Adding Pemberton birds tagged in 2020 & 2023 does not change anything for the survival results - everything is still null
- Because release site and release year aren't entirely covarying, I added release year (alongside time point, release site, and ancestry) as a predictor for detection probability
- For detection probabilities, the difference seems to be primarily between release years, but also a reduction in Lilloet relative to Pemberton - not sure how much to read into that

Survival analysis results:

```
knitr::kable(cjs_out_pemberton%>%filter(startsWith(Factor,"Phi"))%>%
  mutate_if(is.numeric,round,digits=2)%>%
  select(-se)%>%
  rename(Lower_CL=lc1,Upper_CL=uc1))
```

Factor	Estimate	Lower_CL	Upper_CL
Phi.(Intercept)	2.82	2.17	3.46
Phi.release_siteLilloet	1.21	-1.15	3.58
Phi.release_siteSquamish	-0.91	-3.41	1.59
Phi.ancestry	0.29	-0.59	1.17
Phi.release_siteLilloet:ancestry	-2.36	-5.71	1.00
Phi.release_siteSquamish:ancestry	1.35	-1.86	4.56

Detection probability analysis results:

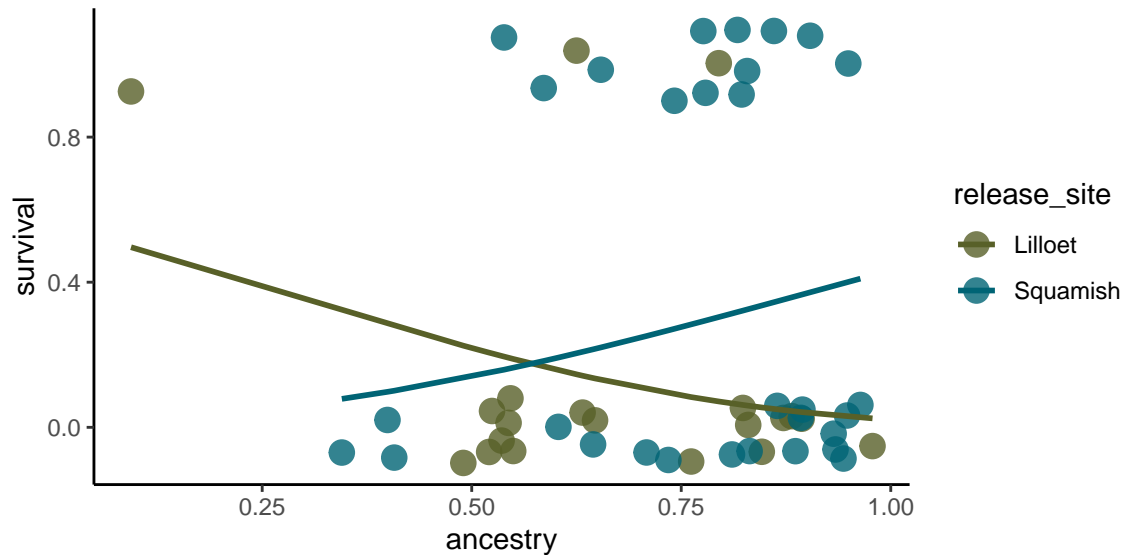
```
knitr::kable(cjs_out_pemberton%>%filter(startsWith(Factor,"p."))%>%
  filter(!startsWith(Factor,"p.time"))%>%
  mutate_if(is.numeric,round,digits=2)%>%
  select(-se)%>%
  rename(Lower_CL=lc1,Upper_CL=uc1))
```

Factor	Estimate	Lower_CL	Upper_CL
p.(Intercept)	-0.41	-0.95	0.13
p.release_siteLilloet	-1.07	-1.77	-0.36
p.release_siteSquamish	0.33	0.01	0.66
p.release_year2023	1.14	0.87	1.42
p.ancestry	0.41	-0.21	1.03

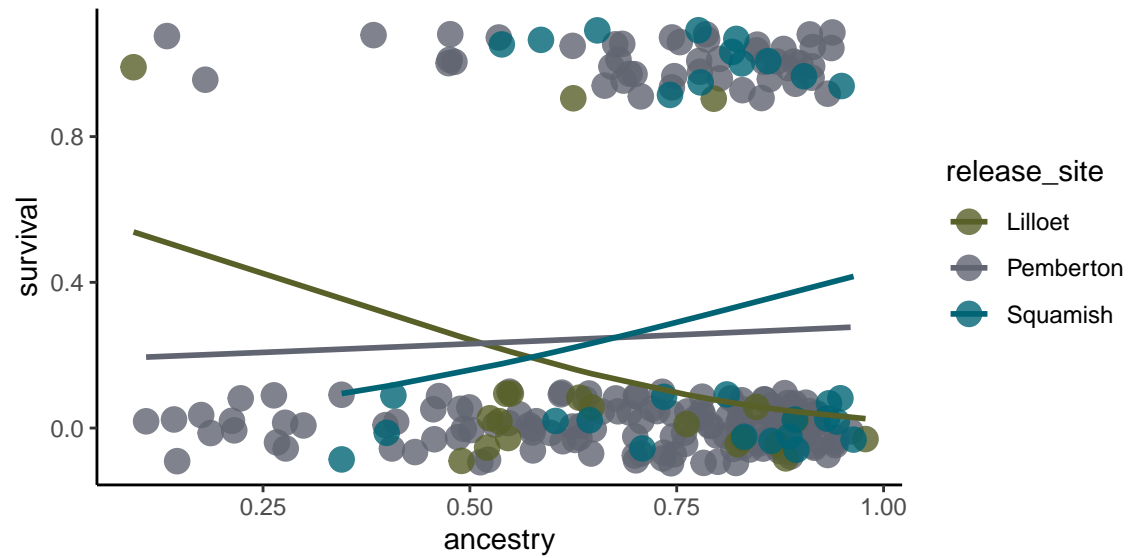
Survival figures

- slopes are based on ancestry x release site predictions from the CJS models
- I think I actually prefer the violin plots because the data are more visible

```
ggplot(birds,aes(x=ancestry,y=survival,
                group=release_site,
                colour=release_site))+
  #geom_smooth(method="lm",alpha=0.18)+
  geom_point(size=4,shape=19,alpha=0.8,position=position_jitter(width=0,height=0.1))+
  geom_line(data=phi,aes(x=ancestry,y=est.adj,colour=release_site),size=1)+
  scale_color_manual(values=natparks.pals("Banff")[c(4,1)])+
  xlab("ancestry")+
  ylab("survival")
```

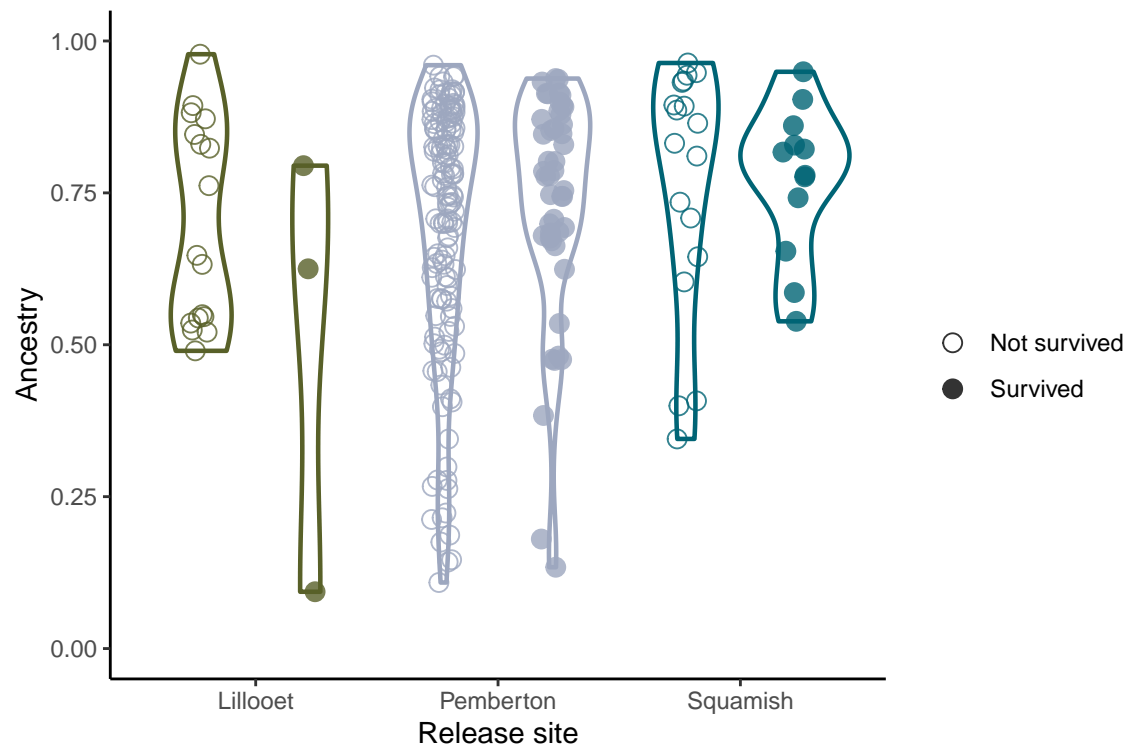


```
ggplot(birds2,aes(x=ancestry,y=survival,
                 group=release_site,
                 colour=release_site))+
  geom_point(size=4,shape=19,alpha=0.8,position=position_jitter(width=0,height=0.1))+
  geom_line(data=phi_pemberton,
            aes(x=ancestry,y=est.adj,colour=release_site),size=1)+
  scale_color_manual(values=natparks.pals("Banff")[c(4,6,1)])+
  xlab("ancestry")+
  ylab("survival")
```



```
gg1<-ggplot(birds2,aes(y=ancestry,x=release_site,
                      group=interaction(as.factor(survival),release_site),
                      colour=release_site,shape=as.factor(survival)))+
  geom_point(size=3,alpha=0.8,
             position=position_jitterdodge(
               jitter.width =0.2,jitter.height=0,dodge.width=0.9))+
  scale_shape_manual(values=c(1,19),name="",labels=c("Not survived","Survived"))+
  scale_color_manual(values=natparks.pals("Banff")[c(4,7,1)],
                    guide="none")+
  geom_violin(fill=NA,aes(group=interaction(survival,release_site)),size=0.8)+
  ylab("Ancestry")+xlab("Release site")+ylim(0,1)+
  scale_x_discrete(labels=c("Lillooet","Pemberton","Squamish"))
```

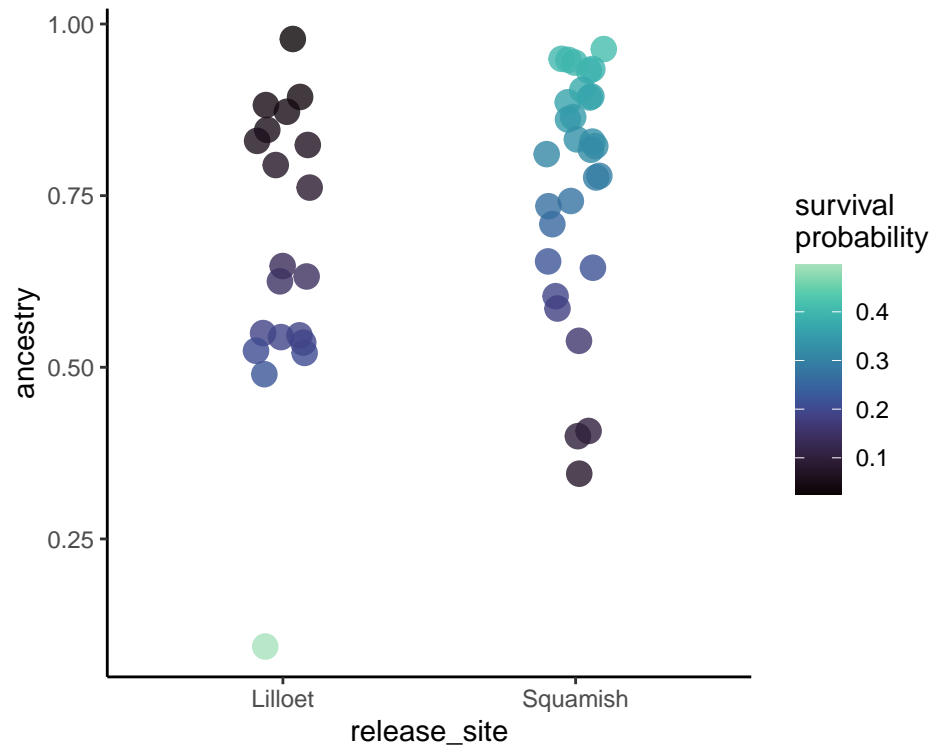
gg1



```
#ggsave("C:/Users/Steph/TAMU_OneDrive/Thrushes/translocation/Fig2.png",
#       width=6,height=4)
```

- Next, points coloured by model-fitted survival probabilities

```
ggplot(phi,aes(x=release_site,y=ancestry,colour=est.adj))+
  geom_jitter(size=4,shape=19,alpha=0.8,width=0.1)+
  viridis::scale_colour_viridis(option="mako",end=0.9,name="survival\nprobability")
```



```
ggplot(phi_pemberton, aes(x=release_site, y=ancestry, colour=est.adj)) +
  geom_jitter(size=4, shape=19, alpha=0.8, width=0.2) +
  viridis::scale_colour_viridis(option="mako", end=0.9, name="survival\nprobability")
```

