

Grizzly Bear Covid Analysis

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Prepare Data for Analysis

Load Data, Functions and Cleanup Data

```
##Load Packages
lapply(c("hrbrthemes", "velox", "raster", "here", "sf", "lme4", "MuMIn", "lubridate",
        "sjPlot", "survival", "gtsummary", "survminer", "tidyverse"),
       require, character.only = TRUE)

#####
##load data
#####
cap <- read.csv(here::here("data", "cap_mb.csv"))
reloc <- read.csv(here::here("data", "reloc_mb.csv"))
```

Add Spatial Attributes

```
##make bear data spatial
reloc <- st_as_sf(reloc,
                 coords = c("X", "Y"),
                 crs = 4326)%>%
  st_transform("+proj=aea +lat_1=50 +lat_2=58.5 +lat_0=45 +lon_0=-126 +x_0=1000000 +y_0=0 +ellps=GRS80")

## HUMAN INFLUENCE INDEX
hii<- raster(here::here("data", "spatial", "hii.tif"))

##make velox (faster)
hiiiv <- velox(hii)

##extract hii to reloc
reloc <- reloc%>%mutate(hii=hiiiv$extract_points(sp = reloc))

rm(hii)

## NDVI
##make smaller
ndvi<- raster(here::here("data", "spatial", "ndvi.tif"))

##make velox (faster)
ndviv <- velox(ndvi)

##extract hii to reloc
reloc <- reloc%>%mutate(ndvi=ndviv$extract_points(sp = reloc))

rm(ndvi)
```

```
###make Tibble
reloc <- reloc%>%
  as_tibble()
```

Add Temporal Attributes

```
reloc <- reloc%>%
  mutate(m=month(DateTimeLocal),
         year=year(DateTimeLocal))
```

Add Individual Attributes

```
reloc <- reloc%>%
  left_join(cap%>%dplyr::select(Name,Sex,Age,EndReason,Born), by="Name")%>%
  mutate(Age=year-Born)
```

Reclassify factors

```
reloc <- reloc%>%
  mutate(m=as.factor(m),
         Name=as.factor(Name))

reloc <- reloc%>%
  filter(m%in%5:11)

reloc <- reloc%>%
  mutate(COVID=case_when(year<2020~"control",year>=2020~"covid"))
```

Prep Monthly Survival Data

```
##summarize live locs by month
reloc.m <- reloc%>%
  mutate(d=day(DateTimeLocal))%>%
  group_by(Name,year,m,Sex,Age,EndReason,covid, COVID)%>%
  summarize(hii=mean(hii,na.rm=TRUE),
            ndvi=mean(ndvi,na.rm=TRUE),
            d=max(d,na.rm=TRUE))%>%
  as_tibble()%>%
  ungroup()

##bind and join last month with live and dead if needed
reloc.m <- reloc.m%>%
  filter(EndReason%in%"Mortality")%>%
  mutate(m=as.numeric(m))%>%
  arrange(Name,-year,-m)%>%
  group_by(Name)%>%
  slice(1)%>%
  mutate(dead=1)%>%
  ungroup()%>%
  dplyr::select(Name,year,m,dead)%>%
```

```
mutate(m=as.factor(m))%>%
right_join(reloc.m, by=c("Name", "year", "m"))%>%
arrange(Name, year, m)%>%
mutate(dead=case_when(is.na(dead)~0, TRUE~dead))
```

Run Models

Habitat Use

```
##Fit Model
m1 <- lmer(hii ~ Age:Sex + COVID + ndvi + (1|m) + (1|Name), data = reloc,
          REML = FALSE)

##Print Output
tbl_regression(m1)
```

| Characteristic | Beta | 95% CI |
|----------------|-------|-------------|
| COVID | | |
| control | | |
| covid | -2.2 | -2.6, -1.9 |
| ndvi | -1.4 | -2.0, -0.76 |
| Age * Sex | | |
| Age * F | -0.14 | -0.32, 0.04 |
| Age * M | 2.6 | 2.2, 3.0 |

```
summary(m1)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: hii ~ Age:Sex + COVID + ndvi + (1 | m) + (1 | Name)
## Data: reloc
##
##          AIC          BIC      logLik deviance df.resid
## 327347.3 327417.3 -163665.6 327331.3    47038
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3755 -0.6938 -0.0872  0.4746  4.2377
##
## Random effects:
## Groups Name Variance Std.Dev.
## Name (Intercept) 383.961 19.595
## m (Intercept) 2.412 1.553
## Residual 60.946 7.807
## Number of obs: 47046, groups: Name, 55; m, 7
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 5.60255 2.92289 1.917
## COVIDcovid -2.24585 0.17418 -12.894
## ndvi -1.40618 0.32823 -4.284
## Age:SexF -0.14447 0.09204 -1.570
```

```
## Age:SexM      2.61347    0.20413   12.803
##
## Correlation of Fixed Effects:
##              (Intr) COVIDc ndvi   Ag:SxF
## COVIDcovid   0.174
## ndvi         -0.088 -0.063
## Age:SexF     -0.239 -0.547   0.046
## Age:SexM     -0.343 -0.328   0.034   0.319

##Plot Results
# plot_model(
#   m1,
#   sort.est = TRUE,
#   title = "",
#   axis.title=c("Parameter estimates"))+
#   geom_hline(yintercept = 0, linetype="dotted")+
#   ggtitle("Coefficients Measuring use of Human Influenced Habitats")+
#   theme_ipsum()

##get % change
##mean hii to start
mean(reloc%>%filter(COVID%in%"control")%>%pull(hii))

## [1] 14.75639
#14.75639

##hii dropped by -2.24585 during covid based on glmm, so:
(-2.24585/14.75639)*100

## [1] -15.21951
#15% decline in hii use.
```

Run Cox Proportional Hazard Survival Models

```
##Fit Model
surv <- coxph(Surv(d, dead)~ Age*Sex + COVID + ndvi +
              cluster(Name), data = reloc.m)

##Test Assumptions
print(cox.zph(surv))

##              rho  chisq      p
## Age           0.622  1.1363 0.2864
## SexM          0.370  1.5393 0.2147
## COVIDcovid   -0.431  2.8698 0.0903
## ndvi         -0.172  0.0617 0.8039
## Age:SexM     -0.619  1.1426 0.2851
## GLOBAL       NA    3.3155 0.6515

##Print Output
tbl_regression(surv)
```

| Characteristic | log(HR) | 95% CI | p-value |
|----------------|---------|--------------|---------|
| Age | -0.50 | -0.82, -0.17 | 0.003 |
| Sex | | | |
| F | | | |
| M | -0.50 | -3.1, 2.1 | 0.7 |
| COVID | | | |
| control | | | |
| covid | 0.64 | -1.2, 2.4 | 0.5 |
| ndvi | 1.6 | -2.3, 5.5 | 0.4 |
| Age * Sex | | | |
| Age * M | 0.21 | -0.19, 0.61 | 0.3 |

```
summary(surv)
```

```
## Call:
## coxph(formula = Surv(d, dead) ~ Age * Sex + COVID + ndvi + cluster(Name),
##       data = reloc.m)
##
##      n= 367, number of events= 10
##
##              coef exp(coef) se(coef) robust se      z Pr(>|z|)
## Age          -0.4985   0.6074   0.2366   0.1661 -3.000   0.0027 **
## SexM          -0.5036   0.6043   1.5619   1.3145 -0.383   0.7016
## COVIDcovid    0.6361   1.8892   0.8682   0.9221  0.690   0.4903
## ndvi          1.6109   5.0073   3.3200   1.9967  0.807   0.4198
## Age:SexM      0.2079   1.2311   0.3060   0.2041  1.019   0.3084
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## Age              0.6074      1.6463   0.43861   0.8412
## SexM              0.6043      1.6547   0.04596   7.9465
## COVIDcovid       1.8892      0.5293   0.31003  11.5115
## ndvi              5.0073      0.1997   0.10000 250.7270
## Age:SexM         1.2311      0.8123   0.82521   1.8366
##
## Concordance= 0.838 (se = 0.093 )
## Rsquare= 0.042 (max possible= 0.267 )
## Likelihood ratio test= 15.6 on 5 df,  p=0.008
## Wald test              = 17.4 on 5 df,  p=0.004
## Score (logrank) test = 11.84 on 5 df,  p=0.04,   Robust = 8.74  p=0.1
##
## (Note: the likelihood ratio and score tests assume independence of
##       observations within a cluster, the Wald and robust score tests do not).
##Plot Results
# plot_model(surv)+
# ggtitle("Mortality Hazard Coefficients")+
# geom_hline(yintercept = 1, linetype="dotted")+
# theme_ipsum()
```

```
##get % change

pre.surv <- exp(-predict(surv,
  newdata=data.frame(Age=mean(reloc.m$Age),Sex="F", COVID="control", ndvi=mean(reloc.m$ndvi),
  type="expected"))^6 ##6 month active season,

pre.surv <- pre.surv * ((1-0.003)^6) ## den survival

post.surv <- exp(-predict(surv,
  newdata=data.frame(Age=mean(reloc.m$Age),Sex="F", COVID="covid", ndvi=mean(reloc.m$ndvi),
  type="expected"))^6 ##6 month active season,

post.surv <- post.surv * ((1-0.003)^6) ## den survival

((pre.surv-post.surv)/pre.surv)*100

## [1] 2.304182
```

Summary

Habitat Use

I show that grizzly bears (*Ursus arctos*) appeared to shift their habitat use to less human influenced, or “wilder” areas (human influence variable, the response variable, hii) during COVID-19 lockdowns (covid variable). The % decrease in human influenced habitats during covid was 15%. This is likely due to increased human recreation around the valley, which was seen a large spike in local tourism and local use of the landscape. The t-statistic for this effect is -12.894

Survival

There was no detectable change in survival of bears during the COVID-19 lockdowns. The z value for this effect is 0.690. The % change was a 2.3% increase in annual survival.