

Annexure I

R script

```
library(readr)
library(lme4)
library(spm)
#Read in file
bear_presence <- read.csv("E:/R studio/Sloth_bear_R2019_R2020.csv")
#Convert binary variables to factors
bear_presence$`Season` <- as.factor(bear_presence$Season)
bear_presence$`SB presence sign` <- as.factor(bear_presence$SB.presence.sign)
bear_presence$`Presence of food` <- as.factor(bear_presence$Presence.of.food)
bear_presence$`Habitat Type` <- as.factor(bear_presence$Habitat.Type)
bear_presence$`Zizyphus spp` <- as.factor(bear_presence$Zizyphus.spp)
bear_presence$`Cassia Fistula` <- as.factor(bear_presence$Cassia.Fistula)
bear_presence$`Grewia Flavesecnes` <- as.factor(bear_presence$Grewia.Flavesecnes)
bear_presence$`Diosyros melanoxyton` <- as.factor(bear_presence$Diosyros.melanoxyton)
```

#Data visualization

Hide

```
plot(bear_presence$`SB presence sign`~bear_presence$Season)
plot(bear_presence$Season~bear_presence$`Presence of food`)

#Because all the habitat variables are exactly the same between seasons, we really cannot do much beyond account for those differences.

mcnemar.test(bear_presence$`SB presence sign`,bear_presence$Season)

#lm1=glmer(bear_presence$SB.presence.sign~bear_presence$Season+(1|bear_presence$S..No.),family = binomial)
lm1=glmer(bear_presence$SB.presence.sign~bear_presence$Season+ (1|bear_presence$S..No.),family = binomial)

summary(lm1)

plot(lm1)
```

```
library(readr)
```

Results

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
library(spm)
```

```
#Read in file
```

```
bear_presence <- read.csv("E:/R studio/Sloth_bear_R2019_R2020.csv")
```

```
#Convert binary variables to factors
```

```
bear_presence$`Season` <- as.factor(bear_presence$Season)
```

```
bear_presence$`SB presence sign` <- as.factor(bear_presence$SB.presence.sign)
```

```
bear_presence$`Presence of food` <- as.factor(bear_presence$Presence.of.food)
```

```
bear_presence$`Habitat Type` <- as.factor(bear_presence$Habitat.Type)
```

```
bear_presence$`Zizyphus spp` <- as.factor(bear_presence$Zizyphus.spp)
```

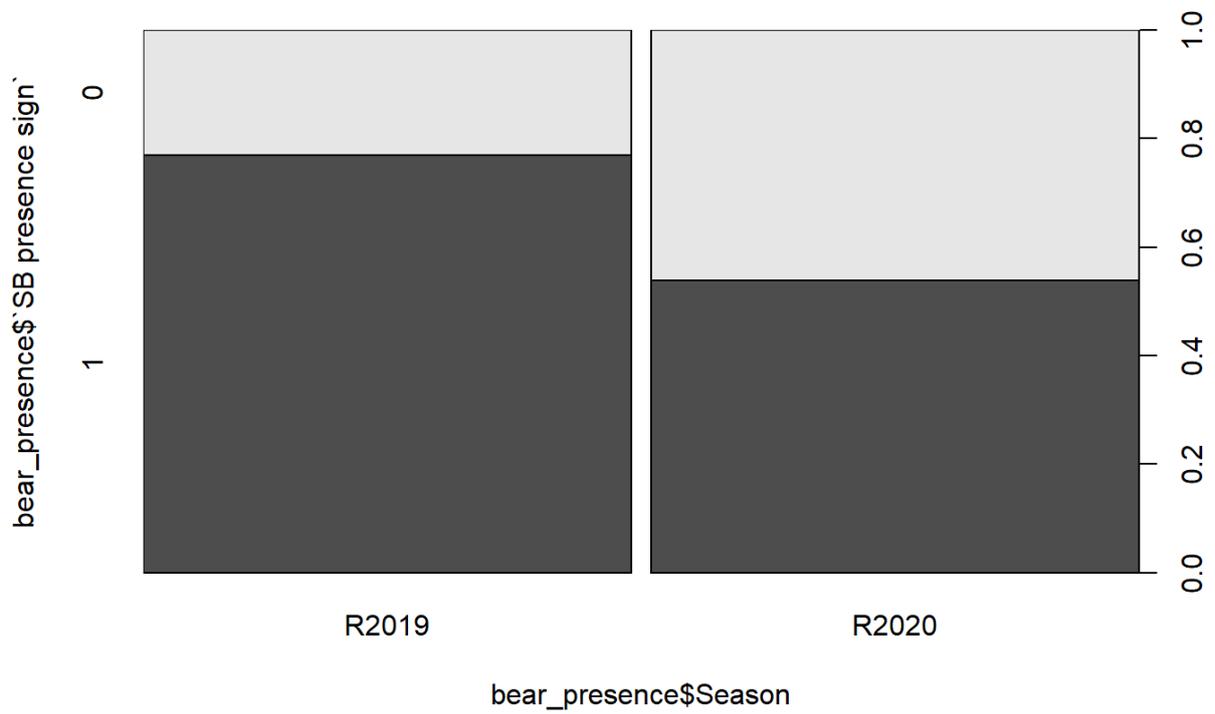
```
bear_presence$`Cassia Fistula` <- as.factor(bear_presence$Cassia.Fistula)
```

```
bear_presence$`Grewia Flavesecnes` <- as.factor(bear_presence$Grewia.Flavesecnes)
```

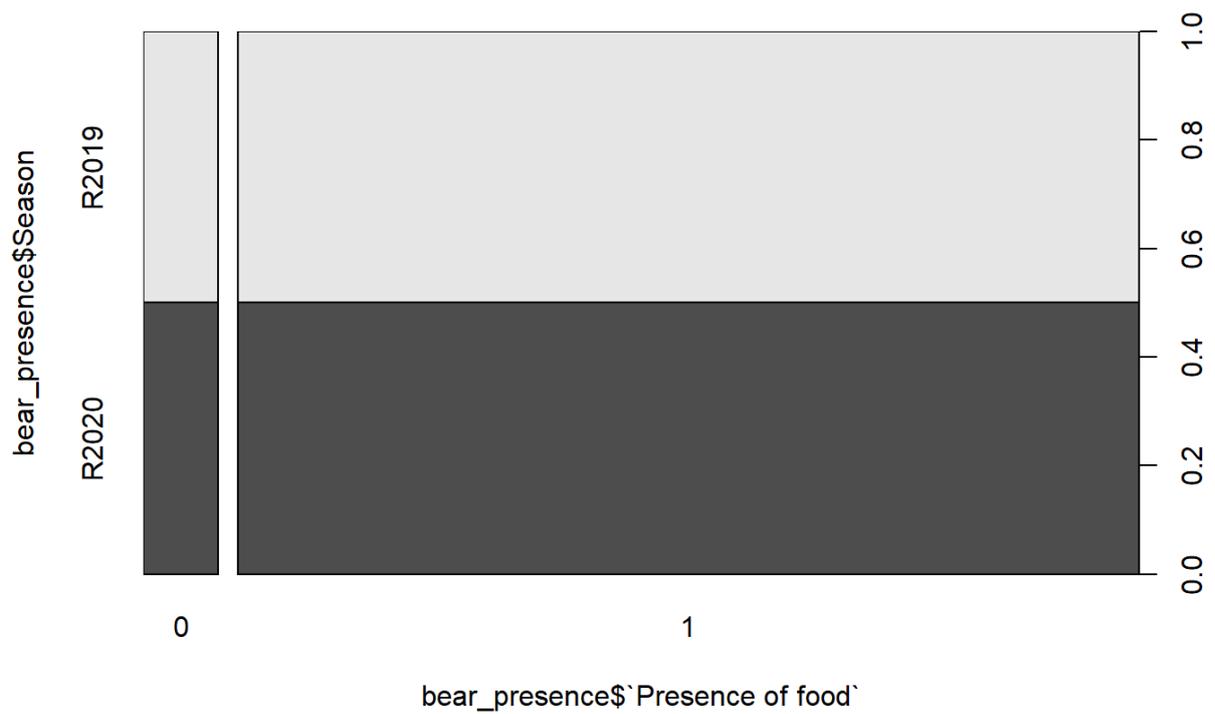
```
bear_presence$`Diosyros melanoxyton` <- as.factor(bear_presence$Diosyros.melanoxyton)
```

```
#Data visualization
```

```
plot(bear_presence$`SB presence sign`~bear_presence$Season)
```



```
plot(bear_presence$Season~bear_presence$`Presence of food`)
```



#Because all the habitat variables are exactly the same between seasons, we really cannot do much beyond account for those differences.

```
mcnemar.test(bear_presence$`SB presence sign`,bear_presence$Season)
```

```
##
```

```
## McNemar's Chi-squared test with continuity correction
```

```
##
```

```
## data: bear_presence$`SB presence sign` and bear_presence$Season
```

```
## McNemar's chi-squared = 1.5312, df = 1, p-value = 0.2159
```

```
#lm1=glmer(bear_presence$SB.presence.sign~bear_presence$Season+(1|bear_presence$S..No.),family = binomial)
```

```
lm1=glmer(bear_presence$SB.presence.sign~bear_presence$Season+(1|bear_presence$S..No.),family = binomial)
```

```
summary(lm1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
```

```
## Approximation) [glmerMod]
```

```
## Family: binomial ( logit )
```

```
## Formula: bear_presence$SB.presence.sign ~ bear_presence$Season + (1 |
```

```
## bear_presence$S..No.)
```

```
##
```

```
## AIC BIC logLik deviance df.resid
```

```
## 69.1 75.0 -31.6 63.1 49
```

```
##
```

```
## Scaled residuals:
```

```
## Min 1Q Median 3Q Max
```

```
## -1.8329 -0.9661 0.3780 0.7173 1.0351
```

```
##
```

```
## Random effects:
```

```
## Groups Name Variance Std.Dev.
```

```
## bear_presence$S..No. (Intercept) 1.022 1.011
```

```
## Number of obs: 52, groups: bear_presence$S..No., 26
```

```
##
```

```
## Fixed effects:
```

```
## Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept) 1.4707 0.6618 2.222 0.0263 *
```

```
## bear_presence$SeasonR2020 -1.2808 0.7469 -1.715 0.0864 .
```

```
## ---  
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Correlation of Fixed Effects:  
##      (Intr)  
## br_p$SR2020 -0.768  
plot(lm1)
```

Annexure II

Table. S. 1 (a). Pair wise matrix used for calculating the weighted sum for resistance score.

Layers	Conflict zone	Land use land cover	Road	Rail	Settlements	Slope	Water bodies	Forest
Conflict zone	1	2	3	3	3	3	3	5
LU/LC	0.50	1	3	3	2	3	2	5
Roads	0.50	0.33	1	0.25	1	2	2	3
Rails	0.33	0.33	0.25	1	0.33	2	3	3
Settlements	0.33	0.5	1	3.03	1	3	3	5
Slope	0.33	0.33	0.50	0.5	0.33	1	2	5
Water bodies	0.33	0.5	0.50	0.33	0.33	0.5	1	4
Forests	0.20	0.20	0.33	0.33	0.20	0.2	0.25	1
SUM	3.53	5.20	9.58	11.45	8.20	14.7	16.25	31

Table. S.2. (b). Standardized Decision Matrix used for calculating resistance score.

Standardized Decision matrix									Sum	Weight (%)	Weighted criteria
Conflict zone	0.28	0.57	0.85	0.85	0.85	0.85	0.85	1.42	6.51	23.02	0.81
LU/LC	0.14	0.28	0.85	0.85	0.57	0.85	0.57	1.42	5.52	19.52	0.69
Road	0.14	0.09	0.28	0.07	0.28	0.57	0.57	0.85	2.85	10.09	0.36
Rail	0.09	0.09	0.07	0.28	0.09	0.57	0.85	0.85	2.90	10.26	0.36
Settlements	0.09	0.14	0.28	0.86	0.28	0.85	0.85	1.42	4.77	16.88	0.60
Slope	0.09	0.09	0.14	0.14	0.09	0.28	0.57	1.42	2.83	10.01	0.35
Water bodies	0.09	0.14	0.14	0.09	0.09	0.14	0.28	1.13	2.12	7.51	0.27
Forest	0.06	0.06	0.09	0.09	0.06	0.06	0.07	0.28	0.77	2.72	0.10
SUM									28.28	100	3.53

Table. S.3. (c). Normalised decision Matrix used for calculating consistency index and ratio

Conflict zone	0.81	1.38	1.07	1.09	1.79	1.06	0.80	0.48	8.48	10.42
LU/LC	0.41	0.69	1.07	1.09	1.19	1.06	0.53	0.48	6.52	9.45
Road	0.41	0.23	0.36	0.09	0.60	0.71	0.53	0.29	3.21	8.99
Rail	0.27	0.27	0.09	0.36	0.20	0.71	0.80	0.29	2.98	8.23
Settlements	0.27	0.34	0.36	1.10	0.60	1.06	0.80	0.48	5.01	8.39
Slope	0.27	0.23	0.18	0.18	0.20	0.35	0.53	0.48	2.42	6.85
Water bodies	0.27	0.34	0.18	0.12	0.20	0.18	0.27	0.38	1.94	7.31
Forest	0.16	0.14	0.12	0.12	0.12	0.07	0.07	0.10	0.89	9.29